

Curriculum Vitae

Nina Ariadne Sokolov

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EDUCATION

- 2018- Present **Ph. D in Integrative Biology**, University of California, Berkeley
- Supervisor: Dr. Mike Boots
- 2012- 2016 **B.Sc. Honors in Biology with Distinction**, University of Toronto
- Ecology and Evolutionary Biology Specialist

ACADEMIC AWARDS

- 2018 NSERC Canada Graduate Scholarships - Master's Award (Offered)
- 2017 NSF Graduate Research Fellowship Program - Honorable Mention
- 2016 Undergraduate Global Change Sciences Internship
- 2015 NSERC Undergraduate Student Research Award

RESEARCH EXPERIENCE

- Oct. 2016- **Research Assistant**, Harvard University
June 2018 **Supervisor:** Prof. Hopi Hoekstra
Burrowing was observed in two closely related deer mouse species that exhibit different behaviors. The digging behavior and characteristics of the burrow between species were quantified. These phenotypes are being correlated with potential candidate genes and regions of the brain.
Duties: Managing mice colonies; behavioral assays, filming/scoring behaviors; DNA extraction, PCR, library prep; lab management, field work in Florida.
- Sept. 2016- **Research Internship**, Harvard University
June 2018 **Supervisor:** Prof. Brian Farrell
Surveys revealed the presence of two species of mosquito hybridizing: *A. triseriatus* - a vector for diseases- while *A. hendersoni* is not. A morphometric tool was created to identify hybrids in the wild.
Duties: Mosquito egg collecting, counting, and offspring rearing; identification of insects based on morphology and genetic analysis; R; DNA extractions, PCR
- Sept. 2016- **Research Internship**, Harvard University
June 2018 **Supervisor:** Prof. Naomi Pierce
The genus *Vanessa* varies wildly in their migratory behavior. Geographically restricted species are sisters to migratory species, suggesting that migratory behavior is an evolutionary liable trait. Climatic data was combined with distributional ranges to reconstruct ancestral niches using R to study the role of historical competition on speciation to test hypotheses on migration evolution.
Duties: Preparing samples for museum collections; creating datasets of current species distributions with GIS; summarizing climatic variables from WorldClim; reconstructing ancestral niches using R
- May 2016- **Research Assistant**, Global Change Sciences Internship, University of Toronto
Aug. 2016 **Supervisor:** Prof. Arthur Weis
Breeding populations of *Brassica rapa* with a phenological mismatch in flowering time lead to decreased rates of hybridization. The feasibility of rescuing northern populations through assisted gene flow was determined to hinge on the ability to match flowering time of resident and migrant populations.

- May- Aug. 2015 **Duties:** Planted and reared over 6,000 offspring of controlled and open pollinated crosses to create purebred/hybrid lines; phenotypic characteristics of offspring measured as metric of hybridization; linear discriminant analysis run in R.
Research Assistant, NSERC USRA Project, University of Toronto
Project title: Experimental Evolution on Sexual Reproduction.
Supervisor: Prof. Aneil Agrawal
Significance/novelty/results: The goal was to further our understanding on the effects of migration and meta-population dynamics on the evolution of sexual reproduction. Preliminary results suggest that high levels of migration confer an increased propensity for sex.
- Oct. 2013- May 2015 **Duties:** Designed experimental evolution project on rotifers. Colony management; manual transfer of rotifers as migration events; density counts; sex assays, growth assays; trained team of undergraduates to assist with research.
Work Study, University of Toronto
Supervisors: Prof. Aneil Agrawal; Dr. Pepijn Luijckx
Generated inbred lines of rotifers to test Hill-Robertson interference effect.
Duties: Grew/maintained populations of rotifers; fitness, growth, and sexual propensity assays; created inbred isogenic lines of rotifers; grew/counted algae as food preparations; assisted PhD students and Postdoc.
- May-Aug. 2012 **Research Assistant**, Clarkson University, Potsdam, NY
Supervisors: Prof. Craig Woodworth
Significance/novelty/results: Fungal toxin treatment on human skin cells in vitro and mouse skin cells in vivo caused shrinking of aging skin cells. This resulted in disappearance of age-related fine lines on mouse skin.
Duties: Cultured/maintained human skin epithelial cells; measured size and growth of cells through time.

PUBLICATIONS and PRESENTATIONS

- *Poster:* Kiszewski, A.E., **Sokolov, N.A.** Detecting Hybrid Individuals in Crosses between *Aedes triseriatus* and *hendersoni* mosquitoes with Linear Discriminant Analysis. Society for Vector Ecology Conference – Yosemite, CA, 2018.
- *In review:* Bonner, C.; **Sokolov, N.A.**; Westover, S.; Ho, M.; Weis, A. Divergent mating phenology between residents and migrants impedes hybridization: experimental tests, and implications for Assisted Gene Flow. *Journal of Biological Conservation*.
- *Presentation:* Sokolov, Nina. “Exploring the efficacy of assisted gene flow in promoting adaptation to a changing climate.” CGCS Research Fair - University of Toronto, 2016.
- Sokolov, I., Guz, N.V., Iyer, S., Hewitt, A., **Sokolov, N.A.**, Erlichman, J.S., Woodworth, C.D. 2015. Recovery of aging-related size increase of skin epithelial cells: *in vivo* mouse and *in vitro* human study. *PLOS One* 10(3): e0122774.

OTHER PROFESSION-RELATED EXPERIENCE AND SKILLS

- 2018 - Volunteer science communicator for the CLEAR Project (Communication, Literacy & Education for Agricultural Research)
- 2018 - Volunteer teacher for BASIS (Bay Area Scientists in Schools)
- 2017 - Member of the Cambridge Entomological Club
- 2015 - Volunteer facilitator in the hands-on ‘Life in Crisis: Schad Gallery of Biodiversity’ for the Royal Ontario Museum.
- 2014 - Volunteer core tutor in the Saturday Program

Modeling the impact of honey bee importation on viral prevalence in wild bees

Populations of honeybees are declining, but the dynamics of most other bee species are not known. Infectious diseases are major contributors to this decline. Honey bees are traded and now distributed almost worldwide for crop pollination. Areas of high commercial honeybee density can accidentally introduce emergent parasites that have the potential to spill over into bordering populations of wild bees. This could represent a major cause of mortality of wild bees wherever managed bees are maintained. I plan to address the question of, how far from high density honeybee sites do we find evidence of ecologically important pathogens such as deformed wing virus (DWV), and how fast would this virus spread? At what point do we see peak prevalence? What is the impact of honey bee population density fluctuating through importation events? I aim to generate spatially explicit models of pathogen spillover to determine rate of spread from domesticated bees and the prevalence of disease that would arise in wild bees. Using insect-pathogen models with additional space and time parameters I aim to predict the spatial prevalence of the virus near honeybee populations in which the density is fluctuating through time to mimic importation events. The rate of spread outwards from the source population will be determined. Ecologically relevant factors will be parameterized such as the following: the differences in symptoms going from sub-lethal to lethal effects to mimic the variation in DWV virulence. The rate at which the virus breaks down when it exists in the pollen during environmental transmission. The rate at which the bees are foraging and could increase viral deposition.

This will increase understanding of the impact that common practice of mass importing honey bee populations for crop pollination on disease, both within honeybees, and out into wild populations. This work will help to bolster quantification of disease risk factors, and anthropogenic impacts on pollinators to inform proper management and intervention strategies on pollinators. My overarching goal is to compare this model to the results I find in a field system. In that project I aim to empirically track temporal dynamics of honeybee and wild bee viruses at a range of human impacted sites across the span of a year. I propose to fit epidemiological models to my surveillance data to estimate the force of infection and characterize changes through time. This will pinpoint high risk periods of disease transmission from honeybees to wild bees. Multiple interventions can be modeled such as determining a threshold for importation that can decrease spillover of pathogens into wild populations. Together both lines of evidence, from mathematical to empirical, will provide calculated strategies to minimize disease transmission and subsequent bee losses.

Nina Sokolov – Statement of Interest

Up until now, my main experiences in the scientific realm has come from working in the lab or in the field. I have worked in a range of systems, from experimental evolution of rotifers, to behavioral genetics of deer mice. My first stint in disease ecology occurred recently when I worked on two local species of mosquitoes which are known to interbreed and share habitats but differ in their competencies for transmission of a pathogen, Lacrosse encephalitis virus. This is what initially got my mind buzzing on what environmental factors impact disease transmission and how are pathogens existing within a community context. Now that I have started graduate school I have narrowed down on my research topics where I aim to address gaps in our knowledge regarding the effect of human impact on infectious diseases in wild bee communities. I want to focus on the breadth of insect diversity in this group and ask questions about how are diseases being transmitted amongst wild bee species and what environmental factors are impacting that transmission? What is the role of the domesticated honey bee in this landscape? In the lab I have joined I have started to become acquainted with the world of mathematical modeling, and I can see how powerful of a tool this would be for addressing my research goals. This workshop is especially unique as it matches my goals by approaching epidemiological issues from an ecological perspective. Additionally, this workshop would elevate my coding skills, because up till now my training in R and Python has all been self-taught. To continue being a successful biologist I think it is crucial that I gain a firmer training in coding languages to analyze the data I aim to collect to produce the most compelling results. In the short term my goals for my PhD are to empirically quantify spatiotemporal viral dynamics in honeybees and wild bees, and to determine the impact of large-scale honeybee importation for crop pollination on these dynamics. I plan to generate models that will describe the patterns of disease spread during spillover events from honey bee to wild bee populations. Then I will compare that to my empirical data to determine which modelled parameters are most important for disease spread. In the long term it will provide me with a theoretical tool kit to employ upon my field and empirical data that I will be collecting through my research career. Through the lens of community ecology, I aim to create a predictive framework of intervention strategies for mitigation of infectious diseases in honey bees and wild bees. This will be critical for agricultural, as the maximal crop yield has been found occur from pollination by wild bees working in concert with honeybees, and not honeybees alone. From an ecological perspective it is important to maintain diversity during the time of a changing climate. Preserving a diverse contingent of wild pollinators, each offering a combination of behavioral and physiological adaptations, will allow for maximizing ecosystem stability. Therefore, I find it imperative to use as many pieces of evidence, including mathematics, to inform the most ecologically sound intervention strategies. This workshop would be exactly the training I need to attain my research goals, and to tackle the gaps in knowledge surrounding wild bee epidemiology.