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Potential Environmental and Ecological Effects of Global Climate Change on Venomous Terrestrial Species in the Wilderness

Needleman, RK; Neylan, IP; Erickson, T, 2018

Introduction Climate change has been scientifically documented, and its effects on wildlife have been prognosticated. We sought to predict the overall impact of climate change on venomous terrestrial species. We hypothesize that given the close relationship between terrestrial venomous species and climate, a changing global environment may result in increased species migration, geographical redistribution, and longer seasons for envenomation, which would have repercussions on human health. **Methods** A retrospective analysis of environmental, ecological, and medical literature was performed with a focus on climate change, toxinology, and future modeling specific to venomous terrestrial creatures. Species included venomous reptiles, snakes, arthropods, spiders, and Hymenoptera (ants and bees). Animals that are vectors of hemorrhagic infectious disease (eg, mosquitos, ticks) were excluded. **Results** Our review of the literature indicates that changes to climatic norms will have a potentially dramatic effect on terrestrial venomous creatures. Empirical evidence demonstrates that geographic distributions of many species have already shifted due to changing climatic conditions. Given that most terrestrial venomous species are ectotherms closely tied to ambient temperature, and that climate change is shifting temperature zones away from the equator, further significant distribution and population changes should be anticipated. For those species able to migrate to match the changing temperatures, new geographical locations may open. For those species with limited distribution capabilities, the rate of climate change may accelerate faster than species can adapt, causing population declines. Specifically, poisonous snakes and spiders will likely maintain their population numbers but will shift their geographic distribution to traditionally temperate zones more often inhabited by humans. Fire ants and Africanized honey bees are expected to have an expanded range distribution due to predicted warming trends. Human encounters with these types of creatures are likely to increase, resulting in potential human morbidity and mortality. **Conclusions** Temperature extremes and changes to climatic norms may have a dramatic effect on venomous terrestrial species. As climate change affects the distribution, populations, and life histories of these organisms, the chance

Expanding insect pollinators in the Anthropocene

Ghisbain, G; Gerard, M; Wood, TJ; Hines, HM; Michez, D, 2021

Global changes are severely affecting pollinator insect communities worldwide, resulting in repeated patterns of species extirpations and extinctions. Whilst negative population trends within this functional group have understandably received much attention in recent decades, another facet of global changes has been overshadowed: species undergoing expansion. Here, we review the factors and traits that have allowed a fraction of the pollinating entomofauna to take advantage of global environmental change. Sufficient mobility, high resistance to acute heat stress, and inherent adaptation to warmer climates appear to be key traits that allow pollinators to persist and even expand in the face of climate change. An overall flexibility in dietary and nesting requirements is common in expanding species, although niche specialization can also drive expansion under specific contexts. The numerous consequences of wild and domesticated pollinator expansions, including competition for resources, pathogen spread, and **hybridization** with native wildlife, are also discussed. Overall, we show that the traits and factors involved in the success stories of expanding pollinators are mostly species specific and context dependent, rendering generalizations of 'winning traits' complicated. This work illustrates the increasing need to consider expansion and its numerous consequences as significant facets of global changes and encourages efforts to monitor the impacts of expanding insect pollinators, particularly exotic species, on natural ecosystems.

SIMULATING RANGE EXPANSION: MALE SPECIES RECOGNITION AND LOSS OF PREMATING ISOLATION IN DAMSELFIES

Wellenreuther, M; Tynkynen, K; Svensson, EI, 2010

Prolonged periods of allopatry might result in loss of the ability to discriminate against other formerly sympatric species, and can lead to heterospecific matings and **hybridization** upon secondary contact. Loss of premating isolation during prolonged allopatry can operate in the opposite direction of reinforcement, but has until now been little explored. We investigated how premating isolation between two closely related damselfly species, *Calopteryx splendens* and *C. virgo*, might be affected by the expected future northward range expansion of *C. splendens* into the allopatric zone of *C. virgo* in northern Scandinavia. We simulated the expected secondary contact by presenting *C. splendens* females to *C. virgo* males in the northern allopatric populations in Finland. Premating isolation toward *C. splendens* in northern allopatric populations was compared to sympatric populations in southern Finland and southern Sweden. Male courtship responses of *C. virgo* toward conspecific females showed limited geographic variation, however, courtship attempts toward heterospecific *C. splendens* females increased significantly from sympatry to allopatry. Our results suggest that allopatric *C. virgo* males have partly lost their ability to discriminate against heterospecific females. Reduced premating isolation in allopatry might lead to increased heterospecific matings between taxa that are currently expanding and shifting their ranges in response to climate change.

Climate change-induced hybridization in flying squirrels

Garroway, CJ; Bowman, J; Cascaden, TJ; Holloway, GL; Mahan, CG; Malcolm, JR; Steele, MA; Turner, G; Wilson, PJ, 2010

There is now unequivocal evidence for global climate change; however, its potential impacts on evolutionary processes remain unclear. Many species have responded to contemporary climate change through shifts in their geographic range. This could lead to increased sympatry between recently diverged species; likely increasing the potential for **hybridization**. Recently, following a series of warm winters, southern flying squirrels (*Glaucomys volans*) in Ontario, Canada rapidly expanded their northern range limit resulting in increased sympatry with the closely related northern flying squirrel (*Glaucomys sabrinus*). This provided the opportunity to test the prediction that contemporary climate change can act as a catalyst creating conditions for the formation of **hybrid** zones. Following extensive sampling and molecular analyses (nuclear and mitochondrial DNA), we identified the occurrence of **hybridization** between sympatric *G. sabrinus* and *G. volans*. There was evidence of backcrossing but not of extensive introgression, consistent with the hypothesis of recent rather than historic **hybridization**. To our knowledge, this is the first report of **hybrid** zone formation following a range expansion induced by contemporary climate change. This is also the first report of **hybridization** between North American flying squirrel species.

The ecological interaction of the mountain pine beetle and jack pine budworm in the boreal forest

Colgan, LJ; Erbilgin, N, 2010

As climate change facilitates the range and host expansion of insect species into new ecosystems, the development of new strategies for managing and preventing biological invasion is receiving considerable interest. In recent years, the range of the mountain pine beetle (*Dendroctonus ponderosae* Hopkins) has expanded from lodgepole pine-dominated forests east of the Rocky Mountains into lodgepole x jack pine **hybrid** forest of western Alberta, and may soon invade jack pine forests of the boreal. Our understanding of factors contributing colonization of jack pine by mountain pine beetle is far from complete and several factors may limit its spread in these forests, including tree resistance and competitors. Among these, the jack pine budworm (*Choristoneura pinus pinus* Freeman) is one of the most important insect enemies of jack pine and an outbreak defoliator that potentially weakens jack pine trees, which may make them more susceptible to MPB attacks. To develop

effective management strategies in the face of the short-run impacts of climate change, we need an in-depth understanding of factors influencing establishment and survival of the beetle in jack pine forests.

Asymmetric hybridization in *Cordulegaster* (Odonata: Cordulegasteridae): Secondary postglacial contact and the possible role of mechanical constraints

Solano, E; Hardersen, S; Audisio, P; Amorosi, V; Senczuk, G; Antonini, G, 2018

Two *Cordulegaster* dragonflies present in Italy, the Palaearctic and northern distributed *Cordulegaster boltonii* and the endemic to the south of the peninsula *Cordulegaster trinacriae*, meet in central Italy and give rise to individuals of intermediate morphology. By means of mitochondrial and nuclear markers and of Geometric Morphometrics applied to sexual appendages, we defined i) the geographical boundaries between the two species in Italy and ii) we determined the presence, the extent, and the genetic characteristics of the **hybridization**. Genetic data evidenced asymmetric **hybridization** with the males of *C. trinacriae* able to mate both interspecifically and intraspecifically. The results contrast with expectations under neutral gene **introgression** and sexual selection. This data, along with the morphological evidence of significant differences in size and shape of sexual appendages between the males of the two species, seem indicative of the role of mechanical constraints in intraspecific matings. The origin of the two species is dated about to 1.32 Mya and the **hybridization** resulted related to range expansion of the two species after Last Glacial Maximum and this led to the secondary contact between the two taxa in central Italy. At last, our results indicate that the range of *C. trinacriae*, a threatened and protected species, has been moving northward probably driven by climate changes. As a result, the latter species is currently intruding into the range of *C. boltonii*. The **hybrid** area is quite extended and the **hybrids** seem well adapted to the environment. From a conservation point of view, even if *C. trinacriae* has a strong genetic identity, the discovery of **hybridization** between the two species should be considered in a future species management.

Potential for interspecific hybridization between *Zizina emelina* and *Zizina otis* (Lepidoptera: Lycaenidae)

Sakamoto, Y; Yago, M, 2017

Environmental changes such as global warming and biological invasion caused by human activities raise the possibility of secondary contact between the endangered butterfly species *Zizina emelina* and its sibling species *Zizina otis* in Japan. To assess the possible risks from their habitats overlapping, we investigated the potential for **hybridization** and the development of F1 individuals. We observed successful mating of the two sibling species under artificial conditions. The presence of a postzygotic **hybridization** barrier was supported by the delay of larval development only in females; a delay did not occur in males. Existence of the barrier was also supported by a decreased egg hatching rate in one brood; this was likely associated with infection with *Wolbachia*, a bacterium manipulating the reproductive capability of its host. The size and wing markings of F1 **hybrid** individuals were intermediate between those of the two species. These results suggest that, if *Z. emelina* and *Z. otis* are distributed sympatrically in the future, there is a possibility of **introgression** and reproductive interference between the two species, which would increase the risk of decline of each species.

Northern range expansion of European populations of the wasp spider *Argiope bruennichi* is associated with global warming correlated genetic admixture and population-specific temperature adaptations

Krehenwinkel, H; Tautz, D, 2013

Poleward range expansions are observed for an increasing number of species, which may be an effect of global warming during the past decades. However, it is still not clear in how far these expansions reflect simple geographical shifts of species ranges, or whether new genetic adaptations play a role as well. Here, we analyse the expansion of the wasp spider *Argiope bruennichi* into Northern Europe during the last century. We have used a range-wide sampling of contemporary populations and historical specimens from museums to trace the phylogeography and genetic changes associated with the range shift. Based on the analysis of mitochondrial, microsatellite and SNP markers, we observe a higher level of genetic diversity in the expanding populations, apparently due to admixture of formerly isolated lineages. Using reciprocal transplant experiments for testing overwintering tolerance, as well as temperature preference and tolerance tests in the laboratory, we find that the invading spiders have possibly shifted their temperature niche. This may be a key adaptation for survival in Northern latitudes. The museum samples allow a reconstruction of the invasion's genetic history. A first, small-scale range shift started around 1930, in parallel with the onset of global warming. A more massive invasion of Northern Europe associated with genetic admixture and morphological changes occurred in later decades. We suggest that the latter range expansion into far Northern latitudes may be a consequence of the admixture that provided the genetic material for adaptations to new environmental regimes. Hence, global warming could have facilitated the initial admixture of populations and this resulted in genetic lineages with new habitat preferences.

Anthropogenic cause of range shifts and gene flow between two grasshopper species revealed by environmental modelling, geometric morphometrics and population genetics

Sivyer, L; Morgan-Richards, M; Koot, E; Trewick, SA, 2018

The range of a species is controlled by biotic and abiotic factors; both could have changed recently due to human activity. We used environmental modelling, morphometric and genetic data to interpret ecological responses at the species boundary of a pair of New Zealand grasshoppers with very different ranges; one widespread (*Phaulacridium marginale*) and one restricted to semi-arid central/southern South Island (*Phaulacridium otagoense*). Climate- and habitat-based distribution models for grasshoppers in the past (last glacial maximum), present and future (2070), in concert with modelling of vegetation patterns imply range and demographic expansion of *P. marginale* and stability of *P. otagoense*. mtDNA sequence revealed four main lineages with pronounced differences in genetic diversity and geographical range. The widespread lineage associated with *P. marginale* revealed a signature of range expansion but regionally restricted lineages were geographically structured at a fine scale. Within the narrow geographical range of *P. otagoense*, three mtDNA lineages resulted in high diversity, more typical of large stable populations. Geometric analysis of pronotum shape identified individuals from a region of sympatry with mixed characteristics. Mismatch of phenotype, mtDNA lineage and nuclear DNA sequence indicates **introgression** between grasshopper species now in contact. This appears to be accompanied by *P. otagoense* range reduction through ecological competition. Deforestation by people starting approximate to 800 years ago best explains range change and resulting **hybridisation** of these grasshoppers. Anthropogenic habitat modification can have indirect consequences on insect biodiversity and conservation by enabling **introgression** between formerly separate populations and species.

Colonization and reproduction of potential competitors with mountain pine beetle in baited logs of a new host for mountain pine beetle, jack pine

Smith, ZM; Chase, KD; Takagi, E; Kees, AM; Aukema, BH, 2021

The mountain pine beetle (*Dendroctonus ponderosae* Hopkins) is a bark beetle that is native to pine forests of western North America and the Black Hills of South Dakota. Recent eastward range expansion into stands of jack pine (*Pinus banksiana*) and associated **hybrids** with lodgepole pine (*Pinus contorta*) in western Canada has created concern that the insect will continue moving eastward. In the Great Lakes region, mountain pine beetle would encounter novel species of pines and associated insect fauna; interactions with which are largely unexplored. We baited logs of jack pine with lures for mountain pine beetle and *Ips grandicollis* (Eichhoff) alone and in combination in a 2 x 2 factorial design in the Black Hills of South Dakota. Both insects occur in this region, but not jack pine, a common species in the Great Lakes region of North America at risk of invasion by mountain pine beetle. We measured attraction and reproduction of insects that colonized the logs. *Ips*

grandicollis were significantly more attracted to logs of jack pine baited with their aggregation pheromone, ipsenol, than unbaited logs or those baited with pheromones of mountain pine beetle and myrcene, a host volatile. Colonization by *I. grandicollis* was inhibited by the presence of lures for mountain pine beetle. We also found larvae of longhorn borers, likely *Monochamus* spp., infesting logs. These borers, which act as competitors and facultative predators of bark beetles, were significantly attracted to logs baited with ipsenol over those baited with lures for mountain pine beetle. Our results suggest that if mountain pine beetle were to invade the Great Lakes Region, common bark and woodboring species such as *I. grandicollis* and longhorn borers would not compete with mountain pine beetles at tree-colonizing stages, and thus could pose little resistance to invasion.

Phytochemicals as mediators for host range expansion of a native invasive forest insect herbivore

Erbilgin, N, 2019

Mountain pine beetle (MPB) has recently invaded jack pine forests in western Canada. This invasion signifies a climate change-induced range expansion by a native insect. The mechanism underlying this invasion is unknown, but likely involves phytochemicals that play critical roles in MPB biology. Thus far, studies have investigated the compatibility of jack pine chemistry with beetles and their microbial symbionts. I have identified three phytochemical mechanisms that have likely facilitated the host range expansion of MPB. First, jack pine chemistry is overall similar to that of the historical hosts of MPB. In particular, jack pine chemistry is compatible with beetle pheromone production, aggregation on host trees and larval development. Furthermore, the compatibility of jack pine chemistry maintains beneficial interactions between MPB and its microbial symbionts. Second, compared with historical hosts, the novel host not only has lower concentrations of toxic and repellent defense chemicals, but also contains large concentrations of chemicals promoting host colonization by MPB. These patterns are especially pronounced when comparing novel hosts with well-defended historical hosts. Finally, before MPBs arrived in jack pine forests, they invaded a zone of **hybrids** of novel and historical hosts that likely improved beetle success on jack pine, as **hybrids** show chemical characteristics of both hosts. In conclusion, the phytochemistry of jack pine has likely facilitated the biological invasion of this novel host by MPB.

A climate model of the red imported fire ant, *Solenopsis invicta* Buren (Hymenoptera: Formicidae): Implications for invasion of new regions, particularly Oceania

Sutherst, RW; Maywald, G, 2005

The paucity of empirical data on processes in species life cycles demands tools to extract insight from field observations. Such insights help inform policy on invasive species and on impacts of climate change at regional and local scales. We used the CLIMEX model to infer the response of the red imported fire ant, *Solenopsis invicta* Buren (Hymenoptera: Formicidae), to temperature and moisture from its range in the United States. We tested hypotheses on the mechanisms that limit the distribution of the ant and estimated the potential global area at risk from invasion. The ant can spread further in the United States, including north along the west coast, where patterns of infestation will differ from those in the east. We analyzed the risk of colonization in Australia and New Zealand, where the ant was recently discovered. The patterns of infestation of the ant in Oceania will differ from those in the eastern United States, with slower growth and less winter mortality. This study adds to earlier temperature-based models by incorporating a moisture response; by replacing arbitrary categories of colony size to predict overwintering success with a site-specific model based on the balance between annual growth and survival; and by comparing different hypotheses on low temperature-related mechanisms that limit the geographical distribution. It shows how the response of a species to climate can be synthesized from field observations to provide useful insights into its population dynamics. Such analyses provide a basis for making decisions on regional management of invasive species and an informative context for local studies.

Wolbachia-driven selective sweep in a range expanding insect species

Deng, JC; Assandri, G; Chauhan, P; Futahashi, R; Galimberti, A; Hansson, B; Lancaster, LT; Takahashi, Y; Svensson, EI; Duploux, A,

Background Evolutionary processes can cause strong spatial genetic signatures, such as local loss of genetic diversity, or conflicting histories from mitochondrial versus nuclear markers. Investigating these genetic patterns is important, as they may reveal obscured processes and players. The maternally inherited bacterium *Wolbachia* is among the most widespread symbionts in insects. *Wolbachia* typically spreads within host species by conferring direct fitness benefits, and/or by manipulating its host reproduction to favour infected over uninfected females. Under sufficient selective advantage, the mitochondrial haplotype associated with the favoured maternally-inherited symbiotic strains will spread (i.e. hitchhike), resulting in low mitochondrial genetic variation across the host species range. Method The common bluetail damselfly (*Ischnura elegans*: van der Linden, 1820) has recently emerged as a model organism for genetics and genomic signatures of range expansion during climate change. Although there is accumulating data on the consequences of such expansion on the genetics of *I. elegans*, no study has screened for *Wolbachia* in the damselfly genus *Ischnura*. Here, we present the biogeographic variation in *Wolbachia* prevalence and penetrance across Europe and Japan (including samples from 17 populations), and from close relatives in the Mediterranean area (i.e. *I. genei*: Rambur, 1842; and *I. saharensis*: Aguesse, 1958). Results Our data reveal (a) multiple *Wolbachia*-strains, (b) potential transfer of the symbiont through **hybridization**, (c) higher infection rates at higher latitudes, and (d) reduced mitochondrial diversity in the north-west populations, indicative of hitchhiking associated with the selective sweep of the most common strain. We found low mitochondrial haplotype diversity in the *Wolbachia*-infected north-western European populations (Sweden, Scotland, the Netherlands, Belgium, France and Italy) of *I. elegans*, and, conversely, higher mitochondrial diversity in populations with low penetrance of *Wolbachia* (Ukraine, Greece, Montenegro and Cyprus). The timing of the selective sweep associated with infected lineages was estimated between 20,000 and 44,000 years before present, which is consistent with the end of the last glacial period about 20,000 years. Conclusions Our findings provide an example of how endosymbiont infections can shape spatial variation in their host evolutionary genetics during postglacial expansion. These results also challenge population genetic studies that do not consider the prevalence of symbionts in many insects, which we show can impact geographic patterns of mitochondrial genetic diversity.

Differential effects of short-term winter thermal stress on diapausing tiger swallowtail butterflies (*Papilio* spp.)

Scriber, JM; Maher, E; Aardema, ML,

It is generally thought that insects inhabiting lower latitudes are more severely impacted by changes in their thermal environment than are high latitude species. This is attributed to the wider range of temperatures to which high-latitude species are exposed. By contrast, low-latitude species have typically evolved in more thermally stable environments with a narrower range of temperature variation. However, deviation from this pattern can occur and here we report that under variable winter conditions a higher latitude species may be more sensitive to thermal variation than its lower latitude sister species. Using split broods, we examined the survival and adult emergence success of diapausing pupae of *Papilio canadensis* and *P. glaucus*, as well as a unique, recombinant **hybrid** population (late-flight) to short periods of mid-winter cold and heat stress. Our results indicate that the higher latitude, univoltine populations (*P. canadensis* and late-flights) exhibit lower pupal survival than the lower latitude, facultative diapauser (*P. glaucus*) for all mid-winter thermal stress treatments, both high and low. Size differences alone do not appear to account for the observed differences in survival or metabolic costs in these three phenotypes, as late-flight individuals are similar in size to *P. glaucus*. We attribute the observed differences in survival and weight loss to potential metabolic differences and variation in the intensity of diapause, in addition to divergent adaptation to winter precipitation levels (e.g. snow cover) and the influences this may have on microhabitat temperature moderation.

Mountain pine beetle host range expansion threatens the boreal forest

Cullingham, CI; Cooke, JEK; Dang, S; Davis, CS; Cooke, BJ; Coltman, DW, 2011

The current epidemic of the mountain pine beetle (MPB), an indigenous pest of western North American pine, has resulted in significant losses of lodgepole pine. The leading edge has reached Alberta where forest composition shifts from lodgepole to jack pine through a **hybrid** zone. The susceptibility of jack pine to MPB is a major concern, but there has been no evidence of host-range expansion, in part due to the difficulty in distinguishing the parentals and their **hybrids**. We tested the utility of a panel of microsatellite loci optimized for both species to classify lodgepole pine, jack pine and their **hybrids** using simulated data. We were able to accurately classify simulated individuals, and hence applied these markers to identify the ancestry of attacked trees. Here we show for the first time successful MPB attack in natural jack pine stands at the leading edge of the epidemic. This once unsuitable habitat is now a novel environment for MPB to exploit, a potential risk which could be exacerbated by further climate change. The consequences of host-range expansion for the vast boreal ecosystem could be significant.

~~The Lodgepole x Jack Pine Hybrid Zone in Alberta, Canada: A Stepping Stone for the Mountain Pine Beetle on its Journey East Across the Boreal Forest?~~

Lusebrink, I; Erbilgin, N; Evenden, ML, 2013

Historical data show that outbreaks of the tree killing mountain pine beetle are often preceded by periods of drought. Global climate change impacts drought frequency and severity and is implicated in the range expansion of the mountain pine beetle into formerly unsuitable habitats. Its expanded range has recently reached the lodgepole x jack pine **hybrid** zone in central Alberta, Canada, which could act as a transition from its historical lodgepole pine host to a jack pine host present in the boreal forest. This field study tested the effects of water limitation on chemical defenses of mature trees against mountain pine beetle-associated microorganisms and on beetle brood success in lodgepole x jack pine **hybrid** trees. Tree chemical defenses as measured by monoterpene emission from tree boles and monoterpene concentration in needles were greater in trees that experienced water deficit compared to well-watered trees. Myrcene was identified as specific defensive compound, since it significantly increased upon inoculation with dead mountain pine beetles. Beetles reared in bolts from trees that experienced water deficit emerged with a higher fat content, demonstrating for the first time experimentally that drought conditions benefit mountain pine beetles. Further, our study demonstrated that volatile chemical emission from tree boles and phloem chemistry place the **hybrid** tree chemotype in-between lodgepole pine and jack pine, which might facilitate the host shift from lodgepole pine to jack pine.

~~Spatial genetic structure of the mountain pine beetle (*Dendroctonus ponderosae*) outbreak in western Canada: historical patterns and contemporary dispersal~~

Samarasekera, GDNG; Bartell, NV; Lindgren, BS; Cooke, JEK; Davis, CS; James, PMA; Coltman, DW; Mock, KE; Murray, BW, 2012

Environmental change has a wide range of ecological consequences, including species extinction and range expansion. Many studies have shown that insect species respond rapidly to climatic change. A mountain pine beetle epidemic of record size in North America has led to unprecedented mortality of lodgepole pine, and a significant range expansion to the northeast of its historic range. Our goal was to determine the spatial genetic variation found among outbreak population from which genetic structure, and dispersal patterns may be inferred. Beetles from 49 sampling locations throughout the outbreak area in western Canada were analysed at 13 microsatellite loci. We found significant north-south population structure as evidenced by: (i) Bayesian-based analyses, (ii) north-south genetic relationships and diversity gradients; and (iii) a lack of isolation-by-distance in the northernmost cluster. The north-south structure is proposed to have arisen from the processes of postglacial colonization as well as recent climate-driven changes in population dynamics. Our data support the hypothesis of multiple sources of origin for the outbreak and point to the need for population specific information to improve our understanding and management of outbreaks. The recent range expansion across the Rocky Mountains into the jack/lodgepole **hybrid** and pure jack pine zones of northern Alberta is consistent with a northern British Columbia origin. We detected no loss of genetic variability in these populations, indicating that the evolutionary potential of mountain pine beetle to adapt has not been reduced by founder events. This study illustrates a rapid range-wide response to the removal of climatic constraints, and the potential for range expansion of a regional population.

~~Effects of introgression on the genetic population structure of two ecologically and economically important conifer species: lodgepole pine (*Pinus contorta* var. *latifolia*) and jack pine (*Pinus banksiana*)~~

Cullingham, CI; Cooke, JEK; Coltman, DW, 2013

Forest trees exhibit a remarkable range of adaptations to their environment, but as a result of frequent and long-distance gene flow, populations are often only weakly differentiated. Lodgepole and jack pine **hybridize** in western Canada, which adds the opportunity for **introgression** through **hybridization** to contribute to population structure and (or) adaptive variation. Access to large sample size, high density SNP datasets for these species would improve our ability to resolve population structure, parameterize **introgression**, and separate the influence of demography from adaptation. To accomplish this, 454 transcriptome reads for lodgepole and jack pine were assembled using Newbler and MIRA, the assemblies mined for SNPs, and 1536 SNPs were selected for typing on lodgepole pine, jack pine, and their **hybrids** (N = 536). We identified population structure using both Bayesian clustering and discriminate analysis of principle components. Introgressed SNP loci were identified and their influence on observed population structure was assessed. We found that introgressed loci resulted in increased differentiation both within lodgepole and jack pine populations. These findings are timely given the recent mountain pine beetle population expansion in the **hybrid** zone, and will facilitate future studies of adaptive traits in these ecologically important species.

~~The influence of variation in host tree monoterpene composition on secondary attraction by an invasive bark beetle: Implications for range expansion and potential host shift by the mountain pine beetle~~

Burke, JL; Carroll, AL, 2016

The range of mountain pine beetle (*Dendroctonus ponderosae*) has expanded in recent years to include many evolutionarily naive forests in western Canada. These forests include novel populations of the principal host species, lodgepole pine (*Pinus contorta*), the novel species jack pine (*Pinus banksiana*), and their **hybrids** (*P. contorta* x *P. banksiana*). These novel forests are chemically and physically different than native forests, and recent studies have shown beetle reproductive performance is enhanced in these novel habitats. We conducted a field experiment to determine the effect of differing host chemistry, specifically alpha-pinene content, on secondary attraction by foraging mountain pine beetles. Alpha-pinene is the precursor molecule for the production of trans-verbenol, the main aggregation pheromone for this beetle species. We found that elevated relative concentrations of alpha-pinene in bolts significantly increased their attractiveness to in situ mountain pine beetles. Seventy-five percent of attacks were found on infested bolts with the most alpha-pinene relative to other monoterpenes. Other measures of terpene chemistry between bolt types could not explain the pattern of attacks. This result suggests that elevated concentrations of alpha-pinene could increase the rate of aggregation and attack success by the mountain pine beetle in novel pine forests. Newly invaded **hybrid** and jack pine in the western boreal forest are reported to contain 3-4 times the relative concentration of alpha-pinene than lodgepole pines in forests in which the beetle has coevolved. These elevated concentrations may help the mountain pine beetle overcome some of the potential restraints for establishment and spread in the boreal forest, such as low pine volume and connectivity, and continue expanding its range. Crown Copyright (C) 2015 Published by Elsevier B.V. All rights reserved.

~~Eco-genomic analysis of the poleward range expansion of the wasp spider *Argiope bruennichi* shows rapid adaptation and genomic admixture~~

Krehenwinkel, H; Rodder, D; Tautz, D, 2015

Poleward range expansions are commonly attributed to global change, but could alternatively be driven by rapid evolutionary adaptation. A well-documented example of a range expansion during the past decades is provided by the European wasp spider *Argiope bruennichi*. Using ecological niche modeling, thermal tolerance experiments and a genome-wide analysis of gene expression divergence, we show that invasive populations have adapted to novel climatic conditions in the course of their expansion. Their climatic niche shift is mirrored in an increased cold tolerance and a population-specific and functionally differentiated gene expression response. We generated an *Argiope* reference genome sequence and used population genome resequencing to assess genomic changes associated with the new climatic adaptations. We find clear genetic differentiation and a significant admixture with alleles from East Asian populations in the invasive Northern European populations. Population genetic modeling suggests that at least some of these introgressing alleles have contributed to the new adaptations during the expansion. Our results thus confirm the notion that range expansions are not a simple consequence of climate change, but are accompanied by fast genetic changes and adaptations that may be fuelled through admixture between long separated lineages.

~~Mountain Pine Beetles Colonizing Historical and Naive Host Trees Are Associated with a Bacterial Community Highly Enriched in Genes Contributing to Terpene Metabolism~~

Adams, AS; Aylward, FO; Adams, SM; Erbilgin, N; Aukema, BH; Currie, CR; Suen, G; Raffa, KF, 2013

The mountain pine beetle, *Dendroctonus ponderosae*, is a subcortical herbivore native to western North America that can kill healthy conifers by overcoming host tree defenses, which consist largely of high terpene concentrations. The mechanisms by which these beetles contend with toxic compounds are not well understood. Here, we explore a component of the hypothesis that beetle-associated bacterial symbionts contribute to the ability of *D. ponderosae* to overcome tree defenses by assisting with terpene detoxification. Such symbionts may facilitate host tree transitions during range expansions currently being driven by climate change. For example, this insect has recently breached the historical geophysical barrier of the Canadian Rocky Mountains, providing access to naive tree hosts and unprecedented connectivity to eastern forests. We use culture-independent techniques to describe the bacterial community associated with *D. ponderosae* beetles and their galleries from their historical host, *Pinus contorta*, and their more recent host, **hybrid** *P. contorta*-*Pinus banksiana*. We show that these communities are enriched with genes involved in terpene degradation compared with other plant biomass-processing microbial communities. These pine beetle microbial communities are dominated by members of the genera *Pseudomonas*, *Rahnella*, *Serratia*, and *Burkholderia*, and the majority of genes involved in terpene degradation belong to these genera. Our work provides the first metagenome of bacterial communities associated with a bark beetle and is consistent with a potential microbial contribution to detoxification of tree defenses needed to survive the subcortical environment.

~~The contribution of genetics and genomics to understanding the ecology of the mountain pine beetle system~~

Cullingham, CI; Janes, JK; Hamelin, RC; James, PMA; Murray, BW; Sperling, FAH, 2019

Environmental change is altering forest insect dynamics worldwide. As these systems change, they pose significant ecological, social, and economic risk through, for example, the loss of valuable habitat, green space, and timber. Our understanding of such systems is often limited by the complexity of multiple interacting taxa. As a consequence, studies assessing the ecology, physiology, and genomics of each key organism in such systems are increasingly important for developing appropriate management strategies. Here we summarize the genetic and genomic contributions made by the TRIA project—a long-term study of the mountain pine beetle (*Dendroctonus ponderosae* Hopkins) system encompassing beetle, fungi, and pine. Contributions include genetic and genomic resources for species identification, sex determination, detection of selection, functional genetic analysis, mating system confirmation, **hybrid** stability tests, and integrated genetic studies of multiple taxa. These resources and subsequent findings have accelerated our understanding of the mountain pine beetle system, facilitating improved management strategies (e.g., enhancements to stand susceptibility indices and predictive models) and highlighting mechanisms for promoting resilient forests. Further, work from the TRIA project serves as a model for the increasing number and severity of invasive and native forest insect outbreaks globally (e.g., Dutch elm disease and thousand cankers disease).

~~Adaptive governance in a complex social-ecological context: emergent responses to a native forest insect outbreak~~

Abrams, J; Huber-Stearns, H; Steen-Adams, M; Davis, EJ; Bone, C; Nelson, MF; Moseley, C, 2021

In contrast to traditional structures of state-centric bureaucratic administration, **hybrid** networks of state and non-state actors are believed to possess the advantages of greater adaptability in the face of environmental change as well as greater legitimacy in contested socio-political settings. Between 1998 and 2016, pine forests throughout the western United States experienced the largest and most destructive outbreak of the native mountain pine beetle (*Dendroctonus ponderosae*) on record, with most of the affected forests located on lands owned and managed by the U.S. government as national forests. Socio-political responses to this event in many geographies included the emergence of local to regional **hybrid** networks that provided direction and resources for responding to the disturbance event. In this study, we analyze the ability of governance networks to adapt in the face of the insect outbreak across four regional geographies: The Black Hills region of South Dakota and Wyoming; northern Colorado; northeastern Washington; and southwestern Montana. Specifically, we ask what factors accounted for divergent governance responses in the four cases and to what extent the emergent governance dynamics in each case facilitated lasting, long-term adaptation. Our results highlight governance trajectories as products of their respective histories and of feedback cycles among socio-political, institutional, and technological variables. By analyzing the origin, characteristics, and persistence of institutional change, this research contributes a comparative perspective on the adaptive potential of networks as functions of influences from multiple spatial and temporal scales.

~~Rapid evolution of *Ophraella communa* cold-tolerance in new low-temperature environments~~

Tian, ZQ; Chen, GM; Zhang, Y; Ma, C; Tian, ZY; Gao, XY; Chen, HS; Guo, JY; Zhou, ZS, 2022

Low winter temperatures severely stress newly arriving insect species. Adaptive evolutionary changes in cold tolerance can facilitate their establishment in new environments. *Ambrosia artemisiifolia*, a noxious invasive plant, occurs throughout China. *Ophraella communa*, a biological control agent of *A. artemisiifolia*, mainly occurs in southern China. However, in 2012, it established populations in Beijing (39.98 degrees N, 115.97 degrees E) following introduction from Laibin (23.62 degrees N, 109.37 degrees E), implying cold adaptation. The mechanisms underlying its rapid evolution of cold tolerance remain unknown. We investigated the levels of cryoprotectants and energy reserves in adult *O. communa* from two latitudes. In high-latitude insects, we found high trehalose, proline, glycerol, total sugar, and lipid levels; five potential genes (*Tret1a*, *Tret1b*, *Tret1-2*, *P5CS*, and *GST*), responsible for regulating cold tolerance and involved in trehalose transport, proline biosynthesis, and glutathione S-transferase activation, were highly expressed. These **hybridisation** changes could facilitate cold temperature adaptation. We demonstrate the genetic basis underlying rapid adaptation of cold tolerance in *O. communa*, explaining its extension to higher latitudes. Thus, specialist herbivores can follow host plants by adapting to new temperature environments via rapid genetic evolution.

~~Experimental studies of adaptation in *Clarkia xantiana*. II. Fitness variation across a subspecies border~~

Geber, MA; Eckhart, VM, 2005

Because the range boundary is the locale beyond which a taxon fails to persist, it provides a unique opportunity for studying the limits on adaptive evolution. Adaptive

constraints on range expansion are perplexing in view of widespread ecotypic differentiation by habitat and region within a species' range (regional adaptation) and rapid evolutionary response to novel environments. In this Study of two parapatric subspecies, *Clarkia xantiana* ssp. *xantiana* and *C. x.* ssp. *parviflora*, we compared the fitness of population transplants within their native region, in a non-native region within the native range, and in the non-native range to assess whether range expansion might be limited by a greater intensity of selection on colonists of a new range versus a new region within the range. The combined range of the two subspecies spans a west-to-east gradient of declining precipitation in the Sierra Nevada of California, with ssp. *xantiana* in the west being replaced by ssp. *parviflora* in the east. Both Subspecies had significantly higher fitness in the native range (range adaptation), whereas regional adaptation was weak and was found only in the predominantly outcrossing ssp. *xantiana* but was absent in the inbreeding ssp. *parviflora*. Because selection intensity on transplants was Much stronger in the non-native range relative to non-native regions, there is a larger adaptive barrier to range versus regional expansion. Three of five sequential fitness components accounted for regional and range adaptation, but only one of them, survivorship from germination to flowering, contributed to both. Flower number contributed to regional adaptation in ssp. *xantiana* and fruit Set (number of fruits per flower) to range adaptation. Differential survivorship of the two taxa or regional Populations of ssp. *xantiana* in non-native environments was attributable. in part, to biotic interactions, including competition, herbivory, and pollination. For example. low fruit set in ssp. *xantiana* in the east was likely due to the absence of its principal specialist bee pollinators in ssp. *parviflora*'s range. Thus, convergence on self-fertilization may be necessary for ssp. *xantiana* to invade ssp. *parviflora*'s range. but the evolution of outcrossing would not be required for ssp. *parviflora* to invade ssp. *xantiana*'s range.

Characterizing the physical and genetic structure of the lodgepole pine-jack pine hybrid zone: mosaic structure and differential introgression

Cullingham, CI; James, PMA; Cooke, JEK; Coltman, DW, 2012

Understanding the physical and genetic structure of **hybrid** zones can illuminate factors affecting their formation and stability. In north-central Alberta, lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia*) and jack pine (*Pinus banksiana* Lamb) form a complex and poorly defined **hybrid** zone. Better knowledge of this zone is relevant, given the recent host expansion of mountain pine beetle into jack pine. We characterized the zone by genotyping 1998 lodgepole, jack pine, and **hybrids** from British Columbia, Alberta, Saskatchewan, Ontario, and Minnesota at 11 microsatellites. Using Bayesian algorithms, we calculated genetic ancestry and used this to model the relationship between species occurrence and environment. In addition, we analyzed the ancestry of **hybrids** to calculate the genetic contribution of lodgepole and jack pine. Finally, we measured the amount of gene flow between the pure species. We found the distribution of the pine classes is explained by environmental variables, and these distributions differ from classic distribution maps. **Hybrid** ancestry was biased toward lodgepole pine; however, gene flow between the two species was equal. The results of this study suggest that the **hybrid** zone is complex and influenced by environmental constraints. As a result of this analysis, range limits should be redefined.

Cross-species outlier detection reveals different evolutionary pressures between sister species

Cullingham, CI; Cooke, JEK; Coltman, DW, 2014

Lodgepole pine (*Pinus contorta* var. *latifolia*) and jack pine (*Pinus banksiana*) **hybridize** in western Canada, an area of recent mountain pine beetle range expansion. Given the heterogeneity of the environment, and indications of local adaptation, there are many unknowns regarding the response of these forests to future outbreaks. To better understand this we aim to identify genetic regions that have adaptive potential. We used data collected on 472 single nucleotide polymorphism (SNP) loci from 576 tree samples collected across 13 lodgepole pine-dominated sites and four jack pine-dominated sites. We looked at the relationship of genetic diversity with the environment, and we identified candidate loci using both frequency-based (ARLEQUIN and BAYESCAN) and correlation-based (MATSAM and BAYENV) methods. We found contrasting relationships between environmental variation and genetic diversity for the species. While we identified a number of candidate outliers (34 in lodgepole pine, 25 in jack pine, and 43 interspecific loci), we did not find any loci in common between lodgepole and jack pine. Many of the outlier loci identified were correlated with environmental variation. Using rigorous criteria we have been able to identify potential outlier SNPs. We have also found evidence of contrasting environmental adaptations between lodgepole and jack pine which could have implications for beetle spread risk.

A Comprehensive and Dated Phylogenomic Analysis of Butterflies

Espeland, M; Breinholt, J; Willmott, KR; Warren, AD; Vila, R; Toussaint, EFA; Maunsell, SC; Aduse-Poku, K; Talavera, G; Eastwood, R; Jarzyna, MA; Guralnick, R; Lohman, DJ; Pierce, NE; Kawahara, AY,

Butterflies (Papilionoidea), with over 18,000 described species [1], have captivated naturalists and scientists for centuries. They play a central role in the study of speciation, community ecology, biogeography, climate change, and plant-insect interactions and include many model organisms and pest species [2, 3]. However, a robust higher-level phylogenetic framework is lacking. To fill this gap, we inferred a dated phylogeny by analyzing the first phylogenomic dataset, including 352 loci (> 150,000 bp) from 207 species representing 98% of tribes, a 35-fold increase in gene sampling and 3-fold increase in taxon sampling over previous studies [4]. Most data were generated with a new anchored **hybrid** enrichment (AHE) [5] gene kit (BUTTERFLY1.0) that includes both new and frequently used (e.g., [6]) informative loci, enabling direct comparison and future dataset merging with previous studies. Butterflies originated around 119 million years ago (mya) in the late Cretaceous, but most extant lineages diverged after the Cretaceous-Paleogene (K-Pg) mass-extinction 65 mya. Our analyses support swallowtails (Papilionidae) as sister to all other butterflies, followed by skippers (Hesperiidae) + the nocturnal butterflies (Hedylidae) as sister to the remainder, indicating a secondary reversal from diurnality to nocturnality. The whites (Pieridae) were strongly supported as sister to brush-footed butterflies (Nymphalidae) and blues + metalmarks (Lycaenidae and Riodinidae). Ant association independently evolved once in Lycaenidae and twice in Riodinidae. This study overturns prior notions of the taxon's evolutionary history, as many long-recognized subfamilies and tribes are para- or polyphyletic. It also provides a much-needed backbone for a revised classification of butterflies and for future comparative studies including genome evolution and ecology.

Predicting hybridisation as a consequence of climate change in damselflies

Nava-Bolanos, A; Sanchez-Guillen, RA; Wellenreuther, M; Munoz, J; Torres-Pachon, M; Novelo-Gutierrez, R; Cordoba-Aguilar, A, 2019

Climate change is a key stressor for species. Two major consequences of climate-induced range shifts are the formation of new areas of geographic overlap (i.e. sympatry) and an increased probability of **hybridisation** in the de novo created contact zones. One method to effectively quantify the potential of **hybridisation** is to integrate ecological niche modelling and the propensity to **hybridisation** based on genetic divergence. In this paper, we have applied this methodology to predict **hybridisation** outcomes following different scenarios of climate change in 30 species of *Argia* damselflies. We (i) investigated how climate change may affect species' distributions; (ii) quantified if changed distributions generate new areas of sympatry between species; (iii) calculated the propensity to **hybridise** based on genetic divergence between species; and (iv) integrated these data to predict the future potential of species to **hybridise**. We found that the distribution of 29 of the 30 species was affected by a change in climate which led to a general increase in sympatric overlap among species. The degree of genetic divergence among the 108 species' combinations ranged from 0.06% to 0.36%. Based on the sympatric overlap and genetic divergence, it can be predicted that 97 of the species pairs are likely to **hybridise** in the future. Our results are useful to forecast how highly diverse and closely related groups, such as *Argia* damselflies, may respond to a change in climate and how this can impact the potential of species mixing under a scenario of increased global warming.

Agricultural insect hybridization and implications for pest management

Correa, AS; Cordeiro, EMG; Omoto, C, 2019

Biological invasions, the expansion of agricultural frontiers, and climate change favor encounters of divergent lineages of animals and plants, increasing the likelihood of **hybridization**. However, **hybridization** of insect species and its consequences for agroecosystems have not received sufficient attention. Gene exchange between distinct and distant genetic pools can improve the survival and reproduction of insect pests, and threaten beneficial insects in disturbed agricultural environments. **Hybridization** may be the underlying explanation for the recurrent pest outbreaks and control failures in putative **hybrid** zones, as suspected for bollworm, corn borer, whiteflies, and stink bugs. Reliable predictions of the types of changes that can be expected in pest insect genomes and fitness, and of their impacts on the fate of species and populations remain elusive. Typical steps in pest management, such as insect identification, pest monitoring, and control are likely affected by gene flow and adaptive **introgression** mediated by **hybridization**, and we do not have ways to respond to or mitigate the problem. To address the adverse effects of farming intensification and global trade, we must ensure that current integrated pest management programs incorporate up-to-date monitoring and diagnostic tools. The rapid identification of **hybrids**, quantification of levels of **introgression**, and in-depth knowledge of what genes have been transferred may help to explain and predict insect population outbreaks and control failures in the future. (c) 2019 Society of Chemical Industry

Hybridization rate and climate change: are endangered species at risk?

Sanchez-Guillen, RA; Munoz, J; Hafernik, J; Tierney, M; Rodriguez-Tapia, G; Cordoba-Aguilar, A, 2014

Many species are altering their geographic range due to climate change creating new sympatric populations of otherwise allopatric populations. We investigated whether climate change will affect the distribution and thus the pattern of **hybridization** between two pairs of closely related damselfly species [*Ischnura damula* and *I. demorsa*, and *I. denticollis* and *I. gemina* (this, an endangered species)]. Thus, we estimated the strength of pre and postmating reproductive barriers between both pairs of species, and we predicted future potential distribution under four different Global Circulation Models and a realistic emissions scenario of climate change by using maximum entropy modelling technique. Our results showed that reproductive isolation (RI) is complete in *I. damula* x *I. demorsa* individuals: F-1 (first generation) **hybrids** are produced but do not reach sexual maturation. However, RI in *I. denticollis* x *I. gemina* **hybrids** is high but incomplete and unidirectional: only *I. gemina* females produced F-1 **hybrids** which mate with males and females of *I. denticollis* and between them producing BC1 (back-crosses) and F-2 (second generation) viable **hybrids**. Maximum entropy models revealed a northern and westward shift and a general reduction of the potential geographic ranges. Based on the pattern of **hybridization**, for *I. damula* and *I. demorsa* there is a current threat as well as a rapid displacement and/or extinction of *I. gemina* by *I. denticollis*. However, the current pattern of extinction may not continue due to the contraction in ranges of the four species.

Positive and Negative Impacts of Non-Native Bee Species around the World

Russo, L,

Though they are relatively understudied, non-native bees are ubiquitous and have enormous potential economic and environmental impacts. These impacts may be positive or negative, and are often unquantified. In this manuscript, I review literature on the known distribution and environmental and economic impacts of 80 species of introduced bees. The potential negative impacts of non-native bees include competition with native bees for nesting sites or floral resources, pollination of invasive weeds, co-invasion with pathogens and parasites, genetic **introgression**, damage to buildings, affecting the pollination of native plant species, and changing the structure of native pollination networks. The potential positive impacts of non-native bees include agricultural pollination, availability for scientific research, rescue of native species, and resilience to human-mediated disturbance and climate change. Most non-native bee species are accidentally introduced and nest in stems, twigs, and cavities in wood. In terms of number of species, the best represented families are Megachilidae and Apidae, and the best represented genus is Megachile. The best studied genera are *Apis* and *Bombus*, and most of the species in these genera were deliberately introduced for agricultural pollination. Thus, we know little about the majority of non-native bees, accidentally introduced or spreading beyond their native ranges.

Seasonal Migration of *Pantala flavescens* Across the Bohai Strait in Northern China

Cao, LZ; Fu, XW; Hu, CX; Wu, KM, 2018

Pantala flavescens (Fabricius 1798) (Odonata: Libellulidae) is one of the most common species of migratory dragonflies. *P. flavescens* adults were captured by a searchlight trap on Beihuang Island (BH Island; 38 degrees 24'N, 120 degrees 55'E) from 2003 to 2016, where there is no freshwater. This inspired our research to analyze the pattern of seasonal migration and population dynamics. Stable hydrogen isotope measurement and the **Hybrid** Single Particle Lagrangian Integrated Trajectory (HYSPLIT) were used to simulate the migration pathway of *P. flavescens* between different breeding habitats. The results showed that there was no significant difference among population numbers of this overseas migration across years ($F_{13,F-2161} = 0.85$, $P = 0.604$); however, the numbers were significantly different across months ($F_{5,F-2161} = 3.91$, $P = 0.003$). Our geospatial natal assignment model suggested that *P. flavescens* trapped on BH were originated in different geographical regions and might have three movement strategies: wandering around northern China and north-bound (positive) and south-bound (negative) movements. Among them, the majority were engaged in wandering around northern China. Model simulations suggested that *P. flavescens* toured around BH. The results contribute to the knowledge of *P. flavescens* population ecology in a large-scale geographic region and will aid in the prediction and interpretation of insect migration patterns in response to climate change.

Aspects, Including Pitfalls, of Temporal Sampling of Flying Insects, with Special Reference to Aphids

Loxdale, HD, 2018

Since the advent and widespread use of high-resolution molecular markers in the late 1970s, it is now well established that natural populations of insects are not necessarily homogeneous genetically and show variations at different spatial scales due to a variety of reasons, including **hybridization/introgression** events. In a similar vein, populations of insects are not necessarily homogenous in time, either over the course of seasons or even within a single season. This of course has profound consequences for surveys examining, for whatever reason/s, the temporal population patterns of insects, especially flying insects as mostly discussed here. In the present article, the topics covered include climate and climate change; changes in ecological niches due to changes in available hosts, i.e., essentially, adaptation events; **hybridization** influencing behaviour-host shifts; infection by pathogens and parasites/parasitoids; habituation to light, sound and pheromone lures; chromosomal/genetic changes affecting physiology and behaviour; and insecticide resistance. If such phenomena, i.e., aspects and pitfalls are not considered during spatio-temporal study programmes, which is even more true in the light of the recent discovery of morphologically similar/identical cryptic species, then the conclusions drawn in terms of the efforts to combat pest insects or conserve rare and endangered species may be in error and hence end in failure.

Evolution of insect-plant relationships: chemical constraints, coadaptation, and concordance of insect/plant traits

Scriber, JM, 2002

Co-adaptations, co-evolution, and co-speciation between herbivores and their host plants have been topics of interest for several decades. Difficulties in deciphering these relationships as well as physiological, biochemical, and ecological adaptations of herbivorous insects themselves are discussed here in relation to biotic and abiotic environmental factors that create temporal as well as spatial mosaics of genetic variation. **Hybridization** was shown in swallowtail butterflies (Papilio) (Lepidoptera: Papilionidae) to produce some trait concordance, but mostly independent geographic trait clines (physiological, biochemical, and morphological). Strong and extensive genetic **introgression** of *Liriodendron tulipifera* detoxification abilities was documented northward across the **hybrid** zone, presumably as a result of regional climate warming only during the last 3-4 years. These and other genetic novelties produced by **hybridization** may be important in speciation processes, and they also emphasize the difficulties identifying appropriate taxonomic classifications for discussing any species concept. Host plant detoxification abilities (as 'key innovations') are shown capable of rapid movement between different polyphagous herbivore species independently of the host plant availability and well beyond the insect species geographical range distribution. Part of the difficulty associated with ecologically categorizing herbivore species and identifying affiliated adaptations for host plant use may be related to independent movement of various 'species-diagnostic' traits. Climate-driven local selection regimes could help generate the dynamic variation observed for co-adapted, co-evolved, or non-adapted genotypes, and may produce the confusing and changing patterns of geographic mosaics seen within and among closely related herbivores. Experimental analyses of several factors that could explain the asymmetrical shapes of trait clines across the **hybrid** zone for tiger swallowtail butterflies are discussed.

Evolutionary consequences of climate-induced range shifts in insects

Sanchez-Guillen, RA; Cordoba-Aguilar, A; Hansson, B; Ott, J; Wellenreuther, M, 2016

Range shifts can rapidly create new areas of geographic overlap between formerly allopatric taxa and evidence is accumulating that this can affect species persistence. We review the emerging literature on the short- and long-term consequences of these geographic range shifts. Specifically, we focus on the evolutionary consequences of novel species interactions in newly created sympatric areas by describing the potential (i) short-term processes acting on reproductive barriers between species and (ii) long-term consequences of range shifts on the stability of **hybrid** zones, **introgression** and ultimately speciation and extinction rates. Subsequently, we (sill) review the empirical literature on insects to evaluate which processes have been studied, and (fr) outline some areas that deserve increased attention in the future, namely the genomics of **hybridisation** and **introgression**, our ability to forecast range shifts and the impending threat from insect vectors and pests on biodiversity, human health and crop production. Our review shows that species interactions in de novo sympatric areas can be manifold, sometimes increasing and sometimes decreasing species diversity. A key issue that emerges is that climate-induced **hybridisations** in insects are much more widespread than anticipated and that rising temperatures and increased anthropogenic disturbances are accelerating the process of species mixing. The existing evidence only shows the tip of the iceberg and we are likely to see many more cases of species mixing, Mowing range shifts in the near future.

A de-novo genome assembly and annotation of the southern flying squirrel (*Glaucomys volans*)

Wolf, JF; Bowman, J; Keobouasone, S; Taylor, RS; Wilson, PJ; Sethuraman, A, 2022

Northern (*Glaucomys sabrinus*) and southern (*Glaucomys volans*) flying squirrels are widespread species distributed across North America. Northern flying squirrels are common inhabitants of the boreal forest, also occurring in coniferous forest remnants farther south, whereas the southern flying squirrel range is centered in eastern temperate woodlands. These two flying squirrel species exhibit a **hybrid** zone across a latitudinal gradient in an area of recent secondary contact. *Glaucomys* **hybrid** offspring are viable and can successfully backcross with either parental species, however, the fitness implications of such events are currently unknown. Some populations of *G. sabrinus* are endangered, and thus, interspecific **hybridization** is a key conservation concern in flying squirrels. To provide a resource for future studies to evaluate **hybridization** and possible **introgression**, we sequenced and assembled a de novo long-read genome from a *G. volans* individual sampled in southern Ontario, Canada, while four short-read genomes (two *G. sabrinus* and two *G. volans*, all from Ontario) were resequenced on Illumina platforms. The final genome assembly consisted of approximately 2.40Gb with a scaffold N50 of 455.26Kb. Benchmarking Universal Single-Copy Orthologs reconstructed 3,742 (91.2%) complete mammalian genes and genome annotation using RNA-Seq identified the locations of 19,124 protein-coding genes. The four short-read individuals were aligned to our reference genome to investigate the demographic history of the two species. A principal component analysis clearly separated resequenced individuals, while inferring population size history using the Pairwise Sequentially Markovian Coalescent model noted an approximate species split 1 million years ago, and a single, possibly recently introgressed individual.

Climate-Induced Range Shifts and Possible Hybridisation Consequences in Insects

Sanchez-Guillen, RA; Munoz, J; Rodriguez-Tapia, G; Arroyo, TPF; Cordoba-Aguilar, A, 2013

Many ectotherms have altered their geographic ranges in response to rising global temperatures. Current range shifts will likely increase the sympatry and **hybridisation** between recently diverged species. Here we predict future sympatric distributions and risk of **hybridisation** in seven Mediterranean ischnurid damselfly species (*I. elegans*, *I. fountaineae*, *I. genei*, *I. graellsii*, *I. pumilio*, *I. saharensis* and *I. senegalensis*). We used a maximum entropy modelling technique to predict future potential distribution under four different Global Circulation Models and a realistic emissions scenario of climate change. We carried out a comprehensive data compilation of reproductive isolation (habitat, temporal, sexual, mechanical and gametic) between the seven studied species. Combining the potential distribution and data of reproductive isolation at different instances (habitat, temporal, sexual, mechanical and gametic), we infer the risk of **hybridisation** in these insects. Our findings showed that all but *I. graellsii* will decrease in distributional extent and all species except *I. senegalensis* are predicted to have northern range shifts. Models of potential distribution predicted an increase of the likely overlapping ranges for 12 species combinations, out of a total of 42 combinations, 10 of which currently overlap. Moreover, the lack of complete reproductive isolation and the patterns of **hybridisation** detected between closely related ischnurids, could lead to local extinctions of native species if the **hybrids** or the introgressed colonising species become more successful.

Combining virtual and in-place field crews to model pollinator species shift in the Greater Yellowstone Ecosystem

Whipple, S; Rohlf, A; Vasquez, CD; Dominguez, D; Bowser, G; Halliwell, P,

Insect pollinators (bees and butterflies) face global challenges as climate change impacts species occurrence (or extinction) within managed and protected areas. While species decline is predicted for invertebrate species, especially in sensitive ecosystems such as high alpine systems, little is known about species responses to climate change. This study seeks to understand the impact of climate change on pollinators in high elevation ecosystems, specifically within Yellowstone and Grand Teton National Parks. These parks are connected protected areas in the United States that act as a large reservoir for conserving species, including pollinators. Students performing research amidst the COVID-19 pandemic were divided into two virtual teams (bug team and climate team) to assess historic climate data, natural history collections and plant/pollinator data from Yellowstone and Grand Teton National Parks. Each team was tasked with addressing the larger question of climate change impacts on pollinators within protected areas while also gaining interpersonal, collaborative learning skills through their experience. This paper highlights two case studies tied to pollinator decline. The first assesses citizen science and natural history collection databases to predict and field test species occurrence within the parks. The second identifies suitable habitats for species occurrence locations. Lastly, this paper emphasizes the learning outcomes students had from virtual and **hybrid** field settings and offers suggestions for applications towards field-based research efforts.

The role of latitudinal, genetic and temperature variation in the induction of diapause of *Papilio glaucus* (Lepidoptera: Papilionidae)

Ryan, SF; Valella, P; Thivierge, G; Aardema, ML; Scriber, JM,

A key adaptation in insects for dealing with variable environmental conditions is the ability to diapause. The tiger swallowtail butterflies, *Papilio glaucus* and *P. canadensis* are ideal species to explore the genetic causes and population genetic consequences of diapause because divergence in this trait is believed to be a salient factor in maintaining a **hybrid** zone between these species. Yet little is known about the factors that influence diapause induction in this system. Here we explored how spatial (latitudinal), environmental (temperature) and genetic (**hybridization**) factors affect diapause induction in this system. Specifically, a series of growth chamber experiments using wild caught individuals from across the eastern United States were performed to: (1) evaluate how critical photoperiod varies with latitude, (2) isolate the stage in which induction occurs, (3) test whether changes in temperature affected rates of diapause induction, and (4) explore how the incidence of diapause is affected in **hybrid** offspring. We find that induction occurs in the larval stage, is not sensitive to a relatively broad range of temperatures, appears to have a complex genetic basis (i.e., is not simply a dominant trait following a Mendelian inheritance pattern) and that the critical photoperiod increases by 0.4 h with each increasing degree in latitude. This work deepens our understanding of how spatial, environmental and genetic variation influences a key seasonal adaptation (diapause induction) in a well-developed ecological model system and will make possible future studies that explore how climatic variation affects the population dynamics and genetics of this system.

DRIVERS OF HYBRIDIZATION IN A 66-GENERATION RECORD OF COLIAS BUTTERFLIES

Jahner, JP; Shapiro, AM; Forister, ML, 2012

Hybridization significantly affects the ecology and evolution of numerous plant and animal lineages. Most studies have focused on endogenous drivers of **hybridization** and neglected variation in exogenous factors, such as seasonal weather patterns. In this study, we take advantage of a unique dataset consisting of records of **hybridization** between the butterflies *Colias eurytheme* and *C. eriphyle* (Pieridae) for 66 generations (22 years) to investigate the importance of seasonal weather on the production and survival of **hybrid** offspring. Important seasonal weather variables for each parental species and **hybrid** offspring were determined using model averaging, and these weather variables, along with butterfly abundances, were analyzed using path analysis. The most important drivers of **hybridization** were the abundance of *C. eriphyle*, summer minimum temperature, and spring maximum temperature. In contrast, the abundance of *C. eurytheme* and weather variables prior to the current flight season were relatively unimportant for variation in **hybrid** abundance. Parental abundances were mostly driven by weather variables prior to the flight season possibly because these variables affect host plant quality. Our results suggest that exogenous, climatic factors can influence **hybridization** in natural systems, and that these factors can act both directly on **hybrid** abundance and indirectly through the population dynamics of parental species.

Modeling diesel engine fueled with tamanu oil—Diesel blend by hybridizing neural network with firefly algorithm

Rao, YKSS; Krishna, BB, 2019

Research works are ongoing in mixing the biologically synthesized oil with the diesel for reducing the effect of global warming and climate change. From the review study, it is noted that the blended biodiesels require more assert about their practical viability. So, the non-edible Tamanu oil is synthesized and it is blended with diesel and its emission characteristics, engine performance and combustion characteristics are studied in our previous work. This paper attempts to model the diesel engine fueled with tamanu oil biodiesel blend. The proposed model exploits the context of neural network and the firefly algorithm is used to train it. After analyzing the various characteristics of the diesel engine, the acquired data is subjected to a proposed FF-NM method. The simulated results are statistically evaluated and the proposed modeling method is proved to be better than the other NM. (C) 2018 Published by Elsevier Ltd.

Ecology and conservation of the British Swallowtail butterfly, *Papilio machaon britannicus*: old questions, new challenges and potential opportunities

Collins, NM; Barkham, PJ; Blencowe, M; Brazil, A; Kelly, A; Oldfield, S; Strudwick, T; Vane-Wright, RI; Stewart, AJA, 2020

The British Swallowtail, *Papilio machaon britannicus*, is an iconic flagship for its unique but now restricted and fragmented fenland ecosystem in the UK's Norfolk Broads. Occurrence in 1 km² recording squares fell by 56% over the period of 1974-2014 and by 13% in 2005-2014, but the breeding populations, mainly confined to reserves, have increased in size. Climate change-induced sea-level rise and consequent seawater incursion into the Norfolk Broads represent a significant existential threat to the butterfly. Translocation to more secure fenland sites is recommended; several are being restored or recreated through stakeholder partnerships in East Anglia and Somerset. Well-researched introduction and management of the foodplant, Milk-parsley, is essential for such translocations to succeed. A better understanding is needed of the genetic structuring of the British Swallowtail populations using modern sequencing technologies, in particular to elucidate the significance of gene flow in relation to the viability of introductions to small or isolated sites. In a species in which **hybridisation** is commonplace across the Holarctic, the continued influx and future spread in Britain of the continental subspecies *Papilio machaon gorganus* may present a threat to the genetic integrity of subspecies *britannicus*, despite their differences in habitat and larval foodplants.

Simultaneous Quaternary radiations of three damselfly clades across the Holarctic

Turgeon, J; Stoks, R; Thum, RA; Brown, JM; McPeck, MA, 2005

If climate change during the Quaternary shaped the macroevolutionary dynamics of a taxon, we expect to see three features in its history: elevated speciation or extinction rates should date to this time, more northerly distributed clades should show greater discontinuities in these rates, and similar signatures of those effects should be evident in the phylogenetic and phylodemographic histories of multiple clades. In accordance with the role of glacial cycles, speciation rates increased in the Holarctic *Enallagma* damselflies during the Quaternary, with a 4.25 x greater increase in a more northerly distributed clade as compared with a more southern clade. Finer-scale phylogenetic analyses of three radiating clades within the northern clade show similar, complex recent histories over the past 250,000 years to produce 17 Nearctic and four Palearctic extant species. All three are marked by nearly synchronous deep splits that date to approximately 250,000 years ago, resulting in speciation in two. This was soon followed by significant demographic expansions in at least two of the three clades. In two, these expansions seem to have preceded the radiations that have given rise to most of the current biodiversity. Each also produced species at the periphery of the clade's range. In spite of clear genetic support for reproductive isolation among almost all species, mtDNA signals of past asymmetric **hybridization** between species in different clades also suggest a role for the evolution of mate choice in generating reproductive isolation as species recolonized the landscape following deglaciation. These analyses suggest that recent climate fluctuations resulted in radiations driven by similar combinations of speciation processes acting in different lineages.

Does including physiology improve species distribution model predictions of responses to recent climate change?

Buckley, LB; Waaser, SA; MacLean, HJ; Fox, R, 2011

Thermal constraints on development are often invoked to predict insect distributions. These constraints tend to be characterized in species distribution models (SDMs) by calculating development time based on a constant lower development temperature (LDT). Here, we assessed whether species-specific estimates of LDT

based on laboratory experiments can improve the ability of SDMs to predict the distribution shifts of six U. K. butterflies in response to recent climate warming. We find that species-specific and constant (5 degrees C) LDT degree-day models perform similarly at predicting distributions during the period of 1970-1982. However, when the models for the 1970-1982 period are projected to predict distributions in 1995-1999 and 2000-2004, species-specific LDT degree-day models modestly outperform constant LDT degree-day models. Our results suggest that, while including species-specific physiology in correlative models may enhance predictions of species' distribution responses to climate change, more detailed models may be needed to adequately account for interspecific physiological differences.

Hybrid zones: windows on climate change

Taylor, SA; Larson, EL; Harrison, RG, 2015

Defining the impacts of anthropogenic climate change on biodiversity and species distributions is currently a high priority. Niche models focus primarily on predicted changes in abiotic factors; however, species interactions and adaptive evolution will impact the ability of species to persist in the face of changing climate. Our review focuses on the use of **hybrid** zones to monitor responses of species to contemporary climate change. Monitoring **hybrid** zones provides insight into how range boundaries shift in response to climate change by illuminating the combined effects of species interactions and physiological sensitivity. At the same time, the semipermeable nature of species boundaries allows us to document adaptive **introgression** of alleles associated with response to climate change.

Hybridisation and climate change: brown argus butterflies in Britain (Polyommatus subgenus Aricia)

Mallet, J; Wynne, IR; Thomas, CD, 2011

1. Distribution changes brought about by climate change are likely to alter levels of **hybridisation** between related taxa, and may threaten some species.
2. Nuclear (Tpi) and mitochondrial (cytB) DNA sequence data give evidence for **introgression** between two related Polyommatus (subgenus Aricia) butterfly species in a 150-200 km wide overlap zone in northern England and North Wales. A history of **hybridisation** is evident from the mixture of genotypes present within this region: some populations contain southern-origin (Polyommatus agestis) mtDNA and northern-origin (Polyommatus artaxerxes) Tpi alleles, and many populations contain mixtures of Tpi alleles.
3. The timing of the original **hybridisation** is unknown, but could be immediately post-glacial or much more recent in origin.
4. Both species are now beginning to shift northwards, associated with recent climatic warming.
5. It is thus expected that anthropogenic climate change will unleash a new spate of **hybridisation**, potentially threatening the long-term survival of the northern species in Britain.

The roles of hybridization and habitat fragmentation in the evolution of Brazil's enigmatic longwing butterflies, Heliconius nattereri and H. hermathena

Massardo, D; VanKuren, NW; Nallu, S; Ramos, RR; Ribeiro, PG; Silva-Brandao, KL; Brandao, MM; Lion, MB; Freitas, AVL; Cardoso, MZ; Kronforst, MR, 2020

Background Heliconius butterflies are widely distributed across the Neotropics and have evolved a stunning array of wing color patterns that mediate Mullerian mimicry and mating behavior. Their rapid radiation has been strongly influenced by **hybridization**, which has created new species and allowed sharing of color patterning alleles between mimetic species pairs. While these processes have frequently been observed in widespread species with contiguous distributions, many Heliconius species inhabit patchy or rare habitats that may strongly influence the origin and spread of species and color patterns. Here, we assess the effects of historical population fragmentation and unique biology on the origins, genetic health, and color pattern evolution of two rare and sparsely distributed Brazilian butterflies, Heliconius hermathena and Heliconius nattereri. Results We assembled genomes and re-sequenced whole genomes of eight H. nattereri and 71 H. hermathena individuals. These species harbor little genetic diversity, skewed site frequency spectra, and high deleterious mutation loads consistent with recent population bottlenecks. Heliconius hermathena consists of discrete, strongly isolated populations that likely arose from a single population that dispersed after the last glacial maximum. Despite having a unique color pattern combination that suggested a **hybrid** origin, we found no genome-wide evidence that H. hermathena is a **hybrid** species. However, H. hermathena mimicry evolved via **introgression**, from co-mimetic Heliconius erato, of a small genomic region upstream of the color patterning gene cortex. Conclusions Heliconius hermathena and H. nattereri population fragmentation, potentially driven by historical climate change and recent deforestation, has significantly reduced the genetic health of these rare species. Our results contribute to a growing body of evidence that **introgression** of color patterning alleles between co-mimetic species appears to be a general feature of Heliconius evolution.

Global diversity of mayflies (Ephemeroptera, Insecta) in freshwater

Barber-James, HM; Gattolliat, JL; Sartori, M; Hubbard, MD, 2008

The extant global Ephemeroptera fauna is represented by over 3,000 described species in 42 families and more than 400 genera. The highest generic diversity occurs in the Neotropics, with a correspondingly high species diversity, while the Palaearctic has the lowest generic diversity, but a high species diversity. Such distribution patterns may relate to how long evolutionary processes have been carrying on in isolation in a bioregion. Over an extended period, there may be extinction of species, but evolution of more genera. Dramatic extinction events such as the K-T mass extinction have affected current mayfly diversity and distribution. Climatic history plays an important role in the rate of speciation in an area, with regions which have been climatically stable over long periods having fewer species per genus, when compared to regions subjected to climatic stresses, such as glaciation. A total of 13 families are endemic to specific bioregions, with eight among them being monospecific. Most of these have restricted distributions which may be the result of them being the relict of a previously more diverse, but presently almost completely extinct family, or may be the consequence of vicariance events, resulting from evolution due to long-term isolation.

Differences in Thermal Tolerance between Parental Species Could Fuel Thermal Adaptation in Hybrid Wood Ants

Martin-Roy, R; Nygard, E; Nouhaud, P; Kulmuni, J, 2021

Genetic variability is essential for adaptation and could be acquired via **hybridization** with a closely related lineage. We use ants to investigate thermal adaptation and the link between temperature and genetic variation arising from **hybridization**. We test for differences in cold and heat tolerance between Finnish Formica polyctena and Formica aquilonia wood ants and their naturally occurring **hybrids**. Using workers, we find that the parental individuals differ in both cold and heat tolerances and express thermal limits that reflect their global distributions. **Hybrids**, however, cannot combine thermal tolerance of parental species as they have the same heat tolerance as F. polyctena but not the same cold tolerance as F. aquilonia. We then focus on a single **hybrid** population to investigate the relationship between temperature variation and genetic variation across 16 years using reproductive individuals. On the basis of the thermal tolerance results, we expected the frequency of putative F. polyctena alleles to increase in warm years and F. aquilonia alleles to increase in cold years. We find support for this in **hybrid** males but not in **hybrid** females. These results contribute to understanding the outcomes of **hybridization**, which may be sex specific or depend on the environment. Furthermore, genetic variability resulting from **hybridization** could help **hybrid** wood ants cope with changing thermal conditions.

Constructing a hybrid species distribution model from standard large-scale distribution data

Singer, A; Schweiger, O; Kuhn, I; Johst, K, 2018

Species range shifts under climate change have predominantly been projected by models correlating species observations with climatic conditions. However, geographic range shifting may depend on biotic factors such as demography, dispersal and species interactions. Recently suggested **hybrid** models include these factors. However, parameterization of **hybrid** models suffers from lack of detailed ecological data across many taxa. Further, it is methodologically unclear how to upscale ecological information from scales relevant to ecological processes to the coarser resolution of species distribution data (often 100 km²) or even 2500 km²). We tackle these problems by developing a novel modelling and calibration framework, which allows **hybrid** model calibration from (static) presence-absence data that is available for many species. The framework improves understanding of the influence of biotic processes on range projections and reveals critical sources of uncertainty that limit projection reliability. We demonstrate its performance for the case of the butterfly *Titania's Fritillary* (*Boloria titania*).

~~A New Hybrid Butterfly Optimization Algorithm for Green Vehicle Routing Problem~~

Utama, DM; Widodo, DS; Ibrahim, MF; Dewi, SK, 2020

In the industrial sector, transportation plays an essential role in distribution. This activity impacts climate change and global warming. One of the critical problems in distribution is the green vehicle routing problem (G-VRP). This study focuses on G-VRP for a single distribution center. The objective function is to minimize the distribution costs by considering fuel costs, carbon costs, and vehicle use costs. This research aims to develop the **hybrid** butterfly optimization algorithm (HBOA) to minimize the distribution costs on G-VRP. It was inspired by the butterfly optimization algorithm (BOA), which was by combining the tabu search (TS) algorithm and local search swap and flip strategies. BOA is a new metaheuristic algorithm that has been successfully applied in various engineering fields. Experiments were carried out to test the parameters of the proposed algorithm and vary the speed of vehicles. The proposed algorithm was also compared with several procedures of prior study. The experimental results proved that the HBOA could minimize the total distribution cost compared to other algorithms. Moreover, the computation time is also included in the analysis.

~~Mitochondrial DNA Suggests the Introduction of Honeybees of African Ancestry to East-Central Europe~~

Oleksa, A; Kusza, S; Tofilski, A, 2021

Simple Summary In Europe, a well-known threat to the conservation of honeybee diversity is the loss of genetic uniqueness of local populations due to beekeepers' preference for a few genetic lineages. However, due to climate change and large-scale ongoing movement of breeding individuals, the expansion of bees of African origin could represent another threat. This issue has not yet been recognised in detail, although bees bearing African mitochondrial DNA occur in South-West and South Europe due to natural gene flow. Here, we determine the diversity of mitochondrial DNA in honey bees from East-Central Europe. We sequenced the COI-COII region in 427 bees sampled along two 900 km transects (17.5 degrees N and 23 degrees E). We found that 1.64% of bees (95% CI: 0.66-3.35%) had African mitochondrial DNA. It is unlikely that their presence in the area resulted from natural migration but instead human-driven introductions of **hybrids** of African ancestry. This expansion deserves more attention, as it may contribute to the dissemination of undesirable traits, parasites and diseases. In Europe, protecting the genetic diversity of *Apis mellifera* is usually perceived in the context of limiting the spread of the evolutionary C-lineage within the original range of the M-lineage. However, due to climate change and large-scale ongoing movement of breeding individuals, the expansion of bees from the African A-lineage could represent another threat. This issue has not yet been investigated in detail, although A-mitotypes occur in South-West and South Europe due to natural gene flow. Here, we determine the diversity of mtDNA in honey bees from East-Central Europe. We sequenced the COI-COII region in 427 bees sampled along two 900 km transects (17.5 degrees N and 23 degrees E). We found that 1.64% of bees (95% CI: 0.66-3.35%) had A-mitotypes. It is unlikely that their presence in the area resulted from natural migration but instead human driven introductions of **hybrids** of African ancestry. This expansion deserves more attention, as it may contribute to the dissemination of undesirable traits, parasites and diseases.

~~Applying genetic methods to identify northern and southern flying squirrels and determine conservation needs~~

Rogic, A; Dubois, G; Tessier, N; Pare, P; Canac-Marquis, P; Lapointe, FJ, 2016

The two species of flying squirrels found in North America are the northern (*Glaucomys sabrinus*) and the southern (*G. volans*) flying squirrel. Both species have wide range distributions across North America, yet differences in their preferred habitat result in few areas of sympatry. Climate change however, has shifted the southern flying squirrel's range limit further north, thus allowing the two species to encounter each other more frequently. *Glaucomys volans* is the more competitive of the two, and also carries a nematode parasite (*Strongyloides robustus*) proven to be deleterious towards its sister species. The northern incursion of the southern flying squirrel may therefore dislodge its sister species from its original distribution. With *G. sabrinus* considered endangered in different parts of North America, and *G. volans* listed as "concerned" in its northernmost limit, the two species require close monitoring. Morphological identification is often challenging for incomplete and juvenile specimens, therefore we developed a molecular identification protocol using mitochondrial and nuclear markers in tandem to help distinguish each species. These protocols were tested on *Glaucomys* individuals located elsewhere in Canada and the USA to ensure the validity of the designed primers. Moreover, employing our methods may detect F1 **hybrids**. To assess the current genetic portrait of *G. sabrinus* populations in Quebec before the potential invasion of its sister species, a preliminary population genetics study using seven microsatellite loci was also realized. The various conservation and management implications are discussed.

~~Simulation Optimization of Reservoir Water Quality under Climate Change~~

Azadi, F; Ashofteh, PS; Shokri, A; Loaiciga, HA, 2021

Increasing population and water use, rising pollution of water resources, and climate change affect the quantity and quality of water resources. Reservoir operation is an important tool for water supply that can be optimized by simulation-optimization considering the impact of climate change on water quality. This study presents a simulation-optimization approach linking the CE-QUAL-W2 hydrodynamic model with the firefly algorithm k-nearest neighbor (FA-KNN) model to obtain optimal reservoir discharges to achieve water quality objectives under climate change conditions. The developed algorithm overcomes the computational burden of CE-QUAL-W2. The FA-KNN **hybrid** algorithm is employed to optimize the total dissolved solids (TDS) while achieving computational efficiency beyond what could be achieved with CE-QUAL-W2 simulations alone. This paper's approach is evaluated with the Aidoghmouth Reservoir (East Azerbaijan, Iran). Overall, 36 simulation-optimization scenarios for dry and wet years under baseline and climate change conditions are evaluated by considering three initial water levels for the reservoir (minimum, average, and normal) and three thresholds for assessing the **hybrid** algorithm. The TDS released from the reservoir in wet years would be acceptable for agricultural use; in dry years, on average, the TDS would not be acceptable for 24 days per year under climate change. The reservoir in winter undergoes complete mixing; it becomes stratified in spring and summer, and it is close to complete mixing in the autumn. The highest TDS in the reservoir would occur during the summer in dry years under climate change, reaching TDS of approximately 2,645 g/m³. (C) 2021 American Society of Civil Engineers.

~~Social thermoregulation does not explain heterospecific nesting in North American flying squirrels~~

Olson, MN; Bowman, J; Burness, G, 2018

Contemporary climate change has increased range overlap between northern (*Glaucomys sabrinus*) and southern (*Glaucomys volans*) flying squirrels, which has in turn led to interspecific **hybridization**. Mating in flying squirrels begins in late winter, at a time when squirrels tend to thermoregulate socially (i.e. they huddle in communal nests for warmth). We tested the hypothesis that the proximate cause of **hybridization** was a requirement for social thermoregulation that would lead squirrels at the range periphery to nest socially with heterospecifics. We conducted a captive preference experiment with pairs of same-sex, wild-caught flying squirrels to test the relative frequency of conspecific and heterospecific nesting. Contrary to our expectations, ambient temperature did not predict the willingness of squirrels to thermoregulate socially. Instead, *G. volans* nested as a conspecific pair in all trials, whereas *G. sabrinus* nested in conspecific pairs less often than *G. volans*. Heterospecific pairs occurred less often than conspecific pairs of either species. A low level of heterospecific social nesting occurred in all conditions and at all times of year, however, suggesting that the behaviour of social nesting is not a perfect reproductive barrier and might lead to some opportunities for **hybridization**.

Phylogeography of spruce beetles (*Dendroctonus rufipennis* kirby) (Curculionidae: Scolytinae) in north america

Maroja, LS; Bogdanowicz, SM; Wallin, KF; Raffa, KF; Harrison, RG, 2007

Tree-feeding insects that are widespread in north temperate regions are excellent models for studying how past glaciations have impacted differentiation and speciation. We used mitochondrial DNA (mtDNA) sequences and allele frequencies at nine microsatellite loci to examine genetic population structure across the current range of the spruce beetle (*Dendroctonus rufipennis*), an economically important insect in North America. Two major haplotype groups occur across northern North America, from Newfoundland to Alaska, on white spruce (*Picea glauca*), and a third distinctive haplotype group occurs throughout the Rocky Mountains on Engelmann spruce (*Picea engelmannii*). The two mtDNA lineages found in northern populations are 3-4% divergent from each other and from the lineages found in the Rocky Mountains. Analyses of microsatellite data also suggest the existence of major population groupings associated with different geographical regions. In the Pacific Northwest, concordant contact zones for genetically distinct populations of spruce beetles and their principal hosts appear to reflect recent secondary contact. Although we could detect no evidence of historical mtDNA gene flow between allopatric population groups, patterns of variation in the Pacific Northwest suggest recent **hybridization** and **introgression**. Together with the pollen record for spruce, they also suggest that beetles have spread from at least three glacial refugia. A minimum estimate of divergence time between the Rocky Mountain and northern populations was 1.7 Myr (million years), presumably reflecting the combined effects of isolation during multiple glacial cycles.

Stable *Heliconius* butterfly hybrid zones are correlated with a local rainfall peak at the edge of the Amazon basin

Rosser, N; Dasmahapatra, KK; Mallet, J, 2014

Multilocus clines between Mullerian mimetic races of *Heliconius* butterflies provide a classic example of the maintenance of **hybrid** zones and their importance in speciation. Concordant **hybrid** zones in the mimics *Heliconius erato* and *H. melpomene* in northern Peru were carefully documented in the 1980s, and this prior work now permits a historical analysis of the movement or stasis of the zones. Previous work predicted that these zones might be moving toward the Andes due to selective asymmetry. Extensive deforestation and climate change might also be expected to affect the positions and widths of the **hybrid** zones. We show that the positions and shapes of these **hybrid** zones have instead remained remarkably stable between 1985 and 2012. The stability of this interaction strongly implicates continued selection, rather than neutral mixing following secondary contact. The stability of cline widths and strong linkage disequilibria (gametic correlation coefficients $R_{\max} = 0.35-0.56$ among unlinked loci) over 25 years suggest that mimetic selection pressures on each color pattern locus have remained approximately constant (s approximately to 0.13-0.40 per locus in both species). Exceptionally high levels of precipitation at the edge of the easternmost Andes may act as a population density trough for butterflies, trapping the **hybrid** zones at the foot of the mountains, and preventing movement. As such, our results falsify one prediction of the Pleistocene Refugium theory: That the ranges of divergent species or subspecies should be centered on regions characterized by maxima of rainfall, with **hybrid** zones falling in more arid regions between them.

Spruce budworm (*Choristoneura* spp.) biotype reactions to forest and climate characteristics

Volney, WJA; Fleming, RA, 2007

The spruce budworm (*Choristoneura fumiferana*) is the most destructive insect defoliator of forests in North America. Climatic influences on this species' life history are considered a major factor in restricting the extent and intensity of outbreaks. We examine the life history traits of the spruce budworm and related *Choristoneura* populations with respect to forecasting the conifer-feeding responses of these insects in changing environments. Analysis of the evolutionary relationships between *Choristoneura* entities, including their **hybridization**, genetic distances, and their degree of sympatry leads us to distinguish 15 possible *Choristoneura* 'biotypes'. Population trend has been associated with recruitment to the feeding stage, and two indicators of recruitment, egg weights and phenological development, are both 'biotype' and climate dependent. Among Abietoid feeding 'biotypes' and among spruce budworm populations, those from locations with extreme winters tend to have heavier eggs than those from the more benign environments. In spruce budworm, this genetically based adaptation allows populations to increase their potential recruitment substantially where winters are mild. All biotypes feed on the newly developed shoots of their host trees in spring, and are thus vulnerable to the uncertain timing of budbreak. Genetic control of spring emergence is weak so larvae from a single family typically exit from hibernacula over a prolonged period. This guarantees some synchronization with budburst. However, **hybrid** populations have high heritabilities. This allows rapid adaptation to new conditions (e.g. mixed host-species stands). Geographic variation in phenological development after establishing feeding sites is largely genetically controlled. The importance of variation in these traits is examined with respect to competing population dynamics theories to evaluate their utility in forecasting future trends in defoliation. We finish with a plea for jointly using alternative approaches in forecasting spatiotemporal patterns of defoliation.

Topologies of climate change: actor-network theory, relational-scalar analytics, and carbon-market overflows

Blok, A, 2010

Climate change is quickly becoming a ubiquitous socionatural reality, mediating extremes of sociospatial scale from the bodily to the planetary. Although environmentalism invites us to 'think globally and act locally', the meaning of these scalar designations remains ambiguous. This paper explores the topological presuppositions of social theory in the context of global climate change, asking how carbon emissions 'translate' into various sociomaterial forms. Staging a meeting between Tim Ingold's phenomenology of globes and spheres and the social topologies of actor-network theory (ANT), the paper advances a 'relational-scalar' analytics of spatial practices, technoscience, and power. As technoscience gradually constructs a networked global climate, this 'grey box' comes to circulate within fluid social spaces, taking on new shades as it **hybridizes** knowledges, symbols, and practices. Global climates thus come in multiple interfering versions, and we need to pay attention to both continuities and overflows, as illustrated in the paper by controversies surrounding transnational carbon markets. The relational-scalar analytics of ANT, I contend, are well suited to navigating such shifting terrains, a task central to the intellectual as well as practical challenges raised by the climate crisis.

Elevated temperature increases reproductive investment in less preferred mates in the invasive European corn borer moth

Enos, AN; Kozak, GM, 2021

Rapidly changing environments may weaken sexual selection and lead to indiscriminate mating by interfering with the reception of mating signals or by increasing the costs associated with mate choice. If temperature alters sexual selection, it may impact population response and adaptation to climate change. Here, we examine how differences in temperature of the mating environment influence reproductive investment in the European corn borer moth (*Ostrinia nubilalis*). Mate preference in this species is known to be related to pheromone usage, with assortative mating occurring between genetically distinct E and Z strains that differ in the composition of female and male pheromones. We compared egg production within and between corn borer lines derived from four different populations that vary in pheromone composition and other traits. Pairs of adults were placed in a mating environment that matched the pupal environment (ambient temperature) or at elevated temperature (5 degrees C above the pupal environment). At ambient temperature, we found that within-line pairs produced eggs sooner and produced more egg clusters than between-line pairs. However, at elevated temperature, between-line pairs produced the same number of egg clusters as within-line pairs. These results suggest that elevated temperature increased investment in matings with typically less preferred, between-line mates. This increased investment could result in changes in gene flow among corn borer populations in warming environments.

Interaction between global warming potential, durability, and structural properties of fiber-reinforced concrete with high waste materials inclusion

Nguyen, W; Martinez, DM; Jen, G; Duncan, JF; Ostertag, CP, 2021

Concrete production requires significant consumption of raw materials and is a major contributor to global greenhouse gas emissions. Because concrete is placed in varied, damage-inducing conditions, its durability performance is crucial for allowing the material to reach its intended service life and avoid premature replacement. In this multidisciplinary research program, a concrete is developed for both reduced environmental impact and enhanced durability compared to conventional solutions. These goals are realized through a novel combination of design parameters: recycled concrete aggregates (RCA) that increase reuse of construction demolition waste; a high-volume fly ash (HVFA) matrix that further incorporates industrial waste products while reducing portland cement content; and internal fiber reinforcement that increases composite crack resistance. The resulting high-performance concrete, designated as green **hybrid** fiber-reinforced concrete (GHyFRC), contains 39% waste materials by volume and is evaluated by life cycle assessment (LCA), exposure to a corrosive environment for 4.3 years, and structural loading. Corrosion activity of steel rebar embedded within GHyFRC was reduced through the low chloride permeability of a high-volume fly ash matrix and fiber reinforcement that limited crack propagation, maintaining the low designed matrix permeability. GHyFRC can be a more sustainable alternative to concrete under certain conditions by contributing to greater retention of flexural strength after corrosion has begun and lowering global warming potential (GWP) when normalized by flexural strength.

Biological invasions and pollinator decline

Montero-Castano, A; Calvino-Cancela, M; Rojas-Nossa, S; De la Rua, P; Arbetman, M; Morales, CL, 2018

Biological invasions are among the main threats to biodiversity, and pollinators are not exempt from such threat. Here, we review the mechanisms through which animal and plant invasive species may affect pollinators, either directly or indirectly. We classified these mechanisms in four groups: (a) changes in habitat quantity or quality, (b) predation, (c) pathogen spread and (d) genetic **introgression**. We review the impacts of these mechanisms on the behaviour, demography and evolution of native pollinators and their communities. In addition, we highlight some current knowledge gaps about the effect of biological invasions on pollinators and suggest some measures to minimize such effects.

HETEROSIS, COMBINING ABILITY AND GENE ACTION STUDIES IN CUCUMBER FOR DIFFERENT BIOTIC STRESSES TO DEVELOPE RESISTANT

Thakur, M; Kumar, R; Kansal, S, 2019

Biotic stress is the major constrains for the realization of crop yield potential. As climate change progresses, the spread and intensity of biotic stress is expected to increase, with increased probability of crops being exposed to stress. Shielding crops from stress requires a better understanding of the plant's response and its genetic architecture. The dearth of research pertaining to the heterosis, combining ability and gene action studies for insect-pest (fruit fly) and disease incidences (powdery and downy mildew) in cucumber compels us to undertake this study. The experimental material comprised 15 F-1 crosses, developed by crossing 6 genotypes during the year 2015. Parents and the 15 **hybrids**, along with standard check (KH-1), were planted in a randomized complete block design during the year 2016 for screening against different insect-pest and diseases under natural field conditions. In the present studies, genotypes PI-618860, UHF-CUC-1, UHF-CUC-2 and Khira-75 and crosses Khira-75 x PI-618860, Khira-75 x UHF-CUC-1 and Khira-75 x UHF-CUC-2 were found superior in response to insect-pest and disease incidences. Further, gene action studies indicated predominant role of non-additive gene action governing all the traits under study.

Distribution of the Main Apis mellifera Mitochondrial DNA Lineages in Italy Assessed Using an Environmental DNA Approach

Utzeri, VJ; Ribani, A; Taurisano, V; Banque, CHI; Fontanesi, L, 2021

Simple Summary The conservation of the genetic diversity of the native honey bee subspecies is a hot topic in many European countries. Mitochondrial DNA (mtDNA) analyses can provide some information that is useful to monitor the genetic integrity of *Apis mellifera* populations. A preliminary distribution of the main honey bee mitotypes in Italy was obtained more than 20 years ago. In this study we obtained an updated and more detailed distribution map of the main groups of honey bee mitotypes using an unconventional method that exploits the information derived from the environmental DNA contained in the honey. The results were quite different from the picture taken two decades ago. The African mtDNA lineage was spread all over Italy and not only in Sicily, where it is mainly attached to the *A. m. siciliana* subspecies, and where it was identified in the previous investigation. A reduction in the frequency of the M lineage was also evident, and, on the other hand, a counterbalanced increase in the C mitotypes was observed in regions all over. The obtained results provided an updated distribution map of the A, C and M groups of mitotypes in Italy, which could be a starting point to design appropriate conservation programs for native honey bee subspecies. Growing interest has been emerging on the need to monitor the genetic integrity of the European *Apis mellifera* subspecies that could be threatened by the human-mediated dispersion of non-native populations and lines. Mitochondrial DNA (mtDNA) lineages can provide useful information for this purpose. In this study, we took advantage of the environmental DNA (eDNA) contained in the honey, which can be analyzed to detect the main groups of mitotypes of the honey bees that produced it. In this study, we applied this eDNA to produce a distribution map all over the Italian peninsula and the two major islands (Sicily and Sardinia) of the following three honey bee mtDNA lineages: A, C and M. A total of 607 georeferenced honey samples, produced in all Italian regions, was analyzed to detect these lineages. The A lineage was widespread in Sicily, as expected, considering that *A. m. siciliana* carries the African lineage. Surprisingly, this lineage was also reported in about 14% of all other samples produced in almost all continental regions, and in Sardinia. The applied method obtained an updated distribution map of honey bee mtDNA lineages that could be useful to design policies for the conservation of Italian honey bee genetic resources.

A hybrid ant lion optimization chicken swarm optimization algorithm for charger placement problem

Deb, S; Gao, XZ,

Transportation electrification is known to be a viable alternative to deal with the alarming issues of global warming, air pollution, and energy crisis. Public acceptance of Electric Vehicles (EVs) requires the availability of charging infrastructure. However, the optimal placement of chargers is indeed a complex problem with multiple design variables, objective functions, and constraints. Chargers must be placed with the EV drivers' convenience and security of the power distribution network being

taken into account. The solutions to such an emerging optimization problem are mostly based on metaheuristics. This work proposes a novel metaheuristic considering the **hybridization** of Chicken Swarm Optimization (CSO) with Ant Lion Optimization (ALO) for effectively and efficiently coping with the charger placement problem. The amalgamation of CSO with ALO can enhance the performance of ALO, thereby preventing it from getting stuck in the local optima. Our **hybrid** algorithm has the strengths from both CSO and ALO, which is tested on the standard benchmark functions as well as the above charger placement problem. Simulation results demonstrate that it performs moderately better than the counterpart methods.

Evidence for spatial clines and mixed geographic modes of speciation for North American cherry-infesting *Rhagoletis* (Diptera: Tephritidae) flies

Doellman, MM; Saint Jean, G; Egan, SP; Powell, THQ; Hood, GR; Schuler, H; Bruzese, DJ; Glover, MM; Smith, JJ; Yee, WL; Goughnour, R; Rull, J; Aluja, M; Feder, JL, 2020

An important criterion for understanding speciation is the geographic context of population divergence. Three major modes of allopatric, parapatric, and sympatric speciation define the extent of spatial overlap and gene flow between diverging populations. However, mixed modes of speciation are also possible, whereby populations experience periods of allopatry, parapatry, and/or sympatry at different times as they diverge. Here, we report clinal patterns of variation for 21 nuclear-encoded microsatellites and a wing spot phenotype for cherry-infesting *Rhagoletis* (Diptera: Tephritidae) across North America consistent with these flies having initially diverged in parapatry followed by a period of allopatric differentiation in the early Holocene. However, mitochondrial DNA (mtDNA) displays a different pattern; cherry flies at the ends of the clines in the eastern USA and Pacific Northwest share identical haplotypes, while centrally located populations in the southwestern USA and Mexico possess a different haplotype. We hypothesize that the mitochondrial difference could be due to lineage sorting but more likely reflects a selective sweep of a favorable mtDNA variant or the spread of an endosymbiont. The estimated divergence time for mtDNA suggests possible past allopatry, secondary contact, and subsequent isolation between USA and Mexican fly populations initiated before the Wisconsin glaciation. Thus, the current genetics of cherry flies may involve different mixed modes of divergence occurring in different portions of the fly's range. We discuss the need for additional DNA sequencing and quantification of prezygotic and postzygotic reproductive isolation to verify the multiple mixed-mode hypothesis for cherry flies and draw parallels from other systems to assess the generality that speciation may commonly involve complex biogeographies of varying combinations of allopatric, parapatric, and sympatric divergence.

Asymmetrical thermal constraints on the parapatric species boundaries of two widespread generalist butterflies

Mercader, RJ; Scriber, JM, 2008

1. The sibling species *Papilio glaucus* and *Papilio canadensis* meet in a narrow **hybrid** zone believed to be maintained by temperature thresholds acting independently on both species. The present study tests if this assertion is true for the cold-adapted species, *P. canadensis*, which is presumed to be limited by the effect of high temperatures in late summer and/or autumn on pupal survival. 2. Three experiments were conducted examining the effects of: (i) short periods of high temperature stress in autumn, (ii) prolonged warm temperatures in autumn, and (iii) temperatures simulating warmer winters/longer springs upon the survival of *P. canadensis* and *P. glaucus*. 3. Results indicated that short periods of high temperatures did not induce the high C mortality rates required to be the key factor limiting the range of *P. canadensis*. However, *P. canadensis* did exhibit a considerably lower tolerance to high temperature extremes, prolonged warm temperatures in autumn, and conditions simulating shorter/warmer winters than *P. glaucus*. 4. Differences in temperature tolerance throughout the pupal stage are likely to be a significant factor in maintaining the southern range limit of *P. canadensis*. Further warming as may occur during climate change, particularly in winter and spring, will likely affect the dynamics of southerly populations of *P. canadensis*.
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Analysis of a contact area between two distinct evolutionary honeybee units: an ecological perspective

Canovas, F; De la Rua, P; Serrano, J; Galian, J, 2014

Determining the relationships between environmental variables and genetic diversity is critical to understand the processes that drive evolution in species-contact areas. We employed a combination of modeling approaches and multivariate statistical analyses to analyze mtDNA diversity in a **hybrid** zone between two evolutionary lineages of honeybees in order to interpret the microevolutionary processes that led to the observed spatial pattern of diversity. The model located the west European honeybee lineage mainly across temperate areas characterized by mild winters and high water availability throughout the year, whereas the African lineage was mainly associated with warmer and drier areas. Selection could be playing an important role in shaping the life history evolution, particularly affecting the mitochondria, and also resulting in hitchhiking effects on particular regions of the mitochondrial genome.

Influence of drought on plant performance through changes in belowground tritrophic interactions

Guyot, A; Hibbard, BE; Holzkamper, A; Erb, M; Robert, CAM, 2018

Climate change is predicted to increase the risk of drought in many temperate agroecosystems. While the impact of drought on aboveground plant-herbivore-natural enemy interactions has been studied, little is known about its effects on belowground tritrophic interactions and root defense chemistry. We investigated the effects of low soil moisture on the interaction between maize, the western corn rootworm (WCR, *Diabrotica virgifera*), and soil-borne natural enemies of WCR. In a manipulative field experiment, reduced soil moisture and WCR attack reduced plant performance and increased benzoxazinoid levels. The negative effects of WCR on cob dry weight and silk emergence were strongest at low moisture levels. Inoculation with entomopathogenic nematodes (EPNs, *Heterorhabditis bacteriophora*) was ineffective in controlling WCR, and the EPNs died rapidly in the warm and dry soil. However, ants of the species *Solenopsis molesta* invaded the experiment, were more abundant in WCR-infested pots and predated WCR independently of soil moisture. Ant presence increased root and shoot biomass and was associated with attenuated moisture-dependent effects of WCR on maize cob weight. Our study suggests that apart from directly reducing plant performance, drought can also increase the negative effects of root herbivores such as WCR. It furthermore identifies *S. molesta* as a natural enemy of WCR that can protect maize plants from the negative impact of herbivory under drought stress. Robust herbivore natural enemies may play an important role in buffering the impact of climate change on plant-herbivore interactions.

An Efficient Ant Colony System Approach for New Energy Vehicle Dispatch Problem

Liang, D; Zhan, ZH; Zhang, YC; Zhang, J, 2020

As a powerful measure to alleviate greenhouse gas emissions and global warming issue, new energy vehicle (NEV) has aroused extensive attention from the whole society in recent years. In the past few decades, many studies have been conducted on the dispatch of traditional fuel-driven vehicles. As a means of transportation, NEV has the characteristics of fuel-driven vehicles, but the dispatch is different because of its unique refueling manner. With the popularization of NEV, its unique dispatch research is imminent. This paper comprehensively considers electricity and charging piles during the NEV dispatch (NEVD) process. An NEVD framework containing a novel dispatch model is proposed, which elaborates the application service of NEV. To the best of our knowledge, this study is the first to combine NEVD with service system. Based on the formulated model, an efficient ant colony system (EACS) approach enhanced by pre-selection strategy and local pruning strategy is designed to dispatch NEVs to passengers. Experiments are carried out to investigate the applicable scenarios of ACS-based algorithms. The results verify that the proposed EACS algorithm is an effective and efficient approach to solve the NEVD problem.

~~Local adaptation and rapid evolution of aphids in response to genetic interactions with their cottonwood hosts~~

Wooley, SC; Smith, DS; Lonsdorf, EV; Brown, SC; Whitham, TG; Shuster, SM; Lindroth, RL, 2020

Several studies have demonstrated the ecological consequences of genetic variation within a single plant species. For example, these studies show that individual plant genotypes support unique composition of the plants' associated arthropod community. By contrast, fewer studies have explored how plant genetic variation may influence evolutionary dynamics in the plant's associated species. Here, we examine how aphids respond evolutionarily to genetic variation in their host plant. We conducted two experiments to examine local adaptation and rapid evolution of the free-feeding aphid *Chaitophorus populicola* across genetic variants of its host plant, *Populus angustifolia*. To test for local adaptation, we collected tree cuttings and aphid colonies from three sites along an elevation/climate gradient and conducted a reciprocal transplant experiment. In general, home aphids (aphids transplanted onto trees from the same site) produced 1.7-3.4 times as many offspring as foreign aphids (aphids transplanted onto trees from different sites). To test for rapid evolution, we used 4 clonally replicated aphid genotypes and transplanted each onto 5 clonally replicated *P. angustifolia* genotypes. Each tree genotype started with the same aphid genotype composition. After 21 days (similar to two aphid generations), aphid genotype composition changed (i.e., aphids evolved) and some tree genotypes supported unique evolutionary trajectories of aphids. These results suggest that plant evolution in response to human perturbation, such as climate change and invasive species, will also result in evolutionary responses in strongly interacting species that could cascade to affect whole communities.

Insect Hybridization and Climate Change

Larson, EL; Tinghitella, RM; Taylor, SA, 2019

Contemporary global change is altering ecosystems at an unprecedented pace and scale. This critical period is a crisis for biodiversity, but the perturbations caused by global environmental change also offer new opportunities to study the evolution of species boundaries—their persistence, formation, or collapse—over rapid evolutionary timescales. Increasing temperature means and fluctuations have the potential to alter gene flow between species through changes in species distributions, interactions, life history, and temperature-dependent behavior. This is particularly true for insects, whose geographic ranges, behaviors, and life history traits are temperature dependent. Here, we review the potential for climate change to influence gene flow and species boundaries between closely related insect species. We focus on studies that have tracked changes in climate and insect distributions and/or have evaluated temperature dependent reproductive barriers between species.

~~Genetic differentiation across a latitudinal gradient in two co-occurring butterfly species: revealing population differences in a context of climate change~~

Zakharov, EV; Hellmann, JJ, 2008

Genetic differentiation within a species' range is determined by natural selection, genetic drift, and gene flow. Selection and drift enhance genetic differences if populations are sufficiently isolated, while gene flow precludes differentiation and local adaptation. Over large geographical areas, these processes can create a variety of scenarios, ranging from admixture to a high degree of population differentiation. Genetic differences among populations may signal functional differences within a species' range, potentially leading to population or ecotype-specific responses to global change. We investigated differentiation within the geographical range of two butterfly species along a broad latitudinal gradient. This gradient is the primary axis of climatic variation, and many ecologists expect populations at the poleward edge of this gradient to expand under climate change. Our study species inhabit a shared ecosystem and differ in body size and resource specialization; both also find their poleward range limit on an island. We find evidence for divergence of peripheral populations from the core in both taxa, suggesting the potential for genetic distinctiveness at the leading edge of climate change. We also find differences between the species in the extent of peripheral differentiation with the smaller and more specialized species showing greater population divergence (microsatellites and mtDNA) and reduced gene flow (mtDNA). Finally, gene flow estimates in both species differed strongly between two marker types. These findings suggest caution in assuming that populations are invariant across latitude and thus will respond as a single ecotype to climatic change.

~~Evolution, not transgenerational plasticity, explains the adaptive divergence of acorn ant thermal tolerance across an urban-rural temperature cline~~

Martin, RA; Chick, LD; Yilmaz, AR; Diamond, SE, 2019

Although studies increasingly disentangle phenotypic plasticity from evolutionary responses to environmental change, few test for transgenerational plasticity in this context. Here, we evaluate whether phenotypic divergence of acorn ants in response to urbanization is driven by transgenerational plasticity rather than evolution. F2 generation worker ants (offspring of laboratory-born queens) exhibited similar divergence among urban and rural populations as field-born worker ants, suggesting that evolutionary divergence rather than transgenerational plasticity was primarily responsible for shifts toward higher heat tolerance and diminished cold tolerance in urban acorn ants. **Hybrid** offspring from matings between urban and rural populations also indicated that evolutionary divergence was likely the primary mechanism underlying population differences in thermal tolerance. Specifically, thermal tolerance traits were not inherited either maternally or paternally in the **hybrid** pairings as would be expected for strong parental or grandparental effects mediated through a single sex. Urban-rural **hybrid** offspring provided further insight into the genetic architecture of thermal adaptation. Heat tolerance of **hybrids** more resembled the urban-urban pure type, whereas cold tolerance of **hybrids** more resembled the rural-rural pure type. As a consequence, thermal tolerance traits in this system appear to be influenced by dominance rather than being purely additive traits, and heat and cold tolerance might be determined by separate genes. Though transgenerational plasticity does not appear to explain divergence of acorn ant thermal tolerance, its role in divergence of other traits and across other urbanization gradients merits further study.

~~An integrative revision of the subgenus Liophloeodes (Coleoptera: Curculionidae: Entiminae: Polydrusini): taxonomic, systematic, biogeographic and evolutionary insights~~

Waclawik, B; Nugnes, F; Bernardo, U; Gebiola, M; Przybycien, M; Lachowska-Cierlik, D, 2021

The subgenus *Liophloeus* Weise, 1894 of *Liophloeus* Germar, 1817 (Coleoptera: Curculionidae: Entiminae: Polydrusini) consists of five morphologically similar species traditionally diagnosed based on the shape of the aedeagus. However, traits of the genital apparatus exhibit substantial and overlapping inter- and intraspecific variation. All five species have the same ecological requirements and occur in central and eastern Europe, mostly in montane areas. The focus of this work was to verify the taxonomic status and validity of *Liophloeodes* species using a combination of molecular and morphometric techniques. Specimens were collected from the entire distribution range and initially assigned to a species according to the aedeagal shape. Genetic diversity and phylogeny of the subgenus were studied using three molecular markers (two ribosomal, 28S-D2 and ITS2, and one mitochondrial, COI). Moreover, several morphological characters were used for multivariate morphometric analyses. Finally, presence and prevalence of bacterial endosymbionts among species were investigated. Phylogenies based on ribosomal markers suggest that traditional species are correctly delimited, whereas COI phylogeny suggests **hybridization** and **introgression** occurring between *Liophloeodes* species. Morphometric analyses confirmed low interspecific diversity. Two major bacterial endosymbionts, *Rickettsia* and *Wolbachia*, were detected in many populations. We argue that *Liophloeodes* consists of young lineages whose evolution and diversification was possibly mediated by cyclic climate change events.

Elevated ozone modifies the feeding behaviour of the common leaf weevil on hybrid aspen through shifts in developmental, chemical, and structural properties of leaves

Freiwald, V; Haikio, E; Julkunen-Tiitto, R; Holopainen, JK; Oksanen, E, 2008

In this study, we tested the impact of moderately elevated ozone (O-3) - 1.5 x ambient, equivalent to predicted near-future ozone concentrations - on the feeding behaviour of the common leaf weevil *Phyllobius pyri* L. (Coleoptera: Curculionidae), on two **hybrid** aspen [*Populus tremula* x *Populus tremuloides* (Salicaceae)] clones (clones 55 and 110) differing in ozone sensitivity using the open-air ozone exposure site in Kuopio, Finland. Three host-selection tests (test between treatments, test between clones, and test between treatments* clones) with common leaf weevil females were carried out in the laboratory in the 2nd year of ozone exposure. The beetles were offered two (four for the tests between treatments and clones) freshly cut leaf discs from first flush leaves. After 24 h, the beetles were removed and the leaf disc area consumed was measured. In the field, the unfolding of the buds was followed and samples were taken for anatomical and chemical (salicylates, condensed tannins, nitrogen, and water content) leaf analyses. *Phyllobius pyri* significantly preferred leaves from clone 55 to those from clone 110 in the ambient air treatment, whereas this preference was less evident under elevated ozone. Leaves from ozone-exposed trees were significantly preferred to leaves grown in ambient air. Our results suggest that the preference of clone 55 and of ozone-exposed leaves can be explained by phenotypic properties of the plant and prevailing ozone concentration through shifts in leaf development process, phenolic composition, and leaf thickness.

Towards sustainable micro and nano composites from fly ash and natural fibers for multifunctional applications

Pappu, A; Thakur, VK, 2017

Manufacturing of petroleum based synthetic materials, exploitation of timber products from forest reserves, improper management of industrial wastes and natural resources greatly persuade the environmental contaminations and global warming. To find viable solutions and reduce such alarming issues, innovative research work on recycling of unutilized materials such as fly ash and natural cellulosic polymers has been reported in this work to develop advanced sustainable **hybrid** micro/nano composites. In this study, the use of natural cellulosic sisal fibers with fly ash has enhanced the tensile properties and surface finish of composites. Fly ash particulates acted as fillers, additives, as well as surface-finishing medium and sisal fibers as reinforcing elements in achieving glossy finish sustainable composites. The developed composites have been found to be stronger than wood, plastics and have many opportunities for multifunctional applications. (C) 2017 Published by Elsevier Ltd.

Genetic and firefly metaheuristic algorithms for an optimized neuro-fuzzy prediction modeling of wildfire probability

Jaafari, A; Termeh, SVR; Bui, DT, 2019

In the terrestrial ecosystems, perennial challenges of increased frequency and intensity of wildfires are exacerbated by climate change and unplanned human activities. Development of robust management and suppression plans requires accurate estimates of future burn probabilities. This study describes the development and validation of two **hybrid** intelligence predictive models that rely on an adaptive neuro-fuzzy inference system (ANFIS) and two metaheuristic optimization algorithms, i.e., genetic algorithm (GA) and firefly algorithm (FA), for the spatially explicit prediction of wildfire probabilities. A suite of ten explanatory variables (altitude, slope, aspect, land use, rainfall, soil order, temperature, wind effect, and distance to roads and human settlements) was investigated and a spatial database constructed using 32 fire events from the Zagros ecoregion (Iran). The frequency ratio model was used to assign weights to each class of variables that depended on the strength of the spatial association between each class and the probability of wildfire occurrence. The weights were then used for training the ANFIS-GA and ANFIS-FA **hybrid** models. The models were validated using the ROC-AUC method that indicated that the ANFIS-GA model performed better (AUC(success rate) = 0.92; AUC(prediction rate) = 0.91) than the ANFIS-FA model (AUC(success rate) = 0.89; AUC(prediction rate) = 0.88). The efficiency of these models was compared to a single ANFIS model and statistical analyses of paired comparisons revealed that the two meta-optimized predictive models significantly improved wildfire prediction accuracy compared to the single ANFIS model (AUC(success rate) = 0.82; AUC(prediction rate) = 0.78). We concluded that such predictive models may become valuable toolkits to effectively guide fire management plans and on-the-ground decisions on firefighting strategies.

Alkali Activated Hybrid Concrete Based on Fly Ash and Its Application in the Production of High-Class Structural Blocks

Rojas-Duque, O; Espinosa, LM; Robayo-Salazar, RA; de Gutierrez, RM, 2020

This article reports the production and characterization of a **hybrid** concrete based on the alkaline activation of a fly ash (FA) of Colombian origin, which was added with 10% Portland cement (OPC) in order to promote the compressive strength development at room temperature. The alkali-activated **hybrid** cement FA/OPC 90/10 was classified as a low heat reaction cement (type LH), according to American Society of Testing Materials, ASTM C1157; the compressive strength was of 31.56 MPa and of 22.68 MPa (28 days) at the levels of paste and standard mortar, respectively, with an initial setting time of 93.3 min. From this binder, a **hybrid** concrete was produced and classified as a structural type, with a compressive strength of 23.16 MPa and a flexural modulus of rupture of 5.32 MPa, at 28 days of curing. The global warming potential index (GWP 100), based on life cycle analysis, was 35% lower than the reference concrete based on 100% OPC. Finally, its use was validated in the manufacture of a solid block-type construction element, which reached a compressive strength of 21.9 MPa at 28 days, exceeding by 40.6% the minimum strength value established by the Colombia Technical Standard, NTC 4026 (13 MPa) to be classified as high class structural blocks.

Large and small scale geographic structures affecting genetic patterns across populations of an Alpine butterfly

Trense, D; Hoffmann, AA; Fischer, K, 2021

Understanding factors influencing patterns of genetic diversity and the population genetic structure of species is of particular importance in the current era of global climate change and habitat loss. These factors include the evolutionary history of a species as well as heterogeneity in the environment it occupies, which in turn can change across time. Most studies investigating spatio-temporal genetic patterns have focused on patterns across wide geographic areas rather than local variation, but the latter can nevertheless be important particularly in topographically complex areas. Here, we consider these issues in the Sooty Copper butterfly (*Lycaena tityrus*) from the European Alps, using genome-wide SNPs identified through RADseq. We found strong genetic differentiation within the Alps with four genetic clusters, indicating western, central, and eastern refuges, and a strong reduction of genetic diversity from west to east. This reduction in diversity may suggest that the southwestern refuge was the largest one in comparison to other refuges. Also, the high genetic diversity in the west may result from (a) admixture of different western refuges, (b) more recent demographic changes, or (c) **introgression** of lowland *L. tityrus* populations. At small spatial scales, populations were structured by several landscape features and especially by high mountain ridges and large river valleys. We detected 36 outlier loci likely under altitudinal selection, including several loci related to membranes and cellular processes. We suggest that efforts to preserve alpine *L. tityrus* should focus on the genetically diverse populations in the western Alps, and that the dolomite populations should be treated as genetically distinct management units, since they appear to be currently more threatened than others. This study demonstrates the usefulness of SNP-based approaches for understanding patterns of genetic diversity, gene flow, and selection in a region that is expected to be particularly vulnerable to climate change.

Research and application of association rule algorithm and an optimized grey model in carbon emissions forecasting

Accurate carbon emissions forecasting plays a pivotal role in reducing global warming by providing references to formulate emission reduction policies. Although numerous studies have focused on forecasting China's carbon emissions, the results of different methods are contradicting, because they are based on different data and use different parameters. This paper aims to propose a **hybrid** carbon emissions forecasting model based on multi-factor identification to offer reliable forecasting results. First, association rule algorithm was applied to find influencing factors and analyse their joint effects on carbon emissions from the perspective of time and space. Energy consumption, economic growth, industrial structure, foreign direct investment, and urbanization are proven to be the five major factors that can cause an increase in carbon emissions. Second, a multivariate grey model optimized by firefly algorithm was utilized to conduct carbon emissions forecasting under different scenarios. Empirical results indicated that the proposed **hybrid** model had the best performance compared to other methods. If no effective measures are taken, it is difficult for China to realize its goal for carbon emissions reduction in 2020.

Tick-borne pathogens, including Crimean-Congo haemorrhagic fever virus, at livestock markets and slaughterhouses in western Kenya

Chiuya, T.; Masiga, D.K.; Falzon, L.C.; Bastos, A.D.S.; Fevre, E.M.; Villinger, J., 2021

Vectors of emerging infectious diseases have expanded their distributional ranges in recent decades due to increased global travel, trade connectivity and climate change. Transboundary range shifts, arising from the continuous movement of humans and livestock across borders, are of particular disease control concern. Several tick-borne diseases are known to circulate between eastern Uganda and the western counties of Kenya, with one fatal case of Crimean-Congo haemorrhagic fever (CCHF) reported in 2000 in western Kenya. Recent reports of CCHF in Uganda have highlighted the risk of cross-border disease translocation and the importance of establishing inter-epidemic, early warning systems to detect possible outbreaks. We therefore carried out surveillance of tick-borne zoonotic pathogens at livestock markets and slaughterhouses in three counties of western Kenya that neighbour Uganda. Ticks and other ectoparasites were collected from livestock and identified using morphological keys. The two most frequently sampled tick species were *Rhipicephalus decoloratus* (35%) and *Amblyomma variegatum* (30%); *Ctenocephalides felis* fleas and *Haematopinus suis* lice were also present. In total, 486 ticks, lice and fleas were screened for pathogen presence using established molecular workflows incorporating high-resolution melting analysis and identified through sequencing of PCR products. We detected CCHF virus in *Rh. decoloratus* and *Rhipicephalus* sp. cattle ticks, and 82 of 96 pools of *Am. variegatum* were positive for *Rickettsia africae*. Apicomplexan protozoa and bacteria of veterinary importance, such as *Theileria parva*, *Babesia bigemina* and *Anaplasma marginale*, were primarily detected in rhipicephaline ticks. Our findings show the presence of several pathogens of public health and veterinary importance in ticks from livestock at livestock markets and slaughterhouses in western Kenya. Confirmation of CCHF virus, a *Nairovirus* that causes haemorrhagic fever with a high case fatality rate in humans, highlights the risk of under-diagnosed zoonotic diseases and calls for continuous surveillance and the development of preventative measures.

Role of *Sesamia nonagrioides* and *Ostrinia nubilalis* as Vectors of *Fusarium* spp. and Contribution of Corn Borer-Resistant Bt Maize to Mycotoxin Reduction

Arias-Martin, M.; Haidukowski, M.; Farinos, G.P.; Patino, B., 2021

Maize expressing Cry1Ab insecticidal toxin (Bt maize) is an effective method to control *Sesamia nonagrioides* and *Ostrinia nubilalis*, the most damaging corn borers of southern Europe. In this area, maize is prone to *Fusarium* infections, which can produce mycotoxins that pose a serious risk to human and animal health, causing significant economic losses in the agrifood industry. To investigate the influence of corn borer damage on the presence of *Fusarium* species and their mycotoxins, Bt maize ears and insect-damaged ears of non-Bt maize were collected from commercial fields in three Bt maize growing areas in Spain, and differences in contamination were assessed. Additionally, larvae of both borer species were collected to evaluate their role as vectors of these molds. Non-Bt maize ears showed significantly higher presence of *F. verticillioides*, *F. proliferatum*, and *F. subglutinans* than Bt maize ears. For the first time, *Fusarium* species have been isolated from larvae of the two species. The most frequently found mycotoxins in ears were fumonisins, with non-Bt ears being significantly more contaminated than those of Bt maize. High levels of fumonisins were shown to correlate with the occurrence of corn borers in the ear and the presence of *F. verticillioides* and *F. proliferatum*.

Multi-layer perceptron hybrid model integrated with the firefly optimizer algorithm for windspeed prediction of target site using a limited set of neighboring reference station data

Deo, R.C.; Ghorbani, M.A.; Samadianfard, S.; Maraseni, T.; Bilgili, M.; Biazar, M., 2018

Long-term windspeed prediction is crucial for establishing the viability of wind as a clean energy option, including the selection of wind farm locations, feasibility studies on energy potential and the operation of wind energy conversion systems with minimal investment risk. To deliver this vital societal need, data-inexpensive artificial intelligence models relying on historical inputs can be a useful scientific contrivance by energy analysts, engineers and climate-policy advocates. In this paper, a novel approach is adopted to construct a multilayer perceptron (MLP) **hybrid** model integrated with the Firefly Optimizer algorithm (MLP-FFA) trained with a limited set of historical (monthly) data (2004-2014) for a group of neighboring stations to predict windspeed at target sites in north-west Iran. Subsequently, the MLP-FFA model is developed to minimize the error rate of the resulting **hybrid** model and applied at each of the eight target sites one-by-one (namely: Tabriz, Jolfa, Sarab, Marand, Sahand, Kaleybar, Maraghe and Miandeh) such that the seven neighboring (reference) sites are used for training and the remainder eighth site for testing purposes. To ascertain conclusive results, the **hybrid** model's ability to predict windspeed at each target site is cross-validated with the MLP model without the FFA optimizer and the statistical performance is benchmarked with root mean square error (RMSE), mean absolute error (MAE), Nash-Sutcliffe efficiency (E-Ns), Willmott's Index (d) and the Legates and McCabe's Index (E-1), including relative errors. For all eight target sites, the testing performance of the MLP-FFA model is found to be significantly superior than the classical MLP, resulting in lower values of the RMSE (0.202-0.50 ms⁻¹) relative to 0.236-0.664 ms⁻¹) and larger values of ENs, d and E1 (0.686-0.953 vs. 0.529-0.936, 0.874-0.976 vs. 0.783-0.966, 0.417-0.800 vs. 0.303-0.748). Despite a more accurate performance of **hybrid** models tested at each target site, the preciseness registered a distinct geographic signature with the least accurate result (for Kaleybar) and the most accurate result (for Jolfa). To accord with this result, we conclude that the utilization of the FFA as an add-in optimizer in a **hybrid** data-intelligent model leads to a significant improvement in the predictive accuracy, presumably due to the optimal weights attained in the hidden layer that allows a more robust feature extraction process. Accordingly, we establish that the **hybrid** MLP-FFA model can be explored further in a problem of long-term windspeed prediction with reference station input data, and feasibility studies on wind energy investments in data-scarce regions where a limited set of neighboring reference site data can be employed to forecast the target site windspeed. (C) 2017 Elsevier Ltd. All rights reserved.

Simulating Climate Change Impacts on Hybrid Poplar and Black Locust Short Rotation Coppices

Seserman, D.M.; Pohle, I.; Veste, M.; Freese, D., 2018

In Brandenburg, north-eastern Germany, climate change is associated with increasing annual temperatures and decreasing summer precipitation. Appraising short rotation coppices (SRCs), given their long-time planning horizon demands for systematic assessments of woody biomass production under a considerable spectrum of climate change prospects. This paper investigates the prospective growth sensitivity of poplar and black locust SRCs, established in Brandenburg to a variety of weather conditions and long-term climate change, from 2015 to 2054, by a combined experimental and simulation study. The analysis employed (i) a biophysical, process-based model to simulate the daily tree growth and (ii) 100 realisations of the statistical regional climate model STAR 2K. In the last growing period, the simulations showed that the assumed climate change could lead to a decrease in the woody biomass of about 5 Mg ha⁻¹ (18%) for poplar and a decrease of about 1.7 Mg ha⁻¹ (11%) for black locust trees with respect to the median observed in the reference period. The findings corroborate the potential tree growth vulnerability to prospective climatic changes, particularly to changes in water availability and underline the importance of coping management strategies in SRCs for forthcoming

Testing historical explanations for gradients in species richness in heliconiine butterflies of tropical America

Rosser, N; Phillimore, AB; Huertas, B; Willmott, KR; Mallet, J, 2012

We compiled a large database of 58 059 point locality records for 70 species and 434 subspecies of heliconiine butterflies and used these data to test evolutionary hypotheses for their diversification. To study geographical patterns of diversity and contact zones, we mapped: (1) species richness; (2) mean molecular phylogenetic terminal branch length; (3) subspecies richness and the proportion of specimens that were subspecific **hybrids**, and (4) museum sampling effort. Heliconiine species richness is high throughout the Amazon region and peaks near the equator in the foothills and middle elevations of the eastern Andes. Mean phylogenetic terminal branch length is lowest in the eastern Andes and tends to be low in species-rich areas. By contrast, areas of high subspecies richness, where subspecies overlap in range and/or **hybridize**, are concentrated along the course of the Amazon River, with the eastern Andes slopes and foothills relatively depauperate in terms of local intraspecific phenotypic diversity. Spatial gradients in heliconiine species richness in the Neotropics are consistent with the hypothesis that species richness gradients are driven at least in part by variation in speciation and/or extinction rates, resulting in observed gradients in mean phylogenetic branch length, rather than via evolutionary age or niche conservatism alone. The data obtained in the present study, coupled with individual case studies of recently evolved *Heliconius* species, suggest that the radiation of heliconiine butterflies occurred predominantly on the eastern slopes of the Andes in Colombia, Ecuador, and Peru, as well as in the upper/middle Amazon basin. (C) 2012 The Linnean Society of London, Biological Journal of the Linnean Society, 2012, 105, 479497.

ALIEN PHYTOPHAGOUS INSECT AND MITE SPECIES ON WOODY PLANTS IN CROATIA

Matosevic, D; Zivkovic, IP, 2013

Alien species are defined as species living outside of their natural range and outside of their natural dispersal potential. When an alien species enters a novel environment and has negative ecological and economical impact it becomes invasive species. Alien species are considered as one of the major threats to biodiversity after habitat destruction and enormous damage is done by them to ecosystems and economies. They have been described as an outstanding global problem. Economic damages associated with alien species in several countries in the world amount to about 5 % of the world GNP. Numerous alien insect species, many introduced only in the last 200 years, have become successfully established in various ecosystems in Europe, 1541 species of alien invertebrates are already present, 94 % of them are arthropods and 90 % of them are insects. More than half of the alien invertebrates are phytophagous (52 %) and 30 % of them infest trees and shrubs. Basic knowledge of the identity, origin, pathway, time of introduction of alien species is essential for assessing the threats from alien species and the first requirement when assessing the impact of alien species on ecosystems is to make an alien species inventory of a certain territory or country. Such studies are needed to assess which taxonomic or bio-ecological groups of alien insects are more successful invaders or more harmful to environment and economy. Croatia lacks such an inventory. Even though Croatia was included in most recent and comprehensive study of alien terrestrial arthropodes in Europe, Croatian references with first records were totally missing. There is no up-to-date list of phytophagous alien insect species on woody plants in Croatia. The aim of this paper is to provide up-to-date comprehensive list of known phytophagous alien insect and mite species on woody plants in Croatia with all relevant Croatian references. The starting point for compiling the list of alien species of phytophagous insects on woody plants in Croatia was a book "Alien Terrestrial Arthropodes of Europe" and database DAISIE. These are primary online resources on alien insect species available to the public and first qualified reference system on invasive alien species for the European region. We compiled the list by searching many sources of forestry, agricultural and taxonomic entomological peer-reviewed literature in Croatia, checklists and primary research publications on alien insect species. The references in these sources were examined for additional relevant publications. A total of 101 phytophagous alien species (98 insect species from 6 orders and 3 mite species from subclass Acarina) on woody plants were recorded (Table 1) and they are already present in Croatian entomofauna. They were dominated by Hemiptera (56.4 %), Lepidoptera (14.9 %), Hymenoptera (12.9 %), followed by Diptera (5.9 %) and Coleoptera (5.9 %), Acarina (3 %) and Thysanoptera (1 %)(Figure 1). One third (33.7 %) of the alien species in Croatia originate from Asia, 26.7 % from North America while 12.9 % are of tropical origin (Figure 2). From the 101 established alien insect species in Croatia, an increase in the number of introductions can be noted in the first decade of 21st century (Figure 3). Agricultural lands are the most frequently invaded habitats by alien phytophagous insects in Croatia (56.4 %), followed by parks and gardens (28.7 %) and woodlands and forests (14.9 %)(Figure 4). Order Hemiptera clearly dominates as it includes some of the most successful invaders (57 %) on woody plants in Croatia. Similar results were obtained at a country level for Hungary, Great Britain, Italy, Slovenia and Europe in general. This outcome can be attributed to the fact that species of this order remain undetected and are easily transported due to their tiny size in concert with the intensive trade in agricultural commodities. The occurrence of other orders (Lepidoptera 14 %, Hymenoptera 13 %, Diptera 6 %, Coleoptera 6 %, and Thysanoptera 1 %) is slightly different from other European countries. Results from several investigations have shown strong positive correlations between the number of alien insects per European country and the volume of manufactured and agricultural imports, road network size, the GDP and the geographic size. In contrast, alien species richness was not correlated with the total or percentage of forest cover. The number of alien insects is positively correlated with country surface area, and bordering the sea does not influence the number of alien insect species which is quite important for Croatia. There is a strong correlation between the number of alien insect species and the total amount of imports and level of international trade of the country. It can be predicted that the number of established alien insect species will grow as Croatia shows constant increase of traded commodities with other European and non-European countries. In this review we have listed alien insect species that have not yet been recorded for Croatia on European level. These are *Oxycarenus lavaterae*; *Massilieurodes chitendeni*; *Adelges* (*Dreyfusia*) *nordmannianae*; *Pineus* (*Eopineus*) *strobi*; *Protopulvinaria pyriformis*; *Dryocosmus kuriphilus*; *Platygaster robiniae*; *Aproceros leucopoda*; *Rhyzobius lophanthae*; *Rodolia cardinalis*; *Harmonia axyridis*; *Xylosandrus germanus*; *Caloptilia roscipennella*; *Caloptilia azaleella*; *Phyllocnistis citrella*; *Argyresthia thuiella*; *Cydalima perspectalis*; *Dasineura gleditchiae*; *Ceratitis capitata*; *Rhagoletis cingulata* and *Drosophila suzukii*. Some of them are novel and only recently introduced alien species whereas some of them are present for decades in Croatia but due to the lack of a comprehensive and regularly updated inventory of alien species they have not been listed before. This also makes this up-to-date list of alien phytophagous insects in Croatia valuable. Our results have shown that Asia is the main region of origin of alien insects established in Croatia (33 %), followed by North America (27 %). The trends are similar in other European countries and Europe in general. A rapid increase in the number of new alien species introduction per year in Croatia is noticeable from the years 2007-2012 (6.4 species/year) compared to 2002-2007 (1.8 species/year) (Figure 3). In Europe, an average of 17.5 new species of insects per year was recorded between 2000 and 2007, while this value was only 8.1 from 1950 to 1974. In Europe twice as many new insect species were observed per year on trees and shrubs during the period 2000-2007 (6.3 species) compared to 1960-1979 (3.4 species). The differences between the number of new alien species/year in Europe and Croatia are probably due to differences in sampling efforts, country surface, volume of traded goods etc but the rapidly increasing trend is obvious. More than 80 % of alien insect species in Croatia (57 % on agricultural lands and 28 % in parks and gardens) have been established in man-made habitats (Figure 4). Only 15 % of alien insect species in Croatia have established themselves in natural environments (forests and woodlands) which is almost the same percentage as on European level. It is a common observation that simple, disturbed, man-made habitats are more easily invaded by insects and other invaders than complex, undisturbed, natural habitats. Alien insects linked to human environments and activities (e.g. ornamental plants, bonsais, seeds, large potted trees, cut flowers, vegetables, fruits) are more likely to be carried by human transports into a new region than insects living in natural areas. A study has shown that bonsais carry a more diverse alien insect fauna than timber and that ornamental plants constitute "miniature" ecosystems which may host a large variety of insects that have the potential to damage other woody plants as well. Almost 90 % of alien invertebrates in Europe were introduced unintentionally through human activities, mostly as contaminants of a commodity. In Europe, ornamental plant trade contributes significantly more than forestry products to the invasion of alien forest insects. As interception data have not been analysed in this paper, a research of such data for alien insect species and trade volumes in horticultural plants in Croatia is strongly needed. There is a strong suspicion that ornamental plants are one of main pathways of introduction of alien insects to Croatia due to the increase of the imported volumes from year to year. Alien insect species are known for being serious pests worldwide and they can impact habitats which they invade in several ways. Alien insects can affect native biodiversity through direct actions: phytophagous insects feeding on plants, a predator or a parasitoid attacking host, an alien species **hybridizing** with a native species or indirect actions: vectoring diseases, competing for food, or sharing natural enemies with native species. This research has shown that dangerous pests that can cause direct economic costs have invaded and are spreading in Croatia (Table 1). Due to high percentage of alien insect on agricultural lands (outdoor and in glasshouses) in Croatia (Figure 4) the yield losses of alien insect species on agricultural crops in Croatia must be considerable. Alien insects can have serious negative impact on forests, woodlands and urban parks. Some potentially damaging forest and urban pests have already established themselves in Croatia. In countries where the percentage of forest cover is high (Croatia around 44 %) the damage from alien insects is expected to be considerable. Most introductions of alien insects are unintentional and unpredictable. Less than 20 % of the alien invertebrates in Europe have been intercepted before their arrival. There are several harmful phytophagous alien species approaching the borders of Croatia: *Agrilus planipennis* which could pose serious threat to Croatian lowland oak

ecosystems, *Anoplophora* sp. which is spreading rapidly in Northern Italy. Some of the most polyphagous alien insect species, such as *Drosophila suzukii*, have only recently been discovered in Croatia. This study has also shown a time lag between arrival and first record of an alien species which has direct implications on successful eradication measures. Climate change may directly influence establishment and colonisation of alien insect species in new territories-from other continents to Europe and from warmer European regions of Europe further north. Global warming is likely to influence establishment and spread of alien insect species from subtropical and tropical areas (24 % found in Croatia) especially on the Mediterranean coast. One of the main factors, globalisation, will definitely influence the upward trend of introduction and spread of new alien species in Croatia which will negatively influence economy and ecosystems.

Hybridization of Two Major Termite Invaders as a Consequence of Human Activity

Chouvenc, T; Helmick, EE; Su, NY, 2015

While **hybridization** of an invasive species with a native species is a common occurrence, **hybridization** between two invasive species is rare. Formosan subterranean termites (*Coptotermes formosanus*) and Asian subterranean termites (*C. gestroi*) are both ecologically successful and are the two most economically important termite pests in the world. Both species have spread throughout many areas of the world due to human activity; however, their distributions overlap in only three narrow areas because of distinct ecological requirements. In south Florida, where *C. formosanus* and *C. gestroi* are both invasive, the dispersal flight seasons of both species overlapped for the first time on record in 2013 and 2014. Pairings of heterospecific individuals were readily observed in the field and *C. gestroi* males preferentially engaged in mating behavior with *C. formosanus* females rather than females from their own species. In the laboratory, heterospecific and conspecific pairings had an equal colony establishment rate, but heterospecific incipient colonies had twice the growth rate of conspecific incipient colonies, suggesting a potential case of **hybrid** vigor. As all prezygotic barriers were lifted between the two species in the field, the apparent absence of post-zygotic barriers in the laboratory raises the possibility for introgressive **hybridization** in south Florida. While laboratory observations remain to be confirmed in the field, and the alate **hybrid** fertility is currently unknown, our results raise a tangible concern about the **hybridization** of two major destructive pest species. Such **hybridization** would likely be associated with a new economic impact.

Environmental and economic performances of municipal solid waste incineration fly ash low temperature utilization: An integrated hybrid life cycle assessment

Zheng, RF; Wang, Y; Liu, ZX; Zhou, JZ; Yue, Y; Qian, GR, 2022

Detoxification and utilization of municipal solid waste incineration fly ash (MSWIFA) with low temperature pretreatment, low environmental burden and low cost have become more and more popular topics in the world. Based on integrated **hybrid** life cycle assessment, this study compares the environmental and economic performance of MSWIFA low-temperature utilization with the cement kiln co-processing technique when the scenarios with or without salt recovery were considered. The result shows that the **hybrid** integrated life cycle assessment captures larger environmental and economic benefits of MSWIFA utilization than traditional method due to extending the system boundary to the entire economy. Especially, the avoiding in global warming, primary energy demand and human toxicity from the economic input-output system account for 15%-53%, 26%-65%, and 93%-96% of total impacts, respectively. Additionally, the **hybrid** model captures a considerable avoidance of cost for MSWIFA treatment. When adopting salt recovery, except for human toxicity, the environmental credit of low-temperature utilization is 3.19-12.64 times higher than that of cement kiln co-processing. Moreover, because of the saving of chemicals and energy, the environmental and economic credit of scenarios without salt recovery is significantly higher than that of scenarios with salt recovery. Findings of this study provide scientific foundations to promote the low-temperature utilization of MSWIFA, as well as multiple solutions on ash-washing wastewater treatment.

Nexus on climate change: agriculture and possible solution to cope future climate change stresses

Shahzad, A; Ullah, S; Dar, AA; Sardar, MF; Mehmood, T; Tufail, MA; Shakoor, A; Haris, M, 2021

The changing climate scenarios harshen the biotic stresses including boosting up the population of insect/pest and disease, uplifting weed growth, declining soil beneficial microbes, threaten pollinator, and boosting up abiotic stresses including harsh drought/waterlogging, extremisms in temperature, salinity/alkalinity, abrupt rainfall pattern)) and ultimately affect the plant in multiple ways. This nexus review paper will cover four significant points viz (1) the possible impacts of climate change; as the world already facing the problem of food security, in such crucial period, climatic change severely affects all four dimensions of food security (from production to consumption) and will lead to malnutrition/malnourishment faced by low-income peoples. (2) How some major crops (wheat, cotton, rice, maize, and sugarcane) are affected by stress and their consequent loss. (3) How to develop a strategic work to limit crucial factors, like their significant role in climate-smart breeding, developing resilience to stresses, and idiosyncratic breeding. Additionally, there is an essence of improving food security, as much of our food is wasted before consumption for instance post-harvest losses. (4) Role of biotechnology and genetic engineering in adaptive **introgression** of the gene or developing plant transgenic against pests. As millions of dollars are invested in innovation and research to cope with future climate change stresses on a plant, hence community base adaptation of innovation is also considered an important factor in crop improvements. Because of such crucial predictions about the future impacts of climate change on agriculture, we must adopt measures to evolve crop.

Adaptation of Forest Management Regimes in Southern Sweden to Increased Risks Associated with Climate Change

Subramanian, N; Bergh, J; Johansson, U; Nilsson, U; Sallnas, O, 2016

Even though the growth rates of most tree species in Sweden is expected to increase in the near future as a result of climate change, increased risks of damage by storms and various pests and pathogens, notably root rot and bark beetles, may also occur. Thus, forest management practices such as changes to thinning regimes, reductions in rotation lengths, and switching to other species (native or exotic) may represent adaptive management strategies to increase the resistance and resilience of Swedish forests to climate change. Clearly, thorough analyses examining the effects of anticipated climatic changes on damage levels, and the potentially relieving effects of possible management adaptations are needed before implementing such changes. In this study, damage caused by storms, root rot and bark beetles (single and in various combinations) under selected climate and management scenarios were simulated in Norway spruce (*Picea abies* (L.) Karst.) stands. The results indicate that reductions in thinning intensity and rotation lengths could improve both volume production and profitability in southern Sweden. In addition, cultivation of rapidly growing species, such as **hybrid** larch (*Larix x marschlinii* Coaz.) and **hybrid** aspen (*Populus tremula* L. x *P. tremuloides* Michx.), could be as profitable as Norway spruce cultivation, or even more profitable. However, slow-growing species, such as Silver birch (*Betula pendula* Roth), Downy birch (*Betula pubescens* Ehrh.) and European beech (*Fagus sylvatica* L.) indicated low economic output in terms of Land Expectation Value.

Mechanical Properties and Water Absorption Capacity of Hybrid GFRP Composites

Badaruzzaman, WHW; Dabbagh, NMR; Salleh, KM; Saharuddin, EN; Radzi, NFM; Azham, MAA; Sani, SFA; Zakaria, S, 2022

Hybrid glass fibre reinforced polymer (GFRP) composites have been used for decades in various engineering applications. However, it has a drawback with its application in marine/flood environments due to a lack of water resistance and frail mechanical stability. Floods have been considered one of the most periodic hazards that could hit urban areas, due to climate change. The present paper aims to address this gap and to investigate the mechanical properties (tensile, compressive, and flexural strength) and water absorption capacity of **hybrid** GFRP composite comprising woven E-glass fabric and epoxy resin, various reinforcing

materials (kenaf and coconut fibres), and various filler materials (fly ash, nano-silica, and calcium carbonate (CaCO₃). The composites with 30 wt.% GFRP, 50 wt.% resin, 15 wt.% fly ash, 5 wt.% CaCO₃, 10 wt.% GFRP, 60 wt.% resin, and 30 wt.% fly ash showed the lowest water absorption property of 0.45%. The results revealed that the GFRP composite reinforced kenaf fibres with nano-silica, fly ash, and CaCO₃ improved the water absorption resistance. At the same time, GFRP reinforced the coconut fibres with fly ash, and kenaf fibres with CaCO₃ showed no favourable impact on water absorption. The identification of a **hybrid** GFRP composite with various reinforcing materials and fillers would assist future developments with a more compatible, enhanced, and reliable water-resistant composite, specifically for structural applications in flood-prone areas.

Hybrid effects in field populations of the African monarch butterfly, *Danaus chrysippus* (L.) (Lepidoptera: Nymphalidae)

Smith, DAS; Bennie, JJ; Gordon, IJ; Martin, S; Ileri, P; Omufwoko, KS; Ffrench-Constant, RH, 2021

Heterosis, Haldane and Bateson-Dobzhansky-Muller effects have been widely documented amongst a range of plants and animals. However, typically these effects are shown by taking parents of known genotype into the laboratory and measuring components of the F₂ progeny under laboratory conditions. This leaves in doubt the real significance of such effects in the field. Here we use the well-known colour pattern genotypes of the African monarch or queen (*Danaus chrysippus*), which also control wing length, to test these effects both in the laboratory and in a contact zone in the field. By measuring the wing lengths in animals of known colour pattern genotype we show clear evidence for all three **hybrid** effects at the A and BC colour patterning loci, and importantly, that these same effects persist in the same presumptive F₁s when measured in **hybrid** populations in the field. This demonstrates the power of a system in which genotypes can be directly inferred in the field and highlights that all three **hybrid** effects can be seen in the East African contact zone of this fascinating butterfly.

An overview and experimental study on hybrid binders containing date palm ash, fly ash, OPC and activator composites

Al-Kutti, W; Nasir, M; Johari, MAM; Islam, ABMS; Manda, AA; Blaisi, NI, 2018

Global warming due to high greenhouse gasses emission coupled with excessive energy involved in concrete manufacturing process is indeed an alarming threat. To overcome the problem, numerous researches have been carried out to partially replace ordinary Portland cement (OPC) with supplementary cementitious materials (SCMs) that includes agricultural or industrial solid wastes, development of alternative binder known as geopolymer concrete made of one or more pure SCMs using alkaline activators and elevated temperature curing or by development of **hybrid** cement system that incorporates alkaline activation of OPC-based SCMs. This study aims to: (1) carry out an overview on: CO₂ emission by construction industry; alternate cement systems such as partial replacement, geopolymers and most importantly **hybrid** binders; as well as identification of date palm ash (DPA) as a potential waste material and (2) develop novel **hybrid** alkali activated binders with a combination of agro-industrial waste to form binary and ternary mortar binders cured under water up to 28-days. The utilized SCMs include fly ash (FA), ground date palm ash (GDPA) i.e. alkali activated or raw DPA i.e. non-activated. These **hybrid** and non **hybrid** binders were compared through physical properties such as strength and workability along with microstructural properties by hydration products and pore volume. X-ray diffraction (XRD) technique was employed to get the mineral composition; phase decomposition of unreacted water, C-S-H/C-A-SH gel and Ca(OH)₂ had been studied by Thermogravimetric analysis (TGA) while nitrogen adsorption test determined surface area of particles as well as pore volume of the paste. The results revealed potential use of DPA as a strong and sustainable material in ternary blend with FA and OPC in conventional non-**hybrid** binder that can efficiently maximize clinker replacement without energy utilization in alkaline activation. (C) 2017 Elsevier Ltd. All rights reserved.

Range limits in sympatric cryptic species: a case study in *Tetramorium* pavement ants (Hymenoptera: Formicidae) across a biogeographical boundary

Cordonnier, M; Bellec, A; Dumet, A; Escarguel, G; Kaufmann, B, 2019

In the context of climate changes, factors that determine the distribution patterns of European species of the ubiquitous ant genus *Tetramorium* were investigated. The study took place along a steep North-South climatic gradient across the boundary between the European Continental and Mediterranean biogeographical regions spanning 460 km along the Rhone valley, France. Ants from 1690 *Tetramorium* colonies were collected in 19 sampling zones. Species were identified using an integrative approach based on a two-step process combining nuclear DNA (14 microsatellite markers), morphological examination and mitochondrial DNA cytochrome oxidase I sequencing. The impact of climate on species distribution patterns was tested using bioclimatic variables. Species discrimination was successful, despite a complex situation with cryptic species, inter-specific **hybridisation** and uneven sampling across species. Our results showed a strong effect of latitude, temperature and rainfall on the distribution of three of four species. *Tetramorium semilaeve* was found only south of the boundary, in warmer and dryer sites; *Tetramorium caespitum* extended north and 70 km south of the boundary and favoured colder sites with strong seasonal variation. *Tetramorium immigrans* was absent from the northernmost sampling zones and favoured warmer and wetter sites. *Tetramorium moravicum* was mostly found close to the boundary, but without significant climatic preferences. The fundamental role of climate as a factor limiting the ranges of these species at a major biogeographical boundary is confirmed. Monitoring range limits of these strongly climate-dependant species may offer exciting insights on the impact of climate changes on species distributions.

Assisted Migration Field Tests in Canada and Mexico: Lessons, Limitations, and Challenges

Saenz-Romero, C; O'Neill, G; Aitken, SN; Lindig-Cisneros, R, 2021

Assisted migration of forest tree populations through reforestation and restoration is a climate change adaptation strategy under consideration in many jurisdictions. Matching climates in which seed sources evolved with near future climates projected for plantation sites should help reduce maladaptation and increase plantation health and productivity. For threatened tree species, assisted migration outside of the species range could help avert extinction. Here, we examine lessons, limitations, and challenges of assisted migration through the lens of three assisted migration field trials of conifers in Canada and Mexico: *Pinus albicaulis* Engelm., an endangered subalpine tree species in the mountains of western North America; the *Picea glauca* (Moench) Voss x *P. engelmannii* Parry ex Engelm **hybrid** complex, of great economic and ecological importance in western Canada, and *Abies religiosa* (Kunth) Schldtl. & Cham., a tree species that provides overwintering sites for the monarch butterfly. We conclude that: (a) negative impacts of climate change on productivity of *Picea glauca* x *P. engelmannii* may be mitigated by planting seed sources from locations that are 3 degrees C mean coldest month temperature warmer than the plantation; (b) it is possible to establish *Pinus albicaulis* outside of its current natural distribution at sites that have climates that are within the species' modelled historic climatic niche, although developing disease-resistant trees through selective breeding is a higher priority in the short term; (c) *Abies religiosa* performs well when moved 400 m upward in elevation and local shrubs (such as *Baccharis conferta* Kunth) are used as nurse plants; (d) new assisted migration field trials that contain populations from a wide range of climates tested in multiple disparate climates are needed, despite the costs; and (e) where naturalization of a migrated tree species in recipient ecosystem is viewed as undesirable, the invasive potential of the tree species should be assessed prior to large scale establishment, and stands should be monitored regularly following establishment.

Forecasting CO₂ emissions in Hebei, China, through moth-flame optimization based on the random forest and extreme learning machine

Sun, W; Wang, YW; Zhang, CC, 2018

The surge of carbon dioxide emission plays a dominant role in global warming and climate change, posing an enormous threat to the development of human being and a profound impact on the global ecosystem. Thus, it is essential to analyze the carbon dioxide emission change trend through an accurate prediction to inform

reasonable energy-saving emission reduction measures and effectively control the carbon dioxide emission from the source. This paper proposed a **hybrid** model by combining the random forest and extreme learning machine together for the carbon dioxide emission forecasting in this paper; the random forest is applied for influential factors analysis and the extreme learning machine for the prediction. To improve the performance of the prediction model, moth-flame optimization is adopted to optimize initial weight and bias in extreme learning machine. A case study whose data is derived from Hebei Province, China, during the period 1995-2015 is conducted to verify the effectiveness of the proposed model. Results show that the novel model outperforms the compared parallel models in carbon dioxide emission prediction and has the potential to improve the accuracy of CO₂ emission forecasting.

Different Responses in Geographic Range Shifts and Increase of Niche Overlap in Future Climate Scenario of the Subspecies of *Melipona quadrifasciata* Lepeletier

Teixeira, KO; Silveira, TCL; Harter-Marques, B, 2018

Climate change is suggested to be one of the possible drivers of decline in pollinators. In this paper, we applied an ecological niche model to modeling distributional responses in face of climate changes for the subspecies of *Melipona quadrifasciata* Lepeletier. This species is divided into two subspecies based on difference in the yellow tergal stripes, which are continuous in *M. q. quadrifasciata* and interrupted in *M. q. anthidioides*. The geographic distribution of each subspecies is also distinct. *M. q. quadrifasciata* is found in colder regions in the Southern states of Brazil, whereas *M. q. anthidioides* is found in habitats with higher temperatures, suggesting that ecological features, such as adaption to distinct climatic conditions may take place. Thus, the possibility of having different responses in geographic range shifts to future climate scenario would be expected. This study aimed to investigate the effects of climate changes on the distribution of the two *M. quadrifasciata* subspecies in Brazil, using an ecological niche model by the MaxEnt algorithm. Our results indicate that the subspecies showed clear differences in geographic shift patterns and increased climate niche overlap in the future scenarios. *M. q. anthidioides* will have the potential for an increase of suitable climatic conditions in the Atlantic Forest, and towards the Pampa biome, while *M. q. quadrifasciata* will suffer a reduction of adequate habitats in almost all of its current geographic distribution. Given the potential adverse effects of climate changes for this subspecies, conservation actions are urgently needed to avoid that it goes extinct.

Trade-offs across densities and mixture proportions in lodgepole pine-hybrid spruce plantations

Barbeito, I; Eskelson, BNI; Carsky, G, 2021

Monocultures tend to yield higher total stand volumes and are simple to manage. Yet, mixed species stands may result in similar stand volumes while providing benefits such as mitigating damage from insects and disease. To understand the effects of stand density and species mixture and their interactions on stand yield, tree size and morphology, and damage in monocultures and mixtures, we analyzed a 25-year-old experiment in interior British Columbia, Canada. The lodgepole pine (PI)-interior **hybrid** spruce (Sx) experiment included three densities?1000, 1500, and 2000 stems per hectare (SPH)?and five species mixtures?1:0, 3:1, 1:1, 1:3, and 0:1 PI:Sx. Results 25 years after stand establishment showed that stand volume was significantly larger with an increasing proportion of PI across all stand densities. PI had 10% larger diameters in the 1000 SPH than in the 2000 SPH and when mixed with Sx (1:1). PI had larger crowns in mixtures regardless of density. Mixture proportion did not affect gall rust incidence or stem form in PI, but reduced attack in Sx by spruce weevil. Our findings suggest that mixing PI-Sx and high planting density decrease weevil attacks in Sx, which reduce loss in timber quality. Yet, PI quality may decrease when mixed with Sx, due to larger PI crowns. These results may be used to improve the implementation of management strategies that decrease trade-offs between yields, desired market tree sizes, and timber loss from pest and pathogens, while making the stands more resilient to further climate change impact.

Genetic architecture and phenotypic plasticity of thermally-regulated traits in an eruptive species, *Dendroctonus ponderosae*

Bentz, BJ; Bracewell, RR; Mock, KE; Pfrender, ME, 2011

Phenotypic plasticity in thermally-regulated traits enables close tracking of changing environmental conditions, and can thereby enhance the potential for rapid population increase, a hallmark of outbreak insect species. In a changing climate, exposure to conditions that exceed the capacity of existing phenotypic plasticity may occur. Combining information on genetic architecture and trait plasticity among populations that are distributed along a latitudinal cline can provide insight into how thermally-regulated traits evolve in divergent environments and the potential for adaptation. *Dendroctonus ponderosae* feed on *Pinus* species in diverse climatic regimes throughout western North America, and show eruptive population dynamics. We describe geographical patterns of plasticity in *D. ponderosae* development time and adult size by examining reaction norms of populations from multiple latitudes. The relative influence of additive and non-additive genetic effects on population differences in the two phenotypic traits at a single temperature is quantified using line-cross experiments and joint-scaling tests. We found significant genetic and phenotypic variation among *D. ponderosae* populations. Simple additive genetic variance was not the primary source of the observed variation, and dominance and epistasis contributed greatly to the genetic divergence of the two thermally-regulated traits. **Hybrid** breakdown was also observed in F-2 **hybrid** crosses between northern and southern populations, further indication of substantial genetic differences among clinal populations and potential reproductive isolation within *D. ponderosae*. Although it is unclear what maintains variation in the life-history traits, observed plasticity in thermally-regulated traits that are directly linked to rapid numerical change may contribute to the outbreak nature of *D. ponderosae*, particularly in a changing climate.

Damage by the pine weevil *Hyllobius abietis* to seedlings of two native and five introduced tree species in Sweden

Wallertz, K; Nordenhem, H; Nordlander, G, 2014

There is increasing interest in using introduced species in Swedish forestry in response to climate change, but it is important to assess their resistance to native pests. Thus, we compared the extent of pine weevil feeding on two dominant native conifers, Scots pine (*Pinus sylvestris* L.) and Norway spruce (*Picea abies* (L.) Karst.), the non-host deciduous broadleaf **hybrid** aspen (*Populus x wettsteinii* Hamet-Ahti) and four introduced conifers: Douglas fir (*Pseudotsuga menziesii* (Mirb.) Franco), **hybrid** larch (*Larix x marschlinii* Coaz), Sitka spruce (*Picea sitchensis* (Bong.) Carriere) and lodgepole pine (*Pinus contorta* Douglas ex Loudon). The extent of feeding damage on seedlings and its effect on their vitality were examined in a field study in south-central Sweden and a laboratory experiment, which gave largely consistent results. Generally, the species most heavily attacked by the pine weevil, in both experiments, were Douglas fir and Sitka spruce. In the field experiment pine weevils killed or severely damaged significantly higher proportions of Douglas fir and Sitka spruce seedlings (60%) than any other species except Norway spruce (49%). Among conifer seedlings the proportions of killed or severely damaged seedlings were lowest for Scots pine and **hybrid** larch (27%) and Lodgepole pine (36%). The results indicate that most conifer species planted on young clear-cuttings in Sweden need some kind of pine weevil protection, and the possibility that introducing new tree species might increase damage caused by pests must be considered. For instance, widespread use of **hybrid** aspen could reduce damage by pine weevils, but increase damage by other, untested pests or pathogens.

Climate driven range shift prompts species replacement

Warren, RJ; Chick, LD; DeMarco, B; McMillan, A; De Stefano, V; Gibson, R; Pinzone, P, 2016

Climate change prompts warm-tolerant species upward and poleward to either displace or replace cold-tolerant species. Warm-tolerant species may replace cold-tolerant individuals with upward migration, or cold-tolerant genes if the species **hybridize**. We examined genetic and morphological differences between low elevation,

warm-tolerant (*Aphaenogaster rudis*) and high elevation cold-tolerant (*A. picea*) ant species that form an upward-shifting ecotone in the southern Appalachian Mountains (USA). The *A. picea/A. rudis* ecotone shifted upward ca. 200 m between the decades 1970 and 2010, and characteristic morphological traits appeared muddled where the species met, suggesting **hybridization**. However, ~~we found no evidence of genetic hybridization~~, and the trait most associated with species identity, pigmentation, remained so across the environmental gradients. Conversely, femur length did not differentiate well between species identities, and it shifted across the environmental gradients. These results suggest that the cold tolerant *A. picea*, associated with high-elevation and high-latitude, was replaced by the warm-tolerant, low elevation *A. rudis* species. As such, these results suggest that less competitive cold-tolerant species may be replaced by more competitive cold-intolerant species with climate warming.

~~Can local adaptation explain varying patterns of herbivory tolerance in a recently introduced woody plant in North America?~~

Long, RW; Bush, SE; Grady, KC; Smith, DS; Potts, DL; D'Antonio, CM; Dudley, TL; Fehlberg, SD; Gaskin, JF; Glenn, EP; Hultine, KR,

Patterns of woody-plant mortality have been linked to global-scale environmental changes, such as extreme drought, heat stress, more frequent and intense fires, and episodic outbreaks of insects and pathogens. Although many studies have focussed on survival and mortality in response to specific physiological stresses, little attention has been paid to the role of genetic heritability of traits and local adaptation in influencing patterns of plant mortality, especially in non-native species. *Tamarix* spp. is a dominant, non-native riparian tree in western North America that is experiencing dieback in some areas of its range due to episodic herbivory by the recently introduced northern tamarisk leaf beetle (*Diorhabda carinulata*). We propose that genotype x environment interactions largely underpin current and future patterns of *Tamarix* mortality. We anticipate that (i) despite its recent introduction, and the potential for significant gene flow, *Tamarix* in western North America is generally adapted to local environmental conditions across its current range in part due to **hybridization** of two species; (ii) local adaptation to specific climate, soil and resource availability will yield predictable responses to episodic herbivory; and (iii) the ability to cope with a combination of episodic herbivory and increased aridity associated with climate change will be largely based on functional tradeoffs in resource allocation. This review focusses on the potential heritability of plant carbon allocation patterns in *Tamarix*, focussing on the relative contribution of acquired carbon to non-structural carbohydrate (NSC) pools versus other sinks as the basis for surviving episodic disturbance. Where high aridity and/or poor edaphic position lead to chronic stress, NSC pools may fall below a minimum threshold because of an imbalance between the supply of carbon and its demand by various sinks. Identifying patterns of local adaptation of traits related to resource allocation will improve forecasting of *Tamarix* population susceptibility to episodic herbivory.

~~The Role of Population and Half-Sib Family on Driving Suitable Functional Traits for *Quercus suber* L. Forest Restoration~~

Morcillo, L; Moutahir, H; Cortina, J; Vilagrosa, A, 2020

Research Highlights:Seedlings of different *Quercus suber* L. populations and half-sib families differ in their response to multiple stressors, which may have consequences on the future distribution of this Mediterranean species.**Background and Objectives:**Global change will likely increase the frequency and severity of drought in drylands. Plant species' distributions will largely depend on their ability to respond to the combined effect of drought and other environmental stressors. Genetic diversity in morpho-functional traits are key components of this response. Yet, information on the response to multiple stresses is scarce for many iconic species. The present study assessed the variability in the response of populations and half-sib families of a Mediterranean acidophilous tree, cork oak, to drought and changes in soil conditions.**Materials and Methods:**We sampled acorns of half-sib families from two cork oak populations genetically introgressed with the alkaline-tolerant species *Quercus ilex* L., and from a non-introgressed cork oak population located in its core habitat. We germinated the acorns and subjected seedlings to contrasted levels of water availability and additions of calcium and magnesium carbonate, and assessed their morpho-physiological response.**Results:**Response to drought and soil chemistry composition differed between populations and families. For some traits, introgressed populations responded similarly to drought than the non-introgressed population. Conversely, the response to soil chemistry was not clearly related to **introgression**. When considering half-sib families within populations, the population effect diminished, which revealed the importance of intra-population variation. However, relevant traits for water scarcity adaptations, such as specific leaf area and root:shoot ratio, remained significantly different at the population level, which highlights the relevance of these traits for management.**Conclusions:**Our study shows that the adaptive management and restoration of cork oak forests should consider not only geographic provenances, but also half-sib lines within populations.

~~Evaluating the effects of climate and land use change on the future flood susceptibility in the central region of Vietnam by integrating land change modeler, machine learning methods~~

Nguyen, HD; Dang, DK; Nguyen, QH; Bui, QT; Petrisor, AI,

The crucial importance of land cover and use changes and climate changes for worldwide sustainability results from their negative effects on flood risk. In a watershed, a particularly important research question concerning the relationship between land use and climate change and the flood risk is the subject of controversy in the literature. This study aims to assess the effects of land use and climate change on the flood susceptibility in the watershed Nhat Le-Kien Giang, Vietnam using machine learning and Land Change Modeler. The results show that Social Ski Driver Optimization (SSD), Fruit Fly Optimization (FFO), Sailfish Optimization (SFO), and Particle Swarm Optimization (PSO) successfully improve the Support Vector Machine (SVM) model's performance, with a value of the Area Under the Receiver Operating Characteristic curve (AUC) > 0.96. Among them, the SVM-FFO model was better with the value of AUC of 0.984, followed by SVM-SFO (AUC = 0.983), SVM-SSD (AUC = 0.98), SVM-PSO (AUC = 0.97), respectively. In addition, the areas with high and very high flood susceptibility in the study area increased by about 30 km² from 2020 to 2050 with the SVM-FFO model. Our results underline the consequences of unplanned development. Thus, by applying the theoretical framework of this study, decision makers can take sound more planning measures, such as avoiding construction in areas often affected by floods, etc. Although in this study flood susceptibility is studied in a Central Coast province, the results can be applied to other rapidly developing and flood-prone provinces of Vietnam.

~~Phylotranscriptomic Insights into the Diversification of Endothermic *Thunnus* Tunas~~

Ciezarek, AG; Osborne, OG; Shipley, ON; Brooks, EJ; Tracey, SR; McAllister, JD; Gardner, LD; Sternberg, MJE; Block, B; Savolainen, V, 2019

Birds, mammals, and certain fishes, including tunas, opahs and lamnid sharks, are endothermic, conserving internally generated, metabolic heat to maintain body or tissue temperatures above that of the environment. Bluefin tunas are commercially important fishes worldwide, and some populations are threatened. They are renowned for their endothermy, maintaining elevated temperatures of the oxidative locomotor muscle, viscera, brain and eyes, and occupying cold, productive high-latitude waters. Less cold-tolerant tunas, such as yellowfin tuna, by contrast, remain in warm-temperate to tropical waters year-round, reproducing more rapidly than most temperate bluefin tuna populations, providing resiliency in the face of large-scale industrial fisheries. Despite the importance of these traits to not only fisheries but also habitat utilization and responses to climate change, little is known of the genetic processes underlying the diversification of tunas. In collecting and analyzing sequence data across 29,556 genes, we found that parallel selection on standing genetic variation is associated with the evolution of endothermy in bluefin tunas. This includes two shared substitutions in genes encoding glycerol-3 phosphate dehydrogenase, an enzyme that contributes to thermogenesis in bumblebees and mammals, as well as four genes involved in the Krebs cycle, oxidative phosphorylation, β -oxidation, and superoxide removal. Using phylogenetic techniques, we further illustrate that the eight *Thunnus* species are genetically distinct, but found evidence of mitochondrial genome **introgression** across two species. Phylogeny-based metrics highlight conservation needs for some of these species.

Modelling bark beetle disturbances in a large scale forest scenario model to assess climate change impacts and evaluate adaptive management strategies

Seidl, R; Schelhaas, M.J; Lindner, M; Lexer, M.J, 2009

To study potential consequences of climate-induced changes in the biotic disturbance regime at regional to national scale we integrated a model of *Ips typographus* (L. Scol. Col.) damages into the large-scale forest scenario model EFISCEN. A two-stage multivariate statistical meta-model was used to upscale stand level damages by bark beetles as simulated in the **hybrid** forest patch model PICUS v1.41. Comparing EFISCEN simulations including the new bark beetle disturbance module against a 15-year damage time series for Austria showed good agreement at province level (RA(2) between 0.496 and 0.802). A scenario analysis of climate change impacts on bark beetle-induced damages in Austria's Norway spruce [*Picea abies* (L.) Karst.] forests resulted in a strong increase in damages (from 1.33 MmA(3)A a(-1), period 1990-2004, to 4.46 MmA(3)A a(-1), period 2095-2099). Studying two adaptive management strategies (species change) revealed a considerable time-lag between the start of adaptation measures and a decrease in simulated damages by bark beetles.

Innate and Introduced Resistance Traits in Genetically Modified Aspen Trees and Their Effect on Leaf Beetle Feeding

Hjalten, J; Axelsson, EP; Julkunen-Tiitto, R; Wennstrom, A; Pilate, G,

Genetic modifications of trees may provide many benefits, e. g. increase production, and mitigate climate change and herbivore impacts on forests. However, genetic modifications sometimes result in unintended effects on innate traits involved in plant-herbivore interactions. The importance of intentional changes in plant defence relative to unintentional changes and the natural variation among clones used in forestry has not been evaluated. By a combination of biochemical measurements and bioassays we investigated if insect feeding on GM aspens is more affected by intentional (induction Bt toxins) than of unintentional, non-target changes or clonal differences in innate plant defence. We used two **hybrid** wildtype clones (*Populus tremula* x *P. tremuloides* and *Populus tremula* x *P. alba*) of aspen that have been genetically modified for 1) insect resistance (two Bt lines) or 2) reduced lignin properties (two lines COMT and CAD), respectively. Our measurements of biochemical properties suggest that unintended changes by GM modifications (occurring due to events in the transformation process) in innate plant defence (phenolic compounds) were generally smaller but fundamentally different than differences seen among different wildtype clones (e. g. quantitative and qualitative, respectively). However, neither clonal differences between the two wildtype clones nor unintended changes in phytochemistry influenced consumption by the leaf beetle (*Phratora vitellinae*). By contrast, Bt induction had a strong direct intended effect as well as a post experiment effect on leaf beetle consumption. The latter suggested lasting reduction of beetle fitness following Bt exposure that is likely due to intestinal damage suffered by the initial Bt exposure. We conclude that Bt induction clearly have intended effects on a target species. Furthermore, the effect of unintended changes in innate plant defence traits, when they occur, are context dependent and have in comparison to Bt induction probably less pronounced effect on targeted herbivores.

Climate change has different predicted effects on the range shifts of two hybridizing ambush bug (Phymata, FamilyReduviidae, Order Hemiptera) species

Zhang, VM; Punzalan, D; Rowe, L, 2020

Aim A universal attribute of species is that their distributions are limited by numerous factors that may be difficult to quantify. Furthermore, climate change-induced range shifts have been reported in many taxa, and understanding the implications of these shifts remains a priority and a challenge. Here, we use Maxent to predict current suitable habitat and to project future distributions of two closely related, parapatrically distributed *Phymatas* species in light of anthropogenic climate change. Location North America. Taxon *Phymata americana* Melin 1930 and *Phymata pennsylvanica* Handlirsch 1897, Family: Reduviidae, Order: Hemiptera. Methods We used the maximum entropy modeling software Maxent to identify environmental variables maintaining the distribution of two *Phymatas* species, *Phymata americana* and *Phymata pennsylvanica*. Species occurrence data were collected from museum databases, and environmental data were collected from WorldClim. Once we gathered distribution maps for both species, we created binary suitability maps of current distributions. To predict future distributions in 2050 and 2070, the same environmental variables were used, this time under four different representative concentration pathways: RCP2.6, RCP4.5, RCP6.0, and RCP8.5; as well, binary suitability maps of future distributions were also created. To visualize potential future **hybridization**, the degree of overlap between the two *Phymatas* species was calculated. Results The strongest predictor to *P. americana* ranges was the mean temperature of the warmest quarter, while precipitation of the driest month and mean temperature of the warmest quarter were strong predictors of *P. pennsylvanica* ranges. Future ranges for *P. americana* are predicted to increase northwestward at higher CO₂ concentrations. Suitable ranges for *P. pennsylvanica* are predicted to decrease with slight fluctuations around range edges. There is an increase in overlapping ranges of the two species in all future predictions. Main conclusions These evidences for different environmental requirements for *P. americana* and *P. pennsylvanica* account for their distinct ranges. Because these species are ecologically similar and can **hybridize**, climate change has potentially important evolutionary ramifications. Overall, our results are consistent with effects of climate change that are highly variable across species, geographic regions, and over time.

Climate Warming Since the Holocene Accelerates West-East Communication for the Eurasian Temperate Water Strider Species *Aquarius paludum*

Ye, Z; Yuan, JJ; Damgaard, J; Berchi, GM; Cianferoni, F; Pintar, MR; Olosutean, H; Zhu, XX; Jiang, K; Yang, X; Fu, SY; Bu, W.J, 2022

Holocene climate warming has dramatically altered biological diversity and distributions. Recent human-induced emissions of greenhouse gases will exacerbate global warming and thus induce threats to cold-adapted taxa. However, the impacts of this major climate change on transcontinental temperate species are still poorly understood. Here, we generated extensive genomic datasets for a water strider, *Aquarius paludum*, which was sampled across its entire distribution in Eurasia and used these datasets in combination with ecological niche modeling (ENM) to elucidate the influence of the Holocene and future climate warming on its population structure and demographic history. We found that *A. paludum* consisted of two phylogeographic lineages that diverged in the middle Pleistocene, which resulted in a "west-east component" genetic pattern that was probably triggered by Central Asia-Mongolia aridification and Pleistocene glaciations. The diverged western and eastern lineages had a second contact in the Holocene, which shaped a temporary **hybrid** zone located at the boundary of the arid-semiarid regions of China. Future predictions detected a potentially novel northern corridor to connect the western and eastern populations, indicating west-east gene flow would possibly continue to intensify under future warming climate conditions. Further integrating phylogeographic and ENM analyses of multiple Eurasian temperate taxa based on published studies reinforced our findings on the "west-east component" genetic pattern and the predicted future northern corridor for *A. paludum*. Our study provided a detailed paradigm from a phylogeographic perspective of how transcontinental temperate species differ from cold-adapted taxa in their response to climate warming.

Selective pollination by fungus gnats potentially functions as an alternative reproductive isolation among five *Arisaema* species

Matsumoto, TK; Hirobe, M; Sueyoshi, M; Miyazaki, Y, 2021

Background and Aims Interspecific difference in pollinators (pollinator isolation) is important for reproductive isolation in flowering plants. Species-specific pollination by fungus gnats has been discovered in several plant taxa, suggesting that they can contribute to reproductive isolation. Nevertheless, their contribution has not been studied in detail, partly because they are too small for field observations during flower visitation. To quantify their flower visitation, we used the genus *Arisaema* (Araceae) because the pitcher-like spathe of *Arisaema* can trap all floral visitors. Methods We evaluated floral visitor assemblage in an altitudinal gradient including five *Arisaema* species. We also examined interspecific differences in altitudinal distribution (geographic isolation) and flowering phenology (phenological isolation). To exclude the effect of interspecific differences in altitudinal distribution on floral visitor assemblage, we established ten experimental plots including the five *Arisaema* species in high- and low-altitude areas and collected floral visitors. We also collected floral visitors in three additional sites. Finally, we estimated the strength and contribution of these three reproductive barriers using a unified formula for reproductive isolation. Key Results Each *Arisaema* species selectively

attracted different fungus gnats in the altitudinal gradient, experimental plots and additional sites. Altitudinal distribution and flowering phenology differed among the five *Arisaema* species, whereas the strength of geographic and phenological isolations were distinctly weaker than those in pollinator isolation. Nevertheless, the absolute contribution of pollinator isolation to total reproductive isolation was weaker than geographic and phenological isolations, because pollinator isolation functions after the two early-acting barriers in plant life history. Conclusions Our results suggest that selective pollination by fungus gnats potentially contributes to reproductive isolation. Since geographic and phenological isolations can be disrupted by habitat disturbance and interannual climate change, the strong and stable pollinator isolation might compensate for the weakened early-acting barriers as an alternative reproductive isolation among the five *Arisaema* species.

Interaction of submergence tolerance and drought yield QTLs (Sub1 and qDTYs) enhances morpho-physiological traits and survival of rice (*Oryza sativa* L.) under submergence

Ikmal, AM; Noraziyah, AS; Wickneswari, R; Amira, I; Ellina, ZPD,

Ascertaining gene flow patterns in livestock populations of developing countries: a case study in Burkina Faso goat

Traore, A; Alvarez, I; Fernandez, I; Perez-Pardal, L; Kabore, A; Ouedraogo-Sanou, GMS; Zare, Y; Tamboura, HH; Goyache, F, 2012

Background: **Introgression** of Sahel livestock genes southwards in West Africa may be favoured by human activity and the increase of the duration of the dry seasons since the 1970's. The aim of this study is to assess the gene flow patterns in Burkina Faso goat and to ascertain the most likely factors influencing geographic patterns of genetic variation in the Burkina Faso goat population. Results: A total of 520 goat were sampled in 23 different locations of Burkina Faso and genotyped for a set of 19 microsatellites. Data deposited in the Dryad repository: <http://dx.doi.org/10.5061/dryad.41h46j37>. Although overall differentiation is poor ($F_{ST} = 0.067 \pm 0.003$), the goat population of Burkina Faso is far from being homogeneous. Barrier analysis pointed out the existence of: a) genetic discontinuities in the Central and Southeast Burkina Faso; and b) genetic differences within the goat sampled in the Sahel or the Sudan areas of Burkina Faso. Principal component analysis and admixture proportion scores were computed for each population sampled and used to construct interpolation maps. Furthermore, Population Graph analysis revealed that the Sahel and the Sudan environmental areas of Burkina Faso were connected through a significant number of extended edges, which would be consistent with the hypothesis of long-distance dispersal. Genetic variation of Burkina Faso goat followed a geographic-related pattern. This pattern of variation is likely to be related to the presence of vectors of African animal trypanosomosis. Partial Mantel test identified the present Northern limit of trypanosome vectors as the most significant landscape boundary influencing the genetic variability of Burkina Faso goat ($p = 0.008$). The contribution of Sahel goat genes to the goat populations in the Northern and Eastern parts of the Sudan-Sahel area of Burkina Faso was substantial. The presence of perennial streams explains the existence of trypanosome vectors. The South half of the Nakambe river (Southern Ouagadougou) and the Mouhoun river loop determined, respectively, the Eastern and Northern limits for the expansion of Sahelian goat genes. Furthermore, results from partial Mantel test suggest that the **introgression** of Sahelian goat genes into Djallonke goat using human-influenced genetic corridors has a limited influence when compared to the biological boundary defined by the northern limits for the distribution of the tsetse fly. However, the genetic differences found between the goat sampled in Bobo Dioulasso and the other populations located in the Sudan area of Burkina Faso may be explained by the broad goat trade favoured by the main road of the country. Conclusions: The current analysis clearly suggests that genetic variation in Burkina Faso goat: a) follows a North to South clinal; and b) is affected by the distribution of the tsetse fly that imposes a limit to the Sahelian goat expansion due to their trypanosusceptibility. Here we show how extensive surveys on livestock populations can be useful to indirectly assess the consequences of climate change and human action in developing countries.

Climate Change: Implications for Stakeholders in Genetic Resources and Seed Sector

Singh, RP; Prasad, PVV; Reddy, KR, 2015

The characteristic of climatic change is increase in the frequency of extreme events that are likely to decrease crop yield. The geographic areas that are currently most food-insecure are likely to be most affected by changing climates. Climate change is likely to affect all dimensions of crop production. Agricultural crop production depends upon the timely availability of good-quality seeds in adequate quantity at affordable prices to the farming communities. Genetic diversity and breeding for improved stress-tolerant genotypes are key elements in tackling climate change. Plant genetic resources (PGRs) are important sources for developing new and improved varieties. The loss of these genetic resources due to climate change will deprive source of diversity and tolerance. Currently, more emphasis has been placed for ex situ conservation, while equally if not more urgency is required to conserve the PGRs in situ. At present, a number of international agreements are enforced for germplasm exchange and utilization. Some of the important methods to develop and disseminate new cultivars include breeding new crop varieties for wider adaptation under adverse climatic conditions using both classical and modern approaches and seed production through participatory approaches. Participatory breeding programs have successfully led to the development and dissemination of varieties in cereals. Seed industry plays an important role in increasing productivity of crops. The adverse effect of climate change on the seed industry can be minimized by developing efficient seed management systems: breeding, seed production, seed certification, and seed trade. Some efficient systems include adjustment of crop calendars for quality seed production, management of pollinators, strengthening **hybrid** seed production, postharvest management of seed, seed treatment technologies, seed processing, and seed storage. For faster and timely development, partnerships (public and private) at various levels (regional and international) are crucial. There is an urgent need to strengthen both formal and informal seed systems including characterization of environment to find suitable geographic regions for quality seed production. For seed certification, harmonization of various international seed certification schemes/programs and seed testing procedures are essential. This will also help in efficient and safe movement of seed. To influence seed trade, the effective management of intellectual property rights, sanitary and phytosanitary certificates in addition to management of trade barriers, are all of prime importance for growth of the seed industry. In both developed and developing nations, public investments in plant breeding and seed industry are on the decline. This trend needs to be reversed by emphasizing the need to increase research funding to all stakeholders of genetic resources and seed industry to develop strategies to mitigate the negative impacts of climate change on agricultural systems.

Fumonisin in Serbian Corn: Long-time Assessment under Actual Climate Change Conditions

Jaksic, S; Zivkov-Balos, M; Janic, I; Abramovic, B, 2019

Maize samples collected in Serbia during a period of seven years were investigated on the presence of fumonisins. Concentration of fumonisins was determined by validated direct competitive Enzyme Linked Immunosorbent Assay method. This method was in accordance with European Union requirements, therefore accredited and performed in the Serbian accredited official laboratory. Summary analysis of all obtained results revealed fumonisins contamination in 82% of the total of 291 maize samples with average contamination being 1.515 mg/kg. An increase in the percentage of contaminated samples (from 51 to 100%), as well as an increase in mean fumonisin concentration in positive samples (from 0.227 to 3.281 mg/kg) and median values in positive samples (from 0.070 to 2.140 mg/kg) was noticed during the observation period. Although in Serbia there is no regular control of fumonisins in corn for animal feeding, long-term results indicate their wide distribution in this grain. Since the data on climate elements show change in temperature and precipitation in relation to multiannual average on the territory of Serbia, further research on the effects of climate change on the development of mold, the appearance of insects and the production of toxins are necessary in order to check the resistance of currently grown **hybrids** in the territory of Serbia on fungal growth and fumonisins production.

Pleistocene climate change promoted rapid diversification of aquatic invertebrates in Southeast Australia

Hawltischek, O; Hendrich, L; Espeland, M; Toussaint, EFA; Genner, MJ; Balke, M, 2012

Background: The Pleistocene Ice Ages were the most recent geohistorical event of major global impact, but their consequences for most parts of the Southern hemisphere remain poorly known. We investigate a radiation of ten species of *Sternopriscus*, the most species-rich genus of epigean Australian diving beetles. These species are distinct based on genital morphology but cannot be distinguished readily by mtDNA and nDNA because of genotype sharing caused by incomplete lineage sorting. Their genetic similarity suggests a Pleistocene origin. Results: We use a dataset of 3858 bp of mitochondrial and nuclear DNA to reconstruct a phylogeny of *Sternopriscus* using gene and species trees. Diversification analyses support the finding of a recent rapid speciation event with estimated speciation rates of up to 2.40 species per MY, which is considerably higher than the proposed average rate of 0.16 species per MY for insects. Additionally, we use ecological niche modeling and analyze data on habitat preferences to test for niche divergence between species of the recent *Sternopriscus* radiation. These analyses show that the species can be characterized by a set of ecological variables referring to habitat, climate and altitude. Conclusions: Our results suggest that the repeated isolation of populations in glacial refugia might have led to divergent ecological adaptations and the fixation of morphological traits supporting reproductive isolation and therefore may have promoted speciation. The recent *Sternopriscus* radiation fulfills many characteristics of a species flock and would be the first described example of an aquatic insect species flock. We argue that the species of this group may represent a stage in speciation past the species flock condition because of their mostly broad and often non-overlapping ranges and preferences for different habitat types.

~~One, two or more species? Mitonuclear discordance and species delimitation~~

Despres, L, 2019

Delimiting species boundaries is central to understand ecological and evolutionary processes, and to monitor biodiversity patterns over time and space. Yet, most of our current knowledge on animal diversity and phylogeny relies on morphological and mitochondrial (mt) DNA variation, a popular molecular marker also used as a barcode to assign samples to species. For morphologically undistinguishable sympatric species (cryptic species), the congruence of several independent markers is necessary to define separate species. Nuclear markers are becoming more accessible, and have confirmed that cryptic species are widespread in all animal phyla (Fiser, Robinson, & Malard, 2018). However, striking differences between the mitochondrial and nuclear variation patterns are also commonly found within single species. Mitonuclear discordance can result from incomplete lineage sorting, sex-biased dispersal, asymmetrical **introgression**, natural selection or Wolbachia-mediated genetic sweeps. But more generally, the distinct mode of transmission of these two types of markers (maternal vs. biparental) is sufficient to explain their distinct sensitivity to purely demographic events such as spatial range and population size fluctuations over time. In a From the Cover manuscript in this issue of *Molecular Ecology*, Hijonosa et al. (2019) show that highly divergent mtDNA lineages coexist in a widespread European butterfly (Figure 1). None of the hundreds of nuclear markers analyzed was associated with mt lineages, nor was Wolbachia variation. These findings rule out the presence of cryptic species but shed light on complex demographic history of lineage divergence/fusion during the Pleistocene climatic fluctuations, and pave the way to a better integration of both mt and nuclear information in demographic models.

~~The Role of Agrotechnical Factors in Shaping the Health of Maize Plants (Zea mays L.)~~

Szulc, P; Ambrozy-Deregowska, K; Mejza, I; Kobus-Cisowska, J; Ligaj, M; Krauklis, D, 2021

The article presents the results of 3-year field studies, whose purpose was to assess the impact of maize sowing method, type of cultivar and NP fertiliser sowing method on the health of maize plants. Changing weather conditions during the study years significantly differentiated the percentage of maize plants damaged by pests and affected by diseases. The positive effect of the row method of NP fertiliser application in maize cultivation not only reduced plant infestation by *Fusarium* diseases, but also reduced Frit fly (*Oscinella frit* L.) pressure. The "stay-green" **hybrid** was characterized by a significantly lower susceptibility to feeding of the European corn borer (*Ostrinia nubilalis* Hbn.) compared to the traditional cultivar. Sowing maize of the traditional cultivar using the direct sowing system increased damage to plants caused by Frit fly larvae (*Oscinella frit* L.) compared to sowing into soil cultivated in a traditional way. For the "stay-green" type, the method of soil preparation for sowing did not significantly affect the pressure of this pest. A simplified method of soil preparation for sowing maize should give preference to cultivating "stay-green" varieties.

~~The priming of periodical cicada life cycles~~

Grant, PR, 2005

Periodical cicadas in the genus *Magicicada* have unusually long life cycles for insects, with periodicities of either 13 or 17 years. Biologists have explained the evolution of these prime number period lengths in terms of resource limitation, enemy avoidance, **hybridization** and climate change. Here, I question two aspects of these explanations: that the origin of the life cycles was associated with Pleistocene ice age events, and that they evolved from shorter life cycles through the lengthening of nymphal stages in annual increments. Instead, I suggest that these life cycles evolved earlier than the Pleistocene and involved an abrupt transition from a nine-year to a 13-year life cycle, driven, in part, by interspecific competition.

~~Marine Geopolymer Concrete: A Hybrid Curable Self-Compacting Sustainable Concrete for Marine Applications~~

Rahman, SK; Al-Ameri, R, 2022

Featured Application This research work features the mechanical properties of a novel marine geopolymer concrete that can be used under marine exposure conditions without any strength deterioration. Marine environments are widely addressed as a serious threat to coastal concrete structures due to higher repair and rehabilitation costs. The rising concerns of climate change and related issues also require marine structures to be resilient and sustainable at the same time. Geopolymer concrete has been given more significant consideration as an alternative, reporting better resistance to harsh and hazardous environmental exposure, including sulphate attacks, chloride attacks, and freeze-thaw climates. This study investigated the mechanical properties of fly ash (FA) and ground granulated blast furnace slag (GGBFS)-based self-compacting geopolymer concrete (SCGC), subjected to short term ambient and marine curing conditions. The mechanical performance, inclusive of compressive strength, tensile strength, and modulus of elasticity under three-month marine exposure compared to an ambient environment, indicates that the SCGC mix offered an increase in strength. It is reported that the compressive strength of SCGC increased to the range of 50 MPa after marine exposure in comparison to the 40 MPa strength after 28-day curing. A similar increase in indirect tensile strength and modulus of elasticity were observed for the test specimens, with no signs of leaching of salts under marine exposure. Thus, the current SCGC acts as a sustainable construction material in counteracting the threats of marine degradation in civil structural components.

~~Using a novel assessment framework to evaluate protective functions and timber production in Austrian mountain forests under climate change~~

Maroschek, M; Rammer, W; Lexer, MJ, 2015

In Central European mountain forests, timber production and the protection of infrastructure and settlements against gravitational natural hazards are key forest ecosystem services (ES). The quantitative assessment of mountain forest ES for management planning and decision support is a particular challenge, due to

manifold involved spatial scales from tree to slope and landscape level. We present an assessment framework to analyze and communicate the effect of management and climate change on the provision of selected ES in mountain forests. Core element is the spatially explicit **hybrid** forest ecosystem model PICUS. Remote sensing data and inventories are combined to generate realistic fine-grained forest landscapes with single tree resolution as input to PICUS. Landscape-level planning of silvicultural prescriptions employs geographic information systems functionalities (locate skyline corridors and treatment areas, prescribe silvicultural operations based on tree-level attributes) and produces management maps, which are interpreted by PICUS and executed in course of simulation runs. Model output is imported into a spatially explicit landscape assessment tool to assess the protective effect of vegetation. In a 250 ha case study in the Eastern Alps in Austria, the assessment framework is demonstrated to evaluate effects of climate change and management on timber production and protection against landslides and snow avalanche release. Climate change had, depending on climate and management scenario both, positive and negative impacts on desired ES. Key factor for ES provisioning in the case study was the interaction of bark beetle disturbances, legacies of past land-use practices and forest management.

~~Kernel Ridge Regression Hybrid Method for Wheat Yield Prediction with Satellite-Derived Predictors~~

Ahmed, AAM; Sharma, E; Jui, SJJ; Deo, RC; Nguyen-Huy, T; Ali, M, 2022

Wheat dominates the Australian grain production market and accounts for 10-15% of the world's 100 million tonnes annual global wheat trade. Accurate wheat yield prediction is critical to satisfying local consumption and increasing exports regionally and globally to meet human food security. This paper incorporates remote satellite-based information in a wheat-growing region in South Australia to estimate the yield by integrating the kernel ridge regression (KRR) method coupled with complete ensemble empirical mode decomposition with adaptive noise (CEEMDAN) and the grey wolf optimisation (GWO). The **hybrid** model, 'GWO-CEEMDAN-KRR,' employing an initial pool of 23 different satellite-based predictors, is seen to outperform all the benchmark models and all the feature selection (ant colony, atom search, and particle swarm optimisation) methods that are implemented using a set of carefully screened satellite variables and a feature decomposition or CEEMDAN approach. A suite of statistical metrics and infographics comparing the predicted and measured yield shows a model prediction error that can be reduced by ~20% by employing the proposed GWO-CEEMDAN-KRR model. With the metrics verifying the accuracy of simulations, we also show that it is possible to optimise the wheat yield to achieve agricultural profits by quantifying and including the effects of satellite variables on potential yield. With further improvements in the proposed methodology, the GWO-CEEMDAN-KRR model can be adopted in agricultural yield simulation that requires remote sensing data to establish the relationships between crop health, yield, and other productivity features to support precision agriculture.

~~Variation in susceptibility of Eucalyptus grandis and selected hybrid clones to two termite species Macrotermes bellicosus and M. subhyalinus in Uganda~~

Nakabonge, G; Matovu, B, 2021

The maximum productivity of plantation forestry and its role in climate change mitigation, adaptation and resilience cannot be met without proper management. Termites in the genus *Macrotermes* have been reported as a major challenge to *Eucalyptus* plantation forestry establishment. The current study evaluated the susceptibility of four *Eucalyptus* **hybrid** clones: GU 7, GC 796, GC 550 and GC 796/2, and *E. grandis* Hill ex Maid. to the most damaging *Macrotermes bellicosus* (Smeathman) and *Macrotermes subhyalinus* (Rambur) to identify tolerant material that can be planted in high incidence areas. The study involved exposure of moisture dry pieces of wood from *E. grandis* and the four **hybrid** clones to damage by *M. bellicosus* and *M. subhyalinus*. Results confirmed that *M. bellicosus* is the most aggressive. Results further revealed that *E. grandis* and GC 550 are the most susceptible whereas GC 796 is the most tolerant clone. The findings from the study will contribute to improved management of termites by planting tolerant material in high risk areas.

~~Long-term cloud forest response to climate warming revealed by insect speciation history~~

Salces-Castellano, A; Stankowski, S; Arribas, P; Patino, J; Karger, DN; Butlin, R; Emerson, BC,

~~Plantation forests, climate change and biodiversity~~

Pawson, SM; Brin, A; Brockerhoff, EG; Lamb, D; Payn, TW; Paquette, A; Parrotta, JA, 2013

Nearly 4 % of the world's forests are plantations, established to provide a variety of ecosystem services, principally timber and other wood products. In addition to such services, plantation forests provide direct and indirect benefits to biodiversity via the provision of forest habitat for a wide range of species, and by reducing negative impacts on natural forests by offsetting the need to extract resources. There is compelling evidence that climate change is directly affecting biodiversity in forests throughout the world. These impacts occur as a result of changes in temperature, rainfall, storm frequency and magnitude, fire frequency, and the frequency and magnitude of pest and disease outbreaks. However, in plantation forests it is not only the direct effects of climate change that will impact on biodiversity. Climate change will have strong indirect effects on biodiversity in plantation forests via changes in forest management actions that have been proposed to mitigate the effects of climate change on the productive capacity of plantations. These include changes in species selection (including use of species mixtures), rotation length, thinning, pruning, extraction of bioenergy feedstocks, and large scale climate change driven afforestation, reforestation, and, potentially deforestation. By bringing together the potential direct and indirect impacts of climate change we conclude that in the short to medium term changes in plantation management designed to mitigate or adapt to climate change could have a significantly greater impact on biodiversity in such plantation forests than the direct effects of climate change. Although this hypothesis remains to be formally tested, forest managers worldwide are already considering new approaches to plantation forestry in an effort to create forests that are more resilient to the effects of changing climatic conditions. Such change presents significant risks to existing biodiversity values in plantation forests, however it also provides new opportunities to improve biodiversity values within existing and new plantation forests. We conclude by suggesting future options, such as functional zoning and species mixtures applied at either the stand level or as fine-scale mosaics of single-species stands as options to improve biodiversity whilst increasing resilience to climate change.

~~New double decomposition deep learning methods for river water level forecasting~~

Ahmed, AAM; Deo, RC; Ghahramani, A; Feng, Q; Raj, N; Yin, ZL; Yang, LS, 2022

Forecasting river water levels or streamflow water levels (SWL) is vital to optimising the practical and sustainable use of available water resources. We propose a new deep learning **hybrid** model for SWL forecasting using convolutional neural networks (CNN), bi-directional long-short term memory (BiLSTM), and ant colony optimisation (ACO) with a two-phase decomposition approach at the 7-day, 14-day, and 28-day forecast horizons. The newly developed CBiLSTM method is coupled with complete ensemble empirical mode decomposition with adaptive noise (CEEMDAN) and variational mode decomposition (VMD) methods to extract the most significant features within predictor variables to build a **hybrid** CVMD-CBiLSTM model. We integrate three distinct datasets (satellite-derived, climate mode indices, and ground-based meteorological observations) to improve the forecasting capability of the CVMD-CBiLSTM model, applied at nineteen different gauging stations in the Australian Murray River system. This proposed model returns a significantly accurate performance with 98% of all prediction errors within less than ± 0.020 m and a low relative root mean square of 0.08%, demonstrating its superiority over several benchmark models. The results show that using the new **hybrid** deep learning algorithm with ACO feature selection can significantly improve the accuracy of forecasted river water levels, and therefore, the method is attractive for adopting remote sensing data to the model ground-based river flow for strategic water savings planning initiatives and dealing with climate change-induced extreme events such as drought events.

~~Susceptibility of eucalypt taxa to a natural infestation by *Leptocybe invasa*~~

da Silva, PHM; Junqueira, LR; de Araujo, MJ; Wilcken, CF; Moraes, MLT; de Paula, RC, 2020

Recently, pest occurrence in forest plantations has been increasing influenced by genotypes and environmental conditions such as climate change, thus impacting production negatively. In 2008, the exotic pest *Leptocybe invasa* (Hym: Eulophidae), known as the blue gum chalcid, was introduced in Brazil causing damage to eucalypt plantations in many regions of the country. To this end, this study evaluated the susceptibility of *Eucalyptus camaldulensis* (one seedlot), *E. grandis* (four seedlots), *E. urophylla* (four seedlots), and the "E. urograndis" **hybrid** (*E. urophylla* x *E. grandis*) (three seedlots) exposed to a natural infestation by *L. invasa* in two seasons (winter and summer). The attack on seedlings was classified in terms of severity as healthy (no pest attack), oviposition (only oviposition signs) and gall formation. The results show a significant higher pest incidence in summer compared to winter. Further, *Eucalyptus urophylla* was the least attacked and 90% of the seedlings were healthy whereas *E. grandis* showed the highest number of seedlings with galls. The *E. urograndis* **hybrid** showed intermediate results between the two species. Differences in susceptibility were observed between seedlots within species. *Eucalyptus camaldulensis*, which was expected to have the highest incidence of galls, had a high oviposition incidence (60%) and low gall incidence (< 10%), probably due to its provenance. The susceptibility of the different eucalypt families varied significantly with respect to *L. invasa* infestation, and family heritability ranged from 0.27 to 0.68. The genetic control of *L. invasa* is possible through the selection of tolerant and resistant material, considering the species, provenance, and family.

~~Density-dependent population dynamics of mountain pine beetle in thinned and unthinned stands~~

MacQuarrie, CJK; Cooke, BJ, 2011

Thinning, the selective removal of some trees from a forest, is one way forest managers can reduce the probability that a forest will be susceptible to attack by bark beetles. Although this method has been shown to be effective, it is not clear whether the effect arises when pre-outbreak populations are small or during the epidemic phase when outbreaks are growing. We adopted a population dynamics approach to determine if the effect of limit or basal area thinning could be observed in the form of differential beetle recruitment using lodgepole pine (*Pinus contorta* Dougl. ex Loud.) and ponderosa pine (*Pinus ponderosa* Dougl. ex P. & C. Laws.) mortality data from previously published studies as a proxy measure of mountain pine beetle (*Dendroctonus ponderosae* Hopkins) population size. We found that mountain pine beetle populations exhibit density-dependent population dynamics that are influenced by the silvicultural history of their host's stand. Thinning did not change the epidemic equilibrium but instead caused a shift in dynamics from linear to nonlinear. In a validation test, the models developed for thinned and unthinned stands predicted reproductive rates in independent locations. These data also suggest the epidemic dynamics of mountain pine beetle may be sensitive to perturbations and to systematic trends associated with climate variability and climate change.

~~Phylogeny and evolution of large body size in the rove beetle genus *Phlaeopterus* Motschulsky, 1853 (Coleoptera: Staphylinidae: Omaliinae: Anthophagini)~~

Sikes, DS; Mullen, LJ, 2021

The omaliine rove beetle genus *Phlaeopterus* Motschulsky, 1853 contains 22 species. The genus is distributed across northwestern North America and eastern Asia. These beetles occur primarily along the edges of alpine snowfields and streams, habitats that are particularly sensitive to the impacts of climate change. Two species have not been collected since 1979 and 1984, one of which, *Phlaeopterus bakerensis* Mullen and Campbell, 2018, is a contender for the largest-bodied species among the over 1,600 species of the subfamily Omaliinae. Here, we present the first phylogeny of the genus, using Bayesian and maximum likelihood analyses based on DNA sequences from the mitochondrial gene COI and morphological data. We tested previous taxonomic hypotheses and most were rejected by all three analyses. *Phlaeopterus castaneus* Casey, 1893 is non-monophyletic based on COI sequences and may have **hybridized** with *P. loganensis* Hatch, 1957. We found support for the monophyly of the genus *Phlaeopterus*. Our analyses suggest the common ancestor of the genus had small-bodied adults (maximum body size under 5 mm) with ocelli. Within this small-bodied radiation of species, ocelli were lost once and there were two separate evolutionary transitions to large-bodied adults. Although all the large-bodied species are snowfield-associated and only 25% of the small-bodied species are, we did not find statistical support for a relationship between large body size and use of snowfield habitats. These findings represent the first modern phylogenetic reconstruction of species-level relationships within the rove beetle subfamily Omaliinae using both morphological and molecular data.

~~Using wild relatives and related species to build climate resilience in Brassica crops~~

Quezada-Martinez, D; Nyarko, CPA; Schiessl, SV; Mason, AS, 2021

Climate change will have major impacts on crop production: not just increasing drought and heat stress, but also increasing insect and disease loads and the chance of extreme weather events and further adverse conditions. Often, wild relatives show increased tolerances to biotic and abiotic stresses, due to reduced stringency of selection for yield and yield-related traits under optimum conditions. One possible strategy to improve resilience in our modern-day crop cultivars is to utilize wild relative germplasm in breeding, and attempt to introgress genetic factors contributing to greater environmental tolerances from these wild relatives into elite crop types. However, this approach can be difficult, as it relies on factors such as ease of **hybridization** and genetic distance between the source and target, crossover frequencies and distributions in the **hybrid**, and ability to select for desirable **introgressions** while minimizing linkage drag. In this review, we outline the possible effects that climate change may have on crop production, introduce the Brassica crop species and their wild relatives, and provide an index of useful traits that are known to be present in each of these species that may be exploitable through interspecific **hybridization**-based approaches. Subsequently, we outline how **introgression** breeding works, what factors affect the success of this approach, and how this approach can be optimized so as to increase the chance of recovering the desired **introgression** lines. Our review provides a working guide to the use of wild relatives and related crop germplasm to improve biotic and abiotic resistances in Brassica crop species.

~~Long-term cloud forest response to climate warming revealed by insect speciation history (vol 75, pg 231, 2021)~~

Salces-Castellano, A; Stankowski, S; Arribas, P; Patino, J; Karger, DN; Butlin, R; Emerson, BC, 2021

Montane cloud forests are areas of high endemism, and are one of the more vulnerable terrestrial ecosystems to climate change. Thus, understanding how they both contribute to the generation of biodiversity, and will respond to ongoing climate change, are important and related challenges. The widely accepted model for montane cloud forest dynamics involves upslope forcing of their range limits with global climate warming. However, limited climate data provides some support for an alternative model, where range limits are forced downslope with climate warming. Testing between these two models is challenging, due to the inherent limitations of climate and pollen records. We overcome this with an alternative source of historical information, testing between competing model predictions using genomic data and demographic analyses for a species of beetle tightly associated to an oceanic island cloud forest. Results unequivocally support the alternative model: populations that were isolated at higher elevation peaks during the Last Glacial Maximum are now in contact and **hybridizing** at lower elevations. Our results suggest that genomic data are a rich source of information to further understand how montane cloud forest biodiversity originates, and how it is likely to be impacted by ongoing climate change.

Maize diversity for fall armyworm resistance in a warming world

Singh, GM; Xu, JC; Schaefer, D; Day, R; Wang, ZY; Zhang, F, 2022

Currently, maize (*Zea mays* L.) production is under threat from climate change, drought, and pests such as fall armyworm (FAW) [Spodoptera frugiperda (J.E. Smith) (Lepidoptera: Noctuidae)]. Since its first detection outside of its native range in 2016, FAW has spread into 76 nations across Africa and Asia adversely affecting maize production and, in turn, the livelihoods of millions of smallholder farmers. Thus, there is a strong need for the development of cost-effective and biologically based integrated pest management (IPM) practices including host-plant resistance (HPR). However, most of the commercial maize cultivars have lost some defensive traits through selective breeding for yield during domestication. The majority of the commercially cultivated **hybrids** and cultivars in Asia and Africa are highly susceptible to FAW. Therefore, this review summarizes information about various maize landraces, native germplasm, and crop wild relatives (CWRs) possessing FAW resistance traits and about their potential resistance mechanisms, namely antibiosis, antixenosis, and tolerance. There is clear evidence of FAW resistance acting through diverse mechanisms in several maize landraces, germplasm lines, native populations, and CWRs such as Antigua race, FAW Tuxpeno, Zapalote Chico 2451F, Doce Flor da Serra, FAWCC (C5), CMS 14C, PopG (C2), MpSWCB-4, Mp708, Mp 704, CML 67, and FAW 7050, as well as a few species of teosinte and Tripsacum L. Further, a scheme that outlines strategies and approaches for prebreeding and their **introgression** into elite cultivars for developing FAW-resistant maize is proposed as a possible way forward.

Identification of winter moth (*Operophtera brumata*) refugia in North Africa and the Italian Peninsula during the last glacial maximum

Andersen, JC; Havill, NP; Mannai, Y; Ezzine, O; Dhahri, S; Ben Jamaa, ML; Caccone, A; Elkinton, JS, 2019

Numerous studies have shown that the genetic diversity of species inhabiting temperate regions has been shaped by changes in their distributions during the Quaternary climatic oscillations. For some species, the genetic distinctness of isolated populations is maintained during secondary contact, while for others, admixture is frequently observed. For the winter moth (*Operophtera brumata*), an important defoliator of oak forests across Europe and northern Africa, we previously determined that contemporary populations correspond to genetic diversity obtained during the last glacial maximum (LGM) through the use of refugia in the Iberian and Aegean peninsulas, and to a lesser extent the Caucasus region. Missing from this sampling were populations from the Italian peninsula and from North Africa, both regions known to have played important roles as glacial refugia for other species. Therefore, we genotyped field-collected winter moth individuals from southern Italy and northwestern Tunisia—the latter a region where severe oak forest defoliation by winter moth has recently been reported—using polymorphic microsatellite. We reconstructed the genetic relationships of these populations in comparison to moths previously sampled from the Iberian and Aegean peninsulas, the Caucasus region, and western Europe using genetic distance, Bayesian clustering, and approximate Bayesian computation (ABC) methods. Our results indicate that both the southern Italian and the Tunisian populations are genetically distinct from other sampled populations, and likely originated in their respective refugium during the LGM after diverging from a population that eventually settled in the Iberian refugium. These suggest that winter moth populations persisted in at least five Mediterranean LGM refugia. Finally, we comment that outbreaks by winter moth in northwestern Tunisia are not the result of a recent introduction of a nonnative species, but rather are most likely due to land use or environmental changes.

Interglacial refugia and range shifts of the alpine grasshopper *Stenobothrus coticus* (Orthoptera: Acrididae: Gomphocerinae)

Berger, D; Chobanov, DP; Mayer, F, 2010

A warming climate leads to shifts in distribution ranges to higher latitudes and altitudes. Consequently, cold-adapted alpine species can be trapped in interglacial Holocene refugia on high mountain summits if they fail to expand their ranges to the north. One example is the alpine grasshopper *Stenobothrus coticus*. This species was assumed to be endemic to the southwestern Alps (France, Italy). However, we have found a second refugium in the Rila Mountains in southwestern Bulgaria. Analyses of the mitochondrial gene *co1* and of phenotypic characters from morphology and behaviour did not reveal differences between the two geographically separated populations of *S. coticus* studied. We suppose that *S. coticus* had a wider distribution during colder periods, when its range was expanded to lower altitudes. This hypothesis is supported by the current distribution of the closely related montane *S. rubicundulus*.

The extended consequences of genetic conductivity: Mating distance affects community phenotypes in Norway spruce

Axelsson, EP; Keith, J, 2018

Anthropogenic landscape-level alterations such as habitat fragmentation and long distance translocation of genetic material are currently altering the genetic connectivity and structure of forest tree populations globally. As the susceptibility of individual trees to dependent organisms is often genetically determined, it is possible that these genetic changes may extend beyond individuals to affect associated communities. To test this, we examined how variation in crossing distance among the progeny of 18 controlled crosses of Norway spruce (*Picea abies*) populations occurring across central Sweden affected chemical defense, and subsequently, a small community of galling *Adelges* aphids infecting planted trees at two common garden trails. Although crossing distance did not influence growth, vitality or reproduction in the studied population, it did influence the expression of one candidate defensive chemical compound, apigenin, which was found in higher concentrations within outcrossed trees. We also show that this variation in apigenin induced by crossing distance correlated with susceptibility to one member of the galling community but not the other. Furthermore, the effect of crossing distance on galling communities and the general susceptibility of Norway spruce to infection also varied with environment. Specifically, in the more benign environment, inbred trees suffered greater gall infection than outcrossed trees, which is contrary to general predictions that the effects of inbreeding should be more pronounced in harsher environments. These findings suggest that the effects of variation in crossing distance in forest trees can extend beyond the individual to influence whole communities.

Recent Bibliography on the Optimization of Multi-source Energy Systems

Gaabout, A; Metatla, A; Kelaiaia, R; Bourennani, F; Kerboua, A, 2019

Due to fast increase in the world of the population and global warming, designing efficient and low-polluting or clean energy systems are one of the critical problems of the century. In the recent years, most researchers are focusing on wind and solar energy sources as they freely available, complementary, their costs are becoming competitive, and they are clean. Designing optimally **hybrid** energy is complex as involves various mixed-type variables, tight constraints, and other complexities. In the present paper, we summarize most important optimization works related to the design of **hybrid** PV-wind systems, and present findings on future trends.

Best of both worlds: hybrids of two commercially important pines (*Pinus contorta* x *Pinus banksiana*) combine increased growth potential and high drought tolerance

Bockstette, SW; de la Mata, R; Thomas, BR, 2021

Over 18 million hectares of lodgepole pine (*Pinus contorta* Dougl. var. *latifolia* Engelm.) forests have been affected by a massive mountain pine beetle outbreak in western Canada. The ensuing need for reforestation compels forest managers to deploy more drought-resistant stock in anticipation of a hotter and drier future climate. Recent studies suggest that naturally occurring lodgepole pine x jack pine (*Pinus banksiana* Lamb.) **hybrids** may be more drought-resistant than pure

lodgepole pine. We used single-nucleotide polymorphism markers to determine the level of jack pine **introgression** present in the region J lodgepole pine seed orchard, in northwest Alberta, and we identified six **hybrid** genotypes with 10%-18% jack pine **introgression** for further study. We compared the performance of open-pollinated seedlings of lodgepole, jack, and **hybrid** pines under well-watered and drought conditions in a greenhouse experiment. Seedlings were subjected to repeated drought cycles, withholding water for either 2 or 3 weeks. We found that **hybrid** pines grew significantly faster than lodgepole pine under well-watered conditions while retaining the high tolerance to prolonged drought exhibited by lodgepole pine seedlings, a particularly beneficial combination of traits during the critical stage of establishment. We therefore suggest the deployment of **hybrid** lodgepole pine as a strategy to promote adaptation to hotter and drier future climates.

A Comprehensive Review on the Taxonomy, Ecology, Reproductive Biology, Economic Importance and Conservation Status of Indian Himalayan Rhododendrons

Basnett, S; Ganesan, R,

The Indian Himalaya is characterized by high plant diversity and endemism levels. Here, the genus *Rhododendron* is one of the largest flowering plant genera. The flowering of rhododendrons across elevations in the Himalaya supports insects, birds, and animal movements seasonally. Their diverse life forms and habits also form an important structural component of diverse vegetation types from tropical to temperate forests and alpine thickets. Rhododendrons are also a source of livelihood for many rural communities in the Himalaya. The high ecological and economic significance of rhododendrons in this mountain region qualifies it as an important genus for further investigation and exploration. However, over time, climate change and the ever-increasing demand for natural resources have collectively exerted considerable pressure on Indian Himalayan rhododendrons in their natural habitats. Available data on various aspects of taxonomy, ecology and conservation status are scanty. There is an urgent need to assess the potential ecological and economic benefits that rhododendrons provide to local mountain communities and associated wildlife. This critical review provides comprehensive detail on taxonomy, evolutionary history, ecology, reproductive biology, **hybridization**, economic importance, impact of climate change on its ecology and evolution, and the conservation status of rhododendrons in the Indian Himalaya. Further, we conclude with a discussion of the strategies to be adopted for the conservation of *Rhododendron*-dominated forests in the Indian Himalaya. This comprehensive compilation will open new perspectives for future studies and improve ongoing conservation efforts to manage valuable plant resources.

Research frontiers in sustainable development of energy, water and environment systems in a time of climate crisis

Kilkis, S; Krajacic, G; Duic, N; Montorsi, L; Wang, QW; Rosen, MA; Al-Nimr, MA, 2019

Sustainable energy conversion and management processes increasingly require an integrated approach, especially in the context of addressing the climate crisis. This editorial puts forth related research frontiers based on 28 research articles of the special issue that is dedicated to the 13th Conference on Sustainable Development of Energy, Water and Environment Systems and regional series based on the 1st Latin American and 3rd South East European Conferences. Seven research frontiers are reviewed, the first three of which are (i) sustainable technologies for local energy systems, (ii) energy storage and advances in flexibility and (iii) solar energy penetration across multiple sectors. These research frontiers contain contributions based on renewable energy for waste-water treatment in islands, energy savings across urban built infrastructure, advanced district heating and cooling networks, power-to-gas and hydrogen production technologies, demand response in industrial systems, **hybrid** thermal energy storage, **hybrid** solar energy power plants, novel photovoltaic thermal technologies, and improved solar energy dispatchability. The research frontiers continue with (iv) wind, water based energy and the energy-water nexus, (v) effective valorization and upgrading of resources, (vi) combustion processes and better utilization of heat and (vii) carbon capture, storage and utilization. Significant contributions include innovative wind and hydrokinetic turbines, osmotic power technologies, synergetic solutions for water desalination, efficient catalytic pyrolysis, upgrading to reduce particle pollution, co-processing for alternative fuels, combustion characterization, electricity generation from waste heat sources, advances in heat exchangers and heat transfer, oxy-fuel combustion, post-combustion capture, and fly ash recycling for energy storage material. The research frontiers in this editorial provide ample opportunities to support societal transformations in the next decades to sustain planetary life-support systems.

Larval pattern morphotypes in the Western Palaearctic Hyles euphorbiae complex (Lepidoptera: Sphingidae: Macroglossinae)

Hundsdoerfer, AK; Mende, MB; Harbich, H; Pittaway, AR; Kitching, IJ, 2011

External morphological variation in larval pattern elements in the *Hyles euphorbiae* complex is documented and described from independent samples of numerous populations across Europe and North Africa. Variability in the distribution of black cuticle and other colours was found to be much higher within populations than previously believed and it proved difficult to characterize any species, subspecies and even local population unequivocally using this feature alone. A representative sample of larvae from the Canary Islands, Madeira, North Africa, Iberia, Italy, Germany, Eastern Europe, Malta, Greece and Yemen, is illustrated, supplemented by observations from photographs of larvae from the Middle East and Western Asia. Taxonomy-independent definitions of larval morphotypes demonstrate significant overlap between species. We discuss the results in the context of Western Palaearctic biogeography, postulating several areas of **hybridisation** between the more northern *Hyles euphorbiae* and more southern *H. tithymali* that have led to the mosaic distribution patterns observed, and consider the potential of these moths for tracking the future effects of climate change in the Mediterranean Basin.

GM trees with increased resistance to herbivores: trait efficiency and their potential to promote tree growth

Hjalten, J; Axelsson, EP, 2015

Climate change, as well as a more intensive forestry, is expected to increase the risk of damage by pests and pathogens on trees, which can already be a severe problem in tree plantations. Recent development of biotechnology theoretically allows for resistance enhancement that could help reduce these risks but we still lack a comprehensive understanding of benefits and tradeoffs with pest resistant GM (genetically modified) trees. We synthesized the current knowledge on the effectiveness of GM forest trees with increased resistance to herbivores. There is ample evidence that induction of exogenous *Bacillus thuringiensis* genes reduce performance of target pests whereas upregulation of endogenous resistance traits e.g., phenolics, generates variable results. Our review identified very few studies estimating the realized benefits in tree growth of GM trees in the field. This is concerning as the realized benefit with insect resistant GM plants seems to be context-dependent and likely manifested only if herbivore pressure is sufficiently high. Future studies of secondary pest species and resistance evolution in pest to GM trees should be prioritized. But most importantly we need more long-term field tests to evaluate the benefits and risks with pest resistant GM trees.

The major threats to Atlantic salmon in Norway

Forseth, T; Barlaup, BT; Finstad, B; Fiske, P; Gjoaester, H; Falkegard, M; Hindar, A; Mo, TA; Rikardsen, AH; Thorstad, EB; Vollestad, LA; Wennevik, V, 2017

Atlantic salmon (*Salmo salar*) is an economically and culturally important species. Norway has more than 400 watercourses with Atlantic salmon and supports a large proportion of the world's wild Atlantic salmon. Atlantic salmon are structured into numerous genetically differentiated populations, and are therefore managed at the population level. Long-distance migrations between freshwater and ocean habitats expose Atlantic salmon to multiple threats, and a number of anthropogenic factors have contributed to the decline of Atlantic salmon during the last decades. Knowledge on the relative importance of the different anthropogenic factors is vital for prioritizing management measures. We developed a semi-quantitative 2D classification system to rank the different anthropogenic factors and used this to assess the major threats to Norwegian Atlantic salmon. Escaped farmed salmon and salmon lice from fish farms were identified as expanding population threats,

with escaped farmed salmon being the largest current threat. These two factors affect populations to the extent that they may be critically endangered or lost, with a large likelihood of causing further reductions and losses in the future. The introduced parasite *Gyrodactylus salaris*, freshwater acidification, hydropower regulation and other habitat alterations were identified as stabilized population threats, which have contributed to populations becoming critically endangered or lost, but with a low likelihood of causing further loss. Other impacts were identified as less influential, either as stabilized or expanding factors that cause loss in terms of number of returning adults, but not to the extent that populations become threatened. Management based on population specific reference points (conservation limits) has reduced exploitation in Norway, and overexploitation was therefore no longer regarded an important impact factor. The classification system may be used as a template for ranking of anthropogenic impact factors in other countries and as a support for national and international conservation efforts.

~~Geopolymer-based hybrid foams: Lightweight materials from a sustainable production process~~

Ricciotti, L; Occhicone, A; Petrillo, A; Ferone, C; Cioffi, R; Roviello, G, 2020

The construction industry causes significant environmental impacts in terms of global warming and embodied energy consumption. Concrete is one of the most widely used product in the planet. The development of new materials as alternative to cement could lay the foundations for introducing on the market innovative systems with higher performances and lower environmental impacts. The present research investigates, through a life cycle approach, the environmental impacts of the production process of aerated systems based on innovative Geopolymer-based **Hybrid** Foams (GHF), choosing as system boundary the method "cradle to gate". The environmental impacts of GHF derived from fly ash (GHF-FA) were compared to GHF based on metakaolin (GHF-MK) and commercial Aerated Autoclaved Concrete (AAC) system. The main result shows that GHF-FA has the lowest environmental impact (in terms of CO₂ production), thus it appears as an environmentally friendly material. (C) 2019 Elsevier Ltd. All rights reserved.

~~The effect of developmental temperature fluctuation on wing traits and stressed locomotor performance in *Drosophila melanogaster*, and its dependence on heterozygosity~~

Kjaersgaard, A; Le, N; Demontis, D; Novicic, ZK; Loeschcke, V; Pertoldi, C,

Background: Natural environments fluctuate and all organisms experience some degree of environmental variance. Global climate models predict increasing environmental variance in the future. Yet we do not fully understand how environmental variation affects performance traits. Questions: Does temperature fluctuation during development affect adult size and wing shape in *Drosophila melanogaster*? If so, are the effects predictable? Do they depend on heterozygosity? Do fluctuations in developmental temperature affect adult physiological performance at high temperature? Methods: We tested the effect of one fluctuating (21 degrees C/29 degrees C) and several constant (21 degrees C, 23 degrees C, 25 degrees C, 27 degrees C, 29 degrees C) developmental temperature regimes on three wing morphometric traits (wing length, wing width, and wing shape) in an experiment using three inbred lines of *D. melanogaster* and their first-generation **hybrids**. We also tested the effect of fluctuating and constant developmental temperature on adult locomotor performance at several high and stressful test temperatures (32 degrees C, 34 degrees C, 36 degrees C, 38 degrees C, 40 degrees C). Results: Performance mostly declined if the flies were reared under the fluctuating temperature regime versus the constant temperature regime with the same mean (25 degrees C). Heterozygosity level also affected the traits investigated, with crossbreds usually having higher trait values. Crossbred genotypes compared across constant temperatures also showed greater plasticity in wing aspect. Conclusion: The widespread use of constant developmental temperatures in laboratory experiments may lead to overestimation of performance.

~~High night temperature during maize post-flowering increases night respiration and reduces photosynthesis, growth and kernel number~~

Kettler, BA; Carrera, CS; Sonzogno, FDN; Trachsel, S; Andrade, FH; Neiff, N, 2022

In the last years globally, daily night-time low temperatures have increased more than twice compared with maximum temperatures. There is little evidence about maize growth and yield responses to high night temperature (HNT) under field conditions. In this study, we aimed to (i) evaluate the effect of HNT during post-flowering on kernel number (KN), crop growth rate expressed in chronological days and thermal units (CGR(D) and CGR(TU), respectively), radiation use efficiency (RUE), night respiration (Rn), net photosynthesis (Amax), chlorophyll fluorescence and cell membrane stability (CMS), and (ii) identify associations among the measured physiological traits. Two **hybrids** (Te, temperate; and St, subtropical) were exposed to two thermal conditions from R1 + 2d to R1 + 16d: (i) HNT from 1900 to 0700 h, and (ii) ambient night temperature (ANT). The HNT resulted in reductions in KN (8%), CGR(D) (11%), and CGR(TU) (19%), with non-significant changes in kernel weight and grain yield. Reductions in KN were better explained by drops in CGR(TU) than in CGR(D). Under HNT, Amax significantly decreased ($p < 0.05$; 17%, among experiments and **hybrids**) with insignificant changes in CMS and chlorophyll fluorescence. HNT caused a larger effect on Rn in Te (+40%) than in St. We found a strong negative relationship between Rn and Amax, indicating that high Rn might exhibit an indirect effect on Amax, altering carbon balance and growth.

~~Is Gene Flow Promoting the Reversal of Pleistocene Divergence in the Mountain Chickadee (*Poecile gambeli*)?~~

Manthey, JD; Klicka, J; Spellman, GM, 2012

The Pleistocene glacial cycles left a genetic legacy on taxa throughout the world; however, the persistence of genetic lineages that diverged during these cycles is dependent upon levels of gene flow and **introgression**. The consequences of secondary contact among taxa may reveal new insights into the history of the Pleistocene's genetic legacy. Here, we use phylogeographic methods, using 20 nuclear loci from regional populations, to infer the consequences of secondary contact following divergence in the Mountain Chickadee (*Poecile gambeli*). Analysis of nuclear data identified two geographically-structured genetic groups, largely concordant with results from a previous mitochondrial DNA (mtDNA) study. Additionally, the estimated multilocus divergence times indicate a Pleistocene divergence, and are highly concordant with mtDNA. The previous mtDNA study showed a paucity of sympatry between clades, while nuclear patterns of gene flow show highly varied patterns between populations. The observed pattern of gene flow, from coalescent-based analyses, indicates southern populations in both clades exhibit little gene flow within or between clades, while northern populations are experiencing higher gene flow within and between clades. If this pattern were to persist, it is possible the historical legacy of Pleistocene divergence may be preserved in the southern populations only, and the northern populations would become a genetically diverse **hybrid** species.

~~Impact of Hybrid Electric Aircraft on Contrail Coverage~~

Yin, FJ; Grewe, V; Gierens, K,

~~A multiscale climate emulator for long-term morphodynamics (MUSCLE-morpho)~~

Antolinez, JAA; Mendez, FJ; Camus, P; Vitousek, S; Gonzalez, EM; Ruggiero, P; Barnard, P, 2016

Interest in understanding long-term coastal morphodynamics has recently increased as climate change impacts become perceptible and accelerated. Multiscale,

behavior-oriented and process-based models, or **hybrids** of the two, are typically applied with deterministic approaches which require considerable computational effort. In order to reduce the computational cost of modeling large spatial and temporal scales, input reduction and morphological acceleration techniques have been developed. Here we introduce a general framework for reducing dimensionality of wave-driver inputs to morphodynamic models. The proposed framework seeks to account for dependencies with global atmospheric circulation fields and deals simultaneously with seasonality, interannual variability, long-term trends, and autocorrelation of wave height, wave period, and wave direction. The model is also able to reproduce future wave climate time series accounting for possible changes in the global climate system. An application of long-term shoreline evolution is presented by comparing the performance of the real and the simulated wave climate using a one-line model.

~~Harnessing Diversity in Wheat to Enhance Grain Yield, Climate Resilience, Disease and Insect Pest Resistance and Nutrition Through Conventional and Modern Breeding Approaches~~

Mondal, S; Rutkoski, JE; Velu, G; Singh, PK; Crespo-Herrera, LA; Guzman, C; Bhavani, S; Lan, CX; He, XY; Singh, RP, 2016

Current trends in population growth and consumption patterns continue to increase the demand for wheat, a key cereal for global food security. Further, multiple abiotic challenges due to climate change and evolving pathogen and pests pose a major concern for increasing wheat production globally. Triticaceae species comprising of primary, secondary, and tertiary gene pools represent a rich source of genetic diversity in wheat. The conventional breeding strategies of direct **hybridization**, backcrossing and selection have successfully introgressed a number of desirable traits associated with grain yield, adaptation to abiotic stresses, disease resistance, and bio-fortification of wheat varieties. However, it is time consuming to incorporate genes conferring tolerance/resistance to multiple stresses in a single wheat variety by conventional approaches due to limitations in screening methods and the lower probabilities of combining desirable alleles. Efforts on developing innovative breeding strategies, novel tools and utilizing genetic diversity for new genes/alleles are essential to improve productivity, reduce vulnerability to diseases and pests and enhance nutritional quality. New technologies of high-throughput phenotyping, genome sequencing and genomic selection are promising approaches to maximize progeny screening and selection to accelerate the genetic gains in breeding more productive varieties. Use of cisgenic techniques to transfer beneficial alleles and their combinations within related species also offer great promise especially to achieve durable rust resistance.

~~FLOWERING PHENOLOGY OF SELECTED LINDEN (TILIA L.) TAXA IN RELATION TO POLLEN SEASONS~~

Dabrowska, A; Piotrowska-Weryszko, K; Weryszko-Chmielewska, E; Sawicki, R, 2016

All lindens provide Apidae insects with nectar, pollen, and honeydew. Lindens are important melliferous trees in Poland. The first purpose of the study was to carry out phenological observations of the flowering in ten linden taxa. The second aim was to analyse the content of linden pollen grains in the air of Lublin. A correlation between the parameters of the pollen season and meteorological factors was also determined. This study was conducted in the city of Lublin located in the central-eastern part of Poland. The flowering phenophases were analysed, using the method developed by Lukasiewicz, during the growing seasons of 2012-2015. Aerobiological monitoring, which was based on the volumetric method, was carried out over the 2001-2014 time period. As shown in the study, the flowering period of all the analysed linden taxa lasted 7 weeks, on average, from June 7 to July 24. The average length of the flowering period of the investigated taxa and **hybrids** was in the range of 12-17 days. Their flowering periods overlapped. The atmospheric pollen season lasted, on average, from mid-June to the second 10-day period of July. The highest concentration of airborne pollen was noted at the end of June. The pollen season pattern was significantly affected by temperature and relative air humidity as well as by rainfall in May and June. The investigations indicate a 9-day acceleration of the pollen season, which may be associated with global warming.

~~Characterization of Maize Hybrids (Zea mays L.) for Detecting Salt Tolerance Based on Morpho-Physiological Characteristics, Ion Accumulation and Genetic Variability at Early Vegetative Stage~~

Huqe, MA; Haque, MS; Sagar, A; Uddin, MN; Hossain, MA; Hossain, AZ; Rahman, MM; Wang, XK; Al-Ashkar, I; Ueda, A; El Sabagh, A, 2021

Increasing soil salinity due to global warming severely restricts crop growth and yield. To select and recommend salt-tolerant cultivars, extensive genotypic screening and examination of plants' morpho-physiological responses to salt stress are required. In this study, 18 prescreened maize **hybrid** cultivars were examined at the early growth stage under a hydroponic system using multivariate analysis to demonstrate the genotypic and phenotypic variations of the selected cultivars under salt stress. The seedlings of all maize cultivars were evaluated with two salt levels: control (without NaCl) and salt stress (12 dS m⁻¹) simulated with NaCl for 28 d. A total of 18 morpho-physiological and ion accumulation traits were dissected using multivariate analysis, and salt tolerance index (STI) values of the examined traits were evaluated for grouping of cultivars into salt-tolerant and -sensitive groups. Salt stress significantly declined all measured traits except root-shoot ratio (RSR), while the cultivars responded differently. The cultivars were grouped into three clusters and the cultivars in Cluster-1 such as Prabhat, UniGreen NK41, Bisco 51, UniGreen UB100, Bharati 981 and Star Beej 7Star exhibited salt tolerance to a greater extent, accounting for higher STI in comparison to other cultivars grouped in Cluster-2 and Cluster-3. The high heritability (h^2), > 60%) and genetic advance (GAM, > 20%) were recorded in 13 measured traits, indicating considerable genetic variations present in these traits. Therefore, using multivariate analysis based on the measured traits, six **hybrid** maize cultivars were selected as salt-tolerant and some traits such as Total Fresh Weight (TFW), Total Dry Weight (TDW), Total Na⁺, Total K⁺ contents and K⁺-Na⁺ Ratio could be effectively used for the selection criteria evaluating salt-tolerant maize genotypes at the early seedling stage.

~~Genomic divergence and lack of introgressive hybridization between two 13-year periodical cicadas support life cycle switching in the face of climate change~~

Koyama, T; Ito, H; Fujisawa, T; Ikeda, H; Kakishima, S; Cooley, JR; Simon, C; Yoshimura, J; Sota, T, 2016

Life history evolution spurred by post-Pleistocene climatic change is hypothesized to be responsible for the present diversity in periodical cicadas (Magicicada), but the mechanism of life cycle change has been controversial. To understand the divergence process of 13-year and 17-year cicada life cycles, we studied genetic relationships between two synchronously emerging, parapatric 13-year periodical cicada species in the Decim group, Magicicada tredecim and M. neotredecim. The latter was hypothesized to be of **hybrid** origin or to have switched from a 17-year cycle via developmental plasticity. Phylogenetic analysis using restriction-site-associated DNA sequences for all Decim species and broods revealed that the 13-year M. tredecim lineage is genomically distinct from 17-year Magicicada septendecim but that 13-year M. neotredecim is not. We detected no significant **introgression** between M. tredecim and M. neotredecim/M. septendecim thus refuting the hypothesis that M. neotredecim are products of **hybridization** between M. tredecim and M. septendecim. Further, we found that introgressive **hybridization** is very rare or absent in the contact zone between the two 13-year species evidenced by segregation patterns in single nucleotide polymorphisms, mitochondrial lineage identity and head width and abdominal sternite colour phenotypes. Our study demonstrates that the two 13-year Decim species are of independent origin and nearly completely reproductively isolated. Combining our data with increasing observations of occasional life cycle change in part of a cohort (e.g. 4-year acceleration of emergence in 17-year species), we suggest a pivotal role for developmental plasticity in Magicicada life cycle evolution.

~~Adaptation to a landscape scale mountain pine beetle epidemic in the era of networked governance: the enduring importance of bureaucratic institutions~~

Abrams, JB; Huber-Stearns, HR; Bone, C; Grummon, CA; Moseley, C, 2017

Landscape-scale forest disturbance events have become increasingly common worldwide under the combined influences of climate change and ecosystem

modification. The mountain pine beetle (*Dendroctonus ponderosae*) epidemic that swept through North American forests from the late 1990s through the early 2010s was one of the largest such disturbance events on record and triggered shocks to ecological and economic systems. We analyze the policy and governance responses to this event by focusing on three national forests in the state of Colorado and on the agency responsible for their management, the U.S. Forest Service. We found that the event triggered the formation of new **hybrid** agency/nonagency organizations that contributed both legitimacy and capacity to address the most immediate threats to human safety and infrastructure. Despite the use of a highly networked governance structure, longstanding U.S. Forest Service institutions continued to heavily influence the scope of the response and the means for implementing management activities. We detected relatively limited institutional response at the level of the agency as a whole, even as regional- and local-scale institutions within Colorado showed greater dynamism. Indeed, the changes to agency institutions that were detected were largely consistent with institutional change trajectories already in place prior to the epidemic. Our study points to the importance of institutional persistence and path dependence in limiting the latitude for adaptation to social and environmental shocks.

~~Fuel Burn Reduction of Hybrid Aircraft Employing an Exhaust Heat Harvesting System~~

Hughes, M; Olsen, J, 2022

This study investigates the application of an exhaust gas energy harvesting **hybrid** powertrain to three general aviation aircraft with reciprocating spark-ignition piston engines. The **hybridization** process involves downsizing the internal combustion engine to save weight and installation of an exhaust heat harvesting system composed of a harvester, a generator, lithium-ion traction battery, an electrical conversion system, and an electric motor. Novel calculations for a **hybrid** powertrain performance envelope are presented that estimate the upper limits to the degree of downsizing and mass of the harvester. An organic Rankine cycle (ORC) has been proposed as a potential compact, high-efficiency harvester. Five hydrofluoroolefins (which have no ozone depletion potential and very low global warming potential) are considered as organic fluids for the ORC. It is found that R-1336mzz(Z) performs best in this application. Each ORC design parameter is investigated, and an optimized design with 14.3% thermal efficiency is found. At this efficiency, the internal combustion engine may be downsized up to 34.5%. The fuel burn reduction at this degree of downsizing may be as high as 12.7-14.5%.

~~Tracking diversity and evolutionary pathways of Lebanese oak taxa through plastome analyses~~

Douaihy, B; Saliba, C; Stephan, J; Simeone, MC; Cardoni, S; Farhat, P; Kharat, MBD, 2020

The aim of this study is to better understand the phylogeography and evolution of the Lebanese oaks and to assess the convergence between their morphological and molecular characteristics. We investigated DNA sequence variation in four plastid markers (TrnH-psbA, ycf1, trnK-matK and PetD) of the seven species (three sections) occurring in Lebanon: *Q. calliprinos*, *Q. infectoria*, *Q. kotschyana*, *Q. cedrorum*, *Q. cerris*, *Q. look*, and *Q. ithaburensis*, in addition to *Q. libani* and *Q. cerris* from Syria, and possible **hybrids**. Among the four markers, the TrnH-psbA and trnK-matK loci resulted in the best-resolved genealogies. *Quercus calliprinos* haplotypes clearly belong to the west Asian-eastern Mediterranean 'WAHEA' lineage. *Sect. Cerris* haplotypes are derived variants of the central Mediterranean 'Cerris-Ilex' lineage. *Sect. Quercus* haplotypes were less differentiated and in close connection with the Caucasian primary refugium of white oaks. Despite the low species-level resolution, a gradient in genetic diversity linked to the ecological plasticity of the sampled species was observed. A close relationship of *Q. look* with *Q. cerris* is confirmed. *Quercus kotschyana* seems an ancient stock of closely related and disjunct oak of *sect. Quercus*. Finally, our results confirm the relevance of the Levant region as an important biogeographical crossroad between continents, and its key role in stimulating diversification and preservation of ancient gene pools. Important areas in Lebanon that should be taken into consideration in future conservation strategies are highlighted, to ensure a wider genetic potential of local oak species to face the current climate change.

~~Multiobjective Scheduling of Hybrid Renewable Energy System Using Equilibrium Optimization~~

Dubey, SM; Dubey, HM; Pandit, M; Salkuti, SR, 2021

Due to increasing concern over global warming, the penetration of renewable energy in power systems is increasing day by day. Generators that traditionally focused only on maximizing their profit in the competitive market are now also focusing on operation with the minimum pollution level. The paper proposes a multiobjective model capable of finding a set of trade-off solutions for the joint optimization problem, considering the cost of reserve and curtailment of power from renewable sources. Managing a **hybrid** power system is a challenging task due to its stochastic nature mixed with the objective function and complex practical constraints associated with it. A novel metaheuristic Equilibrium Optimizer (EO) algorithm conceived in the year 2020 utilizes the concept of control volume and mass balance for finding equilibrium state is proposed here for computing the optimal schedule and impact of renewable energy integration on profit and emission for different optimization objectives. In this paper, EO has shown dominant performance over well-established metaheuristic algorithms such as particle swarm optimizer (PSO) and artificial bee colony (ABC). In addition, EO produces well-distributed Pareto-optimal solutions and the fuzzy min-ranking is used as a decision maker to acquire the best compromise solution.

~~Next-generation variety development for sustainable production of arabica coffee (Coffea arabica L.): a review~~

van der Vossen, H; Bertrand, B; Charrier, A, 2015

Arabica coffees (60 % of current world coffee production) are generally sold at considerably better prices than robustas on account of superior beverage quality. However, costs of production are much higher, mainly due to more stringent demands for soil and climatic conditions, crop management, primary processing and control of several pests and diseases including the potentially very destructive coffee leaf rust (CLR) and berry disease (CBD). Breeding for disease resistance in combination with vigour, productivity and quality started in the early 1920s in India, but especially in the second half of the 20th century comprehensive breeding programmes have been implemented in several other coffee producing countries. Many of the resulting CLR- and CBD + CLR-resistant cultivars (true-breeding lines and F1 **hybrids**) meet the required standards of profitable and sustainable crop production. Challenges of more recent date include limited access to additional genetic resources of *Coffea arabica*, breakdown of host resistance to CLR, aggravating insect pest problems and the increasingly negative impact of climate change on arabica coffee production worldwide. This review discusses prospects of breeding and disseminating next generation (**hybrid**) cultivars of arabica coffee for sustainable coffee production under changing conditions of diseases, pests and climate. International networking on coffee breeding will facilitate sharing of resources (financial, genetic) and scientific information, application of genomics-assisted selection technologies, and pre-breeding for specific characters. Breeding and multiplication of new cultivars well adapted to the local environment will continue to be carried out at national or regional levels. A tree crop like arabica coffee does not lend itself to centralized variety development and dissemination on a global scale.

~~Forest genomics: Advancing climate adaptation, forest health, productivity, and conservation~~

Isabel, N; Holliday, JA; Aitken, SN, 2020

Forest ecosystems provide important ecological services and resources, from habitat for biodiversity to the production of environmentally friendly products, and play a key role in the global carbon cycle. Humanity is counting on forests to sequester and store a substantial portion of the anthropogenic carbon dioxide produced globally. However, the unprecedented rate of climate change, deforestation, and accidental importation of invasive insects and diseases are threatening the health

and productivity of forests, and their capacity to provide these services. Knowledge of genetic diversity, local adaptation, and genetic control of key traits is required to predict the adaptive capacity of tree populations, inform forest management and conservation decisions, and improve breeding for productive trees that will withstand the challenges of the 21st century. Genomic approaches have well accelerated the generation of knowledge of the genetic and evolutionary underpinnings of nonmodel tree species, and advanced their applications to address these challenges. This special issue of Evolutionary Applications features 14 papers that demonstrate the value of a wide range of genomic approaches that can be used to better understand the biology of forest trees, including species that are widespread and managed for timber production, and others that are threatened or endangered, or serve important ecological roles. We highlight some of the major advances, ranging from understanding the evolution of genomes since the period when gymnosperms separated from angiosperms 300 million years ago to using genomic selection to accelerate breeding for tree health and productivity. We also discuss some of the challenges and future directions for applying genomic tools to address long-standing questions about forest trees.

A Critical Review of Power Take-Off Wave Energy Technology Leading to the Conceptual Design of a Novel Wave Plus Photon Energy Harvester for Island/Coastal Communities' Energy Needs

Prasad, KA; Chand, AA; Kumar, NM; Narayan, S; Mamun, KA, 2022

As the global interest in renewable energy generation continues, the need to develop new and innovative solutions is being explored every day throughout the world by researchers and innovators. **Hybrid** renewable energy innovations are gaining progressive interest not only because of the threat of climate change but also due to the technological advancements seen in renewables. Ocean waves have immense potential as a renewable energy source, and related technologies have advanced continuously over the past few decades. In response, this paper extensively studies wave energy converters (WECs) based on the power take-off (PTO) technique, and presents a novel **hybrid** wave-plus-photon energy (HWPE) harvester called Wavevoltaics, based on wave and solar energy capture systems for coastal communities' power needs, in line with decarbonization measures. The HWPE harvester uses a simple rack-and-pinion mechanism in combination with solar cell technology to convert the wave energy into usable electrical energy in a water column structural design. This novel HWPE device can be used to provide power for lighting and gadgets for coastal communities that rely heavily on fossil fuels for their lighting and electrical needs. Later in the paper, the challenges faced in **hybrid** wave energy development are presented.

Increasing sustainability for rice production systems

Nawaz, A; Rehman, AU; Rehman, A; Ahmad, S; Siddique, KHM; Farooq, M, 2022

Rice (*Oryza sativa* L.) is the staple food for millions of people in Asia and the world; however, it is also the largest consumer of freshwater resources worldwide. More than 75% of the world's rice is grown under flooded conditions. However, the long-term sustainability of this flooded system is threatened by the rapid changes in climatic events causing erratic rainfall and abiotic stresses, looming water and energy crisis, low nitrogen use efficiency, increasing micronutrient deficiencies, increasing labor costs and reduced labor availability, increased methane emissions, yield stagnation, and the negative effects of rice crops on post-rice crops. The narrow genetic background in rice has also slowed the pace of breeding rice cultivars tolerant to abiotic and biotic stresses which has resulted in yield stagnation. While direct-seeded rice has become popular in developed countries, saving water and labor resources and reducing methane emissions, developing countries in Asia struggle to disseminate direct seeding technologies due to the lack of government support and policy. Weed management in direct seeded rice is still a major bottle neck in wide scale adoption of this rice system in developing world. Mechanical transplanting of rice is gaining momentum in Asia, reducing labor requirements, ensuring timely transplantation, and saving water during initial growth. Nonetheless, government support and strong policy are needed to boost its uptake by providing subsidies to purchase mechanical transplanters and training farmers to use this technology. With deteriorating soil health due to continuous cultivation of rice with cereals in rotation, overuse of synthetic fertilizers, and increased co-occurrence of abiotic and biotic stresses in rice, there is a need to adopt integrated crop management techniques, and to identify genes of interest and quantitative trait loci (QTL) for their **introgression** into desired plants. These interventions will improve the improve biotic and abiotic stress tolerance in rice. There is also a need for extensive campaign and policy support from the government to force farmers to harvest their rice crops using specific rice harvesters that can save the yield losses that occur when using wheat combine harvesters-a common practice in many developing countries.

Selecting hardwood taxa for wood and fibre production in Queensland's subtropics

Lee, DJ; Huth, JR; Osborne, DO; Hogg, BW, 2010

Optimal matching of species to sites is required for a sustainable hardwood plantation industry in the subtropics. This paper reports the performance and adaptation of 60 taxa (species, provenances and **hybrids**) across two rainfall zones and a range of soil types in southern Queensland. Specifically, performance of taxa is compared across five replicated taxon-site matching trials at age 6 y. Three trials are in a 1000-mm y(-1) rainfall zone of the Wide Bay region near Miriam Vale and two in a drier (about 750 mm y(-1)) rainfall zone near Kingaroy in the South Burnett region. In the higher-rainfall zone, the taxa with the fastest growth in the three trials at age 6 y were *Corymbia citriodora* subsp. *variegata* Woondum provenance, which ranked 1st, 6th and 5th respectively; *E. longirostrata* Coomingleh provenance, ranked 3rd, 2nd and 3rd; and two sources of *E. grandis*, Copperlode provenance (ranked 4th and 1st) and SAPPI seed orchard (ranked 6th and 4th), which were planted in only two of the three trials. Similarly, in the lower-rainfall zone, *E. grandis* and its **hybrids** appear promising from the 6-y growth data., This excellent early growth, however, has not continued in either rainfall zone, with these taxa, 8 y after planting, now showing signs of stress and mortality. Based on trial results in these two rainfall zones, the taxon that appears the most promising for sustainable plantation development with high average annual volume index values and low incidence of borer attack is *Corymbia citriodora* subsp. *variegata* (6.7 m(3) ha(-1)). *Eucalyptus grandis* and *E. longirostrata* both have better average annual volume indexes (8.2 m(3) ha(-1) and 7.4 m(3) ha(-1) respectively) but are very susceptible to borer attack. The current and long-term productivity and sustainability of plantation forestry in these rainfall zones is discussed. Further, the implications of predicted climate change (particularly reduced rainfall) for growing trees for fibre production and carbon sequestration are explored.

Basal cold but not heat tolerance constrains plasticity among Drosophila species (Diptera: Drosophilidae)

Nyamukondiwa, C; Terblanche, JS; Marshall, KE; Sinclair, BJ, 2011

Thermal tolerance and its plasticity are important for understanding ectotherm responses to climate change. However, it is unclear whether plasticity is traded-off at the expense of basal thermal tolerance and whether plasticity is subject to phylogenetic constraints. Here, we investigated associations between basal thermal tolerance and acute plasticity thereof in laboratory-reared adult males of eighteen *Drosophila* species at low and high temperatures. We determined the high and low temperatures where 90% of flies are killed (ULT90 and LLT90, respectively) and also the magnitude of plasticity of acute thermal pretreatments (i.e. rapid cold-and heat-hardening) using a standardized, species-specific approach for the induction of hardening responses. Regression analyses of survival variation were conducted in ordinary and phylogenetically informed approaches. Low-temperature pretreatments significantly improved LLT90 in all species tested except for *D. pseudoobscura*, *D. mojavensis* and *D. borealis*. High-temperature pretreatment only significantly increased ULT90 in *D. melanogaster*, *D. simulans*, *D. pseudoobscura* and *D. persimilis*. LLT90 was negatively correlated with low-temperature plasticity even after phylogeny was accounted for. No correlations were found between ULT90 and LLT90 or between ULT90 and rapid heat-hardening (RHH) in ordinary regression approaches. However, after phylogenetic adjustment, there was a positive correlation between ULT90 and RHH. These results suggest a trade-off between basal low-temperature tolerance and acute low-temperature plasticity, but at high temperatures, increased basal tolerance was accompanied by increased plasticity. Furthermore, high-and low-temperature tolerances and their plasticity are clearly decoupled. These results are of broad significance to understanding how organisms respond to changes in habitat temperature and the degree to which they can

adjust thermal sensitivity.

Eco-efficient alkali-activated cement based on red clay brick wastes suitable for the manufacturing of building materials

Robayo-Salazar, RA; Mejia-Arcila, JM; de Gutierrez, RM, 2017

The objective of this study was to obtain **hybrid**-type binders at room temperature (25 degrees C) from the alkaline activation of a red clay brick waste and the addition of a reduced amount ($\leq 30\%$) of Portland cement. Different types of activators were used, including solids (Na_2SO_4 , Na_2CO_3 , NaOH) and liquids ($\text{Na}_2(2)\text{SiO}(3)\text{xH}(2)\text{O}$). The results highlight the possibility of obtaining an eco-efficient, **hybrid** cement with compressive strengths of up to 102 MPa at 28 days and reductions of up to 73% in the global warming potential (expressed in $\text{kg. CO}_2\text{ eq/MPa}$) associated with a Portland cement paste. Based on the optimum **hybrid** cement, a mortar was developed and used as a base material for the production of block and paver construction elements that comply with construction industry standards. (C) 2017 Elsevier Ltd. All rights reserved.

Effect of humidity and temperature on the performance of three strains of *Aphalara itadori*, a biocontrol agent for Japanese Knotweed

Fung, C; Gonzalez-Moreno, P; Pratt, C; Oliver, TH; Bouchier, RS; Gonzalez-Suarez, M, 2020

Japanese knotweed (*Fallopia japonica*) is a highly damaging invasive species affecting UK infrastructure and biodiversity. Under laboratory conditions, the psyllid *Aphalara itadori* has demonstrated its potential to be a successful biocontrol agent for *F. japonica*. However, this potential has not materialised in the field where long-term establishment of *A. itadori* has been unsuccessful and faces the added challenge of climate change. Intraspecific variation (variation among individuals of a species) has been shown to support establishment in alien species and improve resilience to changing environmental conditions. Here we propose it could improve the performance of biocontrols. To test this possibility we compared the performance and impact on *F. japonica* of three strains of *A. itadori* with different genetic backgrounds, including a newly created **hybrid**. We hypothesize that genetic variability would be increased in **hybrids** resulting in greater biocontrol effectiveness (greater impact on plant growth). We also explored the potential influence of changing climate on performance, testing all strains under two humidity conditions (with the same temperature). Contrary to our expectation, the **hybrid** strain had the worst performance (slowest development rate and lower survival from egg to adult emergence) under both environmental conditions. Exposure to different strains of *A. itadori* did not result in consistent differences in plant growth, suggesting similar biocontrol effectiveness among strains. Under the drier, more stressful, conditions plants exposed to *A. itadori* had fewer leaves and accumulated less above-ground biomass. Overall, our results suggest that genetic variability may not be the key to improve *A. itadori* biocontrol effectiveness, but that predicted climate change, which anticipates drier and hotter summers in the UK, could reduce the growth potential of *F. japonica* when exposed to *A. itadori*.

Using Cellular Automata Approach to Optimize the Hydropower Reservoir Operation of Folsom Dam

Goharian, E; Azizipour, M; Sandoval-Solis, S; Fogg, G, 2021

While hydropower in California is one the main sources of renewable energy, population growth has continuously increased demand for energy. In addition, recent droughts reduced the amount of available water behind the hydropower dams to provide the water head needed to run the turbines in hydropower plants. A more sustainable alternative, instead of developing new infrastructure, is to enhance the daily operation of reservoirs to support hydropower generation. This study suggests a new optimal operation policy for Folsom Reservoir in California and hydropower plants, which maximizes hydropower generation and reduces flood risk. This study demonstrates the application of the cellular automata (CeA) approach to optimize the daily hydropower operation of Folsom Reservoir. The reservoir operation is a nonlinear problem, where the hydropower generation and elevation-area-storage functions are the main nonlinearity to accurately represent the daily operation of the system. Moreover, the performance of the CeA approach under two extreme climate conditions, wet and dry, was evaluated and compared to the operation during normal conditions. Results showed that the CeA approach provides more efficient solutions in comparison to the commonly used evolutionary optimization algorithms. For the size of the non-linear optimization problem designed in this study, CeA outperformed genetic algorithm for finding optimal solutions for different climate conditions. Results of CeA showed that although the annual average inflow to the reservoir during the dry period was about 30% less than the normal condition, CeA offered about a 20% reduction in average hydropower generation. The new operation policy offered by CeA can partly compensate for the loss of the snowpack in California's Sierra Nevada under a warming climate. The approach and its outcomes support an informed decision-making process and provide practical reservoir operational guideline to remediate the adverse effects of hydroclimatic changes in the future.

Drivers of emerging fungal diseases of forest trees

Ghelardini, L; Pepori, AL; Luchi, N; Capretti, P; Santini, A, 2016

In order to prevent emerging infective diseases (EIDs), which increasingly threaten trees of agro-forest and urban ecosystems, a thorough understanding of the factors causing them is necessary. In this paper we reviewed the current knowledge about the changes in the interplay between environment (with its components climate and human activity), pathogens and host plants that drive fungal EIDs of forest trees. We described seven groups of drivers that may be involved individually or together, at once or successively, in the emergence of an infective disease, and we illustrated them by examples. In the past century plant EIDs mostly resulted from the introduction of alien pathogens to new geographic areas as a consequence of international trade (i). However, other factors also played an important role, as for instance climate change (ii), which acts as a strong evolutionary force potentially enhancing the fitness or driving the expansion of the distribution range of pathogens, and/or weakening host plants i.e. predisposing them to infection. Global trade made geographically isolated pathogens spread beyond their natural range and **hybridize** with related species. **Hybridization** (iii) between previously isolated fungal pathogens has driven the emergence of new organisms with different and/or wider host range than the parental species. In some cases EIDs were caused by a hypervirulent strain of a known pathogen or by a completely new species, whose origin is still unclear (iv), which might be due to the development of novel traits or the acquisition of virulence from other species through horizontal gene transfer (HGT). The sudden appearance of unforeseen diseases may be driven by cryptic disease agents, i.e. microorganisms indistinguishable from known species except for unapparent traits involved in pathogenesis, by pathogens with an extended latency period, or by endophytes capable of turning into pathogens after environment changes (v). New associations between introduced insect vectors and native tree pathogens (vi), or vice versa, may result into more efficient transmission and extended host- or geographic range of pathogens. The global use of intensively managed forest plantations (vii) of non-native trees or of a small number of clones of the same species over huge areas has increased the attacks by pathogens, which were accidentally introduced and/or adapted to new hosts. While the idea of totally preventing new EIDs appears unrealistic, it may be possible to reduce their occurrence, and the related damages and costs, by managing the drivers of disease emergence. (C) 2016 Elsevier B.V. All rights reserved.

Evolutionary relationships within European *Monochamus* (Coleoptera: Cerambycidae) highlight the role of altitude in species delineation

Koutroumpa, FA; Rougon, D; Bertheau, C; Lieutier, F; Roux-Morabito, G, 2013

Phylogenetic relationships within the European *Monochamus* (Coleoptera: Cerambycidae) remain understudied despite their increasing importance in the Pine Wood Nematode spread in Europe. To clarify the delimitation and the evolutionary history of the two main European *Monochamus* species, *Monochamus galloprovincialis* and *Monochamus sutor*, as well as their sub-species, a comparative study using morphological, molecular, and biogeographical criterions was conducted. Four

morphological characters, including a newly-described morphological character on the male genitalia, separated the two species. Additionally, molecular data revealed twelve and two single nucleotide polymorphisms in cytochrome oxidase c subunit I and 28S, respectively, supporting species segregation. By contrast, incongruence between morphological and genetic results did not allow discriminating the sub-species of *M. galloprovincialis* and *M. sutor*, even though mitochondrial DNA revealed intraspecific differentiation, mostly consenting to a multiple refugia origin. Within-species variability was explained to a large extent by biogeography (i.e. altitude, climate). These different ecological adaptations within beetle species, together with potential climate change impact, increase the risk of spreading the nematode across Europe to novel conifer hosts and challenge the European biosecurity. (c) 2013 The Linnean Society of London, Biological Journal of the Linnean Society, 2013, 109, 354376.

~~Biological Flora of the British Isles: *Ophrys sphegodes*~~

Jacquemyn, H; Hutchings, MJ, 2015

This account presents information on all aspects of the biology of *Ophrys sphegodes* Mill. that are relevant to understanding its ecological characteristics and behaviour. The main topics are presented within the framework of the Biological Flora of the British Isles: distribution, habitat, communities, responses to biotic factors, responses to environment, structure and physiology, phenology, floral and seed characteristics, herbivores and disease, history and conservation. Native to Britain, *O. sphegodes* used to be more widely distributed throughout south-eastern England, but is now mainly restricted to the counties of Dorset, East Sussex and Kent. It is widespread throughout the western parts of central and southern Europe, and is common in Spain, France and Italy. Further east, it occurs in Bulgaria and Greece, including most of the Mediterranean islands, and extends into southern Russia, Turkey and northern Iran. *Ophrys sphegodes* grows on calcareous, nutrient-poor substrates and rarely under any shade. It is most common in ancient, heavily grazed grassland on chalk and Jurassic limestone, but it also occurs in disturbed habitats, horizontally oriented rock floors in limestone quarries, on old limestone quarry spoil heaps, and in lightly trampled calcareous grasslands on maritime cliffs. *Ophrys sphegodes* multiplies predominantly by sexual reproduction. Vegetative multiplication occasionally occurs through survival or splitting of the old tuber. In the UK, the species is almost exclusively pollinated by males of the solitary bee *Andrena nigroaenea*. Male bees are attracted by complex floral bouquets emitted by the flowers that strongly resemble pheromones produced by female *A. nigroaenea*. Fruit production is generally low, and in most populations, <15% of the flowers produce capsules. *Ophrys sphegodes* is reproductively isolated from other species in the genus by strong pre-mating barriers, most notably temporal (differences in flowering time) and floral (different pollinators) isolation. In particular, differences in floral odour appear to underlie floral isolation. Nonetheless, several **hybrids** involving *O. sphegodes* have been described in Britain and elsewhere in Europe. The range of *O. sphegodes* in Britain declined dramatically in the twentieth century, leading to its extinction in twelve vice-counties. Losses were mainly due to ploughing of grassland and changes in fertilizer and grazing regimes. Its range has increased somewhat in recent years. However, increases in spring temperature due to climate warming may seriously threaten the species in Britain by disrupting the close relationship between *O. sphegodes* flowering time and the phenology of flight of its prime pollinator, leading to reproductive failure.

~~Finding common ground in the debate between carbon tax and cap-and-trade policies~~

Cleetus, R, 2011

Swift and deep reductions in emissions of greenhouse gases, chiefly carbon dioxide, are necessary to help avoid some of the most devastating effects of climate change. One aspect of US climate policy that is particularly contentious is the issue of the best economic tool to employ to reduce emissions: a carbon tax or a cap-and-trade system. This unnecessarily polarized debate has damaged the effectiveness of climate policy supporters in securing climate legislation. The logical way forward is a **hybrid** of the two policies—an approach incorporated in some of the recent climate bills, though it was not properly explained or highlighted. This approach would be a practical starting point when the United States next takes up a climate bill, the author writes.

~~Optimum design of hybrid renewable energy systems: Overview of different approaches~~

Erdinc, O; Uzunoglu, M, 2012

Public awareness of the need to reduce global warming and the significant increase in the prices of conventional energy sources have encouraged many countries to provide new energy policies that promote the renewable energy applications. Such renewable energy sources like wind, solar, hydro based energies, etc. are environment friendly and have potential to be more widely used. Combining these renewable energy sources with back-up units to form a **hybrid** system can provide a more economic, environment friendly and reliable supply of electricity in all load demand conditions compared to single-use of such systems. One of the most important issues in this type of **hybrid** system is to optimally size the **hybrid** system components as sufficient enough to meet all load requirements with possible minimum investment and operating costs. There are many studies about the optimization and sizing of **hybrid** renewable energy systems since the recent popular utilization of renewable energy sources. In this concept, this paper provides a detailed analysis of such optimum sizing approaches in the literature that can make significant contributions to wider renewable energy penetration by enhancing the system applicability in terms of economy. (C) 2011 Elsevier Ltd. All rights reserved.

~~The contribution of Anatolia to European phylogeography: the centre of origin of the meadow grasshopper, *Chorthippus parallelus*~~

Korkmaz, EM; Lunt, DH; Ciplak, B; Degerli, N; Basibuyuk, HH, 2014

Aim *Chorthippus parallelus* is one of the classic model systems for studying genetic structure and phylogeography in the Western Palaearctic. Here, we investigate the regional genetic differentiation of *C. parallelus* and evaluate the historical and evolutionary processes responsible for such genetic structuring, test the nature of the Turkish Straits system as a barrier to dispersal, and explore the contribution of Anatolian populations to the biodiversity of the Western Palaearctic. Location Western Palaearctic. Methods We incorporated sequence data from dense sampling of the phylogeographically important Anatolian region with both previous and newly obtained data of the nuclear fragment cpnI-1 and the mitochondrial fragment COI-tRNA^{Leu}-COII. In total, 1049 sequences of cpnI-1 from 33 regions were analysed to investigate the genetic diversity, genetic structuring and phylogeography of *C. parallelus* across its distributional range. The mtDNA region was additionally used to test whether the Turkish Straits system acts as a barrier. Results The analyses revealed that not all southern refugial populations of *C. parallelus* have contributed equally to the post-glacial recolonization of Europe. Four genetic clusters across the species' range were recovered: cluster A (eastern part of the Anatolian Diagonal); cluster B (western part of the Anatolian Diagonal); cluster C (Spain, Italy, southern Balkans, west part of Anatolia and Russia); and cluster D (covering the entire distributional range of the species). The Turkish Straits system has been a weak barrier to dispersal by *C. parallelus*, allowing gene flow from Anatolia to the Balkans. Main conclusions The current patterns of genetic structuring of *C. parallelus* were best explained by multiple expansion and contraction events. Anatolia has been well connected to the Balkans, contributing genetically to the establishment of central and northern European populations prior to the Holocene. The Anatolian refugium is suggested to be the centre of origin for Western Palaearctic *C. parallelus* diversity rather than a Balkan refugium.

~~Morpho-Physiological and Genomic Evaluation of Juglans Species Reveals Regional Maladaptation to Cold Stress~~

Ebrahimi, A; Lawson, SS; McKenna, JR; Jacobs, DF, 2020

Climate change may have unpredictable effects on the cold hardiness of woody species planted outside of their range of origin. Extreme undulations in temperatures may exacerbate susceptibility to cold stress, thereby interfering with productivity and ecosystem functioning. *Juglans* L. and their naturally occurring interspecific F1

hybrids, are distributed natively across many temperate regions, and *J. regia* has been extensively introduced. Cold hardiness, an environmental and genetic factor yet to be evaluated in many native and introduced *Juglans* species, may be a limiting factor under future climate change and following species introductions. We evaluated cold hardiness of native North American and Eastern Asian *Juglans* along with *J. regia* genotypes using field data from the Midwestern United States (Indiana), controlled freezing tests, and genome sequencing with close assessment of *Juglans* cold hardy genes. Many *Juglans* species previously screened for cold-hardiness were genotypes derived from the Midwest, California, and Europe. In 2014, despite general climate adaptation, Midwestern winter temperatures of -30 degrees C killed *J. regia* originating from California; however, naturalized Midwestern *J. regia* survived and displayed low damage. **Hybridization** of *J. regia* with black walnut (*J. nigra*) and butternut (*J. cinerea*) produced F1s displaying greater cold tolerance than pure *J. regia*. Cold hardiness and growth are variable in Midwestern *J. regia* compared to native *Juglans*, East Asian *Juglans*, and F1 **hybrids**. Phylogeny analyses revealed that *J. cinerea* sorted with East Asian species using the nuclear genome but with North American species using the organellar genome. Investigation of selected cold hardy genes revealed that *J. regia* was distinct from other species and exhibited less genetic diversity than native *Juglans* species. Average whole genome heterozygosity and Tajima's D for cold hardy genes was low within *J. regia* samples and significantly higher for **hybrid** as well as *J. nigra*. We confirmed that molecular and morpho-physiological data were highly correlated and thus can be used effectively to characterize cold hardiness in *Juglans* species. We conclude that the genetic diversity within local *J. regia* populations is low and additional germplasm is needed for development of more regionally adapted *J. regia* varieties.

Climatic effects on population declines of a rare wetland species and the role of spatial and temporal isolation as barriers to hybridization

Rohde, K; Hau, Y; Kranz, N; Weinberger, J; Elle, O; Hochkirch, A, 2017

Climate change and climatic extremes may affect species directly or indirectly. While direct climatic effects have been intensively studied, indirect effects, such as increasing **hybridization** risk, are poorly understood. The goal of our study was to analyse the impact of climate on population dynamics of a rare habitat specialist, *Chorthippus montanus*, as well as the fine-scale spatial overlap with a sympatric habitat generalist, *Chorthippus parallelus* and the dispersion of **hybrids**. We were particularly interested in the role of spatiotemporal overlap on heterospecific encounter frequencies. We conducted high-precision mark-recapture studies on two sites over 7 years and genotyped 702 individuals of two *C. montanus* generations to detect **hybrids**. We tested the performance of three programs (structure, new**hybrids** and adegenet) and accepted only **hybrids** detected by the two best performing programs. We then tested for correlations between yearly population trends and climatic variables. Furthermore, we analysed the spatial dispersion of both taxa and the **hybrids** to calculate variation in spatial and temporal overlap and infer heterospecific encounter probabilities. Our results revealed that droughts during the egg phase and rainy weather during nymphal development were strongly correlated with population declines in the habitat specialist. The highest **hybridization** rate (196%) was found in the population with lowest population size. The combined effects of spatial and temporal niche overlap decreased heterospecific encounter probabilities to 42-76% compared to 20-28% and 11-19% calculated alone from phenology or spatial overlap respectively. **Hybrids** were detected in areas of higher heterospecific encounter probability, mainly at the edge of the specialists' occupied habitat in areas with intermediate soil moisture conditions compared to the parental species. This illustrates that the combination of spatial and temporal segregation provides an effective barrier to **hybridization**. However, the high **hybridization** rate in one of the populations suggests that this function may decrease with decreasing population size. This supports the hypothesis that climatic extremes threaten rare species directly by reducing reproductive success and may indirectly increase **hybridization** risk. A is available for this article.

Somatic hybrids of *Sinapis alba* plus *Brassica juncea*: study of backcross progenies for morphological variations, chromosome constitution and reaction to *Alternaria brassicae*

Kumari, P; Singh, KP; Bisht, D; Kumar, S, 2020

The wild relatives of crops represent a rich reservoir of genes for introducing resilience to climate change into cultivated crops. To introgress genes from *Sinapis alba*, a wild relative of Brassicaceae, into *Brassica juncea*, a cultivated member of this family, we initially produced somatic **hybrids** between the two species and then produced a large number of backcross populations involving the two somatic **hybrids** (H1 and H2) with *Brassica juncea*. BC1 progeny were morphologically very similar. However, when they were challenged inoculated with a highly virulent *Alternaria brassicae* (ITCC No. 2542) culture under in vivo and in vitro conditions in two growing seasons, they showed wide variations in their disease reaction. Of the 40 BC1 lines tested in one season, 36 showed a resistant reaction. BC1F2 progenies derived from these resistant BC1 plants also showed resistance to *Alternaria brassicae*, indicating stable inheritance of the resistant phenotype. However, BC1F2 progenies showed a wide variation in morphological traits, including plant height, basal branching, leaf thickness, trichome density on leaves and stem. BC1 plants were examined by genomic in-situ **hybridization** (GISH) to determine their chromosome constitution. All five plants were found to possess 12 strong **hybridization** signals upon **hybridization** with a FITC-labeled *S. alba*-specific probe. GISH studies on BC1F2 plants indicated localized signals in addition to 12 full chromosome **hybridization** signals, suggesting alien **introgressions** into *B. juncea* that requires further validation. The BC2 generation was found to possess half of the haploid set of alien chromosomes. The BC1F2 and BC2 generations were further screened against *A. Brassicaceae* and found to be resistant/tolerant.

Quantification of the Environmental Benefits of Ultrafine/Nanotitanium Dioxide Photocatalyst Coatings for Concrete Pavement Using Hybrid Life Cycle Assessment

Hassan, MM, 2010

The use of titanium dioxide (TiO2) ultrafine particulates as coating for concrete pavement have received considerable attention in recent years as these coatings can trap and absorb organic and inorganic air pollutants by a photocatalytic process. Despite these promising benefits, the promotion of TiO2 coatings based on a single factor such as air quality does not provide a complete evaluation of this technology and may omit critical environmental factors that should be considered in the selection of sustainable materials. The objective of this study was to determine the life-cycle assessment of TiO2 coating technology based on a **hybrid** life-cycle methodology. To achieve this objective, a life-cycle inventory that quantifies the energy, abiotic raw material inputs, and emission of TiO2 coatings from cradle to grave were developed. Based on this inventory, life-cycle impact assessment of TiO2 coatings for concrete pavement was conducted using the BEES impact assessment model. The use of titanium dioxide coating reduces the concentration of harmful pollutants by a photocatalytic process, and therefore, reduces the environmental impacts in four main categories: acidification, eutrophication, criteria air pollutants, and smog formation. However, during the production phases and due to the consumption of fossil energy, titanium dioxide will cause an increase in global warming, fossil fuel depletion, water intake, ozone depletion, and impacts on human health. Based on the overall environmental performance of this product, life-cycle assessment shows that titanium dioxide coating has an overall beneficial effect on the environment.

Evaluation of climate-related carbon turnover processes in global vegetation models for boreal and temperate forests

Turner, M; Beer, C; Ciais, P; Friend, AD; Ito, A; Kleidon, A; Lomas, MR; Shaun, QG; Rademacher, TT; Schaphoff, S; Tum, M; Wiltshire, A; Carvalhais, N, 2017

Turnover concepts in state-of-the-art global vegetation models (GVMs) account for various processes, but are often highly simplified and may not include an adequate representation of the dominant processes that shape vegetation carbon turnover rates in real forest ecosystems at a large spatial scale. Here, we evaluate vegetation carbon turnover processes in GVMs participating in the Inter-Sectoral Impact Model Intercomparison Project (ISI-MIP, including HYBRID4, JeDi, JULES, LPJmI, ORCHIDEE, SDGVM, and VISIT) using estimates of vegetation carbon turnover rate (*k*) derived from a combination of remote sensing based products of biomass and net primary production (NPP). We find that current model limitations lead to considerable biases in the simulated biomass and in *k* (severe underestimations by all models except JeDi and VISIT compared to observation-based average *k*), likely contributing to underestimation of positive feedbacks of the northern forest carbon balance to climate change caused by changes in forest mortality. A need for improved turnover concepts related to frost damage, drought, and insect outbreaks to better reproduce observation-based spatial patterns in *k* is identified. As direct frost damage effects on mortality are usually not accounted for in these GVMs,

simulated relationships between k and winter length in boreal forests are not consistent between different regions and strongly biased compared to the observation-based relationships. Some models show a response of k to drought in temperate forests as a result of impacts of water availability on NPP, growth efficiency or carbon balance dependent mortality as well as soil or litter moisture effects on leaf turnover or fire. However, further direct drought effects such as carbon starvation (only in HYBRID4) or hydraulic failure are usually not taken into account by the investigated GVMs. While they are considered dominant large-scale mortality agents, mortality mechanisms related to insects and pathogens are not explicitly treated in these models.

~~Climatic changes and potatoes: How can we cope with the abiotic stresses?~~

Handayani, T; Gilani, SA; Watanabe, KN, 2019

Climate change triggers increases in temperature, drought, and/or salinity that threaten potato production, because they necessitate specific amounts and quality of water, meanwhile lower temperatures generally support stable crop yields. Various cultivation techniques have been developed to reduce the negative effects of drought, heat and/or salinity stresses on potato. Developing innovative varieties with relevant tolerance to abiotic stress is absolutely necessary to guarantee competitive production under sub-optimal environments. Commercial varieties are sensitive to abiotic stresses, and substantial changes to their higher tolerance levels are not easily achieved because their genetic base is narrow. Nonetheless, there are several other possibilities for genetic enhancement using landraces and wild relatives. The complexity of polysomic genetics and heterozygosity in potato hamper the phenotype evaluation over abiotic stresses and consequent conventional **introgression** of tolerance traits, which are more challenging than previous successes shown over diseases and insects resistances. Today, potatoes face more challenges with severe abiotic stresses. Potato wild relatives can be explored further using innovative genomic, transcriptomic, proteomic, and metabolomic approaches. At the field level, appropriate cultivation techniques must be applied along with precision farming technology and tolerant varieties developed from various breeding techniques, in order to realize high yield under multiple stresses.

~~Experimental evidence for heritable reproductive time in 2 allochronic populations of pine processionary moth~~

Branco, M; Paiva, MR; Santos, HM; Burban, C; Kerdelhue, C, 2017

Phenology allows organisms to overcome seasonally variable conditions through life-cycle adjustment. Changes in phenology can drastically modify the evolutionary trajectory of a population, while a shift in the reproductive time may cause allochronic differentiation. The hypothesis of heritable reproductive time was experimentally tested, by studying a unique population of the pine processionary moth *Thaumetopoea pityocampa* (Den. & Schiff.) which has a shifted phenology, and however co-occurs with the typical population following the classical life cycle. When populations of both types were reared under controlled conditions, the reproductive time was maintained asynchronous, as observed in the field. The shifted population was manipulated in the laboratory to reproduce later than usual, yet the offspring emerged in the next year at the expected dates thus coming back to the usual cycle. **Hybrids** from crosses performed between the 2 populations showed an intermediate phenology. From the emergence times of parents and offspring, a high heritability of the reproductive time ($h = 0.76$) was observed. The offspring obtained from each type of cross was genetically characterized using microsatellite markers. Bayesian clustering analysis confirmed that **hybrids** can be successfully identified and separated from the parental genetic classes by genotyping. Findings support the hypothesis that, for this particular population, incipient allochronic speciation is due to a heritable shift in the reproductive time that further causes assortative mating and might eventually cause ecological adaptation/maladaptation in response to environmental changes.

~~Assessment of thermal and energy performance of thermally efficient sustainable wall system for Malaysian low cost housing~~

Raut, AN; Gomez, CP, 2018

Thermal performance of building envelope has been of great Importance in determining the indoor thermal environment mainly due to the impact of existing global warming issues. Thus there is a need to provide wall system with better thermal performance than conventional wall systems. The focus of the research is to tackle the twin issues of sustainability and thermal performance of building wall systems for low-cost housing. Fiber reinforced mortar (FRM), and thermally enhanced sustainable **hybrid** (TESH) bricks were developed by optimizing the mix design using Glass Powder, Palm Oil Fly Ash, and Oil Palm Fibers. Both the FRM and TESH bricks, which constitute the TESH wall system, were analyzed for physical, mechanical and thermal performance and they comply with the various codes of practice for building materials. Heat transfer simulation was performed to determine the thermal performance of the newly developed TESH. The temperature distribution and rate of heat transfer through the wall system was found to be significantly lower than conventional wall systems. Also, the energy consumption analysis suggested 10.6% energy reduction for TESH wall system over conventional wall system. The total energy costing for the building was also reduced by 10.2% for TESH wall system.

~~Established and new technologies reduce increasing pest and pathogen threats to Eucalypt plantations~~

Wingfield, MJ; Roux, J; Slippers, B; Hurley, BP; Garnas, J; Myburg, AA; Wingfield, BD, 2013

Plantation forestry based on *Eucalyptus* spp. has grown dramatically during the past 100 years, mainly in the tropics and southern hemisphere where these trees are non-native. Early plantations were affected by pests and pathogens, although damage was generally minimal. This is a situation that is changing dramatically with serious pest and pathogen problems now emerging regularly and often times causing very serious damage. Given the growing movement of people and products around the world, this is a trend that is certain to continue and the threat of diseases and insect damage is now seen as one of the most important constraints to the future sustainability of Eucalypt plantation forestry globally. While this is a very troubling situation, there are also reasons to be optimistic. Established technologies such as breeding and selection of disease and insect resistant species and **hybrids**; enhanced through vegetative propagation have already shown substantial promise to reduce damage. Likewise, biological control is being effectively used to reduce damage due to invasive alien insect pests. New technologies including DNA-based tools for identification, detection and monitoring of pest and pathogens are increasingly valuable. Similarly, the growing availability of genome sequences for Eucalypts and for their pests and pathogens will increasingly add to our capacity to reduce damage. While there are unknown dangers such as the impact of climate change on the damage caused by pests and pathogens, we believe that continual and realistic investment in technology will ensure long term sustainability of Eucalypt plantation forestry. Failure to invest wisely will result in the collapse of plantation enterprises and concomitant loss in investments. (c) 2012 Elsevier B.V. All rights reserved.

~~Overview of Risk Factors and Strategies for Management of Insect-Derived Ear Injury and Aflatoxin Accumulation for Maize Grown in Subtropical Areas of North America~~

Pruter, LS; Weaver, M; Brewer, MJ, 2020

Pest and disease risk factors causing maize yield and kernel quality issues in subtropical areas of North America (between 35 degrees N and 23.5 degrees N latitude) are reviewed: preharvest *Aspergillus flavus* (Link) (Deuteromycetes: Moniliales) infection and propagation in maize ears and ear injury principally caused by *Helicoverpa zea* (Boddie) and *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae). Risk is affected by potentially interacting factors of maize genetics, ear feeding with insects, fungal inoculum and growth, and weather (rainfall, temperature, and humidity). This review gives special attention to integration of the most

efficient pest and disease management strategy combinations and the potential interaction of insect ear feeding and *A. flavus* occurrence. Management strategies reviewed include maximizing partial genetic resistance to *A. flavus* and selection of appropriate **hybrids** for the area, biological control of *A. flavus* using non-aflatoxigenic strains, avoiding pests and diseases using cultural practices like early planting, and reducing *H. zea* and *S. frugiperda* ear injury using Bt transgenes. Understanding the combined influences and identifying combined management approaches may lead to reduced aflatoxin risk and maintaining yield. This review focuses on subtropical areas of North America because the amount of maize produced in warm environments within or similar to subtropical maize production areas is likely to increase due to projected increases in demand for maize and predicted increases in temperature may increase pest and disease risk.

A review on plant diversity and forest management of European beech forests

Schulze, ED; Aas, G; Grimm, GW; Gossner, MM; Walentowski, H; Ammer, C; Kuhn, I; Bouriaud, O; von Gadow, K, 2016

The impact of historical and present drivers on forest biodiversity is poorly understood. A better understanding is mandatory to ensure conservation and appropriate management of biodiversity and ecosystem functions in the face of climate warming and increasing demand for wood products. Here, we assess forest management strategies for maintaining plant biodiversity in Central European beech forests, with a focus on Germany. We show that (1) diversity of the German vascular plant flora increased exponentially during the Holocene reaching 3874 species mainly through apomictic and **hybrid** speciation. Vascular plant species confined to forests comprise about 10 % of this flora. No loss in vascular plants restricted to forests occurred over the past 250 years despite of forest management; (2) the indigenous arboreal flora has a low diversity (64 tree species) compared with other continents due to environmental changes in the last 2 million years; (3) forest management has maintained a high plant diversity in the past. It should be an aim of silviculture to ensure this in the future; and (4) only 22 of the indigenous tree species are commercially used; nine of these commercially used species are threatened by diseases. We introduce the concept of palaeo-neophytes to address genera that existed in Central Europe during the latest Cenozoic. The introduction of species of palaeo-neophytic genera and sub Mediterranean species is discussed as a measure to buffer negative effects on native species caused by climate change and spread of novel diseases.

Inuit Modern Sculpture from the Arctic

McMaster, G, 2011

In response to new thinking about the North, Inuit Modern situates its major themes within the context of a rapidly changing Arctic. It considers how Inuit have dealt with the swift transition from a traditional lifestyle to the current disturbing complexities of globalization and climate change. It describes how Inuit art reflects the reciprocal stimulus of contact with Euro-Canadians and concurrently analyzes the birth and evolution of a modernist Inuit aesthetic that springs from an ancient cultural context and, through acculturation, creates an exciting new **hybridized** art form.

Revising the EU ETS and CORSIA in times of the COVID-19 pandemic: challenges for reducing global aviation emissions

Mai, DTT, 2021

Since fast-growing emissions from the aviation sector have become a major contributor to climate change, global efforts have been undertaken to reduce them effectively. The European Union Emissions Trading System (EU ETS) and the Carbon Offsetting and Reduction Scheme for International Aviation (CORSIA) are two existing market-based measures (MBMs) for addressing aviation emissions, whose implementation has been affected by the Coronavirus 2019 (COVID-19) pandemic. This article aims to examine challenges that the pandemic has posed on both systems by assessing the policy options for revising the EU ETS provisions on aviation, as well as the political debates regarding amendment to the CORSIA design in June 2020. Key policy insights From the environmental, economic and international perspectives, none of the six policy options proposed in the Inception Impact Assessment regarding future implementation of CORSIA alongside the EU ETS is optimal to achieving the EU's multiple goals in revising its ETS. This article recommends the adoption of a **hybrid** option, which would help maintain international intra-EU/European Free Trade Association (EFTA) flights under the EU ETS scope to achieve EU climate targets and at the same time still integrate some features of CORSIA's design in implementation. Concerning the reduction of free allowances for aviation, the swift phase-out option should be considered in conjunction with plans to develop sustainable aviation fuels (SAFs). While long-term effects of the pandemic on the effectiveness of CORSIA remain to be seen, its immediate impacts can be noticed in the weakening of this scheme's credibility and stability in implementation.

Promoting low-carbon city through industrial symbiosis: A case in China by applying HPIMO model

Dong, L; Fujita, T; Zhang, H; Dai, M; Fujii, M; Ohnishi, S; Geng, Y; Liu, Z, 2013

China launched low-carbon city strategy to respond global climate change. Industrial symbiosis (IS) could generate both economic and environmental benefits in clustered industries and communities. This research shed light on how industrial symbiosis contributes to city's low-carbon development. An urban-level **hybrid** physical input and monetary output (HPIMO) model which covers physical energy inputs and air pollutants emissions, is established for addressing case study in a Chinese typical industrial city (Liuzhou). Based on current energy consumption and industrial symbiosis and the application of HPIMO model, scenarios related to industrial symbiosis, including waste plastics recycling, scrap tires recycling, flying ash recycling and biomass utilization are explored. Results show that compared with business-as-usual (BAU) scenario, IS can reduce solid wastes and further contribute to the co-benefits of energy saving, CO₂ emissions reduction and air pollutants reduction. The finding is critical for national low-carbon strategy. Finally, policy implications to support the ever-improvement of IS promotion in China are proposed and discussed. (C) 2013 Elsevier Ltd. All rights reserved.

Biomass Yield and Economic, Energy and Carbon Balances of *Ulmus pumila* L., *Robinia pseudoacacia* L. and *Populus x euroamericana* (Dode) Guinier Short-Rotation Coppices on Degraded Lands under Mediterranean Climate

Alesso, SP; Tapias, R; Alaejos, J; Fernandez, M, 2021

The steadily increasing demand for energy and concerns about climate change have prompted countries to promote the use of renewable energy sources, including lignocellulosic biomass. In this context, this work aims to assess the biomass production for energy purposes in crops with short rotation, as well as its effect on soil properties. Deciduous tree species were used, mainly Siberian elm (*Ulmus pumila* L.), black locust (*Robinia pseudoacacia* L.) and a **hybrid** poplar clone (*Populus x euroamericana* (Dode) Guinier, clone 'AF2'). Four field trials were implemented, under two different types of Mediterranean climate, where highly productive taxa were tested, in addition to the mixed planting of a nitrogen-fixing species with a non-fixing one. Short-rotation coppices (SRCs) of these taxa yield about 12-14 t ha⁻¹ year⁻¹ of high-quality dry woody biomass, when fertilizers and irrigation water are supplied; generate 205-237 GJ ha⁻¹ year⁻¹ net and earnings of about EUR 1.5 per EUR 1 invested; and sequester into the soil 0.36-0.83 t ha⁻¹ year⁻¹ of C and 57 kg ha⁻¹ year⁻¹ of N. Therefore, these species raised as SRCs could improve degraded soils if the crop is properly managed, resulting in favorable economic, energy and CO₂ emission balances. The use of mixed plantations can bring economic and environmental gains, and the biomass transformation into high-quality chips or pellets gives it added value.

Predicting spatio-temporal *Culicoides imicola* distributions in Spain based on environmental habitat characteristics and species dispersal

Peters, J; Waegeman, W; Van Doninck, J; Ducheyne, E; Calvete, C; Lucientes, J; Verhoest, NEC; De Baets, B, 2014

The use of distance variables expressing the likelihood of species occurrence at a given site in relation to the distance to observed species presence is demonstrated to improve species distribution models, especially when combined with environmental variables which relate species occurrence to the environmental habitat characteristics. In this study we developed models to predict the spatio-temporal distribution of *Culicoides imicola*, which is the main transmission vector for the bluetongue virus in the Mediterranean region. We investigated (i) the importance of the environmental habitat characterization by means of bioclimatic variables, (ii) the effect of different distance variables to model the dispersal process, and (iii) the suitability of two different parameter identification procedures to determine the distance variables for species distribution modeling. Results showed that niche-based species distribution models, which only use environmental data, could estimate the occurrence of *Culicoides imicola* accurately, given that environmental data of the period of high species abundance (April until October) was included. The use of these models may therefore be hampered for predictive risk assessment aiming to estimate the probabilities and magnitude of undesired effects caused by the occurrence of *C. imicola*. Species distribution models accounting for species dispersal in addition to the environmental habitat characteristics, i.e. **hybrid** models, did provide accurate predictions of *C. imicola* distributions well before the onset of the season of high species abundance. A Gaussian or negative exponential function of the distance to presence locations was most suitable to model insect dispersal. The enhanced predictive capacity of these models potentially leads towards an increased model applicability in risk assessment and disease control. (C) 2014 Elsevier B.V. All rights reserved.

Fitness and maternal effects in hybrids formed between transgenic oilseed rape (*Brassica napus* L.) and wild brown mustard [*B. juncea* (L.) Czern et Coss.] in the field

Di, K; Stewart, CN; Wei, W; Shen, BC; Tang, ZX; Ma, KP, 2009

BACKGROUND: Gene flow between crops and weedy relatives depends on the survivorship and reproduction of early-generation **hybrids** in a field environment. The primary aim of this study was to compare the fitness of transgenic crop x wild **hybrids** with their parental types and a non-transgenic crop type in the field under enhanced temperature and humidity. RESULTS: Transgenic insect-resistant oilseed rape (*Brassica napus* L.), wild brown mustard [*B. juncea* (L.) Czern et Coss.], their **hybrids** and non-transgenic *B. napus* were grown in such a way as to mimic field conditions after harvest under which volunteer plants might appear in agricultural settings. Factor analysis revealed that vegetative growth characteristics explained most of the observed differences among plant types. Wild brown mustard had the highest fitness during its entire life history. **Hybrids** had intermediate composite fitness and lowest reproductive fitness. The **hybrid** and the wild weed shared similar vegetative growth characteristics and seed dormancy in their respective progenies. CONCLUSION: These data indicate that there might be enhanced persistence of the transgene in warmer climates. The absence of fitness cost of the transgenes might allow transgenes to persist in ecosystems. These data will contribute to risk assessments of transgene persistence and weed management against the backdrop of global climate change. (C) 2009 Society of Chemical Industry

Source or Sink? A comparison of Landfire- and FIA-based estimates of change in aboveground live tree carbon in California's forests

Holland, TG; Stewart, W; Potts, MD,

Forests play a central role in addressing climate change, and accurate estimates of forest carbon are critical for the development of actions that reduce emissions from forests and that maximize sequestration by forests. Methodological challenges persist regarding how best to estimate forest carbon stocks and flux at regulatory-relevant scales. Using California, USA as a case study, we compare two approaches to stock-difference forest carbon estimation for aboveground live trees: one based on ground inventories and one on land cover classification of remotely-sensed data. Previous work using ground inventory data from the Forest Inventory and Analysis Program (FIA) showed net aboveground carbon (AGC) sequestration by live trees in California forests, while estimates using land cover classification from the Landscape Fire and Resource Management Planning Tools (Landfire) showed net reductions in live tree AGC over a similar time period. We examined the discrepancy by re-analyzing the FIA inventory data through the lens of a category-change analysis based on Landfire. This analysis showed more than 50% of the live tree AGC in fewer than 4% of Landfire-equivalent categories and that the overwhelming majority (>80%) of forest area did not change height category between measurement periods. Despite the lack of categorical change, the majority of FIA plots increased in both 95th percentile tree height and in live tree AGC. These findings suggest that an approach based on observing categorical changes risks undercounting AGC sequestration resulting from growth and thus overstating the relative importance of AGC reductions that result from disturbances. This would bias AGC flux estimates downward, leading us to validate the conclusion that live trees in California were a net sink of aboveground carbon in the decade ending in 2016. Our findings suggest an inventory-based or **hybrid** approach is preferable to methods that depend on categorical bins for estimating AGC in disturbance-prone forest ecosystems.

A computational intelligence based maximum power point tracking for photovoltaic power generation system with small-signal analysis

Senapati, MK; Pradhan, C; Calay, RK,

There are multiple peak functions in its output power characteristic curve of a photovoltaic (PV) array under partial shading conditions (PSCs), the perturb and observe (P&O) may fail to track the global maximum power point (GMPP). Therefore, a reliable maximum power point tracking (MPPT) technique is essential to track the GMPP within an appropriate time. This article proposes a **hybrid** technique by combining an evolutionary optimization technique, namely the modified invasive weed optimization (MIWO) with the conventional P&O algorithm to enhance the search performance for the maximum power output of the PV system. MIWO executes in the initial stages of the tracking followed by the P&O at the final stages in the MPPT search process. The combined approach ensures faster convergence and better search to the GMPP under rapid climate change and PSCs. The search performance of the **hybrid** MIWO+P&O technique is examined on a standalone PV system through both MATLAB/Simulink environment and experimentally using dSPACE (DS1103)-based real-time microcontroller hardware setup. The performance of the proposed **hybrid** MPPT scheme is compared with the recent state-of-the-art MPPPT techniques. In addition, the small-signal analysis of the PV system is carried out to evaluate the loop robustness of the controller design. For a given set of system parameters, simulations for the small-signal model and robustness studies are analyzed to verify the results. The overall results justify the efficacy of the proposed **hybrid** MPPT algorithm.

Integrating production scheduling, maintenance planning and energy controlling for the sustainable manufacturing systems under TOU tariff

Cui, WW; Sun, HL; Xia, BX, 2020

Climate change pushes the operation managers to take account of energy-saving issues in their decision-making of production scheduling and maintenance planning (PSMP). We address a PSMP problem for a single machine system under Time-of-Use electricity tariff. We consider two objectives including the makespan that measures the service level and the total energy cost that measures the energy sustainability. Both objectives are considered in a bi-objective mathematical model that is further solved using a novel heuristic algorithm consisting of two layers based on the problem decomposition. The inner layer problem, which is solved by a branch & bound algorithm, is to optimise the decision variables of preventive maintenance and machine's setup. The outer layer problem, which is solved by a **hybrid** NSGA-II algorithm, is to optimise the sequence of jobs and the amount of inserted buffer time. The effectiveness and efficiency of the algorithm are demonstrated by a series of numerical experiments. The Pareto frontier can serve as a tool for managers to consider energy cost explicitly in making decisions. It is observed in some scenarios that reducing energy cost will not increase the makespan.

Species-specific macroinvertebrate responses to climate and land use scenarios in a Mediterranean catchment revealed by an integrated modelling approach

Sultana, J; Recknagel, F; Nguyen, HH, 2020

Climate and land use changes are altering flow and nutrient regimes in catchments that affect stream habitats and aquatic biodiversity. This study applied an integrated modelling approach to quantify the impacts of climate and land use scenarios on the macroinvertebrate community in Sixth Creek catchment, South Australia. Gradient forest (GF) determined flow as most important driver affecting macroinvertebrate assemblages, and identified most flow-sensitive species based on highest cumulative importance along flow gradients. A catchment model developed using the Soil and Water Assessment Tool (SWAT) simulated flow under the following scenarios: (1) deforestation, (2) reforestation, (3) climate change, and (4) a 10% increased urbanisation as projected by local authorities over the next 30 years. The urbanisation scenario predicted a 2% increase of average flow compared to 17% flow increase predicted by the deforestation scenario. In contrast, diminished monthly flow was suggested by both the climate change scenarios due to declining precipitation and higher temperatures, and the reforestation scenario most likely due to declining surface run-off. In reforestation and climate change scenarios, SWAT results predicted the highest decline in flow during late autumn and late spring, which may shift this unusual permanent flowing stream towards intermittency. The **Hybrid** Evolutionary Algorithm (HEA) was used to develop flow-driven models for population dynamics of taxa identified by GF as flow sensitive i.e. Hydrobiidae spp., Austrocerca tasmanica, Offadens spp., Cloeon spp., Micronecta spp. and Tasmanocoenis tillyardi based on 14 years of data monitored at a representative stream site of Sixth Creek. The HEA models achieved coefficients of determination $r(2)$ between 0.85 and 0.97 for predicted vs. observed abundances. While the abundance of Cloeon spp. diminished in all scenarios, it was most affected by low flow predictions of the climate change scenario. Hydrobiidae spp. appeared most tolerant to altered flow conditions by reaching highest abundances at high flow conditions caused by deforestation and urbanisation. Overall, this study highlighted the non-linear response of species within the commonly used Ephemeroptera, Plecoptera and Trichoptera (EPT) grouping and a need to redirect focus of such studies from community to species level. The integrated modelling approach based on GF, SWAT and HEA proved to be suitable for simulating complex species-specific macroinvertebrate responses to relevant climate and land use scenarios. Learning more about these interrelationships is a prerequisite for sustainable catchment management.

Registration of Tepary Germplasm with Multiple-Stress Tolerance, TARS-Tep 22 and TARS-Tep 32

Porch, TG; Beaver, JS; Brick, MA, 2013

High ambient temperature and drought stress as a result of climate change are increasingly critical factors affecting agriculture, specifically grain legume production. Tepary bean (*Phaseolus acutifolius* A. Gray), a drought- and heat-tolerant species closely related to common bean (*P. vulgaris* L.), has long been employed by Native Americans for production in regions prone to abiotic stress. In addition to abiotic stress, common bacterial blight [caused by *Xanthomonas axonopodis* pv. *phaseoli* (Smith) Dye] and seed weevils [*Acanthoscelides obtectus* (Say)] are widespread yield and storage constraints worldwide, respectively. TARS-Tep 22 (Reg. No. GP-288, PI 666350) and TARS-Tep 32 (Reg. No. GP-289, PI 666351) were developed by the USDA-ARS, the University of Puerto Rico Agricultural Experiment Station, and Colorado State University. The tepary bean germplasms were selected for multiple stress tolerances, including high-temperature and drought stresses and resistance to bacterial blight and seed weevils, and for larger seed size and more erect architecture. TARS-Tep 22 represents the first published release of improved tepary as a result of **hybridization** and selection, and TARS-Tep 32 is a single plant selection from a landrace (PI 477033) from Arizona. The use of this improved germplasm by farmers in production zones affected by abiotic and/or biotic stress or by breeding programs can potentially increase yields of this newly rediscovered crop.

Greenhouse gas emissions from ratoon rice fields among different varieties

Song, KF; Zhang, GB; Ma, J; Peng, SB; Lv, SH; Xu, H, 2022

Ratoon rice (RR) is a practice originating from the stubble left after the previous main rice crop (MR) harvested. Planting RR is of great significance to increase grain production and ensure food security. However, few reports are available on the response of RR varieties to greenhouse gas emissions. A field experiment was conducted to comprehensively estimate the CH₄ and N₂O emissions among RR varieties in Southwest China. Five varieties were adopted in the experiment: Hanyou 73 (HY), Taiyou 390 (TY), Jingliangyouhuazhan (JLY), Yuxiang 203 (YX), and Fengliangyouxiangyihao (FLY). The CH₄ and N₂O emissions from the RR seasons accounted for 23–24% and 10–27% of total emissions from the MR+RR seasons, respectively. The significant reduction in CH₄ emissions during the RR seasons was caused by low temperature, short growth period, and low aboveground biomass. Considering both CH₄ and N₂O emissions, the global warming potential of JLY was as high as 10.95 t CO₂-eq ha⁻¹ in the MR+RR seasons, but the total yields were significantly higher than those of other varieties by 8–16%, and thereby the greenhouse gas intensity (GHGI) of JLY was the lowest at 1.10 t CO₂-eq t⁻¹ yield. The findings demonstrate that JLY is a suitable ratoon rice variety with the highest yield and lowest GHGI. Furthermore, it is possible to reduce greenhouse gas emissions through the innovation of high-yielding rice varieties to adapt to future climate changes and ensure food security.

Modelling tree mortality by bark beetle infestation in Norway spruce forests

Seidl, R; Baier, P; Rammer, W; Schopf, A; Lexer, MJ, 2007

Disturbances play a major role in forest ecosystems, they are main constituents of forest dynamics and are often a relevant driver in forest management decisions. The European Spruce Bark Beetle (*Ips typographus* L. Col. Scol.) is one of the major biotic disturbances in Norway spruce (*Picea abies* (L.) Karst.) forests. In this contribution a sub-model of disturbances by *I. typographus* was developed and integrated in the existing **hybrid** forest patch model PICUS v1.4. The new disturbance sub-model builds on a recently developed phenology model for risk assessment of outbreaks of *I. typographus* (PHENIPS) and elements from an existing predisposition assessment system (PAS). Model parameterisation was based on data from 28 Nor-way spruce stands in Austria. In a preliminary model evaluation a comprehensive sensitivity analysis at sites along an elevation gradient in the Eastern Alps is presented. Sensitivity over the elevation gradient was found to be highest and strongly nonlinear with regard to the thermal environment. Furthermore, in accordance with general expectations and observations simulated damages were high under colline and submontane conditions and strongly decreased over the elevation transect. Based on the results of the simulation experiments it is concluded that the presented model is a promising tool to analyse the dynamic interaction of disturbances by *I. typographus*, environmental conditions and forest structure as affected by natural forest development and management interventions. Limitations of the model and possible approaches for extensive validation against empirical damage data are discussed. (c) 2007 Elsevier B.V. All rights reserved.

"Cradle-to-Gate" assessment of material-related embodied carbon: A design-stage stratagem for mid-rise housing in Sri Lanka

Jayawardana, AS; Perera, NGR; Perera, LASR, 2021

Achieving low carbon buildings is seen as a key concept in order to reduce carbon emission and mitigate climate change. In contrast to operational emission, material related embodied carbon (EC) in the built environment plays a pivotal role, with the continuous consumption of high carbon emitting materials. This research relates to the 'Cradle-to-Gate' system boundary, while limiting its focus on building design stage decisions. A **hybrid** analysis approach was adopted a bottom-up process with steps encompassing mass analysis, EC calculation, highlighting carbon hotspots, and ultimately the identification of critical building components. As a case study, multi-storey housing was selected as a critical building typology, in Sri Lanka. The results reveal 'walls' as a carbon hotspot that needs to be explored in strategies for mitigation. Substantial EC savings were seen in the selection of fly ash blocks as an alternate material to clay brick or cement block. Changes to the configuration of walls, specifically, bonding patterns and non inclusion of a plaster layer, also showed savings. This paper, contributes to the understanding of material selection implications in the cradle-to-gate stage for the reduction of carbon emissions in mid-rise housing, in the context of Sri Lanka. (C) 2020 Elsevier B.V. All rights reserved.

Optimal energy management for hybrid electric aircraft

Leite, JPSP; Voskuil, M, 2020

Purpose In recent years, increased awareness on global warming effects led to a renewed interest in all kinds of green technologies. Among them, some attention has been devoted to **hybrid**-electric aircraft - aircraft where the propulsion system contains power systems driven by electricity and power systems driven by hydrocarbon-based fuel. Examples of these systems include electric motors and gas turbines, respectively. Despite the fact that several research groups have tried to design such aircraft, in a way, it can actually save fuel with respect to conventional designs, the results hardly approach the required fuel savings to justify a new design. One possible path to improve these designs is to optimize the onboard energy management, in other words, when to use fuel and when to use stored electricity during a mission. The purpose of this paper is to address the topic of energy management applied to **hybrid**-electric aircraft, including its relevance for the conceptual design of aircraft and present a practical example of optimal energy management. Design/methodology/approach To address this problem the dynamic programming (DP) method for optimal control problems was used and, together with an aircraft performance model, an optimal energy management was obtained for a given aircraft flying a given trajectory. Findings The results show how the energy onboard a **hybrid** fuel-battery aircraft can be optimally managed during the mission. The optimal results were compared with non-optimal result, and small differences were found. A large sensitivity of the results to the battery charging efficiency was also found. Originality/value The novelty of this work comes from the application of DP for energy management to a variable weight system which includes energy recovery via a propeller.

Legume genetic resources: management, diversity assessment, and utilization in crop improvement

Upadhyaya, HD; Dwivedi, SL; Ambrose, M; Ellis, N; Berger, J; Smykal, P; Debouck, D; Duc, G; Dumet, D; Flavell, A; Sharma, SK; Mallikarjuna, N; Gowda, CLL, 2011

Grain legumes contribute significantly to total world food production. Legumes are the primary source of dietary proteins in many developing countries, where protein hunger and malnutrition are widespread. Grain legumes germplasm constitute similar to 15% of the 7.4 M accessions preserved globally. Nearly, 78% of the CGIAR's, 0.217 M accessions, have been characterized, compared to 34% of national genebank collections. Interestingly, limited data on grain quality are available as the primary focus has been on morpho-agronomic traits. Clearly, more resources should be targeted on biochemical evaluation to identify nutritionally rich and genetically diverse germplasm. The formation of core and mini core collections has provided crop breeders with a systematic yet manageable entry point into global germplasm resources. These subsets have been reported for most legumes and have proved useful in identifying new sources of variation. They may however not eliminate the need to evaluate entire collections, particularly for very rare traits. Molecular characterization and association mapping will further aid to insights into the structure of legume diversity and facilitate greater use of collections. The use of high resolution elevational climate models has greatly improved our capacity to characterize plant habitats and species' adaptive responses to stresses. Evidence suggests that there has been increased use of wild relatives as well as new resources resulting from mutagenesis to enhance the genetic base of legume cultigens.

Design and implementation of a hybrid MLP-GSA model with multi-layer perceptron-gravitational search algorithm for monthly lake water level forecasting

Ghorbani, MA; Deo, RC; Karimi, V; Kashani, MH; Ghorbani, S, 2019

Lakes are primitive water holding geographic structures containing most the fresh water on the Earth's surface, but the recent trends show that climate change can potentially lead to a significant aberration in the Lake water level and its overall pristine state, and therefore, could also threaten the source of freshwater. The ability to forecast the lake water is a paramount decision-making and risk-reduction task, and this is required to retain the sustainability of the natural environment, and to reduce the risk to the local and global food chain, recreation activities, agriculture and ecosystems. In this study, we have designed and evaluated a new **hybrid** forecasting model, integrating the gravitational search algorithm (GSA), as a heuristic optimization tool, with the Multilayer Perceptron (MLP-GSA) algorithm to forecast water level in Winnepesaukee and Cypress Lakes in the United States of America. The performance of the resulting **hybrid** MLP-GSA model is benchmarked and compared with the traditional MLP trained with Levenberg-Marquadt back propagation learning algorithm, two other intelligent **hybrid** models (MLP-PSO and MLP-FFA) and also two stochastic models namely, ARMA and ARIMA models. In this case study, the monthly time scale water level data from 1938 to 2005 and 1942 to 2011 for the Lakes Winnepesaukee and Cypress, respectively, were applied to train and evaluate the MLP-GSA model. The best input combinations of the standalone (MLP) and the **hybrid** MLP-GSA forecasting models were determined by sensitivity analysis of historical water level training data for 1-month lead forecasting. The **hybrid** MLP-GSA model was evaluated independently with statistical score metrics: coefficient of correlation, coefficient of efficiency, the root mean square and relative root mean square errors, and the Bayesian Information Criterion. The results showed that the **hybrid** MLP-GSA4 and MLP-GSA5 model (where the 4 and 5 months' of lagged input combinations of Lake water level data were utilized as the model inputs) performed more accurately than the ARIMA, ARMA, MLP4, MLP-PSO4 and MLP-FFA4 models for the Cypress Lake and ARIMA, ARMA, MLP5, MLP-PSO5 and MLP-FFA5 models for the Winnepesaukee lake, respectively. This study ascertained the robustness of **hybrid** MLP-GSA over ARMA, ARIMA, MLP, MLP-PSO and MLP-FFA for the forecasting of Lake water level. The high efficacy of the **hybrid** MLP-GSA model over the other applied models, indicate significant implications of its use in water resources management, decision-making tasks, irrigation management, management of hydrologic structures and sustainable use of water for agriculture and other necessities.

Climatic and Genotypic Effects for Grain Yield in Maize under Stress Conditions

Romay, MC; Malvar, RA; Campo, L; Alvarez, A; Moreno-Gonzalez, J; Ordas, A; Revilla, P, 2010

Climate change is expected to affect agriculture. Yield stability across environments is a critical breeding goal when dealing with unstable climate and input reductions in farming systems. The objective of this study was to determine climatic and genetic factors contributing to genotype (G), environment (E), and genotype x environment (GE) variability for maize (*Zea mays* L.) grain yield under some stress conditions like drought, cold, and pest attack. A large sample of panish maize populations was evaluated along with checks at three diverse locations during 3 yr. Factorial regression was performed to obtain a biological explanation of the G, E, and GE interaction for yield. The commercial **hybrids** had more yield and stability than most populations; therefore, breeding programs focusing on yield have released **hybrids** with high yield and stability under stress conditions. The populations with a reasonable compromise between yield and stability were Andoain and Lira. The main genotypic covariate was kernel depth followed by ear length, although other covariates were important for each location. The main climatic covariates for yield were related to days with mean temperature over 15 degrees C and maximum temperature in September, but they were not consistent across locations. Therefore, if yield under stress conditions is a breeding goal, several climatic variables, especially those related to high temperatures, and genotypic traits such as kernel depth and ear length should be considered.

Effect of morpho-physiological traits on grain yield of sorghum grown under stress at different growth stages, and stability analysis

Sankarapandian, R; Audilakshmi, S; Sharma, V; Ganesamurthy, K; Talwar, HS; Patil, JV, 2013

Recent trends in climate change resulting in global warming and extreme dry spells during rainy seasons are having a negative impact on grain and fodder production in rain-fed crops in India. Understanding the mechanisms of drought tolerance at various growth stages will help in developing tolerant genotypes. Crosses were made between elite and drought-tolerant sorghums, and F-2 and F-3 progenies were evaluated for drought tolerance in multiple locations. Twenty-five F-4/F-5 derivatives along with drought-tolerant check plants (two high-yielding genotypes showing moderate drought tolerance: C43 (male parent of the commercial **hybrid**

CSH 16, tolerant to drought) and CSV 17, (a pure line commercial cultivar released for drought-prone areas) were screened for drought tolerance under a factorial randomized block design with three replications during the rain-free months of April-June in 2007 and 2008 at Tamil Nadu Agricultural University, Kovilpatti, India. In each generation/year, four trials were conducted and water stress at different phases of crop growth, viz. vegetative, flowering and post-flowering (maturity), was imposed by withholding irrigation. Observations were recorded on grain and straw yields, plant height, number of roots, root length, leaf relative water content (LRWC), chlorophyll content and stomatal conductance under all treatments. The traits, grain yield, plant height, average root length and stomatal conductance showed significant mean sums of squares (SSs) for genotypexenvironment (GxE), suggesting that genotypes had significant differential response to the changing environments. Significant mean SSs due to GxE (linear) were obtained for straw yield, LRWC and chlorophyll content, indicating that the variability is partly genetic and partly influenced by environment. Grain yield was correlated with chlorophyll content ($r=0.43$) at the vegetative stage, with number of roots ($r=0.49$), LRWC ($r=0.51$), chlorophyll content ($r=0.46$) and stomatal conductance ($r=0.51$) at the pre-flowering stage, and with LRWC ($r=0.50$) and stomatal conductance ($r=0.40$) at the post-flowering stage, under water stress. Partial least square (PLS) analysis showed that different traits were important for grain yield under water stress at different growth stages. Pyramiding the genes for the traits responsible for high grain yield under stress will help in developing stable genotypes at different stages of plant growth.

Effects of temperature increase on the epidemiology of three major vector-borne viruses

Reynaud, B; Delatte, H; Peterschmitt, M; Fargette, D, 2009

The epidemiologies of Maize streak virus (MSV), Maize stripe virus (MSpV), and Maize mosaic virus (MMV) were compared in La Reunion over a three year-period. Disease incidence caused by each virus was assessed, and the leaf and planthopper vector populations (*Cicadulina mbila* and *Peregrinus maidis*) were estimated in weekly sowings of the temperate, virus-susceptible maize **hybrid** INRA 508 and of the composite resistant cv. IRAT 297. MSV caused the most prevalent disease and MMV the least, with lower incidences in cv. IRAT 297 than in INRA 508. For each plant-virus-vector combination, (a) disease incidence was positively correlated to vector abundance, often with 1 month of time lag; (b) annual periodicity of disease incidence and of vector numbers was consistent with highest autocorrelations and a time lag of 12 months, (c) vector numbers and disease incidence were closely associated with temperature fluctuations, both remaining relatively constant below 24 °C and increasing rapidly above this threshold temperature. By contrast, relationships with rainfall and relative humidity (RH) were less consistent. Overall, 63 to 80% of the variance of disease incidence was explained through stepwise regression with vector number, temperature, and sometimes also rainfall or RH. The simple epidemiological model proposed underlines the close link between increased temperature and possible (re-) emergence of these three diseases in a maize cropping area.

Niche divergence of two closely related *Carbula* species (Insecta: Hemiptera: Pentatomidae) despite the presence of a hybrid zone

Liu, HX; Ye, Z; Liang, JY; Wang, SJ; Bu, WJ, 2018

1. The extent to which ecologically divergent selection acts to maintain species boundaries in the presence of **hybridisation** and gene flow is not well understood. Two parapatric taxa, *Carbula humerigera* (Uhler) and *Carbula putoni* (Jakovlev), were used to test the extent to which niche differentiation might sustain divergence of related taxa despite ongoing gene flow. 2. Mitochondrial [cytochrome c oxidase subunit I (COI), cytochrome c oxidase subunit II (COII) and cytochrome b (Cytb)] and nuclear [elongation factor 1- α (EF-1)] markers were sequenced from 383 individuals. Clusters of morphological variations were estimated and visualised using principal component analysis (PCA). Haplotype networks were constructed using median-joining and neighbour-net algorithm methods. Gene flows were estimated using migrate-n analyses. Suitable habitats for each species and their sympatric distribution were predicted with ecological niche modelling (ENM). Niche comparisons were conducted using Schoener's D and Warren's I. In addition, PCA, multivariate analysis of variance (manova) and discriminant function analysis were used to test ecological differentiation. 3. Morphological clusters and network analysis indicated that samples were generally divided into three groups (*C. humerigera*, *C. putoni* and **hybrids**). Ongoing gene flow was detected among the three groups, with abundant magnitudes in the sympatric region. Niche comparison and statistical analysis showed ecological differentiation between *C. humerigera* and *C. putoni*. Two potential **hybrid** zones were predicted in the ENM reconstruction, located along the Yanshan-Taihang-Qinling and Taishan mountains. 4. These results reveal a geographically delineated **hybrid** zone between *C. humerigera* and *C. putoni*. These two closely related *Carbula* species still live in different ecological niches despite **hybridisation** and ongoing gene flow.

Multi-depot vehicle routing problem for large-scale disaster relief in drought scenarios: The case of the Brazilian northeast region

Vieira, YEM; Bandeira, RAD; da Silva, OS, 2021

Emergency water trucking (EWT) is the reactive response to address droughts most adopted by developing countries. Consequently, as droughts are becoming more frequent, severe, and longer due to climate change, there has been an increasing demand for EWT. However, when applied on a large scale to geographically dispersed rural populations, EWT requires the use of a significant vehicle fleet, leading to higher operational costs. It thus becomes crucial to propose solutions that guarantee EWT's financial and technical viability. Therefore, this paper proposes a two-step procedure to address the problem of large-scale water distribution to drought-affected populations. In step one, we use the transportation problem to assign a set of demand points to water sources, and, in step two, we model the problem as Capacitated Vehicle Routing Problems. Moreover, we also explore in this paper possibilities of using a new **hybridizing** Ant Colony Optimization metaheuristic with Random Variable Neighborhood Descent (MACS-RVND) to search for efficient solutions, in terms of the total distance and number of vehicles used, for large scale EWT. Hence, in the second step of the developed procedure, results from the MACS-RVND are compared with those obtained by Clarke and Wright heuristics with 2-opt, and with results from an Adaptive Large Neighborhood Search approach proposed by Erdogan. The procedure was then applied to a real water distribution case in the Brazilian semi-arid region. Results are compared with the actual procedures adopted in Brazilian water distribution, showing that the developed procedure can promote more efficient, economic, and equitable water distribution.

Yield of early white cabbage grown under mulch and non-mulch conditions with low populations of onion thrips (*Thrips tabaci* Lindeman)

Trdan, S; Znidarcic, D; Kac, M; Vidrih, M, 2008

The damage caused by *Thrips tabaci* to a susceptible **hybrid** of early white cabbage was studied in field experiments undertaken during 2004 and 2005. The three treatments tested were beds of cabbage mulched with: (1) barley straw, (2) hay, and (3) black polyethylene (PE) sheeting. Bare-soil (un-mulched) beds were used as the control treatment. One early and one late experiment were performed in both years. In the early experiments, the mulches were applied at the start of the experiment, whereas in the late experiments the soil was first covered with black polyethylene for approximately 1 month. In both years, the springs were cold and wet, and so the thrips appeared late and their numbers were low. The highest mean actual weight and trimmed weight were recorded for cabbage grown in 2005 under PE mulch (actual early: 995g, actual late: 1184 g, trimmed early: 870g, trimmed late: 1056 g). Year 2004 gave lower values (110g for both variables) under barley straw and hay mulch (165g and 160g, respectively). There was no evidence of an allelopathic effect of water extracts of either barley straw or hay.

Screening brinjal (*Solanum melongena*) accessions conserved in the National Genebank collected from states adjoining Bangladesh for adventitious presence of EE1 event

Systematic management of Plant Genetic Resources (PGRs) is the key to sustainable agriculture for food and nutritional security and in mitigating climate change. The National Genebank (NGB) at ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi, acts as a repository of PGRs for future use. This study aimed at screening for the adventitious presence of transgenes in brinjal (*Solanum melongena* L.) accessions conserved in the NGB. The study targeted the collections made during 2007-2016 from areas adjacent to Bangladesh (Assam, Meghalaya, Mizoram, Tripura and West Bengal), where field trials of Bt brinjal event EE1 were conducted during 2005-2012 and commercial cultivation of this event was permitted in 2013. There could be an apprehension of both unintentional **introgression** and transboundary movement through borders. Adventitious presence of transgenes was checked in a set of 96 accessions of brinjal employing Polymerase Chain Reaction (PCR) and real-time PCR assays. As event EE1 carries cryIIAc gene for insect resistance with Cauliflower Mosaic Virus (CaMV) promoter (P-35S) and marker genes (nptII and aadA), so these genetic elements were targeted for qualitative GM testing. Based on the test results, transgenes were not detected in brinjal accessions conserved in NGB. Our study showed that brinjal and wild species collected from adjoining areas of Bangladesh, post field trials and release, do not contain the event EE1. The study presents an efficient and reliable method to ensure conservation of GM-free germplasm in the NGB.

~~Experimental hybridization in allopatric species of the *Drosophila repleta* group (Diptera: Drosophilidae): implications for the mode of speciation~~

Colines, B; Soto, IM; de Panis, DN; Padro, J, 2018

The Pleistocene refugia theory proposes that recurrent expansions and contractions of xerophytic vegetation over periods of climate change affected the evolution of cactophilic *Drosophila* in South America. The resulting demographic fluctuations linked to the available patches of vegetation should have been prone to bottlenecks and founder events, affecting the fate of gene pool dynamics. However, these events also promoted the diversification of cacti, creating an ecological opportunity for host specialization. We tested the hypothesis of ecological speciation in the *Drosophila buzzatii* group. We assessed adaptive footprints and examined the genetic architecture of fitness-related traits in the sibling allopatric species *D. koepferae* and *D. antonietae*. The results are in line with the idea that these species evolved under different ecological scenarios. Joint-scaling analysis comparing both species and their **hybrids** revealed that additive genetic variance was the major contributor to phenotypic divergence, but dominance, epistasis and maternal effects were also important factors. Correlation analysis among functionally related traits suggested divergent selection on phenotypic integration associated with fitness. These findings support the hypothesis of adaptive evolution driving the phylogenetic radiation of the group through independent events of host shifts to chemically complex columnar cacti.

~~A success story: water primroses, aquatic plant pests~~

Thouvenot, L; Haury, J; Thiebaut, G, 2013

Aquatic ecosystems are currently invaded by non-indigenous aquatic plants. A major challenge for biological invasion research is to develop the ability to predict the spread of species. Throughout the world, *Ludwigia peploides* subsp. *montevidensis* and *Ludwigia grandiflora* subsp. *hexapetala* are now considered to be two of the most invasive aquatic plants. This paper reviews the scientific knowledge about these species, their ecological and socio-economic impacts and methods of management. Water primrose possesses some advantageous biological traits, such as rapid growth rate, efficient reproductive capacity, high plasticity in growth response, broad ecological tolerance and allelopathic compounds which might explain its expansion and colonization of numerous ecosystems. Much attention must be paid to *Ludwigia grandiflora* subsp. *hexapetala* and *Ludwigia peploides* subsp. *montevidensis*. According to climatic models, global warming will further increase the spread of these species in Europe. Copyright (c) 2013 John Wiley & Sons, Ltd.

~~Morpho-physiological evaluation of tomato genotypes under high temperature stress conditions~~

Shaheen, MR; Ayyub, CM; Amjad, M; Waraich, EA, 2016

BACKGROUND: Tomato (*Solanum lycopersicum* L.) is an important but heat-sensitive vegetable crop. The losses in tomato production associated with heat stress are aggravating further under a global warming scenario. The present study was designed to investigate the comparative performance of tomato genotypes under high temperature stress. Tomato genotypes (191) were exposed to the controlled conditions of high temperature (40/32 degrees C day/night temperature). Different morphological (shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, root dry weight and number of leaves), physiological (photosynthetic rate, transpiration rate, water use efficiency, stomatal conductance to water, sub-stomatal CO₂ and leaf temperature) and SPAD value (chlorophyll content) were recorded to check the diversity among genotypes against heat stress. **RESULTS:** All the genotypes showed a significantly variable response in almost all the attributes under high-temperature conditions. Correlation among the variables provided a clear understanding of the phenomena involved. Based on all the attributes studied, genotypes L00090 and L00091 were found to be the most heat tolerant compared to other genotypes, whereas CLN1462A and CLN 1466E were found to be comparatively sensitive. **CONCLUSION:** It was concluded that the studied attributes were genotype dependent, and significant diverse performance was noted. The findings of this study pave the way towards the selection of tolerant genotypes, not only for use under high-temperature conditions but also to employ them in breeding programs to produce heat-tolerant **hybrids**. (c) 2015 Society of Chemical Industry

~~The capacitated pollution routing problem with pickup and delivery in the last mile~~

Tan, YY; Deng, L; Li, LX; Yuan, F, 2019

Purpose With the increasing awareness of global warming and the important role of last mile distribution in logistics activities, the purpose of this paper is to build an environmental and effective last mile distribution model considering fuel consumption and greenhouse gas emission, vehicle capacity and two practical delivery service options: home delivery (HD) and pickup site service (PS). This paper calls the problem as the capacitated pollution-routing problem with pickup and delivery (CPRPPD). The goal is to find an optimal route to minimize operational and environmental costs, as well as a set of optimal speeds over each arc, while respecting capacity constraints of vehicles and pickup sites. **Design/methodology/approach** To solve this problem, this research proposes a two-phase heuristic algorithm by combining a **hybrid** ant colony optimization (HACO) in the first stage and a multiple population genetic algorithm in the second stage. First, the HACO is presented to find the minimal route solution and reduce distribution cost based on optimizing the speed over each arc. **Findings** To verify the proposed CPRPPD model and algorithm, a real-world instance is conducted. Comparing with the scenario including HD service only, the scenario including both HD and PS option is more economical, which indicates that the CPRPPD model is more efficient. Besides, the results of speed optimization are significantly better than before. **Practical implications** - The developed CPRPPD model not only minimizes delivery time and reduces the total emission cost, but also helps logistics enterprises to establish a more complete distribution system and increases customer satisfaction. The model and algorithm of this paper provide optimal support for the actual distribution activities of logistics enterprises in low-carbon environment, and also provide reference for the government to formulate energy-saving and emission reduction policies. **Originality/value** This paper provides a great space for the improvement of carbon emissions in the last mile distribution. The results show that the distribution arrangement including HD and PS services in the last mile adopting speed optimization can significantly reduce the carbon emission. Additionally, an integrated real-world instance is applied in this paper to illustrate the validity of the model and the effectiveness of this method.

~~A Combination of Metaheuristic Optimization Algorithms and Machine Learning Methods Improves the Prediction of Groundwater Level~~

Groundwater is a crucial source of water supply in drought conditions, and an auxiliary water source in wet seasons. Due to its increasing importance in view of climate change, predicting groundwater level (GWL) needs to be improved to enhance management. We used adaptive neuro-fuzzy inference systems (ANFIS) to predict the GWL of the Urmia aquifer in northwestern Iran under various input scenarios using precipitation, temperature, groundwater withdrawal, GWL during the previous month, and river flow. In total, 11 input patterns from various combinations of variables were developed. About 70% of the data were used to train the models, while the rest were used for validation. In a second step, several metaheuristic algorithms, such as genetic algorithm (GA), particle swarm optimization (PSO), and colony optimization for continuous domains (ACOR), and differential evolution (DE) were used to improve the model and, consequently, prediction performance. The results showed that (i) RMSE, MAPE, and NSE of 0.51 m, 0.00037 m, and 0.86, respectively, were obtained for the ANFIS model using all input variables, indicating a rather poor performance, (ii) metaheuristic algorithms were able to optimize the parameters of the ANFIS model in predicting GWL, (iii) the input pattern that included all input variables resulted in the most appropriate performance with RMSE, MAPE, and NSE of 0.28 m, 0.00019 m, and 0.97, respectively, using the ANFIS-ACOR hybrid model, (iv) results of Taylor's diagram ($CC = 0.98$, $STD = 0.2$, and $RMSD = 0.30$), as well as the scatterplot ($R^2 = 0.97$), showed that best prediction was achieved by ANFIS-ACOR, and (v) temperature and evaporation exerted stronger influence on GWL prediction than groundwater withdrawal and precipitation. The findings of this study reveal that metaheuristic algorithms can significantly improve the performance of the ANFIS model in predicting GWL.

~~Growing scattered broadleaved tree species in Europe in a changing climate: a review of risks and opportunities~~

Hemery, GE; Clark, JR; Aldinger, E; Claessens, H; Malvolti, ME; O'Connor, E; Raftoyannis, Y; Savill, PS; Brus, R, 2010

Scattered broadleaved tree species such as ashes (*Fraxinus excelsior* L. and *Fraxinus angustifolia* Vahl.), black alder (*Alnus glutinosa* (L.) Gaertn.), birches (*Betula pendula* Roth. and *Betula pubescens* Ehrh.), elms (*Ulmus glabra* Huds., *Ulmus laevis* Pall. and *Ulmus minor* Mill.), limes (*Tilia cordata* Mill. and *Tilia platyphyllos* Scop.), maples (*Acer campestre* L., *Acer platanoides* L. and *Acer pseudoplatanus* L.), wild service tree (*Sorbus domestica* L. and *Sorbus torminalis* L. Crantz), walnuts (*Juglans regia* L., *Juglans nigra* L. and **hybrids**) and wild cherry (*Prunus avium* L.) are important components of European forests. Many species have high economic, environmental and social values. Their scattered distributions, exacerbated in many cases by human activity, may make them more vulnerable to climate change. They are likely to have less ability to reproduce or adapt to shifting climate space than more widespread species. The general impacts of climate change on these scattered species are reviewed. Some specific risks and opportunities are highlighted for each species, although there is considerable uncertainty and therefore, difficulty in quantifying many specific risks and/or impacts on scattered broadleaved tree species.

~~Biotechnology for Jatropha improvement: A worthy exploration~~

Moniruzzaman, M; Yaakob, Z; Khatun, R, 2016

Comfortable life, economic growth, industrialisation, global warming, energy security and sustainable environment are burning issues facing modern civilisation. The availability of adequate renewable energy is in demand. *Jatropha* is being explored as a potential biofuel crop candidate because of its biodiesel production potential, high oil content, rapid growth, easy propagation, drought tolerant nature, relatively less irrigation and agricultural inputs, insect and pest resistance. However, previous programmes for *Jatropha* plantation did not satisfy the expectation because of the absence of a good commercial variety, large scale propagation without evaluating the planting material, knowledge gap and consideration as low a impute crop. Lack of systematic breeding programmes, the inexistence of a collaboration between scientists in this field, the unavailability of desired germplasm and more importantly less variability within the species are the constraints for the conventional breeding for a *Jatropha* improvement programme. Biological techniques have proven records for the improvement of many crops. *Jatropha* "organogenesis", which has insignificant contribution to genetic improvement, is studied. Several genomic and transgenic studies have been reported, but it is still far behind in comparison to other crops. It is time to investigate somaclonal variation, in vitro selection and haploid breeding for *Jatropha* improvement. Resequencing and transcriptome analysis are necessary for high density linkage map and a good reference genome. Genome wide association studies (GWAS) and genomic selection (GS) are pending. Genetic engineering, particularly to increase female flowers in inflorescence, eliminates the toxic component and increases tolerance to diseases, insects and pests should be given priority. (C) 2015 Elsevier Ltd. All rights reserved.

~~MITIGATION OF CLIMATE CHANGE EFFECT IN SWEET PEPPER (*Capsicum annuum* L.) THROUGH ADJUSTMENT OF PLANTING TIME~~

Saqib, M; Anjum, MA, 2021

Sweet pepper (*Capsicum annuum* L.) is one of the most popular and high value vegetable crops grown for its immature fruits throughout the world. In Pakistan it is cultivated as warm season crop in open fields during summer and in plastic tunnels during winter. Optimum planting date in sweet pepper production is key to better yield as it determines the period of maximum crop potential, efficient use of resources, lesser competition of plants with weeds and insect pests. It is the need of time to understand the negative impact of climate change on phenological development of sweet pepper. Therefore, the current study was designed to mitigate the effect of climate on growth and yield of sweet pepper cultivars at agro-ecological area of Multan, Pakistan by adjusting planting date. Three transplanting dates (viz. February 15th, March 2nd and March 16th) were evaluated during year 1 whereas five transplanting dates (viz. February 1st, February 15th, March 2nd, March 16th and April 1st) were assessed during year 2. There were three sweet pepper cultivars (Ganga, Winner and Savio) under study. Overall plant growth (stem height, average canopy diameter, number of leaves per plant and fresh and dry mass of plant parts) was significantly higher in the earliest planting dates (viz. February 1st in year 1 and February 1st in year 2) and it reduced as the planting was delayed. Plant yield, number of fruits and average fruit weight were also significantly higher in the earliest planting dates, and significantly lesser in later planting dates. During year 1, the effect of cultivar was prominent, and Winner performed better regarding growth characteristics while the effect was non-significant on yield attributes except average fruit weight which was also significantly higher in Winner as compared with other two cultivars. During year 2, cv. Winner performed better in growth attributes, whereas significantly greater number of fruits was found in cv. Savio, average fruit diameter was greater in cv. Winner and average fruit length was higher in cv. Ganga. It is concluded that nursery of sweet pepper should be planted in 1st week of February to achieve maximum growth and yield of fruits. In cultivar selection, cv. Winner should be preferred among sweet pepper **hybrids**.

~~Rice varietal improvement for Mediterranean France~~

Clement, G; Louvel, D, 2013

In France, rice is grown mainly near the Mediterranean Sea, in the Camargue. An irrigated system based on direct seeding on wet land is used. Occurrence of cold periods throughout the crop cycle (April/May-September/October) and the risk of soil salinization are the most important constraints. Since 1988, CIRAD and CFR have been implementing a rice breeding program for the Camargue. It aims at creating cultivars fitting the needs of rice farmers (yield potential and stability), the rice industry (milling and processing qualities) and consumers (cooking and taste qualities). Varieties grown in the region belong to the japonica subspecies of *Oryza sativa*. **Hybridization** is the basis for creation of variability. Progenies are selected using the pedigree method associated or not with haploidiploidisation applied to the first generation. Marker-assisted selection has recently been introduced to improve selection efficacy for resistance to fungal diseases occurring erratically in relation to climate. So far, 25 varieties have been registered in the European Official Catalogue, of which 5 have proven particularly successful among farmers. Progress achieved for germination in anaerobic conditions, resistance to stem borers, grain shape and other qualities, including aroma, are presented. Prospects in relation to new objectives such as weed control and adaptation to climate change are also presented.

The establishment of hybrids of the *Daphnia longispina* complex explained by a mathematical model incorporating different overwintering life history strategies

Griebel, J; Utz, M; Hermisson, J; Wolinska, J, 2018

Interspecific **hybridization** (i.e. mating between species) occurs frequently in animals. Among cyclical parthenogens, **hybrids** can proliferate and establish through parthenogenetic reproduction, even if their sexual reproduction is impaired. In water fleas of the *Daphnia longispina* species complex, interspecific **hybrids** hatch from sexually produced dormant eggs. However, fewer **hybrid** genotypes contribute to the dormant egg bank and their hatching rate from dormant eggs is reduced, compared to eggs resulting from intraspecific crosses. Therefore, *Daphnia* **hybrids** would benefit from adaptations that increase their survival over winter as parthenogenetic lineages, avoiding the need to re-establish populations after winter from sexually produced dormant eggs. Here, we constructed a mathematical model to examine the conditions that could explain the frequently observed establishment of **hybrids** in the *D. longispina* species complex. Specifically, we compared the outcome of **hybrid** and parental taxa competition given a reduced contribution of **hybrids** to hatchlings from the sexually produced dormant egg bank, but their increased ability to survive winter as parthenogenetic lineages. In addition, different growth rates of parental species and differences in average annual temperatures were evaluated for their influence on **hybrid** production and establishment. Our model shows that increased overwinter performance as parthenogenetic females can compensate for reduced success in sexual reproduction, across all tested scenarios for varying relative growth rates of parental species. This pattern holds true for lower annual temperatures, but at higher temperatures **hybrids** were less successful. Consequently, **hybrids** might become less abundant as temperatures rise due to climate change, resulting in reduced diversity and faster differentiation of the parental species.

Characterizing multiple linkages between individual diseases, crop health syndromes, germplasm deployment, and rice production situations in India

Reddy, CS; Laha, GS; Prasad, MS; Krishnaveni, D; Castilla, NP; Nelson, A; Savary, S, 2011

Five groups of crop health syndromes, four production situations, and three patterns of germplasm deployment were identified and characterized from a data set consisting of information from 129 Indian districts, which were surveyed in 2005 as part of the Production-Oriented Surveys conducted by the Directorate of Rice Research of the Indian Council of Agricultural Research. ANOVAs and MANOVAs indicated that these groupings from hierarchical cluster analyses correspond to clearly different levels of disease and animal pest injuries (crop health syndromes): of crop rotation, crop management, agricultural resources, and inputs (production situations): and of deployment of traditional, high yielding, or **hybrid** plant material (patterns of germplasm deployment). Correspondence analysis and discriminant analyses further indicated that crop health syndromes, and their change, are strongly associated with production situations, and patterns of germplasm deployment. A few specific hypotheses were tested, indicating that false smut is statistically associated with the involvement of **hybrid** rice in patterns of germplasm deployment. This highlights the need for research on the biology and the epidemiology of this disease in order to develop suitable management tools. Importantly, this work shows that national surveys, such as the Production-Oriented Surveys conducted by the Directorate of Rice Research, generate extremely valuable information to guide research and development through the characterization of production environments, contexts, and crop health responses, in times of unprecedented agricultural change. This work concurs with earlier results obtained at the field level, and thus opens important methodological questions regarding the up- and down-scaling of information between different scales (e.g., field, district). We propose that our ability to predict emerging diseases and crop health syndromes in the face of global and climate change will necessarily entail our ability to link different scales, where a range of different processes, biological and socio-economic, take place. (C) 2010 Elsevier B.V. All rights reserved.

Heat stress induced responses in local and multinational maize hybrids for morphophysiological and kernel quality traits

Yousaf, MI; Bhatti, MH; Maqbool, MA; Ghani, A; Akram, M; Ibrar, I; Khan, A; Khan, RAH; Kohli, SA; Siddiq, MA; Khalid, MU, 2021

Heat stress is one of the major causes of low kernel yield of maize in Pakistan as compared to other countries like United State of America, Turkey, Canada, Argentina and China. To overcome this problem, the current study was designed to evaluate heat stress induced responses in maize **hybrids** for morpho-physiological and kernel quality related traits. The research was conducted at Maize and Millets Research Institute (MMRI), Yusufwala, Pakistan for three consecutive spring seasons (2017, 2018 and 2019). Maize **hybrids** were sown under two heat regimes: (i) normal sowing and (ii) sowing under heat stress (late sowing) for each spring seasons. Results revealed highly significant ($P < 0.05$) differences among maize **hybrids** for kernel yield and related traits under both conditions and for all three seasons. Moreover, 11% to 36% reduction in kernel yield was observed during heat stress compared to normal sowing. Highest average percentage reduction was observed in local **hybrid** YH-5532 (28.7%) followed by all the three multinational **hybrids** NK-8711 (27.3%), P-1543 (23.4%) and DK-6724 (21.2%), respectively. This reduction in kernel yield was attributed to the reduction in thousand kernel weight (4.8% to 17.2%), number of kernels per ear (4.7% to 13.3%), net photosynthetic rate (11% to 24.9%) and shelling percentage (up to 4.7%) as revealed by biplot analysis. Biplot analysis further unveiled that two local maize **hybrids** YH-5507 and YH-5427 were the most productive and heat tolerant **hybrids** under both conditions and for three consecutive seasons. Therefore, these **hybrids** are recommended general cultivation especially in heat prone areas.

Mosquitoes established in Lhasa city, Tibet, China

Liu, QY; Liu, XB; Cirendunzhu; Woodward, A; Pengcuociren; Bai, L; Baimaciwang; Sang, SW; Dazhen; Wan, FJ; Zhou, L; Guo, YH; Wu, HX; Li, GC; Lu, L; Wang, J; Dawa; Chu, C; Xiraoruodeng, 2013

Background: In 2009, residents of Lhasa city, Tibet Autonomous Region (TAR), China reported large numbers of mosquitoes and bites from these insects. It is unclear whether this was a new phenomenon, which species were involved, and whether these mosquitoes had established themselves in the local circumstances. Methods: The present study was undertaken in six urban sites of Chengguan district Lhasa city, Tibet. Adult mosquitoes were collected by bed net trap, labor hour method and light trap in August 2009 and August 2012. The trapped adult mosquitoes were initially counted and identified according to morphological criteria, and a proportion of mosquitoes were examined more closely using a multiplex PCR assay. Results: 907 mosquitoes of the *Culex pipiens* complex were collected in this study. Among them, 595 were females and 312 were males. There was no significant difference in mosquito density monitored by bed net trap and labor hour method in 2009 and 2012. Of 105 mosquitoes identified by multiplex PCR, 36 were pure mosquitoes (34.29%) while 69 were **hybrids** (65.71%). The same subspecies of *Culex pipiens* complex were observed by bed net trap, labor hour method and light trap in 2009 and 2012. Conclusion: The local *Culex pipiens* complex comprises the subspecies *Cx. pipiens pipiens*, *Cx. pipiens pallens*, *Cx. pipiens quinquefasciatus* and its **hybrids**. Mosquitoes in the *Cx. pipiens* complex, known to be, potentially, vectors of periodic filariasis and encephalitis, are now present from one season to the next, and appear to be established in Lhasa City, TAR.

Increased root herbivory under elevated atmospheric carbon dioxide concentrations is reversed by silicon-based plant defences

Frew, A; Allsopp, PG; Gherlenda, AN; Johnson, SN, 2017

1. Predicted increases in atmospheric concentrations of CO₂ may alter the susceptibility of many plants to insect herbivores due to changes in plant nutrition and defences. Silicon plays a critical role in plant defence against herbivores, so increasing such silicon-based defences in plants may help remediate situations where plants become more susceptible to herbivores. 2. Sugar cane (*Saccharum* spp. **hybrid**) was subjected to fully factorial treatment combinations of ambient (aCO₂) or elevated (eCO₂) atmospheric CO₂ concentrations; ambient silicon or silicon supplementation; insect-free or subject to root herbivory by greyback canegrub (*Dermolepida albohirtum*). A glasshouse study was used to determine how these factors affected rates of photosynthesis, growth, chemistry (concentrations of silicon, carbon, nitrogen and non-structural carbohydrates). Changes in canegrub mass were determined in the glasshouse pot study, together with more detailed assessment of how eCO₂ and silicon supplementation affected performance and feeding behaviour

(relative growth rate and relative consumption) in a 24-h feeding efficiency assay. 3. Elevated CO₂ and silicon supplementation increased rates of photosynthesis (+32% and 14%, respectively) and sugar cane biomass (+45% and 69%, respectively). Silicon supplementation increased silicon concentrations in both leaves and roots by 54% and 75%, respectively. eCO₂ caused root C:N to increase by 12%. 4. Canegrub performance and consumption increased under eCO₂; relative growth rate (RGR) increased by 116% and consumed 57% more root material (suggestive of compensatory feeding). Silicon application reversed these effects, with large decreases in mass change, RGR and root consumption (65% less root mass consumed). 5. Synthesis and applications. Our results suggest future atmospheric carbon dioxide concentrations could lead to increased crop damage by a below-ground herbivore. Increasing bioavailable silicon in soil stimulated silicon-based defences which dramatically decreased herbivory and herbivore performance. Our findings suggest future pest management strategies could benefit from characterising deficiencies in bioavailable silicon in agricultural soils and targeted application of silicon fertilisers. Moreover, future breeding programmes should exploit variation in silicon uptake between cultivars to enhance silicon uptake in new crop varieties. Silicon-based plant defence proved to be highly beneficial for remediating the negative effects of atmospheric change on sugar cane susceptibility to herbivory and could be applicable in other crops.

~~Drought and Saline Stress Tolerance Induced in Somatic Hybrids of Solanum chacoense and Potato Cultivars by Using Mismatch Repair Deficiency~~

Molnar, I; Cozma, L; Denes, TE; Vass, I; Vass, IZ; Rakosy-Tican, E, 2021

Global climate change, especially when involving drought and salinity, poses a major challenge to sustainable crop production, causing severe yield losses. The environmental conditions are expected to further aggravate crop production in the future as a result of continuous greenhouse gas emissions, causing further temperature rise and leading to increased evapotranspiration, severe drought, soil salinity, as well as insect and disease threats. These suboptimal growth conditions have negative impact on plant growth, survival, and crop yield. Potato is well known as a crop extremely susceptible to drought, which is primarily attributed to its shallow root system. With potato being the fourth major food crop, increasing potato productivity is thus important for food security and for feeding global population. To maintain a sustainable potato production, it is necessary to develop stress tolerant potato cultivars that cope with the already ongoing climate change. The aim of our study is to analyze the response of potato somatic **hybrids** to drought and salt stress under in vitro conditions; the somatic **hybrids** studied are the wild relative *Solanum chacoense* (+) *Solanum tuberosum*, with or without mismatch repair deficiency (MMR). Upon this selection of drought and salt tolerant genotypes, somatic **hybrids** and their parents were phenotyped on a semi-automated platform, and lines tolerant to medium water scarcity (20% compared to 60% soil water capacity) were identified. Although none of the parental species were tolerant to drought, some of the MMR-deficient somatic **hybrids** showed tolerance to drought and salt as a new trait.

~~Phylogeographic structure without pre-mating barriers: Do habitat fragmentation and low mobility preserve song and chorus diversity in a European bushcricket?~~

Mahamoud-Issa, M; Marin-Cudraz, T; Party, V; Greenfield, MD, 2017

When animal species have a strong phylogeographic structure questions arise on the origin, maintenance and future evolutionary trajectory of that structure. One prediction is that phenotypic differences among populations serve as pre-mating barriers should secondary contact occur. Post-mating barriers may also function and ensure further separation of the populations. We tested these predictions in an acoustic insect, the European bushcricket *Ephippiger diurnus*, that is geographically distributed in separated, genetically isolated populations distinguished by pronounced differences in male songs and chorusing and female preferences for song. We staged mixed-population choruses to examine how males sing when in the company of other populations, and we released females in these choruses to assess their preference for or aversion toward males of their own population versus a different one. We also paired males and females of the same and different populations to test mating success, spermatophore transfer, and oviposition in the various pairings. In most cases males sang as effectively when accompanied by males from another population as when in a single-population chorus, and females overall expressed little aversion toward males from a different population. Inter-population pairs did not mate less frequently, transfer smaller spermatophores, or deposit fewer or smaller eggs than pairs of males and females from the same population. We infer that pre-mating barriers play little role in maintaining phylogeographic structure despite the acoustic differences between populations. Rather, the structure probably reflects the fragmented distribution of suitable habitat and the low mobility of both juveniles and adults. Thus, if secondary contact does occur, and we predict that it will in several key locations owing to ongoing environmental change, coalescence of populations and reduction of genetic and acoustic diversity may follow.

~~Effects of Soil Amendment With Wood Ash on Transpiration, Growth, and Metal Uptake in Two Contrasting Maize (*Zea mays* L.) Hybrids to Drought Tolerance~~

Romdhane, L; Ebinezer, LB; Panozzo, A; Barion, G; Dal Cortivo, C; Radhouane, L; Vamerli, T, 2021

Wood ash as a soil amendment has gained wide spread acceptance in the recent years as a sustainable alternative to chemical fertilizers, although information regarding the effects of its application on maize growth and yield in the context of climate change and increasing drought severity is lacking till date. In the present study, field and pot trials were carried out at the experimental farm of the University of Padova at Legnaro (NE Italy) in a silty-loam soil in order to investigate the effects of soil amendment with wood ash (0.1% w/w, incorporated into the 0.2-m top soil) on the bioavailability of mineral elements and their uptake by maize. Characteristics analyzed included plant growth, leaf transpiration dynamics, and productivity in two contrasting **hybrids**, P1921 (drought sensitive) and D24 (drought tolerant). Wood ash contained relevant amounts of Ca, K, Mg, P, and S, and hazardous levels of Zn (732 mg kg⁻¹), Pb (527 mg kg⁻¹), and Cu (129 mg kg⁻¹), although no significant changes in total soil element concentration, pH, and electrical conductivity were detected in open field. Ash application led to a general increasing trend of diethylene triamine penta-acetic acid (DTPA)-extractable of various elements, bringing to higher grain P in D24 **hybrid**, and Zn and Ni reductions in P1921 **hybrid**. Here, the results demonstrated that ash amendment enhanced shoot growth and the number of leaves, causing a reduction of harvest index, without affecting grain yield in both **hybrids**. The most relevant result was a retarded inhibition of leaf transpiration under artificial progressive water stress, particularly in the drought-tolerant D24 **hybrid** that could be sustained by root growth improvements in the field across the whole 0-1.5 m soil profile in D24, and in the amended top soil in P1921. It is concluded that woody ash can be profitably exploited in maize fertilization for enhancing shoot and root growth and drought tolerance, thanks to morphological and physiological improvements, although major benefits are expected to be achieved in drought tolerant **hybrids**. Attention should be paid when using ash derived by metal contaminated wood stocks to avoid any health risk in food uses.

~~Natural wind-driven ultra-compact and highly-efficient hybridized nanogenerator for self-sustained wireless environmental monitoring system~~

Rahman, MT; Salauddin, M; Maharjan, P; Rasel, MS; Cho, H; Park, JY, 2019

Owing to the climate change and energy crisis, harvesting energy from our surroundings and the construction of self-powered wireless environmental monitoring systems are promising approaches in modern times. In this paper, an ultra-compact highly efficient miniaturized windmill comprising a **hybridized** nanogenerator (MW-HNG) is reported based on three conversion mechanisms i.e. triboelectric nanogenerator (TENG), piezoelectric nanogenerator (PENG), and electromagnetic generator (EMG). The MW-HNG is designed as a 3D-printed fully-enclosed structure for the natural wind energy harvesting by converting into rotational motion: all harvesting units reside in a common rotation system to effectively and simultaneously produce electricity. At a wind speed of 6 m/s, the flexible-blade-based **hybridization**-mode (contact-lateral sliding-separation-contact) TENG and coupled PENG can generate maximal power values of 1.67 mW and 1.38 mW at optimal load resistances of 10 M Ω and 330 K Ω , respectively. In contrast, the multipole-magnet-based EMG can obtain a maximal output power of 268.6 mW at 180 Ω . The MW-HNG demonstrates a quick charging ability for capacitors and the capability to feed hundreds of LEDs. Further, a self-powered wireless sensor system is developed for real-time environmental monitoring by combining an MW-HNG, a customized power management circuit, and wireless sensor unit (a smartphone to display sensor data). Our proposed MW-HNG is suitable for self-powered wireless sensor networks (WSNs) in the subway system by generating high-

power electrical output from moving-induced wind mechanical energy.

Adaptive radiation within New Zealand endemic species of the cockroach genus *Celatoblatta* Johns (Blattidae): a response to Plio-Pleistocene mountain building and climate change

Chinn, WG; Gemmell, NJ, 2004

The South Island of New Zealand offers unique opportunities to study insect evolution due to long-term physical isolation, recent alpine habitats and high levels of biotic endemism. Using DNA sequence data from cytochrome oxidase subunit 1, we investigated the phylogeographical pattern among 10 endemic cockroach species within the genus *Celatoblatta* Johns (Blattidae). We tested the hypothesis that an ancestral cockroach species underwent rapid speciation in response to major climatic differentiation induced by mountain building. Results suggest that speciation was a twofold process, with an interspecific radiation of Pliocene/Pleistocene age followed by intraspecific diversification during the mid Pleistocene. Average genetic distance (maximum likelihood GTR + I + Gamma) was 9.17%, with a maximum of 14.5%. Data revealed eight deep well-supported branches, each with terminal clades. Six clades were differentiated according to morphological species, while the seventh was composed of three sympatric species. We consider the latter to be a phylogenetic species, possibly as a result of hybridization within a defined geographical area. This finding seriously challenges species distinctions for these three cockroach species. Correlation between genetic distances and a Climate Similarity Index (CSI) was negative, suggesting that species found in similar habitats are also genetically closely related. A Mantel test on within-clade genetic distances vs. linear geographical distance was positive, suggesting allopatric isolation for those haplotypes. We present a model of speciation for South Island *Celatoblatta*.

Appraisal of Salt Tolerance under Greenhouse Conditions of a Cucurbitaceae Genetic Repository of Potential Rootstocks and Scions

Modarelli, GC; Rouphael, Y; De Pascale, S; Oztekin, GB; Tuzel, Y; Orsini, F; Gianquinto, G, 2020

Soil salinization due to climate change and intensive use of water and soil is increasing exponentially. Cucurbitaceae species are cultivated worldwide and the identification of salinity tolerant genotypes to be used as rootstock or scion for securing yield stability in salt affected agricultural areas is a research priority. In the present greenhouse study, we assessed the response to salinity (0 mM a non-salt control and 150 mM NaCl dissolved in the nutrient solution) in the seedlings of 30 genotypes of cucurbits grown in a floating hydroponic system. The species tested included 16 genotypes of *Cucumis melo* L. (CM1-16), 6 *Citrullus vulgaris* Schrad. (CV1-6), 2 interspecific hybrids of *Cucurbita maxima* Duch. x *Cucurbita moschata* Duch. (CMM-R1 and 2), 4 bottle gourd (*Lagenaria siceraria* (Molina) Standl. (LS1-4)), 1 *Cucurbita moschata* Duch. (CM051-17), and 1 *Luffa* (*Luffa cylindrica* Mill. (LC1)) species. Results highlighted different morphological and physiological traits between the species and genotypes and a different response to salt stress. We identified *C. maxima* x *C. moscata* interspecific hybrid CMM-R2, melon genotypes CM6, CM7, CM10, and CM16 together with watermelon genotypes CV2 and CV6 and bottle gourd LS4 as salt tolerant genotypes and possible candidates as salt resistant rootstock to be introduced in grafting programs.

Tree species selection revisited for plantations in the Interior Cedar-Hemlock zone of southern British Columbia

Vyse, A; Cleary, MR; Cameron, IR, 2013

We provide results from two trials comparing performance of species of known provenance planted on logged sites in the southern Interior Cedar-Hemlock biogeoclimatic zone of southern British Columbia 20 and 26 years after establishment. The commonly used plantation species, lodgepole pine (*Pinus contorta* var. *latifolia*), interior spruce (a naturally occurring hybrid between *Picea glauca* and *P. engelmannii*) and Douglas-fir (*Pseudotsuga menziesii* var. *glauca*), survived as well as, but grew more slowly than, western larch (*Larix occidentalis*), western white pine (*Pinus monticola*) and ponderosa pine (*Pinus ponderosa*), and faster than western redcedar (*Thuja plicata*). Site index values were generally higher than published values for similar sites. Numerous pests affected all species in the trials. Mountain pine beetle (*Dendroctonus ponderosae*) caused heavy mortality in lodgepole pine in part of one trial, and Armillaria root disease caused widespread damage to western larch and Douglas-fir in the other trial. Western white pine from local seed sources were severely damaged by white pine blister rust (*Cronartium ribicola*) in both trials but a rust-resistant seed source used in one trial survived better. Frost damage reduced survival and growth of Douglas-fir in one trial and may have affected western white pine. Survival of two planted broadleaves (*Betula papyrifera*) and a hybrid of black cottonwood (*Populus trichocarpa*) and black poplar (*Populus nigra*) was severely reduced by drought. The results support ongoing efforts to broaden the number of species used in British Columbia reforestation programs.

Evolutionary history of two endemic Appalachian conifers revealed using microsatellite markers

Potter, KM; Frampton, J; Josserand, SA; Nelson, CD, 2010

Fraser fir (*Abies fraseri* [Pursh] Poir.) and intermediate fir (*Abies balsamea* [L.] Mill. var. *phanerolepis* Fern.) exist in small populations in the Appalachian highlands of the southeastern United States. We used ten nuclear microsatellite markers to quantify genetic variation within Fraser fir and intermediate fir, and to examine their evolutionary relationships with the widespread balsam fir (*Abies balsamea* [L.] Mill.). We found little genetic differentiation among these taxa, suggesting that Fraser fir might best be classified as a variety of balsam fir. The results further appear to reject the hypothesis that intermediate fir was of hybrid origin between two comparatively distantly related species. Low levels of genetic diversity suggest that intermediate fir and Fraser fir have undergone at least some genetic degradation since post-Pleistocene isolation. The results may prove important for in situ and ex situ gene conservation efforts for Fraser fir and intermediate fir, which are imperiled by an exotic insect and by global climate change.

Genetic traits leading to invasion: plasticity in cold hardiness explains current distribution of an invasive agricultural pest, *Tetranychus evansi* (Acari: Tetranychidae)

Migeon, A; Auger, P; Hufbauer, R; Navajas, M, 2015

Among the factors limiting species distribution, low temperatures play a key role for tropical invasive species in temperate areas. Susceptibility to cold winter conditions has been recognized as the limiting factor in Europe for *Tetranychus evansi*, an invasive spider mite feeding on Solanaceous plants originated from tropical South America and now present on every continent except Australia. Two genetically distinct lineages of this species were introduced to Europe; one (lineage 1) is widely distributed, while the other (lineage 2) has a limited distribution. Whether this difference corresponds to differences in cold hardiness is evaluated here by assessing phenotypic response of *T. evansi* to the winter conditions that the mite encounters in the coldest parts of the current invaded area. We designed the thermal regimes to mimic winter conditions, including temperature fluctuations between day and night (L:D 8:16, 12:4 degrees C) and exposed mites to this regime for 5, 10 or 15 weeks. We tested *T. evansi* from three locations, one from the tropical native area (Piracicaba, Brazil) and two, corresponding to the two introduced lineages, from the temperate invaded area (lineage 1 from Nice and lineage 2 from Perpignan, France). After 5 weeks of treatment, mites from all the locations showed high survival rates but the two introduced populations grew, producing more than one offspring per female. After 10 weeks, survival rates declined for mites from Brazil and Perpignan, but not Nice. After 15 weeks, only the mites from Nice survived and produced offspring. Thus, mites belonging to the widespread lineage 1 exhibit increased cold tolerance suggesting broader adaptability, helping to explain its current geographical distribution.

The strategic importance of applied tree conservation programs to the forest industry in South Africa

Dvorak, W, 2012

Because of anticipated adverse climatic change and resulting increases in disease and insect attacks in forest plantations in the future, forest industries must maintain broad genetic bases for adaptability and pest resistance. Since the early 1980s, the South African forest industry has obtained genetic material of 25 pine and eucalypt species that represent more than 4 200 trees from 260 natural populations around the world through its participation in Camcore (International Tree Breeding and Conservation Program) at North Carolina State University, USA. This combined genetic testing and conservation program has identified new productive pine species, such as *P. tecunumanii* and *P. maximinoi*, that grow well and are resistant in the seedling stage to the pitch canker fungus (*Fusarium circinatum*). Because of the industry's foresight to assemble genetic material and test alternate species over the last three decades, it was well prepared to immediately develop more-resistant pine **hybrids** such as *P. patula* x *P. tecunumanii* when the pitch canker situation became problematic. The South African forest industry has collectively worked together to established special 20-40 ha conservation parks across the country to hold and protect the original genetic material collected in Central America, Mexico and South-east Asia. Species are conserved in the parks at the population level and are represented by a minimum of 10 open-pollinated families, five trees per family across two sites. The design is based on maintaining an effective population size of approximately 30 with the goal to capture alleles at high frequencies as well as to include a number of rare alleles in the ex situ plantings. The overlying goal is to maintain well-adapted genetic material for future deployment.

Conservation implications of anthropogenic impacts on visual communication and camouflage

Delhey, K; Peters, A, 2017

Anthropogenic environmental impacts can disrupt the sensory environment of animals and affect important processes from mate choice to predator avoidance. Currently, these effects are best understood for auditory and chemosensory modalities, and recent reviews highlight their importance for conservation. We examined how anthropogenic changes to the visual environment (ambient light, transmission, and backgrounds) affect visual communication and camouflage and considered the implications of these effects for conservation. Human changes to the visual environment can increase predation risk by affecting camouflage effectiveness, lead to maladaptive patterns of mate choice, and disrupt mutualistic interactions between pollinators and plants. Implications for conservation are particularly evident for disrupted camouflage due to its tight links with survival. The conservation importance of impaired visual communication is less documented. The effects of anthropogenic changes on visual communication and camouflage may be severe when they affect critical processes such as pollination or species recognition. However, when impaired mate choice does not lead to **hybridization**, the conservation consequences are less clear. We suggest that the demographic effects of human impacts on visual communication and camouflage will be particularly strong when human-induced modifications to the visual environment are evolutionarily novel (i.e., very different from natural variation); affected species and populations have low levels of intraspecific (genotypic and phenotypic) variation and behavioral, sensory, or physiological plasticity; and the processes affected are directly related to survival (camouflage), species recognition, or number of offspring produced, rather than offspring quality or attractiveness. Our findings suggest that anthropogenic effects on the visual environment may be of similar importance relative to conservation as anthropogenic effects on other sensory modalities.

THE STUDY OF MODERN HYBRIDS OF GRAIN SORGHUM IN THE CONDITIONS OF THE STEPPE ZONE

Baranovsky, AV; Kapustin, SI; Kapustin, AS, 2019

In modern conditions of global climate change towards warming, in order to guarantee the provision of an increasing population of the planet with food, and especially grain, the issue of selecting the most productive, drought-resistant and heat-resistant crops becomes very urgent. One of such promising plants is sorghum grain, the main products of which are used for food, fodder and technical purposes. Almost every year, this crop in the steppe arid regions significantly exceeds traditional spring crops - oats, barley, corn and millet. In the State Register of Breeding Achievements Approved for Use in Russia for 2019, 120 domestic and foreign varieties and **hybrids** of grain sorghum were registered. The purpose of the research is to study the productivity of modern **hybrids** of sorghum grain in the soil and climatic conditions of the steppe zone on the basis of the Lugansk National Agrarian University in the crop rotation of the Department of Agriculture and Environmental Ecology (2016-2018). As a result of the studies, the most productive and maximally adapted crop varieties were established, which have the highest manufacturability and guaranteed maturation by the end of the growing season. In all the studied **hybrids**, no shedding of grain from panicles was recorded, even when the plants were stopped. The greatest damage to the leaves of cereal aphids was found in the wetter 2016. The average productivity of grain sorghum in the favorable year was 6.2 t / ha, in the arid year 2018 - 5.01 t / ha. On average, in 2016-2018, the highest yields (over 6.0 t / ha of grain) were obtained for early-ripening **hybrids** Frisket and PR88Y20 and mid-early Puma Star, Solarius and Bianka. These developments can be successfully implemented in agricultural production of the steppe regions of the North Caucasus region.

Flower age expressed in thermal time: is nectar secretion synchronous with pistil receptivity in oilseed rape (*Brassica napus* L.)?

Chabert, S; Lemoine, T; Cagnato, MR; Morison, N; Vaissiere, BE, 2018

Floral longevity can vary substantially with temperature in a given plant species. Thermal time has been widely used to measure developmental age of plants and poikilothermic organisms. We tested whether thermal time was suitable to express flower age to characterise the duration of pistil receptivity and that of nectar secretion in undisturbed flowers of oilseed rape (OSR), and whether these two functional processes were synchronous. Flower age was measured in a male fertile **hybrid** F-1 line and in its male sterile (MS) parental line to determine if the presence of pollen affected the nectar secretion period. Hand pollinations and nectar samplings were conducted throughout the lifespan of OSR flowers on several flower cohorts from plants grown under tunnels under various temperature conditions. The number of seeds produced per flower was used as a proxy to assess the level of pistil receptivity at the time of hand-pollination. Thermal time was more suitable than calendar time to express OSR flower age. A phase of maturity followed by a phase of senescence took place in the two processes, and both proceeded faster as temperature increased. Nectar was secreted during the phase of full pistil receptivity, and, in the MS line, was then reabsorbed during the gradual decline of pistil receptivity. However, the nectar secretion period was extended beyond the onset of pistil senescence in the F-1 line. OSR flowers invest in nectar secretion to attract insect pollinators at least to cover the whole receptivity period of their female part. Nectar secretion may be prolonged in pollen-laden male fertile flowers to attract insect pollinators longer to ensure as long as possible the probability of their pollen being disseminated. Flower senescence is triggered by pistil senescence, while the presence of pollen in anthers acts as an inhibitor and therefore delays flower senescence. Thermal time should henceforth be used to express more universally the age of plant organs and to model the duration of processes in relation to temperature, especially in the advent of global warming.

Effects of forest management on biodiversity in temperate deciduous forests: An overview based on Central European beech forests

Schulze, ED, 2018

This overview of relationships between biodiversity and management focuses on Central European *Fagus* forests. Present management and conservation activities are embedded in the geographic and historic background of Central European forest flora, including endangered, protected, and plant species for which Germany has taken special responsibility to ensure their future survival. Managed and unmanaged forests are compared with respect to plants and other organisms. Based on the floristic background, management for climate change and consequences of conservation on a global ecological footprint will be discussed. The Central European tree

flora contains only about 7% of the tree diversity of East Asia. Only a few genera re-migrated to Central Europe after the Pleistocene, while others were lost during the Pleistocene, e.g. the genus *Pseudotsuga*. In this study the forest flora is characterized by specialized plant species that only grow in forests. These forest specialists contribute only 10% of the plant species of the total German flora. This fraction is even less (4-5%) for Romania which is generally regarded as a region with close to "natural" forest conditions. Also, the forest flora of Germany and Romania contains fewer apomictic and **hybrid** plant species than the non-forest flora. No forest plant species have gone extinct in Germany in the past 250 years, which is the time since the first floristic documentation of a plant species that was lost in Thuringia, despite intense forest use including changes in dominant tree species. With respect to the Natura 2000 goals of maintaining species diversity of Europe, the deciduous forest, as managed by rotation forestry, contain more protected and endangered species, and species for which Germany has taken responsibility than protected forest. Forests managed with permanent forest cover (so-called "management close-to-nature") contain fewer plant species than age-class (rotation) forestry. The abundance of dead wood-fungi and of soil bacteria is higher in rotation forest than in protected forests. For the initial phase of decay, a dead wood experiment identified two important tree species, *Carpinus betulus* and *Picea abies*, as the most preferred tree species for xylobionts. *Carpinus* has the most diverse fungal flora among all wood types and is a typical species for managed forests. The Natura 2000 habitat types were defined by plant species, but the assessment of ecosystem health is based on bird species in Central Europe. A time series extending from 1927 until 2015 indicates that most non-migratory forest bird species show an increasing abundance since 1970. Adding migrating and rare bird species populations resulted in constant average abundances since 1970. There is no evidence that sustainable forest management has led to decreased biodiversity in Central Europe. In view of climate change and increasing presence of tree diseases, Europe should avoid enlarging its ecological footprint by taking Central European forests out of management.

~~SCREENING OF WHEAT-THINOPYRUM BESSARABICUM ADDITION AND TRANSLOCATION LINES FOR DROUGHT TOLERANCE~~

Shafqat, N; Ahmed, H; Shehzad, A; Chaudhry, SK; Shah, SH; Islam, M; Khan, W; Masood, R; Khan, U, 2019

Domestication of the crop plants has narrowed the genetic base of the crops and thereby mounting their exposure towards global climate change, disease and insect epidemics. Genetic variability of modern days crops must be broadened to make crop production more sustainable against various biotic and abiotic stresses which are posturing major threats to the world. It is therefore, crucial to identify novel additional sources of durable resistance. Wheat wild relatives have provided valuable sources of genetic diversity for various biotic, abiotic and quality components. In this respect wide **hybridization** has become a promising breeding method for introducing new variability in crop plants by using the crop wild relatives. In the present research work wheat-Th. Bessarabicum amphiploid, addition and translocation lines have been screened. These genetic stocks were exposed to 15% polyethylene glycerol (PEG) stress, to find out the drought tolerant addition and translocation lines by studying different physiological parameters. The screening of drought stress revealed that addition lines 2JJ, 4JJ, 5JJ, 7JJ and translocation line Tr-7 exhibited tolerance attitude towards water deficient conditions.

~~The impact of climate on flowering in the High Arctic –The case of Dryas in a hybrid zone~~

Hoye, TT; Ellebjerg, SM; Philipp, M, 2007

The extreme seasonality of the High Arctic creates very different flowering conditions for plants in areas of early and late snowmelt. Therefore, future reproductive responses to climate change may be dependent on the timing of snowmelt. We combined genetic, morphological, and long-term monitoring data on *Dryas* from a High Arctic **hybrid** zone of *D. integrifolia* and *D. octopetala* to assess whether climate variation influenced flowering differently in areas of early and late snowmelt, and whether this could have a genetic origin. We found a non-linear relationship between timing of snowmelt and flowering. The duration of the period between snowmelt and the onset of flowering (pre-floration interval) varied with the date of snowmelt. Shorter pre-floration intervals were associated with warmer average temperature during the pre-floration intervals in both early and late melting plots. However, the pre-floration interval was much shorter in early than in late plots at the same average temperature. Likewise, the interannual variation in flower abundance differed between early and late melting plots. Flower abundance was negatively influenced by frost after snowmelt in the year of flowering in early plots. In late plots, flower abundance was positively influenced by the length of the previous growing season. We identified two morpho-types in the study area, but their distribution and genetic differentiation was not related to the snowmelt gradient. We conclude that the different flowering responses found along the snowmelt gradient are a result of environmental variation. Based on our results and projected climatic change for the study area, we predict that the onset of flowering will advance and flower abundance will increase in areas of early snowmelt. In areas of late snowmelt, the onset of flowering will remain unchanged or be delayed and flower abundance will decrease.

~~Ecological vulnerability analysis for suppression of *Drosophila suzukii* by gene drives~~

Lalyer, CR; Sigsgaard, L; Giese, B, 2021

Synthetic gene drives are transgenic constructs that aim to bias heredity and thereby influence the characteristics and fate of populations regarding abundance and evolution. Aside from irreversible effects in ecosystems that could be triggered by the release of a gene drive, research on confinable drives or even the reversibility of gene drives is underway and shows first success under laboratory conditions. However, their effectiveness under realistic conditions is not entirely clear unless first test releases have taken place. Since a potentially irreversible intervention into ecosystems is created, a prospective assessment is needed. We present an approach of prospective ecological vulnerability analysis for the proposed control of the invasive pest *Drosophila suzukii* by using gene drives. The analysis considers the accidental spread of the gene drive to the native habitat of *Drosophila suzukii*, with a focus on Japan. It contains a mapping of potential impacts as a consequence of the suppression of the insect. Multiple cascading effects were identified including the potential spread of the gene drive in geographic range or potential **hybridization** with non-target species. Determining the vulnerability of an ecosystem requires information regarding specific characteristics at different organizational levels. The vulnerability analysis of an affected ecosystem will initially serve to identify gaps in knowledge. Reducing complexity and breaking down the potential events that might arise from a gene drive population suppression enables to better understand endpoints i.e. concrete effects. Three potential effects have been selected for a specific analysis of the vulnerability of populations and species. A high vulnerability was obtained for the suppression of non-target (native) populations of *Drosophila suzukii* as well as for a decrease in specialized parasitoid abundance. The paper proposes the outline of a comprehensive prospective approach to understand the susceptibility of an ecosystem to unintended and irreversible harm.

~~Sustainable intensification of transgenic cotton in India –A review~~

Singh, RJ, 2017

World population is projected to reach over nine billion by the year 2050, and ensuring fiber security while mitigating environmental impacts represent a major agricultural challenge. Conventional cotton (*Gossypium* sp) production technologies had significant effects on the environment and farm profitability in the past. New era transgenic or Bt cotton production technology can be used to simultaneously reduce the environmental footprint and enhance the profitability of cotton production. Information on these two sustainability aspects of transgenic cotton is missing in the scientific literature. Here, we review the potential advantages of insect tolerance Bt insect resistant technology used in **hybrid** cotton by comparing with the major cereal based rotations in India. Our results suggested that by using this technology, there was significant reduction in pesticide use roughly by 40%, and yield advantages of 30-40%. These resulted in saving on fossil fuels and decreasing CO₂ emissions-which are major bonus for climate change mitigation. During the last decade, significant increase in cotton area and production in India is attributed to better returns realized by the farmers, which were largely due to better management practices followed to grow transgenic cotton. Most of the studies conducted in India, concluded that Bt-cotton is more efficient in input use and had a lower environmental impact quotient, which indicates less damage to the environment than non-Bt-cotton. However, Bt-cotton based cropping systems have less profitability and energy efficiency in comparison to the major cereal based rotations in India due to lesser productivity potential of cotton crop particularly in rain-fed ecosystems. This was mainly attributed to the lesser dissemination of

proven energy-efficient research technologies to the farmer's fields. Although, Bt-cotton can contribute to a "sustainable intensification" strategy favoured by many science academies worldwide, which allows productivity/production to be increased in the current crop land, thereby saving forests and biodiversity.

Grape phylloxera (*Daktulosphaira vitifoliae*)—a review of potential detection and alternative management options

Benheim, D; Rochfort, S; Robertson, E; Potter, ID; Powell, KS, 2012

The management options for grape phylloxera, *Daktulosphaira vitifoliae*, a monophagous insect pest of *Vitis* species are reviewed. Although in a worldwide context, grape phylloxera is managed predominantly by the use of resistant rootstocks developed through conventional breeding of **hybrid** crosses of American *Vitis* species, this management aspect is largely excluded from the review so that emerging technologies in the field of detection, quarantine and alternative management are discussed. In some viticulture regions of the world, where grape phylloxera's geographic distribution is limited (e.g. Australia), the pest is managed through a combination of surveillance, detection and quarantine. Although some alternative management options for grape phylloxera exist they have received relatively limited research attention because of the relative success of resistant rootstocks. The resilience of resistant rootstocks as the primary management option could also be challenged in the future by host-plant interactions with diverse grape phylloxera clonal lineages and by potential impacts of climate change on both grapevine and grape phylloxera distribution. A range of control options exist which could be integrated into an improved management system for grape phylloxera. Priority areas for future evaluation and further development include early detection techniques, investigation into the use of biological control agents and development of an integrated approach to grapevine phylloxera management.

Biological Flora of the British Isles: *Ulmus glabra*

Thomas, PA; Stone, D; La Porta, N, 2018

1. This account presents information on all aspects of the biology of *Ulmus glabra* Hudson (wych elm) that are relevant to understanding its ecological characteristics and behaviour. The main topics are presented within the standard framework of the Biological Flora of the British Isles: distribution, habitat, communities, responses to biotic factors, responses to environment, structure and physiology, phenology, floral and seed characters, herbivores and disease, history and conservation. 2. *Ulmus glabra* is a large forest tree, and often an important canopy tree in ancient and semi-natural woodlands. It is primarily native to the north and west of Britain and much of mainland Europe. It is the only elm native to Ireland. It is the most distinct of the British elms in that it rarely suckers and sets abundant viable seed. Although found on limestone screes and cliffs, and hedgerows, it is primarily a woodland tree, especially on moist, basic soils. In many secondary woodlands, it often co-occurs with *Acer pseudoplatanus* and has ecological needs that are similar to *Fraxinus excelsior*. 3. *Ulmus glabra* has clusters of c. 25 hermaphrodite flowers appearing before the leaves on previous year's growth. Seeds are wind-dispersed, falling in April to July, but remain viable for only a few days. Nevertheless, seedling establishment can be abundant. **Hybrid**isation with other northern European elms is common but **hybrids** are notoriously difficult to identify and therefore probably under-recorded. 4. The health and survival of wych elm in Europe has been seriously compromised since the 1970s due to Dutch elm disease caused by the fungus *Ophiostoma novo-ulmi*, transmitted by elm bark beetles (*Scolytus* spp.). To the south of its Scottish stronghold, many elms are reduced to small trees regrowing from basal sprouts or seeds. These trees tend to be reinfected once trunk diameter exceeds 10 cm. Fortunately for its long-term survival, seed production usually begins a number of years before they are reinfected.
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Banks Grass Mite (*Acari: Tetranychidae*) Suppression May Add to the Benefit of Drought-Tolerant Corn Hybrids Exposed to Water Stress

Ruckert, A; Golec, JR; Barnes, CL; Ramirez, RA, 2021

Spider mite (*Acari: Tetranychidae*) outbreaks are common on corn grown in the arid West. Hot and dry conditions reduce mite development time, increase fecundity, and accelerate egg hatch. Climate change is predicted to increase drought incidents and produce more intense temperature patterns. Together, these environmental shifts may cause more frequent and severe spider mite infestations. Spider mite management is difficult as many commercially available acaricides are ineffective due to the development of resistance traits in field mite populations. Therefore, alternative approaches to suppress outbreaks are critically needed. Drought-tolerant plant **hybrids** alleviate the challenges of growing crops in water-limited environments; yet, it is unclear if drought-tolerant **hybrids** exposed to water stress affect mite outbreaks under these conditions. We conducted a greenhouse experiment to evaluate the effect of drought-tolerant corn **hybrids** on Banks grass mite [*Oligonychus pratensis* Banks (*Acari: Tetranychidae*)], a primary pest of corn, under optimal irrigation and water-stress irrigation. This was followed by a 2-yr field study investigating the effect of drought-tolerant corn **hybrids** exposed to the same irrigation treatments on Banks grass mite artificially infested on **hybrids** and resident spider mite populations. Results showed that water-stressed drought-tolerant **hybrids** had significantly lower Banks grass mite and resident spider mite populations than water-stressed drought-susceptible **hybrids**. Interestingly, water-stressed drought-tolerant **hybrids** had equal Banks grass mite populations to drought-susceptible and drought-tolerant **hybrids** under optimal irrigation. We posit that planting drought-tolerant **hybrids** may suppress spider mite outbreaks in water-challenged areas.

An explicit test of Pleistocene survival in peripheral versus nunatak refugia in two high mountain plant species

Pan, D; Hulber, K; Willner, W; Schneeweiss, GM, 2020

Pleistocene climate fluctuations had profound influence on the biogeographical history of many biota. As large areas in high mountain ranges were covered by glaciers, biota were forced either to peripheral refugia (and possibly beyond to lowland refugia) or to interior refugia (nunataks). However, nunatak survival remains controversial as it relies solely on correlative genetic evidence. Here, we test hypotheses of glacial survival using two high alpine plant species (the insect-pollinated *Pedicularis asplenifolia* and wind-pollinated *Carex fuliginosa*) in the European Alps. Employing the iDDC (integrative Distributional, Demographic and Coalescent) approach, which couples species distribution modelling, spatial and temporal demographic simulation and Approximate Bayesian Computation, we explicitly test three hypotheses of glacial survival: (a) peripheral survival only, (b) nunatak survival only and (c) peripheral plus nunatak survival. In *P. asplenifolia* the peripheral plus nunatak survival hypothesis was supported by Bayes factors (BF > 100), whereas in *C. fuliginosa* the peripheral survival only hypothesis, although best supported, could not be unambiguously distinguished from the peripheral plus nunatak survival hypothesis (BF = 5.58). These results are consistent with current habitat preferences (*P. asplenifolia* extends to higher elevations) and the potential for genetic swamping (i.e., replacement of local genotypes via **hybridization** with immigrating genotypes [expected to be higher in the wind-pollinated *C. fuliginosa*]). Although the persistence of plants on nunataks during glacial periods has been debated and studied over decades, this is one of the first studies to explicitly test the hypothesis instead of solely using correlative evidence.

Why new crop technology is not scale neutral A critique of the expectations for a crop-based African Green Revolution

Fischer, K, 2016

Poverty reduction during the Asian Green Revolution has been attributed to the inherent scale neutrality of new crop varieties making them equally beneficial to small-scale and large-scale farmers. The term 'scale-neutral' is now reappearing in debates on agricultural development in Africa with claims that crop technology is inherently scale-neutral and that African smallholders will significantly benefit from new crop varieties not specifically developed for their contexts. Using a social shaping of technology (SST) perspective and the concept of biological embeddedness, this paper critically examines whether it is helpful to describe crop technology as scale neutral when drawing lessons from the Asian Green Revolution about how new crop technology can be of benefit to African smallholders. The paper

describes how political commitment, rather than inherently scale-neutral crops, was central for the outcome of the Asian Green Revolution. It also highlights that while the effects of crop biology are often disregarded in adoption studies, biology significantly affected the ability of Green Revolution crop technology to benefit smallholders, and continues to do so today. Using maize and GM crops as examples, this paper suggests that GM crops in their current form have reinforced a technological trajectory established with **hybrid** technology and directed it away from smallholder practices and agroecologies. Consequently, describing crop technology as inherently scale-neutral is not helpful for understanding how crop technology works in Africa today and prevents important lessons being learned from the Asian Green Revolution. (C) 2016 Elsevier B.V. All rights reserved.

Targeted Capture Sequencing in Whitebark Pine Reveals Range-Wide Demographic and Adaptive Patterns Despite Challenges of a Large, Repetitive Genome

Syring, JV; Tennesen, JA; Jennings, TN; Wegrzyn, J; Scelfo-Dalbey, C; Cronn, R, 2016

Whitebark pine (*Pinus albicaulis*) inhabits an expansive range in western North America, and it is a keystone species of subalpine environments. Whitebark is susceptible to multiple threats - climate change, white pine blister rust, mountain pine beetle, and fire exclusion - and it is suffering significant mortality range-wide, prompting the tree to be listed as 'globally endangered' by the International Union for Conservation of Nature and 'endangered' by the Canadian government. Conservation collections (in situ and ex situ) are being initiated to preserve the genetic legacy of the species. Reliable, transferrable, and highly variable genetic markers are essential for quantifying the genetic profiles of seed collections relative to natural stands, and ensuring the completeness of conservation collections. We evaluated the use of **hybridization**-based target capture to enrich specific genomic regions from the 27 GB genome of whitebark pine, and to evaluate genetic variation across loci, trees, and geography. Probes were designed to capture 7,849 distinct genes, and screening was performed on 48 trees. Despite the inclusion of repetitive elements in the probe pool, the resulting dataset provided information on 4,452 genes and 32% of targeted positions (528,873 bp), and we were able to identify 12,390 segregating sites from 47 trees. Variations reveal strong geographic trends in heterozygosity and allelic richness, with trees from the southern Cascade and Sierra Range showing the greatest distinctiveness and differentiation. Our results show that even under non-optimal conditions (low enrichment efficiency; inclusion of repetitive elements in baits), targeted enrichment produces high quality, codominant genotypes from large genomes. The resulting data can be readily integrated into management and gene conservation activities for whitebark pine, and have the potential to be applied to other members of 5-needle pine group (*Pious* subsect. *Quinquefolia*) due to their limited genetic divergence.

Windthrow Detection in European Forests with Very High Resolution Optical Data

Einzmann, K; Immitzer, M; Bock, S; Bauer, O; Schmitt, A; Atzberger, C, 2017

With climate change, extreme storms are expected to occur more frequently. These storms can cause severe forest damage, provoking direct and indirect economic losses for forestry. To minimize economic losses, the windthrow areas need to be detected fast to prevent subsequent biotic damage, for example, related to beetle infestations. Remote sensing is an efficient tool with high potential to cost-efficiently map large storm affected regions. Storm Niklas hit South Germany in March 2015 and caused widespread forest cover loss. We present a two-step change detection approach applying commercial very high-resolution optical Earth Observation data to spot forest damage. First, an object-based bi-temporal change analysis is carried out to identify windthrow areas larger than 0.5 ha. For this purpose, a supervised Random Forest classifier is used, including a semi-automatic feature selection procedure; for image segmentation, the large-scale mean shift algorithm was chosen. Input features include spectral characteristics, texture, vegetation indices, layer combinations and spectral transformations. A **hybrid**-change detection approach at pixel-level subsequently identifies small groups of fallen trees, combining the most important features of the previous processing step with Spectral Angle Mapper and Multivariate Alteration Detection. The methodology was evaluated on two test sites in Bavaria with RapidEye data at 5 m pixel resolution. The results regarding windthrow areas larger than 0.5 ha were validated with reference data from field visits and acquired through orthophoto interpretation. For the two test sites, the novel object-based change detection approach identified over 90% of the windthrow areas (≥ 0.5 ha). The red edge channel was the most important for windthrow identification. Accuracy levels of the change detection at tree level could not be calculated, as it was not possible to collect field data for single trees, nor was it possible to perform an orthophoto validation. Nevertheless, the plausibility and applicability of the pixel-based approach is demonstrated on a second test site.

Trophic interactions in a changing world: modelling aboveground-belowground interactions

Schroter, D; Brussaard, L; De Deyn, G; Poveda, K; Brown, VK; Berg, MP; Wardle, DA; Moore, J; Wall, DH, 2004

The rate and scale of human-driven changes can exert profound impacts on ecosystems, the species that make them up and the services they provide that sustain humanity. Given the speed at which these changes are occurring, one of society's major challenges is to coexist within ecosystems and to manage ecosystem services in a sustainable way. The effect of possible scenarios of global change on ecosystem services can be explored using ecosystem models. Such models should adequately represent ecosystem processes above and below the soil surface (aboveground and belowground) and the interactions between them. We explore possibilities to include such interactions into ecosystem models at scales that range from global to local. At the regional to global scale we suggest to expand the plant functional type concept (aggregating plants into groups according to their physiological attributes) to include functional types of aboveground-belowground interactions. At the scale of discrete plant communities, process-based and organism-oriented models could be combined into **"hybrid"** approaches that include organism-oriented mechanistic representation of a limited number of trophic interactions in an otherwise process - oriented approach. Under global change the density and activity of organisms determining the processes may change non-linearly and therefore explicit knowledge of the organisms and their responses should ideally be included. At the individual plant scale a common organism-based conceptual model of aboveground-belowground interactions has emerged. This conceptual model facilitates the formulation of research questions to guide experiments aiming to identify patterns that are common within, but differ between, ecosystem types and biomes. Such experiments inform modelling approaches at larger scales. Future ecosystem models should better include this evolving knowledge of common patterns of aboveground-belowground interactions. Improved ecosystem models are necessary tools to reduce the uncertainty in the information that assists us in the sustainable management of our environment in a changing world. (C) 2004 Elsevier GmbH. All rights reserved.

Spatio-temporal dynamics of the *Allonemobius fasciatus*-*A. socius* mosaic hybrid zone: a 14-year perspective

Britch, SC; Cain, ML; Howard, DJ, 2001

Long-term studies of **hybrid** zones can provide valuable insight into a number of questions that have long attracted the attention of evolutionists. These questions range from the stability and fate of **hybrid** zones to the relative fitness of **hybrids**. In this paper we report the results of a 14-year survey of the *Allonemobius fasciatus*-*Allonemobius socius* **hybrid** zone. Populations were collected intensively in 1986 and 1987 and then more sporadically through the end of the 1980s and throughout the 1990s. By documenting changes in the genetic composition of populations near and within the zone during this period of time we assessed: the strength of the reproductive isolation between the two species; the relative growth rates (which can be considered a surrogate of relative fitness) of genotype classes corresponding to **hybrids** and to pure species individuals; and, the power of single-year and multi-year measurements of relative growth rates to predict changes in the genetic composition of mixed populations through time. In brief, we found very large year-to-year variation in the relative growth rates of pure species and **hybrid** individuals. This variation may reflect the fact that both species are at the edge of their range and perhaps at the limits of their ability to deal with environmental perturbations. As a consequence of the variation, even multi-year estimates of relative growth rates often provided imprecise predictions regarding the future genotypic composition of mixed populations. Despite our limited ability to predict the dynamics of individual populations, some trends are apparent. *A. socius*, the southern species, has clearly increased in frequency along a transect through the Appalachian Mountains, indicating that the zone is moving north in this region. In contrast, the zone appeared to be more stable along the East Coast transect. Within mixed populations, character-index profiles are often bimodal and stable through time, indicating relatively strong reproductive isolation between the two species that is not being reinforced, nor is it breaking down.

Photocatalytic Systems for CO₂ Reduction: Metal-Complex Photocatalysts and Their Hybrids with Photofunctional Solid Materials

Kumagai, H; Tamaki, Y; Ishitani, O, 2022

CONSPECTUS: Photocatalytic CO₂ reduction is a critical objective in the field of artificial photosynthesis because it can potentially make a total solution for global warming and shortage of energy and carbon resources. We have successfully developed various highly efficient, stable, and selective photocatalytic systems for CO₂ reduction using transition metal complexes as both photosensitizers and catalysts. The molecular architectures for constructing selective and efficient photocatalytic systems for CO₂ reduction are discussed herein. As a typical example, a mixed system of a ring-shaped Re(I) trinuclear complex as a photosensitizer and fac-[Re(bpy)(CO)(3)](OC₂H₄N(C₂H₄OH)(2)) as a catalyst selectively photocatalyzed CO₂ reduction to CO with the highest quantum yield of 82% and a turnover number (TON) of over 600. Not only rare and noble metals but also earth abundant ones, such as Mn(II), Cu(I), and Fe(II) can be used as central metal cations. In the case using a Cu(I) dinuclear complex as a photosensitizer and fac-Mn(bpy)(CO)(3)Br as a catalyst, the total formation quantum yield of CO and HCOOH from CO₂ was 57% and TONCO+HCOOH exceeded 1300. Efficient supramolecular photocatalysts for CO₂ reduction, in which photosensitizer and catalyst units are connected through a bridging ligand, were developed for removing a diffusion control on collisions between a photosensitizer and a catalyst. Supramolecular photocatalysts, in which Ru(N^πN)(3)-type photosensitizer and Re(I) or Ru(II) catalyst units are connected to each other with an alkyl chain, efficiently and selectively photocatalyzed CO₂ reduction in solutions. Mechanistic studies using time-resolved IR and electrochemical measurements provided molecular architecture for constructing efficient supramolecular photocatalysts. A Ru(II)-Re(I) supramolecular photocatalyst constructed according to this molecular architecture efficiently photocatalyzed CO₂ reduction even when it was fixed on solid materials. Harnessing this property of the supramolecular photocatalysts, two types of **hybrid** photocatalytic systems were developed, namely, photocatalysts with light-harvesting capabilities and photoelectrochemical systems for CO₂ reduction. Introduction of light-harvesting capabilities into molecular photocatalytic systems should be important because the intensity of solar light shone on the earth's surface is relatively low. Periodic mesoporous organosilica, in which methyl acridone groups are embedded in the silica framework as light harvesters, was combined with a Ru(II)-Re(I) supramolecular photocatalyst with phosphonic acid anchoring groups. In this **hybrid**, the photons absorbed by approximately 40 methyl acridone groups were transferred to one Ru(II) photosensitizer unit, and then, the photocatalytic CO₂ reduction commenced. To use water as an abundant electron donor, we developed **hybrid** photocatalytic systems combining the metal-complex photocatalysts with semiconductor photocatalysts that display high photooxidation powers, in which two photons are sequentially absorbed by the metal-complex photosensitizer and the semiconductor, resulting in both high oxidation and reduction power. Various types of dye sensitized molecular photocathodes comprising the p-type semiconductor electrodes and the supramolecular photocatalysts were developed. Full photoelectrochemical cells combining these dye-sensitized molecular photocathodes and n-type semiconductor photoanodes achieved CO₂ reduction using only visible light as the energy source and water as the reductant. Drastic improvement of dye-sensitized molecular photocathodes is reported. The results presented in this Account clearly indicate that we can construct very efficient, selective, and durable photocatalytic systems constructed with the metal-complex photosensitizers and catalysts. The supramolecular-photocatalyst architecture in which the photosensitizer and the catalyst are connected to each other is useful especially on the surface of solid owing to rapid electron transfer from the photosensitizer to the catalyst. On basis of these findings, we successfully constructed **hybrid** systems of the supramolecular photocatalysts with photoactive solid materials. These **hybridizations** can add new functions to the metal-complex photocatalytic systems, such as water oxidation and light harvesting.

Conservation biology of banksias: insights from natural history to simulation modelling

Lamont, BB; Enright, NJ; Witkowski, ETF; Groeneveld, J, 2007

We have studied the ecology and conservation requirements of Banksia species in the species-rich sandplains of south-western Australia for 25 years. Loss of habitat through land-clearing has had the greatest impact on their conservation status over the last 50 years. Ascertaining optimal conditions for conservation management in bushland requires detailed knowledge of the species under consideration, including demographic attributes, fire regime, growing conditions and interactions with other species. Where populations have been fragmented, seed production per plant has also fallen. The group most vulnerable to the vagaries of fire, disease, pests, weeds and climate change are the non-sprouters, rather than the resprouters, with population extinction so far confined to non-sprouting species. Recent short-interval fires (< 8 years) appear to have had little impact at the landscape scale, possibly because they are rare and patchy. Fire intervals exceeding 25-50 years can also lead to local extinction. Up to 200 viable seeds are required for parent replacement in Banksia hookeriana when growing conditions are poor (low post-fire rainfall, commercial flower harvesting) and seed banks of this size can take up to 12 years to be reached. Seed production is rarely limited by pollinators, but interannual seasonal effects and resource availability are important. Genetic diversity of the seed store is quickly restored to the level of the parents in B. hookeriana. Florivores and granivores generally reduce seed stores, although this varies markedly among species. In Banksia tricuspidis, black cockatoos actually increase seed set by selectively destroying borers. Potential loss of populations through the root pathogen Phytophthora cinnamomi also challenges management, especially in the southern sandplains. Prefire dead plants are a poor source of seeds for the next generation when fire does occur. Harvesting seeds and sowing post-fire have much to commend them for critically endangered species. Bare areas caused by humans can result in ideal conditions for plant growth and seed set. However, in the case of B. hookeriana/B. prionotes, disturbance by humans has fostered **hybridisation**, threatening the genetic integrity of both species, whereas fine-textured soils are unsuitable for colonisation or rehabilitation. Few viable seeds become seedlings after fire, owing to post-release granivory and herbivory and unsuitable germination conditions. Seedling-competitive effects ensure that season/intensity of fire is not critical to recruitment levels, except in the presence of weeds. Water availability during summer-autumn is critical and poses a problem for conservation management if the trend for declining rainfall in the region continues. Our simulation modelling for three banksias shows that the probability of co-occurrence is maximal when fire is stochastic around a mean of 13 years, and where fire-proneness and post-fire recruitment success vary in the landscape. Modelling results suggest that non-sprouting banksias could not survive the pre-European frequent-fire scenario suggested by the new grass-tree technique for south-western Australia. However, we have yet to fully explore the conservation significance of long-distance dispersal of seeds, recently shown to exceed 2.5 km in B. hookeriana.

Genetic Diversity for Wheat Improvement as a Conduit to Food Security

Mujeeb-Kazi, A; Kazi, AG; Dundas, I; Rasheed, A; Ogbonnaya, F; Kishii, M; Bonnett, D; Wang, RRC; Xu, S; Chen, PD; Mahmood, T; Bux, H; Farrakh, S, 2013

Genetic diversity is paramount for cultivated crops genetic improvement, and for wheat this resides in three gene pools of the Triticeae. In wheat, access to this diversity and its exploitation is based upon the genetic distance of the wild species relatives from the wheat genomes. For several decades, these wide crosses have been a reservoir of novel variation for wheat improvement. Among these, close relatives of the primary gene pool have been preferred since this ensures successful gene transfer as they permit homologous genetic exchanges to occur between related genomes, as exemplified by the A and D genome diploid progenitors. One strategy has been based upon first producing genetic stocks that capture the potential of the diploids via bridge crossing where the D genome synthetic hexaploid wheats (2n = 6x = 42, AABBDD) are exploited. The synthetics are products of crosses between elite durum wheat cultivars (Triticum turgidum) and various Aegilops tauschii accessions. Similarly, the diversity of the A and B genomes has also been assembled as AABBAA (T. turgidum/A genome diploids Triticum boeoticum, Triticum monococcum, Triticum urartu) and AABBBB (SS) (T. turgidum/Aegilops speltoides). The utilization of these useful diversity for various biotic/abiotic stresses including in the development of molecular tools for enhancing breeding efficiency has been in the forefront of wheat improvement over the past two decades. Additional strategy employed includes the direct crosses between parental diploids and recipient wheat cultivars extended to give even swifter products by top- or backcrossing the F-1 combinations with either durum or bread wheats. Relatively less progress has been made in the use of genes from tertiary gene pool often involving "intergeneric crosses." The potency of potentially useful diversity in tertiary gene pool warrants further exploitation of this resource. Presented here are major facets of intergeneric **hybridization** embracing a taxonomic consideration of genetic diversity within the Triticeae, the exploitation protocols, prebreeding strategies, and some of the outputs from distant **hybridization** with a major focus on wheat/alien chromosomal exchanges classed as "translocations" such as T1BL.1RS and to a lesser degree the T1AL.1RS Robertsonian translocations. This chapter also attempts to relate the exploitation of the Triticeae genetic diversity with wheat productivity as a means of addressing diverse stress constraints that if pursued will provide yield enhancing outputs necessary for overriding environmental limitations of climate change, unpredictable incidences of biotic stresses, and catalyzing gains for food security with wheat.

Modelling West Nile virus transmission risk in Europe: effect of temperature and mosquito biotypes on the basic reproduction number

Vogels, CBF; Hartemink, N; Koenraadt, CJM, 2017

West Nile virus (WNV) is a mosquito-borne flavivirus which has caused repeated outbreaks in humans in southern and central Europe, but thus far not in northern Europe. The main mosquito vector for WNV, *Culex pipiens*, consists of two behaviourally distinct biotypes, *pipiens* and *molestus*, which can form **hybrids**. Differences between biotypes, such as vector competence and host preference, could be important in determining the risk of WNV outbreaks. Risks for WNV establishment can be modelled with basic reproduction number (R0) models. However, existing R0 models have not differentiated between biotypes. The aim of this study was, therefore, to explore the role of temperature-dependent and biotype-specific effects on the risk of WNV establishment in Europe. We developed an R0 model with temperature-dependent and biotype-specific parameters, and calculated R0 values using the next-generation matrix for several scenarios relevant for Europe. In addition, elasticity analysis was done to investigate the contribution of each biotype to R0. Global warming and increased mosquito-to-host ratios can possibly result in more intense WNV circulation in birds and spill-over to humans in northern Europe. Different contributions of the *Cx. pipiens* biotypes to R0 shows the importance of including biotype-specific parameters in models for reliable WNV risk assessments.

Overwintering, cold tolerance and supercooling capacity comparison between *Liriomyza sativae* and *L. trifolii*, two invasive leafminers in China

Zhang, QK; Wu, SY; Wang, HH; Xing, ZL; Lei, ZR, 2022

Liriomyza sativae Blanchard and *Liriomyza trifolii* (Burgess) are two highly polyphagous pests that successively invaded China in the 1990s and 2000s, respectively, threatening vegetable and horticultural plants. Competitive displacement of *L. sativae* by *L. trifolii* occurred during the expansion process of the latter in southern China, while whether *L. trifolii* can expand their range to northern China remains unclear. Overwintering and cold tolerance capacity largely determine the species distribution range and can affect species displacement through overwintering and phenology. In this study, we compared the overwintering potential, cold tolerance and supercooling point (SCP) between these two leafminer species. Our results showed that *L. trifolii* can overwinter at higher altitudes than *L. sativae*. In addition, we found that they can both successfully overwinter in greenhouses in northern China, and the overwintering capacity of *L. trifolii* was higher than that of *L. sativae*. Moreover, the extreme low-temperature survival of *L. trifolii* was significantly higher than that of *L. sativae*, and the SCP of the former was lower than that of the latter. We thus conclude that the overwintering and cold tolerance capacity of *L. trifolii* is much better than that of *L. sativae*. Our findings indicate that *L. trifolii* has the potential to displace *L. sativae* and expand its range to northern China. Moreover, our results have important implications for predicting overwinter ranges and developing management strategies for invasive leafminers in China.

Diversity of mosquito fauna (Diptera, Culicidae) in higher altitude regions of Croatia

Busic, N; Kucinic, M; Merdic, E; Bruvo-Madaric, B, 2021

Global climate change and the accompanying rise in temperature could affect the biology and ecology of a number of vectors, including mosquitoes. High altitude areas that were previously unsuitable for the spread of mosquito vector populations could become suitable. The aim of this research was to study the distribution of mosquito species in higher altitude regions of Croatia. Samples were collected in three areas: Slavonian Mountains, Gorski Kotar, and Middle Velebit. Specimens were morphologically determined and confirmed by DNA barcoding and other genetic markers and showed the presence of 16 species belonging to six genera. The most abundant species were the *Culex pipiens* complex with 50% of the collected specimens. Both *pipiens* (Linnaeus, 1758) and *molestus* (Forsk., 1775) biotypes and their **hybrids** were identified within the complex, followed by *Culex torrentium* (Martini, 1925) (20.2%), *Culiseta longiareolata* (Macquart, 1838) (8.5%), and the invasive species *Aedes japonicus* (Theobald, 1901) (7.8% of the total number of collected specimens). The remaining 12 species made up 14.7% of the collected specimens. Intraspecific COI p-distances were within the standard barcoding threshold for OTUs, while interspecific genetic distances were much higher, confirming the existence of barcoding gaps. Mosquito fauna of Croatian mountains showed a moderate variety and made 30.8% of the total number of recorded mosquito species in Croatia thus far.

ANALYSIS OF PROPAGATION FOR IMPULSIVE REACTION-DIFFUSION MODELS

Fazly, M; Lewis, M; Wang, H, 2020

We study a **hybrid** impulsive reaction-advection-diffusion model given by a reaction-advection-diffusion equation composed with a discrete-time map in space dimension n is an element of N . The reaction-advection-diffusion equation takes the form $u(t)((m)) = \text{div}(A \text{ del } u((m)) - qu((m))) + f(u((m)))$ for (x, t) is an element of $R-n \times (0, 1)$, for some function f , a drift q , and a diffusion matrix A . When the discrete-time map is local in space we use $N-m(x)$ to denote the density of population at a point x at the beginning of reproductive season in the m th year, and when the map is nonlocal we use $u(m)(x)$. The local discrete-time map is $\{u((m))(x, 0) = g(N-m(x))$ for x is an element of $R-n$, $N-m+1(x) := u((m))(x, 1)$ for x is an element of $R-n$ for some function g . The nonlocal discrete time map is $\{u((m))(x, 0) = u(m)(x)$ for x is an element of $R-n$, $u(m+1) : g(\int(Rn) K(x - y)u((m))(y, 1)dy)$ for x is an element of $R-n$, when K is a nonnegative normalized kernel. Here, we analyze the above model from a variety of perspectives so as to understand the phenomenon of propagation. We provide explicit formulas for the spreading speed of propagation in any direction e is an element of $R-n$. Due to the structure of the model, we apply a simultaneous analysis of the differential equation and the recurrence relation to establish the existence of traveling wave solutions. The remarkable point is that the roots of spreading speed formulas, as a function of drift, are exactly the values that yield blow-up for the critical domain dimensions, just as with the classical Fisher's equation with advection. We provide applications of our main results to impulsive reaction-advection-diffusion models describing periodically reproducing populations subject to climate change, insect populations in a stream environment with yearly reproduction, and grass growing logistically in the savannah with asymmetric seed dispersal and impacted by periodic fires.

Traditional agricultural management of Kam Sweet Rice (*Oryza sativa* L.) in southeast Guizhou Province, China

Liu, CH; Wang, YJ; Ma, XD; Cui, D; Han, B; Xue, DY; Han, LZ, 2022

Background The Dong people mainly live in Hunan, Guangxi and Guizhou provinces, China, with a long history of glutinous rice cultivation, among which Kam Sweet Rice (KSR) is a group of rice landraces that has been domesticated for thousands of years by the Dong people. The core distribution area of KSR is Liping, Congjiang and Rongjiang County of southeast, Guizhou Province. Paddy fields, forests, livestock and cottages have formed a special artificial wetland ecosystem in local area, and the Dong people have also formed a set of traditional farming systems of KSR for variety breeding, field management, and soil and water conservation. However, this traditional agricultural management has not been reported at multiple levels based on landraces, species and ecosystems. Methods Fieldwork was conducted in ten villages in southeast Guizhou from 2019 to 2021. A total of 229 informants were interviewed from the villages. Semi-structured and key informant interviews were administered to collect ethnoecological data on the characteristics and traditional utilization of KSR, traditional farming systems and agricultural management of the Dong people. Results (1): A total of 57 KSR landraces were recorded as used by the Dong people in southeast Guizhou. We analyzed the cultural importance index (CII) of all KSRs. KSR with high CII often has a pleasant taste, special biological characteristics of cold resistance, disease and insect resistance and high utilization in the traditional culture of Dong people. (2) There is a clear division of labor between men and women in the breeding, seed retention, field management and grain storage management of different landraces of KSR in Dong communities. In order to resist natural disasters and insect pests, the cultivation of KSR is usually managed by multi-variety mixed planting. These agricultural management modes are the result of Dong people's understanding and adaptation to the local natural geographical environment, as well as the experience and wisdom crystallization of Dong people's long-term practice. (3) The traditional farmland of Dong People is a typical artificial wetland ecosystem that is planted with mixed KSR landraces with rich traditional wisdom. In addition, the economic benefit of the rice-fish-duck

symbiotic system was 3.07 times that of **hybrid** rice alone; therefore, the rice-fish-duck system not only has the function of maintaining soil, water and ecological balance but also improves the income of Dong people. Conclusion KSR is a special kind of rice that has been domesticated and cultivated by Dong people for thousands of years. Dong people have also formed traditional agriculture dominated by KSR cultivation. The traditional agricultural management of Dong people provides suitable habitats for flora and fauna with biodiversity protection, and convenient conditions for rational utilization and distribution of water resources were also provided. This traditional management mode is of great significance for environmental protection, climate change response, community resource management, sustainable utilization and agricultural transformation in modern society. Therefore, we call for interdisciplinary research in natural and social sciences, in-depth study of the ecological culture of ethnic areas, and sort out treasures conducive to the development of all mankind.

~~The Arrival of the Northern House Mosquito *Culex pipiens* (Diptera: Culicidae) on Newfoundland's Avalon Peninsula~~

Chaulk, AC; Carson, KP; Whitney, HG; Fonseca, DM; Chapman, TW, 2016

Culex pipiens L., the northern house mosquito, is the primary vector of West Nile virus to humans along the east coast of North America and thus the focus of much study. This species is an urban container-breeding mosquito whose close contact with humans and flexibility in host choice has led to its classification as a "bridge vector"; that is, it is thought to move zoonotic diseases to humans from vertebrate reservoirs. While this invasive species is now well documented in its established range, which expanded in 2001 to include Canada, the existence of populations of this species along the fringes of its range are less well known. Here we report, using morphological and genetic techniques, the existence of two locations where *Cx. pipiens* exists in Newfoundland in both expected and unexpected sites based on projected habitat suitability on the island.

~~Biological Flora of the British Isles: *Sorbus torminalis*~~

Thomas, PA, 2017

1. This account presents information on all aspects of the biology of *Sorbus torminalis* (L.) Crantz (Wild Service-tree) that are relevant to understanding its ecological characteristics and behaviour. The main topics are presented within the standard framework of the Biological Flora of the British Isles: distribution, habitat, communities, responses to biotic factors, responses to environment, structure and physiology, phenology, floral and seed characters, herbivores and disease, history and conservation. 2. *Sorbus torminalis* is an uncommon, mostly small tree (but can reach 33 m) native to lowland England and Wales, and temperate and Mediterranean regions of mainland Europe. It is the most shade-tolerant member of the genus in the British Isles, and as a result, it is more closely associated with woodland than any other British species. Like other British *Sorbus* species, however, it grows best where competition for space and sunlight is limited. Seedlings are shade tolerant but adults are only moderately so. This, combined with its low competitive ability, restricts the best growth to open areas. In shade, saplings and young adults form a sapling bank, showing reproduction and extensive growth only when released. *Sorbus torminalis* tolerates a wide range of soil reaction (pH 3.5-8.0) but grows best on calcareous clays and thin soils over limestone. 3. *Sorbus torminalis* is a sexual, diploid, non-apomictic species that has **hybridised** with a number of other *Sorbus* species to form microspecies. The hermaphrodite flowers are primarily insect pollinated. Seed production is reliable only in warm years, especially at the edge of its range, although even then seed viability is low. The fruits are primarily dispersed by carnivorous mammals. Seeds display embryo dormancy but most will germinate the first spring after falling. 4. This tree is very tolerant of short droughts but only moderately tolerant of frost, hence its southerly and lowland distribution. It faces no particular individual threats although the small size of most populations makes it susceptible to habitat loss and fragmentation, particularly through the loss of open coppiced areas. As a consequence, it appears to be declining throughout Britain and Europe despite its wide range of historical uses and the high value of its timber. The extent to which these losses will be offset by increases due to climate change is unknown.
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~~Effects of Warm Winter Temperature on the Abundance and Gonotrophic Activity of *Culex* (Diptera: Culicidae) in California~~

Reisen, WK; Thiemann, T; Barker, CM; Lu, HL; Carroll, B; Fang, Y; Lothrop, HD, 2010

Culex tarsalis Coquillett, *Cx. quinquefasciatus* Say, and *Cx. pipiens* L. were collected during the warm winter of 2009 using dry ice-baited and gravid traps and walk-in red boxes positioned in desert, urban, and agricultural habitats in Riverside, Los Angeles, Kern, and Yolo Counties. Temperatures exceeded the preceding 50 yr averages in all locations for most of January, whereas rainfall was absent or below average. Abundance of *Culex* Species in traps during January ranged from 83 to 671% of the prior 5 yr average in all locations. Few females collected resting were in diapause during January based on follicular measurements. Evidence for early season gonotrophic activity included the detection of freshly bloodfed, gravid, and parous females in resting collections, gravid oviposition site-seeking females in gravid female traps, and nulliparous and parous host-seeking females at dry ice-baited traps. Female *Culex* seemed to employ multiple overwintering strategies in California, including larval and adult quiescence, adult female diapause, and all intermediate situation with adult females collected with enlarged follicles, but without evident vitellogenesis. West Nile, St. Louis, or western equine encephalitis viruses were not detected in 198 pools of adults or 56 pools of adults reared from field-collected immatures collected during January and February 2009. Our preliminary data may provide insight into how climate change may extend the mosquito season in California.

~~*Bursaphelenchus xylophilus*: opportunities in comparative genomics and molecular host-parasite interactions~~

Jones, JT; Moens, M; Mota, M; Li, HM; Kikuchi, T, 2008

Most *Bursaphelenchus* species are fungal feeding nematodes that colonize dead or dying trees. However, *Bursaphelenchus xylophilus*, the pine wood nematode, is also a pathogen of trees and is the causal agent of pine wilt disease. *B. xylophilus* is native to North America and here it causes little damage to trees. Where it is introduced to new regions it causes huge damage. The most severely affected areas are found in the Far East but more recently *B. xylophilus* has been introduced into Portugal and the potential for damage here is also high. As incidence and severity of pine wilt disease are linked to temperature we suggest that climate change is likely to exacerbate the problems caused by *B. xylophilus* and, in addition, will extend (northwards in Europe) the range in which pine wilt disease can occur. Here we review what is currently known about the interactions of *B. xylophilus* with its hosts, including recent developments in our understanding of the molecular biology of pathogenicity in the nematode. We also examine the potential developments that could be made by more widespread use of genomics tools to understand interactions between *B. xylophilus*, bacterial pathogens that have been implicated in disease and host trees.

~~Dieback of riparian alder caused by the *Phytophthora alni* complex: projected consequences for stream ecosystems~~

Bjelke, U; Boberg, J; Oliva, J; Tattersdill, K; McKie, BG, 2016

Alder trees (*Alnus* spp.) are key nitrogen-fixing riparian species in the northern hemisphere. Inputs of nitrogen-rich leaf litter from alder into stream food webs can contribute significantly to nitrogen dynamics at local and landscape scales. Alder trees also provide habitats for terrestrial and aquatic organisms, and help stabilize river banks. Recently, substantial declines in alder stands have occurred along streams in Europe, with damages observed in some parts of North America also. A major driver has been the invasive oomycete pathogen *Phytophthora alni* species complex, which can spread rapidly along stream networks. This review synthesises information on the pathogen, processes of spread and infection, and its impacts on alder. We further address the potential ecosystem-level and management

consequences of the decline of alder, and highlight research needs. The alder dieback caused by *P. alni* is associated with reductions in shade and quality and quantity of leaf litter. A decline in the structural integrity of branches and roots further threatens bank stability. Stream banks dominated by other tree species or no trees at all will result in ecosystem-level changes both above and below the waterline. The *P. alni* taxonomic complex includes different species with varying phenotypes. An improved understanding of their environmental tolerances, virulence and evolution, along with the processes regulating the spread and impacts of the pathogen, would assist in identification of the riparian and stream systems most vulnerable not only to invasion but also to the heaviest disease outbreaks and ecosystem-level impacts. Within the *P. alni* complex, the highly pathogenic **hybrid** species *P. x alni* is favoured by mild winters and warm, but not excessively hot summer temperatures suggesting possible changes in distribution and level of impact under future global climate change.

~~Bio-economics of Indian hybrid Bt cotton and farmer suicides~~

Gutierrez, AP; Ponti, L; Kranthi, KR; Baumgartner, J; Kenmore, PE; Gilioli, G; Boggia, A; Cure, JR; Rodriguez, D, 2020

Background The implementation of **hybrid** Bt cotton unique to India has been heralded as a grand success by government agencies, seed companies and other proponents, and yet yields have stagnated at low levels and production costs have risen 2.5-3-fold. The low-yield **hybrid** cotton system of India contributes thousands of farmer suicides to the annual national toll. Conceptual and methodological barriers have hindered bioeconomic analysis of the ecological and social sustainability of such cross-scale agro-ecological problems in time and geographic space, under global technology and climate change. As a paradigm shift, we use conceptually simple, parameter-sparse, theoretically based, mechanistic, weather-driven physiologically based demographic models (PDBMs) to deconstruct the bio-economics of the Indian cotton system. Results Our analysis of Indian **hybrid** cotton system explains some extant ecological and economic problems, and suggests a viable solution. Specifically, the model accurately captured the age-stage mass dynamics of rainfed and irrigated cotton growth/development and the interactions with the key pest pink bollworm across five south-central Indian states, and enabled identification of proximate bioeconomic factors responsible for low yield and their relationship to farmer suicides. The results are reinforced by analysis of Ministry of Agriculture annual state-level data. We explain why short-season, high-density non-GM cotton is a highly viable solution for Indian cotton farmers in rainfed and irrigated cotton areas of the five states, and possibly nationally. The transition from a theoretical bioeconomic construct to a real-world regional bioeconomic analysis proved seamless. Conclusions The **hybrid** long-season Bt technology for rainfed and irrigated cotton is unique to India, and is a value capture mechanism. This technology is suboptimal leading to stagnant yields, high input costs, increased insecticide use, and low farmer incomes that increase economic distress that is a proximate cause of cotton farmer suicides. The current GM Bt technology adds costs in rainfed cotton without commensurate increases in yield. Non-GM pure-line high-density short-season varieties could double rainfed cotton yield, reduce costs, decrease insecticide use, and help ameliorate suicides. The GM **hybrid** technology is inappropriate for incorporation in short-season high-density varieties.

~~Importation biological control of invasive fire ants with parasitoid phorid flies progress and prospects~~

Chen, L; Morrison, LW, 2021

Twenty-two known species of Pseudacteon flies (Diptera: Phoridae) are parasitoids of South American fire ants in the *Solenopsis saevissima* (Smith) complex. Phorid flies of different sizes and with differing activity patterns have been released in the United States to control two imported fire ant species-*Solenopsis richteri* and *Solenopsis invicta*-and their **hybrid**. Six highly host-specific Pseudacteon species have been successfully established at dozens of release sites and most are now widely distributed across areas infested by imported fire ants. This complex of released fly species is expected to weaken the competitive vigor of fire ant colonies through both direct and indirect effects, and eventually reduce the abundance of imported fire ants. To date, however, few studies have attempted to document the effect of these parasitoids on host ants in the field, and future research should focus on the overall magnitude of reduction in host ant populations. Knowledge gained from the successful importation and establishment of South American phorid flies in the US can provide guidance for utilization of these parasitoid flies for biological control of *S. invicta* in other introduced ranges, and aid the search for additional importation biological control agents of pest ants in general.

~~Parallel evolution in sympatric, hybridizing species: performance of Colias butterflies on their introduced host plants~~

Porter, AH; Levin, EJ, 2007

Shared ancestry and **introgression** can contribute to genetic similarity between **hybridizing** species, and it is generally difficult to disentangle these causes. However, shared ancestry plays a more limited role in traits that have recently undergone parallel directional selection in the two species, permitting the role of **introgression** to be better understood. The butterflies *Colias eurytheme* (Boisduval) and *Colias philodice* (Godart) (Lepidoptera, Pieridae) are native to North America and have shifted their host ranges in parallel onto several introduced weedy and agricultural legumes. These butterflies **hybridize** at moderate rates throughout their range, and there is a strong possibility that they could be sharing host-associated adaptations. We split families of each species among nine introduced, prospective hosts and measured survivorship, larval duration, pupal weight, and a new variable, effective daily growth rate (DGR), analogous to a compound daily interest rate in economics. We found strong effects of host, sex, and family (species), but negligible effects of the hosts *species interaction that would indicate species-specific differences in performance on different hosts. We found species-specific life-history differences: C. eurytheme matured significantly later and reached a significantly larger body size than C. philodice while growing at the same DGR. Protandry was strong, and males, in addition to pupating sooner than females, grew significantly faster than females as measured by DGR. We measured broad-sense heritabilities and genetic correlations for host-associated performance variables. Most pairwise comparisons of performance among hosts and most pairwise comparisons between performance variables showed positive genetic correlations, except survivorship where little heritability was found. Nevertheless, a factorial multivariate analysis of variance of G-matrices showed highly significant species, host, and hostspecies interactions, suggesting differentially evolving genetic architectures underlying host adaptation in these two species, despite the small differences in overall performance. At least some of the genes affecting host performance in Colias are likely to be in the small, species-diagnostic regions and not shared via introgression between these hybridizing species. For biologists interested in the evolutionary ecology of their host associations, including applied biologists managing their agricultural pest potential, C. eurytheme and C. philodice are most usefully studied as if they were a single polymorphic species wherever they co-exist. In studying species that hybridize readily with a sympatric congener, it may often be necessary to include the second species in the experimental design.*

~~Distribution of Pseudacteon spp. (Diptera: Phoridae), biological control agents of Solenopsis spp. (Hymenoptera: Formicidae), in Louisiana and associated prevalence of Kneallhazia solenopsae (Microsporidia: Thelohaniidae)~~

Meszaros, A; Oi, DH; Valles, SM; Beuzelin, JM; Reay-Jones, FPF; Johnson, SJ, 2014

Phorid flies, Pseudacteon spp. (Diptera: Phoridae), have been released in the United States since 1996 as biological control agents for imported fire ants, *Solenopsis invicta* Buren, *Solenopsis richteri* Forel, and their **hybrid** (Hymenoptera: Formicidae). A statewide survey was conducted in Louisiana during 2009 and 2010 to determine the distribution of Pseudacteon tricuspidis Borgmeier and Pseudacteon curvatus Borgmeier, and to quantify the potential spatial association between the two species. Additionally, collected phorid flies were tested for the microsporidium Kneallhazia (=Thelohania) solenopsae (Knell, Allen, and Hazard), another natural enemy of fire ants, to establish an account of the pathogen's distribution and prevalence in phorid fly populations. *P. tricuspidis* and *P. curvatus* have expanded their range from four and three separate release sites, respectively, in Louisiana. By 2010, *P. tricuspidis* and *P. curvatus* occupied approximately 86,600 and 111,900 km(2), respectively. Overall, *P. curvatus* was more abundant than *P. tricuspidis*, with 41.9 +/- 7.3 (SE) and 9.8 +/- 1.5 (SE) females, respectively, collected on average per sampling site in 2009. Spatial Analysis by Distance IndicEs (SADIE) suggested aggregation for the two phorid fly species. *P. tricuspidis* collections were positively associated with *P. curvatus* collections, indicating that gaps and clusters of both species generally overlapped. *K. solenopsae* was detected in 22 of 64 parishes, and among 124 collection sites tested, 19% yielded positive responses for *K. solenopsae*. *P. tricuspidis* males and females and *P. curvatus* females were found to harbor *K. solenopsae*. This study is the first to detect *K. solenopsae* in *P. tricuspidis*. (C) 2014 Elsevier Inc. All rights reserved.

Adaptive maintenance of European alleles in the Brazilian Africanized honeybee

Harpur, BA, 2017

The Anthropocene is an epoch hallmarked by intensified human intrusion across ecosystems. One such intrusion is the movement and re-introduction of long-separated populations. By facilitating **introgression** - intraspecific genetic admixture - secondary contact can facilitate range expansion and the establishment of invasive species. The proximate mechanisms through which **introgression** facilitates expansion are rarely known (Bock et al., 2015; Rius & Darling, 2014), but managed species provide a useful avenue for exploration. Bee-keepers have been interbreeding highly diverged honeybee clades for centuries, often to introduce "useful" phenotypic variation to their stocks. Across the Western honeybee's (*Apis mellifera*) European range, this practice has not resulted in range expansion (Moritz, Hartel, & Neumann, 2005). In the Americas, however, **introgression** of European with African subspecies resulted in a widely publicized invasive population: The Africanized honeybee (AHB). In this issue of Molecular Ecology, Nelson, Wallberg, Simoes, Lawson, and Webster (2017) have made the first step towards understanding how this invasive species successfully spread across the Americas.

Worker Size, Geographical Distribution, and Introgressive Hybridization of Invasive *Solenopsis invicta* and *Solenopsis richteri* (Hymenoptera: Formicidae) in Tennessee

Pandey, M; Addesso, KM; Archer, RS; Valles, SM; Baysal-Gurel, F; Ganter, PF; Youssef, NN; Oliver, JB, 2019

Worker size and geographical distribution of red imported fire ants (*Solenopsis invicta* Buren), black imported fire ants (*Solenopsis richteri* Forel), and their **hybrid** (*S. invicta* x *S. richteri*) (Hymenoptera: Formicidae) were evaluated from colonies sampled across Tennessee. The fire ant species and **hybrid** status were determined using cuticular hydrocarbon and venom alkaloid indices obtained from gas chromatography and mass spectrometry. **Hybrids** were the most common fire ant throughout Tennessee. With the exception of a few isolated *S. invicta* samples, only **hybrids** were found in east Tennessee, and **hybrids** predominated in middle Tennessee. In west Tennessee, mixed populations of *S. richteri* and **hybrids** were found. **Hybrids** were more common in west Tennessee than a survey performed a decade earlier. No statistical differences were detected in the average inter-colonial worker size of *S. richteri* and **hybrids**. Likewise, average worker size was not related to geographic location in Tennessee. The similarity in average worker size among **hybrid** colonies with a wide range of cuticular hydrocarbon and venom alkaloid values suggests **introgression** was not impacting ant size in colonies sampled throughout Tennessee.

Molecular and ecological signatures of an expanding hybrid zone

Wellenreuther, M; Munoz, J; Chavez-Rios, JR; Hansson, B; Cordero-Rivera, A; Sanchez-Guillen, RA, 2018

Many species are currently changing their distributions and subsequently form sympatric zones with **hybridization** between formerly allopatric species as one possible consequence. The damselfly *Ischnura elegans* has recently expanded south into the range of its ecologically and morphologically similar sister species *Ischnura graellsii*. Molecular work shows ongoing **introgression** between these species, but the extent to which this species mixing is modulated by ecological niche use is not known. Here, we (1) conduct a detailed population genetic analysis based on molecular markers and (2) model the ecological niche use of both species in allopatric and sympatric regions. Population genetic analyses showed chronic **introgression** between *I. elegans* and *I. graellsii* across a wide part of Spain, and admixture analysis corroborated this, showing that the majority of *I. elegans* from the sympatric zone could not be assigned to either the *I. elegans* or *I. graellsii* species cluster. Niche modeling demonstrated that *I. elegans* has modified its environmental niche following **hybridization** and genetic **introgression** with *I. graellsii*, making niche space of introgressed *I. elegans* populations more similar to *I. graellsii*. Taken together, this corroborates the view that adaptive **introgression** has moved genes from *I. graellsii* into *I. elegans* and that this process is enabling Spanish *I. elegans* to occupy a novel niche, further facilitating its expansion. Our results add to the growing evidence that **hybridization** can play an important and creative role in the adaptive evolution of animals.

An Updated List of Ants of Alabama (Hymenoptera: Formicidae) with New State Records

Macgown, JA; Booher, D; Richter, H; Wetterer, JK; Hill, JG, 2021

A 2005 review compiled a list of 155 ant species plus the **hybrid** fire ant *Solenopsis invicta* X *richteri* from Alabama. Here, we add an 38 additional species based on both published and unpublished records and revised identifications raising the total to 193 species and one **hybrid**. Of these, 32 species and one **hybrid** are considered exotic to the state. We present county level maps of species richness and collection efforts for native and exotic ants highlighting areas of special concern for conservation and invasion risks.

The distribution and range expansion of Africanized honey bees (*Apis mellifera*) in the state of Yucatan, Mexico

Quezada-Euan, JGG; Echazarreta, CM; Paxton, RJ, 1996

Africanized honey bees (*Apis mellifera*) first arrived in the neotropical Mexican state of Yucatan in 1987. We documented the distribution and spread of Africanized honey bees at 15 localities across Yucatan by sampling worker honey bees from more than 280 managed colonies per year from 1990 to 1994, and from over 60 feral colonies per year at the same localities from 1992 to 1994. Colonies were classified morphometrically, using the criteria of Rinderer et al (1993a) for managed colonies and using modified probabilities for feral colonies. Africanized honey bees spread from the south, and by 1991 were found throughout Yucatan in managed colonies. By 1994, 52% of managed colonies were classified as pure Africanized and, assuming linearity in the rate of Africanization, all managed colonies are projected to be Africanized by mid-1997. Feral colonies showed evidence of Europeanization in 1992 but, by 1994, they were classified as Africanized. The slower pace of Africanization of managed colonies than that predicted for Yucatan may have arisen from extensive **hybridization** between the incoming Africanized honey bees and the large resident European honey bee population of the state, which contained among the highest densities of managed European colonies in the world before 1987. As yet, there is no evidence of a reduction in honey production in Yucatan.

Evolution of novel mimicry rings facilitated by adaptive introgression in tropical butterflies

Enciso-Romero, J; Pardo-Diaz, C; Martin, SH; Arias, CF; Linares, M; McMillan, WO; Jiggins, CD; Salazar, C, 2017

Understanding the genetic basis of phenotypic variation and the mechanisms involved in the evolution of adaptive novelty, especially in adaptive radiations, is a major goal in evolutionary biology. Here, we used whole-genome sequence data to investigate the origin of the yellow hindwing bar in the *Heliconius cydno* radiation. We found modular variation associated with hindwing phenotype in two narrow noncoding regions upstream and downstream of the *cortex* gene, which was recently identified as a pigmentation pattern controller in multiple species of *Heliconius*. Genetic variation at each of these modules suggests an independent control of the dorsal and ventral hindwing patterning, with the upstream module associated with the ventral phenotype and the downstream module with the dorsal one. Furthermore, we detected **introgression** between *H. cydno* and its closely related species *Heliconius melpomene* in these modules, likely allowing both species to

participate in novel mimicry rings. In sum, our findings support the role of regulatory modularity coupled with adaptive **introgression** as an elegant mechanism by which novel phenotypic combinations can evolve and fuel an adaptive radiation.

Distribution and rapid range expansion of the introduced willow sawfly *Nematus oligospilus* Forster (Hymenoptera: Tenthredinidae) in Australasia

Caron, V; Ede, F; Sunnucks, P; O'Dowd, DJ, 2014

The willow sawfly, *Nematus oligospilus* Forster (Hymenoptera: Tenthredinidae), has been introduced inadvertently across temperate regions in the Southern Hemisphere, including New Zealand and Australia, where it has dispersed extremely rapidly. A host specialist herbivore, at high population densities it can defoliate and damage introduced willows (*Salix* spp.), many species of which are invasive weeds in Australasia. In this study, we show that in just 10 years, the distribution of *N. oligospilus* has expanded across most of south-eastern Australia and south-western Western Australia and, in less than 15 years across both the North and South Islands of New Zealand. The relative population density of *N. oligospilus* varied widely within both geographic regions. The distribution of *N. oligospilus* was still expanding in Australia where high densities resulted in widespread willow defoliation. In contrast, the distribution of the willow sawfly had reached fully across both the North and South Islands in New Zealand, but its density had declined from the early stage of invasion. All willow taxa surveyed were utilized by the willow sawfly, but host preferences were apparent, especially for the *S. fragilis*/*S. x rubens* **hybrid** complex. Many factors, including natural enemies, willow range expansion and environmental conditions are likely to affect the long-term population dynamics and spread of *N. oligospilus* in Australia.

Statewide Survey of Imported Fire Ant (Hymenoptera: Formicidae) Populations in Tennessee

Oliver, JB; Vander Meer, RK; Ochieng, SA; Youssef, NN; Pantaleoni, E; Mrema, FA; Vail, KM; Parkman, JP; Valles, SM; Haun, WG; Powell, S, 2009

Imported fire ants (*Solenopsis* spp.; Hymenoptera: Formicidae) occupy 54 counties (similar to 5.4 million ha) in Tennessee. To better understand the fire ant species distribution in Tennessee, the state was divided into 16.1 x 16.1 km grids, and a single colony was sampled for cuticular hydrocarbon and venom alkaloid analyses within each grid. A total of 387 samples was processed from which 9 (2.3%), 167 (43.2%), and 211 (54.5%) were identified as red (*Solenopsis invicta* Buren), black (*Solenopsis richteri* Forel), or **hybrid** (*S. invicta* x *S. richteri*) imported fire ants, respectively. The *S. invicta* was only found near metropolitan Nashville in Davidson and Williamson counties and at one site in Decatur Co. All samples east of Franklin Co. were identified as **hybrids**. Tennessee counties west of Lincoln were predominantly *S. richteri* (86.5%) as opposed to **hybrid** (13.0%) and *S. invicta* (0.5%). The exception was Hardin Co., which was predominantly **hybrid**. Counties containing both **hybrid** and *S. richteri* (all in the middle and western part of the state) included Bedford, Decatur, Franklin, Giles, Hardeman, Hardin, Haywood, Lawrence, Lincoln, Marshall, Maury, McNairy, Perry, and Wayne. The *S. invicta* samples collected from one Williamson Co. site were determined to be polygynous and infected with the *Solenopsis invicta* virus (genotype SINV-1A). This was the first detection of polygynous imported fire ant in Tennessee. The SINV-1A virus was also a new find at the time of detection, but has been previously reported. The survey results are being used to direct current and future biological control efforts against imported fire ants in Tennessee.

Cleaner fish escape salmon farms and hybridize with local wrasse populations

Faust, E; Halvorsen, KT; Andersen, P; Knutsen, H; Andre, C, 2018

The genetic impact of farmed fish escaping aquaculture is a highly debated issue. However, non-target species, such as cleaner fish used to remove sea lice from farmed fish, are rarely considered. Here, we report that wild corkscrew wrasse (*Symphodus melops*), which are transported long distances to be used as cleaner fish in salmon farms, escape and **hybridize** with local populations. Recently, increasing numbers of corkscrew wrasse have been reported in Flatanger in Norway, north of its described distribution range, an area heavily relying on the import of cleaner fish from Skagerrak. Using genetic markers identified with 2bRAD sequencing, we show that, although the Flatanger population largely is a result of a northward range expansion, there is also evidence of considerable gene flow from southern populations in Skagerrak and Kattegat. Of the 40 corkscrew wrasses sampled in Flatanger, we discovered two individuals with clear southern genotypes, one first generation **hybrid**, and 12 potential second-generation **hybrids**. In summary, we provide evidence that corkscrew wrasse escape from fish farms and **hybridize** with local populations at the leading edge of an ongoing range expansion. Although the magnitude and significance of escapees warrant further investigation, these results should be taken into consideration in the use of translocated cleaner fish.

Inheritance patterns of photoperiodic diapause induction in *Leptinotarsa decemlineata*

Lehmann, P; Margus, A; Lindstrom, L, 2016

Photoperiod is a reliable indicator of season and an important cue that many insects use for phenological synchronization. Undergoing range expansion insects can face a change in the local photoperiod to which they need to resynchronize. Rapid range expansion can be associated with rapid photoperiodic adaptation, which can be associated with intense selection on strongly heritable polygenic traits. Alternatively, it is proposed that, in insects with an XO sex-determination system, genes with large effect residing on the sex chromosome could drive photoperiodic adaptation because the gene or genes are exposed to selection in the sex carrying only a single X-chromosome. The present study seeks to understand which of these alternatives more likely explains the rapid photoperiodic adaptation in European Colorado potato beetles *Leptinotarsa decemlineata* Say. Diapause induction is assessed in beetles from a northern and a southern population, as well as from reciprocal **hybrid** crosses between the northern and southern population, when reared at an intermediate length photoperiod. The crosses within population display the expected responses, with the northern and southern populations showing high and low diapause propensity, respectively. The **hybrids** show intermediate responses in all studied traits. No clear difference in the responses in **hybrids** depending on the latitudinal origin of their father or mother is detected, even though partial paternal line dominance is seen in the responses of male beetles in one **hybrid** cross. These results therefore indicate that, in *L. decemlineata*, photoperiodic diapause induction is strongly heritable, and has an additive polygenic autosomal background.

Plant hybrid zones and insect host range expansion

Pilson, D, 1999

The **hybrid** bridge hypothesis suggests that plant **hybrids** "bridge" the genetic gap between actual and potential host species, and that, for this reason, herbivorous insects are more likely to evolve an expanded host range in the presence of **hybrids**. While intuitively appealing, the hypothesis has two implicit assumptions: that phenotypic gaps between potential hosts limit host range, and that characters controlling host use are additively inherited in plant **hybrids**. Evaluation of these assumptions suggests that operation of the **hybrid** bridge hypothesis is relatively uncommon. In addition, the hypothesis has not been well integrated into existing theoretical and empirical work on the evolution of host range in herbivorous insects. Proper evaluation of the hypothesis will require information on the effect of plant **hybridization** on both insect preference and insect performance. Ecological and genetic factors affecting range expansion in both **hybrids** and novel parents also require evaluation.

Colonization history and population differentiation of the Honey Bees (*Apis mellifera* L.) in Puerto Rico

Acevedo-Gonzalez, JP; Galindo-Cardona, A; Avalos, A; Whitfield, CW; Rodriguez, DM; Uribe-Rubio, JL; Giray, T, 2019

Honey bees (*Apis mellifera* L.) are the primary commercial pollinators across the world. The subspecies *A. m. scutellata* originated in Africa and was introduced to the Americas in 1956. For the last 60 years, it **hybridized** successfully with European subspecies, previous residents in the area. The result of this **hybridization** was called Africanized honey bee (AHB). AHB has spread since then, arriving to Puerto Rico (PR) in 1994. The honey bee population on the island acquired a mosaic of features from AHB or the European honey bee (EHB). AHB in Puerto Rico shows a major distinctive characteristic, docile behavior, and is called gentle Africanized honey bees (gAHB). We used 917 SNPs to examine the population structure, genetic differentiation, origin, and history of range expansion and colonization of gAHB in PR. We compared gAHB to populations that span the current distribution of *A. mellifera* worldwide. The gAHB population is shown to be a single population that differs genetically from the examined populations of AHB. Texas and PR groups are the closest genetically. Our results support the hypothesis that the Texas AHB population is the source of gAHB in Puerto Rico.

Regional divergence and mosaic spatial distribution of two closely related damselfly species (*Enallagma hageni* and *Enallagma ebrium*)

Bourret, A; McPeck, MA; Turgeon, J, 2012

North American *Enallagma* damselflies radiated during the Pleistocene, and species differ mainly by reproductive structures. Although morphologically very different, *Enallagma hageni* and *Enallagma ebrium* are genetically very similar. Partitioning of genetic variation (AFLP), isolation by distance and clustering analyses indicate that these morphospecies are locally differentiated genetically. Spatial analyses show that they are rarely sympatric at local sites, and their distributions form a mosaic of patches where one is clearly dominant over hundreds of square kilometers. However, these morphospecies are also not genetically more similar when they are sympatric, indicating that **hybridization** is probably not occurring. Given that these morphospecies are ecologically equivalent, strong assortative mating, reproductive interference and fast post-glacial recolonization may explain the origin and maintenance of these distributional patches across eastern North America. By limiting opportunities for gene flow, reproductive interference may play an unsuspected role in accelerating genetic differentiation in the early phases of nonecological speciation.

Restoration of an endangered plant, *Hygrophila pogonocalyx*, leads to an adaptive host shift of the chocolate pansy (*Junonia iphita iphita*)

Tan, WH; Liu, TH; Lin, YK; Hsu, YF, 2014

Anthropogenic introduction of a plant species may cause novel encounters between the plant and local herbivores, and initiate evolutionary changes in host plant usage by herbivores. Until recently the endemic aquatic plant *Hygrophila pogonocalyx* was endangered and had a restricted distribution in Taiwan. Massive restoration efforts since 1997 have led to an expansion of the plant's distribution and a novel encounter between it and an Asian butterfly, the chocolate pansy, *Junonia iphita* (Nymphalidae). This butterfly appears to have colonized *H. pogonocalyx*, switching from its original host, *Strobilanthes penstemonoides* var. *formosana*. In the present study, we aimed to investigate whether the utilization of *H. pogonocalyx* as a host plant has initiated a differentiation between butterflies using the novel and the original hosts. To this purpose we collected butterflies from patches of the two host plants which grow sympatrically. We tested oviposition preference for the two hosts and larval performance on them. Female adults exhibited distinct oviposition preference toward the host plant their mothers preferred. Offspring showed greater survivorship and pupal weight when fed on the host plant their mothers preferred. Male adults displayed territorial behaviors on the host plant that their mothers had preferred. Finally, the survival rate of offspring produced from cross-mating between individuals with different host plant preference was lower than that of non-**hybrids**. Taken together, we suggest that genetic differentiation has occurred between individuals preferring *H. pogonocalyx* versus *S. penstemonoides* as host plants via host shifting. This process was likely induced by the mass restoration of the formerly rare and endangered plant species. (C) 2014 Elsevier GmbH. All rights reserved.

Selection of entomopathogenic fungus *Beauveria bassiana* (Deuteromycotina: Hyphomycetes) for the biocontrol of *Dendroctonus ponderosae* (Coleoptera: Curculionidae, Scolytinae) in Western Canada

Rosana, ARR; Pokorny, S; Klutsch, JG; Ibarra-Romero, C; Sanichar, R; Engelhardt, D; van Belkum, MJ; Erbilgin, N; Bohlmann, J; Carroll, AL; Vederas, JC, 2021

The mountain pine beetle, *Dendroctonus ponderosae*, has infested over similar to 16 Mha of pine forests in British Columbia killing >50% of mature lodgepole pine, *Pinus contorta*, trees in affected stands. At present, it is functionally an invasive species in Alberta, killing and reproducing in evolutionarily naive populations of lodgepole pine (*P. contorta*), novel jack pine (*P. banksiana*), and their **hybrids**. The entomopathogenic fungus *Beauveria bassiana* has shown some potential as a biocontrol agent of several bark beetle species. In this study, nine isolates of *B. bassiana* were examined for insect virulence characteristics, including conidiation rate, pigmentation, and infection rate in laboratory-reared *D. ponderosae*, to assess for their potential as biocontrol agents. The strains were categorized into three phenotypic groups based on pigmentation, conidial density, and myceliation rate. Virulence screening utilizing insect-based agar medium (*D. ponderosae* and European honeybee *Apis mellifera* carcasses) revealed no difference in selection of fungal growth. However, infection studies on *D. ponderosae* and *A. mellifera* showed contrasting results. In vivo *A. mellifera* infection model revealed similar to 5% mortality, representing the natural death rate of the hive population, whereas laboratory-reared *D. ponderosae* showed 100% mortality and mycosis. The LT50 (median lethal time 50) ranges from 2 to 5 +/- 0.33 days, and LT100 ranges from 4 to 6 +/- 0.5 days. We discuss the selective advantages of the three phenotypic groups in terms of virulence, pigmentation, conidial abundance, and tolerance to abiotic factors like UV and host tree monoterpenes. These results can further provide insights into the development of several phenotypically diverse *B. bassiana* strains in controlling the spread of the invasive *D. ponderosae* in Western Canada.

HYBRIDIZATION BETWEEN EUROPEAN AND AFRICANIZED HONEY-BEES IN THE NEOTROPICAL YUCATAN PENINSULA

RINDERER, TE; STELZER, JA; OLDROYD, BP; BUCO, SM; RUBINK, WL, 1991

A population genetic analysis of honey bees of the Mexican neotropical Yucatan peninsula shows that the range expansion of Africanized bees there has involved extensive introgressive **hybridization** with European bees. Yucatan honey bee populations now include many colonies with intermediate morphologies. Genotypes of mitochondria have disassociated from historically correlated Africanized or European morphology, producing diverse phenotypic associations. This suggests that the size of resident European populations may be important in explaining previously reported asymmetrical **hybridization**. Evidence of natural **hybridization** is encouraging for the use of genetic management to mitigate the effects of Africanized bees in the United States.

Phylogeography of *Pogonomyrmex barbatus* and *P. rugosus* harvester ants with genetic and environmental caste determination

Mott, BM; Gadau, J; Anderson, KE, 2015

We present a phylogeographic study of at least six reproductively isolated lineages of new world harvester ants within the *Pogonomyrmex barbatus* and *P. rugosus* species group. The genetic and geographic relationships within this clade are complex: Four of the identified lineages show genetic caste determination (GCD) and

are divided into two pairs. Each pair has evolved under a mutualistic system that necessitates sympatry. These paired lineages are dependent upon one another because their GCD requires interlineage matings for the production of F1 **hybrid** workers, and intralineage matings are required to produce queens. This GCD system maintains genetic isolation among these interdependent lineages, while simultaneously requiring co-expansion and emigration as their distributions have changed over time. It has also been demonstrated that three of these four GCD lineages have undergone historical **hybridization**, but the narrower sampling range of previous studies has left questions on the **hybrid** parentage, breadth, and age of these groups. Thus, reconstructing the phylogenetic and geographic history of this group allows us to evaluate past insights and hypotheses and to plan future inquiries in a more complete historical biogeographic context. Using mitochondrial DNA sequences sampled across most of the morphospecies' ranges in the U.S.A. and Mexico, we conducted a detailed phylogeographic study. Remarkably, our results indicate that one of the GCD lineage pairs has experienced a dramatic range expansion, despite the genetic load and fitness costs of the GCD system. Our analyses also reveal a complex pattern of vicariance and dispersal in *Pogonomyrmex* harvester ants that is largely concordant with models of late Miocene, Pliocene, and Pleistocene range shifts among various arid-adapted taxa in North America.

Differential rates of invasion in three related alien oak gall wasps (Cynipidae: Hymenoptera)

Walker, P; Leather, SR; Crawley, MJ, 2002

Three related species of oak gall wasps, *Andricus corruptrix* (Schlechtendal), *A. kollari* (Hartig) and *A. lignicola* (Hartig) have entered Britain since the introduction of Turkey oak, *Quercus cerris* L. in 1735. Their lifecycles involve alternating generations between an agamic generation on the native oak species (*Q. petraea*, *Q. robur* and their **hybrid** *Q. x. rosacea*), and a smaller, sexual generation on the alien *Q. cerris*. In examining the distributions of these insects and *Q. cerris*, we hypothesized that: (1) the invasion will spread more rapidly in places where both host trees are equally abundant than through regions where one of the tree species is substantially less common than the other; (2) interspecific competition between these bud-galling species will lead to a negative correlation between their abundances at a particular site; (3) differential recruitment of natural enemies from the native hymenopteran fauna will slow the rate of spread in a species-specific manner. *A. kollari* arrived nearly 200 years ago and is now found throughout the British Isles, wherever Turkey oak is grown. *A. lignicola* and *A. corruptrix* have been here for 30 years, after establishing in S. E. England. *A. lignicola* is in its final rapid stages of range expansion across England, southern Scotland and N.E. Scotland. *A. corruptrix* is just beginning to spread through Central and S. W. England. It has occupied proportionally fewer sites behind its invasion front than have the other two species, but is no less abundant at these sites. Nevertheless, distance leaps of up to 50 km were identified in *A. lignicola* in N.E. Scotland, and the possibility of long-distance transport of infected trees through the horticulture and forestry trades remains. The co-occurrence of mature individuals of both host *Quercus* species does appear to have increased their rates of colonization in *A. lignicola* and *A. corruptrix*. There is no evidence, however, to suggest that interspecific competition between the three alien gall formers is an important factor in determining their distributions and abundance within their invaded ranges. All three species have recruited parasitoids and inquilines rapidly from the native fauna; attack rates were highly variable, but showed no evidence of density dependence across sites.

Comparative Cutaneous Water Loss and Desiccation Tolerance of Four *Solenopsis* spp. (Hymenoptera: Formicidae) in the Southeastern United States

Ajayi, OS; Appel, AG; Chen, L; Fadamiro, HY, 2020

The high surface area to volume ratio of terrestrial insects makes them highly susceptible to desiccation mainly through the cuticle. Cuticular permeability (CP) is usually the most important factor limiting water loss in terrestrial insects. Water loss rate, percentage of total body water (%TBW) content, CP, and desiccation tolerance were investigated in workers of four *Solenopsis* species in the southeastern USA. We hypothesized that tropical/subtropical ants (*S. invicta* and *S. geminata*) will have lower CP values and tolerate higher levels of desiccation than temperate ants (*S. richteri* and *S. invictaxS. richteri*). The %TBW content was similar among species. *Solenopsis invicta* had a 1.3-fold and 1.1-fold lower CP value than *S. invictaxS. richteri* and *S. richteri*, respectively. *Solenopsis geminata* had a 1.3-fold lower CP value than *S. invictaxS. richteri*, and a 1.2-fold lower CP value than *S. richteri*. The LT(50) values (lethal time to kill 50% of the population) ranged from 1.5 h (small *S. geminata*) to 8.5 h (large *S. invicta*). Desiccation tolerance ranged between 36 and 50 %TBW lost at death and was not related to a species' location of origin. This study is the first report of water relations of *S. invictaxS. richteri*. It demonstrates that desiccation stress differentially can affect the survival of different *Solenopsis* species and implies that environmental stress can affect the distribution of these species in the southeastern USA.

Out of the forest: past and present range expansion of a parthenogenetic weevil pest, or how to colonize the world successfully

Rodriguero, MS; Lanteri, AA; Guzman, NV; Guedes, JVC; Confalonieri, VA, 2016

Previous research revealed complex diversification patterns in the parthenogenetic weevil *Naupactus cervinus*. To understand the origin of clonal diversity and successful spreading of this weevil, we investigated its geographic origin and possible dispersal routes and whether parthenogens can persist in habitats under unsuitable environmental conditions. This study is based on samples taken throughout a broad area of the species' range. We used both mitochondrial and nuclear markers and applied phylogenetic and network analyses to infer possible relationships between haplotypes. Bayesian phylogeographic analyses and ecological niche modeling were used to investigate the processes that shaped genetic diversity and enabled the colonization of new geographic areas. Southeastern Brazil emerges as the original distribution area of *N. cervinus*. We detected two range expansions, one along natural corridors during the Pleistocene and the other in countries outside South America during recent times. Isolation due to climate shifts during the early Pleistocene led to diversification in two divergent clades, which probably survived in different refugia of the Paranaense Forest and the Parana River delta. The origin of the clonal diversity was probably a complex process including mutational diversification, **hybridization**, and secondary colonization. The establishment of *N. cervinus* in areas outside its native range may indicate adaptation to drier and cooler conditions. Parthenogenesis would be advantageous for the colonization of new environments by preventing the breakup of successful gene combinations. As in other insect pests, the present distribution of *N. cervinus* results from both its evolutionary history and its recent history related to human activities.

Comparisons of mountain pine beetle (*Dendroctonus ponderosae* Hopkins) reproduction within a novel and traditional host: effects of insect natal history, colonized host species and competitors

McKee, FR; Huber, DPW; Aukema, BH, 2013

1 During host-breadth expansion, phytophagous insects incur risk from potentially deleterious novel host environments at the same time as potentially securing a potential escape in space or time from competing species. 2 Bark beetles reproduce under the bark of stems and branches of mature, stressed or moribund trees, and may suffer high mortality from plant defences and inter- and intraspecific competition. 3 An epidemic of mountain pine beetle (*Dendroctonus ponderosae* Hopkins) in western Canada has extended to over 18.1 million hectares of lodgepole pine (*Pinus contorta* Douglas ex. Loudon) forests. 4 In some areas, mountain pine beetles have been found to reproduce within interior **hybrid** spruces [*Picea glauca* (Moench) Voss x *engelmannii* Parry ex. Engelmann], a normally rare occurrence. 5 Using mountain pine beetles reared from naturally-infested interior **hybrid** spruce and lodgepole pine hosts, we examined the effect of female natal species and colonized host species on the ability to attract mates and reproduce within spruce and pine logs deployed as a choice assay in a field setting. Additionally, we examined whether the arrival and reproduction of competitors such as pine engravers (*Ips* spp.) was associated with reduced brood production. 6 Females reared from pine and spruce exhibited similar reproductive potentials. Recruitment and establishment of ovipositional galleries, larval galleries and pupal chambers were similar in the typical and novel hosts. 7 Reproduction by mountain pine beetles in spruce, although successful, was significantly lower than in pine. This reduction occurred despite spruce logs being almost entirely free of competing secondary beetles.

Complex inheritance of larval adaptation in *Plutella xylostella* to a novel host plant

Henniges-Janssen, K; Reineke, A; Heckel, DG; Groot, AT, 2011

Studying the genetics of host shifts and range expansions in phytophagous insects contributes to our understanding of the evolution of host plant adaptation. We investigated the recent host range expansion to pea, in the pea-adapted strain (P-strain) of the crucifer-specialist diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae). Larval survivorship on the novel host plant pea and a typical crucifer host (kale) was measured in reciprocal F-1, F-2 and backcrosses between the P-strain and a strain reared only on crucifers (C-strain). Reciprocal F-1 **hybrids** differed: offspring from P-strain mothers survived better on pea, indicating a maternal effect. However, no evidence for sex-linkage was found. Backcrosses to the P-strain produced higher survivorship on pea than C-strain backcrosses, suggesting recessive inheritance. In a linkage analysis with amplified fragment length polymorphism markers using P-strain backcrosses, two, four and five linkage groups contributing to survival on pea were identified in three different families respectively, indicating oligogenic inheritance. Thus, the newly evolved ability to survive on pea has a complex genetic basis, and the P-strain is still genetically heterogeneous and not yet fixed for all the alleles enabling it to survive on pea. Survivorship on kale was variable, but not related to survivorship on pea. This pattern may characterize the genetic inheritance of early host plant adaptation in oligophagous insect species. *Heredity* (2011) 107, 421-432; doi:10.1038/hdy.2011.27; published online 15 June 2011

Genetic population structure and hybridization in two sibling species, *Tomoplagia reticulata* and *Tomoplagia pallens* (Diptera: Tephritidae)

Abreu, AG; Solferini, VN,

Tomoplagia reticulata and *T. pallens* are sibling species that are specialists on *Eremanthus glomerulatus*. Besides adult terminalia, they show slight morphological differences and distinct geographic distributions. Once, however, they were found sympatrically. Using data from allozyme and mtDNA, we examined patterns of intra- and interspecific genetic structure, and investigated the possible occurrence of gene flow between them. Both species showed low diversity and high genetic structure, which can be linked to their high degree of specialization. Larval development occurs within flower heads, tissues that are available only during a short period of the year. Afterward, as they do not hibernate, they probably suffer a great reduction in population size, which leads to low genetic diversity. As monophagous insects, their population structure may correspond to the fragmented distribution of *E. glomerulatus*, which could isolate fly populations and increase inbreeding within them. One population exhibited a mixed genetic composition, compatible with one **hybridization** season when species were sympatric. This **hybridization** seems to be a rare event, due to *T. pallens* unusual range expansion.

A holocenic and dynamic hybrid zone between two cactophilic *Drosophila* species in a coastal lowland plain of the Brazilian Atlantic Forest

Barrios-Leal, DY; Menezes, RST; Ribeiro, JV; Bizzo, L; de Sene, FM; Neves-da-Rocha, J; Manfrin, MH, 2021

Hybridization and **introgression** are processes that contribute to shaping biological diversity. The factors promoting the formation of these processes are multiples but poorly explored in a biogeographical and ecological context. In the southeast coastal plain of the Brazilian Atlantic Forest, a **hybrid** zone was described between two closely related cactophilic species, *Drosophila antonietae* and *D. serido*. Here, we revisited and analysed specimens from this **hybrid** zone to evaluate its temporal and spatial dynamic. We examined allopatric and sympatric populations of the flies using independent sources of data such as mitochondrial and nuclear sequences, microsatellite loci, morphometrics of wings and male genitalia, and climatic niche models. We also verified the emergence of the flies from necrotic tissues of collected cacti to verify the role of host association for the population dynamics. Our results support the existence of a **hybrid** zone due to secondary contact and limited to the localities where the two species are currently in contact. Furthermore, we detected asymmetric bidirectional **introgression** and the maintenance of the species integrity, ecological association and morphological characters, suggesting selection and limited **introgression**. Considering our paleomodels, probably this **hybrid** zone is recent and the contact occurred during the Holocene to the present day, favoured by range expansion of their populations due to expansion of open and dry areas in eastern South America during palaeoclimatic and geomorphological events.

Adaptive introgression of herbivore resistance traits in the weedy sunflower *Helianthus annuus*

Whitney, KD; Randell, RA; Rieseberg, LH, 2006

The role of **hybridization** in adaptive evolution is contentious. While many cases of adaptive trait **introgression** have been proposed, the relevant traits have rarely been identified, resulting in a lack of clear examples of this process. Here, we examine a purported case of adaptive **introgression** in which the annual sunflower *Helianthus annuus annuus* has captured alleles from a congener (*Helianthus debilis*) to form a stabilized **hybrid**, *Helianthus annuus texanus*. We tested the hypotheses that herbivore resistance traits have introgressed from *H. debilis* to *H. annuus* and have increased adaptation in the latter. In two common gardens, fitness (estimated by seed production) was on average 55% higher in *H. a. texanus* than in *H. a. annuus*. For *H. a. texanus*, three damage traits (of seven tested) differed significantly from the *H. a. annuus* parent in one or both sites and were shifted in the direction of the more resistant *H. debilis*. Natural selection favored *H. a. debilis* BC 1 **hybrids** (synthesized to mimic the ancestors of *H. a. texanus*) with *H. debilis* - like resistance to seed midges *Neolasioptera helianthis* and to receptacle/seed feeding *Lepidoptera* at one or both sites. Assuming similar herbivore pressures in the past, these results suggest that **introgression** of biotic resistance traits was important in the adaptation of *H. annuus* to central and southern Texas.

Is the last glaciation the only relevant event for the present genetic population structure of the meadow brown butterfly *Maniola jurtina* (Lepidoptera : Nymphalidae)?

Schmitt, T; Rober, S; Seitz, A, 2005

Phylogeographical studies are available for a considerable number of European species, but few analyses exist for temperate species with very large and fairly continuous populations that are also absent from Northern Europe. Therefore, we studied the butterfly *Maniola jurtina* as a model for this group. The species has two major genetic lineages (mean genetic distance between lineages: 0.033; F-CT: 0.052), most probably evolving in glacial differentiation centres in the western and eastern Mediterranean. The onset of this differentiation might have been the beginning of the last glacial stage maximum some 40 kyr BP. A **hybrid** zone between these two lineages exists in western Central Europe. No genetic substructures have been found within the two lineages (F-SC: 0.017) and average genetic distances are very small. Therefore, it is highly probable that postglacial expansion was of the phalanx type. There is, at most, very limited differentiation at regional and local scales. However, the genetic diversity within populations is high (means: A: 2.68; H-E: 17.2%; P: 78%), as would be predicted for such a common species. Comparison of these results with a published allozyme analysis revealed a similar phylogeographical pattern, but lower genetic diversity in the latter. Morphological patterns of wings and genitalia show similar geographical patterns as allozyme data. (c) 2005 The Linnean Society of London.

The genetic structure of hawthorn-infesting *Rhagoletis pomonella* populations in Mexico: implications for sympatric host race formation

Michel, AP; Rull, J; Aluja, M; Feder, JL, 2007

The genetic origins of species may not all trace to the same time and place as the proximate cause(s) for population divergence. Moreover, inherent gene-flow barriers separating populations may not all have evolved under the same geographical circumstances. These considerations have lead to a greater appreciation of

the plurality of speciation: that one geographical mode for divergence may not always be sufficient to describe a speciation event. The apple maggot fly, *Rhagoletis pomonella*, a model system for sympatric speciation via host-plant shifting, has been a surprising contributor to the concept of speciation mode plurality. Previous studies have suggested that past **introgression** of inversion polymorphism from a hawthorn-fly population in the trans-Mexican volcanic belt (EVTM) introduced diapause life-history variation into a more northern fly population that subsequently contributed to sympatric host race formation and speciation in the United States (US). Here, we report results from a microsatellite survey implying (i) that volcanic activity in the eastern EVTm may have been responsible for the initial geographical isolation of the Mexican and northern hawthorn-fly populations c. 1.57 mya; and (ii) that flies in the Sierra Madre Oriental Mountains (SMO) likely served as a conduit for past gene flow from the EVTm into the US. Indeed, the microsatellite data suggest that the current US population may represent a range expansion from the northern SMO. We discuss the implications of these findings for sympatric race formation in *Rhagoletis* and speciation theory.

~~More northern than ever thought: refugia of the Woodland Ringlet butterfly *Erebia medusa* (Nymphalidae: Satyrinae) in Northern Central Europe~~

Besold, J; Schmitt, T, 2015

Extra-Mediterranean refugia are climatically buffered and locally restricted habitat zones, which enable temperate species to survive the harsh climatic conditions of at least the last ice age north of the typical Mediterranean retreats. Applying polymorphic allozyme loci, we analyse the late Wurm glacial and postglacial range dynamics of the temperate butterfly species *Erebia medusa* in eastern Central Europe near to its present northern distribution limit. We analysed the genetic structure of 36 *E. medusa* populations (n=1508) from the Northern Carpathians and Sudety Mountains and the surrounding areas in eastern Germany, southern Poland, Czech Republic, Slovakia and north-eastern Hungary. We used various descriptive statistics and explorative cluster analyses on an individual, population and group level. The genetic diversities of the populations mostly correspond with those known from samples in other parts of the species distribution range. The differentiations among population groups are in the order of magnitude of other butterfly species evolving genetic lineages over at least one glacial-interglacial cycle. From four different genetic lineages, three lineages supported the existence of extra-Mediterranean refugia postulated in previous studies. The fourth lineage indicated one exceptionally northern extra-Mediterranean refuge in southern Poland, strongly separated from the more southern centres by the Sudety Mountains and Northern Carpathians; however, its postglacial origin out of a Transylvanian refuge cannot be ruled out completely. The genetic substructure of the Polish populations mirrors their dynamics of expansion and retraction caused by climatic oscillation during the late Wurm ice age. This pattern was further supported by a within-lineage **hybrid** zone in south-central Poland established between two groups of populations on either side, most probably resulting from final postglacial range expansion.

~~The butterfly *Danaus chrysippus* (L) in East Africa: Polymorphism and morph ratio clines within a complex, extensive and dynamic hybrid zone~~

Smith, DAS; Owen, DF; Gordon, IJ; Lowis, NK, 1997

Samples of the polymorphic butterfly *Danaus chrysippus* are analysed from six well separated sites in East Africa. Morph-ratio clines are described for four diallelic genes A, B, C and L, each of which influences the visual phenotype. Each of the four clines has a different orientation, consistent with an hypothesis that the polymorphism originated from **hybridization** between a number of polytypic demes which have at various times undergone range expansion. Allopatric subspeciation in isolated Pleistocene refugia is postulated. The phenotype of each geographical race is shared with one of the morphs within the **hybrid** zone; other sympatrically maintained polymorphic forms are normally confined to the **hybrid** zone. Wright's isolation-by-distance model best explains the present distribution of gene frequencies. Morph-ratios differ significantly between the sexes and are sometimes associated with heterozygote excess; gametic and genotypic disequilibria are general throughout the region and suggest the clines are maintained by strong natural selection. Seasonal cycling of phenotype frequency is believed to result from extensive migratory movements rather than natural selection. Female-biased sex-ratio, which is also seasonal, and Haldane rule effects, result from **hybrid** breakdown when genetically distinct demes meet and interbreed. Oscillating sex-ratios and frequency of colour genes are functionally linked by negative feedback. The polymorphism owes its origin to allopatric evolution but is now maintained sympatrically. (C) 1997 The Linnean Society of London.

~~Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of *Albugo candida*, a generalist parasite~~

McMullan, M; Gardiner, A; Bailey, K; Kemen, E; Ward, BJ; Cevik, V; Robert-Seilaniantz, A; Schultz-Larsen, T; Balmuth, A; Holub, E; van Oosterhout, C; Jones, JDG, 2015

How generalist parasites with wide host ranges can evolve is a central question in parasite evolution. *Albugo candida* is an obligate biotrophic parasite that consists of many physiological races that each specialize on distinct Brassicaceae host species. By analyzing genome sequence assemblies of five isolates, we show they represent three races that are genetically diverged by similar to 1%. Despite this divergence, their genomes are mosaic-like, with similar to 25% being introgressed from other races. Sequential infection experiments show that infection by adapted races enables subsequent infection of hosts by normally non-infecting races. This facilitates **introgression** and the exchange of effector repertoires, and may enable the evolution of novel races that can undergo clonal population expansion on new hosts. We discuss recent studies on **hybridization** in other eukaryotes such as yeast, *Heliconius* butterflies, Darwin's finches, sunflowers and cichlid fishes, and the implications of **introgression** for pathogen evolution in an agro-ecological environment.

~~Host and geography together drive early adaptive radiation of Hawaiian planthoppers~~

Goodman, KR; Prost, S; Bi, K; Brewer, MS; Gillespie, RG, 2019

The interactions between insects and their plant host have been implicated in driving diversification of both players. Early arguments highlighted the role of ecological opportunity, with the idea that insects "escape and radiate" on new hosts, with subsequent hypotheses focusing on the interplay between host shifting and host tracking, coupled with isolation and fusion, in generating diversity. Because it is rarely possible to capture the initial stages of diversification, it is particularly difficult to ascertain the relative roles of geographic isolation versus host shifts in initiating the process. The current study examines genetic diversity between populations and hosts within a single species of endemic Hawaiian planthopper, *Nesosydne umbratica* (Hemiptera, Delphacidae). Given that the species was known as a host generalist occupying unrelated hosts, Clermontia (Campanulaceae) and Pipturus (Urticaceae), we set out to determine the relative importance of geography and host in structuring populations in the early stages of differentiation on the youngest islands of the Hawaiian chain. Results from extensive exon capture data showed that *N. umbratica* is highly structured, both by geography, with discrete populations on each volcano, and by host plant, with parallel radiations on Clermontia and Pipturus leading to extensive co-occurrence. The marked genetic structure suggests that populations can readily become established on novel hosts provided opportunity; subsequent adaptation allows monopolization of the new host. The results support the role of geographic isolation in structuring populations and with host shifts occurring as discrete events that facilitate subsequent parallel geographic range expansion.

~~The Effect of Water Limitation on Volatile Emission, Tree Defense Response, and Brood Success of *Dendroctonus ponderosae* in Two Pine Hosts, Lodgepole, and Jack Pine~~

Lusebrink, I; Erbilgin, N; Eyenden, ML, 2016

The mountain pine beetle (MPB; *Dendroctonus ponderosae*) has recently expanded its range from lodgepole pine forest into the lodgepole x jack pine **hybrid** zone in central Alberta, within which it has attacked pure jack pine. This study tested the effects of water limitation on tree defense response of mature lodgepole and jack pine (*Pinus contorta* and *Pinus banksiana*) trees in the field. Tree defense response was initiated by inoculation of trees with the MPB associated fungus *Grosmannia*

clavigera and measured through monoterpene emission from tree boles and concentration of defensive compounds in phloem, needles, and necrotic lesion tissues. Lodgepole pine generally emitted higher amounts of monoterpenes than jack pine; particularly from fungal-inoculated trees. Compared to non inoculated trees, fungal inoculation increased monoterpene emission in both species, whereas water treatment had no effect on monoterpene emission. The phloem of both pine species contains (-)-alpha-pinene, the precursor of the beetle's aggregation pheromone, however lodgepole pine contains two times as much as jack pine. The concentration of defensive compounds was 70-fold greater in the lesion tissue in jack pine, but only 10-fold in lodgepole pine compared to healthy phloem tissue in each species, respectively. Water-deficit treatment inhibited an increase of L-limonene as response to fungal inoculation in lodgepole pine phloem. The amount of myrcene in jack pine phloem was higher in water-deficit trees compared to ambient trees. Beetles reared in jack pine were not affected by either water or biological treatment, whereas beetles reared in lodgepole pine benefited from fungal inoculation by producing heavier female offspring. Female beetles that emerged from jack pine bolts contained more fat than those that emerged from lodgepole pine, even though lodgepole pine phloem had a higher nitrogen content than jack pine phloem. These results suggest that jack pine chemistry is suitable for MPB pheromone production and aggregation on the host tree.

Cuticular hydrocarbon chemistry, an important factor shaping the current distribution pattern of the imported fire ants in the USA

Xu, M; Lu, ZK; Lu, YY; Balusu, RR; Ajayi, OS; Fadamiro, HY; Appel, AG; Chen, L, 2018

Two sibling species, *Solenopsis richteri* and *S. invicta*, were both introduced into the southern USA from South America in the early 20th century. Today, *S. richteri* occupies higher latitudes and colder areas, while *S. invicta* occupies lower latitudes. Between the distributions of the two species, there is a large area of viable **hybrid** (*S. richteri* x *S. invicta*) populations. This study aimed to characterize the forces driving this distribution pattern and the underlying mechanisms. Cuticular hydrocarbons (CHCs) of freshly killed workers of *S. invicta*, **hybrids**, and *S. richteri* were removed using hexane. Both intact and CHCs-extracted workers were subjected to a constant rate of increasing temperature from 10 to 60 degrees C to obtain relative water loss and the water loss transition temperature (Tc-ant). Mass loss and Tc-ant were both significantly increased with CHCs removal. We then examined the CHC composition of three species. CHC profiles of *S. richteri* are characterized by significant amounts of short-chain (C-23-C-27) saturated and unsaturated hydrocarbons. In contrast, profiles of *S. invicta* consist primarily of long chain (C-27-C-29) saturated hydrocarbons; unsaturated alkenes are completely lacking. **Hybrid** fire ants show intermediate profiles of the two parent species. We measured the melting point (T-m) and water-loss transition temperature of CHC blends (Tc-CHC) of different ant species colonies using differential scanning calorimetry (DSC) and an artificial membrane system, respectively. There were 3-5 T(m)s of each CHCs sample of different ant colonies due to their complex chemistry. The highest T(m)s (T(m-max)s) of CHCs samples from *S. invicta* and the **hybrid** were significantly higher than that from *S. richteri*. The correlation between Tc-CHC and Tm-max obtained from the same CHCs sample was highly significant. These results reveal that species having higher T-c and Tm-max retain more water under relatively higher temperature, and consequently are able to occupy warmer environments. We conclude that CHC chemistry plays a role in shaping current distribution patterns of *S. richteri*, *S. invicta* and their **hybrid** in the United States.

Scent of a break up: phylogeography and reproductive trait divergences in the red-tailed bumblebee (*Bombus lapidarius*)

Lecocq, T; Dellicour, S; Michez, D; Lhomme, P; Vanderplanck, M; Valterova, I; Rasplus, JY; Rasmont, P, 2013

Background: The Pleistocene climatic oscillations are considered as a major driving force of intraspecific divergence and speciation. During Ice Ages, populations isolated in allopatric glacial refugia can experience differentiation in reproductive traits through divergence in selection regimes. This phenomenon may lead to reproductive isolation and dramatically accentuates the consequences of the climatic oscillations on species. Alternatively, when reproductive isolation is incomplete and populations are expanding again, further mating between the formerly isolated populations can result in the formation of a **hybrid** zone, genetic **introgression** or reinforcement speciation through reproductive trait displacements. Therefore changes in reproductive traits driven by population movements during climatic oscillations can act as an important force in promoting pre-zygotic isolation. Notwithstanding, divergence of reproductive traits has not been approached in the context of climatic oscillations. Here we investigate the impact of population movements driven by climatic oscillations on a reproductive trait of a bumblebee species (*Bombus lapidarius*). We characterise the pattern of variation and differentiation across the species distribution (i) with five genes (nuclear and mitochondrial), and (ii) in the chemical composition of male marking secretions (MMS), a key trait for mate attraction in bumblebees. Results: Our results provide evidence that populations have experienced a genetic allopatric differentiation, in at least three main refugia (the Balkans, Centre-Eastern Europe, and Southern Italy) during Quaternary glaciations. The comparative chemical analyses show that populations from the Southern Italian refugium have experienced MMS differentiation and an incipient speciation process from another refugium. The meeting of Southern Italian populations with other populations as a result of range expansion at a secondary contact zone seems to have led to a reinforcement process on local MMS patterns. Conclusions: This study suggests that population movement during Quaternary climatic oscillations can lead to divergence in reproductive traits by allopatric differentiation during Ice Ages and by reinforcement during post-glacial recolonization.

Tracking invasions of a destructive defoliator, the gypsy moth (*Erebidae: Lymantria dispar*): Population structure, origin of intercepted specimens, and Asian introgression into North America

Wu, YK; Bogdanowicz, SM; Andres, JA; Vieira, KA; Wang, BD; Cosse, A; Pfister, SE, 2020

Genetic data can help elucidate the dynamics of biological invasions, which are fueled by the constant expansion of international trade. The introduction of European gypsy moth (*Lymantria dispar* *dispar*) into North America is a classic example of human-aided invasion that has caused tremendous damage to North American temperate forests. Recently, the even more destructive Asian gypsy moth (mainly *L. d. asiatica* and *L. d. japonica*) has been intercepted in North America, mostly transported by cargo ships. To track invasion pathways, we developed a diagnostic panel of 60 DNA loci (55 nuclear and 5 mitochondrial) to characterize worldwide genetic differentiation within *L. dispar* and its sister species *L. umbrosa*. Hierarchical analyses supported strong differentiation and recovered five geographic groups that correspond to (1) North America, (2) Europe plus North Africa and Middle East, (3) the Urals, Central Asia, and Russian Siberia, (4) continental East Asia, and (5) the Japanese islands. Interestingly, *L. umbrosa* was grouped with *L. d. japonica*, and the introduced North American population exhibits remarkable distinctiveness from contemporary European counterparts. Each geographic group, except for North America, shows additional lower-level structures when analyzed individually, which provided the basis for inference of the origin of invasive specimens. Two assignment approaches consistently identified a coastal area of continental East Asia as the major source for Asian invasion during 2014-2015, with Japan being another source. By analyzing simulation and laboratory crosses, we further provided evidence for the occurrence of natural Asian-North American **hybrids** in the Pacific Northwest, raising concerns for **introgression** of Asian alleles that may accelerate range expansion of gypsy moth in North America. Our study demonstrates how genetic data contribute to bio-surveillance of invasive species with results that can inform regulatory management and reduce the frequency of trade-associated invasions.

Spatial and genetic structure of the lodgepole x jack pine hybrid zone

Burns, I; James, PMA; Coltman, DW; Cullingham, CI, 2019

In north-central Alberta, lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia*) and jack pine (*Pinus banksiana* Lamb.) form a mosaic **hybrid** zone, the spatial extent of which remains poorly defined. We sought to refine the genetic and geographic distribution of this **hybrid** zone in western North America to provide information important in predicting future risk of mountain pine beetle (*Dendroctonus ponderosae* Hopkins) outbreaks. We used 29 single nucleotide polymorphism (SNP) markers to discriminate lodgepole pine, jack pine, and their **hybrids**. We compared and contrasted spatial patterns of **hybridization** in northern and southern forest zones based on the colonization history of the two species. We found that patterns of **introgression** were more similar between the zones than expected by chance, but there were significant differences between these regions at specific loci. Using logistic regression, we created a robust predictive model to distinguish among lodgepole pine, jack pine, and their **hybrids** using a combination of geographic and environmental predictors. Using model selection based on Akaike

information criterion, we found that location, elevation, and moisture are important predictors for species class. Quantification of the genetic differences between these two regions, combined with an accurate model for predicting the spatial distribution of lodgepole pine, jack pine, and their **hybrids**, provides essential information for continued effective management of forest resources.

~~Fecundity of a native herbivore on its native and exotic host plants and relationship to plant chemistry~~

Marko, MD; Newman, RM,

The host range expansion of the specialist milfoil weevil, *Euhrychiopsis lecontei*, from the native *Myriophyllum sibiricum* (northern watermilfoil) to invasive *M. spicatum* (Eurasian watermilfoil) is one of the few examples of a native insect herbivore preferring, growing and surviving better on a nonindigenous host plant than it does on its native host plant. The milfoil weevil's preference for the nonindigenous plant can be induced during juvenile development or through exposure to Eurasian watermilfoil as an adult. We evaluated how the fecundity of the milfoil weevil was affected over time by juvenile and adult exposure to the native, invasive and invasive x native **hybrid** milfoils and whether fecundity was correlated with host plant quality. Weevils reared on Eurasian watermilfoil laid more eggs than those reared on northern or **hybrid** watermilfoils. When weevils were collected from and exposed to milfoils collected directly from a lake, Eurasian-reared weevils had higher fecundity and greater preference for Eurasian over northern watermilfoil. When weevils were reared on and allowed to oviposit on milfoils grown in a common environment, the differences in fecundity and preference for Eurasian over northern or **hybrid** watermilfoils diminished. In Eurasian-northern experiments, milfoil weevils laid more than 80% of their eggs on Eurasian watermilfoil, but that value decreased when plants from common environments were used. Despite this preference, most weevils continued to use both hosts indicating that a complete host switch is unlikely. Weevils showed no oviposition preference between Eurasian and **hybrid** milfoils. The milfoil weevil had higher fecundity on Eurasian watermilfoil, which had a higher concentration of carbon, polyphenols and lignin than did northern watermilfoil, which had a higher concentration of ash. The milfoil weevil's preference for Eurasian watermilfoil was affected by changes in plant chemistry, and ash appeared to act as a deterrent to oviposition on northern watermilfoil. The milfoil weevil can modify its response based on host-plant chemistry.

~~Potential Geographic Distributions and Successful Invasions of Parthenogenetic Broad-Nosed Weevils (Coleoptera: Curculionidae) Native to South America~~

Lanteri, AA; Guzman, NV; Del Rio, MG; Confalonieri, VA, 2013

Ten species of parthenogenetic broad-nosed weevils (Coleoptera: Curculionidae: Entiminae) native to Argentina, southern Brazil, and Uruguay were selected for niche modeling analysis based on climatic data and altitude, to evaluate their potential range expansion inside and outside South America. The selected species belong to five genera of the tribe Naupactini affecting economically important crops. Until present, five of the 10 species analyzed here have invaded prairies and steppes of countries outside South America (Australia, New Zealand, Mexico, United States, and South Africa): *Aramigus tessellatus* (Say), *Atrichonotus sordidus* (Hustache), *Atrichonotus taeniatus* (Berg), *Naupactus leucoloma* Boheman, and *Naupactus peregrinus* (Buchanan). Our niche modeling analyses performed with MAXENT demonstrated that these areas would be also suitable for *Aramigus conirostris* (Hustache), *Eurymetopus fallax* (Boheman), *Pantomorus auripes* Hustache, *Pantomorus ruizi* (Brethes), and *Pantomorus viridisquamosus* (Boheman), consequently, they also have the potential to invade areas outside their native ranges, mainly in southeastern United States, some European countries (e.g., Portugal, France, and southern England), South Africa, New Zealand, and southeastern Australia. All the studied species share similar environmental requirements, the most important variables being the Mean Temperature of Driest Quarter, the Annual Mean Temperature and Isothermality. Long distance dispersal through commercial trade, and parthenogenetic reproduction would increase the threat of these weevils to crop production worldwide.

~~Potential novel hosts for the lily leaf beetle *Lilioceris lili* Scopoli (Coleoptera: Chrysomelidae) in eastern North America~~

Ernst, C; Cappuccino, N; Arnason, JT, 2007

1. Introduced insects often incorporate native plants into their diets and might be expected to show a predilection for novel hosts that are phylogenetically related to their normal hosts. The lily leaf beetle, *Lilioceris lili* (Coleoptera: Chrysomelidae), is an introduced pest of cultivated lilies. Oviposition behaviour, larval behaviour, and development of *L. lili* was examined on a range of potential host plants, as well as on the normal host, Asiatic **hybrid** lilies *Lilium* sp. 2. Neonate larval feeding behaviour was quantified on 15 food plant species: 10 from the Liliales, three from the Asparagales and two eudicots. Larvae fed plants closely related to the genus *Lilium* were more likely to initiate feeding, less likely to abandon their food leaf, and consumed more leaf area. 3. In no-choice tests, females oviposited on the novel hosts *Lilium philadelphicum*, *Medeola virginiana*, *Clintonia borealis*, *Streptopus amplexifolius*, and *Polygonatum biflorum*; however, all but *L. philadelphicum* received very few eggs. Non-*Lilium* novel hosts were not used for oviposition when presented along with Asiatic lilies in choice tests. 4. A single individual was reared to the adult stage on the novel host *S. amplexifolius*. Several larvae survived to the pupal stage on *M. virginiana*, although no adults emerged from those pupae. Larvae reared on the native wood lily *L. philadelphicum* performed equally well or better than on the Asiatic cultivar. 5. Our results indicate that the lily leaf beetle poses a threat to native Liliaceae. Several native *Lilium* species, including *L. philadelphicum*, are threatened or endangered in certain jurisdictions throughout their range; these species should be monitored closely for colonisation by the beetle.

~~Hybridization and range expansion in tamarisk beetles (*Diorhabda* spp.) introduced to North America for classical biological control~~

Stahlke, AR; Bitume, EV; Ozsoy, ZA; Bean, DW; Veillet, A; Clark, MI; Clark, EI; Moran, P; Hufbauer, RA; Hohenlohe, PA, 2022

With the global rise of human-mediated translocations and invasions, it is critical to understand the genomic consequences of **hybridization** and mechanisms of range expansion. Conventional wisdom is that high genetic drift and loss of genetic diversity due to repeated founder effects will constrain introduced species. However, reduced genetic variation can be countered by behavioral aspects and admixture with other distinct populations. As planned invasions, classical biological control (biocontrol) agents present important opportunities to understand the mechanisms of establishment and spread in a novel environment. The ability of biocontrol agents to spread and adapt, and their effects on local ecosystems, depends on genomic variation and the consequences of admixture in novel environments. Here, we use a biocontrol system to examine the genome-wide outcomes of introduction, spread, and **hybridization** in four cryptic species of a biocontrol agent, the tamarisk beetle (*Diorhabda carinata*, *D. carinulata*, *D. elongata*, and *D. sublineata*), introduced from six localities across Eurasia to control the invasive shrub tamarisk (*Tamarix* spp.) in western North America. We assembled a de novo draft reference genome and applied RADseq to over 500 individuals across laboratory cultures, the native ranges, and the introduced range. Despite evidence of a substantial genetic bottleneck among *D. carinulata* in N. America, populations continue to establish and spread, possibly due to aggregation behavior. We found that *D. carinata*, *D. elongata*, and *D. sublineata* **hybridize** in the field to varying extents, with *D. carinata* x *D. sublineata* **hybrids** being the most abundant. Genetic diversity was greater at sites with **hybrids**, highlighting potential for increased ability to adapt and expand. Our results demonstrate the complex patterns of genomic variation that can result from introduction of multiple ecotypes or species for biocontrol, and the importance of understanding them to predict and manage the effects of biocontrol agents in novel ecosystems.

~~Population genetic analyses of complex global insect invasions in managed landscapes: a *Leptocybe invasa* (Hymenoptera) case study~~

Dittrich-Schroder, G; Hoareau, TB; Hurley, BP; Wingfield, MJ; Lawson, S; Nahrung, HF; Slippers, B, 2018

Increased rates of movement and the accumulation of insects establishing outside their native range is leading to the 'global homogenization' of agricultural and

forestry pests. We use an invasive wasp, *Leptocybe invasa* (Hymenoptera: Eulophidae), as a case study to highlight the rapid and complex nature of these global invasions and how they can complicate management options. To trace the invasion history of *L. invasa* globally, we characterised the genetic diversity within and between populations from its origin and invaded regions using mitochondrial and nuclear markers. Three mitochondrial Haplogroups were identified, of which two are likely different species that appear to have been independently introduced into different parts of the world. One type (Mitochondrial Haplogroup 1) occurs globally, and is the exclusive type found in Europe, the Middle East, South America and most of Africa. The second type (Mitochondrial Haplogroup 2) co-occurs with the first-type in Laos, South Africa, Thailand and Vietnam, while a third type (Mitochondrial Haplogroup 3) occurs exclusively in Australia, its native range. The distinction of the two invasive Haplogroups was supported by analysis of newly developed simple sequence repeat (microsatellite) markers in populations from 13 countries. Further analyses using clustering methods and approximate Bayesian computation suggested the occurrence of **hybridisation** in the Laos population and revealed that an unsampled population was the origin of Mitochondrial Haplogroup 1. The analyses also showed little genetic differentiation within the invasive populations, suggesting a limited original introduction from a very small population followed by rapid, global range expansion in a stepwise fashion. Results of this study should provide some guidelines for characterizing invasion pathways of new invasive insect pests.

~~Genetics of the butterfly *Danaus chrysippus* (L.) in a broad hybrid zone, with special reference to sex ratio, polymorphism and intragenomic conflict~~

Smith, DAS; Gordon, IJ; Depew, LA; Owen, DF, 1998

The aposematic savanna butterfly *Danaus chrysippus* seems to be an exception to the rule that Batesian models and Mullerian mimics are not polymorphic. Throughout Asia and in much of Africa the species is in fact monomorphic and polytypic, as expected. It is, however, polymorphic for 3-4 colour genes over a large area of central and eastern Africa, where deviant sex ratios and non-Mendelian segregations also occur. All-female broods are widespread and frequent, often outnumbering bisexual progenies and giving rise to heavily female-biased populations. Full and partial sex linkage, which is not controlled from the X or Y chromosomes, and male-biased broods also occur. Genetical analysis for the BC-autosome carrying colour genes suggests there are two: probably mitochondrial, cytotypes (microbe-induced early male death syndrome is considered unlikely) and an autosomal, incompatibility (I) gene, two alleles of which are male-specific killers. F2 and backcross matings by females heterozygous at the I-locus give progenies which are either thelygenic, all males dying at or soon after hatching, or bisexual but showing full or partial sex linkage. Male death is attributed to nuclear-cytoplasmic incompatibility (NCI). Females achieve reversion from a thelygenic to a bisexual line by mating with males of compatible (maternal) cytotype. A second NCI system causes meiotic drive in female oogenesis for a cytoplasmically compatible A-autosome, with no effect on SR. The array or, non-Mendelian segregations for sex and two autosomes, with switching between bisexual and unisexual lineages, indicates autosomal intragenomic conflict with the outcome that one autosome is preserved from elimination in females, and the other condemned in dead males. The geographical distribution of the colour marker genes suggests, that the polymorphisms have a **hybrid** origin involving several once allopatric subspecies: some of which have divergent cytotypes. Secondary contact probably followed range expansion induced by the periodic spread of savanna during the Pleistocene and massive deforestation by man in recent times. The unusual extent of, the **hybrid** zone is attributed to the large number of subspecies involved in its origin, and to **introgression** promoted by the butterfly's extensive migratory activity. (C) 1998 The Linnean Society of London.

~~Phylogeography of Fischer's blue, *Tongeia fischeri*, in Japan: Evidence for introgressive hybridization~~

Jeratthitikul, E; Hara, T; Yago, M; Itoh, T; Wang, M; Usami, S; Hikida, T, 2013

The widespread lycaenid butterfly *Tongeia fischeri* is distributed from eastern Europe to northeastern Asia and represented by three geographically isolated populations in Japan. In order to clarify the phylogeographic history of the species, we used sequences of three mitochondrial (COI, Cyt b and ND5) and two nuclear (Rp15 and Ldh) genes of 207 individuals collected from 55 sites throughout Japan and five sites on the Asian continent. Phylogenetic trees and the median-joining network revealed six evolutionary mitochondrial haplotype clades, which corresponded to the geographic distribution of the species. Common ancestors of Japanese *T. fischeri* might have come to Japan during the mid-Pleistocene by multiple dispersals of continental populations, probably via a land bridge or narrow channel between western Japan and the Korean Peninsula. The geographical patterns of variation of mitochondrial and nuclear markers are discordant in northeastern Kyushu, possibly as a result of introgressive **hybridization** during the ancient contact between the Kyushu and Shikoku populations in the last glacial maximum. The phylogeographic pattern of *T. fischeri* in Japan are probably related to the geological history, Pleistocene climatic oscillations and distribution of the host plant. (C) 2012 Elsevier Inc. All rights reserved.

~~POSTGLACIAL EXPANSION AND GENOME SUBDIVISION IN THE EUROPEAN GRASSHOPPER *CHORTHIPPUS PARALLELUS*~~

COOPER, SJB; IBRAHIM, KM; HEWITT, GM, 1995

A noncoding nuclear DNA marker sequence (Cpn1-1) was used to investigate subdivision in the grasshopper *Chorthippus parallelus* and deduce postglacial expansion patterns across its species range in Europe. Investigation of the spatial distribution of 71 Cpn1-1 haplotypes and estimation of levels of genetic differentiation (K-ST values) between populations and geographic regions provided evidence for subdivision of *C. parallelus* into at least five major geographic regions and indicated that the French form of *C. parallelus* originated after range expansion from a Balkan refugium. Further evidence for subdivision of *C. parallelus* between Italy and northern Europe suggests that the Alps may have formed a significant barrier to gene flow in this grasshopper.

~~Patterns of trait divergence between populations of the meadow grasshopper, *Chorthippus parallelus*~~

Tregenza, T; Pritchard, VL; Butlin, RK, 2000

To understand the process of speciation, we need to identify the evolutionary phenomena associated with divergence between populations of the same species. A powerful approach is to compare patterns of trait differences between populations differing in their evolutionary histories. A recent study of genetic divergence between populations of the meadow grasshopper *Chorthippus parallelus*, from different locations around Europe has allowed us to use this species to investigate which aspects of evolutionary history are associated with divergence in morphology and mating signals. During the last glaciation *C. parallelus* was confined to a number of refugia in southern Europe and has subsequently recolonized the northern part of the continent. This process of isolation followed by range expansion has created populations differing markedly in their evolutionary pasts-some have been isolated from one another for thousands of years, others have undergone repeated founder events, and others now live in sympatry with a closely related species. Using laboratory-reared grasshoppers from 12 different populations with a range of evolutionary histories, we quantify differences in morphology, chemical signals, and male calling-song. The observed pattern of divergence between these populations is then compared with the pattern predicted by hypotheses about what drives divergence. This comparison reveals that long periods in allopatry and processes associated with repeated founder events are both strongly associated with divergence.

~~AN UNUSUAL MITOCHONDRIAL DNA POLYMORPHISM IN THE *CHORTHIPPUS BIGUTTULUS* SPECIES GROUP (ORTHOPTERA, ACRIDIDAE)~~

MASON, DJ; BUTLIN, RK; GACESA, P, 1995

Mitochondrial DNA restriction fragment patterns have been used to investigate the *Chorthippus biguttulus* group: a group of morphologically similar grasshopper species with very distinct male calling songs. Ten haplotypes were identified in 21 populations, representing six species. Haplotype diversity was as great within

species, and in same case within populations, as it was among species and no clear geographical patterns of haplotype distribution were revealed. In the light of grasshopper range changes since the last glaciation it is unlikely that these data can be explained entirely by the retention of ancestral polymorphism. This suggests that **hybridization** has occurred during periods of grasshopper range expansion since the last glacial maximum, allowing mtDNA transfer between populations that have previously diverged in allopatry.

Genetic heterogeneity, reproductive isolation and host preferences in mealy aphids of the *Hyalopterus pruni* complex (Homoptera: Aphidoidea)

Mosco, MC; Arduino, P; Bullini, L; Barbagallo, S, 1997

Three taxa were detected by allozyme markers within the mealy aphids of the *Hyalopterus pruni* complex, having different cultivated *Prunus* species as main primary hosts. The genetically closer *H. pruni* and *H. amygdali* A (D-Nei = 0.10) never share primary hosts, whereas *H. amygdali* A and B (D-Nei = 0.32) may occasionally share them, producing few F-1 **hybrids**. The three species proved reproductively isolated in the field, with no gene exchange. Their speciation seem to have occurred long before the agricultural revolution, crop colonization representing a host range expansion rather than a host shift, as in sympatric speciation.

Origin of Pest Lineages of the Colorado Potato Beetle (Coleoptera: Chrysomelidae)

Izzo, VM; Chen, YH; Schoville, SD; Wang, C; Hawthorne, DJ, 2018

Colorado potato beetle (*Leptinotarsa decemlineata* Say [Coleoptera: Chrysomelidae]) is a pest of potato throughout the Northern Hemisphere, but little is known about the beetle's origins as a pest. We sampled the beetle from uncultivated *Solanum* host plants in Mexico, and from pest and non-pest populations in the United States and used mitochondrial DNA and nuclear loci to examine three hypotheses on the origin of the pest lineages: 1) the pest beetles originated from Mexican populations, 2) they descended from **hybridization** between previously divergent populations, or 3) they descended from populations that are native to the Plains states in the United States. Mitochondrial haplotypes of non-pest populations from Mexico and Arizona differed substantially from beetles collected from the southern plains and potato fields in the United States, indicating that beetles from Mexico and Arizona did not contribute to founding the pest lineages. Similar results were observed for AFLP and microsatellite data. In contrast, non-pest populations from the states of Colorado, Kansas, Nebraska, New Mexico, and Texas were genetically similar to U.S. pest populations, indicating that they contributed to the founding of the pest lineages. Most of the pest populations do not show a significant reduction in genetic diversity compared to the plains populations in the United States. We conclude that genetically heterogeneous beetle populations expanded onto potato from native *Solanum* hosts. This mode of host range expansion may have contributed to the abundant genetic diversity of contemporary populations, perhaps contributing to the rapid evolution of climate tolerance, host range, and insecticide resistance.

Colonization ability of two invasive weevils with different reproductive modes

Guzman, NV; Lanteri, AA; Confalonieri, VA, 2012

The flightless weevils *Naupactus leucoloma* and *Naupactus xanthographus* (Coleoptera: Curculionidae: Naupactini), which are native to and partially co-distributed in South America, apparently have asexual and bisexual reproductive modes, respectively. We used two different molecular markers to elucidate the effects of these reproductive modes on the colonization ability and genetic variability of both species. First, we investigated the occurrence of clonal reproduction in the putative parthenogenetic species (i.e. significant bias in sex ratio) and second, whether parthenogenesis was associated with higher colonization ability and low levels of genetic variability in marginal environments compared with those of the bisexual species. We assessed the central and marginal areas of distribution of these species with ecological niche modeling that includes environmental variables and with landscape interpolation of molecular variability. Our results support the idea that parthenogenetic species are more successful than bisexual ones in colonizing new environments. *N. leucoloma* is most probably apomictic, and would have recently experienced significant population growth concomitant with an important geographic range expansion to distant areas with moderately suitable environmental conditions. On the other hand, the populations of the bisexual species, *N. xanthographus*, seem to have maintained fairly constant sizes, expanding its geographic distribution to locations close to the proposed ancestral area.

Genetic structure, admixture and invasion success in a Holarctic defoliator, the gypsy moth (*Lymantria dispar*, Lepidoptera: Erebiidae)

Wu, YK; Molongoski, JJ; Winograd, DF; Bogdanowicz, SM; Louyakis, AS; Lance, DR; Mastro, VC; Harrison, RG, 2015

Characterizing the current population structure of potentially invasive species provides a critical context for identifying source populations and for understanding why invasions are successful. Non-native populations inevitably lose genetic diversity during initial colonization events, but subsequent admixture among independently introduced lineages may increase both genetic variation and adaptive potential. Here we characterize the population structure of the gypsy moth (*Lymantria dispar* Linnaeus), one of the world's most destructive forest pests. Native to Eurasia and recently introduced to North America, the current distribution of gypsy moth includes forests throughout the temperate region of the northern hemisphere. Analyses of microsatellite loci and mitochondrial DNA sequences for 1738 individuals identified four genetic clusters within *L. dispar*. Three of these clusters correspond to the three named subspecies; North American populations represent a distinct fourth cluster, presumably a consequence of the population bottleneck and allele frequency change that accompanied introduction. We find no evidence that admixture has been an important catalyst of the successful invasion and range expansion in North America. However, we do find evidence of ongoing **hybridization** between subspecies and increased genetic variation in gypsy moth populations from Eastern Asia, populations that now pose a threat of further human-mediated introductions. Finally, we show that current patterns of variation can be explained in terms of climate and habitat changes during the Pleistocene, a time when temperate forests expanded and contracted. Deeply diverged matrilineages in Europe imply that gypsy moths have been there for a long time and are not recent arrivals from Asia.

Influence of water deficit on the molecular responses of *Pinus contorta* x *Pinus banksiana* mature trees to infection by the mountain pine beetle fungal associate, *Grosmannia clavigera*

Arango-Velez, A; Gonzalez, LMG; Meents, MJ; El Kayal, W; Cooke, BJ; Linsky, J; Lusebrink, I; Cooke, JEK, 2014

Conifers exhibit a number of constitutive and induced mechanisms to defend against attack by pests and pathogens such as mountain pine beetle (*Dendroctonus ponderosae* Hopkins) and their fungal associates. Ecological studies have demonstrated that stressed trees are more susceptible to attack by mountain pine beetle than their healthy counterparts. In this study, we tested the hypothesis that water deficit affects constitutive and induced responses of mature lodgepole pine x jack pine **hybrids** (*Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm. ex S. Wats. x *Pinus banksiana* Lamb.) to inoculation with the mountain pine beetle fungal associate *Grosmannia clavigera* (Robinson-Jeffrey and Davidson) Zipfel, de Beer and Wingfield. The degree of stress induced by the imposed water-deficit treatment was sufficient to reduce photosynthesis. *Grosmannia clavigera*-induced lesions exhibited significantly reduced dimensions in water-deficit trees relative to well-watered trees at 5 weeks after inoculation. Treatment-associated cellular-level changes in secondary phloem were also observed. Quantitative RT-PCR was used to analyze transcript abundance profiles of 18 genes belonging to four families classically associated with biotic and abiotic stress responses: aquaporins (AQPs), dehydration-responsive element binding (DREB), terpene synthases (TPSs) and chitinases (CHIs). Transcript abundance profiles of a TIP2 AQP and a TINY-like DREB decreased significantly in fungus-inoculated trees, but not in response to water deficit. One TPS, Pcb(+)-3-carene synthase, and the Class II CHIs PcbCHI2.1 and PcbCHI2.2

showed increased expression under water-deficit conditions in the absence of fungal inoculation, while another TPS, Pcb(E)-beta-farnesene synthase-like, and two CHIs, PcbCHI1.1 and PcbCHI4.1, showed attenuated expression under water-deficit conditions in the presence of fungal inoculation. The effects were observed both locally and systemically. These results demonstrate that both constitutive and induced carbon-and nitrogen-based defenses are affected by water deficit, suggesting potential consequences for mountain pine beetle dynamics, particularly in novel environments.

Diversification in a fluctuating island setting: rapid radiation of Ohomopterus ground beetles in the Japanese Islands

Sota, T; Nagata, N, 2008

The Japanese Islands have been largely isolated from the East Asian mainland since the Early Pleistocene, allowing the diversification of endemic lineages. Here, we explore speciation rates and historical biogeography of the ground beetles of the subgenus Ohomopterus (genus Carabus) based on nuclear and mitochondrial gene sequences. Ohomopterus diverged into 15 species during the Pleistocene. The speciation rate was 1.92 Ma(-1) and was particularly fast (2.37 Ma(-1)) in a group with highly divergent genitalia. Speciation occurred almost solely within Honshu, the largest island with complex geography. Species diversity is highest in central Honshu, where closely related species occur parapatrically and different-sized species co-occur. Range expansion of some species in the past has resulted in such species assemblages. Introgressive **hybridization**, at least for mitochondrial DNA, has occurred repeatedly between species in contact, but has not greatly disturbed species distinctness. Small-island populations of some species were separated from main-island populations only after the last glacial (or the last interglacial) period, indicating that island isolation had little role in speciation. Thus, the speciation and formation of the Ohomopterus assemblage occurred despite frequent opportunities for secondary contact and **hybridization** and the lack of persistent isolation. This radiation was achieved without substantial ecological differentiation, but with marked differentiation in mechanical agents of reproductive isolation (body size and genital morphology).

Bayesian analysis of molecular variance in pyrosequences quantifies population genetic structure across the genome of Lycaeides butterflies

Gompert, Z; Forister, ML; Fordyce, JA; Nice, CC; Williamson, RJ; Buerkle, CA, 2010

The distribution of genetic variation within and among populations is commonly used to infer their demographic and evolutionary histories. This endeavour has the potential to benefit substantially from high-throughput next-generation sequencing technologies through a rapid increase in the amount of data available and a corresponding increase in the precision of parameter estimation. Here we report the results of a phylogeographic study of the North American butterfly genus Lycaeides using 454 sequence data. This study serves the dual purpose of demonstrating novel molecular and analytical methods for population genetic analyses with 454 sequence data and expanding our knowledge of the phylogeographic history of Lycaeides. We obtained 341 045 sequence reads from 12 populations that we were able to assemble into 15 262 contigs (most of which were variable), representing one of the largest population genetic data sets for a non-model organism to date. We examined patterns of genetic variation using a hierarchical Bayesian analysis of molecular variance model, which provides precise estimates of genome-level $\phi(ST)$ while appropriately modelling uncertainty in locus-specific $\phi(ST)$. We found that approximately 36% of sequence variation was partitioned among populations, suggesting historical or current isolation among the sampled populations. Estimates of pairwise genome-level $\phi(ST)$ were largely consistent with a previous phylogeographic model for Lycaeides, suggesting fragmentation into two to three refugia during Pleistocene glacial cycles followed by post-Pleistocene range expansion and secondary contact leading to introgressive **hybridization**. This study demonstrates the potential of using genome-level data to better understand the phylogeographic history of populations.

The role of gene flow asymmetry along an environmental gradient in constraining local adaptation and range expansion

Fedorka, KM; Winterhalter, WE; Shaw, KL; Brogan, WR; Mousseau, TA,

Theoretically, asymmetric gene flow along an environmental gradient can limit species range expansion by keeping peripheral populations from locally adapting. However, few empirical studies have examined this potentially fundamental evolutionary mechanism. We address this possibility in the cricket Allonemobius socius, which exist along a season-length gradient where the probability of producing a single generation per year (univoltinism) increases with latitude. As the probability of univoltinism increases northwards, populations are expected to hedge their bets by producing a greater proportion of diapause eggs when exposed to a mild diapause cue. However, gene flow from southern populations may disrupt local adaptation in the north by reducing the proportion of diapause eggs (expected to be 100% in pure univoltine environments). This may limit range expansion along the northern periphery where A.socius compete with A.fasciatus, a sister species that exhibits an invariant diapause-only egg-laying strategy. To assess the potential for range limitation, we examined diapause incidence (the proportion of diapause eggs produced under diapause conditions), gene flow symmetry and population structure across nine A.socius populations. We found that gene flow was asymmetric and biased northwards towards the periphery. Furthermore, peripheral populations that inhabited pure univoltine environments produced numerous nondiapause eggs (a southern, bivoltine diapause phenotype), which we assume to be a suboptimal phenotype. These patterns suggest that asymmetric gene flow along the gradient constrains adaptation in peripheral populations, potentially constraining species range expansion.

Radiation with reticulation marks the origin of a major malaria vector

Small, ST; Labbe, F; Lobo, NF; Koekemoer, LL; Sikaala, CH; Neafsey, DE; Hahn, MW; Fontaine, MC; Besansky, NJ, 2020

Advances in genomics have led to an appreciation that **introgression** is common, but its evolutionary consequences are poorly understood. In recent species radiations the sharing of genetic variation across porous species boundaries can facilitate adaptation to new environments and generate novel phenotypes, which may contribute to further diversification. Most Anopheles mosquito species that are of major importance as human malaria vectors have evolved within recent and rapid radiations of largely nonvector species. Here, we focus on one of the most medically important yet understudied anopheline radiations, the Afrotropical Anopheles funestus complex (AFC), to investigate the role of **introgression** in its diversification and the possible link between **introgression** and vector potential. The AFC comprises at least seven morphologically similar species, yet only An. funestus sensu stricto is a highly efficient malaria vector with a pan-African distribution. Based on de novo genome assemblies and additional whole-genome resequencing, we use phylogenomic and population genomic analyses to establish species relationships. We show that extensive interspecific gene flow involving multiple species pairs has shaped the evolutionary history of the AFC since its diversification. The most recent **introgression** event involved a massive and asymmetrical movement of genes from a distantly related AFC lineage into An. funestus, an event that predated and plausibly facilitated its subsequent dramatic geographic range expansion across most of tropical Africa. We propose that **introgression** may be a common mechanism facilitating adaptation to new environments and enhancing vectorial capacity in Anopheles mosquitoes.

Population genetic effects of human-mediated plant range expansions on native phytophagous insects

Oliver, JC, 2006

Anthropogenic changes in organismal distributions have affected many, if not all, terrestrial ecosystems. Anthropogenic plant range expansions (APREs) may have profound effects on the population genetics of native phytophagous insects exploiting recent changes in plant distributions. Here I focus on the important, although often overlooked, effects on insect species which feed on such plants, but do not show evidence of host race formation. This article investigates geographic range expansion and increased interpopulation gene flow, which may occur as a result of phytophagous insects exploiting APREs. The two effects have clear predicted

genetic signatures: (1) geographic range expansion should result in low levels of genetic diversity in new portions of the insect species' range, relative to older, pre-APRE portions of the range and (2) increased interpopulation gene flow will result in reduced population genetic differentiation. Data from the literature are qualitatively consistent with the predictions of one or both population genetic change scenarios. Higher order effects, such as reduced local adaptation, increased spread of resistance in agricultural systems, and **hybridization** among formerly isolated lineages, as evidenced by case studies, and the economic and conservation implications thereof are also discussed. Finally, I outline future approaches for addressing the impact of APREs on native phytophagous insect ecology and discuss the application of these concepts of population genetic change and resultant outcomes to research outside plant-insect interactions.

Contrasting patterns of hybridization in large house spiders (*Tegenaria atrica* group, Agelenidae)

Croucher, PJP; Jones, RM; Searle, JB; Oxford, GS, 2007

The integrity of species is not fixed and may vary geographically. Here we investigate the geographic distributions and interactions of species in the *Tegenaria atrica* group (Araneae: Agelenidae). Detailed mapping of *T. saeva* and *T. gigantea* in England and Wales shows them to be broadly allopatric in southern England with a tightly defined, and possibly long-standing, narrow zone of parapatry in central southern England. In the north of England (Yorkshire), by contrast, the species are broadly sympatric as a result of recent range expansions. GIS techniques are used to map the species distributions and to quantify, for the first time, the intimacy of interspecific interactions. The extent and nature of **hybridization** in these two areas is examined through regression and multivariate analyses of morphology. We show that the relative incidence of **hybridization** is much greater in Yorkshire than within the parapatric zone in the south. Clear patterns of asymmetric **introgression** are observed in both northern and southern England, with a greater impact of *T. gigantea* on *T. saeva* than vice versa. We find no sign of morphological reproductive character displacement at the zone of parapatry that might indicate reinforcement, although we cannot exclude more subtle effects, for example via cuticular pheromones. The integrity of these two species seems to be breaking down in northern England, a process that might gain momentum as the gene pools become more similar.

Geographic patterns of phenotypic diversity in incipient species of North American blister beetles (Coleoptera: Meloidae) are not determined by species niches, but driven by demography along the speciation process

de Jesus-Bonilla, VS; Garcia-Paris, M; Ibarra-Cerdana, CN; Zaldivar-Riveron, A, 2018

The *Epicauta stigmata* complex is a group of blister beetles composed of three parapatric or sympatric species that occur in central Mexico to southern USA: *E. stigmata*, *E. uniforma* and *E. melanochroa*. These species are morphologically very similar, and are mainly distinguished by body colour differences. Here we assessed whether phenotypic divergence in coloration patterns define evolutionary units within the complex. We studied the phylogenetic relationships, demographic history and concordances between morphological and ecological traits in the group. The complex apparently had a demographic history of recent population expansion during the last glacial period 75 000 to 9500 years ago. The three species show no reciprocal monophyly, and thus their allospecificity was not confirmed. The current distribution of haplotypes and the genetic divergences in these taxa can be explained by either recent mitochondrial **introgression** events caused by **hybridization** or by incomplete lineage sorting. Colour pattern differences in the complex are not likely a product of local selection acting over a common genetic background. We suggest that phenotypic divergence in colour patterns during an incipient speciation process might be seen as an enhancing factor of cohesion within each of the three evolutionary units.

Comparative phylogeography of three *Leptocarabus* ground beetle species in South Korea, based on the mitochondrial COI and nuclear 28S rRNA genes

Zhang, AB; Kubota, K; Takami, Y; Kim, JL; Kim, JK; Sota, T, 2006

We analyzed the intraspecific gene genealogies of three *Leptocarabus* ground beetle species (*L. seishinensis*, *L. semiopacus*, *L. koreanus*) in South Korea using sequence data from the mitochondrial cytochrome oxidase subunit I (COI) and nuclear 28S rRNA (28S) genes, and compared phylogeographical patterns among the species. The COI data detected significant genetic differentiation among local populations of all three species, whereas the 28S data showed genetic differentiation only for *L. seishinensis*. The clearest differentiation of *L. seishinensis* among local populations was between the northern and southern regions in the COI clades, whereas the 28S clade, which likely indicates relatively ancient events, revealed a range expansion across the northern and southern regions. *Leptocarabus semiopacus* had the most shallow differentiation of the COI haplotypes, and some clades occurred across the northern and southern regions. In *L. koreanus*, four diverged COI clades occurred in different regions, with partial overlaps. We discuss the difference in phylogeographical patterns among these *Leptocarabus* species, as well as between these and other groups of carabid beetles in South Korea.

Characterizing patterns of introgressive hybridization between two species of *Tyrannus* following concurrent range expansion

Worm, AJ; Roeder, DV; Husak, MS; Fluker, BL; Boves, TJ, 2019

Hybridization between two species typically occurs when allopatric or ecologically dissimilar species expand into areas of secondary contact or habitat transitions. However, as species' ranges shift rapidly in response to environmental change, the potential for novel types of ephemeral **hybrid** zones exists. Here, we document and describe the occurrence, prevalence and symmetry of a previously undocumented **hybrid** zone involving two sympatric, ecologically similar sister species that have been expanding their ranges eastward in the central USA: Scissor-tailed Flycatchers *Tyrannus forficatus* and Western Kingbirds *Tyrannus verticalis*. We identified cases of **hybridization** and **introgression** using analyses of eight microsatellite DNA loci and a single mitochondrial gene. We also evaluated short-term reproductive consequences of **hybridization** for both species by surveying for both species and potential **hybrids** at the periphery of their ranges in northeastern Arkansas and western Tennessee, USA. Genetic data revealed bi-directional backcrossing at the periphery of the species' ranges, including a cryptic **hybrid**. We also analysed DNA of putative 'pure' individuals from other parts of their ranges and detected two cryptic admixed individuals, suggesting backcrossed individuals from the periphery may be dispersing to breed or that **hybridization** events have occurred in the core. Finally, our results suggest that there are no short-term reproductive consequences of **hybridization** for the two species. In total, **hybrid** zones that occur at the edges of expanding, sympatric ranges may be ephemeral; we suggest they play an important role in **introgression** and may have long-standing impacts for sympatric sister species. Exploring the extent of **hybrid** zones such as this for other range-expanding taxa will elucidate whether this type of **hybrid** zone is unique or a common occurrence.

COMPARISONS AMONG MORPHOLOGICAL CHARACTERS AND BETWEEN LOCALITIES IN THE CHORTHIPPUS PARALLELUS HYBRID ZONE (ORTHOPTERA, AGRIDIDAE)

BUTLIN, RK; RITCHIE, MG; HEWITT, GM, 1991

Two subspecies of the grasshopper, *Chorthippus parallelus*, meet and **hybridize** in the Pyrenees. The **hybrid** zone between the two taxa is believed to have formed following range expansion at the end of the last glaciation and to be maintained by a balance between gene flow and selection against **hybrids**. Laboratory F1 **hybrid** males are sterile. We have examined morphological characters in two cols about 200 km apart and compared the positions and widths of clines for these characters both within and between cols. Clines are neither coincident (centred in the same position), nor concordant equal in width) in either col. Furthermore clines are wider and more dispersed in the western col. The lack of concordance can be explained on several models for the maintenance of the **hybrid** zone and is a common

observation. There are many fewer examples of lack of coincidence and this result is more difficult to interpret. We suggest that it is due to a difference in population structure between the cols: a patchy distribution of grasshoppers in the western col produces wider, more dispersed clines while a sharp break in distribution in the eastern col tends to concentrate morphological change over a shorter distance.

A new and a described species of *Cystiphora* (Diptera: Cecidomyiidae) from Japan, with reference to geographically diversified intraspecific populations of *C. taraxaci* and its host range expansion from native Japanese to alien and hybrid species of *Taraxacum* (Asteraceae)

Yukawa, J; Kim, W; Nishino, T; Minami, T; Yamauchi, S; Ogawa, M; Ohara, K, 2021

Two species of *Cystiphora* (Diptera: Cecidomyiidae) are newly recorded from Japan. A gall midge that induces leaf galls on *Taraxacum* species (Asteraceae) is identified as *Cystiphora taraxaci* (Kieffer). Another gall midge that is responsible for leaf galls on *Sonchus brachyotus* (Asteraceae) is described as a new species under the name *Cystiphora hachijounae* Yukawa and Kim based on its incised hypoproct of male terminalia and some of the pupal characteristics. Genetic analysis supported the species identifications and indicated that the Palearctic *C. taraxaci* has long existed in Japan. It has been diversifying geographically into intraspecific populations since at least 2.57 Ma. Our current study argues against the recent invasion of Japan by alien *C. taraxaci* at the time of multiple introductions of European *Taraxacum* species to Japan for use as food (seed oil), forage and greening material during the late 19th century. Genetic analysis of gall-bearing *Taraxacum* plants collected from various localities in Japan indicates that most of them were alien or **hybrid** plants, while native Japanese species were rare, and these plants exhibited polyploidy from 2x to 5x. *Cystiphora taraxaci* is considered to have expanded its host range from native Japanese to alien and **hybrid** species of *Taraxacum* without regard to polyploidy.

Differential success in northwards range expansion between ecotypes of the marble gallwasp *Andricus kollari*: a tale of two lifecycles

Stone, G; Atkinson, R; Rokas, A; Csoka, G; Nieves-Aldrey, JL, 2001

The Marble gallwasp *Andricus kollari* has a native range divided into two geographically separated lifecycles. In Eastern Europe and Turkey, the lifecycle involves a sexual generation on Turkey oak, *Quercus cerris*, while in Iberia and North Africa the sexual generation host is cork oak, *Q. suber*. Over the last 500 years, *A. kollari* has expanded its range into northern Europe, following human planting of *Q. cem*'s from Italy and the Balkans. We ask: (i) what is the genetic relationship between eastern and western distributions of *Andricus kollari*? Can we determine which lifecycle is ancestral, and how long ago they diverged? (ii) To what extent have eastern and western native ranges contributed to northwards range expansion? (iii) Is there any evidence for **hybridization** between the two life cycle types? We present analyses of allozyme data for 13 polymorphic loci and of sequence variation for a 433 bp fragment of the mitochondrial cytochrome b gene. These show: (i) that four haplotype lineages (one in Spain, two in Hungary/Italy and one in Turkey) diverged more or less simultaneously between 1 and 2 million years ago, suggesting the existence of at least four refuges through recent ice age cycles. Our data cannot resolve which lifecycle type is ancestral. (ii) Populations north of putative refuges are divided into two sets. Populations in south-west France are allied to Spain, while all remaining populations in northern Europe have been colonized from Italy and the Balkans. (iii) The transition from one race to another in south-west France is marked by abrupt transitions in the frequency of refuge-specific private alleles and corresponds closely to the northern limit of the distribution of cork oak. Although **hybrids** were detected in north-west France, none were detected where the two lifecycles meet in south-western France. The biology of oak gallwasps predicts that any **hybrid** zone will be narrow and limited to regions where *Q. cem*'s and *Q. suber* meet. Our data suggest that eastern and western *A. kollari* are effectively separate species.

Behavioural and genetic interactions between an endangered and a recently arrived hummingbird

van Dongen, WFD; Lazzoni, I; Winkler, H; Vasquez, RA; Estades, CF, 2013

The invasion or expansion of non-native species into new geographic areas can pose a major threat to the conservation of biodiversity. These threats are augmented when the newly-arrived species interacts with native species that are already threatened by other ecological or anthropogenic processes. Potential interactions can include both competition for scarce resources and reproductive interference, including **hybridisation**. Understanding the dynamics of these interactions forms a crucial component of conservation management strategies. A recent contact zone occurs in the north of Chile between the endangered Chilean woodstar (*Eulidia yarrellii*) and the closely-related and recently-arrived Peruvian sheartail (*Thaumastura cora*), which expanded its range from Peru into Chile during the 1970s. We characterised the interactions between the species by combining population size estimates with molecular, morphological and behavioural data. We show that a low degree of **hybridisation**, but not **introgression**, is occurring between the two species. Despite interspecific morphological similarities, behavioural observations indicate that food niche overlap between the species is relatively low, and that the dietary breadth of sheartails is larger, which may have aided the species' range expansion. Finally, woodstars dominate the sheartails in male-male territorial interactions. However, potentially increased energetic costs for woodstars associated with frequent territorial chases and courtship displaying with sheartails may exacerbate the effects of other threats on woodstar viability, such as human-induced habitat modification. This study highlights the value of implementing multidisciplinary approaches in conservation biology to gain a more complete understanding of interactions between recently-arrived and endangered species.

Host plant range of *Aproceros leucopoda* is limited within Ulmaceae

Vetek, G; Csavas, K; Fail, J; Ladanyi, M, 2022

Although much research has been carried out to develop taxa resistant to Dutch elm disease (DED), newly occurring pests represent a new challenge for the protection of elms (Ulmaceae). The invasive zigzag elm sawfly (*Aproceros leucopoda*) is a recent invader of Asian origin in Europe defoliating elm trees that are otherwise often characterized with major resistance to DED. The range expansion of this pest poses a major threat to elms. The aim of this study was to identify the susceptibility of *Ulmus crassifolia*, *Hemiptelea davidii* and *Zelkova serrata* to this pest by using three different methods (oviposition trials with cut shoots and with plants in pots, and larval feeding trials with plants in pots) to define the performance of *A. leucopoda* on potential hosts. The fact is that *A. leucopoda* was unable to complete its development on either of these three taxa of Ulmaceae, whereas *Ulmus pumila* (the reference during the trials) was again confirmed as a true host of the pest clearly indicating that the host plant range of *A. leucopoda* is probably limited not only to *Ulmus* but also within this genus. Our results may be considered in future resistance breeding programmes, pest risk assessments, and for the selection of Ulmaceae species.

Genetic structure of *Cirsium palustre* (Asteraceae) and its role in host diversification of *Tephritis conura* (Diptera: Tephritidae)

Johannesen, J; Tritsch, C; Seitz, A; Diegisser, T, 2008

Whether or not a host plant is incorporated into a phytophagous insect's diet depends on both the insect's ability to colonize the novel host and the host plant's susceptibility to the insect. The latter, again, will be influenced by the genetic structure of the host plant. *Cirsium palustre* (marsh thistle) is heavily infested by the tephritid fly *Tephritis conura* in northern Britain, whereas infestation is not only absent in southern England, but also absent on the European continent where *T. conura* is common on other *Cirsium*. To understand why regional infestation patterns evolve, we studied how genetic structure and phylogeographic ancestry of *C. palustre* are related to the probability of infestation in Britain. The probability of infestation in Britain was related neither to phylogeographic lineage (two lineages were observed in Europe), nor to introgressive **hybridization** with the original host of *T. conura*, *C. heterophyllum*. However, infested British *C. palustre* were strongly

genetically deprived. British *C. palustre* showed continuous loss of genetic variability towards the northern range edge. The loss was explained best by genetic drift during geographic range expansion, rather than by genetic drift in isolated patches or mating system change from predominately outcrossing to selfing. The phylogeographic pattern of *C. palustre* strongly suggests Scotland as the geographic origin of a recent host-plant expansion of *T. conura*. (C) 2008 The Linnean Society of London, Biological Journal of the Linnean Society, 2008, 95, 221-232.

Genetic Diversity and Thermal Performance in Invasive and Native Populations of African Fig Flies

Comeault, AA; Wang, J; Tittes, S; Isbell, K; Ingley, S; Hurlbert, AH; Matute, DR, 2020

During biological invasions, invasive populations can suffer losses of genetic diversity that are predicted to negatively impact their fitness/performance. Despite examples of invasive populations harboring lower diversity than conspecific populations in their native range, few studies have linked this lower diversity to a decrease in fitness. Using genome sequences, we show that invasive populations of the African fig fly, *Zaprionus indianus*, have less genetic diversity than conspecific populations in their native range and that diversity is proportionally lower in regions of the genome experiencing low recombination rates. This result suggests that selection may have played a role in lowering diversity in the invasive populations. We next use interspecific comparisons to show that genetic diversity remains relatively high in invasive populations of *Z. indianus* when compared with other closely related species. By comparing genetic diversity in orthologous gene regions, we also show that the genome-wide landscape of genetic diversity differs between invasive and native populations of *Z. indianus* indicating that invasion not only affects amounts of genetic diversity but also how that diversity is distributed across the genome. Finally, we use parameter estimates from thermal performance curves for 13 species of *Zaprionus* to show that *Z. indianus* has the broadest thermal niche of measured species, and that performance does not differ between invasive and native populations. These results illustrate how aspects of genetic diversity in invasive species can be decoupled from measures of fitness, and that a broad thermal niche may have helped facilitate *Z. indianus*'s range expansion.

Phylogeography and introgressive hybridization of the ground beetle *Carabus yamato* in Japan based on mitochondrial gene sequences

Nagata, N; Kubota, K; Sota, T, 2007

To study the phylogeography of the ground beetle *Carabus yamato* in Japan, we compared 1,020-bp sequences of the mitochondrial NADH dehydrogenase subunit 5 (ND5) gene from 373 specimens from 37 localities with those of three parapatric species (*C. albrechti*, *C. kimurai*, and *C. japonicus*) that might share mitochondrial lineages with *C. yamato* through introgressive hybridization. We found 81 haplotypes from *C. yamato*. Of these, 17 haplotypes were considered to be of an introgressed lineage from *C. albrechti*, based on the phylogeny and geographic distribution. In addition, one haplotype of *C. kimurai* was likely an introgressant from *C. yamato*. Putative **introgression** events among the four species were restricted to these two directional cases. We analyzed the phylogeography of *C. yamato* using nested clade phylogeographical analysis and population genetic parameters. The mitochondrial lineages of *C. yamato* were estimated to have diverged no more than approximately 1.12 million years ago, implying that the estimated historical events occurred after the Early Pleistocene. *Carabus yamato* was inferred to have experienced a contraction of its distribution range, followed by recent range expansion. Populations in the western and eastern regions, segregated by Ise Bay and the Nobi and Okazaki Plains, diverged in the mitochondrial clades. The northern and most western populations possessed one clade only (except an introgressed lineage), whereas eastern and some southwestern populations possessed several diverged clades, which were considered to be ancestral; these populations may have been associated with refugia during glacial periods.

Thermal niche evolution and geographical range expansion in a species complex of western Mediterranean diving beetles

Hidalgo-Galiana, A; Sanchez-Fernandez, D; Bilton, DT; Cieslak, A; Ribera, I, 2014

Background: Species thermal requirements are one of the principal determinants of their ecology and biogeography, although our understanding of the interplay between these factors is limited by the paucity of integrative empirical studies. Here we use empirically collected thermal tolerance data in combination with molecular phylogenetics/phylogeography and ecological niche modelling to study the evolution of a clade of three western Mediterranean diving beetles, the *Agabus brunneus* complex. Results: The preferred mitochondrial DNA topology recovered *A. ramblae* (North Africa, east Iberia and Balearic islands) as paraphyletic, with *A. brunneus* (widespread in the southwestern Mediterranean) and *A. rufulus* (Corsica and Sardinia) nested within it, with an estimated origin between 0.60-0.25 Ma. All three species were, however, recovered as monophyletic using nuclear DNA markers. A Bayesian skyline plot suggested demographic expansion in the clade at the onset of the last glacial cycle. The species thermal tolerances differ significantly, with *A. brunneus* able to tolerate lower temperatures than the other taxa. The climatic niche of the three species also differs, with *A. ramblae* occupying more arid and seasonal areas, with a higher minimum temperature in the coldest month. The estimated potential distribution for both *A. brunneus* and *A. ramblae* was most restricted in the last interglacial, becoming increasingly wider through the last glacial and the Holocene. Conclusions: The *A. brunneus* complex diversified in the late Pleistocene, most likely in south Iberia after colonization from Morocco. Insular forms did not differentiate substantially in morphology or ecology, but *A. brunneus* evolved a wider tolerance to cold, which appeared to have facilitated its geographic expansion. Both *A. brunneus* and *A. ramblae* expanded their ranges during the last glacial, although they have not occupied areas beyond their LGM potential distribution except for isolated populations of *A. brunneus* in France and England. On the islands and possibly Tunisia secondary contact between *A. brunneus* and *A. ramblae* or *A. rufulus* has resulted in **introgression**. Our work highlights the complex dynamics of speciation and range expansions within southern areas during the last glacial cycle, and points to the often neglected role of North Africa as a source of European biodiversity.

Geographically localised bursts of ribosomal DNA mobility in the grasshopper *Podisma pedestris*

Veltsos, P; Keller, I; Nichols, RA, 2009

We report extraordinary variation in the number and the chromosomal location of ribosomal DNA (rDNA) arrays within populations of the alpine grasshopper *Podisma pedestris*; even greater differences were found between populations. The sites were detected by in situ hybridisation of labelled rDNA to chromosomal preparations. The total number of rDNA sites in an individual varied from three to thirteen. In the most extreme case, individuals from populations only 10 km apart had no rDNA loci in common. A survey of the geographical distribution of this variation identified clusters of populations with relatively similar chromosomal distribution of rDNA loci. These clusters correspond to those identified earlier by analysis of rDNA sequences. To explain this geographical clustering, we reconstructed the post-glacial colonisation of the region by assuming that the species' distribution has ascended to its current altitudinal range as the climate warmed. The reconstruction suggests that each cluster is descended from a colonisation route up a different alpine valley. That history would imply rapid establishment of rDNA differences, conceivably during the last 10 000 years since the last glaciation. The proposal for rapid change is consistent with the extensive within-population variation, which indicates that the processes responsible for the change in rDNA's chromosomal location continue to occur at a higher rate. We discuss whether our reconstruction of colonisation routes implies movement of the **hybrid** zone, which would indicate that a neo-XY sex chromosome system has spread through extant populations. *Heredity* (2009) 103, 54-61; doi: 10.1038/hdy.2009.32; published online 22 April 2009

Genetic mixture of multiple source populations accelerates invasive range expansion

Wagner, NK; Ochocki, BM; Crawford, KM; Compagnoni, A; Miller, TEX, 2017

1. A wealth of population genetic studies have documented that many successful biological invasions stem from multiple introductions from genetically distinct source populations. Yet, mechanistic understanding of whether and how genetic mixture promotes invasiveness has lagged behind documentation that such mixture commonly occurs. We conducted a laboratory experiment to test the influence of genetic mixture on the velocity of invasive range expansion. 2. The mechanistic basis for effects of genetic mixture could include evolutionary responses (mixed invasions may harbour greater genetic diversity and thus elevated evolutionary potential) and/or fitness advantages of between-population mating (heterosis). If driven by evolution, positive effects of source population mixture should increase through time, as selection sculpts genetic variation. If driven by heterosis, effects of mixture should peak following first reproductive contact and then dissipate. 3. Using a laboratory model system (beetles spreading through artificial landscapes), we quantified the velocity of range expansion for invasions initiated with one, two, four or six genetic sources over six generations. Our experiment was designed to test predictions corresponding to the evolutionary and heterosis mechanisms, asking whether any effects of genetic mixture occurred in early or later generations of range expansion. We also quantified demography and dispersal for each experimental treatment, since any effects of mixture should be manifest in one or both of these traits. 4. Over six generations, invasions with any amount of genetic mixture (two, four and six sources) spread farther than single-source invasions. Our data suggest that heterosis provided a 'catapult effect', leaving a lasting signature on range expansion even though the benefits of outcrossing were transient. Individual-level trait data indicated that genetic mixture had positive effects on local demography (reduced extinction risk and enhanced population growth) during the initial stages of invasion but no consistent effects on dispersal ability. 5. Our work is the first to demonstrate that genetic mixture can alter the course of spatial expansion, the stage of invasion typically associated with the greatest ecological and economic impacts. We suggest that similar effects of genetic mixture may be a common feature of biological invasions in nature, but that these effects can easily go undetected.

Phenotypic evolution and the genetic architecture underlying photoperiodic time measurement

Bradshaw, WE; Holzapfel, CM, 2001

A wide variety of higher plants, vertebrates, and arthropods use the length of day to synchronize growth, development, reproduction, dormancy, and migration with the changing seasons. In the pitcher-plant mosquito, *Wyeomyia smithii*, critical photoperiod mediating the onset and maintenance of larval diapause has evolved about 10 standard deviations in mean critical photoperiod between the ancestral, Gulf Coast populations, and the derived, Canadian populations. We are seeking to understand how this evolution has been accomplished at both the genetic and the physiological levels. At the genetic level, average heterozygosity at protein-coding loci decreases with latitude of origin, while genetic variation for photoperiodic response increases with latitude of origin, particularly within the formerly glaciated regions of North America. **Hybridization** experiments reveal widespread genetic differences in critical photoperiod due to epistasis. We ascribe the increase in genetic variation in photoperiodic response, despite directional and stabilizing selection to the contrary, to the release of additive from epistatic variance during successive founder events in *W. smithii*'s northward dispersal following recession of the Laurentide Ice Sheet, and to the resulting genetic drift and reorganization of genetic architectures in descendent populations. At the physiological level, northern populations of *W. smithii*, as well as northern populations of spider mites, flies, moths, and beetles in both North America and Europe show a declining expression of the rhythmic component of photoperiodic response. In *Drosophila melanogaster*, when the epistatic coupling between the period locus and photoperiodic response is disrupted, the critical photoperiod is shifted towards shorter daylengths; analogously in *W. smithii*, when epistatic interactions are disrupted in the recombining generations of **hybrid** populations, the critical photoperiod is shifted towards shorter daylengths. The implications here are (1) that in *W. smithii*, it is the epistatic modification of the photoperiodic response curve by the circadian clock that is being disrupted in the recombining generations and (2) that post-glacial range expansion into the North-Temperate Zone by arthropods in general may involve uncoupling of the circadian and photoperiodic clocks. Despite the tremendous advances that have been made in understanding circadian rhythmicity at the molecular level, virtually nothing is known about how or whether any of the downstream 'clock-controlled genes' connect with photoperiodic time measurement. Except in *W. smithii*, little is known about how this connection changes with seasonal adaptation of photoperiodic response through evolutionary time. It is our goal and desire that our top-down approach to the evolution of photoperiodic time measurement will meet and mesh with the bottom-up approach that is being developed so fruitfully for circadian clocks. (C) 2001 Elsevier Science Ltd. All rights reserved.

Invasion spread of *Operophtera brumata* in northeastern United States and hybridization with *O. bruceata*

Elkinton, JS; Liebhold, A; Boettner, GH; Sremac, M, 2014

We used five methods to estimate the rate of spread of the winter moth, *Operophtera brumata* L., a European Lepidoptera, invading the northeastern USA and occasionally **hybridizing** with the closely related *O. bruceata*. These two species utilize the same sex attractant and pheromone traps capture both species. We estimated spread based on the ratio of the two species captured in pheromone-baited traps. Population boundaries were derived from captures in a grid of traps and spread was estimated as 6.6 km/year based on displacement of population boundaries between 2005 and 2008. Radial spread rate was also estimated as 6.9 km/year from the displacement of boundaries using logistic regression of trap captures along a single east-west transect of traps deployed yearly from 2007 to 2011. We also estimated the rate of spread from the expansion of defoliation mapped during aerial surveys. Based on the displacement of defoliation boundaries from 2005 to 2008, spread rate was estimated as 6.0 km/year. Based on the year of first defoliation, spread was estimated as 4.8 km/year and regression of the square-root of the cumulative area/pi versus time yielded an estimate of 4.7 km/year. All five estimates were similar, and differences reflect the nuances of the data from which they were derived. We discuss here how the occasional **hybridization** with *O. bruceata* may be either retarding or enhancing *O. brumata* spread.

Limited hybridization along a large contact zone between two genetic lineages of the butterfly *Erebia medusa* (Satyrinae, Lepidoptera) in Central Europe

Schmitt, T; Muller, P, 2007

Genetic lineages evolving during glacial isolation frequently come into contact as the result of postglacial range expansions. **Hybridization** often occurs along these contact zones. In Europe, the high mountain systems of the Alps and Pyrenees are well known for their **hybrid** belts. This article studies the contact zone of the Woodland Ringlet *Erebia medusa* in a Hercynian mountain area in the Czech-German border region not exceeding 1500 m a.s.l. **Hybrid** populations between an eastern and a western genetic lineage were detected by AMOVA-based tests, principal component analysis and neighbour joining analysis. Over most of the range of the Czech-German Border Mts, the ridges separate the western and the eastern genetic lineage from each other. However, two important **hybrid** areas were detected: (1) the watershed of the Ohre river in the north-west of that area, a major valley system passing through these mountains and (2) the high plateaux of the Sumava Mts in the south-east, an extended area of high elevation. The location of **hybrid** populations in geographical vicinity to non-**hybrid** populations and the generally low F_{IS} (2.1%) make reduced fitness of **hybrid** individuals little likely. The **hybrid** populations have intermediate genetic diversity between the genetically poor western and the genetically rich eastern lineage populations.

Molecular phylogeography of two Italian sibling species of *Calobius* (Coleoptera, Hydraenidae, Ochthebiinae) inhabiting Mediterranean marine rock-pools

Antonini, G; Audisio, P; Mancini, E; De Biase, A; Tronci, C; Rossetti, G; Trizzino, M, 2010

Marine rock-pools, commonly found along the Mediterranean coasts, are isolated patches of habitat characterised by large spatial and temporal variations. The phylogeography of *Calobius quadricollis* and *C. urbanelliae*, two sibling species of moss beetles (Coleoptera, Hydraenidae) inhabiting Italian temporary marine rock-pool ecosystems, were studied using mitochondrial cytochrome c oxidase subunit I (COI). Our data suggest a strong association between the scored genetic variability and the geographical distribution of populations sampled for both species. These analyses provided evidences of episodic species range expansion and fragmentation, recurrent "flush and crash" and bottleneck episodes probably occurring during the Glacial Cycles. The observed phylogeographical pattern is probably related to the historical and biogeographical processes of Mediterranean areas, as well as both to the ephemeral habitat tipology and limited dispersal ability of these

beetles.

~~Contribution of Larvae Developing on Corn and Dry Beans to the Adult Population of Western Bean Cutworm in Michigan~~

Bunn, DC; de Oliveira, ED; Springborn, F; Gonzalez-Meler, MA; Miller, N, 2021

The western bean cutworm, *Striacosta albicosta* (Smith) (Lepidoptera: Noctuidae), is historically a pest of both corn (*Zea mays* L. (Poales: Poaceae)) and dry beans (*Phaseolus* sp. L. (Fabales: Fabaceae)) in the western Great Plains. However, it has recently undergone an eastward range expansion establishing itself across the Corn Belt in 25 states and 4 Canadian provinces. To mitigate the effects of infestation in Michigan, foliar insecticides are used in dry beans, whereas management of the pest in corn relies more heavily on the use of Bt-expressing **hybrids**. In this study stable carbon isotope analysis was used to determine what crop adult moths developed on as larvae with analysis showing that very few of the adult moths developed on dry beans. These results suggest that beans and corn are not suitable as co-refuges and that mainly adults which developed on corn are contributing to the next generation of western bean cutworm in Michigan.

~~Upslope movements and large scale expansions: the taxonomy and biogeography of the *Coenonympha arcania*–*C. d. arwiniana*–*C. gardetta* butterfly species complex~~

Schmitt, T; Besold, J, 2010

Sibling species groups are suitable models for the understanding of inter and intraspecific processes in taxonomy and biogeography. We analysed 262 individuals from the Alps of the *Coenonympha arcania*–*C. gardetta* species complex by allozyme electrophoresis. These taxa showed high variance amongst populations (F_{ST} 0.391) and strong intertaxon genetic differentiation (FCT: 0.376). Although morphologically similar, *Coenonympha gardetta* and *Coenonympha arcania* clearly differ in their genetic characteristics; the morphologically intermediate taxa *Coenonympha darwiniana* and *Coenonympha darwiniana* *macromma* are genetically well distinguished from each other and the two other taxa. *Coenonympha arcania* and *C. d. macromma* most probably share a common ancestor and evolved by cladogenesis, whereas the taxonomic situation of *C. d. darwiniana* is still unresolved: This taxon might be the result of **hybridization** between *C. arcania* and *C. gardetta* or it might have a common ancestor together with *C. gardetta*. We suggest species rank for all four taxa. The distribution of genetic diversity of these populations and the differentiation amongst populations suggest rather different biogeographical scenarios: *C. arcania* most probably is of Mediterranean origin with postglacial range expansion northwards; *C. gardetta* survived the last ice age in peripheral refugia of the Alps and has spread all over this high mountain system in the postglacial; *C. darwiniana* and *C. macromma* survived the Würm in geographic proximity to their actual distribution areas and only have performed moderate uphill translocations during postglacial warming. (C) 2010 The Linnean Society of London, Zoological Journal of the Linnean Society, 2010, 159, 890–904.

~~Abiotically-Induced Plant Morphological Changes and Host-Range Expansion in Quarantine Evaluations of Candidate Weed Biocontrol Agents: The Case Study *Conchyloctenia hybrida* (Coleoptera: Chrysomelidae)~~

Ghebremariam, TT; Kruger, K; Reinhardt, CF; Robbertse, PJ, 2014

Plant morphological changes mediated by growth conditions are linked to changes in host preference of herbivores. Understanding how these morphological changes influence herbivore feeding is critical in the interpretation of results of host evaluation of candidate weed biocontrol agents in quarantine and improvement of the evaluation system. We determined the effect of plant growth conditions on leaf trichomes and host choice of *Conchyloctenia hybrida* Boheman, an insect adapted to the removal of trichomes before feeding. The study included four *Solanum* species: *Solanum lichtensteinii* Willdenow (natural host of *C. hybrida*), *Solanum mauritianum* Scopoli, *Solanum melongena* L., and *Solanum tuberosum* L.. Plants were grown in either full sun, shade, a glasshouse, or in a growth-chamber. Plants grown in full sun had a higher leaf trichome density than those in shade or controlled environments. *S. mauritianum* had the highest trichome density and thickness of trichome layer. In a multiple-choice test using excised leaves, feeding by *C. hybrida* was higher on *Solanum* plants grown in the controlled environment as compared with full sun. Trichome removal from leaf surfaces of plants grown in full sun, using adhesive tape, was effective for *S. lichtensteinii*, *S. mauritianum*, and *S. melongena*, but not *S. tuberosum*. Leaf consumption by *C. hybrida* increased significantly where manual trichome removal using adhesive tape was effective. Structurally, leaves of *S. tuberosum* have simple trichomes with basal cells sunken into the mesophyll tissue. When using forceps to remove trichomes of *S. tuberosum*, mesophyll and vascular tissue remained attached to the trichomes. Generally, the type, density, and mat-thickness of leaf trichomes determined feeding by *C. hybrida*, but varied with plant species and growth conditions.

~~Mitochondrial DNA phylogeography and population history of *Meladema* diving beetles on the Atlantic Islands and in the Mediterranean basin (Coleoptera, Dytiscidae)~~

Ribera, I; Bilton, DT; Vogler, AP, 2003

The phylogeny and population history of *Meladema* diving beetles (Coleoptera, Dytiscidae) were examined using mitochondrial DNA sequence from 16S ribosomal RNA and cytochrome oxidase I genes in 51 individuals from 22 populations of the three extant species (*M. imbricata* endemic to the western Canary Islands, *M. lanio* endemic to Madeira and *M. coriacea* widespread in the Western Mediterranean and on the western Canaries), using a combination of phylogenetic and nested clade analyses. Four main lineages are observed within *Meladema*, representing the three recognized species plus Corsican populations of *M. coriacea*. Phylogenetic analyses demonstrate the sister relationship of the two Atlantic Island taxa, and suggest the possible paraphyly of *M. coriacea*. A molecular clock approach reveals that speciation within the genus occurred in the Early Pleistocene, indicating that the Atlantic Island endemics are not Tertiary relict taxa as had been proposed previously. Our results point to past population bottlenecks in all four lineages, with recent (Late-Middle Pleistocene) range expansion in non-Corsican *M. coriacea* and *M. imbricata*. Within the Canary Islands, *M. imbricata* seems to have independently colonized La Gomera and La Palma from Tenerife (although a colonization of La Palma from La Gomera cannot be discarded), and *M. coriacea* has independently colonized Tenerife and Gran Canaria from separate mainland lineages. In the Mediterranean basin this species apparently colonized Corsica on a single occasion, relatively early in its evolutionary history (Early Pleistocene), and has colonized Mallorca recently on multiple occasions. On the only island where *M. coriacea* and *M. imbricata* are broadly sympatric (Tenerife), we report evidence of bidirectional **hybridization** between the two species.

~~*Torymus sinensis*: a viable management option for the biological control of *Dryocosmus kuriphilus* in Europe?~~

Gibbs, M; Schonrogge, K; Alma, A; Melika, G; Quacchia, A; Stone, GN; Aebi, A, 2011

The chestnut gall wasp *Dryocosmus kuriphilus* is a global pest of chestnut (*Castanea* spp.). Established as a pest in the mid-twentieth century in Japan, Korea and North America, this species was first reported in Europe in 2002. Following the successful release of a biological control agent *Torymus sinensis* in Japan, this parasitoid species has been released in Italy since 2005. Here we discuss the potential of *T. sinensis* as a viable management option for the biological control of *D. kuriphilus* in central Europe. We suggest that more consideration should be given to determining, (i) the conditions under which *T. sinensis* may attack alternative native gall wasp hosts and (ii) the likelihood of **hybridization** of this species with native *Torymus*. Both issues are central to predicting unassisted range expansion by released *T. sinensis*, and to assess the environmental risks associated with a more widespread release of this species in Europe.

Geographic Distribution of *Bacillus thuringiensis* Cry1F Toxin Resistance in Western Bean Cutworm (Lepidoptera: Noctuidae) Populations in the United States

Coates, BS; Abel, CA; Swoboda-Bhattarai, KA; Palmquist, DE; Montezano, DG; Zukoff, SN; Wang, YZ; Bradshaw, JD; DiFonzo, CD; Shields, E; Tilmon, KJ; Hunt, TE; Peterson, JA,

The western bean cutworm (WBC), *Striacosta albicosta* (Lepidoptera: Noctuidae), can be a severe pest of transgenic corn in the western Plains and Great Lakes regions of North America, including on **hybrids** expressing the *Bacillus thuringiensis* (Bt) Cry1F toxin. The level and geographic distribution of Cry1F resistance are not completely known. Neonate *S. albicosta* from 10 locations between Nebraska and New York state were subjected to dose-response trypsin-activated native Cry1F toxin overlay bioassays. In 2017, the mean estimated lethal concentration causing 50% larval mortality (LC50) ranged from 15.1 to 18.4 $\mu\text{g Cry1F cm}^{-2}$, and were not significantly different among locations. In 2018, LC50 estimates at Scottsbluff, NE (22.0 $\mu\text{g Cry1F cm}^{-2}$) and Watertown, NY (21.7 $\mu\text{g Cry1F cm}^{-2}$) were significantly higher when compared to locations in Michigan (15.8 $\mu\text{g Cry1F cm}^{-2}$). Significantly lower 14-day larval weight among survivors was correlated with higher Cry1F dose. Results from this study indicate that *S. albicosta* survivorship on purified Bt Cry1F toxin shows a relatively even distribution across the native and range expansion areas where seasonal field infestations typically occur.

From sympatry to parapatry: a rapid change in the spatial context of incipient allochronic speciation

Burban, C; Rocha, S; Leblois, R; Rossi, JP; Saune, L; Branco, M; Kerdelhue, C, 2020

Speciation is nowadays recognized as a dynamic process in which the respective roles of forces driving ecological differentiation and reproductive isolation can change through time and space. Incipient speciation events are particularly useful to follow such processes that are not tractable when considering well-differentiated taxa. A promising case study was discovered in the pine processionary moth, *Thaumetopoea pityocampa*, a Mediterranean defoliator of *Pinus* species, for which allochrony acting as an automatic magic trait was recognized as the major driver of an incipient speciation process. In Portugal, a unique population with a shifted phenology, known as the summer population (SP), co-occurs with a population following the typical life cycle, known as the winter population (WP). We monitored male activity of both populations in the Leiria region, i.e. over the whole SP distribution range using a systematic sampling along two transects, and studied Portuguese WPs at a larger geographical scale to explore their genetic diversity and spatial pattern of differentiation. Results showed that the WPs were genetically more diverse than the SP, with a strong pattern of isolation by distance both at large and small spatial scales, while the SP was very homogeneous over its whole range, without signature of its recent spatial expansion. Contrary to our expectations, no F1 **hybrids** were identified, even though we found an extended flight period of the SP, overlapping with the beginning of the WP reproductive period. Interestingly, the SP was found to be mostly limited to the sea shore where the WP is now scarce or absent, which could suggest competitive exclusion. Once clearly occurring in a sympatric context, the allochronic differentiation tends to develop nowadays in parapatry.

Invasion Genetics of the Western Flower Thrips in China: Evidence for Genetic Bottleneck, Hybridization and Bridgehead Effect

Yang, XM; Sun, JT; Xue, XF; Li, JB; Hong, XY, 2012

The western flower thrips, *Frankliniella occidentalis* (Pergande), is an invasive species and the most economically important pest within the insect order Thysanoptera. *F. occidentalis*, which is endemic to North America, was initially detected in Kunming in southwestern China in 2000 and since then it has rapidly invaded several other localities in China where it has greatly damaged greenhouse vegetables and ornamental crops. Controlling this invasive pest in China requires an understanding of its genetic makeup and migration patterns. Using the mitochondrial COI gene and 10 microsatellites, eight of which were newly isolated and are highly polymorphic, we investigated the genetic structure and the routes of range expansion of 14 *F. occidentalis* populations in China. Both the mitochondrial and microsatellite data revealed that the genetic diversity of *F. occidentalis* of the Chinese populations is lower than that in its native range. Two previously reported cryptic species (or ecotypes) were found in the study. The divergence in the mitochondrial COI of two Chinese cryptic species (or ecotypes) was about 3.3% but they cannot be distinguished by nuclear markers. **Hybridization** might produce such substantial mitochondrial-nuclear discordance. Furthermore, we found low genetic differentiation (global $F_{ST} = 0.043$, $P < 0.001$) among all the populations and strong evidence for gene flow, especially from the three southwestern populations (Baoshan, Dali and Kunming) to the other Chinese populations. The directional gene flow was further supported by the higher genetic diversity of these three southwestern populations. Thus, quarantine and management of *F. occidentalis* should focus on preventing it from spreading from the putative source populations to other parts of China.

ASSORTATIVE MATING AND SPATIAL STRUCTURE IN HYBRID ZONES

M'Gonigle, LK; FitzJohn, RG, 2010

The spatial genetic composition of **hybrid** zones exhibits a range of possible patterns, with many characterized by patchy distributions. While several hypothetical explanations exist for the maintenance of these "mosaic" **hybrid** zones, they remain virtually unexplored theoretically. Using computer simulations we investigate the roles of dispersal and assortative mating in the formation and persistence of **hybrid** zone structure. To quantify mosaic structure we develop a likelihood method, which we apply to simulation and empirical data. We find that long distance dispersal can lead to a patchy distribution that assortative mating can then reinforce, ultimately producing a mosaic capable of persisting over evolutionarily significant periods of time. By reducing the mating success of rare males, assortative mating creates a positive within-patch frequency-dependent selective pressure. Selection against heterozygotes can similarly create a rare-type disadvantage and we show that it can also preserve structure. We find that mosaic structure is maintained across a range of assumptions regarding the form and strength of assortative mating. Interestingly, we find that higher levels of mosaic structure are sometimes observed for intermediate assortment strengths. The high incidence of assortment documented in **hybrid** zones suggests that it may play a key role in stabilizing their form and structure.

Large-scale production of porcine mature interleukin-18 (IL-18) in silkworms using a hybrid baculovirus expression system

Muneta, Y; Zhao, HK; Inumaru, S; Mori, Y, 2003

In this report, a **hybrid** baculovirus expression system, which means a **hybrid** virus of the Autographa californica nuclear polyhedrosis virus and the Bombyx mori nuclear polyhedrosis virus, was used for the large-scale production of porcine mature interleukin-18 (IL-18) in silkworms. Two recombinant **hybrid** baculoviruses containing cDNA of the porcine precursor IL-18 and the porcine caspase-1 were constructed and were used to infect silkworm larvae. After the co-infection of the two viruses, porcine mature IL-18 was efficiently produced in the haemolymph. The concentration of IL-18 in the haemolymph was 80-100 $\mu\text{g/ml}$, as determined by porcine IL-18 specific ELISA. This yield was twenty-times more than that of the insect cell expression system described previously. The porcine mature IL-18 produced by the silkworms strongly induced interferon-gamma (IFN-gamma) production from porcine PBMC. An insect factory system for the large-scale production of useful cytokines for livestock animals will be available in the near future.

Species status and phylogeography of two closely related Coptolabrus species (Coleoptera: Carabidae) in South Korea inferred from mitochondrial and nuclear gene sequences

Zhang, AB; Kubota, K; Takami, Y; Kim, JL; Kim, JK; Sota, T, 2005

We investigated the species status and intraspecific phylogeography in South Korea of two ground beetle species, *Coptolabrus jankowskii* and *Coptolabrus smaragdinus* (Coleoptera: Carabidae), using statistical parsimony networks and nested clade analyses based on sequences from the mitochondrial cytochrome oxidase subunit I (COI) and nuclear phosphoenolpyruvate carboxykinase (PepCK) and wingless (Wg) genes. Although traditional parsimony tree construction generally failed to resolve interspecific relationships and construct biologically meaningful genealogies, analysis using statistical parsimony networks yielded statistically significant inter- and intraspecific genealogical structures. We found that although these two species represent a notable case of trans-species polymorphisms in both mitochondrial and nuclear gene sequences, their status as separate species was evidenced by the nonrandom association between species and nested clades at various nesting levels. The exceptional occurrence of shared identical or very similar COI sequences was considered to be the result of introgressive **hybridization**. In addition, range expansion and fragmentation events across the Korean Peninsula and adjacent islands were inferred from nested clade phylogeographical analyses. The COI gene revealed the geographical divergence of major eastern and western clades and historical biogeographical events within each major clade, whereas the nuclear PepCK gene, which did not reveal corresponding east-west clades, indicated past fragmentation and range expansion across wide areas that may have been the result of older biogeographical events. Thus, phylogeographical inferences drawn from analyses of mitochondrial and nuclear genes can reveal different and potentially complementary information about phylogeographical processes.

Plant-herbivore coevolution and plant speciation

Maron, JL; Agrawal, AA; Schemske, DW, 2019

More than five decades ago, Ehrlich and Raven proposed a revolutionary idea that the evolution of novel plant defense could spur adaptive radiation in plants. Despite motivating much work on plant-herbivore coevolution and defense theory, Ehrlich and Raven never proposed a mechanism for their "escape and radiate" model. Recent intriguing mechanisms proposed by Marquis et al. include sympatric divergence, pleiotropic effects of plant defense traits on reproductive isolation, and strong postzygotic isolation, but these may not be general features of herbivore-mediated speciation. An alternate view is that herbivores may impose strong divergent selection on defenses in allopatric plant populations, with plant-herbivore coevolution driving local adaptation resulting in plant speciation. Building on these ideas, we propose three scenarios that consider the role of herbivores in plant speciation. These include (1) vicariance, subsequent coevolution within populations and adaptive divergence between geographically isolated populations, (2) colonization of a new habitat lacking effective herbivores followed by loss of defense and then re-evolution and coevolution of defense in response to novel herbivores, and (3) evolution of a new defense followed by range expansion, vicariance, and coevolution. We discuss the general role of coevolution in plant speciation and consider outstanding issues related to understanding: (1) the mechanisms behind cospeciation of plants and insects, (2) geographic variation in defense phenotypes, (3) how defensive traits and geography map on plant phylogenies, and (4) the role of herbivores in driving character displacement in defense phenotypes of related species in sympatry.

Construction of hybrid *Autographa californica* nuclear polyhedrosis bacmid by modification of p143 helicase

Deo, VK; Hiyoshi, M; Park, EY, 2006

We developed a new **hybrid** nuclear polyhedrosis virus (NPV) bacmid capable of infecting *Spodoptera frugiperda*, *Tricoplusia ni*, and *Bombyx mori*, and *B. mori* cell lines for producing **hybrid** recombinant baculovirus that can carry a gene of interest and express it in a broad range of hosts. A GFP(UV)-beta 1,3-N-acetylglucosaminyltransferase 2 fusion gene was expressed successfully in silkworm larvae using this **hybrid** bacmid. The **hybrid** NPV bacmid provides an altogether simple and realistically feasible method for large-scale applications using silkworm larvae. It can be easily managed in *E. coli*, which has no biohazard safety concerns, in addition to the baculovirus-based expression system. (c) 2006 Elsevier B.V. All rights reserved.

To hybridize or not to hybridize: what separates two genetic lineages of the Chalk-hill Blue *Polyommatus coridon* (Lycaenidae, Lepidoptera) along their secondary contact zone throughout eastern Central Europe?

Schmitt, T; Zimmermann, M, 2012

As a consequence of postglacial range expansion, **hybrid** zones evolved where different genetic lineages met. In this study, we analysed the Chalk-hill Blue *Polyommatus coridon* all along the contact zone of two expansive lineages. This zone stretches from the sandy areas of north-eastern Germany, along the mountain ranges of the German-Czech border and throughout the eastern Alps. We studied allozymes (19 loci) of 38 populations (1542 individuals) and compared these data sets against 15 populations of the western and 15 populations of the eastern lineages and found different degrees of **hybridization**. Thus, the calcareous regions of Thuringia and Sachsen-Anhalt were mostly colonized by the western lineage. The middle mountain ranges between Bavaria and Bohemia represented a strong barrier blocking further expansion and thus completely impeding **hybridization** in this region. More intense **hybridization** was detected in the populations of the eastern Alps, especially in the north-eastern part, where the Danube most probably acted as an expansion corridor for both lineages followed by intensive **hybridization**. In the south-eastern Alps, **hybrid** populations were mostly detected in the easternmost parts and along the larger river valley of Drava and Mur; pure western populations dominated in the other areas of this region. These results show that the degree of **hybridization** along a contact zone is correlated with the ecological demands of a species and the regional physical geographic circumstances. This finding was proved for the Chalk-hill Blue in our study but is also the most likely scenario in most animal and plant species.

Evaluation of Tolerance to *Bacillus thuringiensis* Toxins Among Laboratory-Reared Western Bean Cutworm (Lepidoptera: Noctuidae)

Dyer, JM; Sappington, TW; Coates, BS, 2013

The western bean cutworm, *Striacosta albicosta* (Smith) (Lepidoptera: Noctuidae), is a destructive insect pest of dry beans and corn within its native range of western Nebraska and eastern Colorado. However, since the initiation of an eastward range expansion of *S. albicosta* in the late 1990s, economic damage has been observed in the Midwest, and the species has now reached the Atlantic Coast and Quebec. Economic damage to corn occurs by larval feeding on ears, which is not controlled by commercial transgenic **hybrids** that express *Bacillus thuringiensis* (Bt) Cry1Ab, but partial control is observed by corn varieties that express Cry1 F toxins. Inadequate protocols for laboratory rearing of *S. albicosta* have hindered controlled efficacy experimentation in the laboratory and field. We report an *S. albicosta* rearing methodology used to maintain a laboratory colony for 12 continuous generations. Rearing procedures were adapted for Bt toxin diet-overlay assays, revealing that *S. albicosta* larvae exposed to Bt toxin for 14 d were insensitive to Cry1Ab concentrations up to 25,000 ng/cm(2). In contrast, neonates exposed to Cry1 F toxin at ≥ 250 ng/cm(2), showed reduced developmental rates, with estimated effective concentrations of EC50 = 1,187.5 ng/cm(2) and EC95 = 10,000.5 ng/cm(2). The ability to mass produce this pest insect will enhance fundamental research, including evaluation of control tactics and toxin susceptibility.

DNA taxonomy, phylogeny and Pleistocene diversification of the *Cicindela hybrida* species group (Coleoptera: Cicindelidae)

Cardoso, A; Vogler, AP, 2005

Species delimitation is complicated where morphological variation is continuous or poorly subdivided, but for taxonomic convenience it is common practice to

separate and name geographical groups to capture this variation. DNA-based approaches may be used to test if these groups in fact represent historically divided, discrete species entities. The *Cicindela* **hybrida** complex (Coleoptera: Cicindelidae) is an assemblage of up to seven morphologically recognized species and 15 subspecies with wide distribution in the Palaearctic region. We sequenced a discontinuous segment of 1899 bp of mtDNA including three regions (cox1, rrnL+trnL2+nad1, cob) for a total of 99 specimens from 36 sampling localities across Europe, revealing 48 haplotypes. Four major clades could be identified corresponding to geographical groups from central Iberia, Ukraine, central Europe, and a band from the Atlantic Iberian coast to northern Europe. Taking into account further subdivisions within these clades, four of the six named species included in the analysis were recognizable by applying various procedures for species delimitation. Age estimates from calibrated molecular clocks date the diversification of the **hybrida** group within the past 2 million years (Myr), and the separation of the northern clade within 0.4 Myr. Nested clade analysis revealed the rapid range expansion of the northern group consistent with postglacial dispersal, but we did not find support for specific source population(s) in the postulated southern refugia. The evolutionary framework based on mtDNA sequences is shown to identify species entities as discrete clusters of closely related sequences and provides an objective system for delineating and recognizing hierarchically structured groups. In the case of the *C. hybrida* complex, these groups largely coincided with those established from morphology. The study adds further support to the utility of mtDNA-based sequence profiles (the 'DNA taxonomy') as a rapid and objective synthesis of evolutionary diversity and as reference system for communication.

Rampant non-monophyly of species in *Kniphofia* Moench (Asphodelaceae) suggests a recent Afromontane radiation

Ramdhani, S; Barker, NP; Baijnath, H, 2009

The genus *Kniphofia*, comprising 71 species, has an African-Malagasy distribution, with one species from Yemen. The genus is found predominantly in moist temperate montane grassland and has its centre of diversity in the Drakensberg region of southern Africa. The genus has a complex alpha taxonomy and species relationships are poorly understood. Using a multiple exemplar approach, DNA sequence data from the chloroplast trnT-L spacer and the nuclear internal transcribed spacer region were used in an attempt to resolve phylogenetic relationships. Five cpDNA lineages were recovered, the geographic distributions of which correspond well with previously identified Afromontane centres of diversity and endemism. The data revealed that several morpho-species were non-monophyletic, and this, together with short branch lengths and many identical sequences within each of the five lineages, suggests a recent radiation. We additionally propose that **hybridisation** and/or incomplete lineage sorting may also account for this result. The nrITS region was largely uninformative as many taxa and samples had identical sequences. We hypothesise that *Kniphofia* experienced periods of range expansion, secondary contact and **hybridisation** during Pleistocene glacial periods, followed by contraction, fragmentation and isolation in montane refugia during the warmer interglacial periods.

Species delimitation and invasion history of the balsam woolly adelgid, *Adelges (Dreyfusia) piceae* (Hemiptera: Aphidoidea: Adelgidae), species complex

Havill, NP; Griffin, BP; Andersen, JC; Footitt, RG; Justesen, MJ; Caccone, A; D'Amico, V; Elkinton, JS, 2021

The *Adelges (Dreyfusia) piceae* (Ratzeburg) species complex is a taxonomically unstable group of six species. Three of the species are cyclically parthenogenetic [*Ad. nordmannianae* (Eckstein), *Ad. prelli* (Grossmann), and *Ad. merkeri* (Eichhorn)] and three are obligately asexual [*Ad. piceae*, *Ad. schneideri* (Borner), and *Ad. nebrodensis* (Binazzi & Covassi)]. Some species are high-impact pests of fir (*Abies*) trees, so stable species names are needed to communicate effectively about management. Therefore, to refine species delimitation, guided by a reconstruction of their biogeographic history, we genotyped adelgids from Europe, North America, and the Caucasus Mountains region with 19 microsatellite loci, sequenced the COI DNA barcoding region, and compared morphology. Discriminant analysis of principal components of microsatellite genotypes revealed four distinct genetic clusters. Two clusters were morphologically consistent with *Ad. nordmannianae*. One of these clusters consisted of samples from the Caucasus Mountains and northern Turkey, and the other included samples from this region as well as from Europe and North America, where *Ad. nordmannianae* is invasive. A third cluster was morphologically consistent with *Ad. piceae*, and included individuals from Europe, where it is native, and North America, where it is invasive. In North America, the majority of *Ad. piceae* individuals were assigned to two geographically widespread clones, suggesting multiple introductions. The fourth cluster included individuals morphologically consistent with *Ad. prelli* or *Ad. merkeri*. However, based on genetic assignments, **hybrid** simulations, and approximate Bayesian computation, we find it likely that these are contemporary **hybrids** between *Ad. nordmannianae* and *Ad. piceae* that arose independently in Europe and North America, so we propose that *Ad. prelli* and *Ad. merkeri* are invalid. Finally, we synonymise *Ad. schneideri* (syn.n.) with *Ad. nordmannianae* and designate *Ad. nebrodensis* as subspecies *Ad. piceae nebrodensis* (stat.n.). Our revised taxonomy therefore recognises two species: *Ad. nordmannianae* and *Ad. piceae*, which we estimate to have diverged recently, during one of the last two interglacial periods. Finally, we comment on this species complex being in the midst of transition between sexual and asexual reproduction, a pattern that is probably common in Adelgidae.

A Role for the Anti-Viral Host Defense Mechanism in the Phylogenetic Divergence in Baculovirus Evolution

Nagamine, T; Sako, Y, 2016

Although phylogenetic analysis often suggests co-evolutionary relationships between viruses and host organisms, few examples have been reported at the microevolutionary level. Here, we show a possible example in which a species-specific anti-viral response may drive phylogenetic divergence in insect virus evolution. Two baculoviruses, *Autographa californica* multiple nucleopolyhedrovirus (AcMNPV) and *Bombyx mori* nucleopolyhedrovirus (BmNPV), have a high degree of DNA sequence similarity, but exhibit non-overlapping host specificity. In our study of their host-range determination, we found that BmNPV replication in *B. mori* cells was prevented by AcMNPV-P143 (AcP143), but not BmNPV-P143 (BmP143) or a **hybrid** P143 protein from a host-range expanded phenotype. This suggests that AcMNPV resistance in *B. mori* cells depends on AcP143 recognition and that BmNPV uses BmP143 to escape this recognition. Based on these data, we propose an insect baculovirus co-evolution scenario in which an ancestor of silkworms exploited an AcMNPV-resistant mechanism; AcMNPV counteracted this resistance via P143 mutations, resulting in the birth of BmNPV.

WOLBACHIA AND CYTOPLASMIC INCOMPATIBILITY IN MYCOPHAGOUS DROSOPHILA AND THEIR RELATIVES

WERREN, JH; JAENIKE, J, 1995

Bacterial symbionts belonging to the genus *Wolbachia* are associated with postzygotic reproductive incompatibility in a number of insect species. Using polymerase chain reaction (PCR) amplification of bacterial gene sequences, strains from 10 species belonging to the closely related quinaia, testacea and tripunctata groups of *Drosophila* were screened for the presence of *Wolbachia* in their reproductive tissues. Those screened included the mycophagous species *D. falleni*, *D. recens*, *D. phalerata*, *D. testacea*, *D. neotestacea*, *D. orientacea*, *D. putrida* and *D. tripunctata*, and the nonmycophagous species *D. palustris* and *D. quinaia*. Two species, *D. recens* and *D. orientacea*, were found to be infected with *Wolbachia*. Subsequent tests of four additional strains of *D. recens* found all to be infected with the bacteria. It was established that these bacteria cause partial cytoplasmic incompatibility in *D. recens* by antibiotic curing followed by crosses between cured and uncured strains. Curing was confirmed by a PCR assay. Although most species of insects shown to be infected with *Wolbachia* are cosmopolitan and/or have undergone recent range expansion in association with human activity, *D. recens* and *D. orientacea* are endemic species with specialized ecological habits. Preliminary molecular phylogenetic analysis indicates that, among the species we examined, *D. quinaia* is most closely related to *D. recens*. To determine whether the bacteria are involved in reproductive isolation between these two species, reciprocal crosses were carried out between *D. quinaia* and both infected and uninfected (cured) strains of *D. recens*. Although these species did mate with each other, all interspecific crosses failed to yield **hybrid** progeny, indicating that the bacteria are not responsible for reproductive incompatibility between these species.

~~The inexorable spread of a newly arisen neo-Y chromosome~~

Veltsos, P; Keller, I; Nichols, RA, 2008

A newly arisen Y-chromosome can become established in one part of a species range by genetic drift or through the effects of selection on sexually antagonistic alleles. However, it is difficult to explain why it should then spread throughout the species range after this initial episode. As it spreads into new populations, it will actually enter females. It would then be expected to perform poorly since it will have been shaped by the selective regime of the male-only environment from which it came. We address this problem using computer models of **hybrid** zone dynamics where a neo-XY chromosomal race meets the ancestral karyotype. Our models consider that the neo-Y was established by the fusion of an autosome with the ancestral X-chromosome (thereby creating the Y and the 'fused X'). Our principal finding is that sexually antagonistic effects of the Y induce indirect selection in favour of the fused X-chromosomes, causing their spread. The Y-chromosome can then spread, protected behind the advancing shield of the fused X distribution. This mode of spread provides a robust explanation of how newly arisen Y-chromosomes can spread. A Y-chromosome would be expected to accumulate mutations that would cause it to be selected against when it is a rare newly arrived migrant. The Y can spread, nevertheless, because of the indirect selection induced by gene flow (which can only be observed in models comprising multiple populations). These results suggest a fundamental re-evaluation of sex-chromosome **hybrid** zones. The well-understood evolutionary events that initiate the Y-chromosome's degeneration will actually fuel its range expansion.

~~Throwing Out the Bathwater but Keeping the Baby: Lessons Learned from Purple Loosestrife and Reed Canarygrass~~

Anderson, NO, 2019

Historic ignorance of species' native range, expansion due to unintentional involvement by vectors, and their quiet evolution has caused several invasive species to become "poster children," such as purple loosestrife (*Lythrum salicaria*), reed canarygrass (*Phalaris arundinacea*), and others. Common misconceptions on how these became problematic have involved a variety of causes, including ignorance of species' ability to intercross and create introgressive **hybrids**, lack of insects for control, wind pollination, and intercontinental distribution from their native range. Current research focuses on how misappropriating the historical contexts can reverse our misconceptions of native species being noninvasive and how this affects control by land managers. Purple loosestrife and reed canarygrass will be used as example species to demonstrate challenges that native vs. exotic, intra-, and interspecific differences confer to land managers. Issues such as a lack of phenotypic differences challenge land managers' charge to control invasive individuals yet retain the noninvasives. This is fraught with challenges when native vs. exotic status is invoked or cultural values are entwined. To avoid a monumental impasse, particularly when native and exotic types are phenotypically indistinguishable, this dilemma could be solved via modern techniques using molecular biology.

~~Cactophilic Drosophila in South America: A model for evolutionary studies~~

Manfrin, MH; Sene, FM, 2006

The *Drosophila buzzatii* cluster is composed of seven cactophilic species and their known geographical distribution encompasses the open vegetation diagonal, which includes the morphoclimatic Domains of the Caatinga, Chaco and Cerrado, which are situated between the Amazon and the Atlantic forests. Besides these areas, these cactophilic species are also found in a narrow strip along the Atlantic coast from northeastern Brazil to the southern tip of the country. The hypothesis of vicariant events, defining the core areas of each species, is proposed to explain the historical diversification for the cluster. The intraspecific analysis for the cluster shows a population structure with gene flow restricted by distance, range expansion with secondary contact resulting in **introgression** and sympatry, especially in the limits of the species distribution, polytypic populations and assortative mating in inter population experiments. There is a variation related to these events that depends on the species and geographic origin of the population analyzed. These events are, hypothetically, described as the results of expansion and retraction of the population ranges, as a consequence of their association with cacti, which theoretically follow the expansion and retraction of dry areas during the paleoclimatic oscillations in South America, as that promoted by the glacial cycles of the Quaternary. The *Drosophila buzzatii* cluster is divided into two groups. The first one is composed of *D. buzzatii*, a species that has a broad geographic distribution and no significant differentiation between its populations. The second is the *Drosophila serido* sibling set, which encompasses the others species and is characterized by a significant potential for differentiation.

~~THE GENETIC CONSEQUENCES OF LONG-DISTANCE DISPERSAL DURING COLONIZATION~~

NICHOLS, RA; HEWITT, GM, 1994

Rare long distance dispersal may have little impact on gene frequencies in established populations but it can dramatically increase gene flow during episodes of range expansion. We model the invasion of new territory by genetically distinct populations of the same species to investigate the dynamics of such episodes. If long distance dispersal is sufficiently frequent, the populations do not spread as a wave of advance but instead found intermingled isolates. We argue that this process can explain many otherwise puzzling patterns in the geographical distribution of alleles.

~~Biological Flora of the British Isles: *Coincya monensis* (L.) Greuter & Burdet ssp *monensis* (*Rhynchosinapis monensis* (L.) Dandy ex AR Clapham) and ssp *cheiranthos* (Vill.) Aedo, Leadley & Munoz Garm. (*Rhynchosinapis cheiranthos* (Vill.) Dandy)~~

Hipkin, CR; Facey, PD, 2009

P> This account presents information on all aspects of the biology of *Coincya monensis* (L.) Greuter & Burdet that are relevant to understanding its ecological characteristics and behaviour. The main topics are presented within the standard framework of the Biological Flora of the British Isles: distribution, habitat, communities, responses to biotic factors, responses to environment, structure and physiology, phenology, floral and seed characters, herbivores and disease, history and conservation. *Coincya monensis* is represented in the British flora by two subspecies; ssp. *monensis* is a diploid, endemic taxon largely confined to open, coastal, sand dune habitats along the west coast of Britain; ssp. *cheiranthos* is a tetraploid neophyte (alien) of ruderal and coastal habitats. Both subspecies occur as short-lived perennials in outbreeding, insect-pollinated populations in open, early successional communities. Individuals may perennate as hemicryptophytes with buds in basal rosettes or as chamaephytes with buds in aerial shoot rosettes, but adequate seed production is essential for the long-term maintenance of populations. Seed production by the much larger and more floriferous tetraploid alien populations is much greater than that of the native endemic populations. Neither subspecies is able to compete effectively in late successional, grassland communities. *Coincya monensis* ssp. *monensis* benefits from moderate disturbance by trampling, which helps to maintain open, sandy, semi-fixed dune communities, such as those dominated by Marram Grass (*Ammophila arenaria*). *Coincya monensis* ssp. *monensis* has been designated a scarce plant in the British flora and is a priority species in the UK Biodiversity Action Plan. The main threats to its conservation are loss of habitat through natural successional processes and urban development. *Coincya monensis* ssp. *cheiranthos* is well-established in South Wales where it appears to be undergoing a range expansion. At present there are no known mixed populations of the two subspecies but this remains a possibility if the alien subspecies continues to expand its range. Competition and **hybridisation** between subspecies in mixed populations will present additional problems in the conservation of endemic biodiversity in the British Flora.

~~Ecology and Management of the Western Bean Cutworm (Lepidoptera: Noctuidae) in Corn and Dry Beans Revision With Focus on the Great Lakes Region~~

Smith, JL; DiFonzo, CD; Baute, TS; Michel, AP; Krupke, CH, 2019

The western bean cutworm, *Striacosta albicosta* (Smith) is a native North American pest of corn and dry beans. The historical geographic range of the western bean cutworm covered the western Great Plains states including Colorado, Nebraska, and Wyoming. Since 1999, the geographic range of the western bean cutworm has rapidly expanded eastward across the U.S. Corn Belt and eastern Canada, causing significant and economic damage to corn *Zea mays* (L.) and dry edible beans *Phaseolus* spp., in parts of this region. Since 2010, increasing challenges related to managing this pest in its new range prompted numerous research studies that provided new insights into the biology and management of western bean cutworm. This revision of a previous Journal of IPM profile summarizes new information regarding the ecology and biology of western bean cutworm, and discusses updated recommendations for scouting and management in corn and dry beans, with an emphasis in the expanded geographic range of the Great Lakes region.

~~Monoecious hydrilla-A review of the literature~~

True-Meadows, S; Haug, EJ; Richardson, RJ, 2016

Hydrilla verticillata is a submersed aquatic weed that has become one of most expensive and difficult to manage in the United States. It disrupts water flow, interferes with recreation, displaces native vegetation, and can negatively impact nonplant species. There are two biotypes of hydrilla found in the United States a triploid dioecious and a triploid monoecious biotype. The monoecious biotype is typically found from North Carolina northward and is rapidly spreading, whereas dioecious hydrilla is common further south and is not currently demonstrating significant range expansion. Monoecious hydrilla behaves as a herbaceous perennial with shoots senescing over winter and repopulation occurring through prolific turions. This is in contrast to dioecious hydrilla, which has more persistent stems and root crowns, but produces fewer turions. Monoecious hydrilla turions also sprout at a far greater rate under cooler temperatures than dioecious hydrilla. Differences in biology between the two U.S. biotypes have been reported in genetic profiles, with monoecious biotypes, possibly originating from **hybridization** between two distinct dioecious biotypes. Cryptic speciation of hydrilla biotypes is an interesting consideration that has recently been suggested, and additional research is needed on hydrilla genetic diversity worldwide to determine if this has occurred. The body of research focusing strictly on the monoecious biotype is much smaller than that of the dioecious, as reflected in the literature. Many publications on hydrilla make no mention of biotype; therefore only an educated guess can be made based on study locations to decipher biotype. Thus, as monoecious hydrilla continues to spread and now presents a distinct threat to glacial lakes, additional research focused on this biotype is needed. The impact of latitudinal climate changes on monoecious growth and competition with native plants has not been well documented. The native-species spectrum of northern U.S. lakes is different than in traditional monoecious areas. Research needs to evaluate the ecological impact of hydrilla invasion as well as best management techniques for removing monoecious hydrilla from these plant communities. In addition, although seed production of monoecious hydrilla has been reported, it is poorly understood in situ. Seed production, viability, and potential dispersal also represent areas that have not been adequately documented.

~~Establishment of Striacosta albicosta (Lepidoptera: Noctuidae) as a Primary Pest of Corn in the Great Lakes Region~~

Smith, JL; Baute, TS; Sebright, MM; Schaafsma, AW; DiFonzo, CD, 2018

Western bean cutworm, *Stroacpsta albicosta* Smith (Lepidoptera: Noctuidae), is a pest of corn, *Zea maize* L., and dry edible beans, *Phaseolus* sp. L., native to the western United States. Following the range expansion into the U.S. Corn Belt, pheromone trap monitoring began in the Great Lakes region in 2006. The first *S. albicosta* was captured in Michigan in 2006 and in Ontario, Canada in 2008. Pheromone traps were used to document spread and increasing captures of *S. albicosta* across Michigan and Ontario until 2012. Trapping confirmed the univoltine life cycle of *S. albicosta* in this region and identified peak flight, typically occurring in late July. Overwintering of *S. albicosta* in this region was confirmed by emergence from infested fields and overwintering experiments. Multiple soil textures were infested with prepupae, and recovery was assessed throughout the winter. Overwintering success was not affected by soil texture, however, prepupae were found at greater depths in coarse-textured soils. Soil temperatures at overwintering depths did not reach the supercooling point. Injury to corn by *S. albicosta* increased in incidence, severity and geographic range from 2010 to 2014 in field plots. Decreasing control of injury by Cry 1F corn **hybrids** was observed over time. These findings show that *S. albicosta* has established as a perennial corn pest in the Great Lakes region due to observations of overwintering success and unmanaged injury. We recommend *S. albicosta* obtain primary pest status in this region within regulatory framework and a resistance management plan be required for traits targeting this pest.

~~The campaign to DNA barcode all fishes, FISH-BOL~~

Ward, RD; Hanner, R; Hebert, PDN, 2009

FISH-BOL, the Fish Barcode of Life campaign, is an international research collaboration that is assembling a standardized reference DNA sequence library for all fishes. Analysis is targeting a 648 base pair region of the mitochondrial cytochrome c oxidase I (COI) gene. More than 5000 species have already been DNA barcoded, with an average of five specimens per species, typically vouchers with authoritative identifications. The barcode sequence from any fish, fillet, fin, egg or larva can be matched against these reference sequences using BOLD; the Barcode of Life Data System (<http://www.barcodinglife.org>). The benefits of barcoding fishes include facilitating species identification, highlighting cases of range expansion for known species, flagging previously overlooked species and enabling identifications where traditional methods cannot be applied. Results thus far indicate that barcodes separate c. 98 and 93% of already described marine and freshwater fish species, respectively. Several specimens with divergent barcode sequences have been confirmed by integrative taxonomic analysis as new species. Past concerns in relation to the use of fish barcoding for species discrimination are discussed. These include **hybridization**, recent radiations, regional differentiation in barcode sequences and nuclear copies of the barcode region. However, current results indicate these issues are of little concern for the great majority of specimens.

~~Evolutionary genomics of Culex pipiens: global and local adaptations associated with climate, life-history traits and anthropogenic factors~~

Asgharian, H; Chang, PL; Lysenkov, S; Scobeyeva, VA; Reisen, WK; Nuzhdin, SV, 2015

We present the first genome-wide study of recent evolution in *Culex pipiens* species complex focusing on the genomic extent, functional targets and likely causes of global and local adaptations. We resequenced pooled samples of six populations of *C. pipiens* and two populations of the outgroup *Culex torrentium*. We used principal component analysis to systematically study differential natural selection across populations and developed a phylogenetic scanning method to analyse admixture without haplotype data. We found evidence for the prominent role of geographical distribution in shaping population structure and specifying patterns of genomic selection. Multiple adaptive events, involving genes implicated with autogeny, diapause and insecticide resistance were limited to specific populations. We estimate that about 5-20% of the genes (including several histone genes) and almost half of the annotated pathways were undergoing selective sweeps in each population. The high occurrence of sweeps in non-genic regions and in chromatin remodelling genes indicated the adaptive importance of gene expression changes. We hypothesize that global adaptive processes in the *C. pipiens* complex are potentially associated with South to North range expansion, requiring adjustments in chromatin conformation. Strong local signature of adaptation and emergence of **hybrid** bridge vectors necessitate genomic assessment of populations before specifying control agents.

~~Patterns of mitochondrial variation within and between African malaria vectors, Anopheles gambiae and An. arabiensis, suggest extensive gene flow~~

Anopheles gambiae and *An. arabiensis* are mosquito species responsible for most malaria transmission in sub-Saharan Africa. They are also closely related sibling species that share chromosomal and molecular polymorphisms as a consequence of incomplete lineage sorting or introgressive **hybridization**. To help resolve these processes, this study examined the partitioning of mtDNA sequence variation within and between species across Africa, from both population genetic and phylogeographic perspectives. Based on partial gene sequences from the cytochrome b, ND1 and ND5 genes, haplotype diversity was high but sequences were very closely related. Within species, little or no population subdivision was detected, and there was no evidence for isolation by distance. Between species, there were no fixed nucleotide differences, a high proportion of shared polymorphisms, and eight haplotypes in common over distances as great as 6000 km. Only one of 16 shared polymorphisms led to an amino acid difference, and there was no compelling evidence for nonneutral variation. Parsimony networks constructed of haplotypes from both species revealed no correspondence of haplotype with either geography or taxonomy. This trend of low intraspecific genetic divergence is consistent with evidence from allozyme and microsatellite data and is interpreted in terms of both extensive gene flow and recent range expansion from relatively large, stable populations. We argue that retention of ancestral polymorphisms is a plausible but insufficient explanation for low interspecific genetic divergence, and that extensive **hybridization** is a contributing factor.

The Potential Distribution of Invading *Helicoverpa armigera* in North America: Is It Just a Matter of Time?

Kriticos, DJ; Ota, N; Hutchison, WD; Beddow, J; Walsh, T; Tay, WT; Borchert, DM; Paula-Moreas, SV; Czepak, C; Zalucki, MP, 2015

Helicoverpa armigera has recently invaded South and Central America, and appears to be spreading rapidly. We update a previously developed potential distribution model to highlight the global invasion threat, with emphasis on the risks to the United States. The continued range expansion of *H. armigera* in Central America is likely to change the invasion threat it poses to North America qualitatively, making natural dispersal from either the Caribbean islands or Mexico feasible. To characterise the threat posed by *H. armigera*, we collated the value of the major host crops in the United States growing within its modelled potential range, including that area where it could expand its range during favourable seasons. We found that the annual value of crops that would be exposed to *H. armigera* totalled approximately US\$ 78 billion p.a., with US\$ 843 million p.a. worth growing in climates that are optimal for the pest. Elsewhere, *H. armigera* has developed broad-spectrum pesticide resistance; meaning that if it invades the United States, protecting these crops from significant production impacts could be challenging. It may be cost-effective to undertake preemptive biosecurity activities such as slowing the spread of *H. armigera* throughout the Americas, improving the system for detecting *H. armigera*, and methods for rapid identification, especially distinguishing between *H. armigera*, *H. zea* and potential *H. armigera* x *H. zea* **hybrids**. Developing biological control programs, especially using inundative techniques with entomopathogens and parasitoids could slow the spread of *H. armigera*, and reduce selective pressure for pesticide resistance. The rapid spread of *H. armigera* through South America into Central America suggests that its spread into North America is a matter of time. The likely natural dispersal routes preclude aggressive incursion responses, emphasizing the value of preparatory communication with agricultural producers in areas suitable for invasion by *H. armigera*.

Competitive Interactions and Resource Partitioning Between Northern Spotted Owls and Barred Owls in Western Oregon

Wiens, JD; Anthony, RG; Forsman, ED, 2014

The federally threatened northern spotted owl (*Strix occidentalis caurina*) is the focus of intensive conservation efforts that have led to much forested land being reserved as habitat for the owl and associated wildlife species throughout the Pacific Northwest of the United States. Recently, however, a relatively new threat to spotted owls has emerged in the form of an invasive competitor: the congeneric barred owl (*S. varia*). As barred owls have rapidly expanded their populations into the entire range of the northern spotted owl, mounting evidence indicates that they are displacing, **hybridizing** with, and even killing spotted owls. The range expansion by barred owls into western North America has made an already complex conservation issue even more contentious, and a lack of information on the ecological relationships between the 2 species has hampered recovery efforts for northern spotted owls. We investigated spatial relationships, habitat use, diets, survival, and reproduction of sympatric spotted owls and barred owls in western Oregon, USA, during 2007-2009. Our overall objective was to determine the potential for and possible consequences of competition for space, habitat, and food between these previously allopatric owl species. Our study included 29 spotted owls and 28 barred owls that were radio-marked in 36 neighboring territories and monitored over a 24-month period. Based on repeated surveys of both species, the number of territories occupied by pairs of barred owls in the 745-km² study area (82) greatly outnumbered those occupied by pairs of spotted owls (15). Estimates of mean size of home ranges and core-use areas of spotted owls (1,843ha and 305ha, respectively) were 2-4 times larger than those of barred owls (581ha and 188ha, respectively). Individual spotted and barred owls in adjacent territories often had overlapping home ranges, but interspecific space sharing was largely restricted to broader foraging areas in the home range with minimal spatial overlap among core-use areas. We used an information-theoretic approach to rank discrete-choice models representing alternative hypotheses about the influence of forest conditions, topography, and interspecific interactions on species-specific patterns of nighttime resource selection. Spotted owls spent a disproportionate amount of time foraging on steep slopes in ravines dominated by old (>120 yr) conifer trees. Barred owls used available forest types more evenly than spotted owls, and were most strongly associated with patches of large hardwood and conifer trees that occupied relatively flat areas along streams. Spotted and barred owls differed in the relative use of old conifer forest (greater for spotted owls) and slope conditions (steeper slopes for spotted owls), but we found no evidence that the 2 species differed in their use of young, mature, and riparian-hardwood forest types. Mean overlap in proportional use of different forest types between individual spotted owls and barred owls in adjacent territories was 81% (range=30-99%). The best model of habitat use for spotted owls indicated that the relative probability of a location being used was substantially reduced if the location was within or in close proximity to a core-use area of a barred owl. We used pellet analysis and measures of food-niche overlap to determine the potential for dietary competition between spatially associated pairs of spotted owls and barred owls. We identified 1,223 prey items from 15 territories occupied by spotted owls and 4,299 prey items from 24 territories occupied by barred owls. Diets of both species were dominated by nocturnal mammals, but diets of barred owls included many terrestrial, aquatic, and diurnal prey species that were rare or absent in diets of spotted owls. Northern flying squirrels (*Glaucomys sabrinus*), woodrats (*Neotoma fuscipes*, *N. cinerea*), and lagomorphs (*Lepus americanus*, *Sylvilagus bachmani*) were primary prey for both owl species, accounting for 81% and 49% of total dietary biomass for spotted owls and barred owls, respectively. Mean dietary overlap between pairs of spotted and barred owls in adjacent territories was moderate (42%; range=28-70%). Barred owls displayed demographic superiority over spotted owls; annual survival probability of spotted owls from known-fate analyses (0.81, SE=0.05) was lower than that of barred owls (0.92, SE=0.04), and pairs of barred owls produced an average of 4.4 times more young than pairs of spotted owls over a 3-year period. We found a strong, positive relationship between seasonal (6-month) survival probabilities of both species and the proportion of old (>120 yr) conifer forest within individual home ranges, which suggested that availability of old forest was a potential limiting factor in the competitive relationship between these 2 species. The annual number of young produced by spotted owls increased linearly with increasing distance from a territory center of a pair of barred owls, and all spotted owls that attempted to nest within 1.5km of a nest used by barred owls failed to successfully produce young. We identified strong associations between the presence of barred owls and the behavior and fitness potential of spotted owls, as shown by changes in movements, habitat use, and reproductive output of spotted owls exposed to different levels of spatial overlap with territorial barred owls. When viewed collectively, our results support the hypothesis that interference competition with barred owls for territorial space can constrain the availability of critical resources required for successful recruitment and reproduction of spotted owls. Availability of old forests and associated prey species appeared to be the most strongly limiting factors in the competitive relationship between these species, indicating that further loss of these conditions can lead to increases in competitive pressure. Our findings have broad implications for the conservation of spotted owls, as they suggest that spatial heterogeneity in vital rates may not arise solely because of differences among territories in the quality or abundance of forest habitat, but also because of the spatial distribution of a newly established competitor. Experimental removal of barred owls could be used to test this hypothesis and determine whether localized control of barred owl numbers is an ecologically practical and socio-politically acceptable management tool to consider in conservation strategies for spotted owls. (c) 2013 The Wildlife Society
