KEVIN RILEY AMSES, Ph.D.

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Education

Ph.D. Ecology and Evolutionary Biology **2015 – 2021**
University of Michigan, Ann Arbor, MI, USA

Single cell sequencing facilitates genome-enabled biology in uncultured fungi and resolves deep branches on the fungal tree of life.

M.Sc. Ecology and Evolutionary Biology **2015 – 2016**
University of Michigan, Ann Arbor, MI, USA

B.Sc. Botany, minor in Organic Chemistry **2009 – 2015**
Humboldt State University, Arcata, CA, USA

Relevant Skills

Laboratory skills

1. General laboratory skills
    - Aseptic technique, including the use of various sterilization methods (e.g., autoclave, UV, flame sterilization, filter sterilization, Bacti-Cinerator, etc.) and sterile cabinets (e.g., laminar flow hood, biological safety cabinet, etc.)
    - Preparation and maintenance of stock solutions at desired solute concentrations and pH
    - Light, scanning electron, and transmission electron microscopy, including sample preparation
    - Proficient with general laboratory equipment, including serological or micropipettes of various volumes, centrifuges, vortex machines, water baths, heating elements, incubators, scales, etc.

2. Cultivation of microbial cells and tissues
    - Preparation and dispensation of sterile liquid and solid media
    - Isolation of pure microbial cultures from environmental samples
    - Purification of contaminated microbial cultures via dilution plating, streak plating, etc.
    - Single cell isolation
    - Maintenance and transfer of live and active microbial cultures in liquid or solid media
    - Long term storage (4C and -80C) and cataloging of live microbial cultures

3. Molecular biology
    - Isolation and purification of nucleic acids (DNA and RNA) from microbial cells/tissues at low (i.e., single-cell genomics) and high inputs (i.e., tissue cultures or macroscopic forms)
    - Quality assessment of nucleic acid extracts via NanoDrop spectrophotometer and Qubit fluorometer
    - PCR, including primer design, troubleshooting, and optimization
    - qPCR, including primer design, optimization, and QC of short-read sequencing libraries
    - Gel electrophoresis

- Sanger sequencing, including associated cycle sequencing reactions
- Curation of Sanger-derived chromatograms
- Multiple displacement amplification (single-cell genomics)
- Illumina sequencing library preparation from nucleic acid extracts (transposase-mediated tagmentation and PCR-based adapter incorporation)
- Normalization and pooling of Illumina sequencing libraries according to Qubit fluorometric readings
- Interpretation of BioAnalyzer and TapeStation traces
- CRISPR oligo design

Computational skills

1. General computational fluencies
    - python
    - R, base and tidyverse
    - rust
    - Unix (bash, zsh, etc.)
    - Linux and Mac OS X
    - git and GitHub
    - high performance computing environments

2. Bioinformatic competencies
    - Fluency in commonly used file formats for biological data and conversion between them
    - Quality assessment of raw and processed biological data representations (e.g., reads, assemblies, etc.)
    - Assembly and annotation of prokaryotic and eukaryotic draft genomes from short- and long- read libraries
    - Metagenomics
        - *in silico* isolation of microbial draft genomes from complex backgrounds (bulk metagenomics, single-cell metagenomics, etc.)
        - Complexity assessment of metagenomic read libraries
        - Novel implementations of metagenomic filtering algorithms (e.g., see Amses et al. 2020)
    - Multiple sequence alignment, trimming, filtering, and concatenation
    - Phylogenetic and phylogenomic analyses
        - Compilation and curation of phylogenetic datasets using automated and manual approaches
        - Phylogenetic tree construction, including maximum likelihood, ASTRAL consensus, Bayesian, neighbor-joining, etc.
        - Phylogenetic tree visualization, annotation, and *post hoc* analyses
    - Population genomics and heterozygousity assessment
        - Mapping short- and long- read libraries to reference genomes
        - SNP calling and filtering
        - Clustering of strains by SNP profiles using various established and custom distance metrics, and production of high quality SNP trees
        - Novel implementations of SNP-based genomics analyses (e.g., see Amses et al. 2022*)*
    - Comparative genomics analyses and interpretation (e.g., antiSMASH, interproscan, PFAM, KEGG, GO, dbCAN, etc.)
    - Analysis of RNAseq data for differential expression, transcriptome annotation, or transcript-based improvement of DNA assemblies

3. Data visualization
- Production of high quality and informative visual figures (e.g., Amses et al. 2022; Amses et al. 2020)
- Fluency in various data-driven image visualization libraries:
    - ggplot (R, tidyverse)
    - matplotlib (python)
    - plotly (python implementation)

Software

SCGid: a consensus approach to contig filtering and genome prediction from single cell sequencing libraries of uncultured eukaryotes.

Repository: https://github.com/amsesk/SCGid
Publication: 10.1093/bioinformatics/btz866

Research Experience

Postdoctoral Scholar **2021 – present**
Oregon State University, Corvallis, OR, USA

Project description: Fungi are members of complex natural systems, within which their interactions with other living components of these systems (i.e., symbioses) can play pivotal roles in global patterns of nutrient cycling (e.g., mycorrhizae). The stable, symbiotic colonization of fungal cells by bacteria (i.e., endosymbiotic bacteria) is becoming increasingly recognized in nature, although the implications and histories of these systems remain poorly understood. Our work here generates genome-scale data for pairs of symbiotic partners, the current paucity of which corresponds with the relative novelty of this type of symbiosis to science. With increased sampling in genomic contexts, we can better understand the entangled evolutionary trajectories along which partners coevolve, how novel pairs of partners arise and stabilize over deep time scales, and the functional implications of harboring endosymbiotic bacteria with respect to the host.

Graduate Student **2015 – 2021**
University of Michigan, Ann Arbor, MI, USA

Project description: Most fungi are uncultured, meaning that they have not, and possibly cannot, be isolated in pure laboratory cultures. This simple reality severely complicates biological research in these areas of the fungal tree of life, obscuring their forms, functions, and evolutionary histories. My dissertation research uses single-cell genomics (SCG) to circumvent this central obstacle, sequencing the genomes of uncultured fungi collected as individual cells directly from nature. Genome-scale data in hand, we can resolve blurry areas of the tree of life and characterize the life histories of these dark matter fungi in a genetic context.

Undergraduate Researcher **2014 – 2015**

Humboldt State University, Arcata, CA, USA

Project description: Developed and tested growth systems to detect horizontal gene transfer in *Alicyclobacillus*, a thermophillic, acid-loving bacterial genus isolated from acid hot springs in California. The driving question focused on determining the degree to which horizontal gene transfer occurs in acid hot springs and influences microbial community responses to changing conditions in these dramatic environments.

Undergraduate Researcher **2013 – 2015**

Humboldt State University, Arcata, CA, USA

Project description: Much of the Neotropics remain undeveloped. While we know that the tropics boast diverse populations of plants and animals, fungal diversity remains under-explored. We described and published three new genera of false truffles, entirely new to science, using classical and molecular taxonomic approaches.

Publications

9. **Amses, K.R.**, R. Simmons, J.E. Longcore, S.J. Mondo, K. Seto, G. Jeronimo, A. Bonds, C.A. Quandt, W. Davis, Y. Chang, B.A. Federici, A. Kuo, K. LaButti, J. Pangilinan, W. Andreopoulos, A.J. Tritt, R. Riley, H. Hundley, J. Johnson, A. Lipzen, K. Barry, B.F. Lang, C.A. Cuomo, N.E. Buchler, I.V. Grigoriev, J.W. Spatafora, J.E. Stajich, T.Y. James. 2022. Phylogenomic analysis of zoosporic taxa suggests diploid-dominant life cycles characterized the early evolution of Fungi. *Proc Natl Acad Sci USA*. 119(36):e2116841119. doi: 10.1073/pnas.2116841119.

8. Van Court, R.C., M.S. Wiseman, K.W. Meyer, D.J. Ballhorn, **K.R. Amses**, J.C. Slot, B.T.M. Dentinger, R. Garibay-Orijel, and J.K. Uehling. 2022. Diversity, biology, and history of psilocybin-containing fungi: Suggestions for research and technological development. *Fungal Biol*. 126(4):308-319. doi: 10.1016/j.funbio.2022.01.003.

7. Belasen, A.M., **K.R. Amses**, R.A. Clemons, C. Guilherme Becker, L. Felipe Toledo, and T.Y. James. 2022. Habitat fragmentation in the Brazilian Atlantic Forest is associated with erosion of frog immunogenetic diversity and increased fungal infections. *Immunogenetics*. 74:1–11. doi: 10.1007/s00251-022-01252-x.

6. Jerônimo, G.H., D.R. Simmons, **K.R. Amses,** K. Seto, T.Y. James, C.LA. Pires-Zottarelli, and J.E. Longcore. 2022. *Phytochytrium* and *Sparrowiella*, two new polycentric genera in Cladochytriales. *Mycol Prog*. 21:1–9. doi: 10.1007/s11557-022-01791-3.

5. Alors, D., **K.R. Amses**, T.Y. James, S. Boussiba, A. Zarka. 2022. *Paraphysoderma sedebokerense* GlnS III is essential for the infection of its host *Haematococcus lacustris*. *J Fungi*. 8(6): 561. doi: 10.3390/jof8060561.

4. **Amses, K.R.**, W.J. Davis and T.Y. James. 2020. SCGid: a consensus approach to contig filtering and genome prediction from single cell sequencing libraries of uncultured eukaryotes. *Bioinform*. 36(7): 1994–2000. doi: 10.1093/bioinformatics/btz866.

3. Davis, W.J., **K.R. Amses**, G.L. Benny, D. Carter-House, Y. Chang, I. Grigoriev, M.E. Smith, J.W. Spatafora, J.E. Stajich, T.Y. James. 2019. Genome-scale phylogenetics reveals and monophyletic Zoopagales (Zoopagomycota, Fungi). *Mol Phylogenet Evol*. 133:152–163. doi: 10.1016/j.ympev.2019.01.006.

2. Davis, W.J., **K.R. Amses**, E.S. James, T.Y. James. 2019. A new 18S phylogeny of uncultured predacious fungi (Zoopagales). *Mycologia*. 111(2):291–298. doi: 10.1080/00275514.2018.1546066.

1. Smith, M.E., **K.R. Amses**, T.F. Elliott, K. Obase, M., M.C. Aime, T.W. Henkel. 2015. New sequestrate fungi from Guyana: *Jimtrappea guyanensis* gen. sp. nov., *Castellanea pakaraimophila* gen. sp. nov., and *Costatisporus cyanescens* gen. sp. nov. (Boletaceae, Boletales). *IMA Fungus*. 6(2):297–317. doi: 10.5598/imafungus.2015.06.02.03.

Mentorship Experience

Sloane Crowell | Undergraduate Student **2022 – present**

I hired Sloane as a research assistant in July 2022 and have since been training her in the isolation and cultivation of Mortierellomycotina fungi and downstream molecular techniques (i.e. DNA extraction, PCR, gel electrophoresis, and Sanger sequencing). I have also been mentoring Sloane in project management by giving her significant freedom in managing 300+ samples in various states of our processing pipeline.

Paris Salazar-Hamm, Ph.D. | Postdoctoral Scholar **2022 – present**

Paris joined our lab in January of 2022 with extensive skills in microbiology and molecular genetics, but opportunities for growth in bioinformatics. I have guided her in developing her competencies in Unix, R, and bioinformatics software for processing and visualization large biological datasets.

William Gilmour | Undergraduate Student **2021 – present**

I served as Will’s mentor in an 8-week, USDA-funded summer research internship in 2021. I trained him in computational approaches to study biological data and, specifically, conduct RNAseq-based differential gene analysis. Will has continued to work in the lab where I have trained him in the isolation and cultivation of fungal tissues, and downstream molecular techniques.

Teaching Experience

BOT461: Mycology | Guest Lecturer | October 12, 2022
Zygomycete Fungi: Zoopagomycota
Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR

BDS477/577: Population Genetics | Guest Lecturer | May 17, 2022
Introduction to GitHub

Biological Data Sciences, Oregon State University, Corvallis, OR

BOT461: Mycology | Guest Lecturer | October 11, 2021
Zygomycete Fungi: Zoopagomycota
Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR

BIOL207: Microbiology | Graduate Student Instructor | Fall 2019
Program in Biology, University of Michigan, Ann Arbor, MI

BIOL173: Yeast Evolution | Graduate Student Instructor | Winter 2019
Program in Biology, University of Michigan, Ann Arbor, MI

BIOL305: Introduction to Genetics | Graduate Student Instructor | Winter 2016
Program in Biology, University of Michigan, Ann Arbor, MI

BIOL171: Introduction to Biology | Graduate Student Instructor **|** Fall 2015
Program in Biology, University of Michigan, Ann Arbor, MI

Seminars and Presentations

15. **Amses, K.R.** 2022. Change comes from near and far, from recent symbiotic shifts to deep trends in fungal evolution. Mycological Society of Japan. [Oral Presentation]

14. **Amses, K.R.**, W.J. Davis, N. Reynolds, R. Adeleke, T. Pawlowska, T.Y. James, G. Bonito, J.K. Uehling. 2022. Horizontal transmission and loss-driven evolution in *Mycoavidus*, a *Mortierella*-associated endohyphal bacterium. 31st Fungal Genetics Conference, Asilomar Conference Grounds, Pacific Grove, CA, USA. [Oral Presentation]

13. **Amses, K.R.** 2021. Single cell sequencing facilitates genome-enabled biology in uncultured fungi and resolves deep branches on the fungal tree of life. Biology Seminar Series. Humboldt State University, Arcata, CA, USA. [Oral Presentation]

12. **Amses, K.R.**, W.J. Davis, T.Y. James. 2020. SCGid, a consensus approach to contig filtering and genome prediction from single-cell sequencing libraries of uncultured eukaryotes. Tools and Technology Seminar Series. University of Michigan, Ann Arbor, MI, USA. [Oral Presentation]

11. **Amses, K.R.** and T.Y. James. 2019. Unwrapping the Mummy: Solving the phylogenetic mystery of the arthropod-mummifying fungus. 2019 Mycological Society of America Meeting. Graduate Minneapolis, Minneapolis, MN, USA. [Oral Presentation]

10. **Amses, K.R.**, W.J. Davis, T.Y. James. 2019. SCGid - a bioinformatic tool for scaffold binning and genome prediction from single-cell sequencing libraries. 30th Fungal Genetics Conference, Asilomar Conference Grounds, Pacific Grove, CA, USA. [Poster Presentation]

9. **Amses, K.R.**, W.J. Davis, T.Y. James. 2018. SCGid - a bioinformatic tool for scaffold binning and genome prediction from single-cell sequencing libraries. 2018 International Mycological Congress, Puerto Rico Convention Center, San Juan, PR. [Oral Presentation*]

8. **Amses, K.R.**, T.Y. James. 2017. The genome of the nematode destroying fungi *Stylopage hadra*. 29th Fungal Genetics Conference, Asilomar Conference Grounds, Pacific Grove, CA, USA. [Oral Presentation, Poster Presentation]

7. **Amses, K.R.** 2017. Catch your worm and eat it too: The molecular basis of prey-specificity and predatory ability from independent origins of nematophagy in fungi. Winter 2017 EEB Lunch Seminar Series, University of Michigan, Ann Arbor, MI, USA. [Oral Presentation]

6. **Amses, K.R.**, T.Y. James. 2016. The genome of the nematode destroying fungi *Stylopage hadra*. 2016 Mycological Society of America, Clark-Kerr Campus, University of California, Berkeley, CA, USA. [Oral Presentation]

5. **Amses, K.R.**, T.F. Elliott, M.E. Smith, T.W. Henkel. 2015. New Neotropical genera of ectomycorrhizal sequestrate Boletaceae. Eighth International Conference on Mycorrhiza. Northern Arizona University, Flagstaff, AZ, USA. [Poster Presentation]

4. **Amses, K.R.**, L. Nave. 2014. N cycle and fungal community responses to simulated climate change-induced forest die-off. HSU Botany Talk. Humboldt State University, Arcata, CA, USA. [Oral Presentation]

3. **Amses, K.R.**, L. Nave. 2014. N cycle and fungal community responses to simulated climate change-induced forest die-off. University of Michigan Biological Station – REU Research Symposium. University of Michigan Biological Station, Pellston, MI, USA. [Oral presentation]

2. **Amses, K.R.**, Morgan, B., Egerton-Warburton, L.M. 2013. Root access to underground water sources by tropical canopy trees in the seasonally dry forests of the Yucatan Peninsula, Mexico. HSU Botany Talk. Humboldt State University, Arcata, CA, USA. [Oral Presentation]

1. **Amses, K.R.**, Morgan, B., Egerton-Warburton, L.M. 2013. Root access to underground water sources by tropical canopy trees in the seasonally dry forests of the Yucatan Peninsula, Mexico. Chicago Botanic Garden and Field Museum of Natural History Joint REU Research Symposium. Field Museum of Natural History, Chicago, IL, USA. [Poster Presentation]

Awards, Grants, and Fellowships

National Institutes of Health, National Institute of General Medical Sciences (NIGMS) Postdoctoral Research Associate Training (PRAT) Fellowship (declined) *<u>Proposal Title</u>: Uncovering the hidden diversity of Earth's soil virome with an evolutionary perspective and rigorous computational approach.*	**2021**
Myron P. Backus Award ($1,000), Mycological Society of America	**2020**
Best Student Talk*, International Mycological Congress, San Juan, PR	**2018**
BLOCK Grants ($9,100), University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, MI, USA	**2016 – 2020**
University of Michigan Genetics Training Program Fellow (NIH)	**2016 – 2018**
Pre-Candidacy Rackham Student Research Grant ($1,500), University of Michigan, Rackham Graduate School, Ann Arbor, MI, USA	**2017**
Outstanding Scholarship in Organic Chemistry, Humboldt State University	**2015**
Sterling Sam Botany Award ($400), Humboldt State University	**2014**

Service and Outreach

Search Committee Member **2021**
Ecology and Evolution of Infection Plant Diseases, Department of Botany and Plant Pathology, Oregon State University

Assistant Instructor **2020**
ECR^2: Command-Line Bioinformatics for Beginners Workshop
Sponsored by American Society of Naturalists
asngrads.github.io/2020-07-27-ecr2-online/

Instructor **2017 – 2019**
Girls in Science and Education, Genetics module
University of Michigan, Ann Arbor, MI, USA

Assistant Instructor **2016**
Girls in Science and Education, Genetics module
University of Michigan, Ann Arbor, MI, USA

Peer reviewer for academic journals: Syst Biol, Genome Biol Evol, Microbiol Spectr