Poster Abstracts

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Blooms of the harmful algal species *Heterosigma akashiwo* have risen dramatically in coastal regions, where nutrient supply and flux is highly variable. These blooms have been implicated in massive fish-kills which have led to economic losses in aquaculture operations worldwide, yet there is much debate over the mechanisms and sources of toxicity. *H. akashiwo* has been shown to produce reactive oxygen species, an organic neurotoxin-like compound, and haemolysins, although none of these compounds have been definitively linked to the mortality of finfish. I hypothesize that the ratio of nitrate to phosphate supplied to *H. akashiwo* is the trigger for toxicity and that, in addition to fish-kills, *H. akashiwo* toxins will produce an allelopathic effect. Two strains of *H. akashiwo* were grown in nutrient limited chemostats, at varying nitrate to phosphate ratios, to assess the nutrient regime(s) required for toxicity, allelopathy, and to quantify the toxic compounds. In allelopathy assays, SYTOX Green nucleic acid probe uptake (an indicator of cell death) was less than 10% for cultures of *Rhodomonas salina* inoculated with *H. akashiwo*, regardless of growth condition. Production of haemolysins and hydrogen peroxide were measured and there was no correlation between nutrient ratios, the production of the putative toxins, and allelopathy. These results suggest that *H. akashiwo* is not allelopathic and that the compounds produced by this harmful algal bloom species have an alternative function in the maintenance or formation of blooms.

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The effect of trace-metal limitation on the reactive oxygen species generation of the symbiotic dinoflagellate Symbiodinium (zooxanthellae).

Coral bleaching, the loss of the photosynthetic endosymbionts from corals, is occurring at a rapid rate and is linked to the decline in reef health and global climate change. There is no one mechanism responsible for this decline. The oligotrophic nature of the typical coral reef environment suggests that the algal portion of the coral-zooxanthellae symbiosis may be directly affected by severe nutrient limitation. One mechanism that has drawn attention as a mechanism contributing to coral bleaching is that cells can no longer scavenge the potentially damaging reactive oxygen species (ROS). Many of the enzymes involved in antioxidation are metalloenzymes and therefore sensitive to decreases in the supply of necessary metal cofactors. I hypothesize that low ambient concentrations of dissolved metal co-factors for the metalloenzymes (Fe, Zn, Cu and perhaps Mn) in oligotrophic tropical water restricts the metal-dependent antioxidant defenses in zooxanthellae, and this resource limitation contributes to coral bleaching under high light and elevated temperatures. Nitrogen nutrition was found to affect the growth rate of two Symbiodinium spp (CCMP 2432 and 831) grown in laboratory batch culture. Intracellular ROS, measured by flow cytometry with a fluorescent probe, increased with increasing light levels. These results demonstrate that the growth and general physiology of Symobiodinium can be controlled in the laboratory by varying nutrient supply, and that the production of intracellular ROS can be determined.

Koff, Daniel, Boisvert, Michael J., and Sherry, David F.
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Simultaneous timing of reward production by bumble bees

Recently, we demonstrated bumble bees' ability to time short duration intervals, in the seconds to minutes range (Boisvert & Sherry, 2006; Boisvert, Veal & Sherry, submitted). Here, we examined bumble bees' ability to time two durations simultaneously while foraging. Bumble bees foraged in a low-quality patch comprised of 12 artificial flowers, each providing 2.5 microlitres of 25% sucrose. A fixed duration (either 30 s or 150 s) began with the onset of foraging in the low-quality patch. After the fixed duration elapsed one of two unique high quality flowers (HQFs) provided 40 microlitres of 50% sucrose. Which delay was in force during a foraging bout was randomly determined. Of particular interest was bees' behavior on bouts in which the 150 s delay was in force. If bees learned to time both durations then they would be expected to visit the HQF associated with the 30 s duration before they visited the HQF associated with the longer delay. The probability of visits to the two HQFs should also be expected to peak near the times associated with reward availability, 30 s and 150 s respectively. An analysis of wait times (time elapsed before the first visit to a HQF) indicated that bees visited the HQF associated with the 30 s duration significantly sooner than they visited the HQF associated with the 150 s duration. In addition, the probability of visiting the two HQFs was maximal near the respective delays. The data provide new evidence that bumble bees can simultaneously time two durations associated with reward production.

Paquin, Natalie A.
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Demography and breeding site fidelity in male Golden-winged Warblers (*Vermivora chrysoptera*)

The Golden-winged Warbler (*Vermivora chrysoptera*) is one of the fastest declining passerines in North America and was recently listed as threatened by the Committee on the Status of Endangered Wildlife in Canada. Breeding in early successional habitat, the great majority of the Canadian population resides in south-eastern Ontario. The only known, actively studied Canadian population can be found at the Queen's University Biological Station, where Golden-winged Warbler research has taken place over the last decade. This study compiled demographic data collected over the last five years of research in order to assess the trends in annual return rate as well as in site and territory fidelity in male Golden-winged Warblers. Annual percentages of returning males were not found to differ significantly over the study period. Neither territory nor site fidelity at either scale differed significantly over the same time period.
Factors influencing breeding site fidelity can provide valuable information concerning the dynamics of a local population and the quality of its habitat. This is the first study to examine whether previous nesting success affects annual return rates and breeding site fidelity in male Golden-winged Warblers. However, no significant differences were found between males that were successful and those who failed in the previous year with regards to annual return rate and breeding site fidelity. It is possible that other factors such as site familiarity, overall site quality, and age are also contributing to the probability of return, confounding any clear relationship.

Peso, M., and Richards, M.H.
Brock University
Nestmate recognition in *X. virginica*

Rasic, Gordana, and Keyghobadi, Nusha

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An empirical model system in landscape genetics: the insect inhabitants of pitcher plants

The emerging field of landscape genetics has generated an explosion of work using new tools in addressing questions about the interaction between landscape features and microevolutionary processes. Still, there is a lack of any model systems that can provide general conclusions. Our work will be based on establishing an empirical model system using the specialized insect inhabitants of the carnivorous pitcher plant *Sarracenia purpurea*: the mosquito (*Wyeomyia smithii*), the midge (*Metriocnemus knabi*) and the flesh fly (*Fletcherimyia fletcheri*). Microsatellite loci will be isolated de novo and used to characterize the population genetic structure of the proposed species, starting from a very fine scale (a couple of meters) to a large between-bog scale. Assessing the spatial scale of genetic "graining" will determine the sampling design of future studies, and is critical for the correct interpretation of the experimental results.

Samuelsen, A., and Quinn, J.
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Parent-offspring recognition in smooth-billed anis (*Crotophaga ani*)

Individual recognition between parents and offspring is usually present in avian taxa that occur in high densities, or in which frequency of intraspecific brood parasitism is high. Smooth-billed anis have a unique breeding system, in which multiple females share a joint nest. Subordinates may act as "persistent parasites", laying eggs in the nest of a dominant pair. Consequently, offspring within a nest can be unrelated to each other. Because adults gain no fitness benefits from allocating resources to non-related offspring, ability to identify one's offspring, and adjust parental behaviour accordingly should be selected for. Egg ejection and burial, and preferential provisioning of related young may increase the fitness of individual adults. If sophisticated recognition systems have not yet evolved, indirect ways to estimate relatedness may be present. We will test for individual recognition of eggs (by shape and size) and nestlings (by signature call), as well as for indirect ways to estimate relatedness in anis (e.g. scratching of white calcite coating on eggs, which is correlated with time since laying). Nests of groups in which adults have been identified and parentage has been determined will be audio- and video-monitored. Audio tracks will be analyzed to identify whether there is sufficient variation in nestling calls to allow individual discrimination. Video recordings used in conjunction with nestling growth rates will document whether parents eject unrelated eggs, and preferentially care for related offspring. Furthermore, cross-fostering experiments will be used to test whether un-relatedness can be detected at egg and nestling stages.

Sharma, Arjun, Boisvert, Michael J., and Sherry, David F.
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Do bumble bees remember the location, content and timing of nectar rewards?

Recent evidence indicates that bumble bees can learn the timing of nectar rewards as well as nectar concentrations associated with specific flowers (Boisvert, Veal & Sherry, submitted). Here, we examined whether bumble bees could also remember the spatial location of a high-quality flower (HQF). Bumble bees foraged in a patch of twelve low-quality artifical flowers, each of which contained 2.5 microlitres of 25% sucrose. A fixed 30 s duration began on the first visit to a LQF. Immediately after this duration elapsed, a unique high-quality flower (HQF) provided 40 microlitres of 50% sucrose. Bees completed two blocks of 20 foraging bouts with the 30 s delay. After each block, a test trial examined bees' memory for the location of the HQF

(location-test) or memory for the sucrose concentration typically provided by the HQF (content-test). On the location-test, the HQF was removed immediately following the beginning of the 30 s delay and we recorded the spatial distribution of bees' searches. On the content-test, the HQF provided 40 microlitres of 25% sucrose (rather than the typical 50%) and we examined bees' behavior at the HQF following the delay. On non-test trials, bees' visits to the HQF peaked near 30 s, indicating they learned to time its availability. On location tests bees spent more time searching in the vacant location of the HQF than at other vacant locations nearby. On content tests, bees spent less time on the HQF than they did on the previous trial in which the flower provided 50% sucrose. These data suggest that bumble bees remembered not only the location of the HQF, but also what type of reward it provided and when it provided that reward.

Wilson, John James
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Unmasking hidden butterfly diversity with DNA barcodes

Butterflies are among the most conspicuous invertebrates in terrestrial ecosystems and represent a benchmark group for the assembly of an "encyclopedia of life". We are completing a taxonomic inventory of the Lepidoptera of the Area Conservacion Guanacaste, a reserve in Costa Rica with an estimated 9,600 species of non-leaf-mining lepidopterans. The Nymphalidae make an abundant and attractive component of this diversity, comprising the majority of the Costa Rican butterfly fauna. DNA barcode sequence (COI mtDNA) patterns have flagged numerous records of potential species unknown to science. Distinctive barcode clusters, often supported by ecological or morphological characters, can be used as the basis of 'primary' species hypotheses. In this study we will test fifteen of these hypotheses through genealogical concordance with other molecular sequences. If these clusters represent phylogenetic species and not tokogenetic structure, then this should be corroborated by diagnostic characters in sequences from the nuclear genome.