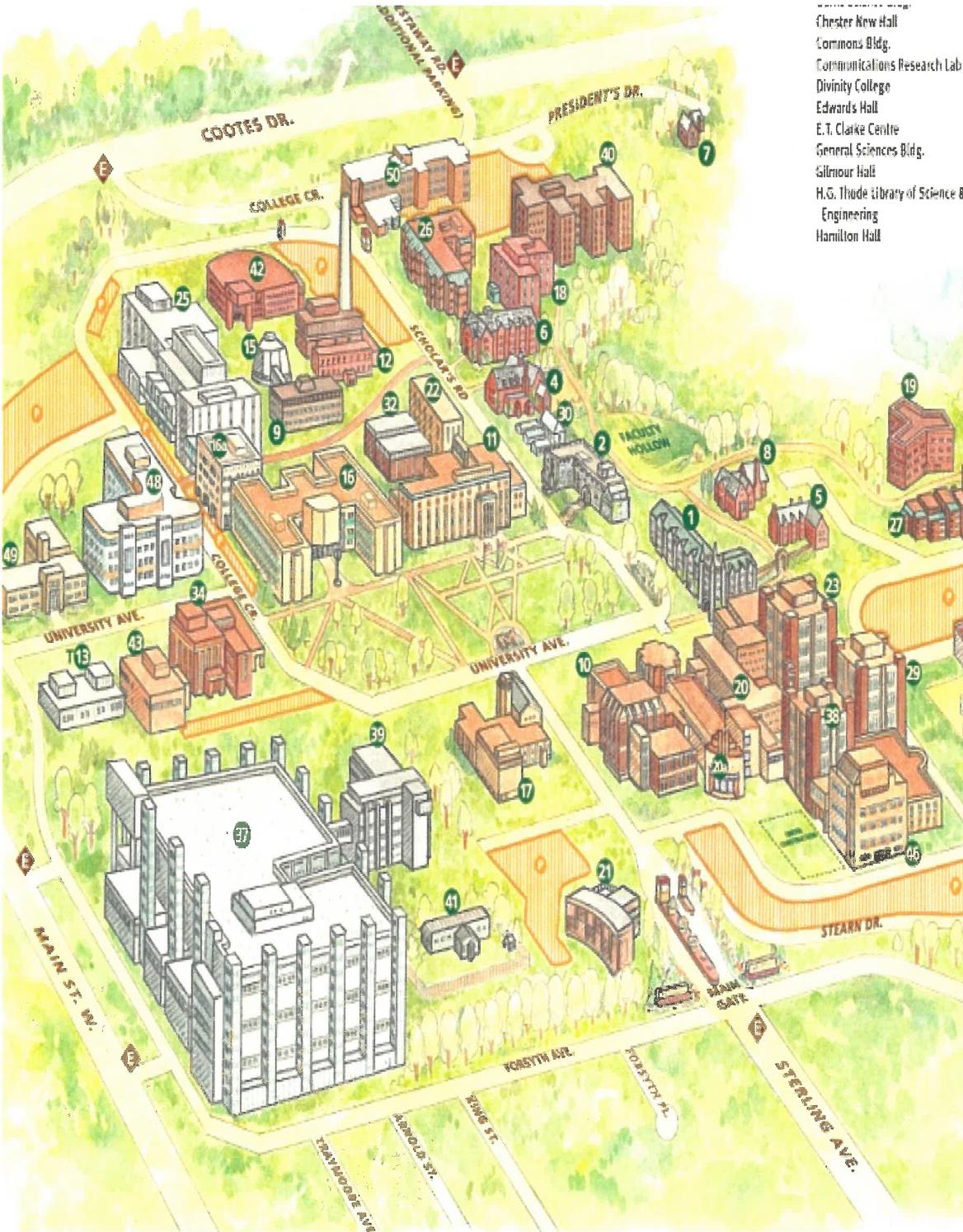


Ontario Ecology & Ethology Colloquium



May 2nd, 3rd & 4th
McMaster University
Hamilton, Ontario

Campus Map



Poster addition

Ecological importance of variation in leaf biomass dynamics among selected Ontario wetland plant species occurring along a north-south

Coulas, J. A. and P. Ryser

Department of Biology, Laurentian University, Sudbury, Ontario, Canada, P3E 2C6

The amount of living and dead plant material present at a given location is limited by the external factors (stress and disturbing agents) acting within the environment. Local factors form the primary selective force acting on a plant species, with successful plants adapting the necessary coping strategies for resource capture, conservation and utilization. It has been established that growth and decomposition parameters are lower in plants adapted to severe environments, yet there is also an indication that this generalized pattern differs for some herbaceous plant forms. In contrast to evergreen species, leaf life spans in herbaceous plants have been shown to decrease with a decreasing growing season length while the relative growth rate increases. It is unclear at this point which external factors are most influential in dictating growth form strategies employed by herbaceous plants. The main goal of this project is to assess the influence that inherent traits (i.e. leaf lifespan, tissue density and litter quality) of individual ecotypes and species play on ecosystem processes of wetlands occurring along a north-south gradient in Ontario. While grown within our outdoor experimental garden in Sudbury, we look to uncover both intra- and interspecific differences in various leaf traits of wetland sedges and grasses adapted to different environments. Wetlands surrounding the areas of Parry Sound, Sudbury, Timmins/Gogama and Moosonee were chosen as study and collection regions as they contained communities of wetland plants that were similar in species composition and nutrient status, yet presented contrasting climatic conditions and different growing season lengths.

Correction

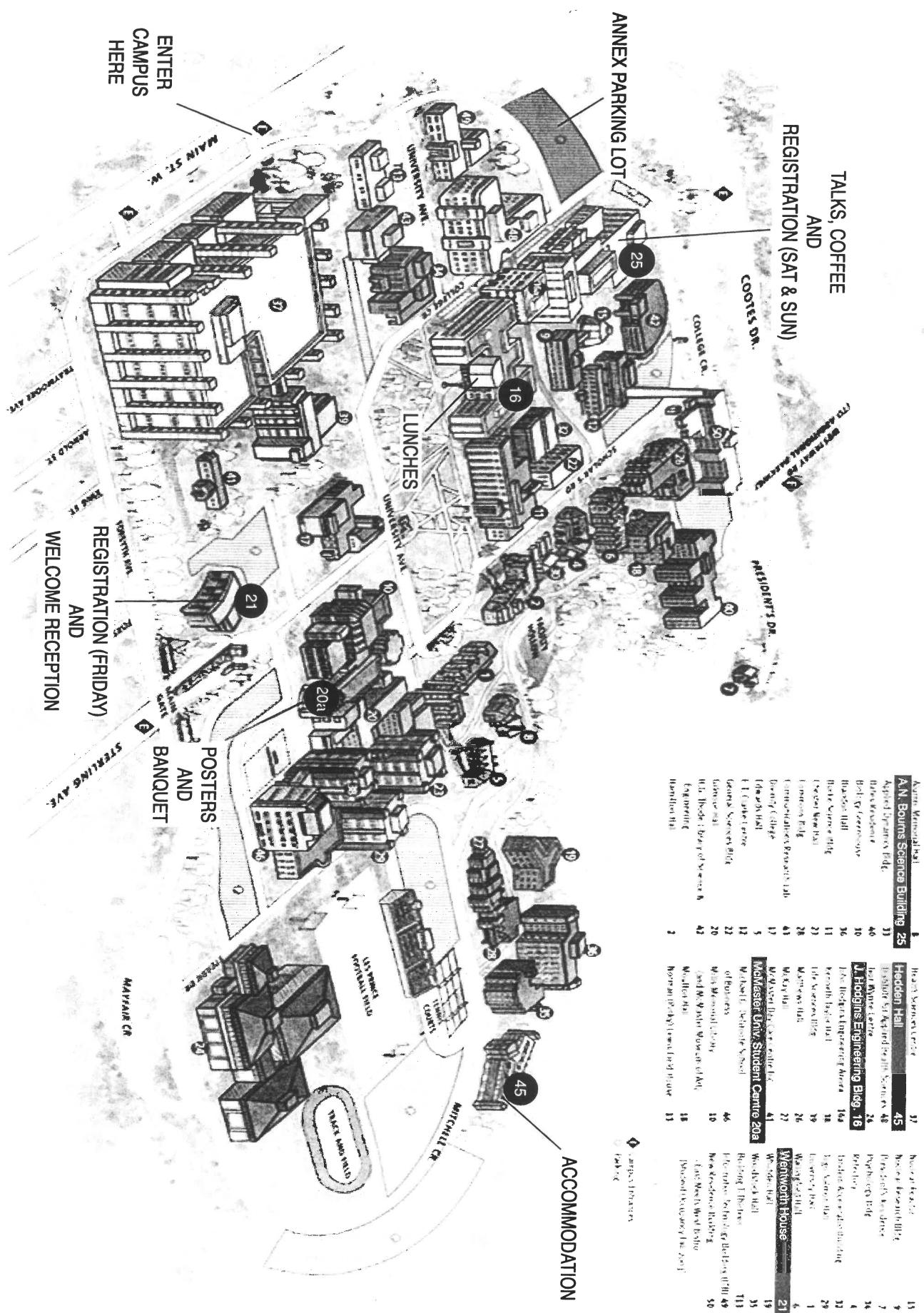
Originally indicated as being presented by the first author, this talk, taking place in talk session 3 (ABB 270) at 4:40 pm will be presented by Beatrix Beisner

Do productivity and biodiversity influence colonization rates of rockpool zooplankton communities?

Hovius, Beisner, Hayward and Kolasa*

OEEC 2003 - McMaster University

CAMPUS MAP



OEEC 2003

May 2nd, 3rd, and 4th 2003

Department of Psychology
McMaster University

Department of Biology
McMaster University

Acknowledgements

A great deal of hard work and an incredible amount of effort goes into organizing a meeting like OEEC. This year because of SARS our original location for the OEEC (McMaster hospital) was changed. Therefore this year's organizing committee had to effectively plan two meetings!!! We wish to thank the fabulous team of committed committee chairs and the entire organizing committees for their time, energy and enthusiasm. You have made this meeting possible.

The OEEC 2003 organizing committee consisted of the following wonderful people

Webpage committee chair, Lisa Debruine

Science committee chair, Julie Desjardins and her committee Marylene Boulet, Sanjay Hirema, Patty Gillis, Sheila McNair, and Jeff Galef,

Fundraising committee chairs, Kelly Stiver and Sean Gregory

Advertising committee chair, Alex Ophir

Logistics committee chair, Eric Bressler and his committee Amanda Aiken, Andrew Clarke, April Haywar and Martin Daly,

Social committee chairs Kamini Persaud and Sean Myles, and their committee Alanna Chaudhry, Emily Kirby, Lesley Reid, Dara Torgerson, and Margo Wilson,

AV committee chair Chris Somers, and his committee Pat Barclay, Mel Huntley, Vicky Kjoss, Titus Seilheimer, and Jim Quinn

This OEEC would not have been possible without the generous financial support from the Psychology and Biology Departments and the Dean of Science. The entire committee wishes to take this opportunity to thank them for making this meeting possible.

The OEEC 2003 Organizing Committee also acknowledges the contributions of the following book publishers and groups: Bistro 1010, Mobix, The Bean Bar, The Phoenix Bar and Eatery, Taylor's Tea Room and Takeaway, Fisher Scientific, Sinauer Associates Inc., CRC Press and Titles Bookstore.

Finally we also want to thank the student volunteers who assisted with registration, convening and audiovisuals.

Looking forward to a great conference.

Sigal Balshine (Psychology Department)
Jim Quinn (Biology Department)

Important Information

Registration Desk

There will be volunteers available to respond to any questions you may have at the Registration desk on Friday night, May 2nd from 5:00 pm in the Wentworth lounge at the Phoenix bar and eatery in Wentworth Hall (#21 on map), on Saturday, May 3rd from 8:00 am in the foyer of the Arthur Bourns Sciences Building (ABB - #25 on map) and on Sunday, May 4th from 8:00 am in the same location as Saturday.

Emergencies and Security

For serious emergencies requiring fire, police or medical assistance, dial 9-911 from any campus telephone. Campus security can be reached from campus phones by dialing 88.

Finding Your Way to the Rooms

All conference activities will be held on the McMaster University main campus in the Arthur Bourns Sciences Building (ABB - #25 on map). A campus maps with pertinent locations have been provided on the inside front cover of these proceedings for your convenience. Room numbers and locations will be clearly indicated once inside the ABB.

Parking

Parking on campus will be available with room rental to those occupying a room on campus while those coming for individual days and those staying on campus can park in any lot for free provided that you arrive after 3:15 pm on Friday, May 2nd and leave before 9:00 am on Monday, May 4th. Parking is strictly enforced in handicap spots and 24-hour reserve spots. We suggest that you park in the lots located on the west campus. These will provide you with the easiest access to ABB and the residences. These parking lots are most easily found by using the Main Street West entrance of the University near the hospital. Please refer to the map provided for further directions.

Session Chairs

Chairs of oral presentation sessions should have received information via email prior to the start of the conference. If you are the chair of a session and have not received any information please see the registration desk or anyone on the organizing committee as soon as possible.

Instructions for Oral Contributed Speakers:

Before your talk: Be sure to have your PC formatted disk with imbedded fonts ready prior to your scheduled talk time. Take your CD to the room where your talk is being held during the break prior to your session to load onto the portable computer. There will be a practice room available (ABB 271) during conference hours. If you wish to use this room, please sign up since there may be multiple presenters interested. Presentations should be no longer than 15 minutes with a 3-minute period allotted for questions prior to your talk. Those using a slide presentation, should have slides prepared in your **own carousel** prior to scheduled talk time and for those using overheads, please bring your overheads with you to your scheduled presentation time.

After your talk: Please be sure to collect all audio-visual materials from the presentation room. Audio-visual volunteers will not be responsible for any materials left in the presentation rooms.

Instructions for Poster Presenters

There will be a single 'official' poster session held on Saturday evening (May 3rd) prior to the banquet and will be held in the McMaster University Student's Centre (MUSC) outside the banquet hall where cocktails will be available before dinner. As presenters, you are expected to attend the poster session and be near your poster during the prescribed time. The poster area will have stands set up and be available to presenters Friday evening (May 2nd) as well as through the day of Saturday May 3rd. Posters should be removed from the display area after the poster session before the end of the banquet. Volunteers will be on hand to assist in installation.

Food and Drink

Coffee breaks will take place in the foyer outside ABB 164 and 165 as well as in the second floor lounge near ABB 270. Providing good weather, lunches will take place in the foyer and the courtyard of Engineering Sciences Building (#16 on map). If weather does not cooperate, lunches will be served in the same locations as coffee. Coffee breaks will take place after both plenary talks and between talk sessions 2 and 3 as well as sessions 5 and 6.

Other Places to Eat and Drink

There are a number of other places to eat and drink on and off campus.

On campus:

The **Student center's Market Place** will be open from 7 am to 10 pm and has a variety of options including, pizza, asian food, sandwiches and Tim Horton's although hours of operation vary from vendor to vendor. The Phoenix is a lively graduate hanging place and will be open for food and drink on Friday night until 2 am. Unfortunately many of the regular places to eat and drink on campus are closed on weekends and out of term.

Off campus:

Across from the Hospital, you will find some convenient options for a quick meal including William's Coffee Pub, Ghazzi's middle eastern food and Gino's Pizza.

Westdale village, situated a few minutes walk east of the University on King Street West, offers a much larger and more attractive selection of dining choices. For example, Bistro 1010 (1010 King St. W. 905/526-6642), an elegant upmarket restaurant in the heart of Westdale Village serves wonderful appetizers, salads and main courses. The Bourbon St. Café (1019 King St. West, 905/526-0888) is a more relaxed and casual restaurants where the portions are large and delicious but service can be slow. The Bean Bar (1012 King St. West, next to the Westdale Cinema 905/524-2326) is an excellent choice, this funky restaurant specializes in mouthwatering desserts. They also have a full dinner menu, liquor license and host live music on a weekly basis. New Village Restaurant (988 King St. West 905/522-4331) is a great family run diner with wholesome and affordable meals served all day long. The Snooty Fox (1011 King St. W. 905/546-0000) is a local favored watering hole with British pub atmosphere combined with inexpensive, tasty filling food. Two favored coffee shops in Westdale visits are the Second Cup (1004 King St. West 905/ 540-1611) and Tim Horton's (951 King St. West 905/521-1533).

McMaster University: Historically, McMaster University is the outgrowth of educational work initiated by Baptists in central Canada as early as the 1830's. Named after Senator William McMaster (1811-1887), who bequeathed substantial funds to endow "a Christian school of learning", the University was incorporated under the terms of an act of the Legislative Assembly of Ontario in 1887. Degree programs began in 1890, with degrees first being conferred in 1894. In 1930 the University moved from Toronto to Hamilton, the forty-first academic session opening on the present site.

Schedule of Events

Friday, May 1st

Time	Event	Location (# on campus map)
17:00	Registration and reception	Wentworth Lounge at Phoenix Bar and Eatery (21)

Saturday, May 2nd

Time	Event	Location (# on campus map)
8:00 -	Registration	Arthur N. Bourns Building (ABB) outside room 102 (25)
9:00	Opening Remarks by Turlough Finan chair of Biology and Ron Racine, Chair of Psychology	ABB room 102 (25)
9:20	Plenary: Paul Hebert with introduction by Jurek Kolasa	ABB room 102 (25)
10:20	Coffee	ABB foyer outside 163 and 165, 2 nd floor faculty lounge (25)
10:40	Talk Session 1	ABB rooms 163, 165 and 270 (25)
12:20	Lunch	Engineering courtyard (16)
13:20	Talk Session 2	ABB rooms 163, 165 and 270 (25)
15:00	Coffee	ABB foyer outside 163 and 165, 2 nd floor faculty lounge (25)
15:20	Talk Session 3	ABB rooms 163, 165 and 270 (25)
17:00	Poster Session and cocktails	McMaster University Student Centre (20)
18:00	Banquet	

Sunday, May 3^d

Time	Event	Location (# on campus map)
9:00	Opening Remarks	ABB room 102 (25)
9:20	Plenary: Nelson Hairston with introduction by Reuven Dukas	ABB room 102 (25)
10:20	Coffee	ABB foyer outside 163 and 165, 2 nd floor faculty lounge (25)
10:40	Talk Session 4	ABB rooms 163, 165 and 270 (25)
12:20	Lunch	Engineering courtyard (16)
13:20	Talk Session 5	ABB rooms 163, 165 and 270 (25)
15:00	Coffee	ABB foyer outside 163 and 165, 2 nd floor faculty lounge (25)
15:20	Talk Session 6	ABB rooms 163, 165 and 270 (25)

Schedule of Talks

Talk Session 1 – Saturday May 3rd 2003

	<i>Plant Ecology Room 270 Chair: R. Dukas</i>	<i>Population Biology Room 163 Chair: A. Schulte-Hostedde</i>	<i>Evolutionary Genetics Room 165 Chair: S. Myles</i>
10:40	Nutrient limitations on plant growth and implications for herbivore forage in arctic marshes <i>Ngai* and Jefferies</i>	The evolution of species geographic range limits <i>Samis* and Eckert</i>	The influence of polyploidy on the fitness of yeast across a range of environments <i>Morrill* and Mable</i>
11:00	Carnivore induced density- and trait-mediated indirect effects cause changes in plant resistance to herbivores <i>Muis* and Thaler</i>	Effects of supplemental food on deer mouse populations <i>Desjardins* and Millar</i>	Characterizing polyploidy in <i>Arabidopsis lyrata</i> using light microscopy and flow cytometry <i>Dart*, Kron and Mable</i>
11:20	Responses to selection on protandry in <i>Chimerion angustifolium</i> <i>Routley* and Husband</i>	Demographic connectivity and sex-biased dispersal in bullfrogs (<i>Rana catesbeiana</i>) <i>Ireland*, Cebek and Berrill</i>	Flow cytometry as a tool used to determine ploidy in the Jefferson Salamander complex <i>Beriault*, Bogart and Mable</i>
11:40	Plant vascular architecture and within-plant spatial patterns in resource quality following herbivory <i>Viswanathan* and Thaler</i>	Effects of extra food on nestling survival in red-backed voles, <i>Clethrionomys gapperi</i> <i>Kasparian* and Millar</i>	Can sexual selection and antagonistic coevolution produce sex difference in autosomal recombination? <i>Lorch*</i>
12:00	Evolution consequences of biological invasion: Do invaders evolve increased vigour? <i>Brown* and Eckert</i>	Prey abundance, availability and anxiety in structured environments <i>Andreuskiw*, Fryxell and Thompson</i>	Novel circling mouse (Cr) appearing in a transgenic growth hormone colony demonstrates behaviour associated with dysregulated striatal dopamine <i>Chaudry*, Szechtman, Rosenfeld and Rollo</i>

Talk Session 2 – Saturday May 3rd 2003

	<i>Population Biology</i> Room 270 Chair: J. Desjardins	<i>Mating Systems / Evolution</i> Room 163 Chair: B. Neff	<i>Conservation Biology</i> Room 165 Chair: J. Quinn
1:20	Antagonistic pleiotropy, mortality source interactions and the evolutionary theory of senescence <i>Williams* and Day</i>	Male (mate) limitation in populations of a key intertidal amphipod <i>Forbes*, McCurdy, Lui and Boates</i>	A world out of balance: Assessing the cause, occurrence and implications of an emerging wildlife pathogen <i>Greer*, Berrill and Wilson</i>
1:40	Social dominance, scent marking and home range quality in the American marten (<i>Martes americana</i>) <i>Herzog*, Fryxell and Thompson</i>	Diploid male production and the population size paradox in common orchid bees <i>Zayed*, Roubik, and Packer</i>	The amazing pulsatile toadfish <i>Wood* and Walsh</i>
2:00	Can sex-specific life history traits be predicted in unsampled populations of yellow perch? <i>Purchase*</i>	What do web vibrations tell widows? <i>Leverette*, Andrade and Mason</i>	Identifying limiting factors for fish species at risk (SAR) in the Sydenham River <i>Poos*, Mandrak and McLaughlin</i>
2:20	Historical trends in body growth of select muskellunge (<i>Esox masquinongy</i>) populations in Ontario <i>Robinson* and Casselman</i>	Why are honeybee (<i>Apis mellifera</i>) drones so large? Comparing fitness components of individuals varying in size <i>McAneney Lannen*, Otis, Hall</i>	Emerging consequences of the sex-biased and trophy-oriented harvest of polar bears <i>Saunders*, de Groot, and Boag</i>
2:40	The similar effect of intrinsic versus extrinsic cycles on mean population densities <i>Brassil*</i>	The effects of intra-specific social interactions on reproductive control and ovarian development in <i>Bombus impatiens</i> Cresson workers <i>Wong*, Cnaani, Thompson</i>	Sentinel mice detect heritable DNA mutations induced by air pollution <i>Somers* and Quinn</i>

Talk Session 3 – Saturday May 3rd 2003

	<i>Community Ecology</i> Room 270 Chair: J. Bogart	<i>Evolution</i> Room 163 Chair: T. Pitcher	<i>Behavioural Ecology</i> Room 165 Chair: R. Gegeair
3:20	Community genetics: The importance of genetic and environmental variation in affecting arthropod community composition on <i>Oenothera biennis</i> <i>Johnson* and Agrawal</i>	Is staying power more important than size? Tests in the Australian redback spider Kasumovic* and Andrade	Worker reproduction in honeybees: A potential two strategy game <i>Abbott*</i>
3:40	The influence of macro-invertebrate predators on the recovery of zooplankton communities in Swan Lake <i>Cooper-Jackson* and Arnott</i>	The effects of condition on the ontogeny of sexually dimorphic traits in the ambush bug <i>Phymata americana</i> Punzalan*, Rowe and Rodd	Effect of the reward properties on learning and choice in free foraging bumblebees <i>Cnaani*</i>
4:00	Spatial and temporal patterns of small stream habitat use by Brook Trout, <i>Salvelinus fontinalis</i> , in Northwestern Ontario <i>Lawrie* and Mackereth</i>	Unseen danger: The fate of a moth on the water surface <i>Guignion*</i>	Predator decrease flower visitation by bees <i>Dukas*</i>
4:20	Removing the confounding effect of habitat specialization reveals stabilizing contribution of diversity to species variability <i>Kolasa* and Li</i>	Tragedy of the commons, trustworthiness and competitive altruism <i>Barclay*</i>	Social and nesting behaviour in the larger carpenter bees <i>Xylocopa</i> <i>Prager*</i>
4:40	Do productivity and biodiversity influence colonization rates of rockpool zooplankton communities? <i>Hovius*, Beisner, Hayward and Kolasa</i>		The social biology of <i>Halictus farinosus</i> <i>Sellars*</i>

Talk Session 4 – Sunday May 4th2003

	<i>Plant reproduction</i> Room 270 Chair: J. Kolasa	<i>Ecology</i> Room 163 Chair: J. Stone	<i>Signal Evolution</i> Room 165 Chair: B. Galef
10:40	Mating system regulation in <i>Chamerion angustifolium</i> <i>Tindall* and Husband</i>	A common genetic basis for food-related behaviours? <i>Fitzpatrick* and Sokolowski</i>	Sex- and context-specific behavioural patterns in response to a complex acoustic signal <i>Guerra*</i>
11:00	Characterizing expression of self-incompatibility alleles in <i>Arabidopsis lyrata</i> <i>Prigoda* and Mable</i>	Ontogenetic changes in diet of coastal marine copepods <i>Finlay * and Roff</i>	Signal evolution in an artificial world <i>Sherratt*, Beatty and Rashed</i>
11:20	Experimental dissection of inbreeding and its adaptive significance in a flowering plant <i>Herlihy* and Eckert</i>	The factors that shape life history variation in the smallmouth bass <i>Dunlop*, Shuter and Rodd</i>	Songs of the Savannah Sparrow (<i>Passerculus sandwichensis</i>): Structure and geographic variation <i>Sung* and Handford</i>
11:40	The importance of geographic isolation in reproductive isolation between diploid and polyploid <i>Chamerion angustifolium</i> <i>Sabara* and Husband</i>	Linking ecosystem-based and single species approaches to marine conservation <i>Evans*, Roff and Hussein</i>	Acoustic cloaking against eared moths during aerial attacks by the bat, <i>Myotis septentrionalis</i> <i>Ratcliffe*, Fullard and Jacobs</i>
12:00	Maternal and paternal effects on the fitness of hybrids between red (<i>Morus rubra L.</i>) and white mulberry (<i>Morus alba L.</i>) <i>Burgess* and Husband</i>	Micro-heterogeneity of natural aquatic microcosms and the effects on biodiversity <i>Reid* and Kolasa</i>	

Practice
in Rm 271

Talk Session 5 – Sunday May 4th 2003

	<i>Evolutionary genetics</i> Room 270 Chair: J. Xu	<i>Community Ecology / Conservation</i> Room 163 Chair: D. Earn	<i>Mating System Evolution</i> Room 165 Chair: L. Rowe
1:20	Phylogenetic analyses of the corbiculate Apinae (Hymenoptera: Apidae) <i>Cardinal* and Packer</i>	Modelling gap formation, neighbourhood interactions and self-organization in a forest <i>Pagnutti*, Anand and Azzouz</i>	Mating type and mitochondrial inheritance in a fungus <i>Yan* and Xu</i>
1:40	Gene genealogical analysis reveals multiple hybridizations in natural populations of a yeast <i>Xu*</i>	Variation in riparian plant community structure: Influences of seed dispersal, regional community mosaics and the local environment <i>Arnold* and Aarssen</i>	The maintenance of sex in coexisting sexual and clonal minnows (<i>Phoxinus</i> sp.) <i>Mee* and Rowe</i>
2:00	Testing a parsimonious, evolutionary explanation for regional-scale variation in species richness <i>Pither* and Aarssen</i>	Sea turtles and forests: What's the connection? <i>Kamel* and Mrosovsky</i>	Fertilized female Japanese Quail weight the costs of sexual harassment differently than unfertilized females <i>Persaud* and Galef</i>
2:20	Evolution of tRNA-Leu genes in animal mitochondrial genomes <i>Higgs*, Jameson, Jow and Rattray</i>	Plant communities in oak savannahs in Ontario: Are we ready for reintroduction of the Karner Blue butterfly (<i>Lycaeides melissa samuelis</i>)? <i>Chan*</i>	Male-male competition in redback spiders (<i>Lactrodectus hasselti</i>) <i>Stoltz* and Andrade</i>
2:40	Mitochondrial DNA and nuclear DNA telling different stories: Evidence from the black-tailed brush lizard <i>Lindell*, Murphy and Mendez de la Cruz</i>	Community disassembly – What causes divergence? <i>Biggers* and Kolasa</i>	Advantage of male self sacrifice in redbacks: Straight sperm transfer or cryptic female choice? <i>Snow* and Andrade</i>

Talk Session 6 – Sunday May 4th 2003

	<i>Evolutionary Genetics Room 270 Chair: P. Higgs</i>	<i>Mating Systems/Evolution Room 163 Chair: P. Barclay</i>	<i>Conservation Biology Room 165 Chair: C. Wood</i>
3:20	A genealogical study of the evolution of sterile polyploids <i>Bruni* and Eckert</i>	The effects of selection and sex-linkage on the evolution of mammalian sperm proteins <i>Torgerson*, Kulathinal and Singh</i>	Exurban development and the nesting success of birds breeding in hardwood forest fragments <i>Phillips*, Nol and Burke</i>
3:40	The evolution of lactase persistence <i>Myles*</i>	On detecting sexually antagonistic coevolution with population crosses <i>Rowe, Cameron* and Day</i>	The effects of forest fragmentation on post-fledging survival and dispersal of a forest songbird <i>Rush* and Stutchbury</i>
4:00	Speciation in sand lizards of the <i>Phrynocephalus versicolor</i> complex (Agamidae) <i>Gozdzik* and Fu</i>	Genome replacement and the maintenance of the unisexual lineage of Ambystoma <i>Ramsden*</i>	Road effects on southern flying squirrels (<i>Glaucomys volans</i>) <i>Judge*, Bednarczuk and Nudds</i>
4:20	Fiordland Tokoeka; a Phylogeographically unique kiwi...or two <i>Burbridge*, Robertson, Colbourne and Baker</i>	Ejaculate feeding expedites oviposition and increases female fecundity in the sexually dimorphic fly <i>Prochyliza xanthostoma</i> (Diptera: Piophilidae) <i>Bonduriansky*, Wheeler and Rowe</i>	The effects of an invasive invertebrate predator, <i>Bythotrephes logimanus</i> , on zooplankton communities recovering from acidification <i>Strecker* and Arnott</i>
5:00	Evolutionary rates and species diversity in Arachnids <i>Barrett*</i>	Genitalic elaboration in guppies (<i>Poecilia reticulata</i>) <i>Cheng*</i>	Nitrogen isotopes and bioerosion surveys on the florida reef tract suggest widespread land-based stress on the reefs <i>Ward-Paige* and Risk</i>

Plenary Abstracts and Profiles

Paul Hebert

Probing Life's Diversity Through DNA Barcodes

Technological advances are providing exciting new opportunities to generate the genomic information needed to probe the relationships of life and the processes important in its diversification. At a practical level, this work offers hope to those frustrated by the slow progress towards the description of life on our planet and the difficulties in gaining identifications. DNA barcodes will soon offer a supplement to the morphological approaches that have revealed the broad outlines of life's diversity. This approach not only promises to revolutionize the business of taxonomy, but will also expedite the inventory of life. Our work has established the feasibility of basing an identification system for animal life upon the analysis of sequence diversity in a single mitochondrial gene.

References

- Hebert, P. D. N., A. Cywinski, S. L. Ball and J. R. deWaard. 2003. Biological identifications through DNA barcodes. *Proc. Roy. Soc. Lond. B* 270: 313-321.
Hebert, P. D. N., S. Ratsingham and J. R. deWaard. 2003. Barcoding animal life: COI divergences among closely allied species. *Proc. Roy. Soc. Lond. B*: in press.

Profile

A native of Kingston, Paul earned his BSc at Queen's University, his PhD at Cambridge and subsequently carried out a PDF at the University of Sydney and the British Museum. He took up a faculty position at Windsor in 1976 where he remained until repositioning to Guelph in 1990 where he now holds a Canada Research Chair in Molecular Biodiversity. He currently serves as Director of CyberNatural Software and as Chairman of the Board at the Huntsman Marine Science Centre. He earlier served as Chair of the Department of Zoology at Guelph and as Director of the Great Lakes Institute at Windsor. He is now leading the establishment of the Biodiversity Institute of Ontario and a national Microgenomics Network. He has received several awards for his involvements in digital media (Pirelli Prize, Richards Education Award, Sony Prize) and for his research in evolutionary biology (Rutherford Fellow, Sigma Xi Excellence in Research, Fellow of the Royal Society of Canada). He has published more than 230 journal articles and book chapters, has edited one book and is a member of the editorial boards of two journals. His laboratory has made important contributions to our understanding of issues such as breeding system evolution and the implications of genome size diversity, largely through studies of aquatic life. However, his work is now solely focused on advancing our understanding of biodiversity through microgenomic analyses.

Nelson Hairston

Role of rapid evolution in trajectories of population cycles in predator-prey systems

The interplay of ecological and evolutionary dynamics on similar time-scales is of growing interest to population biologists. Although accumulating evidence of short-term responses to natural selection in nature has stimulated theoretical studies showing that rapid evolution can alter the trajectories of population size through time, experimental tests are lacking. Using a two-species laboratory-culture system, we tested the proposition that evolution can alter the period and phase relationships of predator-prey dynamics. An explicit model of the dynamic interaction between a unicellular alga and its consumer, a rotifer, suggests that prey evolution in response to predation should lead to population cycles with substantially longer periods and with distinctly different phase relations than those for non-evolving prey. We tested this prediction by manipulating the raw material of evolution, i.e., the clonal diversity of the prey population. A single algal clone (genotype) should produce an evolutionarily "stagnant" population, whereas a multi-clonal algal culture should be evolutionarily "active". Our experimental results confirmed our theory-based prediction that in this system ecological and evolutionary processes take place on the same time-scale. We propose that interpretations of the causes of population oscillations in nature, an active field of enquiry, cannot ignore the potential effects from on-going rapid evolution.

Profile

Dr. Nelson Hairston Jr. is the Frank H. T. Rhodes Professor of Environmental Science, and currently Chair of the Department of Ecology and Evolutionary Biology at Cornell University. He has served on the Cornell faculty since 1985. He received his B.S. from the University of Michigan and his Ph.D. from the University of Washington. His research is on lake ecosystems and the organisms that inhabit them. He has studied the adaptations of zooplankton and fish, and their evolution in response to environmental change, the role of population processes in community dynamics, and the interactions between community dynamics and ecosystem functioning.

Posters

Modelling patterns of Scarlet Fever epidemics in Canada 1924 - 1955
Bailey, S. F. and D. J. D. Earn

The effects of anoxia and pH on the hatching success of *Daphnia ephippia*
Barnett, A. J. D., N. Fesnoux and B. E. Beisner

The population biology of childhood diseases: Predicting outbreak patterns
Bauch, C. T. and D. J. D. Earn

The evolution of conspicuous colouration as a reliable signal of prey defence
Beatty, C. D. and T. N. Sherratt

Effects of population size reduction on genetic variability of reintroduced southern flying squirrels
Bednarczuk, E., T. Nudds and T. Crease

The quantitative genetics of plant physiological traits in *Lobelia* spp.
Caruso, C. M. and H. Maherli

Invasion waves of the Ponto-Caspian crustaceans: Are invasion patterns predictable?
Cristescu, M. E. A. and P. D.N. Hebert

Physiological responses to habitat fragmentation in a threatened migratory song bird on its wintering quarters
De los Santos, J. F. and B. J. M. Stutchbury

Effects of food level and perceived predation risk on foraging behaviour and development rate in a damselfly
Dmitriew, C.

A comparison of microsatellite isolation techniques using avian genomes
Gregory, S. M. and J. S. Quinn

Bee community composition change over a 35-Year period
Grixti, J. C.

Phylogeography and evolution of Alvar species
Hamilton, J.A. and C. G. Eckert

The effect of dissolved organic matter size on the bioaccumulation of mercury in insects
Harding, K. M.

Interactions between dietary copper and dietary sodium in juvenile rainbow trout (*Oncorhynchus mykiss*)
Kjoss, V. A., C. K. Kamunde, S. Niyogi, M. Grosell, and C. M. Wood

The effects of spatial and temporal variation in pH, alkalinity, dissolved organic carbon, and substrate on benthic invertebrate communities in Precambrian shield lakes
Lento, J.

Role of mate attendance by male common Eiders (*Somateria mollissima*) within and between nesting colonies
McKay, K., G. Gilchrist and T. Nudds

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Abstracts

Worker reproduction in honeybees: A potential two strategy game

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In normal honeybee colonies, most workers are sterile but some lay unfertilised eggs that can develop into males (drones). Workers act to suppress worker reproduction and mutually enforce sterility upon each other by an activity called worker policing. Worker policing involves the destruction of worker laid eggs and aggression towards workers with developed ovaries. Despite this, reproductive workers are found in low numbers in normal colonies. It is unclear what forces are maintaining worker reproduction at low levels in honeybees. One possible hypothesis is that it is because worker reproduction is selectively advantageous, but only when rare. In this paper, game theory is used to develop and model the hypothesis that worker reproduction is advantageous only when rare because the probability of a worker laid egg surviving policing, and therefore the benefits of worker reproduction, decreases as the number of reproductive workers increases. Using estimates for all parameters used, this model predicts that 0.7 workers in 10, 000 will be reproductive. Previous studies have estimated that 1 worker in 10, 000 is reproductive (Ratnieks 1993).

Prey abundance, availability, and anxiety in structured environments

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Most studies of prey vulnerability come from laboratory aquatic systems. The common result is reduced vulnerability in structurally complex environments due to impeded predator search and physical refuge for prey. Here we present a terrestrial predator-prey system with the opposite result. We tested the hypothesis that American marten suffer reduced foraging efficiency in structurally simpler forests generated by clearcut logging. From fall 2001 to spring 2002 marten foraging dynamics were studied in logged and unlogged boreal forest of northwestern Ontario. Coarse woody debris and availability of subnivean access were censused along linear transects. Small mammals were censused by live trapping. Marten hunting behavior was examined from snowtracking 34 marten over 100 km, and diets were quantified by scat analysis. Behavioral response of voles to predation risk was measured with giving-up densities. While coarse woody debris levels were higher in unlogged forest, marten selected subnivean access in both forest types. Despite equal small mammal densities, marten encountered and killed prey twice as often in unlogged forest. Giving-up densities of voles were higher in unlogged forest indicating greater fear of predation risk. We conclude that, rather than providing refuge for small mammals, forest structure creates an aggregated and predictably located resource for marten. Second-growth forest therefore represents reduced hunting efficiency. We are calculating prey preferences to test the hypothesis that marten use alternate prey in logged forest where small mammals are less vulnerable.

Variation in riparian plant community structure: Influences of seed dispersal, regional community mosaics and the local environment

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Streams provide a linear, continuous habitat along which community patterns and dynamics have long been examined. The discrete nature of riparian habitat creates a convenient system in which the influence of elusive regional factors such as dispersal and effective regional species pool size can be estimated. If hydrochory, or diaspore transport by water, is the principal means of dispersal along streams then seeds are preferentially dispersed downstream. Models predict that the available species pool is constantly increasing downstream as seeds and species accumulate from upstream communities. We extend this model by predicting that the more community-types the stream traverses, the greater the number of species that can potentially accumulate at the downstream 'sink'. Our hypothesis was that streams flowing through highly heterogeneous landscapes would have the largest species pool available for recruitment, and consequently the highest species richness at the downstream study site. We established study sites on 100 streams that represented a range of upstream heterogeneities and lengths in SE New Brunswick. At each study site we inventoried 60m² of streamside vegetation, and recorded data for local variables hypothesized to influence community structure: canopy cover, channel width, bank slope, and ground cover (rock, moss, soil and litter). Regional factors hypothesized to influence richness were extracted from GIS data. Richness ranged from 21 to 109 species per site. Despite the range in plant richness observed, and the number of local and regional variables considered, we were able to explain very little of the variation in riparian plant richness.

Modelling Patterns of Scarlet Fever Epidemics in Canada 1924 - 1955

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Regular epidemics of Scarlet Fever occurred throughout the first half of the 20th century. We studied weekly and monthly notifications submitted by the Canadian provinces to the Dominion Bureau of Statistics during the period 1924-1955. Spectral analysis of these time series shows that the dominant periods (corresponding to interepidemic intervals) were 1 and 6.25 years, with the longer period playing a greater role in the western provinces. A seasonally forced SEIR model can explain the short period and preliminary analysis suggests that it can also explain the longer period. The one-year period corresponds to the attractor of the model, while the longer period appears to represent transient dynamics that are sustained by demographic stochasticity.

Tragedy of the commons, trustworthiness and competitive altruism

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A "tragedy of the commons" occurs when individuals fail to reach a group-beneficial outcome because of individuals pursuing selfish interests. Altruistic individuals are expected to be outcompeted by selfish individuals who free-ride on the altruists. However, if other people are more likely to trust altruists than free-riders, then altruists can benefit from being altruistic. Furthermore, if only one member of a group can benefit from having an altruistic reputation, then group members may compete to be the most altruistic. In this study, I show that people are

more likely to be altruistic in a cooperative group game when they know that they can benefit from an altruistic reputation in a subsequent dyadic trust game. The more altruistic a person is, the more he or she is trusted. This provides a selection pressure that allows for the evolution of altruism. I also provide some of the first experimental evidence for competitive altruism by showing that people are more likely to persist in being altruistic in a situation where they have to compete to receive the benefits of being altruistic. Thus, opportunities for trust can decrease the likelihood of a tragedy of the commons occurring.

The effects of anoxia and pH on the hatching success of *Daphnia ephippia*

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Anthropogenic input of nutrients from industry and agriculture has enriched many freshwater environments, favoring the dominance of algae. Once algal dominance is established, feedback mechanisms affecting nutrient cycling in lakes can maintain a high algal biomass state. The objective of this study was to determine whether this feedback loop is further reinforced by low recruitment of Daphnia due to low hatching success of ephippial resting eggs under anoxic and/or acidic conditions. A factorial experimental design was used to test the effects of pH and anoxia. Nitrogen bubbling was used to simulate anoxia, while pH was regulated through the use of HCl. The highest proportion hatched occurred in the normoxic/acidic treatment ($0.32 + 0.074$) while the anoxic/acidic treatment exhibited the lowest proportion hatched ($0.22 + 0.059$). None of these treatments were found to be significantly different ($P > 0.05$) when analyzed using a two-factor ANOVA. This suggests either a lack of statistical power or simply that anoxia has no effect on the hatching rate of Daphnia. Future studies can focus on increasing statistical power, mimicking natural conditions more efficiently, or testing the effects of anoxia on a population of Daphnia over multiple generations. The understanding of the processes that inhibit the ability of Daphnia to effectively graze on algae can improve on current lake management techniques.

Evolutionary rates and species diversity in Arachnids

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Genetic change is a necessary component of speciation, but the relationship between rates of speciation and molecular evolution remains unclear. If speciation is associated with greater rates of sequence change then families with high species richness should also show higher rates of genetic divergence. I used phylogenetically independent contrasts to assess the relationship between evolutionary rates and species richness among arachnid families. I found no positive association between evolutionary rate and species richness. In addition, I tested the ability of sequence diversity in a mitochondrial gene, cytochrome c oxidase I (COI), to discriminate between different arachnid families. My results establish that a COI family profile, derived from low-density sampling, can effectively assign newly analysed taxa to the appropriate family. My findings highlight the potential of COI as a biological identification tool, but also signal the need for greater sequence data to test hypotheses about patterns of species diversification and rates of molecular evolution.

The population biology of childhood diseases: Predicting outbreak patterns

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Historical records of incidence of childhood diseases (such as measles, whooping cough, chicken pox and rubella) reveal complex dynamics, and there has been much debate on which mechanisms produce the observed patterns of recurrent outbreaks. For measles, a simple model has indicated that outbreak patterns are determined by seasonal variation in the transmission rate, and are represented by the asymptotic (long-term) behavior of the model. Furthermore, transitions between different outbreak patterns are driven by slow changes in birth rates and vaccination levels. The same analysis can explain the dynamics of chicken pox, but fails for rubella and whooping cough. We show that an additional analysis of the transient (short-term) behavior of the model---together with knowledge of the population size in question---can account for all the observed incidence patterns by predicting how noise-sustained transient dynamics should be manifested in these systems.

The evolution of conspicuous colouration as a reliable signal of prey defence

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While the occurrence of conspicuous (aposematic) traits in defended prey is generally interpreted as a warning signal to potential predators, it is unclear how and why such signals evolved. Current theory suggests that defended prey are conspicuous because it exploits a pre-existing tendency of predators to learn to avoid conspicuous cues more quickly than other cues. Here we tested an alternative theory, namely that warning signals are primarily selected on the basis of their reliability as indicators of defence. To do this, we examined how the attributes of defended (unprofitable) and undefended (profitable) computer-generated prey evolved when they were subject to continued selection by humans. Conspicuous traits readily evolved in defended prey, simply because this allowed them to be readily distinguished from undefended prey. By contrast, undefended prey did not evolve conspicuousness because this rendered them vulnerable to predation. Overall our results show that aposematism readily evolves in artificial systems, and that the primary determinant of the spread of a warning signal is its reliability.

Flow cytometry as a tool used to determine ploidy in the Jefferson salamander complex

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The Jefferson salamander complex has an interesting breeding system which includes diploid, triploid, tetraploid and pentaploid genomic combinations whose ploidy cannot be determined by visual inspection of the animal. In the past a combination of methods was used to determine the ploidy of these cryptic amphibians. Allozyme electrophoresis, chromosome spreads and erythrocyte area are all methods that can be used to determine ploidy but are typically tedious, time consuming and at times inaccurate. Flow cytometry (FCM) is a rapid and highly sensitive method used to measure the nuclear DNA content of cells such as erythrocytes. It has been shown that FCM is more accurate and precise than erythrocyte area and much less time consuming than chromosome spreads. FCM also has the ability to identify mosaicism, a feature

that no other method has yet been able to provide. Although it is more expensive and lacks the ability to discern between the genotypes of hybrids it saves a tremendous amount of time, material and resources. A protocol using tissue samples (tail tips) instead of blood is in the works, in the hope of eventually eliminating the need for sacrificing individuals. Larvae are too small to collect blood from and have the capability to regenerate tail tips, which means that such a protocol would give us the opportunity to study populations accurately and with less interference.

Effects of population size reduction on genetic variability of reintroduced southern flying squirrels

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Demographic bottlenecks or reductions in population size are predicted to result in loss of genetic variability. However, the genetic consequences of demographic bottlenecks, such as those that may occur during translocations, are poorly studied in nature. I used four microsatellite and one mitochondrial DNA marker to test for a recent genetic bottleneck in a population of southern flying squirrels (*Glaucomys volans*) reintroduced to Point Pelee National Park (PPNP), Ontario, in 1993/94. The established population was compared to its source population in Haldimand-Norfolk (H-N). The 2001 PPNP flying squirrel population size was estimated to be 591 (575 – 638) individuals; a six-fold increase from 99 founders over seven years. No signatures of a genetic bottleneck were identified. These findings do not support the conventional wisdom that population bottlenecks result in the loss of genetic variability. Long-term genetic and demographic monitoring of translocated populations may clarify the role of genetic variability in population viability.

Community disassembly – What causes divergence?

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Communities assembled under the same environmental conditions often follow divergent trajectories. Some have postulated that such divergence is due to minute differences in initial conditions; but the question appears to be unresolved. However, in natural systems, differences in environmental conditions strongly influence the community assembly process. In particular, variability in physical conditions has often been suggested as a prominent force in structuring communities. The crucial question emerges then as to what extent community divergence can be attributed to differences in habitat variability. One possible approach to address this question is to tackle it ‘in reverse’. Thus, our approach has been to create ‘maximum’ communities and then follow up on their disassembly as a function of time and local habitat variability. Specifically, we hypothesize that, while communities diverge over time, this divergence will be greater among habitats with greater variability. We test this hypothesis with experimental data from 20 tropical coastal rock pools at Discovery Bay, Jamaica. First, the contents of each rock pool were removed and combined together (in a tank) to form “maximum” assemblages (max S). Next the emptied pools were thoroughly cleaned of propagules and the mixed ‘maximum’ assemblages returned to each pool bringing them to their original volumes. We recorded temperature, salinity, pH, conductivity, and chlorophyll as well as the invertebrate communities for over 2 years at varying intervals. Physical measurements were used to calculate pool variability. Our results indicate that (a) pool richness and abundance declined over time, (b) these declines were associated with the degree of community divergence in each

pool, and (c) that in the later stages of community disassembly, the physical variation of the pools interacted with the time that had elapsed since the beginning of the experiment to determine the magnitude of divergence.

Ejaculate feeding expedites oviposition and increases female fecundity in the sexually dimorphic fly *Prochyliza xanthostoma* (Diptera: Piophilidae)

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In several species of piophilid flies, females expel and ingest sperm and accessory gland fluids after each copulation. This highly unusual behavior is especially interesting in light of recent evidence that ejaculates may be toxic to females. We investigated the effects of ejaculate ingestion on female fitness in the piophilid carrion fly *Prochyliza xanthostoma*: following ejaculate expulsion, females were either permitted or denied the opportunity to ingest the ejaculate, and then either provided with ad lib. food or starved. Three indices of female fitness were recorded: the number of days between mating and first oviposition, the total number of eggs laid, and survival. Fed females laid more eggs and lived longer than starved females. Females permitted to ingest the ejaculate oviposited sooner and laid more eggs than females prevented from ingesting the ejaculate, but ejaculate ingestion did not affect female survival. Thus, ejaculate feeding resulted in direct benefits for *P. xanthostoma* females, and appeared to increase female fitness. The fitness effects of ejaculate ingestion were stronger in fed females than in starved ones, suggesting that these effects are more stimulatory than nutritional. This study provides the only known example of a fitness-enhancing 'nuptial gift' consisting entirely of ejaculate fluids and sperm, and contrasts sharply with recent studies suggesting detrimental effects of ejaculates on females.

The similar effect of intrinsic versus extrinsic cycles on mean population densities

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The long-term mean density of a population across time is a basic measure that is widely used to summarize populations with variable densities. I demonstrate the similar effect of cycling on the mean density, whether the cycling is due to extrinsic or intrinsic noise. Intrinsic cycles are those cycles driven by density dependence or population interactions such as predation. Extrinsic cycles are those driven by random variation in the environment, reflected as variation in a model parameter. The analyses of intrinsic and extrinsic cycles have largely developed along independent lines, however, with regard to the long-term mean density, the effect of intrinsic and extrinsic cycles can be summarized by an examination of density variance. In simple models such as a discrete logistic equation, or the Ricker equation, a similar expression describes the effect of both extrinsic and intrinsic variation on the mean density. In most standard population models, intrinsic or extrinsic variation will decrease the mean density compared to the equilibrium. Depending on the form of non-linearity, variation could lead to an increase in the mean density, as in some formulations of the Beverton-Holt equation. This analysis is extended to two and three species systems, demonstrating how variation interacts with processes such as competition and predation. The similarity of extrinsic and intrinsic variation is based in part on the assumption that external environmental variation is independent among generations. This assumption is examined by looking at the effect of correlated environmental variation.

Evolutionary consequences of biological invasion : Do invaders evolve increased vigour?

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The observation that invasive plants are larger and more fecund in their adventive versus their native range is often reported, although it is unclear as to whether these differences are a result of post-invasion evolution, or a response to improved environmental factors. Here, I investigate evolutionary changes associated with the colonization of North America by the emergent aquatic plant *Butomus umbellatus* (Butomaceae). I used data collected from natural populations to compare flower and seed production between native and introduced plants, and a common greenhouse experiment to compare overall plant vigour, and the respective allocation of resources to sexual and clonal reproduction of introduced versus native populations. My field survey analysis indicates that introduced populations exhibit increased fertility compared to native populations. My greenhouse experiment showed that, on average, seedlings from introduced populations emerged more frequently and had increased plant survival. Furthermore, introduced populations produced inflorescences 3.8 times more often, and produced clonal bulbils 2.8 times more frequently than native populations in experiment 1, and these increases were not due to an increase in total plant biomass. However, increased sexual reproductive capacity in introduced populations does not appear to be a result of adaptive evolution as little genotypic variation was found within and between introduced populations. Consequently, increased multiplication and dispersal of clonal bulbils appears to have been selected during colonization and likely serves as the primary reproductive mode in the spread and colonization of *Butomus umbellatus* in the adventive range.

A genealogical study of the evolution of sterile polyploids

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The importance of polyploidy as an evolutionary force in plant species is widely accepted but relatively unstudied. An increase in genome size may alter key life history traits, allowing polyploids to exhibit novel physiological and ecological traits distinct from their diploid progenitors, promoting polyploid adaptation and establishment. In contrast, uneven polyploidy usually results in sexual sterility which limits the evolutionary persistence and radiation of polyploid lineages. Yet, uneven polyploids sometimes persist via asexual, clonal reproduction and become widespread. Given that asexual triploids are vulnerable to extinction and thus are dependent on their diploid progenitors for recurrent formation, I predicted: 1) On a genealogy, triploids will appear as derived genotypes, and not appear as distinct or ancestral. 2) Triploids should share the majority of their haplotypes with progenitor diploids. 3) Because triploids are ephemeral, they should occur in close geographical proximity to related diploids, sharing identical or very similar haplotypes. To test my predictions, I investigated the evolution of diploids and sterile triploids that co-occur within the aquatic plant species *Butomus umbellatus* (Butomaceae) by screening the chloroplast genome for variation. However, among eight geographically and genetically distinct genotypes no cpDNA variation was detected in sequencing the trnL intron (580bp screened) and restriction enzyme analysis (PCR-RFLP) of the trnH-trnK and trnC-trnS non-coding regions (117bp screened). Thus, *B. umbellatus* appears to have low chloroplast DNA variation, potentially due to stochastic events such as genetic drift, founder effect or a recent bottleneck.

Fiordland Tokoeka; a phylogeographically unique kiwi...or twoBurbidge¹, M. L., H. A. Robertson², R. M. Colbourne² and A. J. Baker¹¹ROM, University of Toronto, Toronto, Ontario, Canada, M5S 3G5²Department of Conservation, New Zealand

The brown kiwi of are comprised of three species distributed across the three main islands of New Zealand. The North Island Brown Kiwi (*Apteryx mantelli*) is found in five allopatric populations on the North Island. The Rowi (*A. rowii*) is found only at Okarito on the west coast of the South Island and the Tokoeka (*A. australis*) is found in two regions in the South Island as well as on Stewart Island. All populations of these species are comprised of one genetic lineage (most are reciprocally monophyletic), except in Fiordland. Here, there are two distinct lineages within 25-30 km of each other. Given that kiwi do not tend to disperse far, and that Fiordland is a mountainous, glaciated region this finding does not seem overly surprising. However, no apparent boundary to gene flow exists between the northern and southern lineages. Even more perplexing, the Haast population (150km to the north on the other side of a geological boundary) is more closely related to the northern Fiordland lineage than either of the Fiordland lineages is to each other. One could then hypothesize that kiwi migrated north from Stewart Island to Fiordland, the Fiordland birds were separated from each other by a glaciation event but the northern ones bypassed the current barrier and continued north to the Haast region. Recent geographically widespread sampling in Fiordland shows that this was not the case; but instead, the processes that created the current genetic patterns in this geologically active region are complex.

Maternal and paternal effects on the fitness of hybrids between red (*Morus rubra* L.) and white mulberry (*Morus alba* L.)

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The ecological and genetic effects of hybridization depend on the nature of differences between parental taxa and their nuclear x nuclear and nuclear x cytoplasmic incompatibilities. Previous studies of hybrids between red mulberry and a more abundant congener, white mulberry (*Morus alba* L.), show large effects on fitness but the underlying basis of these effects is not known. In order to address the role of maternal and paternal effects on fitness, I conducted crosses between red, white and hybrid mulberry in all pairwise combinations. Offspring were compared with respect to fitness measures such as the number of seeds/fruit, percent germination, percent survival and above ground biomass at 12 weeks in a common greenhouse environment (n=1430). Results from this experiment were compared to an additional common garden field experiment (n=315) involving more advanced life history stages (2 years of growth) where similar measures were taken. Results showed significant maternal effects at both early and late stages of development for all fitness traits examined in this study. Paternal effects did not impact fitness and specific maternal x paternal combinations affected only survival. Hybrid fitness in this system may be dependent on the cytoplasmic effects of the maternal genome but less by the nuclear effects of different parental combinations. Therefore, cytoplasmic inheritance may be more important than nuclear contributions to hybrid formation and persistence.

Phylogenetic analyses of the corbiculate Apinae (Hymenoptera: Apidae)

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Relationships among the four tribes of corbiculate apine bees are controversial. Phylogenetic hypotheses based on morphological characters do not agree with those based on molecular data. Furthermore, different morphological and molecular data sets are not always congruent with one another. Thus, a clear resolution has yet to be achieved concerning relationships among the corbiculate bees. In order to help resolve this conflict, more characters need to be added to existing data sets. In all of the morphological analyses to date, the posterior abdominal segments including the sting apparatus have been largely ignored. Recently, a considerable amount of variation in the skeletal parts of the sting apparatus of bees has been found. This suggests the potential of characters derived from the sting apparatus for resolution of the existing conflict surrounding relationships of the corbiculate apine tribes. Preliminary results of cladistic analyses based on morphological characters from the sting apparatus will be presented.

The quantitative genetics of plant physiological traits in *Lobelia* spp.

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Comparative studies suggest that variation in plant physiological traits and variation in the physical environment are frequently correlated. These correlations between phenotype and environment provide indirect evidence for the adaptive evolution of plant physiological traits. Direct evidence that natural selection drives the evolution of plant physiology, however, must be derived from quantitative genetics, which can be used to calculate the magnitude and direction of evolutionary change in response to selection. To determine their potential for adaptive evolution, we measured the genetic architecture of physiological traits in *Lobelia cardinalis* and *L. siphilitica*. These species are sister taxa and differ in ecological breadth. *Lobelia cardinalis* tends to be found in shaded habitats with moist, nutrient-rich soil. *Lobelia siphilitica* is found in a wider variety of habitats, from exposed areas with relatively low soil water availability to habitats characteristic of *L. cardinalis*. When grown in a common garden, a *L. siphilitica* population from a dry site had lower mean A and WUE than a *L. cardinalis* population from a wet site, results opposite to expectations of drought adaptation. There was significant genetic variation for photosynthetic rate (A), stomatal conductance (g), and water use efficiency (WUE) in *L. siphilitica*. In contrast, there was significant genetic variation only for A in *L. cardinalis*. Genetic correlations among these physiological and other life-history traits also differed between species. We discuss the implications of this quantitative genetic variation for the evolution of physiological differences between the *Lobelia* species.

Plant communities in oak savannahs in Ontario: Are we ready for reintroduction of the Karner Blue Butterfly (*Lycaeides melissa samuelis*)?

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The population of the Karner Blue Butterfly has dropped by more than 99% in the past century due to destruction and fragmentation of the oak savannah habitat in North America. In 1991, the butterfly was extirpated in Ontario, which is the only Province where it was found in Canada. Restoration work has been performed upon several oak savannahs in Ontario since then.

Promising results have been obtained, but no systematic scheme has been employed to evaluate the quality of these restored sites and see if they are ready for reintroduction of the Karner Blue. This study tries to evaluate several potential Karner Blue reintroduction sites in Ontario by looking at both biotic (vegetation, especially the larval host plant *Lupinus perennis*, 1st and 2nd brood adult nectar source plants, and tending ant species) and abiotic (temperature, relative humidity and light intensity) aspects. Also, by comparing the biotic and abiotic aspects of these sites with those of the largest Karner Blue sites in the USA, recommendation can be made upon where butterflies should be taken in the USA for reintroduction in Ontario based on the degree of similarity among different sites in terms of vegetation community and microhabitat. Furthermore, comparison will be made when sites are grouped according to their management history so that the effects of different management methods (such as prescribed burn and thinning of the shrub layer) are compared. Recommendations will then be made upon future management strategies of the Ontario sites.

Novel circling mouse (Cr) appearing in a transgenic growth hormone colony demonstrates behaviour associated with dysregulated striatal dopamine

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Numerous genetic variants displaying stereotypic circling behavior have been described in rodents (Pycock et al, 1980). The majority are recessive mutants expressing dopaminergic alterations in the striatum – often with associated vestibular defects (Lee JW, 2001). We describe a novel circling mouse (Cr) with intact vestibular function frequently obtained from our non-transgenic wild type mice (WT). The Cr colony is generated from crosses of WT and transgenic growth hormone mice (TGH). We have characterized Cr with stereotypic circling, head bobbing, hyperkinesia, aggressiveness, and differential responsiveness to behavioural stimuli. The Cr mouse also demonstrates self-mutilating behaviour associated with dysregulated striatal dopamine levels (Saito Y, Takashima S, 2000). TGH are characterized by increased levels of circulating growth hormone and decreased levels of striatal dopamine (Diaz-Torga G, et al, 2002). The purpose of the present study is to identify the response differences between the TGH and Cr mice to dopaminergic drugs. Mice were injected with apomorphine (1.5 mg/kg) and amphetamine (1.0 mg/kg) and placed in a rotometer to assess circling response differences. Post-mortem brain dissection occurred 1 week subsequent to the final injections and striatal dopamine levels were analyzed using high performance liquid chromatography (HPLC). TGH and Cr show potential opposite alterations striatal dopamine levels. Given that dopamine is altered in other rotating genotypes, we hypothesize that frequent generations of Cr may involve unintended selection of genes that counterbalance the consequences of dysregulated striatal dopamine in TGH.

Genitalic elaboration in guppies (*Poecilia reticulata*)

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In the Family Poeciliidae, male genitalia is divergent and has evolved rapidly. In this group, the anal fin is modified to form an intromittent organ, the gonopodium. The distal tip of the gonopodium can have a range of species-specific structures including spines, hooks, claws and serrae. Such elaborate structures can evolve as a result of female choice, sperm competition, and/or antagonistic coevolution. We conducted several experiments to investigate the function of one genitalic structure, the claw, in the guppy (*Poecilia reticulata*). First, we asked whether

the claw was essential for successful insemination with either a) receptive or b) unreceptive females. This was done by removing this small structure from treatment males. Results indicate that males with their claws removed can successfully inseminate receptive females. Results also suggest that claws may be advantageous for males when mating with unreceptive females. Secondly, we tested for clawed-male advantage when females are multiply-mated. Treatment and control males were mated to females that were previously mated with marker males. The proportion of offspring sired by treatment and control males was then measured. Preliminary results suggest that clawed males do not sire higher proportions of offspring than declawed males. If the claw functions to overcome female resistance to mating, then we predict that genitalic structures would be larger and/or more elaborate in populations where females are less likely to mate. To best test this hypothesis, we are carrying out inter-population comparisons of gonopodia.

Effect of the reward properties on learning and choice in free foraging bumblebees

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Bees rapidly learn which of several flower species is more profitable and specialize on the more profitable ones. Vastly more research on bee learning has been done on the properties of the learned cues (like color, shape and scent) than on the properties of the nectar rewards (like nectar volume or concentration), the latter being remarkably poorly studied. In this study we presented to a free foraging bumblebees two different types of equally rewarding artificial flowers. After an initial period of foraging, we changed the profitability of both types making one of them better rewarding than the other by changing sugar concentration, sugar water volume or both. We then compared the learning rate and the choice made by the foraging bee in relation to the reward property that was manipulated. Our results show that bees are faster to respond to a change in rewards sugar concentration than to a change in its volume. Moreover, sugar concentration differences between flowers (40% vs 13%) results in almost complete shift of the foraging bee to the more concentrated type (about 96% of the visits), whether both types offer the same volume (2 μ l) or even if the less concentrated offer higher volume (7 μ l vs 0.85 μ l). Contrary to the sugar concentration differences, when the two types of flower differ in nectar volume (7 μ l vs 0.85 μ l) the flower type that offer the smaller volume still got 22% of the visits.

The influence of macro-invertebrate predators on the recovery of zooplankton communities in Swan Lake, Sudbury, On

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Swan Lake, like many lakes in the Sudbury area, has been affected by atmospheric acid deposition in the past. In recent years, there have been signs of chemical recovery in these lakes, however, biological recovery has been variable. In many lakes fish have been extirpated due to high acidity. This alteration of the aquatic food-web allows macro-invertebrate predators to flourish, but delays the recovery process of the zooplankton community. I conducted both a field mesocosm experiment in Swan Lake and several laboratory feeding experiments to determine the effects of macro-invertebrate predators on zooplankton communities. The invertebrate predator, *Graphoderus liberus* (Say) (Coleoptera) was used in a field enclosure experiment to determine its effect on resident Swan Lake zooplankton and potential zooplankton colonists from a nearby lake, Kelly Lake. Two treatments (*G. liberus* and a control) were established with four replicates each. Enclosures were monitored for five weeks and

changes in abundance, diversity, and richness in zooplankton communities were recorded. The results show that *G. liberus* significantly lowered the overall abundance of zooplankton and of four dominant zooplankton taxa. Richness and diversity of zooplankton were significantly lower in the *G. liberus* predator treatment than in the control treatment. Many of the Kelly Lake colonists declined at the end of the experiment, possibly because of a pH stress. These results show that invertebrate predators have an important impact on recovery of zooplankton community structures and they may be controlling the recovery of damaged lakes.

Invasion waves of the Ponto-Caspian crustaceans: Are invasion patterns predictable?

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The geographical range of the amphipod *Echinogammarus ischnus* and the cladoceran *Cercopagis pengoi* has expanded over the past century from the Ponto-Caspian region to Western Europe, the Baltic Sea and the Great Lakes of North America. The present study explores the phylogeographic patterns of these crustaceans across their current distribution based on an examination of nucleotide diversity in the mitochondrial cytochrome c oxidase subunit I (COI) and NADH dehydrogenase subunit 5 (ND5) genes. Marked genetic divergence exists among populations of *E. ischnus* and *C. pengoi* from the Black and Caspian Seas as well as those from the drainage system of the Black Sea. These interbasin divergences suggest the prolonged geographic isolation of the native populations. By contrast, invading populations of *E. ischnus* and *C. pengoi* are characterized by a lack of genetic variation; a single mitochondrial genotype of Black Sea origin has colonized sites from the Baltic Sea, River Rhine to North America. Despite their contrasting life history strategies, these invading species followed the same route of invasion from the northern Black Sea to the Baltic Sea region and subsequently to North America. This study suggests that human mediated invasion patterns are predictable. The Great Lakes may be more susceptible to Ponto-Caspian invasions than previously thought, since both vagile and poorly dispersing organisms have exploited the same avenues to establish North American populations in similar time frames.

Characterizing polyploidy in *Arabidopsis lyrata* using light microscopy and flow cytometry

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Polyploidy is an important evolutionary process that has had significant effects on the mechanisms of adaptation and speciation in plants, vertebrates and other eukaryotes. Recent studies have suggested that the frequency of polyploidy in angiosperms may be as high as 80%. If this is true, is it safe to assume that current "model" systems are truly diploids exhibiting strict Mendelian inheritance? *Arabidopsis lyrata* has recently become one of the new "model" plants because is thought to be one of the closest relatives of the "model" plant *Arabidopsis thaliana*. *A. lyrata*, like *A. thaliana* was thought to be a purely diploid species, however, recent reports of putatively tetraploid populations of *Arabidopsis lyrata* from various geographical locations suggests that this may not be the case. To confirm these reports, a protocol specific for counting the chromosomes of *A. lyrata* was developed. The chromosome numbers for four populations of *Arabidopsis lyrata* from four different geographical ranges were characterized for ploidy level and compared to DNA content estimates based on flow cytometry. Two tetraploid populations were identified by these methods, reinforcing the importance of characterizing

ploidy in "model" plants. Details about variation in chromosome numbers and DNA content will be discussed.

Physiological responses to habitat fragmentation in a threatened migratory song bird on its wintering quarters

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Migratory songbirds face negative effects because of forest fragmentation in both breeding and wintering grounds. These effects can be indirectly observed as physiological stress as a result of environmental changes, and measured using corticosterone levels as indicators of habitat quality. We studied wintering Hooded warblers (*Wilsonia citrina*) in two different habitats with different fragmentation degree, a well conserved forest in Belize and a highly fragmented landscape in Mexico; to determine fragmentation-related stress among age and sex. We mistnetted 17 warblers in Belize and 22 in Mexico, and collected plasma samples that were stored frozen until assayed using a commercial I125 Corticosterone Radioimmunoassay. A pool of random samples was made to validate corticosterone detection for this species and get a standard curve for corticosterone concentration at different dilutions that ranged from 1:5 to 1:400 obtaining a kit sensibility of 1.25 ng/mL. Corticosterone concentration ranged from 3.85 ng/mL to 55.17 ng/mL respectively, in both sites. Average concentration was higher in the fragmented landscape (Mexico, 27.05 ± 1.2 ng/mL) than in the continuous forest (Belize, 9.85 ± 0.45 ng/mL). There was a significant difference between sites ($p = 0.001$), but no significant difference was found between sexes ($p = 0.438$). This information will be pooled with GIS habitat characteristics to determine a correlation between corticosterone levels and habitat fragmentation indexes in order to get a wider perspective of fragmentation effects on migratory birdsí populations.

Effects of supplemental food on deer mouse populations

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When populations have unlimited resources they are expected to grow exponentially but in reality, natural populations grow logistically and reach a carrying capacity determined by some limited resources. The study of resource limitation stems from how natural populations exhibit logistic growth rather than exponential growth. David Lack was first to suggest that most terrestrial vertebrate populations are constrained by food. The hypothesis that individual reproduction and population growth of *Peromyscus maniculatus* is constrained by food availability was tested using food supplementation. Summer supplementation resulted in an increase in the proportion of young-of-the-year breeding while year-round supplementation resulted in both early spring breeding and an increase in breeding by young-of-the-year.

Together these contributed to a 3.5-fold increase in spring and fall population density relative to controls. Breeding by over-wintered females and winter survival were unaffected by year-round food supplementation. I conclude that late winter food availability may constrain population growth of deer mice but that multiple-factor experiments are required for a full understanding of the population regulation of small mammals.

Effects of food level and perceived predation risk on foraging behaviour and development rate in a damselfly

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Optimal foraging theory predicts that organisms will respond to environmental variation by altering behaviour or life history traits in a way that maximizes fitness. Plasticity of foraging behaviour in response to predation risk is well known in a number of taxa, probably because foraging efficiency often trades off against risk of predation. These plastic responses may also be controlled by external cues, such as temperature or light level to indicate seasonal time constraints, or internal cues such as body size or condition. Using the larvae of the damselfly *Ischnura verticalis*, initial food level was manipulated to simulate time constraint in terms of resource acquisition. It was predicted that in order to reach a minimum size at maturity, individuals raised on a limited food regimen were more likely to increase risky foraging behaviour and development rate relative to individuals raised on an ad libitum diet. Following the food manipulation, damselflies were placed in either a fish predator or control treatment. Activity level, development rate and growth rate were measured for all individuals. Foraging activity was found to be reduced in the predator treatments; however, the food level had no effect on relative activity level. Preliminary results suggest that the growth rate was not affected by predators (possibly because individuals at risk of predation were compensating by increasing foraging activity at night, a period of time during which behaviour was not observed). Data showing the effect of food level and predation on development rate are presently being analyzed.

Predators decrease flower visitation by bees

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Until recently, research on the interactions between pollinators and plants has mostly ignored the effects of pollinators' predators. I will describe my recent experiments indicating that bees are sensitive to perceived danger at flowers, and that flower visitation rate by bees is lower in patches with intense predator activity than in patches with few predators. First, in controlled experiments using artificial flowers, I documented that honeybees preferred apparently safe flowers over equally rewarding flowers associated with perceived danger. Second, in a large-scale field experiment, we found that the bumblebee, *Bombus ternarius*, showed lower visitation rate to milkweed patches with than without crab spiders, *Misumena vatia*. This is the first study documenting negative effects of predators on flower visitation rate by pollinators. Third, I counted 20 times more bumblebees at patches of goldenrod (*Solidago* sp.) farther than close to a large aggregation of bumblebee wolves (*Philanthus bicinctus*). My results suggest that the classic ecological research on flowers and their pollinators should be updated to address the effect of predators on pollinator and plant fitness and the potential evolutionary consequences of such three-level interactions.

The factors that shape life history variation in the smallmouth bass

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We examined the degree of variation in growth and maturity schedule among Ontario

populations of smallmouth bass. Our study included a detailed analysis of two populations in northern Ontario and a broad analysis of life history variation in 40 populations across Ontario. In our detailed study, we compared the reproductive differences between a population with slow individual growth rates and a population with more typical individual growth rates. For our broad analysis of 40 populations, we examined the environmental factors that contributed significantly to life history variation among populations. We determined the relationship between the life history traits of each population and a number of lake-wide, morphological and limnological measures. Our study found evidence that smallmouth bass populations adaptively respond to low food resources by increasing reproductive investment in the form of larger egg sizes and by investing in reproduction earlier in life. We also found a strong relationship between climate and life history traits. This study illustrates the importance of factors such as food availability and climate in shaping life history variation among populations of smallmouth bass. The implication of these findings for life history theory and fisheries management will be discussed.

Linking ecosystem-based and single species approaches to marine conservation

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Due to the recent development of new ecosystem based approaches to marine conservation, we now need to determine links between our traditional (species specific) and new approaches, and to verify our physical proxies used in these ecosystem-based approaches. Ecosystem based approaches for marine conservation use physical parameters to map habitats, which act as surrogates for species assemblages at a particular spatial scale. However, while this type of mapping captures representativeness of the marine environment it may not identify finer scale distinct areas consisting of physical anomalies (e.g. upwelling areas). Preliminary research shows that there is an association between large focal species (those species that we preferentially focus on and are believed to be of high conservation value) and distinctive areas. For example whales will tend to migrate to areas of high prey concentrations, caused by upwelling or gyres, for feeding. Determining if there are physical anomalies (e.g. low temperature, high chlorophyll) occurring at identified areas of importance for focal species, will help in verifying our physical proxy theory. The goal of this study is to determine if we can usefully designate a set of Marine Protected Areas to conserve biodiversity based on the protection of a particular suite of flagship species or their required distinctive habitat. This suite of focal species will be of high conservation value (i.e. endangered species) and their required distinctive habitats will capture a proportion of the habitat types within a region. A gap analysis can then be performed to determine which habitat types were not captured by protecting the focal species. Thus a truly ecosystem based approach should take into account both representative and distinctive areas, which will allow for the integration of traditional approaches into our new ecosystem based approaches to marine conservation.

Ontogenetic changes in diet of coastal marine copepods

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Several studies have focused on the consumption of specific prey items and clearance rates on natural food particles by adult copepods, but few studies have addressed the feeding habits of the earlier stages (copepodites and nauplii). Due to the difference in size among copepod stages, and the dramatic body shape difference between nauplii and copepodites, corresponding difference in diet between these major stages would be expected. This subject was addressed by offering radiolabeled natural food particles (with ³H for heterotrophs and ¹⁴C for autotrophs) to nauplii and copepodites of the copepods in a temperate estuary. By measuring the uptake of the radiolabels by the copepods it was possible to determine clearance rates on different sizes and trophic types of food particles. Preliminary results indicate that all copepod stages consume both heterotrophic and autotrophic prey, and that there is no difference among stages in the lower limit of the size of food consumed. However, the upper size limit of food consumed by nauplii is lower than that of the copepodites and adults. These results indicate that the different developmental stages of copepods will have differential grazing impacts on size fractions of the plankton, that will affect patterns of nutrient cycling in both microbial and 'classical' food webs. Therefore caution should be exercised when extrapolating the diets determined by feeding studies on adult copepods to all members of the copepod.

A common genetic basis for food-related behaviours?

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Despite an immense amount of variation in organisms throughout the animal kingdom many of their genes show substantial conservation in DNA sequence and protein function. Here we explore the potential for a conserved evolutionary relationship between genes and their behavioural phenotypes. To explore this possibility we investigate the evolutionary history of cGMP-dependent protein kinase (PKG) and its possible conserved function in food-related behaviours. First identified for its role in the foraging behaviour of fruit flies, the PKG encoded by the foraging gene has since been associated with the maturation of behaviour (from nurse to forager) in honey bees and the roaming and dwelling food-related locomotion in nematodes. These parallels encouraged us to construct protein phylogenies using 37 PKG sequences that include 19 species. Our analyses suggest five possible evolutionary histories that can explain the apparent conserved link between PKG and behaviour in fruit flies, honey bees and nematodes. Two of these raise the hypothesis that PKG influences the food-related behaviours of a wide variety of animals including vertebrates. Moreover, it appears that the PKG gene was duplicated some time between the evolution of nematodes and a common ancestor of vertebrates and insects whereby current evidence suggests only the for-like PKG might be associated with food-related behaviour.

Male (mate) limitation in populations of a key intertidal amphipodForbes¹, M. R., D. G. McCurdy², K. Lui¹ and J. S. Boates³¹*Department of Biology, Carleton University, Ottawa, Ontario, Canada, K1S 5B6*²*Department of Biology, Albion College, Albion, Michigan, USA, 49224*³*Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada, B4P 2R6*

Mate limitation through social interactions is expected to occur in some populations, but evidence in nature is limited apart from sex role reversed species. Such effects are especially important for species that are of conservation concern. Mate (male) limitation appears to occur in an intertidal amphipod that is a key species for maintenance of biodiversity and ecosystem function. Proportions of ovigerous females decline seasonally at four mudflats in the Bay of Fundy, Canada and that these declines are also associated with reductions in size-specific fecundity. Reduced likelihood of ovigerry and reduced clutch or brood sizes occurred in previous lab experiments where availability of reproductive males was manipulated in relation to timing of receptivity of females. In field populations, sex ratios are distorted in favor of females. Furthermore, proportion of ovigerous females and potential for offspring recruitment is related to density of males of reproductive size, and not to overall amphipod density or amphipod biomass, which should relate to resource acquisition by females. Such mate limitation is not stochastic in nature, but rather is affected by season and is regionally widespread. This seasonal limitation has implications for recruitment in this key species prior to overwintering, which is believed to be a major source of amphipod mortality.

Speciation in sand lizards of the *Phrynocephalus versicolor* complex (Agamidae)

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Populations of *Phrynocephalus frontalis* and *Phrynocephalus przewalski* are isolated by the Yellow River in China's Gobi desert. The two species are distinguished by having different habitat preferences and external morphology. A gene tree constructed from mitochondrial ND2 sequences shows a relatively deep divergence between *P. frontalis* and *P. przewalski*, but certain populations have members in both clades. Allozyme analysis indicates there is no genetic difference between the two species, and suggests hybridization is not occurring. However, observations of intermediate morphologies within contact zones have been made and current work with morphological traits will examine the level of species differentiation. A future study of microsatellite loci will investigate the underlying genetic processes at work in the contact zones.

A World out of balance: Assessing the cause, occurrence and implications of an emerging wildlife pathogen

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An epizootic, systemic disease causing death within wood frog (*Rana sylvatica*) larvae and leopard frog (*Rana pipiens*) metamorphs at three different locations within Southern Ontario has been identified as an iridovirus infection. Amphibians affected were found to exhibit hepatic necrosis and basophilic, cytoplasmic inclusion bodies were observed. Liver tissue samples were found positive by low level PCR amplification of ranavirus (Family: Iridoviridae) major capsid protein (MCP). Positives were confirmed by sequence analysis. Clinically normal, lab raised wood frog egg broods were also found to test weakly positive for ranavirus. Based on field,

histological and molecular investigations, an iridovirus has been identified as a highly infectious viral pathogen causing morbidity and mortality within three Ontario amphibian populations. The population effects of this iridovirus pathogen may be of a magnitude so severe that the occurrence of amphibian population declines in these locations may be inevitable.

A comparison of microsatellite isolation techniques using avian genomes

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Microsatellites consist of tandem repeats of short DNA sequences one to six* base pairs in length. In recent years they have become the molecular marker of choice for such studies as population genetics, genome mapping, and forensics as a result of their high variability, codominant inheritance, and ability to be amplified by the polymerase chain reaction (PCR). Their major downfall, however, is that they often need to be isolated from scratch. Several methods exist for isolation, but the decision as to which one to use is often arbitrary. It is the purpose of this study to compare two of the most common methods: (1) selective hybridization using streptavidin coated magnetic particles, and (2) the more traditional approach using lambda zap. I will compare financial and time costs as well as effectiveness in isolating microsatellites (i.e. total number of microsatellites isolated and fraction of total clones positive for microsatellite repeats) from four distinct avian species. These data should prove useful to researchers selecting an isolation method based on different needs.

Bee community composition change over a 35-year period

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Bees are crucial components of natural and agricultural ecosystems as a result of the pollination services they provide. Recent declines in pollinator populations are increasing the urgency of documenting Canada's bee fauna. Changes in bee distribution patterns as a result of global warming and anthropogenic influences will have major effects upon Canadian ecosystems. My research will be the first that will document these effects (if any) on the bee fauna of Canada, as it will repeat the only historical study on Canadian bee biodiversity. In 1968/1969 a detailed inventory of bee species was conducted in an old field habitat at the Forks of the Credit River. My study is being conducted (between April and October 2002/2003) at exactly the same locality to investigate any changes in species over the intervening 35 years. Additional old field sites in nearby conservation areas (Terra Cotta and Forks of the Credit), as well as the research station, Joker's Hill are being studied for comparative purposes. Comparisons with the two years of original data reveal that bee species richness has declined from 121 species out of 5188 bee specimens collected, to 85 species out of 4307 specimens collected in 2002.

Sex- and context-specific behavioural patterns in response to a complex acoustic signal

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Like other katydid species, male *Conocephalus brevipennis* Scudder (Orthoptera: Tettigoniidae) broadcast species-specific calling song, a signal used to attract distant, sexually receptive females during competitive mate attraction. An atypical characteristic of this species, however, is that both sexes will approach aggregate song, a continuous signal lacking the species-typical

temporal pattern, but manifesting the typical *Conocephalus* spp. ultrasonic carrier frequency band. This phenomenon is particularly unexpected, as there is a sympatric congener whose song is also indistinguishable as an aggregate, making the response to aggregate song non-species-specific. To account for this unusual phonotactic response, and to examine their abilities in discriminating different acoustic signals, both sexes of *C. brevipennis* were presented with various manipulations of conspecific and heterospecific song in single- and two-choice phonotactic bioassays. Results from these experiments suggest that the attraction to aggregate song stems from the benefits of aggregative behaviour, and that once within a group, the phonotactic responses of *C. brevipennis* are mediated by the distinctive features of conspecific song. These responses, however, are both sex- and context-specific.

Unseen danger: The fate of a moth on the water surface

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In response to a high-intensity bat echolocation, eared moths execute evasive behaviours characterised by spirals, erratic flight, and power dives. While the interaction of bats and moths has been intensely studied, little research has been done regarding other nocturnal predators. I examined what the costs are to a moth falling on the water surface as the result of a bat-evasive flight. Eighteen moth species were collected from three locations around Queen's University Biology Station in eastern Ontario. Wing surface area did not correlate with escape success. Upon hitting the water, moths employed two methods of attempted escape; waiting to reach the shore/dock or flying off the surface of the water. There was no trend of either method within family nor according to wing surface area. To test for the use of scales, the escape success of descaled *Lymantria dispar* was compared to sham-operated *L. dispar*. All of the descaled individuals were consumed while 63% of the control individuals escaped. I demonstrate that fish eat moths and do not discriminate between species. I further propose that moths avoid the surface of the water either passively or actively.

Phylogeography and evolution of Alvar species

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Glacial processes have characterized much of the North American landscape, and understanding the impact of these processes on the evolution of temperate species is a central question in population biology, and in the developing field of phylogeography. There has been a recent emergence in research combining molecular and geographic data to understand the impacts of glaciation on the distribution of species, the degree of divergence due to distance barriers and the impacts of glacial refugia on population dynamics. Alvars, which occur in the Great Lakes region, are critically imperiled, open habitats with a thin layer of soil over limestone and are host to a unique collection of flora and fauna including some common western species. This interesting assemblage of plants make alvars a unique system to study the impacts of glaciation and historical population dynamics. I will assess cpDNA variation in three species occurring in western prairies and Ontario/New York alvars; *Geum triflorum*, *Carex richardsonii*, and *Sporobolus heterolepis*. Two theories hypothesize the origin of alvars, the prairie retreat hypothesis suggests that alvars are remnants of prairie that extended east during the recession of the Wisconsin ice front. The range expansion hypothesis suggests that alvars were recently colonized by western prairie species through long distance colonization. This study will address

how these potential historical events have influenced contemporary population genetic structure of alvar communities. This study will also help ongoing alvar conservation and species composition projects by addressing the evolutionary potential of these communities, for which we currently know little.

The effect of dissolved organic matter size on the bioaccumulation of mercury in insects
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Mercury (Hg) in aquatic systems is of concern because it bioaccumulates to a much greater extent than other metals, and has detrimental effects on humans and other top predators that utilize aquatic organisms, particularly fish as a food source. Mercury binds to dissolved organic matter, (DOM) and this may alter its bio-uptake. While this has been shown in several studies, the opposite effect has also been noted, indicating a better understanding of the effects of DOM on Hg bioaccumulation is needed. This proposed research will examine two different aspects of DOM in Hg accumulation, including the effects of DOM size (molecular weight) and photolytic degradation. We will extend the limited information of stream invertebrates using the microcosm design called the "Trent Tube." The water in each microcosm will include DOM from natural sources that has been divided into different molecular weight fractions, and/or exposed to natural sunlight for different periods of time. Mercury will be added to the water prior to addition to the microcosm, and the system will be allowed to stabilize before the addition of the insects. After the conclusion of the study, the chitinous insect exterior will be separated from the cytosolic portion using a centrifuge technique, and the Hg analysis will be performed using ICP-MS.

Experimental dissection of inbreeding and its adaptive significance in a flowering plant
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Inbreeding is a major component of the mating system in many plants and animals, particularly hermaphroditic species. However, inbreeding may occur in several different ways which differ strongly in terms of their ecological causes and evolutionary consequences. In flowering plants, inbreeding can occur through transfer of pollen within the same flower (autogamy), between different flowers on the same plant (geitonogamy), or between related individuals (biparental inbreeding). We experimentally manipulated flowers in 10 populations of columbine, *Aquilegia canadensis*, over two flowering seasons to estimate the relative contribution of each of these modes of inbreeding. We examined how aspects of floral morphology and display, as well as population size and habitat characteristics influence these modes of inbreeding. In all populations, a large proportion of seeds were produced through inbreeding (mean: 76%). Autogamy, geitonogamy and biparental inbreeding all contribute to inbreeding, but the relative contribution of each is highly variable between populations, and between years within populations. In most populations, autogamy was the largest component of inbreeding (mean: 52%), and there was little geitonogamy (mean: 8%). Manipulating flowers to remove the potential for both autogamy and geitonogamy provided a novel method to directly estimate levels of biparental inbreeding. This revealed that on average 15% of seeds are produced through biparental inbreeding. Comparing the inbreeding coefficient of seeds from these plants to that which would result from complete selfing suggests that the relatedness of outcross mates is on average 0.54. Total inbreeding and both measures of biparental inbreeding were strongly influenced by population size.

**Social dominance, scent marking, and home range quality in the American marten
(*Martes americana*)**

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The assumptions of the ideal despotic distribution model are rarely tested experimentally. These assumptions include the existence of some behaviour(s) performed by the resident animal that excludes individuals newly arriving in an area, and that such defence does not vary with the quality of a territory. Here, I test these assumptions in American marten (*Martes americana*). I hypothesized that social dominance (and, thus, exclusion from an area) was communicated through anal scent cues, and that socially dominant marten held areas with higher resource abundance. These hypotheses were tested using a captive marten's responses to anal scent, allowing ranking of marten by dominance status. Home ranges were determined through radio-telemetry, resource levels were sampled at the forest stand type level, and mean resource value was determined across the stand types within the home range of ten marten, allowing ranking of home range quality. Results indicate that variables relating to habitat structure correlated to dominance ranking, and that adults had higher dominance rankings than did juveniles. However, high variability between trials of the same stimuli suggests that signals indicating dominance may be weak within a single sample of scent. I therefore propose a new hypothesis to explain how scent marks may exclude intruders from a territory, the scent density hypothesis (SDH). I contrast the predictions that arise from the SDH with those from two previous hypotheses.

Evolution of tRNA-Leu genes in animal mitochondrial genomes

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Animal mitochondrial genomes usually have two transfer RNAs for Leucine: one, with anticodon UAG, translates the four-codon family CUN, whilst the other, with anticodon UAA, translates the two-codon family UUR. These two genes must differ at the third anticodon position, but in some species the genes differ at many additional sites, indicating that these genes have been independent for a long time. Duplication and deletion of genes in mitochondrial genomes occurs frequently during the evolution of the Metazoa. If a tRNA-Leu gene were duplicated and a substitution occurred in the anticodon, this would effectively turn one type of tRNA into the other. The original copy of the second tRNA type might then be lost by a deletion elsewhere in the genome. There are several groups of species in which the two tRNA-Leu genes occur next to one another (or very close) on the genome, which suggests that tandem duplication has occurred. Here we use RNA-specific phylogenetic methods to determine evolutionary trees for both genes. We present evidence that the process of duplication, anticodon mutation and deletion of tRNA-Leu genes has occurred at least five times during the evolution of the Metazoa - once in the common ancestor of all Protostomes, once in the common ancestor of Echinoderms and Hemichordates, once in the hermit crab, and twice independently in Molluscs.

Do productivity and biodiversity influence colonization rates of rockpool zooplankton communities?

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Environmental productivity influences the availability of resources to potential colonizing species. Similarly, biodiversity or species richness levels have also been correlated with invasibility of communities, owing mainly to a lack of open resource niches with higher richness levels. Zooplankton communities occupying rock pools on the North Coast of Jamaica were used to assemble experimental container communities. We investigated the effects of nutrients and biodiversity on the ability of a native ostracod to colonize artificial pools. Three nutrient levels: ambient, 10X ambient and 100X ambient were crossed with 4 levels of richness: 2, 4, 6, and 7 herbivorous zooplankton species per treatment. Communities were acclimated to the containers for 2 weeks before a competitor colonizer species was introduced to each container. After one month, samples of the full community were taken and complete counts done. Nutrients and species richness showed weak interaction effects on the ability of the ostracod to colonize. Colonization increases with increasing nutrients at low and high biodiversity, but no such pattern appeared for the 4 and 6 species treatments. At 10X ambient nutrients, colonization rates increase with lower richness but, no such pattern in the ambient and 100X ambient treatments. We conclude that the effects of biodiversity and environmental productivity can be complex and that species identity may be more important than richness per se.

Demographic connectivity and sex-biased dispersal in bullfrogs (*Rana catesbeiana*)

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Dispersal is a key factor in the maintenance of metapopulations. In birds and mammals dispersal is often biased towards one sex; such sex-biased dispersal may also operate in amphibian populations. Sex-specific dispersal rates and distances between adjacent wetlands were examined for *Rana catesbeiana*, a prolonged breeder that uses permanent water for their entire life-history. We caught by hand and marked with PIT tags 406 male and 148 female post-metamorphic bullfrogs from 7 quasi-discrete breeding aggregations of equivalent size across two breeding seasons (2001-2002). Breeding aggregations were connected aquatically (5) and non-aquatically (2) over a small spatial scale (~4 km²). 262 frogs were recaptured at least once (191 males and 71 females). The overall sex-ratio was 2.74:1 and recapture probabilities were not significantly different between breeding areas or sex. 89% of recaptured females moved <150 m and 100% moved <200 m. 54% of males moved <150 m, 25% moved >150 m but stayed within the breeding aggregation, and 19% moved between breeding aggregations. 8% of males moved >1500 m aquatically and one moved >1200 m over unsuitable habitat. MtDNA control region analysis for females revealed limited structuring between aquatically connected sites, however the dominant haplotype (67%) was not found in the non-aquatically connected site. These data suggest that post-metamorphic females are highly philopatric and male-biased dispersal may connect breeding aggregations. Using direct (C-M-R) and indirect (genetic) approaches to model anuran metapopulation dynamics will greatly enhance our understanding of bullfrog population biology.

Community genetics: The importance of genetic and environmental variation in affecting arthropod community composition on *Oenothera biennis*

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Genetic and environmental influences on plant resistance are well known to affect insect populations, but their effects on arthropod community composition are not well understood. We tested how plant genotype interacts with the environment between and within habitats to affect herbivory and arthropod community composition. We grew 14 clonal families of *Oenothera biennis* in each of five common gardens. Each common garden represented a unique habitat of *O. biennis*. All arthropod species on plants were identified and counted every 2-4 weeks during the summer. The amount of early season herbivory varied nearly 2-fold between clonal families, but the effects of genetic variation were dependent on environmental variation within habitats. Plant family also affected arthropod diversity, species richness and abundance on individual plants, but in all cases, the effects of family were dependent on the habitat in which plants grew. Species richness and abundance varied by as much as 140% and 280%, respectively, between clonal families within a garden, but genetic variation affected herbivores more strongly than it did predators. Mean species richness was positively correlated ($r = 0.68$) with the proportion of plants within a clonal family that flowered. Plant genetic variation was more important than within-habitat environmental variation in affecting arthropod community composition, but at larger scales, variation between habitats was the most important factor. These results demonstrate that intraspecific genetic variation in plants has large ecological consequences for arthropod communities, but its influence decreases with increasing geographic scale.

Road effects on southern flying squirrels (*Glaucomys volans*)

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We studied the effect of roads on the movements of a nocturnal, gliding rodent, the southern flying squirrel (*Glaucomys volans*). We tested the hypothesis that flying squirrels avoid roads, such that roads restrict normal flying squirrel movements. Traps were arranged in rows on both sides of: 1) a site in continuous forest (control), 2) a roadless gap in forest (to control for the effects of canopy gaps vs. road effects per se), 3) a two-lane (narrow) road and 4) a four-lane (wide) road. We recorded the number, sex and age class of flying squirrels captured in rows of traps at 10, 30 and 50 m from the centre of each site to test for road avoidance; and the frequency of crossings at each site to test for restriction of movement. There were no consistent differences in capture rates of flying squirrels among rows of traps at all sites. However, flying squirrels crossed the wide road less frequently than all other sites. The crossing rates of flying squirrels varied within and between sites depending on age and sex.

Sea turtles and forests: What's the connection?

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Where an animal places its nests has important consequences for its reproductive success, most often through the survival of its offspring. For sea turtles, the environment in which the nest is laid greatly influences the probability of a successful reproductive outcome. With so

much dependent upon the choice of a nest site, it is likely that this behaviour is or has been under strong selection. As little is known about nest site choice in sea turtles, we investigated individual nest placement patterns for female hawksbills nesting at Trois-Îlets, Guadeloupe. In addition, the thermal consequences of the nesting patterns were determined. The nesting patterns revealed that hawksbills nest in thermally diverse habitats. This is of particular relevance as sea turtles display temperature-dependent sex determination, with females being produced at warmer temperatures. Evolutionary and conservation implications in the context of current environmental changes are discussed.

Effects of extra food on nestling survival in red-backed voles, *Clethrionomys gapperi*

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Nestling mortality is typically high among small mammals and food has been suggested as an important limiting factor. The purpose of this study was to examine the effect of food supply on nestling survival in three populations of *Clethrionomys gapperi* in the Kananaskis Valley, Alberta, during the breeding seasons of 2001 and 2002. Breeding females were provided with sunflower seeds during lactation, and nestling survival from birth to emergence from the nest was measured by live trapping. Food supplementation did not increase nestling survival, but newly emerged young from fed mothers were significantly heavier than those from unfed mothers. In addition, nestling survival was male-biased in all populations, and, breeding female densities varied among populations and years. High breeding female densities were associated with high mortality/dispersal of post-emergent young, particularly for female offspring. Results showed that food supply limits nestling growth but it has little effect on nestling survival. It is suggested that any survival advantage incurred from higher nestling growth rates is mitigated by density-dependent mortality/dispersal post-emergence.

Is staying power more important than size?: tests in the Australian redback spider

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Male contests are usually associated with a characteristic set of displays where males can assess their opponents relative fighting ability to determine their probability of winning the contest. Studies generally attribute male success to overall body size or the size of weaponry however, displaying to an opponent carries an energetic cost, and more aggressive displays are more costly. Consequently, energy reserves may play an important role considering these contests can lead to energetic wars of attrition where the loser is determined by the inability to bear the time dependant costs of interaction. In the Australian redback (*Latrodectus hasselti*), there is intense male competition for access to females since up to eight males can settle on a female's web and only two or three males successfully mate. Furthermore, males only get a single mating opportunity since they actively sacrifice themselves during copulation. Therefore, since reproductive success is low, we expect males to fight fatally for access to females. Instead, males rarely show aggression towards one another and scramble compete for access to the female. During these competitions, larger size is not a predictor of male success. We therefore suggest that winners are decided by the ability to outcompete their opponents due to greater energy reserves. In this study we examine whether size dimorphic males differ in energy reserves, and whether similar sized males raised under different feeding regimes differ in energy stores and therefore, competitive ability and mating success.

**Interactions between dietary copper and dietary sodium in juvenile rainbow trout
(*Oncorhynchus mykiss*)**

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Mining and smelting operations contribute to global environmental contamination by discharging metals, including copper (Cu), into aquifers and watersheds. Although Cu is an important trace metal required for proper organismal growth and development, beyond certain concentrations, Cu is toxic. Research on fish has suggested that Cu enters the body via an epithelial sodium (Na) channel; therefore, changes in dietary or waterborne Na concentration ([Na]) may affect the amount of Cu taken up. To investigate whether an increase in dietary [Na] would result in decreased Cu uptake, we exposed juvenile rainbow trout to various levels of Na and Cu in the diet, both in hard and soft water. [Cu] was consistently higher in Cu-fed fish, although differences within treatments were minimal in hard water. In both experiments, liver [Cu] was 6-10-fold higher than in other organs (gill, gut, carcass). In soft water, fish fed the highest [Na] accumulated significantly less Cu in the liver, suggesting that dietary Na may ameliorate the effects of high dietary Cu levels. (Supported by ICA Human Health Program.)

Removing the confounding effect of habitat specialization reveals stabilizing contribution of diversity to species variability

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The question of whether diversity begets stability is important for theoretical and practical reasons. Recently, the relative variability of combined biomass (or abundance) of all the species in a community and the relative variability of constituent populations, N, have been examined as a function of species richness, S. Combined community abundance is stabilized by S. By contrast, the effect of S on population variability continues to elude researchers. Here, we advance these analyses by removing a potentially confounding factor. Assuming that S increases primarily by adding habitat specialists and that specialists vary more than generalists, we deduce that any stabilizing effect S has on population variability may be masked by the contribution of specialists' variability. We test this hypothesis using 49 natural rock pool invertebrate communities. We obtained data on population variability and ecological specialization of all constituent species. We found that relative variability of their populations, CV, depends on the analytic resolution, with only low resolution producing a negative diversity-stability relationship. The fine-resolution analysis initially suggested that CV's were unrelated to S. However, when variability due to species' specialization was factored out, S reduced variability in species N, but only in communities with modest levels of overall absolute variability. Our work demonstrates that species diversity reduces variability of local populations and reduces their risk of extinction.

Spatial and temporal patterns of small stream habitat use by Brook Trout, *Salvelinus fontinalis*, in Northwestern Ontario

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Stream dwelling brook trout populations are widely distributed throughout the coldwater drainage systems they occupy in Northwestern Ontario, including small, tributary streams where they are often the only fish species present. At a watershed scale, brook trout are often found in small streams that flow into larger streams or ponds. These small streams are vulnerable to disturbance from forest management activities because they often do not appear on Ontario Base Maps. Our objectives were to compare the fish community, brook trout population characteristics and habitat characteristics in small (1 km^2 catchment area) and large ($>30 \text{ km}^2$ catchment area) streams and to monitor brook trout movement within and between the two streams. Fish communities were sampled using electrofishing in four small streams and the larger streams into which they flowed. Larger streams had higher mean fish species richness (5.3) than small streams (3.75). Brook trout length ranged from 24-241 mm in large streams and 15-199 mm in small streams where smaller fish were relatively more abundant. Small streams were consistently colder and offered more cover than the larger streams. Two-way weirs were installed at the mouths of the small streams to monitor movement into and out of these streams. Movement of brook trout through the weirs was more frequent in the spring and fall. Movement direction tended to be upstream in the spring and downstream in the fall and was associated with rainfall and stream flow increases. Our results highlight the importance of small streams as brook trout habitat.

The effects of spatial and temporal variation in pH, alkalinity, dissolved organic carbon, and substrate on benthic invertebrate communities in Precambrian Shield lakes

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Use of macroinvertebrates as water quality indicators is limited by a lack of information about their community-based responses to environmental variation over space and time. This study proposes to address this issue through an investigation of the spatial and temporal variation of benthic invertebrate communities in a series of lakes, and its relationship with variation in chemical and physical variables in the water. I will focus on 17 acid-sensitive lakes on the Precambrian Shield that have been sampled since 1988. In particular, the study will evaluate pH, alkalinity, and dissolved organic carbon (DOC), chemical variables strongly affected by acid deposition and whose stability, in the case of pH and alkalinity, is vital to the survival of benthic invertebrate populations. The study will also consider variation in substrate, an important determinant of benthic community structure. Changes in benthic invertebrate community structure will be evaluated on both a spatial and temporal scale. Multivariate statistical analyses will be used to further determine whether a relationship exists between benthic communities and environmental variables. This study will begin to build a foundation of information about DOC interactions, and provide us with more concrete evidence of the relationship between invertebrates and pH and alkalinity.

What do web vibrations tell widows?

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Male courtship provides species recognition cues and/or information about male phenotype used in female mate choice. Male widow spiders transmit vibratory signals through female webs during several hours of courtship. Signals may function to: 1) distinguish males from prey. Females are larger than males and typically respond to web vibration with predatory behaviour. 2) distinguish males from heterospecifics. Mis-matings have been observed, so this would appear to be a risk. 3) signal male quality. Multiple males are frequently observed on female webs. We analyzed the vibratory signals of males of three species, *Latrodectus hesperus*, *L. hasselti*, and *L. mactans*. Signals were compared between species to determine whether they contained species-specific components. To determine whether females might derive information about male phenotype from signals within each species, we analyzed variation in signal components as a function of male metabolic rate, body size and weight. We discuss the implications of this work for the possible roles of pre-copulatory signals in mating behaviour and in speciation within this group.

Mitochondrial DNA and nuclear DNA telling different stories: Evidence from the black-tailed brush lizard

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Due to its long and narrow physiography, the Baja Californian peninsula of northwestern Mexico provides an excellent place to study phylogeny as it relates to geography. A number of studies on mitochondrial DNA reveal concordant genealogical patterns among a wide variety of species. We compare differences in patterns between nuclear DNA and maternally inherited mtDNA in the Black-Tailed Brush Lizard (*Urosaurus nigricaudus*). This common lizard is distributed throughout the peninsula of Baja California. We use nucleotide sequences from the cytochrome b and ATPase 6 regions of the mitochondrial genome to determine the matriarchal genealogy of these lizards. Matriarchal lineages differ by as much as 12 % sequence divergence and nodes on the tree are strongly supported. The mitochondrial patterns strongly contrast with nuclear genomic data from several allozyme loci. Allozyme patterns suggest ongoing gene flow across areas where distinct haplotype lineages are parapatric. This finding has implications for the validity of using maternally inherited markers to estimate intraspecific histories, as commonly pursued in phylogeography. It also impacts on the use of maternal lineages to determine the status of species based on mtDNA alone.

Can sexual selection and antagonistic coevolution produce sex difference in autosomal recombination?

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Across a wide range of taxa (65 species of insects, vertebrates and plants examined), sex differences exist in rates of recombination on autosomes. Typically, males have lower rates than females (42 of 65 species). This sex difference has the potential to give insight into how genomes are structured by selection, refine quantitative trait locus (QTL) maps, and identify

chromosomal regions where candidate genes for traits of interest reside. Of the three hypotheses advanced to explain these sex differences, only one explains reversals in the typical pattern of sex differences. This hypothesis states that sexual selection can produce sex differences in recombination by restricting the number of individuals of one sex able to mate to those with particular alleles spread throughout the genome. Such a restriction would select for reduced recombination whenever genes that give a mating advantage are found on the same chromosome. The original proponents of this hypothesis were not specific about how sexual selection can lead to reduced recombination. I will describe how the dependence of sexually selected traits on condition can clarify this hypothesis. I also will explain how sexually antagonistic coevolution, where male and female interests for which alleles are preferred at particular loci, can increase the sex difference in recombination. Insects that exhibit reversal of typical sex roles, so that females are more competitive for mates and males are more choosy, provide a natural test of the sexual selection hypothesis. I will describe such tests in Mormon crickets (*Anabrus simplex*) with sex role reversal.

Why are honeybee (*Apis mellifera*) drones so large? Comparing fitness components of individuals varying in size

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Honeybee colonies preferentially rear drones in large cells, suggesting that large drones have some reproductive advantage over small males. However, the advantages of large size are unclear. One possibility is that large drones produce superior spermatozoa that out-compete those of smaller males for access to the queen's eggs. Alternatively, large drones may be able to take longer or more mating flights. While earlier experimentation found no difference in the flight characteristics of large and small drones, a positive association between drone size and spermatozoa number was reported. This study verified these findings, and expanded on the aforementioned research by also looking for differences in the length of spermatozoa. Large and small drones were obtained from four colonies with laying workers. Newly emerged drones were marked over a four-day period and placed into a queenless colony. Drones were removed from this colony at 11, 14, 17, 20, 23, 26, 29, and 32 days of age. Once collected, the seminal vesicles were removed and the number of spermatozoa was estimated using a haemocytometer. Small quantities of sperm were then placed on glass slides and air-dried. The length of spermatozoa was measured using an imaging analysis system. The effects of drone size, age, and colony of origin on spermatozoa characteristics are discussed.

Role of mate attendance by male common Eiders (*Somateria mollissima*) within and between nesting colonies

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Birds display a variety of mating systems (promiscuity to monogamy) which involve varying degrees of male attendance. At a Common Eider duck colony in the eastern Canadian arctic, males are seasonally monogamous but appear to exhibit behavioural variations within this mating strategy. First, unlike at other colonies within the circumpolar range of eiders, males come ashore, post-copulation, and attend females during nest searching, laying and early

incubation. Second, because reproductive success varies among pairs throughout the colony, theory suggests that individual males should adjust their attendance behaviour to maximize reproductive success. I am investigating whether and why attendance behaviour varies among colonies and among males within a single colony. Two working hypotheses guide this research: namely that male attendance behaviour varies due to the need for mate guarding (assuring paternity) and/or nest guarding (helping the female search for a quality nest cup and secure it). These hypotheses predict that, in observational and experimental studies, attendance behaviour by males should (1) vary with the quality of the nest site, the probability of nest failure, and time elapsed during laying (as more eggs are laid and incubation starts) and (2) female reproductive success should decrease when males are experimentally removed. Together, the results of these studies at different scales, will allow an assessment of the function of variable male attendance of laying and incubating female eiders.

The maintenance of sex in coexisting sexual and clonal minnows (*Phoxinus* sp.)

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Sex, especially in anisogamous species, is a less efficient method of reproduction than asex. Explaining the widespread occurrence of sexual reproduction is, therefore, an intriguing undertaking. The Red Queen hypothesis invokes the idea that parasites should be under strong selection to infect the most common host genotype. The most common host genotype among coexisting sexual and asexual individuals will most likely be an asexual genotype. There are over 50 known vertebrate species that reproduce asexually. Hybrid dace (*Phoxinus eos-neogaeus*) arose via hybridization between Northern Redbelly dace (*Phoxinus eos*) and Finescale dace (*Phoxinus neogaeus*). The hybrids are all female and reproduce via gynogenesis, an asexual process whereby ova require sperm to stimulate embryogenesis, although syngamy of ovum and sperm does not occur. Hybrids always coexist with one parental species. No two hybrid lineages (i.e. clones) have been found coexisting, and only a single clone has ever been identified in any given study. I will address the question, do Red Queen dynamics between *Phoxinus* and their parasites help balance the cost of sex in sexually reproducing *Phoxinus*? I will also investigate alternative ecological hypotheses for the distribution and abundance of hybrids.

The Spiny Devil Katydids, genus *Panacanthus*: Evolutionary analysis of acoustic behavior and morphological traits

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A cladistic analysis and systematic revision of the genus *Panacanthus* accompanies the description of three new species, with calling songs reported for four species. The evolutionary origin of spines is considered as a defensive mechanism in *Panacanthus*; both morphological and behavioural (i.e. acoustic) traits allow inferences about relationships. Phylogenetic analysis produced one most-parsimonious cladogram 82 steps long, with CI= 0.84. *Panacanthus cuspidatus* and *P. pallicornis* (formerly *Storniza* Walker 1869, *Martinezia* Bolivar 1881) are properly incorporated in *Panacanthus*. On morphology *Panacanthus* is more related to the neotropical *Copiphora* and *Lirometopum* than to the Old-World *Lesina*. Character analysis reveals that in *Panacanthus* the ancestral condition of calling song resonance (the production of musical sounds) has given rise to a more nonresonant (transient) stridulation. A correlation

between the production of more complex sound waves and spinous protection of the body (especially the pronotum) is noted. Since early workers grouped *Panacanthus* with other spiny genera, based on pronotal morphology, we present a critique of the evolutionary and ecological implications of the development of defensive spines in this genus. This approach may be applied to other taxa using a similar protective mechanism. We advise against arrangement of the pronotal, cephalic and femoral armature as a homologous characteristic across subfamilies. Several pronotal processes and modifications evolved independently in other genera of Conocephalinae, Hetrodinae, Pseudophyllinae and Phaneropterinae. The pronotal structure of *Panacanthus* is unique and may be taken as a synapomorphic characteristic of all its species and as an autapomorphic feature of the genus.

The influence of polyploidy on the fitness of yeast across a range of environments

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Polyploidization occurs in several taxa with varying degrees of success and appears to have played a role in the evolutionary histories of most eukaryotes. How do tetraploids compare to diploids with respect to fitness and niche breadth? Are these differences explained by the amount of variation that exists in neodiploid, neotetraploid, evolved diploid, and evolved tetraploid populations? Isogenic diploid and tetraploid populations of the yeast *Saccharomyces cerevisiae* were maintained for 500 generations in a complete nutrient medium at 30°C with selection only for the maintenance of DNA content. Fitness across a range of environments and relative levels of variation were estimated for each of three neodiploid, neotetraploid, evolved diploid, and evolved tetraploid populations. Preliminary results suggest that diploids are more fit than tetraploids when grown at 30°C, but that the diploid advantage disappears in 25°C and 37°C environments. This work may shed some light on the factors that govern the establishment of polyploids, especially along the perimeter of diploid population ranges.

Carnivore induced density- and trait-mediated indirect effects cause changes in plant resistance to herbivores

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Indirect effects are interactions between two species that occur due to the intervention of one or more species. These effects are determined both by changes in density and traits of the intervening species, such as behaviour, morphology and physiology. Such indirect effects are known to be important in many ecological systems. Their influence on plant resistance to herbivores, however, has never been tested. I present results demonstrating that the presence of the predator *Podisus maculiventris* causes changes both in the density and behaviour of the herbivore *Manduca sexta*, and these density- and trait-mediated indirect effects result in changes in resistance in *Solanum ptychanthum*. In the field, *M. sexta* larvae feeding on *S. ptychanthum* in the presence of lethal *P. maculiventris* cause 62 % less damage relative to control plants, whereas the presence of non-lethal predators caused a 38% decrease in damage relative to controls. In the field, lethal *P. maculiventris* caused much higher mortality than did non-lethal predators. Behavioural observations, however, showed that the presence of a predator (either lethal or non-lethal) causes *M. sexta* to feed less and spend more time in defensive postures. Consequently, both lethal and non-lethal predators indirectly caused significant effects on herbivore resistance traits. This affected resistance to subsequent herbivores feeding on the plant, as seen by *M. sexta* lab performance bioassays. Furthermore,

assays of several defensive proteins revealed that carnivore presence indirectly suppressed plant resistance. Overall, the results from this experiment indicate that both density- and trait-mediated indirect effects are important for plant resistance.

The Evolution of lactase persistence

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Most humans are lactose intolerant: the production of lactase in the small intestine declines shortly after weaning. In some individuals however, childhood levels of lactase persist into adulthood. This lactase persistence is inherited in a Mendelian fashion as a dominant trait and varies in frequency among populations. The consensus view is that humans began consuming significant quantities of milk into adulthood only after the domestication of animals ~10,000 years ago. Populations who relied on milk as a main nutritional source co-directed their own biological evolution by creating a selection pressure for the lactase persistence allele. This process of gene-culture coevolution has resulted in the present distribution of worldwide lactase phenotypes, with high frequencies of lactase persistence being found only in populations who have a long history of fresh milk consumption into adulthood. Previous studies have demonstrated that selection has played an important role in establishing the high frequency of lactase persistence in Northern Europe. More recently, a mutation was identified that is likely to be the variant that causes lactase persistence. The present study finds no evidence of strong selection for lactase persistence in a sample of North African Berber. In all but one of the 100 Berber samples, the putatively causal variants occurred on a Northern European genetic background. The one exception forces us to consider the possibility that the lactase persistence allele arose and increased in frequency independently in non-European populations, a hypothesis that meshes well with recent evidence of an independent cattle domestication event in Africa.

Nutrient limitations on plant growth and implications for herbivore forage in arctic marshes

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Marshes grazed by snow geese on the Hudson Bay coast were examined to determine whether a switch from nitrogen- to phosphorus-limited plant growth occurs between the salt marshes and adjacent freshwater marshes. Experimental plots, which were fertilized with N and P in a factorial design, were set up in both salt and freshwater marshes, and plant biomass and tissue nutrient content responses to the fertilization treatments were measured. In the salt marsh, it was found that, when added alone, N and P had non-significant effects on aboveground biomass. However, there was a significant increase in biomass when the nutrients were added together, with nitrogen being the more important element determining the response. In contrast, in the freshwater marsh, the addition of N did not significantly increase aboveground biomass, although there was a significant effect of P additions. No NP interaction was observed in the freshwater site, while in the salt marsh, P became limiting when N availability was supplemented. N:P stoichiometry results also indicated that plant growth in the salt marsh is mainly N-limited, while that in the freshwater marsh is P-limited. In recent decades, destructive feeding by geese has destroyed much of the salt marsh, and the geese have been forced to forage in the freshwater site. This difference in nutrient limitation between the salt and

freshwater marshes means that vegetation available for geese during the post-hatch period is now P- rather than N-limited.

Modeling Mercury (Hg) Mass Balances and Accumulation in Biota in Lakes of the Muskoka River Watershed

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Mercury emissions into the atmosphere from anthropogenic sources have increased Hg levels in aquatic systems in Ontario, resulting in elevated levels in many fish populations. Because this has resulted in human health concerns, it is imperative to understand the factors controlling Hg cycling in the environment and bioaccumulation in fish. In the atmosphere, Hg disperses 1000's of kilometers from point sources before it is deposited on lakes and surrounding watersheds. Although Hg deposition is relatively uniform over large areas, Hg levels in fish vary widely across regions. The relationship between Hg input to lakes and levels in fish is unknown, yet it is important to know what effects emission reductions will have. Dissolved organic carbon (DOC) plays a key role in Hg cycling in aquatic systems because Hg binds to, and is transported by, humic substances. Wetlands are the principle source of DOC in boreal ecosystems, so the extent and nature of wetlands in a watershed controls DOC levels and may thus control Hg fluxes into lakes. We are testing the hypothesis that Hg concentrations in fish are directly related to Hg input to lakes. DOC flux models and a GIS-based model previously derived will be used to develop Hg mass balances for 859 lakes in the Muskoka River watershed. Hg concentrations in fish from a number of lakes are available from the Ontario Sport Fish Contaminant database. Fish Hg levels will be compared with Hg input levels. Using this information, predictions of fish concentrations for the rest of the region will be made and tested. This work may be useful to resource managers and environmental policy makers concerned with protecting aquatic systems and human health. The project will result in a GIS-based approach that potentially permits predictions of Hg levels in lake water and fish from a small number of easily obtained parameters.

Modelling gap formation, neighborhood interactions and self-organization in a forest

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Gap formation in forests is a natural process that is believed to be the key to the maintenance of biodiversity in these ecosystems. Gaps present opportunities for seedling establishment for species which otherwise would be out-competed by dominant species. Gap formation begins with the death of a tree; however, gaps can be of different sizes, depending on the neighbourhood effects of falling trees. Gap formation is also strongly affected by external perturbations like wind, disease and fire. We are working with a cellular automata model proposed by Solé and Manrubia (1997), which attempted (but did not sufficiently succeed) to capture a very interesting observation: gap-size distribution in real forests displays an invariant scaling property, suggesting that forests are in a self-organized, critical state. We improve the implementation of the Solé-Manrubia model, and in addition, show interesting effects of both cell geometry and neighbourhood definition on model dynamics. We discuss the implications of this for cellular automata modeling in ecology.

Solé, R. and Manrubia, S.C. 1997 On forest spatial dynamics with gap formation. *Journal of Theoretical Biology* 187:159-164.

Fertilized female Japanese Quail weight the costs of sexual harassment differently than unfertilized females

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We examined the hypothesis that female Japanese quail avoid the costs due to physically harmful mating when no longer in need of a gamete. Females laying fertilized eggs at the time of testing avoided males and aggregated with other females to a greater extent than females laying eggs that were not fertilized. We interpreted these results as consistent with the hypothesis that once female Japanese quail have secured the benefit of fertilization, they are more likely to evade the costs of sexual harassment.

Exurban development and the nesting success of birds breeding in hardwood forest fragments.

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Housing developments within or adjacent to isolated forest fragments may produce changes in the bird community including reduced abundance and species richness of interior-nesting bird species. Increased rates of nest predation may be partially to blame for these changes. We studied nests of Wood Thrushes (*Hylocichla mustelina*), Ovenbirds (*Seiurus aurocapillus*) and American Robins (*Turdus migratorius*) breeding in 16 woodlots in southern Ontario. Wood Thrushes experienced significantly increased rates of brood parasitism (83% vs. 33%) and parasitism failure (23% vs. 3%) in exurban sites (9-18 houses within 100m of woodlot edge) compared to rural sites (0-3 houses within 100m of woodlot edge). Ovenbirds experienced non-significant increases in brood parasitism in exurban sites compared to rural sites (50% vs. 26%). Neither species experienced changes in seasonal fecundity between treatments. American Robins experienced significantly increased rates of nest predation (48% vs. 25%) and significantly reduced nesting success (94% vs. 97%) in exurban sites compared to rural sites. American Robins breeding in rural woodlots could expect to produce more than twice the number of female fledglings per season as those breeding in exurban woodlots. Compared to rural sites, exurban sites had significantly more edge per unit area (127.8 ± 8.8 m/ha vs. 170.0 ± 10.3 m/ha) and significantly less core area (3.95 ± 0.83 ha vs. 0.43 ± 0.27 ha), since houses were often embedded into woodlot edges. Changes in reproductive parameters may be due to changes in patch variables rather than the addition of houses. Housing developments should be sited away from woodlot edges to minimize changes to physical and ecological properties of woodlots.

Testing a parsimonious, evolutionary explanation for regional-scale variation in species richness.

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Regional patterns in species richness are the manifestation of both ecological and evolutionary processes. Surprisingly few evolutionary hypothesis for such patterns have formally been tested. We evaluate the following prediction that is based on "first-order" evolutionary principles: localities exhibiting environmental conditions that have been spatially common

through time will harbour more species than localities exhibiting rare conditions. The underlying hypothesis is that differential opportunities for speciation among rare and common environmental conditions gives rise to regional variation in diversity. We tested the prediction using an ideal dataset concerning freshwater diatom communities. Temperate lakes in eastern North America are, and have been, predominantly circum-neutral in pH, and oligotrophic to mesotrophic in nutrient status. Diatom species richness measured at the lake scale varied from 26 to 106 across 239 lakes, and showed a unimodal relationship with pH, and a decreasing envelope relationship with increasing nutrient levels (total phosphorus, TP). We assigned each lake an appropriate "commonness" value vis-à-vis pH and TP, and tested whether maximum lake richness increased with increasing commonness. Testing this prediction required non-traditional statistical approaches, including randomization procedures that detected boundary relationships, and quantile regressions. We found strong evidence in support of our prediction for both environmental variables. Differential availability of environmental conditions through space and time provides the most parsimonious explanation for regional-scale variation in freshwater diatom species richness.

Identifying limiting factors for fish species at risk (SAR) in the Sydenham River

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The passage of the Species at Risk Act (Bill C-5) has created the need for improved scientific tools to assess and monitor species at risk (SAR), identify factors that limit their distribution and abundance, and identify their critical habitat requirements. We are using the Sydenham River as a test case to address these needs. The Sydenham is inhabited by 82 fish species, 8 with COSEWIC designations. Our objectives are to identify efficient methods for sampling fish SAR, and to determine the factors that limit their distribution. Fishes were sampled from fifty sites throughout the watershed using a variety of gear types. Corresponding measures of water chemistry, geomorphology, and land use were also made. Backpack electrofishing and seine netting were more efficient at sampling fish SAR than backpack electrofishing alone. Five of the 8 COSEWIC-listed species were collected and three of these, (*Ammocrypta pellucida*, *Fundulus notatus*, *Etheostoma blennioides*), have extended their range. Canonical correspondence analysis was used to determine species -environmental relationships.

Social and nesting behaviour in the large carpenter bees Xylocopa

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Members of the bee genus *Xylocopa*, the large carpenter bees, are traditionally considered solitary. Solitary bees are characterized in part by a limited acceptance of intruders in their nests. Observations, however, suggest that some species are tolerant to conspecifics, suggesting an initial step towards the evolution of sociality. The construction of branched nests is also a factor leading to social interactions. In branched nests, females must share a common nest entrance and thus limited tolerance is required. It can therefore be expected that tolerant species will coincide with branched nests, while intolerant species will be found in unbranched nests. A comparative approach was used to examine the evolution of branched nests and conspecific tolerance. In such an approach, traits are mapped onto an existing phylogeny and analyzed for possible trends. Due to conflicts between existing phylogenies, we created a new total evidence phylogeny. This phylogeny unambiguously accounts for 22 of the 53 commonly

recognized subgenera. These analyses suggest that construction of branched nests and tolerance to conspecifics are ancestral traits in the large carpenter bees. Further, it is shown that there have been multiple reversions in both these traits. Finally, this information is used to make predictions for *Xylocopa virginica* in Ontario.

Characterizing expression of self-incompatibility alleles in *Arabidopsis lyrata*

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Self-incompatibility (SI) is a system used to reduce inbreeding depression in many plant genera. Strong frequency dependant selection maintains a high number of alleles for SI types. Systematic analysis of the evolutionary relationships between alleles requires knowledge of the sequences of a large number of SI alleles. The SI locus of the Brassicaceae is a tightly linked group of multi-allelic genes that determine the SI phenotype of the plant. New alleles at the locus are normally discovered by PCR screening, using conserved regions of the genes. The gene that determines stigma specificity, SRK, is a membrane-bound receptor kinase, and has high sequence similarity to many other genes of this type. In order to determine if a newly amplified sequence is linked to the self-incompatibility phenotype, several controlled crosses must be performed and scored. Identifying the tissue-specific expression pattern of new alleles and comparing it to the expected gene expression pattern for SI genes enables quick identification of new alleles that are likely to be involved in SI phenotype. This method was tested using several alleles in *Arabidopsis lyrata*, a self-incompatible member of the Brassicaceae

Can sex-specific life history traits be predicted in un-sampled populations of yellow perch?

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Effective management of living organisms requires detailed information on life history traits (birth rate, growth rate, mortality rate, maturation age & size, lifespan) of the populations in question. These parameters are often difficult to measure. Yellow perch (*Perca flavescens*) are valued as an important commercial and recreational fishery, as well as a vertebrate model study organism. Population data was obtained for yellow perch from >80 Ontario lakes in an attempt to develop predictive relationships for life history traits with more easily measured variables. Life history traits could be predicted from other population data (e.g., maturation age from the percent of fish mature at a given age) to enable estimation of these parameters in small datasets. In addition, early growth rate and maximum size could be predicted from lake surface area and indices of lake productivity. Maturation size was related to estimates of densities of yellow perch and potential predators. Together with relationships among various life history traits, these results provide a method to estimate parameters influencing maximum sustainable harvest rates in previously un-sampled populations.

**The effects of condition on the ontogeny of sexually dimorphic traits in the ambush bug
*Phymata americana***

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The ambush bug *Phymata americana* exhibits sexual dimorphism in terms of body size and colour pattern. The present study was conducted to determine the extent to which condition (i.e. food availability) influenced age (developmental time) and size (pronotal width) at maturity, as well as the ontogeny of adult colour pattern. We employed computer image analysis software to quantify colour pattern at four different stages (ages) of adulthood. It was found that both condition and sex had significant main effects on adult size. Condition accounted for a significant proportion of variation in developmental time but sex did not. There was no significant interaction between condition and sex with respect to either adult size or developmental time. Both condition and sex had significant main effects on variation in development of adult colour pattern but there was no significant interaction between food level and sex. However, there was a significant interaction between condition and age within individuals. The results demonstrate that sexual size and colour dimorphism persists, regardless of condition, though condition does have independent effects upon these traits. Interestingly, the rate of colour pattern development did not differ between sexes (despite having different absolute values) but the rate of colour pattern development did differ according to condition. These results provide evidence of a condition-dependent, genetic basis for sexual dimorphism in this species and provides a critical starting point for future studies of the evolutionary forces shaping this dimorphism.

Genome replacement and the maintenance of the unisexual lineage of *Ambystoma*

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The unisexual clade of hybrid mole salamanders is comprised of two bisexual species, the jefferson salamander (*Ambystoma jeffersonianum*) and the blue-spotted salamander (*Ambystoma laterale*), as well as all-female nuclear hybrids with varying ploidy levels. It has recently been discovered that the hybrid lineage may be as old as 2-5 million years. There have been conflicting hypotheses concerning the reproductive mechanism utilized that has allowed the lineage to persist longer than any other known unisexual vertebrates. Due to the extremely low variability found in both the isozymes and sequences of these organisms, testing for the presence of mechanisms of recombination have been difficult. This preliminary study utilized newly developed species-specific microsatellite primers to test for the presence of recombination within the egg masses of the unisexuals. Results show the presence of both ploidy elevation and low levels of genetic recombination, indicating that the unisexuals may be utilizing a combination of gynogenetic and hybridogenetic reproductive mechanisms. The successful use of microsatellites in detecting genetic variation between individuals in this system increases the potential for species identification and the ability to estimate population dynamics to levels that were previously impossible.

The evolution of movement behaviour in defended prey

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It is widely recognized that species which possess defence against predators tend to move more slowly and predictably than undefended species. This phenomenon may occur because

defended species are not under such intense selection to avoid predation as undefended species, particularly when fast movement is energetically costly. Alternatively, slow movement in defended prey could reduce the chance of recognition errors by predators. Here we have formally tested these theories for the first time using a system of artificial computer-generated prey, in which individual movement characteristics (step size, time between steps and angular direction) were subject to continued selection by human predators over repeated generations. Defended prey (unprofitable to attack) almost always evolved slower and more predictable movement than undefended prey species (profitable to attack). When prey species were readily distinguishable these differences arose because there was active selection on undefended prey to avoid attack, but no selection on defended prey. When the two prey species were similar in appearance, defended prey were actively selected to move slowly so that they were more readily recognized by potential predators. When the two prey species were morphologically identical, even defended prey evolved rapid movement because it had no other way of avoiding predation.

Acoustic cloaking against eared moths during aerial attacks by the bat, *Myotis septentrionalis*

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The evolutionary arms race between insectivorous bats and moths has fascinated biologists for decades. The singular purpose of the moth's ear (to detect bat echolocation calls) has made this a particularly useful model for study. Due to the simplicity of this sensory organ and the unique qualities of bat echolocation, a spatial sense with which the bat acts both as sender and receiver of information, both systems are popular vehicles for investigation regardless of the arms race that underlies aspects of their evolution. That ears evolved in moths as a direct result of selective pressure by bats is supported by three lines of evidence: they are finely tuned to the frequency ranges of sympatric insectivorous bat communities; are sensitive only to high intensity sounds, and, in almost all species, serve no other function than to inform the central nervous system to initiate evasive flight behaviours. For their part, echolocating, insectivorous bats have three possible means by which to successfully capture eared moths during aerial attacks: through increasing flight speed; by using calls with sound frequencies outside the moths auditory sensitivity, and, by using calls less intense than the threshold required by moths' ears to initiate evasive flight behaviours. Until now, only the first two strategies had been observed. Here we show that the northern long eared bat, *Myotis septentrionalis*, lowers the intensity of its approach phase calls thus 'vanishing' from the moth's auditory experience almost a second before capture.

Micro-heterogeneity of natural aquatic microcosms and the effects on biodiversity

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Environmental heterogeneity is a well established factor promoting biodiversity. Heterogeneity is expressed at various scales; however, there have been no extensive studies examining effects of heterogeneity on species richness at micro-scales. We hypothesized that, by analogy to similar effects at larger scales, greater internal spatial differentiation of habitat conditions enhances species richness. We tested the effects of micro-heterogeneity on invertebrate

species richness and abundance in 49 natural erosional rock pool microcosms on the northern coast of Jamaica. We determined spatial abiotic differentiation within each rock pool by taking measurements of pH, salinity, chloride ion, oxygen, and temperature, within a 5x5cm grid and at different depths, along with size structure of particulate organic matter. Heterogeneity was then expressed as the geometric mean of the standard deviations of these variables. Aquatic invertebrate community data were collected from 1989 to 2002. Richness and abundance were averaged for each pool using these long-term data. Using simple regression analysis we found, surprisingly, that greater local heterogeneity was correlated negatively with richness and positively with abundance. Of the variables examined, heterogeneity in oxygen had the greatest negative effect on species richness. Heterogeneity in Cl had the greatest positive effect on abundance. These results are preliminary and it is possible that other factors (e.g., temporal variability) drive the detected relationship.

Cooperation through interdependence

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Existing theories of cooperation can explain helping among relatives or reciprocating pairs, but it is increasingly being recognized that many behaviours cannot be explained in these terms. Here we show how cooperation is readily established in groups without reciprocity or kinship. We consider a simple two-stage scenario in which individuals first have an option to help others at the expense of their own survival, and are then subjected to a predation process in which their chances of survival increase with group size. We find that altruism is readily established when helping others means that individuals can reduce their own predation risk. We explain this in terms of a 'boomerang effect' whereby the payoff to the altruist is linked to that of its beneficiary. Our results suggest that interdependence between individuals may be an important factor promoting cooperative behaviour.

Historial trends in body growth of select muskellunge (*Esox masquinongy*) populations in Ontario

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Muskellunge (*Esox masquinongy*) management in Ontario has primarily focused on harvest control through minimum size limits, requiring information on the growth potential, responses, and variability of populations. We examined historical muskellunge growth, as recorded in the cleithral bone, in relation to temperature. Growth data were digitally collected from 456 samples from five muskellunge populations, including two populations with larger and longer data sets. Two measures - an index of annual growth and cleithrum size at age eight - were linearly regressed against log-transformed mean daily summer temperatures. There were no significant correlations between temperature and annual growth ($p=0.120$ to 0.762). However, cleithrum size at age eight increased significantly over time (Lake St. Clair $p=0.026$; St. Lawrence River $p<0.0001$); mean temperature and growth over eight-year periods showed a significant but weak relationship for the St. Lawrence River population ($p=0.020$; $r^2=0.055$). Analysis of a significant difference ($p=0.004$) in growth amongst five-year year-class groupings of the St. Lawrence River population showed muskellunge produced from 1975 to 1989 were 9.3% larger than those produced from 1940 to 1959. Temperature has a significant but relatively minor effect on growth of muskellunge, and factors such as prey composition, behavioral

thermoregulation, and handling may override or compensate for this effect.

Characterization of the branchial interaction between lead and calcium in the rainbow trout (*O. mykiss*)

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Characterization of the branchial interaction between lead and calcium in the rainbow trout (*O. mykiss*). Recent evidence has shown that the mechanism of acute toxicity for lead in the rainbow trout is ionoregulatory disruption (Rogers et al., In Press). A component of this toxicity is a disturbance of calcium homeostasis resulting in reduced influx rates and pronounced hypocalcemia. Currently, circumstantial evidence suggests that a Pb/Ca²⁺ antagonism exists. Present studies have confirmed this relationship, as kinetic analysis suggests a competitive interaction exhibiting typical Michaelis-Menten kinetics. In addition, the use of waterborne La³⁺ and Cd, both apical voltage independent calcium channel blockers, significantly reduces the branchial accumulation of Pb while the voltage-dependent channel blockers, nifedipine and verapamil, do not. Pb-induced disruption of Ca²⁺ homeostasis also involves a slower, non-competitive component of Ca²⁺ transport inhibition as Pb does inhibit branchial Ca²⁺-ATPase activity after prolonged acute exposure. Inhibition of activity correlates with gill Pb burden during the same time course.

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Responses to selection on protandry in *Chamerion angustifolium*

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Dichogamy, the temporal separation of gender, is a common feature of flowering plants. Experimental tests of protandry, when male phase precedes female phase, have demonstrated a strong siring advantage for protandrous plants relative to adichogamous plants. However, the evolutionary response to selection for protandry and changes in male-phase duration may be mitigated by the degree of genetic variation for male-phase duration, genetic correlations between male-phase duration and other floral traits, and trade-offs between components of fitness. We detected moderately heritable variation ($h^2=0.27$) for male-phase duration in *Chamerion angustifolium* with a paternal half-sib design. In a selection experiment, two generations of selection shortened male phase duration by 0.76 SD from the parental population to 23.4 hours and lengthened the duration by 2.0 SD to 31.1 hours. This shift in male-phase duration was not correlated with changes in floral size, inflorescence size, or floral display. Although this allows male-phase duration to change freely, we found a trade-off between time allocated to male phase and female phase that may have significant consequences for the evolution of protandry.

On detecting sexually antagonistic coevolution with population crosses

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The results of population crosses on traits such as mating rate, oviposition rate and survivorship are increasingly used to distinguish between modes of coevolution between the sexes. Two key

hypotheses, erected from a verbal theory of sexually antagonistic coevolution, have been the subject of several recent tests. First, statistical interactions arising in between population crosses are suggested to be indicative of a complex signal/receiver system. Second, under sexually antagonistic coevolution females will do "best" when mated with their own males, where best is defined by the weakest response to the signal and the highest fitness. We test these hypotheses by crossing strains generated from a formal model of sexually antagonistic coevolution. Strains differ in the strength of natural selection acting on male and female traits. In our model, we assume sexually antagonistic coevolution of a single male signal and female receptor. The female receptor is treated as a linear preference function where both the slope and intercept of the function can evolve. Our results suggest that neither prediction is consistently supported. Interactions are not diagnostic of complex signal/receiver systems, and even under sexually antagonistic coevolution females may do better mating males of strains other than their own. These results suggest a reinterpretation of several recent experiments and have important implications for developing theories of speciation when sexually antagonistic coevolution is involved.

The effects of forest fragmentation on post-fledging survival and dispersal of a forest songbird

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Many studies have addressed the effects of forest fragmentation on the breeding behavior, fecundity and movement of forest songbirds during the nesting period. However, the effect of forest fragmentation on the post-fledging period has received little attention. One reason why is simply because young birds are extremely vagile and difficult to follow. Hooded warblers have brood division so parents 'split up' and care for a subset of each brood. By radio-tracking attending adults of fledglings from nests within both large (>100 ha), and small (<5 ha) forest fragments, I tested for differences in habitat use due to the sex of the attending adult and/or forest fragment size. I used mark and recapture models to compare the survival rates of the fledglings in relation to their date of fledging, habitat use and parental age. I found fledgling survival did not differ between large and small forest fragments while habitat use was not dependent on forest fragment size or sex of the attending adult. Fledglings cared for by adult females dispersed further than those cared for by males, although all fledglings moved <210 m from the nest during the parental care period. These results suggest that forest fragmentation may not overtly affect the survival or dispersal of fledgling hooded warblers. Although many forest birds are "area-sensitive", my study was the first to test whether the preference for larger fragments occurs because small fragments are detrimental to the post-fledging dispersal and survival of songbirds.

Do pan traps reflect bee phenology?

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Pan traps are a low effort sampling protocol used to collect insects. We examined collection records to determine if pan traps reflect phenological events in populations of bees. Bees were sampled in three locations in Niagara from 10 June to 30 September 2002 and were identified to species. Frequencies of males and females were examined over the course of the field season for species for which enough individuals were collected. Taxa examined were *Ceratina dupla*, *Osmia conjuncta*, *Hylaeus affinis*, *Agapostemon virescens*, *Augochlorella striata*, *Halictus*

confusus, and *Halictus ligatus*. We found that it is possible to infer sociality based on frequencies of individuals in pan trap collections.

The importance of geographic isolation in reproductive isolation between diploid and polyploid *Chamerion angustifolium*

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Genome duplication (polyploidy) theoretically results in instantaneous reproductive isolation between polyploids and their progenitors as a result of strong postzygotic barriers. However, the presence of triploid hybrids in mixed-ploidy populations in nature provides evidence that reproductive isolation may be incomplete. In this study we assessed the role of ecological and geographic differentiation as prezygotic barriers to gene exchange between cytotypes by delineating the range distribution and frequency of occurrence of allopatric and sympatric populations. In the Canadian Rockies, fireweed (*Chamerion angustifolium*) is variable for chromosome number and provides an ideal system to study the influence of chromosome doubling on reproductive isolation. During the summer of 2002, I surveyed fifty-one populations of fireweed throughout Kananaskis Country, Banff and Jasper National Parks. Thirty leaves from each population were collected, ploidy content assessed using flow cytometry and the relative frequency of each cytotype calculated for each population. Forty-one percent of the populations sampled contained only one cytotype (diploid or tetraploid) and a significant relationship was found between the ploidy of allopatric populations and elevation, with tetraploid populations occurring at low elevations and diploid populations at high elevations. In mixed populations cytotype showed no significant relationship with elevation. Triploids were present at a frequency of 0.03 in sympatric populations. These results suggest that geographic differentiation within the contact zone is a strong, but not an exclusive prezygotic barrier to gene flow between ploidy levels.

The evolution of species' geographic range limits

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The geographic range of every species is restricted by a series of ecological and evolutionary factors. The fact of range limits poses a major question: Why doesn't natural selection allow populations at range margins to adapt to their surroundings and spread outward? The gene flow-selection balance (GFSB) model predicts that asymmetric gene flow from large, central populations overwhelms selection in small, marginal populations. An environmental gradient imposes spatially varying selection pressures such that traits conferring high fitness in central environments are under stabilizing selection; but under directional selection in marginal environments, and the degree of local adaptation decreases from central to marginal populations. Marginal populations are in a constant mal-adapted state and, hence; range expansion is constrained. Additional theories such as a lack of appropriate genetic variability at range margins have also been proposed. However, despite the recent surge of theory on the evolution of range limits, there has been little empirical evidence. I am testing the biological importance of current range limit theory to natural plant populations using two coastal dune endemic species, *Camissonia cheiranthifolia* (Onagraceae) and *Abronia umbellata* (Nyctaginaceae). Coastal dune species provide an excellent opportunity for testing range limit theory because they exhibit near one-dimensional geographic ranges as assumed by theoretical models. This system also permits surveys of population demographic and genetic structure and

local adaptation to include a species' entire geographic range. Field surveys of reproductive output and population abundance, chloroplast DNA analysis and common garden experiments are in progress and preliminary findings will be discussed.

Emerging consequences of the sex-biased and trophy-oriented harvest of polar bears

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The harvest of polar bears is an important cultural tradition in Northern Canada. However, the impact of the recent trophy-oriented and sex-biased harvest on the mating system of polar bears is largely unknown. Mark-recapture studies can resolve the demographic consequences but additional tools are needed to characterize variance in reproductive success. The utility of microsatellites for assigning parentage and emerging patterns in the mating system of polar bears will be explored.

The Social Biology of *Halictus farinosus*

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Few sociobiologically relevant data exist for the primitively eusocial halictid bee *Halictus farinosus*. Obtaining these data is important when investigating the origin of social behaviour as eusocial behaviour has evolved within this family at least three times and Halictidae contains species which exhibit varying levels of social organization. Comparisons can therefore be performed between related taxa on the costs and benefits of different levels of social organization. The archetypical eusocial bee phenology in a temperate climate halictid involves a mated queen producing a brood of non-reproductive female workers, who do not produce young, which aid the queen in the production of a second brood. The second brood consists of early emerging males and new queens who emerge a little later. These reproductives mate, and the new queens overwinter and start nests the following year. Over the past two summers I excavated 186 *H. farinosus* nests in northern Utah, obtaining over 1500 bees. Brood productivity per working female ranged from 0 to 14, and the proportion of males in a nest ranged from 0 to 100%. The results of nest contents being measured and dissected suggest that *H. farinosus* does not fit the archetypical eusocial halictid phenology. A high degree of worker mating was recorded, reaching 38% in 2001 with 62% having developed ovaries. In both years nests produced female reproductives before males. Also there is evidence in 2002 of nests being initiated by females produced in the worker brood.

Signal evolution in an artificial world

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It is now widely argued that defended prey have tended to evolve conspicuous ("aposematic") traits because predators more readily learn to avoid defended prey when they are conspicuous. However in his classic text on evolutionary genetics, RA Fisher proposed a very different theory, suggesting that defended prey have evolved conspicuous signals simply because it allows them to be distinguished from undefended prey. Here we investigated how the attributes of defended (unprofitable) and undefended (profitable) computer-generated prey species tended to evolve when they were subject to continued selection by foraging humans. When cryptic forms of both defended and undefended prey were similar in appearance but their conspicuous forms were

not, then undefended prey remained cryptic while defended species evolved their conspicuous form. Indeed in all our trials, defended prey invariably evolved any trait that enabled them to be reliably distinguished from undefended prey, even if such traits were cryptic. When mimicry of defended species was possible, then defended prey evolved unique traits, or characteristics that would make undefended prey more vulnerable. Overall, our work highlights the fact that mutant aposematic forms of defended prey can readily spread from rarity by chance alone, and supports the contention that warning signals are selected to be reliable indicators of defence, rather than to capitalize on any a priori educational biases of predators. If the implications of this study are generally applicable, then the observed psychological receiver biases of contemporary predators towards conspicuous cues may be more of a symptom than a fundamental cause of aposematism.

Advantage of male self sacrifice in redbacks: straight sperm transfer or cryptic female choice?

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Complicity in sexual cannibalism is apparently adaptive for the cannibalized male in the Australian redback spider *Latrodectus hasselti*. Cannibalized males copulate longer than males that are not cannibalized, and copulation duration is positively correlated with paternity. This suggests that longer copulations result in the transfer of more sperm. Alternatively, longer copulations could serve as copulatory courtship and influence cryptic female choice, in which case a correlation between duration and sperm transfer is not necessarily expected. We investigated the relationship between sperm transfer and copulation duration in redbacks to elucidate the mechanism by which cannibalized males achieve a paternity advantage. Copulations were interrupted at three points in the copulatory sequence and sperm release and storage was assessed to determine whether sperm transfer is limited by copulation duration. We found that the paternity advantage enjoyed by males who copulate for longer durations is unlikely to result from the transfer of greater numbers of sperm, as males transfer the majority of their sperm within the first five minutes of copulation. We discuss the implications of these results for understanding sexual sacrifice and mating behaviour in redbacks.

Sentinel mice detect heritable DNA mutations induced by air pollution

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Germline mutation screening at minisatellite DNA loci in Great Lakes herring gulls (*Larus argentatus*) recently showed significantly higher mutation rates in colonies nesting near integrated steel mills than those at rural sites. In addition, mutation frequency was negatively correlated with colony proximity to steel mills. These DNA changes were likely induced by chemical contaminants, but the route of exposure, airborne or aquatic, could not be determined. To address this issue, we exposed sentinel laboratory mice to ambient air for 10 weeks at a site near two integrated steel mills, and simultaneously at a rural site removed from point sources of pollution. We then bred the mice and compared heritable mutation rates at expanded-simple-tandem-repeat (ESTR) DNA loci. We found a near doubling in mutation frequency in steel mice, primarily through the paternal germline, indicating that air pollution in industrial areas near integrated steel mills is a significant route of chemical mutagen exposure. In a follow-up experiment, we exposed mice at the same locations, but included additional groups of animals

that received only HEPA filtered (breathable particles removed) ambient air. Preliminary genetic analyses indicate that HEPA filtration reduces induced ESTR mutation frequency in mice exposed to polluted air. Our results suggest that humans and wildlife living near steel mills worldwide may be at risk of elevated heritable mutation frequency through the inhalation of airborne particles carrying chemical mutagens such as polycyclic aromatic hydrocarbons (PAH).

Response of flower visitors to potential competitors and predators

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Studies assessing the effects of predation risk on pollinator foraging behaviour suggest that foragers may change their behaviour in response to perceived predation risk. But competition or novel object avoidance may confound interpretation of predation avoidance in such studies. The frequency of first visits by nectar-feeding insects to four goldenrod (*Solidago canadensis*) inflorescences each with a different experimental treatment was monitored during thirty-minute trials; treatments were 1) a live ambush bug predator (*Phymata americana*) 2) a pinned worker bumble bee (*Bombus impatiens*) 3) a novel object 4) an unmanipulated goldenrod inflorescence. Of 1296 visitors observed, vespid wasps were the most common (52%), followed by halictid bees (30%), muscoid (7%), and syrphid (6%) flies. Although as a group these visitors showed no overall preference for any of the four treatments a species by treatment interaction was observed. Halictids visited the control more often than other treatments and vespids tended to visit the control less often than other treatments. Other response variables (Shannon diversity, time on inflorescence, and proximity to objects at departure) did not differ among treatments. Syrphid flies on the predator treatment only, showed a negative correlation between time on the inflorescence and departure distance from the predator, suggesting that close predator proximity during long foraging bouts effect departure decisions. Overall, flower visitors (except syrphids) were indifferent in their responses to competitor, predator and novel object treatments.

Male male competition in redback spiders (*Lactrodectus hasselti*)

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In this study the influence of a rival male on measures of male-male agonistic interactions, courtship behavior and mating success was investigated in the Australian redback spider (*Lactrodectus hasselti*). Upon sexual maturity males abandon home webs in search of females. Mate search is very risky for males (83-90% mortality) so an encounter with a female is very valuable. Upon arrival to a females web a male may encounter up to 6 rivals (median=2). Given the high cost of not mating and low probability of finding another mate I predicted that fighting would quickly escalate between rivals, competitive abilities would vary as a function of male size relative to his competitor and males would scramble to copulate quickly to avoid usurpation. The results suggest that a trend existed for larger males to be more aggressive to smaller males, however, not much energy was invested in agonistic behavior. Also, discovered was that smaller males made first contact more often than larger males in mismatch size trials and gained greater mating success (opposite to what was expected). In two male trials, males scramble to copulate quickly compared to single male trials. Although our results suggest that in mismatch trials smaller males gain a greater mating success there may be benefits for the larger males that opt to court longer. Mating contests in *L. hasselti* appear to be a game where

females set the rules but males must always assess their rivals and adopt a strategy dependent on their own relative condition.

The effects of an invasive invertebrate predator, *Bythotrephes longimanus*, on zooplankton communities recovering from acidification.

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Freshwater ecosystems worldwide are endangered by the stresses imposed by human activity. During the past century, sulphur dioxide emissions resulted in the acidification and biological impoverishment of thousands of lakes in North America. International agreements have resulted in emission reductions, improvements in lake pH, and subsequent biological recovery of some lakes. Biological recovery, however, may be influenced by additional stresses, such as the invasion of exotic species. *Bythotrephes longimanus* is a large predatory cladoceran that invaded the Great Lakes in the 1980's from Eurasia. It has since spread into many Canadian and American inland lakes. A field experiment was conducted to test the effects of the invasion of *Bythotrephes* on recovering zooplankton communities in Killarney Park near Sudbury, Ontario. Experimental enclosures were deployed in Kakakise Lake and consisted of 1-m diameter, 8-m deep clear plastic bags, suspended from a wooden frame at the lake surface. The experiment had two treatments: *Bythotrephes* (presence, absence) and zooplankton community (recovered, non-recovered). Total zooplankton abundance decreased in both the recovered and non-recovered enclosures that received the *Bythotrephes* treatment. Several acid-tolerant and acid-sensitive species were differentially affected by the invasion of *Bythotrephes*, depending on what stage of recovery the zooplankton community was in. This suggests that *Bythotrephes* may impede recolonization of acid-sensitive species and decrease acid-tolerant species which sustain zooplankton abundance in acidic conditions. These results will have important implications for the management of recovering lakes and invasive species by providing insight on the effects of an invasion as an additional obstacle to biological recovery.

Songs of the Savannah Sparrow (*Passerculus sandwichensis*): structure and geographic variation

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Song structure and the pattern of geographic variation in Savannah Sparrow (*Passerculus sandwichensis*) were examined at the song and syllable levels. Songs of 153 individuals from 8 populations in Ontario were analyzed with respect to the sequences and similarity of syllables. Except for one male at London, males sang one song type. Two geographic song groups (song themes) appeared and were distributed with clear intergrade patterns from Exeter. Any geographic pattern of song type sharing between populations did not appear. However, syllable dissimilarity among males within and between populations significantly increased as map distance increased. The cluster dendrogram based on syllable similarity between populations closely linked neighboring populations. The final clustering resulted in the populations being separated into two groups, songs of three northern populations and five southern populations, which were predicted from the distribution of song themes. It is suggested that geographic variation of Savannah Sparrow songs is gradual with distance rather than distinct, and two distinct song traditions exist in this study area.

The effects of ecological traits on molecular rates of evolution in fishes

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A general trend of an inverse relationship exists between rates of molecular evolution and body size. This relationship has been shown empirically for mammals and birds, but has never been confirmed for fishes. The underlying mechanism that is governing this trend has also been debated with two hypotheses having been proposed and heavily tested. These hypotheses are the generation time effect and the metabolic rate hypotheses. To test these two hypotheses, different ecological and life history traits have been used as surrogates. This study looked at the possible link between such ecological traits and rates of molecular evolution in fishes. The traits used were body size and mass, median depth of habitat and longevity. Recent literature recommends the use of independent species contrasts to eliminate phylogenetic bias and this method was employed to avoid this possible inaccuracy in analyses. For this study a limited phylogeny of 104 fish species encompassing 13 orders and 39 families produced 21 contrasts for which both sequence and appropriate ecological data exists. Using relative rate tests for the cytochrome c oxidase I (COI) portion of the mtDNA genome, analyses were conducted to test for association between these rates and the four different ecological traits. No significant relationships were found for any of the traits used in this study. However, more directed and extensive taxonomic sampling is needed to increase the number of available contrasts lending more power to the statistical tests and allowing generalizations for all fishes.

Does the genus *Bufo* have a South American origin?

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Species of the genus *Bufo* are distributed worldwide and cover most of the major landmasses, including the Americas, Eurasia, and Africa. It has been proposed that the genus arose in South America and then dispersed as a single radiation to the rest of the continents. Conflicting evidence has suggested that the lineage is much older than originally suggested, and that species of *Bufo* were already present in Africa before the final separation of Gondwanaland. It is felt that species radiation in South America and Africa are of equal magnitude, and that *Bufo* has been long isolated in these two areas. If the genus *Bufo* originated in South America, then a phylogeny of the species should indicate a pattern of radiation up through North America, across Eurasia, and then later into Africa. Regions of the 12S and 16S mitochondrial rRNA genes were amplified and sequenced for phylogenetic analysis of 35 species from the family Bufonidae and an outgroup from Hylidae. Phylogenies were constructed using neighbour-joining, maximum parsimony, and maximum likelihood methods. Although the resultant trees had unresolved portions and the radiation patterns are tentative, there is evidence in support of the species relationships within two major clades from North America and Africa.

Mating system regulation in *Chamerion angustifolium* (Onagraceae)

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Plants regulate the proportions of selfed and outcrossed progeny using a variety of pre- and post-zygotic mechanisms. In the perennial plant *Chamerion angustifolium* few selfed offspring are produced despite wide variation in opportunity for self and outcross pollination. The success of outcross pollen has been attributed to strong inbreeding depression; however, under this

mechanism, relative success of self pollen should be constant. In this study we test, experimentally, whether siring success of self-pollen is conditional upon the frequency of self-pollination and if prezygotic factors are also affecting mating systems in this species. Siring success was examined by altering the proportions of self and outcross pollen on stigmas and assessing siring rate with allozyme markers. Prezygotic selection was evaluated by applying either self or outcross pollen and counting pollen tubes at three positions (top, middle, base) on the style at 3, 6 and 24 hours after pollination. Our data suggest that the siring success of self pollen depends on its frequency in the stigmatic pollen load. Specifically, self pollen fertilized proportionally more seeds when a high percentage (75%) was added to the stigma. In addition, pollen tube number did not differ between self and outcross pollinations, regardless of position in the style and time since pollination. Collectively, these results suggest that relative siring success of self pollen may be conditional upon pollen composition on the stigma. This effect cannot be explained by pre-zygotic effects and suggests that inbreeding depression may also be a frequency dependant mechanism of mating system regulation.

The effects of selection and sex-linkage on the evolution of mammalian sperm proteins

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A growing number of genes involved in sex and reproduction have been demonstrated to be rapidly evolving, suggesting their preferential involvement in speciation. The exact mechanism behind this rapid evolution remains unknown, however multiple factors may be contributing to the overall higher divergence of reproductive genes. One factor may be whether reproductive genes are located on sex chromosomes, as due to their hemizygosity in males, sex-linked genes can evolve slower or faster depending on whether most recessive, or at least partially recessive alleles are deleterious or beneficial. We report that genes expressed solely in spermatozoa represent a highly diverged subset among human and mouse tissue-specific orthologs, and provide evidence that four functionally diverse sperm proteins are under strong adaptive evolution. We also test the hypothesis that sperm-specific genes are evolving faster on the X chromosome compared to autosomes due to selection acting on beneficial mutations. Our combined results highlight the molecular actions of such diverse factors as broad-sense sexual selection and chromosomal location acting on a variety of characters involved in mammalian sperm function, which together drive sperm protein evolution at a faster rate than the rest of the genome. Positive Darwinian selection in rapidly evolving mammalian sperm proteins.

Application of Hidden Markov Models in ecology

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The objectives of this research are: (1) to examine the feasibility of applying HMM's in community ecology and (2) compare the success of 'simple' Markov models vs. HMM's in describing and predicting community responses of vegetation along various disturbance gradients. A simple, stationary Markov model is defined by a vector state description and a state transition matrix. They model perfectly the classic Clementsian view of vegetation recovery in time toward a fixed climax. The convergence to a fixed stable configuration, however, is not realistic in vegetation dynamics involving non-stationary transitions or noise. HMM's are in fact

termed hidden because the sequence of states is not observable; it must be inferred by examining the observation sequence. The observation sequence through time (or space) is the result of a doubly embedded stochastic process. We suggest the application of HMM's for two reasons: (1) they can have multiple states with observations that need not converge on a single configuration and (2) the hidden states allow for the consideration of underlying ecological processes. It seems likely that ecological sequences (in time or space) should be manifestations of hidden states that determine observational probability. The hidden states, however, may not correspond to physical conditions, but may be something more general, such as level of disturbance. Of added interest is the likelihood of occurrence of each state at any given point in time (or space). It is thus suggested that HMM's may provide a better explanatory model for community dynamics.

Plant vascular architecture and within-plant spatial patterns in resource quality following herbivory

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Within-plant spatial heterogeneity can influence the performance or preference of herbivores foraging on plant tissues. Such heterogeneity in resource quality may be caused by herbivory itself, when subsequent induced plant responses vary with distance from the site of damage. An important factor mediating induced responses is thought to be the degree of vascular connectedness between different leaves. Previous studies have found that transport of induced compounds is greatest between leaves with the strongest vascular connections. In this study, we used plant vascular architecture as a framework from which to predict induced changes in resource quality for *Lema trilinea* (Coleoptera: Chrysomelidae) feeding on the host plant *Solanum dulcamara*. The systemic pattern of allocation of dye from a capillary tube inserted onto the petiole of the first true leaf and sections of the stem were used to establish vascular connectivity between different leaves. Induced changes in the activity of two defensive proteins and the performance of *L. trilinea* larvae were measured on plants with the first leaf damaged or undamaged by adult *L. trilinea*. Defensive protein activity and larval performance changed significantly on leaves both strongly and weakly connected to the first leaf, evidence against a simple constraining effect of vascular architecture on the movement of induced compounds. Subsequent experiments showed that predictions based on vascular architecture were upheld at low but not high levels of initial herbivory. The amount of damage imposed by an herbivore may therefore interact with plant vascular architecture to determine changes in resource quality following herbivory.

Nitrogen isotopes and bioerosion surveys on the florida reef tract suggest widespread land-based stress on the reefs

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Cliona delitrix is a destructive, bright orange overgrowing boring sponge that kills coral. Previous work has shown that it is a sewage bioindicator. Field surveys conducted with the Coral Reef Monitoring Project in summer 2001 showed that *C. delitrix* and a closely related sponge, *C. lampa*, are widespread and abundant. Colonies of *C. delitrix* were up to 2m diameter. Coverage by these sponges was highest near areas of dense human habitation, and lowest in remote areas. Study of archival videos has allowed us to document, at nearshore sites, a 3-fold increase in sponge colony numbers and almost a 10-fold increase in sponge area, from 1996 to

2001. The greatest increase in abundance, size, and cover from 1996-2001 occurred in the Upper Keys, where the CRMP found the greatest decline in coral cover. Stable isotopic ratios of Nitrogen in sponge tissues range from 4.0-7.0‰, and identify the importance of terrestrial sources of organic matter. The Florida Reef tract lost 38% of its coral cover between 1996 and 1999, as bioerosion increased. These results suggest that bioerosion estimates are an essential part of any reef-monitoring program, and that concerns of land-based threats on reef environments are accurate.

The effects of male display on female fitness in the waltz fly *Prochyliza xanthostoma*

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Studies on the evolution of female preferences for elaborate male displays have begun to focus on the costs rather than the benefits of expressing a preference. Matings with males who exhibit these displays may directly or indirectly enhance female fitness, and considerable evidence supports this view. Alternatively, male traits may evolve in response to sexual conflict and have negative rather than positive effects on female fitness. Understanding the effects of male displays on female fitness is required for a complete explanation of the evolution of female mating biases. Males of the waltz fly *Prochyliza xanthostoma* exhibit two exaggerated displays; greater head elongation than females and a stereotyped courtship sequence. I investigated the relationship between these male displays and female fitness. Both direct and indirect benefits were assayed. Males were mated to two females and their offspring were similarly mated in order to measure both female and offspring fitness. The results are expected to shed light on the effects of male displays on female fitness in this species.

Antagonistic pleiotropy, mortality source interactions and the evolutionary theory of senescence

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Most theoretical work on the evolution of senescence has assumed that all individuals within a population are equally susceptible to extrinsic sources of mortality. An influential qualitative prediction based on this assumption is Williams' hypothesis, which states that more rapid senescence is expected to evolve when the magnitude of such extrinsic mortality sources is increased. Much evidence suggests, however, that for many groups of organisms externally imposed mortality risk is a function of an organism's internal condition, and hence susceptibility to such hazards. Here we use a model of antagonistic pleiotropy to investigate the consequences that such interactions (between environmental hazard and internal condition) can have for Williams' hypothesis. As with some previous theory examining "non-interactive" extrinsic mortality sources, we find that an increase in "interactive" extrinsic sources of mortality makes it less likely that an individual will survive from birth to any given age, weakening selection against physiological deterioration at all ages and thus favoring more rapid senescence. However, an increase in interactive mortality sources also typically strengthens selection against physiological deterioration at any age given an individual has survived to that age because it reduces the fitness of low condition individuals more than high condition individuals. These opposing effects are not felt equally at all ages, with the latter predominating at early ages. The combined effects can therefore result in the novel prediction that an increase in interactive extrinsic mortality sources can select for slower senescent deterioration early in life

but more rapid deterioration late in life.

The effects of intra-specific social interactions on reproductive control and ovarian development in *Bombus impatiens* Cresson workers

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In order to understand the nature of eusociality in insects, one must have a good foundational knowledge of their natural history and their mechanisms of reproductive control. It has been shown that *Bombus impatiens* require intra-specific social interactions to trigger ovarian development. However, the detailed mechanisms of this social interaction-dependent reproductive control have not been fully explored. Queen-less groups of two workers were constructed to explore the effects of the duration, sequence and types of intra-specific social interaction on reproductive control and ovarian development. Workers were allowed to interact for various durations, sequences and with workers of different ages. Their ovaries were dissected and mean oocyte lengths were measured. We found that four days is the minimum interaction duration for workers to fully develop their ovaries. The effects of the interaction sequence were significant and a particular sequence of interaction resulted in the longest oocyte length. We found that if a newly emerged worker is interacting with an older worker its ovarian development will be inhibited. We also found the workers that interacted with a hive will develop smaller oocytes than the workers that interacted only with workers. The effects of pollen types were also examined and we found that pollen quality significantly affects ovarian development.

The amazing pulsatile toadfish

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Together with a team of collaborators, for almost a decade we have been studying nitrogen metabolism in the gulf toadfish (*Opsanus beta*) which lives in Florida coastal waters. The toadfish is very unusual, because unlike most teleost fish which excrete ammonia all the time, it is facultatively ureotelic, switching to the predominant excretion of urea under a variety of stressful conditions, including simply being confined in a small chamber with an abundant flow of water. Under these conditions, it excretes its entire day's production of urea in a single rapid pulse. Moving from whole animal physiology through biochemistry, molecular biology, ultrastructure, and endocrinology, we have been gradually been dissecting the nature of this phenomenon, but many questions remain, the most interesting of which are the ecological and behavioural significance of this metabolically expensive strategy.

Gene genealogical analysis reveals multiple hybridizations in natural populations of a yeast

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Cryptococcus neoformans is a major pathogen of humans throughout the world. Using commercial monoclonal antibodies to capsular epitopes, strains of *C. neoformans* manifest five distinct serotypes -- A, B, C, D, and AD. Previous studies demonstrated significant divergence

among serotypes A, B, C and D, which are thought to be haploid. In this study, we investigated the origins and evolution of strains of serotype AD. A portion (537 bp) of the laccase gene was cloned and sequenced from 14 strains of serotype AD. Each strain contained two different alleles and sequences for both alleles were obtained. These sequences were compared to those from serotypes A, B, C, and D. This analysis indicated that each of the 14 serotype AD strains contained two phylogenetically distinct haplotypes: one haplotype was highly similar to the serotype A group and the other to the serotype D group. To explain the origins of these serotype AD strains, genealogical analysis is consistent with at least three recent and independent hybridization events. The results demonstrate that the evolution of *C. neoformans* is continuing and dynamic.

Mating type and mitochondrial inheritance in a fungus

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Uniparental mitochondrial inheritance is ubiquitous in anisogamous species. In isogamous species, mitochondria are typically inherited biparentally. However, a previous study demonstrated that mitochondria was uniparentally transmitted in the model isogamous pathogenic yeast *Cryptococcus neoformans*. To begin understanding the mechanisms, this study examined the potential role of the mating type locus (sex genes) on mtDNA inheritance in *C. neoformans*. Through a series of genetic crosses, we constructed strains that differed only in mating type and mitochondrial genotype. These strains were then crossed to produce sexual spores. Among the total of 206 single spores analyzed from six crosses, all but one inherited mtDNA from the MATa parents. Analyses of mating type alleles and mtDNA genotypes of natural hybrids from clinical and natural samples were consistent with the hypothesis that mtDNA is inherited from the MATa parent in *C. neoformans*. To our knowledge, this is the first demonstration that mating type controls mtDNA inheritance in fungi.

Diploid male production and the population size paradox in common widespread orchid bees

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In the Hymenoptera (ants, wasps, and bees), males are normally haploid, however, sterile diploid males do arise from fertilized eggs that are homozygous at the sex locus, and their production has many negative consequences. A recent study on the population genetics of orchid bees showed that several common and widespread species have very high levels of diploid male production. Diploid males are not expected at high frequencies in large populations, and thus we are faced with a paradox: data on diploid male production in orchid bees is anomalous or orchid bees are far less common than observed. Here we show that natural populations of *Euglossa imperialis* have high levels of diploid male production induced by chronically small effective population sizes, the smallest observed for any natural solitary bee population. We found large discrepancies (95% difference) between the census and effective population size, which actually controls genetic diversity at the sex locus. Our findings show that standard census techniques can greatly overestimate the population size of orchid bees, especially with high levels of diploid male production. Also, we discuss the usefulness of diploid male production and effective population size as parameters to detect pollinator declines.

The evaluation of cytochrome c oxidase I (COI) sequence divergence as a potential means of 'barcoding' life

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The demand for species diagnoses is continually rising, however, taxonomic expertise is collapsing. As a result, researchers are currently investigating alternatives for such evaluations. One potential alternative exists in a DNA-based identification system; a procedure which attempts to employ DNA sequences as taxon 'barcodes'. Although many prospects exist, recent evidence suggests cytochrome c oxidase I gene (COI) could serve as the core of a global bioidentification system for animals. To investigate the potential universality of COI, the present case attempted to employ similar methods of current studies in order to gain insight regarding the taxonomic affiliation of 124 fish species. Overall, the present case supported high taxonomic resolution at the species level, however, inconsistent results with familial assemblages. The reduced capacity at higher taxonomic levels can most likely be attributed to systematic error, and should resolve with proper sampling distribution. Thus, despite the promising results obtained in this study, further investigation is required before determining the capacity of COI to act as a diagnostic tool for fish-at-large.



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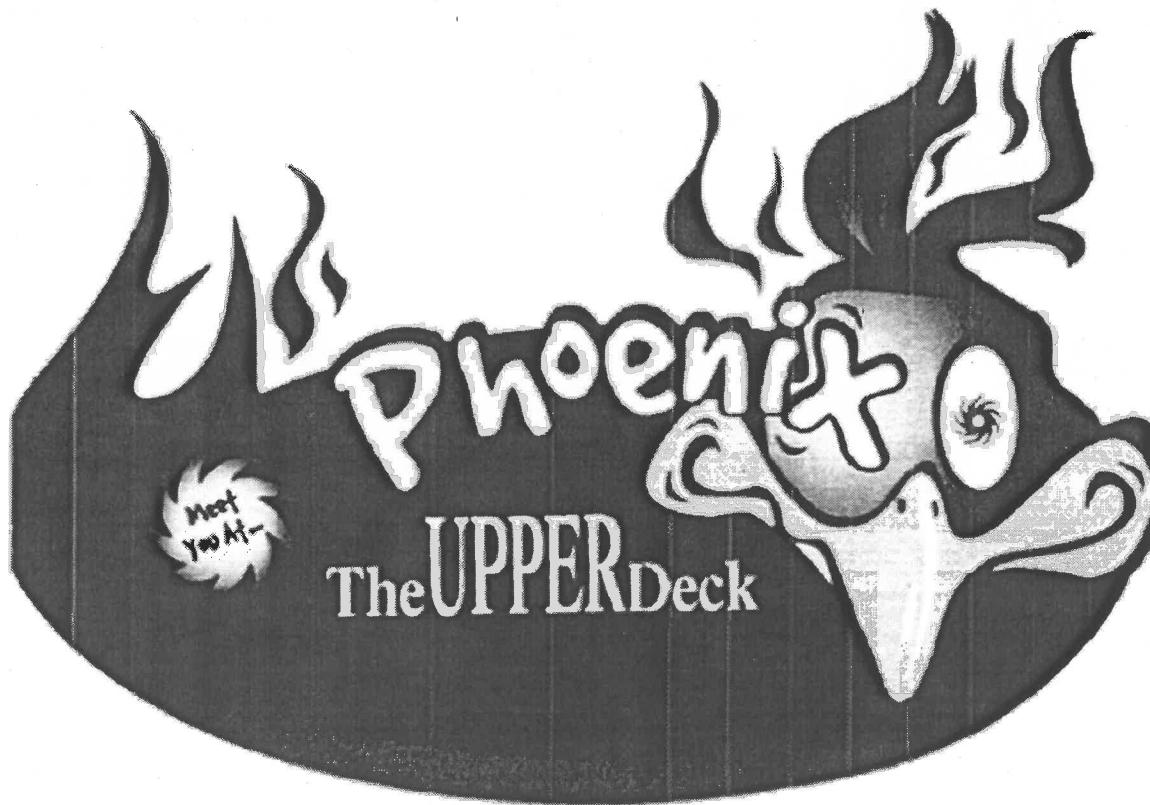


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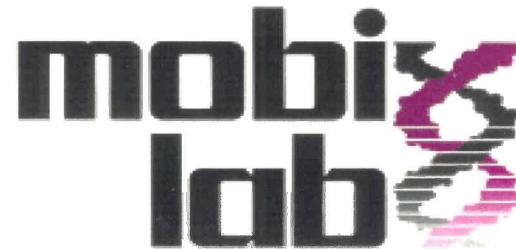
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