Jennafer **Hamlin**

APHL Bioinformatics Fellow

Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA

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I am a scientist with 10+ years of experience in classical genetics, genomics, and evolutionary biology. My training includes using a range of tools - bioinformatics, genomics, population genetics, molecular evolution with experimental design in mind. Over the years as my computational skills increased, the genomes of the organisms I work on get smaller! I, now, work at the interface of public health, tool development, and understanding orgnamisms which can cause to humans.

Education

University of Georgia — *Athens, GA*

Ph.D. in Genetics — *2015*

University of North Carolina - Asheville — *Asheville, NC*

B.S. in Biology — *2010*

Appointments

Centers for Disease Control and Prevention — *Atlanta, GA*

APHL Bioinfomratics Felllow — *Sep-19–Current*

- Tinsel - an Rshiny application for annotating outbreak trees

University of Georgia — *Athens, GA*

Bensasson Lab Post-Doctoral Researcher — *Oct-17–Aug-19*

- Population genomics of yeast

Indiana Unversity — *Bloomingto, IN*

Moyle Lab Post-Doctoral Researcher — *Jun-15–Sep-19*

- Speciation and genomics in wild tomatoes

Skills

Analytical

Genomics, Bioinformatics, Data science, Reproducible research, Statistics, Experimental Design

Programming

R - expert, Bash - expert, AWK - proficient, Python - expert

Tools

Git/Github, High Performance Computing, Conda/Anaconda

Publications

First author

JAP Hamlin, MS Hibbins, LC Moyle — *Evolution Letters*

Assessing biological factors affecting postspeciation introgression — *2020*

JAP Hamlin, GB Dias, CM Bergman, D Bensasson — *G3*

Phased diploid genome assemblies for three strains of Candida albicans from oak trees — *2019*

JAP Hamlin, NA Sherman, LC Moyle — *G3*

Two loci contribute epistastically to heterospecific pollen rejection, a postmating isolating barrier between species — *2017*

JAP Hamlin, TJ Simmonds, ML Arnold — *Biological Journal of the Linnean Society*

Niche conservatism for ecological preference in the Louisiana iris species complex — *2017*

JAP Hamlin, ML Arnold — *Journal of Heredity*

Neutral and Selective Processes Drive Population Differentiation for Iris hexagona — *2015*

JAP Hamlin, ML Arnold — *Ecology and Evolution*

Determining Population Structure and Hybridization for Two Iris Species. — *2014*

Non-first author

ML Arnold, AN Brothers, JAP Hamlin, SJ Taylor, NH Martin — *Reticulate Evolution*

Divergence-with-gene-flow—what humans and other mammals got up to — *2015*

ML Arnold, JAP Hamlin, AN Brothers, ES Ballerini — *Rapidly evolving genes and genetic systems*

Natural hybridization as a catalyst of rapid evolutionary change — *2012*

ML Arnold, ES Ballerini, AN Brothers, JAP Hamlin, CDA Ishibashi, ... — *Plant Ecology & Diversity*

The genomics of natural selection and adaptation: Christmas past, present and future (?). — *2012*

K Marshall, J Hamlin, M Armstrong, J Mendoza, C Lee, D Pieri, R Rivera, ... — *The Bulletin of the Ecological Society of America*

Science for a social revolution: ecologists entering the realm of action — *2011*

Preprints

J Hamlin, LC Moyle — *bioRxiv*

Spatial proximity determines post-speciation introgression in Solanum — *2019*

Presentations

Talks

University of Georgia — *Athens, GA*

Population Genomics of wild and domesticated yeast. — *2018*

Society for the Study of Evolution — *Portland, OR*

No Easy D: Little Evidence for Introgression from Whole-Genome Data in Wild Solanum. — *2017*

Society for the Study of Evolution — *Austin, TX*

Epistasis for Postmating Prezygotic Isolation. — *2016*

Indiana Unviversity Brown Bag — *Bloomington, IN*

Spatial, temporal, and genome-wide patterns of differentiation for the Louisiana iris species complex. — *2015*

Society for the Study of Evolution — *Raleigh, NC*

What Drives Phenotypic and Genetic Divergence for Iris hexagona? — *2014*

Society for the Study of Evolution — *Snowbird, UT*

Comparative Phylogeography of Two Louisiana Irises. — *2013*

Posters

Fungal Genetics Conference — *Pacific Grove, GA*

Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast. — *2019*

Cellular and Molecular Fungal Biology: Gordon Research Conference — *Holderness, NH*

Clinical Saccharomyces cerevisiae are admixed domesticated yeast. — *2018*

Southeastern Population Ecology & Evolutionary Genetics. — *Laural Hill, NC*

Higher Prevalence of Genetic Exchange Given Geographic Proximity. — *2017*

SolGenomics — *Davis, CA*

Two Loci Contribute Epistastically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species. — *2016*

Botany — *Boise, ID*

What Drives Phenotypic and Genetic Divergence for Iris hexagona? — *2014*

American Genetic Association *Guanajuato, Mexico*

Comparative Phylogeography of Two Louisiana Iris Species: Iris fulva and Iris brevicaulis. *2011*

R-Packages

Tinsel

https://github.com/jennahamlin/Tinsel

"An R package for visulizating and annotating phylogenetic trees" *2019*

- Author and maintainer

Mentoring

University of Georgia

- E. Scopel Ferreira Da Costa
- J. Pena
- T. Simmonds
- K. Miler
- J. Foley
- S. Duque
- B. Webb

Indiana University

- A. Huh
- J. Breisch
- S. Henderson
- L. Howser
- C. Plasterer
- D. Shukla
- S. Seo