Susan L. McEvoy

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EDUCATION

Ph.D. in Ecology & Evolutionary Biology   **July 2022**
University of Connecticut, Storrs, CT, USA
Dissertation: *Application of emerging computational and genomic approaches to examine challenges to forest health*
Committee: Pamela Diggle, Elizabeth Jockusch, Rachel O'Neill, Yaowu Yuan, Jill Wegrzyn (chair)

B.S. in Biology   **2002**
Oregon State University, Corvallis, OR, USA

EXPERIENCE

Postdoctoral Scientist in Conservation Genomics   **Jul 2022 - present**
Santa Barbara Botanic Garden
Research Fellow (Courtesy): Rachel Meyer's Lab, Ecology & Evolutionary Biology Department, University of Santa Cruz
Perform the following responsibilities for the project: *Landscape and population genomics of the Gaviota tarplant (Deinandra increscens subsp. villosa; Asteraceae) for long term conservation*:

- Collect sample plant material along the coast in Central California
- Follow protocols for DNA and RNA extraction and library preparation
- Assemble and annotate a reference genome for Gaviota tarplant
- Using DNA resequencing from populations across the native range:
  - Quantify current and historical effective population size and level of inbreeding ○ Quantify degree of isolation versus gene flow
  - Relate allelic variation across landscape to functional annotations, and measure associations between genetic variation, landscape variation, and phenotypic traits
  - Quantify changes in rates of inbreeding, gene flow, and selection over time

Graduate Research Assistant   **Aug 2018 - Jul 2022**
Ecology & Evolutionary Biology, University of Connecticut
Bioinformatic analysis of forest trees, including genome assembly, annotation, comparative genomics, transcriptomics, and methylomics

- Investigated genomic strategies of stress tolerance in *Acer* by generating two genome assemblies and annotations for *Acer saccharum* and *Acer negundo*. Genomic references were used for expression analysis of *A. saccharum* under long-term nutrient stress, and comparative genomics and methylomics
- Assembled and annotated two genomes for *Fagus grandifolia* to investigate genomewide structural variation and examine a candidate locus of Beech bark disease
- Asssisted with assembly, annotation, and methylation profiling of the giant genome *Pinus lambartiana* as a reference for expression and methylation studies on white pine blister rust resistance
- Installed bioinformatic software and provide technical and methodological support to HPC users

Graduate Teaching Assistant   **Jan - Dec 2019**
Ecology & Evolutionary Biology, University of Connecticut
- Instructor for laboratory section of Biol 1108 – Principles of Biology II

Bioinformatician (Faculty Research Associate - Forest Genetics)   **Mar 2017 - Aug 2018**
Forest, Ecosystems, and Society, Oregon State University
Provided bioinformatic support to faculty and the Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC)
- Assembled a transcriptome for *Pinus monticola* and processed the calling of SNPs related to white pine blister rust resistance
- Assisted with creation of SNP genotyping array for Pseudotsuga menziesii
- Wrote code for scripts and modified programs using R, Perl, C#, and Java

Software Developer/Research Assistant   **Apr 2014 - Mar 2017**
Center on Teaching and Learning (CTL), University of Oregon
- Working closely with education researchers, designed and developed web applications and tablet-based instruction tools for the purpose of assessing and tracking student learning and the effectiveness of curricular programs
- Wrote code updating the existing central data system to support integration with new instruction and assessment tools. Extended existing data models and database systems to support new research and development activities

Web Manager   **Aug 2006 – May 2009; Oct 2010 – Apr 2014**
OSU Libraries & University Press, Oregon State University
- Responsible for the web presence of OSU Libraries and Press, including web applications related to resource discovery and access, library instruction, digital collection creation, and

supplementary sites for OSU Press books. Coordinated all aspects of the design and development process to meet deadlines

- Worked with stakeholders to identify content and functional requirements, directed site architecture, layout, and design, wrote code do develop and customize web applications
- Supervised student web developers and graphic designers; provided training to nontechnical staff

Interim Department Head   **May 2009-Oct 2010**
Emerging Technologies and Services, Oregon State University Libraries

- Managed staff including system administrators, programmers, and desktop support to meet departmental goals in areas of technical support
- Served on the Libraries' management team and participated in library reorganization and strategic planning

Forestry Web Communications Coordinator   **June 2003 – Aug 2006**
College of Forestry, Oregon State University

- Responsible for the design and development of the College of Forestry website and associated departmental and program sites
- Communicated standards to college-wide web editors; provided training and resources

AWARDS

2021 CFGA Carl Heimberger Award for Best Student Oral Presentation, Forest Genetics Student and Postdoc Symposium, $1000 CAD

GRANTS

EEB-MNH Botany Award 2021, University of Connecticut, Department of Ecology and Evolutionary Biology ($1500)

The Arnold Arboretum of Harvard University, 2021 Sequencing Award ($9127)

Botanical Society of America, Bill Dahl Graduate Student Research Award, 2020, ($1500)

EEB-MNH Botany Award 2020, University of Connecticut, Department of Ecology and Evolutionary Biology ($1500)

University of Connecticut Institute for Systems Genomics, Linda D. Strausbaugh Fellowship in Genetics and Genomics, 2019 ($1600)

EEB-MNH Botany Award 2019, University of Connecticut, Department of Ecology and Evolutionary Biology, EEB-MNH Botany Award ($1500)

PUBLICATIONS

McEvoy, S. L., Grady, P. G. S., Pauloski, N. Wegrzyn, J., (**2022**). Profiling genome-wide methylation in two maples: fine-scale approaches to detection with nanopore technology. *bioRxiv*.

Vuruputoor, V. S., Monyak, D., Fetter, K. C., Webster, C., Zaman, S., Bhattarai, A., Bennett, J., **McEvoy, S. L**, Shrestha, B., Caballero, M., & Wegrzyn, J. (2022). Welcome to the big leaves: best practices for improving genome annotation in non-model plant genomes. bioRxiv.

McEvoy, S. L., Sezen, U. U., Trouern-Trend, A., McMahon, S. M., Schaberg, P. G., Yang, J., Wegrzyn, J., & Swenson, N. G. (**2021**). Strategies of tolerance reflected in two North American maple genomes. *The Plant Journal*, 109(6), 1591-1613.

Caballero, M., Lauer, E., Bennett, J., Zaman, S., **McEvoy, S.,** Acosta, J., Jackson, C., Townsend, L., Eckert, A., Whetten, R.W. and Loopstra, C., Holliday, J., Mandal, M., Wegrzyn, J., & Isik, F. (**2021**). Toward genomic selection in Pinus taeda: Integrating resources to support array design in a complex conifer genome. *Applications in plant sciences*.

Howe, G. T., Jayawickrama, K., Kolpak, S. E., Kling, J., Trappe, M., Hipkins, V., Ye, T., Guida, S. Cronn, R., Cushman, S., & **McEvoy, S.** (**2020**). An Axiom SNP genotyping array for Douglasfir. *BMC genomics*, *21*(1), 1-17.

PRESENTATIONS

"Investigating beech bark disease resistance: variation and assembly error in two *Fagus grandifolia* genomes" *Plant Genomes Online, April 2022.*

"Genomic characterization and comparison of two maples highlights genes involved in the stress response to acidic soils" *Botanical Society of America (virtual) July 2021.*

"Genomic characterization of two maples highlights genes involved in the stress response to acidic soils across seasons" *Forest Genetics Student and Postdoc Symposium (virtual) May 2021.*

"An integrated and holistic approach to study resilience across forest tree species" *UConn EEB Graduate Symposium (virtual) February 2021*

"Genomic characterization and comparison of two maples highlights genes involved in the stress response to acidic soils" *Botanical Society of America (virtual) July 2020.*

"Sweet Genomes: Assembling, Annotating, and Comparing Three Maples" *EEB UConn Graduate Symposium, Storrs, CT, USA, February 2020.*

"Sweet Genomes: Assembling, Annotating and Comparing Three Maples" *Plant & Animal Genome Conference, San Diego, CA, USA, January 2020.*

"Sweet Genomes: Sequencing, Assembling, and Annotating Two Maples" *EEB UConn Graduate Symposium, Storrs, CT, USA, February 2019.*

POSTERS

"Sweet Genomes: Assembling, Annotating and Comparing Three Maples" *Plant & Animal Genome Conference, San Diego, CA, USA, January 2020.*

"Sweet Genomes: Sequencing, Assembling, and Annotating Three Maples" *Evolution, Providence, RI, USA, June 2019.*

"Sweet Genomes: Sequencing, Assembling, and Annotating Two Maples" *ASPB Northeast Section Annual Meeting, Durham, NH, USA, April 2019.*

"Sweet Genomes: Sequencing, Assembling, and Annotating Two Maples" *Plant & Animal Genome Conference, San Diego, CA, USA, January 2019.*

"Sweet Genomes: Sequencing, Assembling, and Annotating Two Maples" *UMass Plant Biology Graduate Program, Amherst, MA, USA, October 2018.*