

MATTHEW GIBSON

gibsonmatt.github.io

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EDUCATION

Indiana University

2016 - Present

Ph.D. in Evolution, Ecology, and Behavior, minor in bioinformatics

Advisor: Leonie C. Moyle

University of Kansas

2011 - 2016

Bachelor of Science in Genetics, with honors

Thesis: *Connecting the Breeding System to Mating Patterns in Macaronesian Tolpis*

Advisors: Mark E. Mort and Daniel J. Crawford

IN REVIEW/REVISION

Gibson, M.J.S., Crawford, D.J., Mort, M.E., Kerbs, B., Menzes de Sequeira, M., Kelly, J.K. (2020). Genome-wide genotyping estimates mating system parameters in the island species *Tolpis succulenta*. *In review at American Journal of Botany*

Gibson, M.J.S. & Moyle, L.C. (2020). Regional differences in the abiotic environment contribute to genomic divergence within a wild tomato species. *In revision at Molecular Ecology* [BioRxiv: 10.1101/744797]

Gibson, M.J.S., Lourdes Torres, M., & Moyle, L.C. (2020). Local extirpation is pervasive among historical populations of Galpagos endemic tomatoes. *In revision at Evolutionary Ecology* [BioRxiv: 10.1101/744797]

PUBLICATIONS

Jewell, C.P., Zhang, S., **Gibson, M.J.S.**, Tovar-Mendez, A., McClure, B., & Moyle, L.C. (2020). Intraspecific standing variation underlying reproductive barriers between species in the wild tomato clade (*Solanum* sect. *Lycopersicon*). *Accepted at Heredity* [BioRxiv: 10.1101/718544]

Kostyun, J.L., **Gibson, M.J.S.**, King, C.M., & Moyle, L.C. (2019). A simple genetic architecture and low constraint allows rapid floral evolution in a diverse and recently radiating plant genus. *New Phytologist*. doi: 10.1111/nph.15844

Kerbs, B., Ressler, J., Kelly, J.K., Mort, M.E., Santos-Guerra, A., **Gibson, M.J.S.**, Caujape-Castells, J., & Crawford, D.J. (2017). Variation in synthetic interspecific hybrids of *Tolpis* (Asteraceae) in the Canary Islands: novel character combinations, transgressive traits, and phenotypic lines. *Arabidopsis Plants*. 9(5): plx043. doi: 10.1093/aobpla/plx043

PRESENTATIONS

[†] Presenter

- Gibson, M.J.S.[†]**, Lourdes Torres, M., & Moyle, L.C. (2019). Demographic histories of tomato species on the Galpagos islands: genomic consequences of a biological invasion. Contributed presentation. *Galpagos Conservation and Research Symposium*. San Cristobal, Galapagos, Ecuador
- Gibson, M.J.S.[†]**, Lourdes Torres, M., & Moyle, L.C. (2019). Demographic and genomic threats to endemic tomato species on the Galpagos islands: evidence for local hybridization and extinction. Contributed poster. *Plant Sciences Symposium*. Davis, California.
- Hibbins, M.[†], **Gibson, M.J.S.**, Guerrero, R.F., & Hahn, M.W. (2019) Introgression greatly increases the probability of hemiplasy in phylogenetic inference. Poster. *Evolution*. Providence, RI.
- Gibson, M.J.S.[†]** & Moyle, L.C. (2018). Rapid phenotypic evolution is unconstrained by pleiotropy in the florally diverse genus *Jaltomata*. Poster. *American Genetic Association Presidents Symposium*. Toronto, Canada
- Gibson, M.J.S.[†]**, Josephs, E.B., & Moyle, L.C. (2017). Parallel QTL mapping of shared and unique loci for adaptation and reproductive isolation between *Solanum* species. Poster. *Midwest Ecology and Evolution Conference*. Champaign, Illinois, USA
- Gibson, M.J.S.[†]** (2016). Connecting the Breeding System to Mating Patterns in Macaronesian Tolpis. Presentation. *Undergraduate Research Symposium*. Lawrence, Kansas, USA.
- Mort, M.E.[†], Archibald, J.K., **Gibson, M.J.S.**, Bontrager, H., Hauber, D.P., Borges Silva, L., Menezes de Sequeira, Moura, M., Santos-Guerra, A., Kelly, J.K., Gruenstaeudl, M., Juli Caujape-Castells, & Crawford, D.J. (2016). The utility of Multiplexed-Shotgun-Genotyping (MSG) for resolving phylogenetic relationships within and among oceanic archipelagos: an example from Macaronesian Tolpis (Asteraceae). *Island Biology*. Azores, Portugal.
- Mort, M.E.[†], Archibald, J.K., **Gibson, M.J.S.**, Bontrager, H., Hauber, D.P., Borges Silva, L., Menezes de Sequeira, Moura, M., Santos-Guerra, A., Kelly, J.K., Gruenstaeudl, M., Juli Caujape-Castells, & Crawford, D.J. (2016). Analyses of Multiplexed-Shotgun-Genotyping (MSG) data reveal cryptic biodiversity in Macaronesian Tolpis. *Island Biology*. Azores, Portugal.

SOFTWARE

HeIST: Hemiplasy Inference and Simulation Tool. Hibbins, M. & Gibson, M.J.S. 2020.
[<https://github.com/mhibbins/HeIST>]

TEACHING EXPERIENCE

Assistant Instructor, R Programming Boot camp, Indiana University	2019
Guest lecture on climate change and adaptation, BIOL 318 Evolution, Indiana University	2019
Assistant Instructor, BIOL 318 Evolution, Indiana University	2019
Instructor, Our Evolving World, Indiana University	2018-2019
Assistant Instructor, BIOL 111 Evolution and Diversity, Indiana University	2018
Guest lecture on genetic mapping, BIOL 318 Evolution, Indiana University	2017
Assistant Instructor, BIOL 318 Evolution, Indiana University	2017
Assistant Instructor, BIOL 113 Biology Laboratory, Indiana University	2016-2017
Undergraduate Teaching Assistant, Human Anatomy, University of Kansas	2015

AWARDS/HONORS

George W. Brackenridge Fellowship, Indiana University, \$2500	2019
Plant Sciences Symposium Travel Award, UC Davis, \$500	2019
Cleland Plant Science Travel Award, Indiana University, \$500	2018
Summer Institute in Statistical Genetics Scholarship, University of Washington, \$2000	2017
Floyd Plant Biology Fellowship, Indiana University, \$3000	2017-2019
Departmental Honors, University of Kansas,	2016
Undergraduate Research Award, University of Kansas, \$1000	2016
Deans List, University of Kansas	2014-2016

WORKSHOPS

Summer Institute in Statistical Genetics, University of Washington	2017
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PROFESSIONAL EXPERIENCE

Student representative evolution search committee, Indiana University	2019
Student representative EEB hiring committee, Indiana University	2018

VOLUNTEER EXPERIENCE

Mentor, Jim Holland Summer Science Research Program, Indiana University	2018-2019
Mentor, Groups Scholars STEM Program, Indiana University	2016-2017
Natural Science Community Organization, University of Kansas	2015

SOFTWARE PROFICIENCY

Languages: Python, R, and Bash

Life science/genomics: GATK, samtools, BCFtools, BWA, Stacks, iPyrad, R/QTL, Structure, and scikitlearn