Jennafer **Hamlin**

APHL Bioinformatics Fellow

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

jhamlin@cdc.gov | jennahamlin

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, population genetics, molecular evolution all with experimental design in mind. Over the years as my computational skills increased, the genomes of the organisms I work on get smaller! Now, I work at the interface of public health, application development, and understanding organisms that can cause harm to humans with an empahsise of developing reproduciable research.

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 — *19-Sep–Current*

- Developing Tinsel - an Rshiny application for annotating outbreak trees
- Worked with Scicomp for Tinsel to be available on CDC internal server
- Intiated collaboration to make Tinsel part of an open source genomics platform being developed by EDLB

University of Georgia — *Athens, GA*

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

- Directed collaborative research with graduate and undergraduate students
- Collated and streamlined genome mapping for 1000 Saccharomyces cerevisiae isolates as lab resource
- Used an iterative approach to assign 400 genomes to well-defined populations using best practices for population genomics and phylogenetics to validate patterns.
- Resolved haplotypes for Candida albicans genomes and verified with PacBio sequencing

Indiana Unversity — *Bloomingto, IN*

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

- Directed research with faculty, graduate, andundergraduates at IU and with two external universities
- Identified genome-wide trends in 30 genomes for Solanum species using whole genome mapping
- Streamlined genotyping to generate biological replicates. Validate data accuracy using technical replicates along with statistical analyses
- Used linear mixed models and ANOVA to identify differences in targeting, rates, and floral trait differences with biological and technical replicates for a large-scale crossing project

Skills

Analytical

Bioinformatics, Data science, Experimental Design, Genomics, High Performance Computing, Project Management, Quality Control, Reproducible research, Statistics, Technical writing and documentation

Programming

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

Tools

bcftools, blast, bwa, conda/anaconda, fastQC, git/github, quast, samtools, seqtk, spades, vcftools

Publications

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*

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*

JAP Hamlin, ML Arnold — *Ecology and Evolution*

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

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*

Presentations

Talks

Start Writing Manuscripts in Rmarkdown — *Atlanta, GA*

Genomics Interest Group - techincal — *2020*

Build Shiny Apps — *Athens, GA*

Warnell School of Forestry & Natural Resources — *2018*

Population Genomics of wild and domesticated yeast. — *Athens, GA*

University of Georgia — *2018*

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

Society for the Study of Evolution — *2017*

Epistasis for Postmating Prezygotic Isolation. — *Austin, TX*

Society for the Study of Evolution — *2016*

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

Indiana Unviversity Brown Bag — *2015*

What Drives Phenotypic and Genetic Divergence for Iris hexagona? — *Raleigh, NC*

Society for the Study of Evolution — *2014*

Comparative Phylogeography of Two Louisiana Irises. — *Snowbird, UT*

Society for the Study of Evolution — *2013*

Posters

Tinsel - an Rshiny app for phylogenetic tree annotation *Portland, OR*
Association of Public Health Laboratories Annual Meeting *2020*

Tinsel - an Rshiny application for annotating outbreak trees *Atlanta, GA*
Integrated Foodborne Outbreak Response and Management *2020*

Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast. *Pacific Grove, GA*
Fungal Genetics Conference *2019*

Clinical Saccharomyces cerevisiae are admixed domesticated yeast. *Holderness, NH*
Cellular and Molecular Fungal Biology: Gordon Research Conference *2018*

Higher Prevalence of Genetic Exchange Given Geographic Proximity. *Laural Hill, NC*
Southeastern Population Ecology & Evolutionary Genetics. *2017*

Two Loci Contribute Epistastically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species. *Davis, CA*
Solanaceae Conference *2016*

What Drives Phenotypic and Genetic Divergence for Iris hexagona? *Boise, ID*
Botanical Society of America *2014*

Comparative Phylogeography of Two Louisiana Iris Species: Iris fulva and Iris brevicaulis. *Guanajuato, Mexico*
American Genetic Association *2011*

R-Packages

Tinsel - An R package for visulizing and annotating phylogenetic trees *https://github.com/jennahamlin/Tinsel*
Author and maintainer *2019*

Mentoring

University of Georgia graduate students

E. Scopel Ferreira Da Costa
J. Pena

University of Georgia undergraduate students

T. Simmonds
K. Miller
J. Foley
S. Duque
B. Webb

Indiana University graduate students

C. Jewell
M. Gibson

Indiana University undergraduate students

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