

## Research Statement— Jess McLaughlin

Why do we observe specific evolutionary outcomes in one group of organisms, but not others? Often, our predictions based on evolutionary theory fail to capture the full diversity of life. But *why* do we observe the specific variations we do? Why does one group of birds, isolated from its conspecifics, diverge into a distinctive species, while another in the same time and place will still mate with its long-lost sisters? Why do some lizards change to fit a specific habitat type in a pattern seen across other islands in the same archipelago, while others remain generalists? In short, what are the factors that lead to the gaps between our expectations of evolution, and how it actually plays out?

Exploring this space between prediction and outcome is the theme that ties together my research. Drawing on museum collections and large-scale genomic datasets, my research grapples with fundamental questions in the diversification of vertebrates, attempting to understand variations in evolutionary outcomes. I work across multiple vertebrate groups— birds, lizards, and fish— with a research approach built around the keystones of comparative genomics and collections-based research. Currently, my inquiries focus on three areas: the development of reproductive isolation in the birds of lowland Panama, the genomic underpinnings of convergent evolution in Caribbean anoles, and the influence of environmental gradients on gene flow and isolation in the fish *Salminus brasiliensis*. Each of these systems allows me to explore an aspect of these broader themes in more depth, and I plan to continue this approach as I build my research program.

**Comparative genomics**—By comparing multiple taxa that share a common spatial or environmental context— their genetic diversity, the patterns of selection found across their genomes, the architecture of their hybrid zones— we can begin to test what factors intrinsic to these organisms lead to their differing evolutionary trajectories.

The heart of my research program is speciation in lowland Panama. Working with collaborators at the Smithsonian Tropical Research Institute, I have leveraged barcode data to identify widespread cryptic diversity in the birds of Panama, much of which is associated not with clear geographic barriers but with ecological and morphological correlates of dispersal ability such as diet type and hand-wing index<sup>1</sup>. Building on this, I then used loci linked to ultraconserved elements (UCEs) to more closely examine what ecological factors were associated with the development of reproductive isolation in a subset of lowland forest birds, finding that factors such as diet, hand-wing index, and overall genome differentiation played a larger role in predicting the extent of introgression than time in isolation<sup>2</sup>.

I will continue this line of research with whole genome sequencing (WGS) data from 26 species and species-pairs spanning eastern and western Panama. These include the ten taxa from my UCE work, along with other species that span a greater range of taxonomic and ecological breadth while still displaying the same patterns of strong genetic structure between eastern and western Panama. I aim to disentangle how factors arising from diet type, particularly dispersal ability and demographic stability, influence the development of reproductive isolation between populations. While previous research has established the key role of dispersal capability in shaping divergence in birds, as species that are physically limited in their ability to fly long distance are more likely to genetically diverge, my findings indicate that this isn't the full story. I suspect that demographic boom-bust cycles tied with masting cycles in trees drive greater population fluctuations in species reliant on plants, resulting in a fundamentally different pattern of periodic large gene flow events. Related to this, I also plan to test whether different ecological factors are associated with different patterns of selection across

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<sup>1</sup> McLaughlin et al, preprint: <https://doi.org/10.1101/2023.03.15.530646>

<sup>2</sup> McLaughlin and Miller, preprint: <https://doi.org/10.1101/2022.10.25.513737>

the genome— whether specific loci are under selection to maintain barriers despite a contiguous habitat and distribution, or if overall genetic differentiation across the whole of the genome is a greater factor.

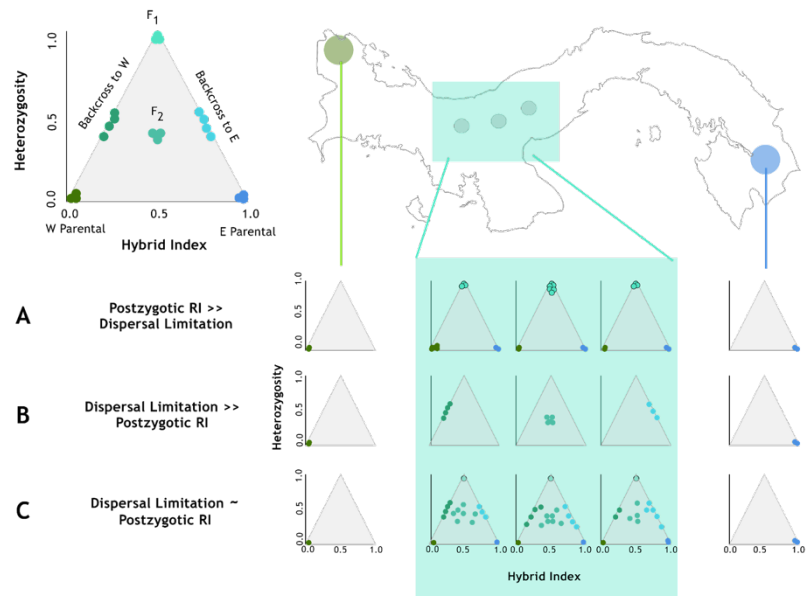
I plan to return to Panama to continue this work, renewing the collaborations with local researchers that were interrupted by the outbreak of COVID-19. During my PhD, I documented a previously little-known area of phylogeographic turnover along the Caribbean coast of Veraguas province<sup>3</sup>. This area appears to be a key region of hybridization in multiple bird species (McLaughlin et al *submitted*), and thus a natural laboratory for understanding how prezygotic factors such as dispersal limitation and postzygotic ones such as genomic compatibility shape the development of hybrid zones. I plan to develop a probe set based on loci identified with my previous WGS sequencing that are fixed in parental populations in eastern and western Panama, and to use this to genotype as many individuals of my focal taxa as possible in a fine-scale transect of this region (Figure 1).

### ***Exploring vertebrate evolution in multiple systems***

While I plan to continue to work in avian speciation, I am broadly trained in other vertebrate taxa. I am continuing my work in convergent evolution in Caribbean *Anolis* lizards, building off my postdoctoral work with Dr. Ian Wang at University of California Berkeley. I am exploring what impact the underlying genomic architecture has on the repeated evolution of distinct ecomorphs, as well as the landscape genomics of several individual species. This well-studied system provides a remarkable opportunity to test whether convergent phenotypes arise primarily from relatively small changes in an ancestral genomic ‘toolkit’, or if there is a large role played by repeated *de novo* changes in a heterogeneous genomic background. Most recently, I have expanded into yet another group of vertebrates, as I begin a second postdoc working with Drs. Lisa Komoroske and Andrew Danylchuk at University of Massachusetts Amherst. Focusing on the golden dorado (*Salminus brasiliensis*), I will be exploring the phylogeography of this widespread species, particularly how population connectivity in the Paraguay River basin is shaped by environmental variables.

Moving forward, I plan to continue collaborating on these systems, while also extending the taxonomic breadth of my core research in Panama, using comparative genomics to better understand the development of reproductive isolation. Panama is known to be home to similar suture zones in fish, amphibians, and reptiles, and I plan to take what I’ve learned in my postdoctoral work and expand my Panama speciation work to these taxa. Ultimately, a key goal of my lab will be in understanding how ecology and speciation are intertwined not just in the birds of this important biogeographic region, but more broadly across animal taxa in Panama.

***Collections-based research and community-driven questions***— Collections are a cornerstone of my research. I am actively involved with efforts to develop novel ways to incorporate specimens into genomics



**Figure 1:** Predicted distribution of admixed individuals across a hypothetical hybrid zone, illustrating how this distribution reflects the relative importance of postzygotic reproductive isolation versus dispersal limitation. In A, postzygotic RI has a much greater influence. Across the whole hybrid zone, parentals of both type and first generation hybrids will be found, but these hybrids are sterile, and do not reproduce. In B, dispersal limitation is the primary factor. Few pure parentals or first generation hybrids will be found; instead, all will be admixed, with backcrosses increasing as you move away from the center. In the final case, neither dispersal limitation nor postzygotic RI are stronger than the other, leading to a hybrid zone with all types across the contact zone. This last case is the most likely to experience reticulation of the lineages in contact.

<sup>3</sup> McLaughlin et al. 2020. *Cotinga* 42:77–81

research, such as retrieving DNA from invertebrate pitfall traps without destroying the specimens themselves<sup>4</sup>. In a world of rapidly changing climate and biodiversity loss, collections are a vital piece in understanding how organisms are responding. I plan to increasingly incorporate historical specimens into my genomics work, and to refine methods for obtaining DNA from these invaluable resources in as minimally invasive a way as possible. I am particularly interested in using specimens from the UA Museum (where I conducted my MSc work) to track how genetic diversity has changed in key subsistence species, partnering with Alaska Native groups to understand how these important species are being impacted by climate change. I would also like to set up a marine metagenomics research program that can be the core of a course-based undergraduate research experience (CURE), building off the similar program I am currently developing at UMass Amherst. I envision my Alaskan research program to be directed by the needs and interests of the communities, particularly Indigenous and rural, and to actively involve these stakeholders in the process as equal collaborators.

***Evidence-based inclusion in STEM***—Sharing my science with as many people as possible is a core component of my research program— not only engaging in public-facing outreach and educational activities, but actively researching how to best do so. This emerging area of my research focuses on two main areas: how best to support inclusion of historically excluded groups in STEM, and how to foster greater engagement in undergraduate learning through research experiences. While both of these are a key part of my teaching and inclusion philosophy, they also form an important component of my scholarly work. Working towards greater equity in STEM requires data, just as our evolutionary hypotheses do, and so I consider my work in this area to be an integral part of my research program instead of an afterthought.

A research area that has recently emerged as a key part of my work is the intersection of biology and transgender, gender-nonconforming, and intersex (TGNCI) rights and inclusion. It is likely not surprising that I have begun working on these topics, as my own career path has been fundamentally shaped by my experience as a nonbinary researcher, but there has been surprisingly little work done on TGNCI inclusion and retention in STEM fields. Personally, I have faced lack of career mobility as more and more states pass laws restricting how TGNCI people can participate in public life, disruptions to my PhD program due to relocating to a safer location, and stigma of being not a “serious researcher” due to my own identity— all usually rooted in faulty understandings of biology, the very topic of my expertise<sup>5</sup>. I am currently working with a group of TGNCI researchers on an invited commentary in *Cell* synthesizing how we are disproportionately impacted by many of the barriers facing early-career researchers, and I will build on this work with more specific surveys on how to best retain TGNCI researchers at every stage of their academic careers with collaborators in the US and UK. My experiences as a trans person working in evolutionary biology have also led to scholarly work on how our societal constructions of binary sex interfere with our ability to understand the diversity of animal sexual systems<sup>6</sup>.

A major strategy that can increase retention of students from historically excluded groups in STEM is early participation in undergraduate research. As discussed above, I am interested in starting a local research project on marine metagenomics. Not only would this generate valuable insights in its own right, which undergraduates would be included in as appropriate as co-authors on publications, but it would create an opportunity to test effective strategies in developing successful CUREs, particularly what structural and instructional features of such programs are most effective in retaining students from historically excluded groups. I’m very excited about the department’s Experiential Learning courses, and I would actively pursue collaborations with other faculty members to analyze what drives the success of these programs.

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<sup>4</sup> Weiser, **McLaughlin**, et al. 2022. *Oikos* e08791.

<sup>5</sup> Sharpe, **McLaughlin**, et al. 2023. *Integr. Comp. Bio.*

<sup>6</sup> **McLaughlin** et al. 2023. *Integr. Comp. Bio.*