Austin H. Patton

Evolutionary Biologist
Postdoctoral Fellow

Berkeley CA, 94703 🏠
(203) 858-2570 ☎
austinhpatton@gmail.com ✉
austinhpatton.github.io 🌐
austinhpatton

I'm an evolutionary biologist specializing in evolutionary genetics and comparative phylogenetics. I received my Ph.D. in Biology from Washington State University and have published in prominent journals including Science, Proceedings of the National Academy of Sciences, and Molecular Biology and Evolution. My projects span multiple biological scales, leveraging phylogenetic methods and high-throughput sequence data to study evolution, whether across entire genera or within populations.

Education

Washington State University	2014-2020	Ph.D., Biology
Warren Wilson College, N.C.	2010-2014	B.S., Biology & Conservation Biology

Experience

2021 - **National Science Foundation Postdoctoral Research Fellow in Biology (PRFB), Martin Lab, Museum of Vertebrate Zoology & Department of Integrative Biology, University of California, Berkeley, CA.**

- Studied young species with ongoing gene-flow to identify candidate genes subject to selective sweeps.
- Estimated population demographic history, identifying candidate introgressed genes.

2020 - 2021 **Postdoctoral Researcher, Martin Lab, Museum of Vertebrate Zoology & Department of Integrative Biology, University of California, Berkeley, CA.**

- Identified candidate fitness associated genes based on a fitness experiment conducted in the wild.
- Constructed genotypic fitness landscapes, quantifying epistasis for fitness.

2014 - 2020 **Ph.D. Student, Storfer Lab, Department of Biological Sciences, Washington State University, Pullman, WA**

- Generated, assembled, & annotated three salamander transcriptomes; identified paralogous and orthologous genes for comparative transcriptomics.
- Assessed sensitivity of demographic reconstruction methods to genome assembly contiguity.
- Studied the macroevolutionary dynamics of adaptive radiation across *Anolis* lizards.
- Extended phylodynamic methods to study transmission dynamics in a transmissible cancer, identifying candidate genes underlying transmission rate variation.

Skills

Code: R (8 years), bash (7 years), Python (1 year).
Statistics: Classical stats, linear/mixed models, genetic demographic modeling, network analysis, Bayesian/Maximum Likelihood phylogenetics, comparative phylogenetics, phylodynamics, genome-scale gene/species tree inference.
Computing: SLURM, PBS, conda, Unix tools, git.
Bench: DNA Extraction, RNA extraction (Kit & TRIzol).
Bioinformatics: Illumina whole genome and transcriptome alignment with BWA. Transcriptome assembly (Trinity), annotation (Trinotate). SNP genotyping with GATK, samtools, ANGSD.

Notable Funding/Awards

***Postdoctoral Research Fellowship in Biology*, 2021 – 2023** – National Science Foundation. Award totaling $138,000. "*Hybridization on the adaptive landscape.*"

***Doctoral Student Achievement Award: Sciences*, 2020** – Washington State University College of Arts and Sciences.

***Brislawn Graduate Fellowship in Biological Sciences*, 2019 –** WSU Graduate Program ($3000).

***Elling Foundation Travel Award (WSU), 2015-2019* –** Awards totaling $11,306.

Select Publications

Full list (21): Google Scholar & Academic CV

A transmissible cancer shifts from emergence to endemism in Tasmanian devils. **Patton** et al., 2020, *Science*. DOI: 10.1126/science.abb9772
When adaptive radiations collide: Different evolutionary trajectories between and within island and mainland lizard clades. **Patton** et al., *PNAS*. DOI: 10.1073/pnas.2024451118
Hybridization alters the shape of the genotypic fitness landscape, increasing access to novel fitness peaks during adaptive radiation. **Patton** et al., 2022, *In Review – eLife*. DOI: 10.1101/2021.07.01.450666
Contemporary demographic reconstruction methods are robust to genome assembly quality: A case study in Tasmanian Devils. **Patton** et al., 2019, *MBE*. DOI: 10.1093/molbev/msz191