Symposium Report

Symposium: Landscape Genetics as a Tool for Managing Human-Impacted Landscapes
Venue: Symposium # S21, held online at IALE meeting – Toronto May 11–14 2020
Funded by: Center for Urban Environments (CUE)

Organizing committee

Cochairs: Hossam Abdel Moniem, Ph.D., PDF, CUE & Lindsay Miles, Ph.D., PDF, UTM
Graduate member: Sophie Breitbart, Ph.D. candidate, UTM

Presentations link (iPoster)

https://2020toronto-ialena.ipostersessions.com/Default.aspx?s=iale_2020_gallery

Attendance

Participants: Nine oral presentations from Canada and USA
Faculty: Lisette Waits, Menalie Murphy, Nusha Keyghobadi, Brad Fedy, William Peterman
Postdocs: Lindsay Miles, Hossam Abdel Moniem
Graduates: Payton Phillips, Felipe Torres

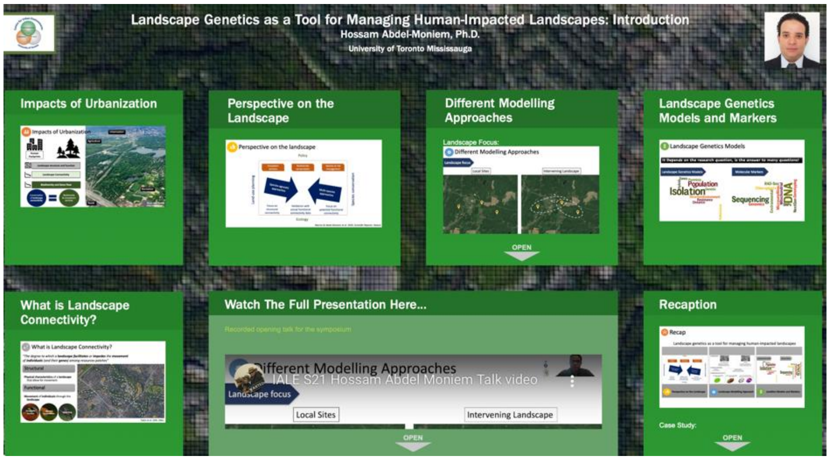
Objectives and Relevance to the CUE

Landscape genetics is an interdisciplinary field that unites population geneticists, landscape ecologists, and spatial statisticians through a common goal: to develop novel research approaches that answer questions about how our dynamic landscapes shape evolutionary processes. A main goal of this symposium is to present current landscape genetics research on different urban-dwelling taxa and discuss how this research can inform policy and practices to better manage our urban and urbanizing landscapes. In addition to building international relationships and facilitating the exchange of ideas among stakeholders, support from the CUE Symposium Grant helped implementing several aspects of CUE's vision. First, the grant allowed participants to share their research with policymakers directly and facilitate the primary, crucial steps of translation from research into applications such as urban designs and laws that prioritize urban sustainability and health for both people and urban biodiversity. Next, the broad audience membership fulfilled CUE's commitment to bridge knowledge across sectors and subdisciplines. Finally, our research and CUE's shared emphasis on maintaining cross-disciplinary relationships spanning the world will remain indefinitely: the success of this field relies on the constant collaboration of researchers in otherwise autonomous disciplines, as well as representatives from government, NGOs, and the private sector, to link research, application, and policy. In conclusion, our symposium tied directly with the CUE mission, and strategic plans and supported professionals and early career scientists and practitioners thriving to achieve these goals with the multidisciplinary field of landscape genetics.

Symposium abstracts:

Landscape genetics as a tool for managing human-impacted landscapes: Symposium opening

Hossam E. Abdel Moniem: PDF; Symposium Chair; CUE-UTM


Landscape Genetics as a Tool for Managing Human-Impacted Landscapes: Introduction
Hossam Abdel-Moniem, Ph.D.
University of Toronto Mississauga

Impacts of Urbanization

Perspective on the Landscape

Different Modelling Approaches

Landscape Genetics Models and Markers

What is Landscape Connectivity?

Watch The Full Presentation Here...

Recorded opening talk for the symposium

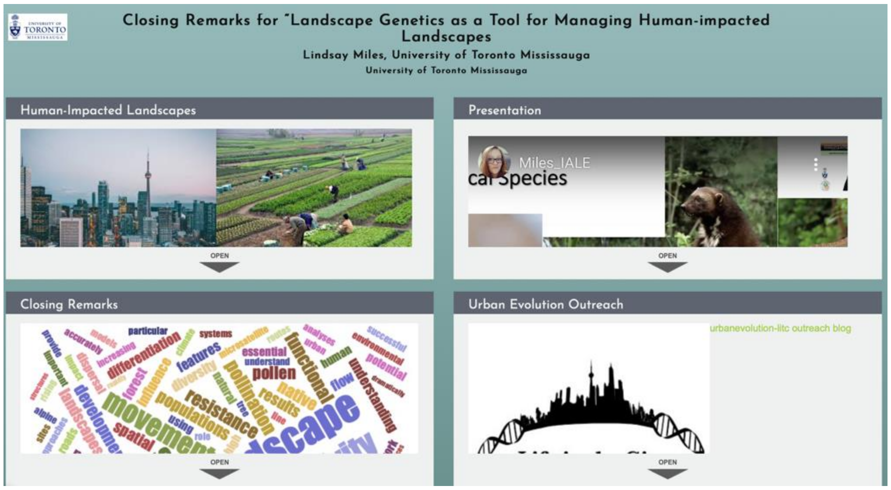
Recaption

Case Study:

By linking landscape ecology and population genetics, the interdisciplinary field of landscape genetics enables us to understand how landscape patterns and ecological processes can shape species population structures. In our rapidly changing landscapes, the human footprint can dramatically affect the connectivity of our natural resources and influence dispersal for species and their genes at the landscape scale. Consequently, we may lose genetic and biological diversity, which is crucial for maintaining ecosystem services and biodiversity markets. Studying how landscape structure and function affect both genetic diversity and spatial distribution of natural populations in complex landscapes has an increasing demand when we try to link research, application, and policy to manage our urban and urbanizing landscapes. Currently, landscape genetics in urban and urbanizing ecosystems is gaining the attention of researchers as a growing field of study. We present a conceptual framework for different landscape perspectives and alternative approaches for quantifying connectivity in landscape genetics research. We discuss how these tools can inform policy and practices to better manage our landscapes.

Landscape Genetics as a Tool for Managing Human-impacted Landscapes: Closing Remarks

Lindsay Miles: PDF; Symposium Cochair; UTM


Closing Remarks for "Landscape Genetics as a Tool for Managing Human-impacted Landscapes
Lindsay Miles, University of Toronto Mississauga
University of Toronto Mississauga

Human-Impacted Landscapes

Presentation

Closing Remarks

Urban Evolution Outreach

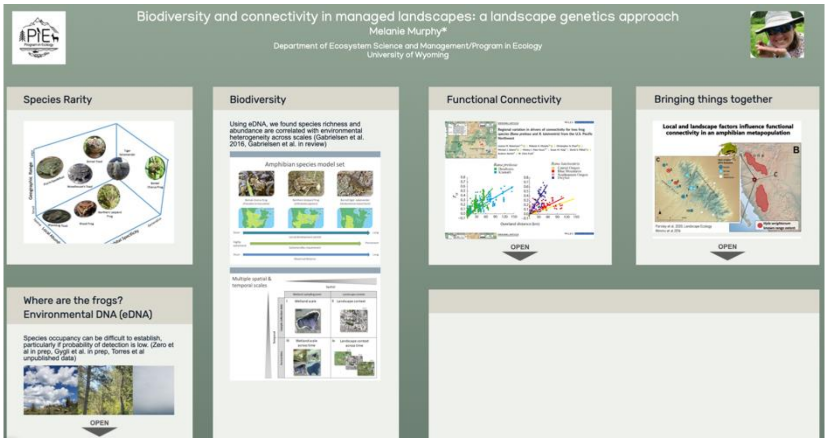
urbanevolution-litc outreach blog

In recent years, humans have drastically altered the natural landscape through agriculture and urban expansion. Here, we have heard that human land-use has contributed to a loss of genetic diversity in a number of organisms of conservation concern. However, we have also heard that urbanization has helped spread non-native species and contributes to the maintenance of high genetic diversity within and between cities. These changes in genetic diversity can influence how these organisms evolve to the changing landscape. The reduced genetic diversity is likely to reduce the adaptive potential and thus these organisms with lower genetic diversity are not likely to persist in the urban environment.

For those organisms like the feral pigeon, rapid land-use change has not reduced genetic diversity and these birds are likely to persist in the urban environment. Given these differing responses to the urban environment, the next step will be to link the identification of corridors and barriers to gene flow. When we can find commonalities in landscape factors that most likely contribute to dispersal, we will be able to manage land-use in a way that promotes gene flow for a variety of taxa of conservation concern.

Distribution and connectivity in managed landscapes: a landscape genetics approach

Melanie Murphy: Associate Professor; University of Wyoming



Biodiversity and connectivity in managed landscapes: a landscape genetics approach

Melanie Murphy*

Department of Ecosystem Science and Management/Program in Ecology

University of Wyoming

Species Rarity

Biodiversity

Using eDNA, we found species richness and abundance are correlated with environmental heterogeneity across scales (Gabrielsen et al. 2016, Gabrielsen et al. in review)

Functional Connectivity

Bringing things together

Local and landscape factors influence functional connectivity in an amphibian metapopulation

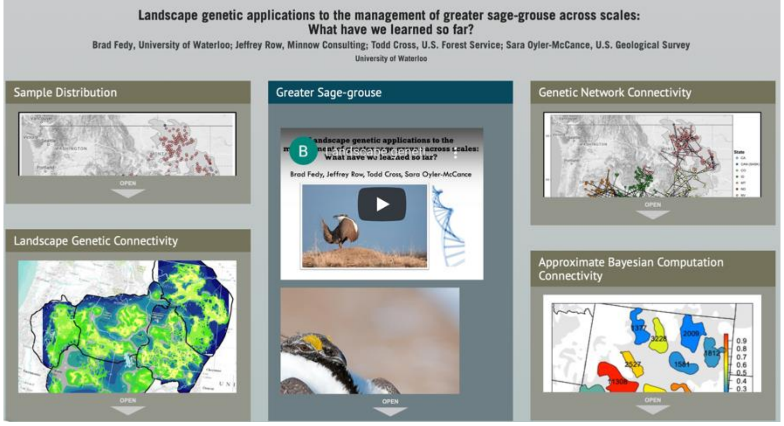
Where are the frogs? Environmental DNA (eDNA)

Species occupancy can be difficult to establish, particularly if probability of detection is low. (Zero et al in prep, Gygli et al. in prep, Torres et al unpublished data)

Understanding distribution and connectivity of species in changing environments is critical for meeting conservation goals. Species rarity may influence both species niche underlying observed distribution and connectivity. Rabinowitz identified these rarity forms using the axes of geographic range (small vs. large), habitat specificity (specialist vs. generalist) and local abundance (sparse vs. dense). Synthesizing across multiple systems, I will address how rarity influences both where species occur and how they are connected in the landscape. I will incorporate occurrence data from environmental DNA (eDNA) to estimate distribution. Then within the distribution, estimate functional connectivity using a variety of neutral genetic data. The models systems presented will cover a range of environmental constraints, anthropogenic influence and taxon.

Landscape genetic applications to the management of greater sage-grouse across scales: What have we learned so far?

Brad Fedy: Associate Professor; University of Waterloo



Landscape genetic applications to the management of greater sage-grouse across scales: What have we learned so far?

Brad Fedy, University of Waterloo; Jeffrey Row, Minnow Consulting; Todd Cross, U.S. Forest Service; Sara Oyler-McCance, U.S. Geological Survey

University of Waterloo

Sample Distribution

Greater Sage-grouse

Landscape genetic applications to the management of greater sage-grouse across scales: What have we learned so far?

Brad Fedy, Jeffrey Row, Todd Cross, Sara Oyler-McCance

Genetic Network Connectivity

Landscape Genetic Connectivity

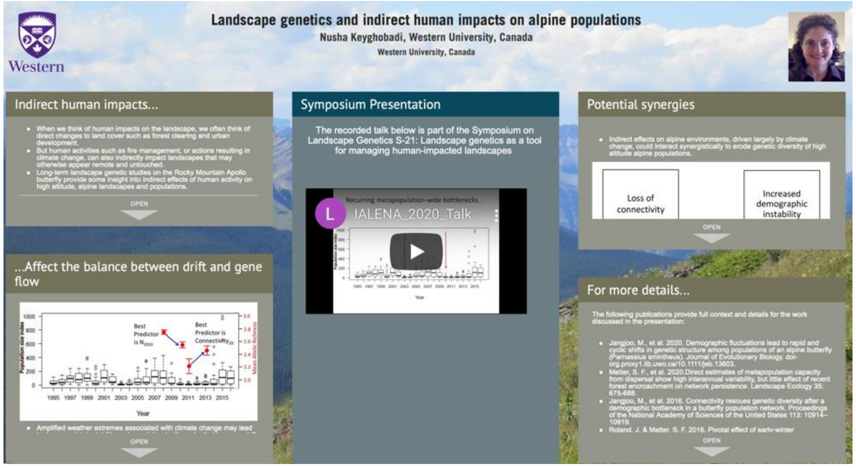
Approximate Bayesian Computation Connectivity

The identification and demographic assessment of biologically meaningful populations is fundamental to species' ecology and management. Additionally, given the significance of animal dispersal to population dynamics and geographic variability, understanding how dispersal is impacted by landscape patterns has major ecological and conservation importance. We used genetic data to define subpopulations, identify the landscape components that most influence connectivity, and assess the role of population connectivity in maintaining genetic diversity for greater sage-grouse (Centrocercus urophasianus) at the state-level. Across the range of the species, we have quantified functional connectivity with network analyses and the development of landscape resistance surfaces using microsatellite genotypes from 6,844 individuals across the 10.7 million km2 range. We have used a combination of these empirical data and extensive simulations to address multiple unique – but related – questions. In this presentation we will summarize the results of this large-scale project and discuss how our contributions have been received and applied by resource management agencies.

Landscape genetics and indirect human impacts on alpine populations

Nusha Keyghobadi: Associate Professor; Western University

Alpine areas are changing dramatically and rapidly under a changing climate. Altered climate and weather regimes can affect populations directly through survival and reproduction, and indirectly by inducing changes in land cover and other landscape features. For high altitude alpine species, rising tree line represents an important indirect impact of a generally warming climate. Over two decades our group has used landscape genetics approaches to explore the potential effects of rising tree line, and loss of connectivity among high altitude alpine meadow habitat, on genetic diversity of the Rocky Mountain apollo butterfly (Parnassius smintheus). I will summarize our findings, highlighting in particular the potential synergy between rising tree line and changing weather patterns (with more frequent extreme meteorological events) in eroding genetic diversity of populations.



Landscape genetics and indirect human impacts on alpine populations
Nusha Keyghobadi, Western University, Canada
Western University, Canada

Indirect human impacts...

- When we think of human impacts on the landscape, we often think of direct changes to land cover such as forest clearing and urban development.
- But human activities such as fire management, or actions resulting in climate change, can also indirectly impact landscapes that may otherwise appear remote and untouched.
- Long-term landscape genetic studies on the Rocky Mountain Apollo butterfly provide some insight into indirect effects of human activity on high altitude, alpine landscapes and populations.

...Affect the balance between drift and gene flow

- Amplified weather extremes associated with climate change may lead

Symposium Presentation

The recorded talk below is part of the Symposium on Landscape Genetics S-21: Landscape genetics as a tool for managing human-impacted landscapes

Potential synergies

- Indirect effects on alpine environments, driven largely by climate change, could interact synergistically to erode genetic diversity of high altitude alpine populations.

Loss of connectivity

Increased demographic instability

For more details...

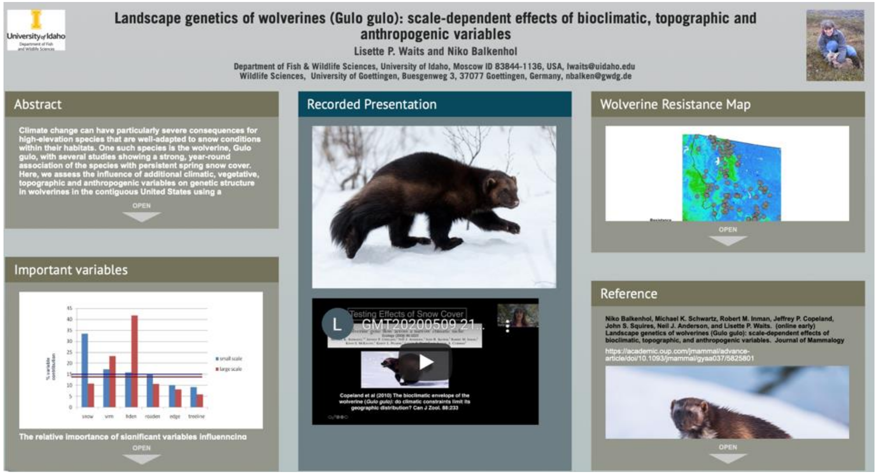
The following publications provide full context and details for the work discussed in the presentation:

- Jangjoo, M., et al. 2020. Demographic fluctuations lead to rapid and cyclic shifts in genetic structure among populations of an alpine butterfly (Parnassius smintheus). Journal of Evolutionary Biology. doi-org.proxy1.lib.uwo.ca/10.1111/jeb.13603.
- Matter, S. F., et al. 2020.Direct estimates of metapopulation capacity from dispersal show high interannual variability, but little effect of recent forest encroachment on network persistence. Landscape Ecology 35: 675-688.
- Jangjoo, M., et al. 2016. Connectivity rescues genetic diversity after a demographic bottleneck in a butterfly population network. Proceedings of the National Academy of Sciences of the United States 113: 10914–10919.
- Roland. J. & Matter. S. F. 2016. Pivotal effect of early-winter

Landscape genetics of wolverines (*Gulo gulo*): scale-dependent effects of bioclimatic, topographic and anthropogenic variables

Lisette Waits: Professor; University of Idaho

Climate change can have particularly severe consequences for high-elevation species that are well-adapted to snow conditions within their habitats. One such species is the wolverine, Gulo gulo, with several studies showing a strong, year-round association of the species with persistent spring snow cover. Here, we assess the influence of additional climatic, vegetative,



Landscape genetics of wolverines (Gulo gulo): scale-dependent effects of bioclimatic, topographic and anthropogenic variables
Lisette P. Waits and Niko Balkenhol
Department of Fish & Wildlife Sciences, University of Idaho, Moscow ID 83844-1136, USA, lwaits@uidaho.edu
Wildlife Sciences, University of Goettingen, Buesgenweg 3, 37077 Goettingen, Germany, nbalken@gwdg.de

Abstract

Climate change can have particularly severe consequences for high-elevation species that are well-adapted to snow conditions within their habitats. One such species is the wolverine, Gulo gulo, with several studies showing a strong, year-round association of the species with persistent spring snow cover. Here, we assess the influence of additional climatic, vegetative, topographic and anthropogenic variables on genetic structure in wolverines in the contiguous United States using a

Important variables

The relative importance of significant variables influenncing

Recorded Presentation

Copeland et al (2010) The bioclimatic envelope of the wolverine (*Gulo gulo*): do climatic constraints limit its geographic distribution? Can J Zool. 88:233

Wolverine Resistance Map

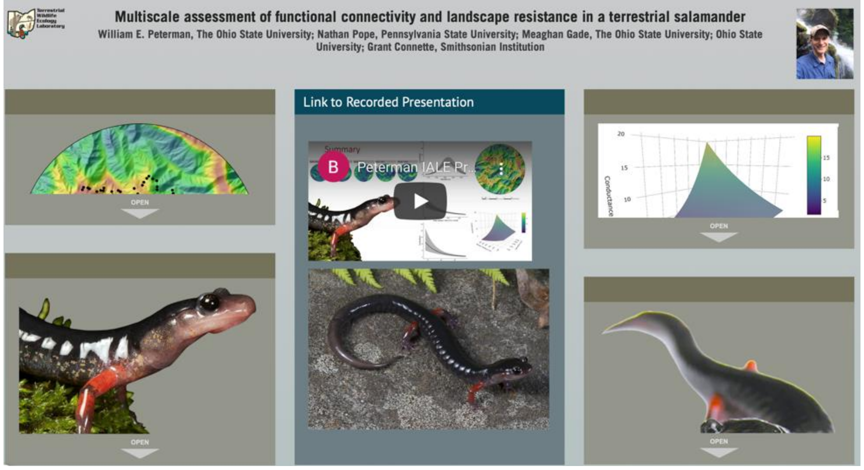
Reference

Niko Balkenhol, Michael K. Schwartz, Robert M. Inman, Jeffrey P. Copeland, John S. Squires, Neil J. Anderson, and Lisette P. Waits. (online early) Landscape genetics of wolverines (Gulo gulo): scale-dependent effects of bioclimatic, topographic, and anthropogenic variables. Journal of Mammalogy
https://academic.oup.com/jmammal/advance-article/doi/10.1093/jmammal/gyaa037/5825801

topographic and anthropogenic variables on genetic structure in wolverines in the contiguous United States using a multivariate, multiscale landscape genetic approach. This approach allows us to detect landscape-genetic relationships due to usual dispersal and mating movements, and also due to less frequent long-distances dispersal. Results suggest that a combination of snow depth, terrain ruggedness, and housing density best predict gene flow in wolverines, and that the relative importance of variables is scale-dependent. Environmental variables were responsible for 78.9% of the explained variation at small scales (i.e., up to ~230 km), and 64.6% at broad scales (i.e., beyond ~ 420 km). In contrast, a null model based only on geographic accounted for only 17.1% and 11.4% of the variation at small and broad scales, respectively. Snow depth was the most important variable for predicting genetic structures overall, and at small scales, where it contributed 42.9% to the variance explained. At broad spatial scales, housing density and terrain ruggedness were most important with contributions to explained variation of 54.6% and 24.9%, respectively. While the small-scale analysis most likely captures gene flow within typical wolverine habitat complexes, the broad-scale analysis reflects long distance dispersal across areas not typically inhabited by wolverines. These findings help to refine our understanding of the processes shaping wolverine genetic structure, which is important for maintaining and improving functional connectivity among remaining wolverine populations.

Multiscale assessment of functional connectivity and landscape resistance in a terrestrial salamander

William E. Peterman:
Assistant Professor; The Ohio State University



Multiscale assessment of functional connectivity and landscape resistance in a terrestrial salamander

William E. Peterman, The Ohio State University; Nathan Pope, Pennsylvania State University; Meaghan Gade, The Ohio State University; Ohio State University; Grant Connette, Smithsonian Institution

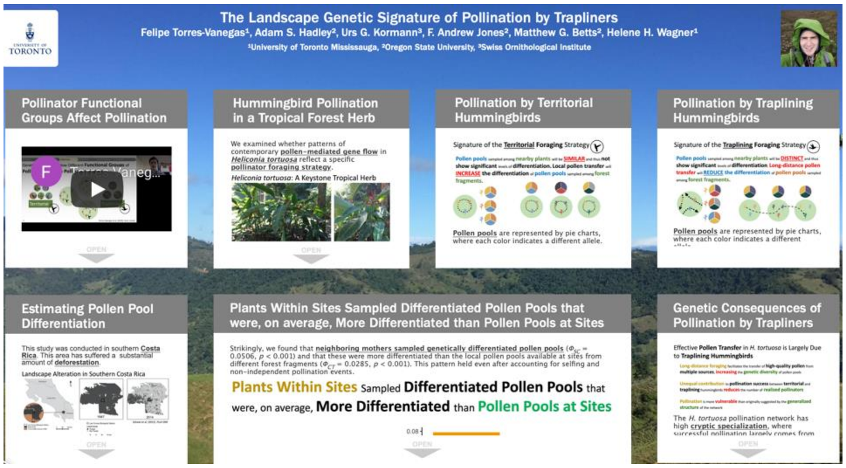
Link to Recorded Presentation

Understanding how organisms move across the landscape is important for developing land use and management strategies that will maintain functional connectivity, which is essential to the long-term persistence of populations on the landscape. However, direct assessment of movement can be difficult or impossible in some systems. The number of individuals present in a population, life history traits, and body size all contribute to the challenge of accurately assessing movement and functional connectivity. Landscape genetics provides a lens through which functional connectivity can be assessed, circumventing many of the obstacles to directly observing movement. When assessing movement, scale is an important, but underappreciated, factor shaping the observed movement patterns. Increasingly, studies are finding that animal movement and habitat selection are multiscale processes, and that there is rarely a single characteristic scale at which wildlife universally respond to landscape or habitat features. Although scale is a cornerstone of landscape ecology, it is infrequently incorporated into landscape genetic analyses. In this study, we conducted a landscape genetic analysis to determine landscape resistance and functional connectivity for the terrestrial salamander Plethodon shermani residing in a working forest landscape in the Southern Appalachian

Mountains. Specifically, we optimized landscape resistance surfaces using combinations of relevant habitat and topographic landscape features, each assessed at multiple spatial scales. The resistance surface that best explained spatial patterns in genetic differentiation was a multiscale combination of aspect, solar exposure, and topographic position. This multiscale resistance surface was vastly better than the same resistance surface created from each landscape variable at its original scale. Our results highlight the importance of incorporating spatial scale in landscape genetic analyses to more accurately assess landscape resistance and functional connectivity across the landscape.

The Landscape Genetic Signature of Pollination by Trapliners

Felipe Torres-Vanegas: PhD Candidate; University of Toronto, Mississauga



The Landscape Genetic Signature of Pollination by Trapliners

Felipe Torres-Vanegas[1], Adam S. Hadley[2], Urs G. Kormann[3], F. Andrew Jones[2], Matthew G. Betts[2], Helene H. Wagner[1]

[1]University of Toronto Mississauga, [2]Oregon State University, [3]Swiss Ornithological Institute

Pollinator Functional Groups Affect Pollination

Hummingbird Pollination in a Tropical Forest Herb

We examined whether patterns of contemporary pollen-mediated gene flow in *Heliconia tortuosa* reflect a specific pollinator foraging strategy.

Heliconia tortuosa: A Keystone Tropical Herb

Pollination by Territorial Hummingbirds

Signature of the Territorial Foraging Strategy

Pollen pools sampled among nearby plants will be SIMILAR and thus not show significant levels of differentiation. Local pollen transfer will INCREASE the differentiation of pollen pools sampled among forest fragments.

Pollen pools are represented by pie charts, where each color indicates a different allele.

Pollination by Traplining Hummingbirds

Signature of the Traplining Foraging Strategy

Pollen pools sampled among nearby plants will be DISTINCT and thus show significant levels of differentiation. Long-distance pollen transfer will REDUCE the differentiation of pollen pools sampled among forest fragments.

Pollen pools are represented by pie charts, where each color indicates a different

Estimating Pollen Pool Differentiation

This study was conducted in southern Costa Rica. This area has suffered a substantial amount of deforestation.

Landscape Alteration in Southern Costa Rica

Plants Within Sites Sampled Differentiated Pollen Pools that were, on average, More Differentiated than Pollen Pools at Sites

Strikingly, we found that neighboring mothers sampled genetically differentiated pollen pools (Φ_{SC} = 0.0506, $p < 0.001$) and that these were more differentiated than the local pollen pools available at sites from different forest fragments (Φ_{CT} = 0.0285, $p < 0.001$). This pattern held even after accounting for selfing and non-independent pollination events.

Plants Within Sites Sampled Differentiated Pollen Pools that were, on average, More Differentiated than Pollen Pools at Sites

Genetic Consequences of Pollination by Trapliners

Effective Pollen Transfer in *H. tortuosa* is Largely Due to Traplining Hummingbirds

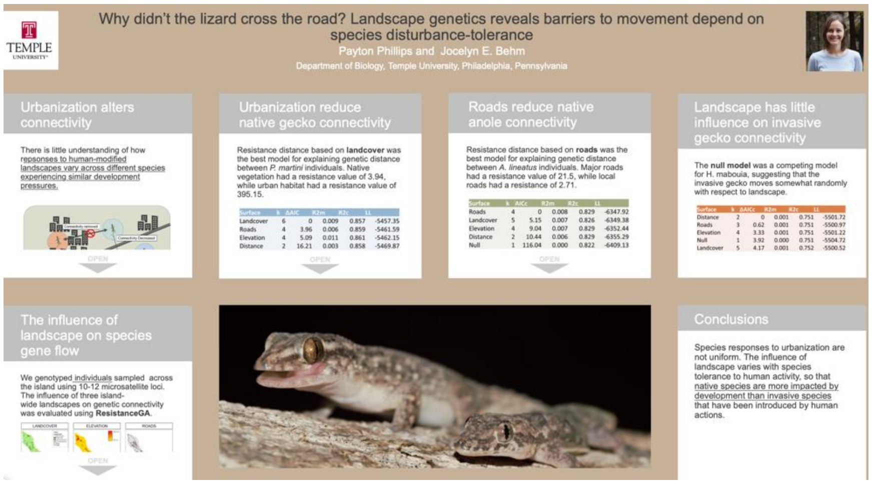
- Long-distance foraging facilitates the transfer of high-quality pollen from multiple sources, increasing the genetic diversity of pollen pools
- Unequal contribution to pollination success between territorial and traplining hummingbirds reduces the number of realized pollinators
- Pollination is more vulnerable than originally suggested by the generalized structure of the network

The *H. tortuosa* pollination network has high cryptic specialization, where

Animal-mediated pollination is essential for the maintenance of plant reproduction, especially in tropical ecosystems, where pollination networks have been thought to have highly generalized structures. However, accumulating evidence suggests that not all floral visitors provide equally effective pollination services, potentially reducing the number of realized pollinators and increasing the cryptic specialization of pollination networks. Thus, there is a need to understand how different functional groups of pollinators influence pollination success. Here, we examined whether patterns of contemporary pollen-mediated gene flow in Heliconia tortuosa are consistent with the foraging strategy of its territorial or traplining hummingbird pollinators. Territorial hummingbirds defend clumps of flowers and are expected to transfer pollen locally. In contrast, traplining hummingbirds forage across longer distances, thereby increasing pollen flow among forest fragments, and are thought to repeatedly visit particular plants. If trapliners indeed visit the same plants repeatedly along their regular routes, this could lead to a situation where neighboring plants sample genetically distinct pollen pools. To test this hypothesis, we genotyped 720 seeds and 71 mother plants from 18 forest fragments at 11 microsatellite loci. We performed TwoGener analysis to test pollen pool differentiation within sites (among neighboring plants within the same forest fragment: ΦSC) and between sites (among forest fragments: ΦCT). We found strong, statistically significant pollen pool differentiation among neighboring mother plants (ΦSC = 0.0506), and weaker, statistically significant differentiation among sites (ΦCT = 0.0285). We interpret this pattern of hierarchical pollen pool differentiation as the landscape genetic signature of the foraging strategy of traplining hummingbirds, where repeatable, long-distance, and high-fidelity routes transfer pollen among particular plants. Although H. tortuosa is also visited by territorial hummingbirds, our results suggest that these pollinators do not contribute substantially to successful pollination, highlighting differences in realized pollination efficiency. This cryptic reduction in the number of realized pollinators potentially increases the vulnerability of pollination success to the decline of populations of traplining hummingbirds, which have been shown to be sensitive to forest fragmentation. We conclude that maintaining habitat connectivity to sustain the foraging routes of trapliners may be essential for the maintenance of pollen-mediated gene flow in human-modified landscapes.

Why didn't the lizard cross the road? Landscape genetics reveals barriers to movement depend on species disturbance-tolerance

Payton Phillips: Graduate Assistant; Temple University



Why didn't the lizard cross the road? Landscape genetics reveals barriers to movement depend on species disturbance-tolerance

Payton Phillips and Jocelyn E. Behm
Department of Biology, Temple University, Philadelphia, Pennsylvania

Urbanization alters connectivity

There is little understanding of how repsonses to human-modified landscapes vary across different species experiencing similar development pressures.

Urbanization reduce native gecko connectivity

Resistance distance based on **landcover** was the best model for explaining genetic distance between *P. martini* individuals. Native vegetation had a resistance value of 3.94, while urban habitat had a resistance value of 395.15.

Surface	k	ΔAIC	R2m	R2c	LL
Landcover	6	0	0.009	0.857	-5457.35
Roads	4	3.96	0.006	0.859	-5461.59
Elevation	4	5.09	0.011	0.861	-5462.15
Distance	2	16.21	0.003	0.858	-5469.87

Roads reduce native anole connectivity

Resistance distance based on **roads** was the best model for explaining genetic distance between *A. lineatus* individuals. Major roads had a resistance value of 21.5, while local roads had a resistance of 2.71.

Surface	k	AICc	R2m	R2c	LL
Roads	4	0	0.008	0.829	-6347.92
Landcover	5	5.15	0.007	0.826	-6349.38
Elevation	4	9.04	0.007	0.829	-6352.44
Distance	2	10.44	0.006	0.829	-6355.29
Null	1	116.04	0.000	0.822	-6409.13

Landscape has little influence on invasive gecko connectivity

The **null model** was a competing model for H. mabouia, suggesting that the invasive gecko moves somewhat randomly with respect to landscape.

Surface	k	ΔAICc	R2m	R2c	LL
Distance	2	0	0.001	0.751	-5501.72
Roads	3	0.62	0.001	0.751	-5500.97
Elevation	4	3.33	0.001	0.751	-5501.22
Null	1	3.92	0.000	0.751	-5504.72
Landcover	5	4.17	0.001	0.752	-5500.52

The influence of landscape on species gene flow

We genotyped individuals sampled across the island using 10-12 microsatellite loci. The influence of three island-wide landscapes on genetic connectivity was evaluated using **ResistanceGA**.

Conclusions

Species responses to urbanization are not uniform. The influence of landscape varies with species tolerance to human activity, so that native species are more impacted by development than invasive species that have been introduced by human actions.

Anthropogenic development creates barriers which reduce population connectivity of native species. However, it is not fully understood how features of urbanization, such as roads, might impact species differently depending on their tolerance to disturbance created by development. We used landscape genetic techniques to understand how development on Curaçao, a biodiverse Caribbean island, alters the movement of three lizard species – two geckos (Hemidactylus mabouia and Phyllodactylus martini) and an anole (Anolis lineatus). These three species represent a gradient of tolerance to human development, with P. martini being an intolerant native species and A. lineatus being a tolerant native species. The invasive gecko, H. mabouia, is highly tolerant to human development and has been spread throughout the Caribbean by human movement and trade. Tissue samples were collected from lizards in urban and natural areas across the island for microsatellite genotyping. Using the R package ResistanceGA, we optimized island-wide resistance surfaces to best explain species movement based on landscape features. We included layers for land use (natural vegetation types, low urbanization, high urbanization), local and major roads, and density of tourist attractions. Local roads most strongly impacted native species, decreasing movement for A. lineatus and P. martini by 3 and 20 times, respectively in accordance with their tolerance to disturbance. These results reinforce the knowledge that roads negatively impact native populations, in this case creating a barrier to movement and reducing genetic connectivity. For the invasive gecko, H. mabouia, the null model was a competing model, suggesting that movement of this species is more random with respect to the environment than that of its native counterparts. This highlights that development may not play a limiting role to the spread of species that have already been introduced by humans, providing them with another advantage over their native counterparts.