Kian Holden Kelly

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Bioinformatics Analyst | PhD Candidate

Bioinformatics Analyst and PhD candidate at University of California Riverside with five years of research experience in next-generation sequencing (NGS) analysis, pipeline development, and molecular biology. Recognized for generating 8 novel genomes and serving as first author to three publications (in prep) involving genomic and metagenomic analysis of fungi. Distinguished as a Chancellor's Fellow and NSF REU Mentor. Graduation expected in September, 2025.

Skills

BIOINFORMATICS

Metabarcoding analysis
Metagenomics
Phylogenetics
Genome assembly and annotation
Comparative genomics
Phylogenomics

SOFTWARE AND PROGRAMMING

R Language
Python
Data visualization
Statistical data analysis
Pipeline development
Nextflow
Bash Scripting
Data wrangling
Git and GitHub
Machine learning (Hidden Markov Models)
Cloud computing
Microsoft Office (Word, PowerPoint, Excel)

MOLECULAR BIOLOGY AND PROTEIN PURIFICATION

PCR (polymerase chain reaction)
Nanopore sequencing
Molecular cloning
Microbial culturing
Membrane protein extraction
CRISPR/Cas9 genome editing
NGS library preparation
DNA amplification and purification
Cell culturing
Viral recombineering
Affinity chromatography
Bacterial artificial chromosome recombineering

Research Experience

GRADUATE STUDENT, UNIVERSITY OF CALIFORNIA RIVERSIDE, CA **SEP '22 – SEP '25**

Generation and analysis of NGS data; sequence classification software development; Jason Stajich Lab

- Generated genomic and metagenomic nanopore and illumina sequence data, resulting in 8 novel fungal genomes and 10,000 taxa identified through metagenomic analysis.
- Performed comparative genomic analysis of extremophilic fungi resulting in the identification of potentially horizontally acquired genes conferring extreme resistance phenotypes.
- Analyzed NGS data using R, and Python, utilizing custom built pipelines resulting in three publications (in preparation)
- Lead developer for sequence classification software using machine learning (Python).
- Obtained first cultures of 15+ undescribed fungal species. Developed strain library of 100+ extreme adapted microbes for bioprospecting use in the National Science Foundation ExFAB Biofoundry.

RESEARCH FELLOW, CORNELL UNIVERSITY, NY **MAY '21 – AUG '21**

National Science Foundation Research Experience for Undergraduates (REU) scholar, Toshi Kawate Lab

- Investigated structure of plant membrane protein NPF3, determining first methods for suitable preparation for cryo-electron microscopy and purification from cultured insect cells.
- Obtained first cryo-electron micrographs of NPF3 along with my mentor, which resulted in the first clear two-dimensional representations of the protein.
- Applied several molecular biology techniques including molecular cloning, cell culturing, transfection, transduction, transposition, membrane protein detergent solubilization, affinity chromatography, size exclusion chromatography, and others.

RESEARCH ASSOCIATE, FORT LEWIS COLLEGE, CO **SEP '19 – MAY '22**

Position in several labs including Caroline Kulesza, David Blake, and Kiesha Carlson labs

- Participated in bacterial artificial chromosome recombineering to generate a Human Cytomegalovirus (HCMV) mutant library.
- Used Golden Gate cloning to create CRISPR plasmids for gene knockout in Arabidopsis suecicia.

Publications

• (In preparation) **Kelly K.,** Wagner C., Coeline C.., Stajich J. (2024). Survey of Moss Biocrust Associated Glomeromycotina Across an Aridity Gradient reveals Widespread, Novel Host Associations. New Phytologist

• (In preparation) **Kelly K.,** Liu X.**,** Croyle J.., Stajich J. (2024) Increased aridity is associated with community shifts toward extreme adapted taxa and reduced diversity in the biocrust mycobiome of Southern California. PLOS ONE

• (In preparation) **Kelly K.,** Croyle J.., Stajich J. (2024) Complete genomic sequence of *Coniochaeta sp.* JDC7 isolate from Mojave Desert moss biocrust. Microbiology Resource Announcements

Software

Personal website: https://g-gnome.github.io/

MAT-PREDICT

Lead developer (project in progress)

- The fungal MAT locus is highly variable in sequence and structure and is sometimes called an "invisible" sequence due to its difficulty to detect in genomes.
- MAT-Predict finds the invisible sequence, reducing the time of MAT locus identification by ~95%.
- Trains Hidden Markov Models based on a curated dataset of fungal mating-type sequences.
- Predicts the genomic coordinates of the fungal mating type sequence.
- Determines the category of mating-type sequence within a fungal genome.
- Utilized: Python, Machine Learning, Hidden Markov Models

Training and Teaching Experience

NSF REU MENTOR **MAY '23 – AUG '23**

- Acted as mentor for an undergraduate student researching metagenomics, microbial culturing, and bioinformatics.

TA, MICROBIOLOGY **JAN '24 – MAY '24**

- Lead weekly discussion sections for 100 students, developing lectures to supplement course content.

LEAD PEER EDUCATOR **SEP '19 – JAN '22**

- Tutored students in all subjects, ran meetings and trainings for other peer educators across several disciplines.

Education

University of California Riverside, Plant Pathology/Microbiology — Ph.D. Sep 2025 (GPA 3.89)
Fort Lewis College — B.S. 2022 (GPA 3.70)

Honors and Activities

President, Ecological Society of America SEEDS program, Fort Lewis College	SEP '19 – MAY '22
Chancellor's Distinguished Fellow, University of California Riverside	AUG '22
GAAN Fellowship, University of California Riverside	SEP '23
Klotz Travel Award, University of California Riverside	JUN '23
Fort Lewis College Undergraduate Research Grant, University of California Riverside	APR '21