

## Susan L. McEvoy

Department of Forest Sciences

University of Helsinki

[susanlmcevoy@gmail.com](mailto:susanlmcevoy@gmail.com)

### EDUCATION

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#### **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

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#### **Postdoctoral Researcher**

**Dec 2023-present**

Population genetics analysis and modeling for the European Union FORGENIUS project.

Spatial transcriptomics and other bioinformatic analyses for GENEOPIN, a study on the mechanics and evolution of polyembryony in *Pinus sylvestris* funded by the Academy of Finland.

#### **Postdoctoral Scientist in Conservation Genomics**

**Jul 2022 – Dec 2023**

Santa Barbara Botanic Garden

As a part of the project "Landscape and population genomics of the Gaviota tarplant (*Deinandra increscens* subsp. *villosa*; *Asteraceae*) for long term conservation":

- Assembled and annotated the reference genome
- Assisted with sample collection and coordination of sequencing

#### **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 characterize genome-wide structural variation and examine a candidate locus of Beech bark disease
- Assisted 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 to 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**

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

**GRANTS**

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

EEB-MNH Botany Award, University of Connecticut, Department of Ecology and Evolutionary Biology, 2019, 2020 & 2021, (\$1500 per year)

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

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

## PUBLICATIONS

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**McEvoy, S. L.**, Meyer, R. S., Hasenstab-Lehman, K. E., & Williams, C. M. (2024). The reference genome of an endangered Asteraceae, *Deinandra increscens* subsp. *villosa*, endemic to the Central Coast of California. *G3: Genes, Genomes, Genetics*, jkae117.

**McEvoy, S. L.**, Grady, P. G. S., Pauloski, N., O'Neill, R Wegrzyn, J., (2024). Profiling genome-wide methylation in two maples: Fine-scale approaches to detection with nanopore technology. *Evolutionary Applications*, 17(4), e13669.

**McEvoy, S. L.**, Lustenhouwer, N., Melen, M. K., Nguyen, O., Marimuthu, M. P., Chumchim, N., Beraut, E., Parker, I. M. & Meyer, R. S. (2023). Chromosome-level reference genome of stinkwort, *Dittrichia graveolens* (L.) Greuter: A resource for studies on invasion, range expansion, and evolutionary adaptation under global change. *Journal of Heredity*, 114(5), 561-569.

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. (2023). Welcome to the big leaves: best practices for improving genome annotation in non-model plant genomes. *Applications in Plant Sciences*, 11(4), e11533.

**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*, 9(6), e11439.

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 Douglas-fir. *BMC genomics*, 21(1), 1-17.

## PRESENTATIONS

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"Conservation genomics of an endangered Asteraceae native to the Central Coast of California." *Botany*, Boise, ID, USA, July 2023

“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” *Botany (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” *Botany (virtual)* July 2020.

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