

## TEA Student Symposium 2017

### Abstracts

**Matt Muzzatti**, University of Guelph

Wing interference patterns (WIPs) - A potential tool for the identification of Sciomyzidae (Diptera) of eastern Canada and the adjacent U.S. states

Wing interference patterns (WIPs) are specific colour patterns developed through thin film interference that appear on translucent insect wings, and are a potential source of useful taxonomic data. The colour sequence in WIPs of Hymenoptera and Diptera is identical to a characteristic sequence of repeated colour bands called the Newton series, and is directly proportionate to wing membrane thickness. WIPs have been used as species-specific taxonomic traits in several Diptera, Hymenoptera, and Hemiptera. For this research project, WIPs were discovered in 84 species across 21 genera of Sciomyzidae (Diptera) from eastern Canada and adjacent U.S. states. Moderate to high interspecific variation and low to moderate intraspecific variation of WIPs was discovered, along with one record of sexual dimorphic WIPs. WIPs of Sciomyzidae are of most value in a taxonomic identification key as a supplemental taxonomic trait to improve difficult couplets, such as those that require examination of internal genitalia.

**Spencer Monkton**, York University

Systematics and biogeography of the sawfly genus *Pristiphora* in the Nearctic

Sawflies are wasp-like plant-feeding insects belonging to the suborder Symphyta, so named for their saw-like ovipositors used to lay eggs in the tissues of plants. Sawflies inhabit all continents except Antarctica, but, in contrast to most living groups, they are most diverse in northern regions, with species richness declining toward the tropics. In the Nearctic, sawflies are recorded from sea level to alpine snowfields and on all parts of the continent, having been collected from as far north as 83.03°N. In particular, the subfamily Nematinae (Tenthredinidae) dominates sawfly diversity in arctic and subarctic regions, where they are frequently the only sawflies present. Larval Nematinae feed on a wide variety of host-plant taxa and employ numerous feeding strategies, thereby occupying a broad range of niches. However, Nearctic sawflies are taxonomically and ecologically poorly known, leaving a substantial gap in our knowledge of northern biodiversity. My PhD research will consist of an integrative study of Nearctic sawfly systematics and biogeography, with a concentration on *Pristiphora*, one of the subfamily's most diverse genera. I will revise the Nearctic species in this genus, continuing the unfinished work of late hymenopterist H. R. Wong, in an effort to catalogue the diversity of these fascinating insects. I also aim to uncover the biogeographic factors dictating distributions of *Pristiphora* in Northern Canada in hopes to better understand the potential responses of these diverse and ecologically relevant insects to a rapidly changing world, especially in that vulnerable region.

**Beverly McClenaghan**, Trent University

Beverly McClenaghan<sup>1</sup>, Erica Nol<sup>1</sup>, Kevin Kerr<sup>2</sup>

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Using DNA barcoding to assess diurnal insect abundance and diversity in agricultural landscapes

Insects represent an abundant food source for other animals in terrestrial systems. The decline of many insectivores, particularly aerial-foraging insectivorous birds, has prompted questions about whether widespread declines in insect populations are the cause of the population decline seen in these predators. Without long-term monitoring of insect populations, we do not know how insect populations have changed. One of the major causes suggested for large-scale insect declines is widespread pesticide use. Pesticides are commonly used in agricultural areas, which are also subject to agricultural intensification. Agricultural intensification has been linked to a decrease in insect abundance and diversity. Our objective was to assess the insect abundance and diversity in agricultural areas, as a measure of food availability for insectivorous birds. Insects were collected using Malaise traps at ten sites in the Peterborough and Kawartha Lakes area. Collection bottles were put on traps at dawn and taken off at dusk to collect diurnal insects only. Insects were collected from April 24<sup>th</sup> – August 28<sup>th</sup>, 2016. Specimens were sorted to morphospecies and representatives of each morphospecies were identified by DNA barcoding. This allowed us to obtain higher taxonomic resolution with less expertise. We identified 1974 different species from 232 families. Insect abundance peaked in early May at all sites while insect diversity peaked between June-July. We have successfully created an inventory of insect diversity that can be used for comparison with other studies and we plan to continue this work by comparing the insect diversity to habitat features.

**Jenny Liu**, University of Guelph

Midges and when they emerge: creating a predictive model of the *Contarinia nasturtii* life cycle

The swede midge (*Contarinia nasturtii* (Kieffer)) is an exotic insect originating from Eurasia, whose feeding has caused a decline of over 60% of Ontario's total canola acreage since 2011. Serious management action must be undertaken to prevent grave ramifications to Canada's \$19.3 billion canola industry, beginning with the development of a reliable forecasting model for swede midge emergence. The objectives of this project are to i) update the development and mortality information for Ontario swede midge populations; ii) revise the current swede midge population dynamics model, entitled MidgEmerge, by incorporating this new information; and iii) use the model to determine environmental conditions for swede midge outbreak. Temperature-dependent rates of development, mortality, viability, and incubation of various swede midge life stages will be elicited using a series of miniature growth chambers at the Saskatoon Research & Development Centre, Agriculture and Agri-Food Canada. The regressions resulting from these data will be incorporated into the MidgEmerge model, which will then be used to compare environmental data between the site of a swede midge outbreak and a site with no outbreak. Including the updated developmental rates is expected to greatly improve

the model's accuracy, and will aid in developing an effective integrated pest management strategy that could help control the swede midge before it severely impacts Canada's main canola-producing regions.

**Kyle D. Doward**, Western University

Where do Ontario True Armyworms Come From? Using stable Hydrogen Isotopes to Study the Origin of *Pseudaletia unipuncta*

In Canada, many lepidopteran pest species, such as the true armyworm (*Pseudaletia unipuncta*), are seasonal migrants. Consequently, as little is known about their origin other than "they come from the south", current management strategies are generally based on pheromone trap catches to estimate the density of immigrants. However, if immigrant populations come from specific areas year after year, one could potentially estimate the size of immigrant populations based on overwintering conditions at the source site.

The existence of a latitudinal continental spatial hydrologic scale for deuterium in precipitation (and thus in the plants growing at different sites) provides a means of determining the natal origin of migrant species. Consequently, I am using hydrogen isotope ratios ( $\delta^2\text{H}$ ) to determine the degree of intra- and inter-year variability in armyworm moths captured in London, ON. Initially, I reared cohorts of larvae on vegetation (*Hordeum vulgare*) treated with water having different concentrations of deuterium to establish the relationship between water  $\delta^2\text{H}$  and wing chitin  $\delta^2\text{H}$ . As there are three periods of armyworm flight activity (immigrants, residents and emigrants) I am now analyzing the wings of field-collected moths that were captured in different years and at different times during the seasons.

Our working hypothesis is that within a year, immigrants captured in spring will have significantly different  $\delta^2\text{H}$  profiles than those in summer and fall, as they will have fed on host plants growing in locations much further south while residents and emigrant populations will have fed on local vegetation. The inter-year comparison will allow me to determine to what extent the origin of immigrants varies from one year to the next.

**Darren Kelly**, University of Guelph

Genome Size Diversity of Coccoidea, Blattodea, and their Relatives

This project is an investigation of the genome size diversity present within Coccoidea (the scale insects), an insect order which contains significant economic pests. The initial goal was to measure these genome sizes for the first time to date, using Feulgen Image Analysis Densitometry, in order to contribute data to the Animal Genome Size Database. The second goal was to analyse genome size against traits associated with extreme pests, as genome size is known to correlate with various properties such as development, body size, and cell division. For pest insects specifically, of interest were parameters such as polyphagy, geographic range size, and reproductive frequency. Genome size was found to correlate positively with body size after correcting for phylogeny, which is a pattern found within a majority of eukaryotes; as genome size increases so does nucleus and cell sizes, which influences overall body size. Genome size also correlated negatively with reproductive frequency after correcting for phylogeny. This correlation provides an inverse interpretation as the pattern found for body size; a smaller genome size allows for

smaller cell sizes, decreasing the time for cellular division and overall development, which are two parameters linked to reproductive frequency. Overall, the present evidence shows that genome size influences body size and reproductive frequency in scale insects, but this is not linked to pest level or how destructive the species is.

**Hayley Yorke**, University of Guelph

Exploration of genome size in theraphosid spiders and 4 previously unsampled arachnid orders

This study seeks to measure genome size in a variety of arachnid taxa including species within such previously unmeasured taxa as Theraphosidae (within infraorder Mygalomorphae), Opiliones, Scorpiones, Amblypygi, and Thelyphonida. Genome size measurements are achieved using Feulgen image analysis densitometry, and are compared with cell size, female adult body size, developmental rate, developmental complexity, and longevity in order to explore and understand possible evolutionary relationships between various arachnid orders. Additionally, a new, non-lethal protocol for extracting haemolymph from live arachnids is adapted from existing techniques with the intent on opening up new avenues of specimen acquisition for future genome size measurements.