Imperial College
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IMPERIAL COLLEGE LONDON

DEPARTMENT OF LIFE SCIENCES

Seminar Diary

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The relevance of taxonomy to Amazon plant diversity estimates

Dr. Domingos Cardoso

In this seminar, Domingos gave us a broad view of the taxonomy to Amazon plant. What I have learned is that based on the GBIF database, there are 11,676 species, 1225 genera of plants on Amazon rainforest, however nearly 50% of plants are incorrectly named, due to they are recorded based on political region, but not geological area. These mistake names result from non Amazonia species biomes, spelling variants and synonyms, non-tree species, not native neo tropical species and non-Amazonia cultivation species. The uncertainty Amazon plant species richness and identity will somehow affect the downstream conservation and evolutionary patterns and processes that drive biodiversity, leaving studies in incomplete and irreproducible conclusions.

In order to solve these problems, they have assembled a comprehensive dataset of Amazonia seed plant species from published sources that includes falsifiable data based on voucher specimens identified by taxonomic specialists. Their list comprises 14,003 species, of which 6,727 are trees, providing a valid starting point for synergy among tropical plant systematists, ecologists and evolution biologista.

Combine with my own experience, I can always find that some mistake named species on some database, because of the reasons that mentioned above. Taxonomy is the foundation of ecology and evolution, and with the development of biotechnology, it also needs constantly self-correction, otherwise it will go into some mistakes or chaos. I'm not surprised that there are some mistakes in those database but did not expect it have this many. So very appreciate their work and also encourages me to self-correction on scientific research.

Earth Observation and Data Science to better Understand and Model Ecosystems under Global Change

Dr. Matthias Forkel

Dr. Matthias Forkel is an environmental scientist who uses satellite observation to study how climate affects ecosystems. He develops and applies remote sensing methods, global ecosystem models, and machine learning approaches. In his speech, he showed us three examples in his research on how approaches from data science help to make use of multiple Earth observation for ecosystem process understanding and modelling.

The first example is the research foucus on mapping increasing cover of vegetation changes across global land and indentifiying the climatic and socioeconomic drivers behind such changes. The changing trends in ecosystem productivity can be quantified using satellite Observation of Normalized Differece vegetation Index (NDVI), while they are differs depending on analyzed satellite dataset, corresponding spatio temporal resolution and applied statistical method. By comparing the performance of wide range of trend estimation methods for long-term NDVI time series, they demonstrated that seasonal trend methods need to be improved against inter-annual variability.

The second example is using satellite observation for modelling to predict wildfires. The developed a new flexible machine learning-based and process-oriented approach (Satelllite Observation to predict Fire Activity, SOFIA) which can use several predictor variables and functional relationships to estiamte burned area. By using this approach, they found out that a high plant productivity in a wet season can cause large burn area in the following dry season and this effect is strongly underestimated by most global vegetation models.

The third example is about phenology. He developed a method to identify phenological metrics like the start and end of the growing season from satellite and ground-based vegetation observation. Futhermore, he improved the representation of phenology in a global vegetation model which helped to

Understanding the effectiveness of indoor based malaria control

Dr. Tom Churcher

Indoor residual spraying (IRS) and long-lasting insecticide treated nets (LLINS) are together contributed to the success of reducing malaria since 2000. However, the substantial reduction in global malaria rebounded in 2016, mainly due to increasing mosquito resistance to pyrethroid insecticides, which are the widely-used class of insecticide for LLINs and IRS. A potential solution is the next-generation bednets and IRS products, piperonyl butoxide (PBO), a syergist that can inhibits specific metabolic enzymes that can detoxify pyrethroid. What's more, several IRS products have recently become available. Novel products need not only show epidemiological impact but also should be recommended based on safety, quality and entomological efficacy data. Hence, Tom's talk outline how to combine entomological data with mathematical models to understand the optimum set of interventions needed to control malaria in a setting.

In Tom's talk, they systematically characterise different IRS product efficacies against mosquito by experimental hut data. Lab trials, hut trials and village trials all demonstrated the pyrethroid-PBO bednets is superior than the traditional pyrethroid bednets. Besides, he investigated the mosquitos' diel behaviour and host diel behaviour and quantify the timing and geographic pattern of mosquito biting activity, and demonstrate the association between host activity and mosquito activity. Overall, they provided a potential effective solution to control malaria with increasing insecticide resistance, though their benefit depends on local factors inculding bednet use, seasonality, endemicity and pyrethroid resistance statusof local mosquito populations.

The screening of formulations does require a lot of trails, Tom's research is a good combination of experimental trials data, statistical analysis and model fitting, truely provided a good standard to help decision makers evaluate IRS product effectivens.

Routes to the resolution of sexual conflict

Dr. Alison Wright

Sexual conflict occurs when males and females have different optimal fitness strategies concerning reproduction, leading to an evolutionary arms race between them. In Alison's presentation, she mainly discussed two topics: i. Does sexual conflict drive sex chromosome formation? ii. Can sexual conflict be resolved by regulatory evolution?

For the first question, firstly, they support the theory that sex chromosome evolve from autosomes, initially with the acquisistion of a sex determining locus. Then, the emergence of sexually antagonistic allele at loci in close proximity to the sex determining locus selects for recombination suppression between sex chromosome, once the recombination is halted on the sex chromosome, the non-recombination region can expand with the acquisistion of additional sexually antagonistic alleles and further recombination suppression. The lack of recombination leads to accumulation of repetitive DNA, which can lead to short-term increase in size but results in large-scale deletion in sex chromosome. They used guppies' colors which are inherited consistent wih Y-linkage as their research object, characterized their sex chromosome and find out how much recombination suppression between them by sequencing.

However, sex chromosome only represents a samll portion of the genome, if the idea about sexual conflict is true, then essentially the locus side with sexually antagonistic alleles should be distributed across whole genome. So they recently tested the realtionship between regulatory evolution and sexual conflict across autosomes and they showed that sex-biased expression in general, and perhaps male-biased expression in particular, is a rapid and effective route to resolve intra-locus sexual conflict.

Breeding system evolution in light of demographic sex biases

Dr. Luke Eberhart-Phillips

Sex ratio variation is an important characteristics of the demographic and evolution study. In particular, adult sex ratio (ASR) shows remarkable variation throughout nature, with birds and mammals tending to have male-biased and female-biased ASRs. In Luke's study, he mainly focused on the demographic pathways that shape sex biase and assess their evolutionary consequences on the parental and mating strategies across several species of *Charadrius* plovers.

Firtly, Luke tried to answer the question that at which point in the life time do these biases emerge? And He reported a detailed individual-based demographic analysis of an intensively studied wild bird population to evaluate origins of sex biases and their consequences on mating strategies and population dynamics. He found that in a polygamous snowy plovers, the primary driver of male-baised sex ratio is sex-specific juvenile survival rather than adults or dependent offspring. And the finding provides support for theories of unbiased sex allocation when sex differences in survival arise after the period of parental investment. Sex biases also strongly influenced population viability, which was significantly overestimated when sex ratio and mating system were ignored. Then he demostrated the significance of sex differences of juvenile survival in determining ASR bias using 6119 individuals from six wild shorebird pupulations.

So it is conceivable that juvenile survival contributes mostly in biased ASR since it is a critical stage in speices development when they are exposed to complicated environment with few survival skills. As for how these biases arises in juvenile survival? We can probably find some intrinsic factors such as sex-diffrent ontogeny and genotype-sex interactions.

Parallel adaptation of rabbit population to myxoma virus

Prof. Frank Jiggins

The myxoma virus was released into wild rabbits in Australia and Europe in the 1950s, while the rabbits in both continents rapidly evolved resistance to the virus. Frank's team investigated the genetic basis of this resistance by comparing the exomes of modern individuals with the historical rabbit specimens collected before the virus release and found out a strong pattern of parallel evolution, with selection on standing genetic variation favoring the same alleles in Australia, France, and the United Kingdom and many of these changes occurred in immunity-related genes.

By sequencing a total of 152 rabbits from Australia, France, and the United Kingdom. Genome-wise polymorphism data analysis showed the colonization route of rabbits is from French to the United Kingdom and then Australia. Genetic variation in historical and modern populations showed that similar patterns of genetic structure and diversity from the same country, more generally, across all SNPs, the allele frequencies of historical and modern population are highly correlated in the three countries. In order to investigate the parallel genetic changes occurred across three countries, they calculated the fixation index between the historical and modern samples for each country and identifide the 1000 SNPs that show the highest fixation index. Moveover, among these SNPs, differentiated in any two populations tend to show elevated fixation in the third population. Desipite the common selection pressure imposed by myxomatosis, they also experienced their distinct selection pressures quantified by Bayesian approach, perhaps due to differences in ecology.

Further investigation into the roles of SNPs subjected to selection revealed two strategies to evolve resistance: selection on the immune system, to increase the potency of the IFN response, reduced the replication of an attenuated strain of MYXV, and changes in host pro-viral proteins that viruses hijack for their own benefit, evaluation of the role of VPS4 found strongly inhibition in MYXV replication.

Reconstructing hyperdiverse food webs: fish gut content metabarcoding as a tool to disentangle trophic interactions on coral reefs

Dr. Jordan Casey

Understanding the role of predators in food webs can be challenging in complicated systems such as coral reefs which composed of small crptic species. DNA based dietary analysis can provide supplement predator removal experiments and provide a high-resolution and large-scale trophic webs of coral fishes in Moorea, French Polynesia (17°30'S, 149°50'W). The study is benefits from Moorea BIOCODE project and the construction of cytochrome c subunit I (COI) sequence library. The Moorea BIOCODE project aims at establishing molecular markers for all non-microbial species of French Polynesia tropical ecosystem and it has identified over 5670 macrobiotic species and constructed species-specific DNA barcode library for most animals.

Identifying species from these samples relies on the ability to match sequences with reference barcodes for taxonomic identification, while ribosomal markers are targeted in most of the previous studies, despite the fact that the mitochondrial Cytochrome c Oxidase subunit I gene(COI) is by far the most widely available sequence region in public reference libraries. Largely because the available universal COI primers target the 658 barcoding region, which is consider to large for sequencing. So, Jordan's team had design a new PCR primer within the higly variable mitochondrial COI region, the "mlCOIintF".

With these primer for species identification in fish gut content, she showed that most of fish species spread out and some species showed high degree dietary hybridization. Moreover, there are limited overlaps among fish family but the NMDS result still showed a cluster pattern. However, only family significantly explained diet partitions while no significant effect of trophic category. Overall, this study revealed a detailed and broad view of food web trophic coral reef system.

Integrating ecology across scales of biological organisation

Dr. Diego Barneche

The main topic of Diego's talk is to discuss how individual-level determinants of metabolism as well as life-history traits affect the energy flux and overall productivity of populations, communities and ecosystems.

The metabolic theory of ecology (MTE) posits that the metabolic rate of organisms is the fundamental biological rate that governs most observed patterns in ecology. It is based on an interpretation of the relationships between body size, body temperature, and metabolic rate across all organisms. To explain the relationship between body mass and temperature, the most known equation is:
$$B = b_0 M^{\frac{3}{4}} e^{-\frac{E}{kT}}$$
where b_0 is a mass-independent normalization constant, M is organism mass, E is activation energy in electronvolts or joules, T is absolute temperature in kelvins ,and k is the Boltzmann constant.

Diego showed a series of studies metabolic framework. The results of relationship between matebolic rate and body mass, and the temperature-dependance energy flux empirically follows the MTE. Meanwhile, he demonstrate that the cost of growth, E_m varies substantially among fishes, and that it may increase with temperature, trophic level and level of activity. Moreover, the system carrying capacity will drop significantly when suffered from extremely heat.

Another important proposition of metabolic theory is how the body size determines the reproductive-energy output. He showed that larger mothers reproduce disproportionately more than smaller mothers contribute disproportionately in fecundity and total reproductive energy, which reset the theory on how reproductive scales with size.

The microbial ecology of bees, and engineering protective microbiomes

Dr. Peter Graystock

Pollinators play a critical role in ecosystem functions and services. Recently, researchers have reported pollinator diversity and abundance decline, especially honeybees and bumblebees in Europe and North America. This decrease may be caused by pathogens, parasites, insecticides, pollutants, habitat fragmentation and climate change. A survey on the prevalence of 5 parasites in 3000 bees and 3000 flowers were carried out in Peters previous research, he detected that 77% commercially imported bumblebee colonies carried several infectious parasites. This may impose detrimental impacts on other indigenous pollinators since the transmission can be facilitated by flowers. Using an experimental approach, Peter indeed proved that flowers can be a hub for parasite transmission.

In Peters talk, he pointed out the significance of gut bacteria of bees. First, the gut bacteria communities vary among host species and is linked to host sociality. Second, gut microbiomes can help reduce parasite virulence. This antagonistic relationship between gut bacteria community and parasite (Crithidia bombi) has been supported by data both from lab and field. However, it is still unclear why gut bacteria can function as a protection of parasite virulence. There may be competition of limited resources when parasites co-exist with gut bacteria. Another possibility is direct interactions between gut bacteria and parasites and leads to parasite fitness decreases. Due to the flaw of experimental design here, researchers can not exclude the possibility that the antibiotic treatment (i.e. host without gut bacteria) led to higher mortality because of lethal toxin effect. Last, bumblebee biome seems to help increase bumblebee tolerance to selenium pollutant in the soil. This ongoing research is trying to address the role microbiome plays in bumblebee survival under selenium threat by testing the metabolic responses in different microbiome combinations. Future work including metatranscriptomics is required to provide a comprehensive understanding of bumblebee microbiome.

Coexistance, community assembly and the N-dimensional hypervolume

Dr. Alex Pigot

'Why are there so many kinds of animals?', this question posed by G.E. Hutchinson remains one of the great challenges in ecology. In Alex's talk, he disscuss their work integrating phylogenies, functional traits and species geographic distributions for the global avian radiation, to understand how ecological niche limits sympatry in birds with a broad-scale and explored how many trait dimensions can describe a avian niche space.

Hutchinson' niche theory was described as a space consisted of both biotic and abiotic variables limiting the species viability. Species morphological traits can be critical variables that constrain species distribution and sympatric pattern. With the availability of high-resolution avian phylogeny and the establish of global avian morphology database, Alex is able to discuss the sympatry pattern in the entire avian clade under a global scale.

Alex and his team revealed that body size is the only strong predictor when explaining coexistence among sister avian species in global scale. But body mass performs poor when it comes to prediction of trophic and foraging niches at larger taxonomic scales. Alex also demonstrated that avian niches are multi-dimensional instead of single linear. These results provide a novel perspective of avian coexistence and community assembly in a broad scale, implying morphological traits such as body size (including body mass and body length) and beak size are of great importance in avian multidimensional niches. This work filled the gaps of previous work focusing on regional or certain clade and suggested that avian niche space have more dimensions compared to plants.

In his recent work, he tired to use random forest to build a classifier for avian foraging niches and achieve around 80% accuracy. But I am kind of confused about his theory about using PCA as a dimensions tool to evaluate the tarit dimensions, because PCA will take all tarits into account for dimensional reduction.

The Evolution of Silver Spoon Effects

Dr. Barbara Tschirren

The life-long reproductive advatange (i.e. increased fitness) enjoyed by an individual that had access to abundant resources during the early. In Barbara's talk, she explained why not all parents provide favorable conditions for their offspring, how parental provisioning experienced by an individual during development affects its own offspring provisioning later in life, and how such cascading parental effects shape the evolution of parental care.

As well as passing on genes, a mother shapes her offsprings phenotype by influencing the environment they experience early in life.However, whether the traits causing these marernal effects also affect their own expression in subsequent generations (cascading maternal effects) and the evolution implicationss of such feedback loops are not well understood. In Barbara's research, they reported that the investment a mother makes in her eggs positively affects the egg investment of her daughter, the size of eggs daughters lay resembles the egg size of their maternal line significantly more than that of their paternal line in Japanese quail, highlighting that egg size is in part maternally inherited. Furthermore, this maternal variance in offspring egg size can be explained by maternal egg size, which can support the presence of a positve cascading effect of maternal egg size on offspring egg size.

By using evolutionary modeling, she further demonstrated that this association between additive genetic and positive cascading maternal effects leads to anamplification effect, accelerating the evolutionary potential of both maternal investment and any other traits in offspring (e.g.,body size) affected by this maternal investment.

Overall, their study provides empirical evidence for positive cascading maternal effects, which by amplifying the amount of variation avaliable for selection to act on, affect the evolutionary potential of both prenatal maternal investment and juvenile body size. Evolutionary models showed that such positive cascading maternal effects only influence evolutionary dynamics in the presence of additive genetic effects.

C.elegan as a tractable host to study natural infections by oomycetes

Dr. Michalis Barkoulas

C.elegan has been extensively used as a model organism in molecular and developmental biology, because of the benefits like short life cycle, easy to cultivate, transparent, simple anatomy and genome, etc. Oomycetes are eukaryotic organisms that inhabit a variety of terrestrial and aquatic enviroments and infect a range of animals and plants. Animals infections by oomycetes have been very litte studied due to paucity of tractable host, so Michalis's lab developed a new pathosystems based on the discovery of natural oomycete infections of C.elegans.

Michalis's lab reported a new natural oomycetes pathogen of C.elegans, M.humicola, which showed some host-specificity infections strategy: budding, hypha growth, sporangia and zoospore release by tractable label FISH (fluorescent in situ hybridisation). Moreover, a novel pathogen-specific immune responses was identified by studying the changes in gene expression with and without exposure to M.humicola infection, which was a previously uncharacterized gene family encoding chitinase-like (CHIL) proteins. They demonstrated that the response is higly specific against M.humicola and antagonizes the infections.

Further, they found that animals overexpressing chil genes showed reduced pathogen attachment, and vice versa. They propose that chil proteins may diminish the ability of the oomycete to infect by hindering pathogen attachment to the host cuticle. By using atomic force microscopy (AFM) to generate force displacement curves whereby the displacement of the cuticle is measured upon delivering quantifiable forces and they found that chil gene overexpression significantly changed the stiffness of cuticle.

Overall, their research developed a new pathosystems to better understand how C.elegans sense and respond to oomycetes.