

Susan L. McEvoy, PhD

Helsinki, Finland

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EDUCATION

Ph.D., Ecology & Evolutionary Biology, University of Connecticut	2022
B.S., Biology, Oregon State University	2002

RESEARCH EXPERIENCE

University of Helsinki, Postdoctoral Researcher 12/2023 – Present
Tanja Pyhäjärvi Lab, Department of Forest Sciences

- Conducting population genetic analyses and modeling in SLiM on behalf of the EU FORGENIUS project.
- Provide bioinformatic expertise for the GENOPIN project on polyembryony in *Pinus sylvestris*.

Santa Barbara Botanic Garden, Genomics Postdoctoral Scientist 07/2022 - 11/2023

- Planned and conducted bioinformatic analyses for conservation genomics of the endangered *Asteraceae*, *Gaviota* tarplant.
- Assembled and annotated a reference genome for *Gaviota* tarplant.
- Coordinated with lab and sequencing centers on library preparation of 960 samples for low coverage sequencing; evaluated results to select 288 samples distributed across geographic occurrences for higher coverage sequencing.

University of Connecticut, Graduate Assistant 08/2018 - 07/2022
Plant Computational Genomics Lab, Dr. Jill Wegrzyn

- Produced research focused on cutting-edge bioinformatic technologies and algorithms, resulting in the dissertation "Application of emerging computational and genomic approaches to examine challenges to forest health."
- Using a variety of sequencing approaches, assembled, annotated, and characterized reference genomes for several forest tree species.
- Conducted an expression study on sugar maple trees subjected to long-term nutrient amendment and identified genes involved in nutrient stress.
- Conducted comparative genomic studies across broadleaf tree species, integrating gene family dynamics, transposable element activity, and methylation profiles called from nanopore sequencing with a focus on nutrient stress genes identified in the expression study.
- Examined structural and single nucleotide variants to identify genotypes associated with resistant phenotypes of beech bark disease in American beech.
- Developed the website for NatureRx, @ UConn, including extensive JavaScript-style customizations for Leaflet map integration of ArcGIS data via API.
- Wrote code in Python and R, installed software on a Linux HPC, shared scripts via Git, and provided bioinformatic guidance and troubleshooting assistance to other HPC users.

Oregon State University, Bioinformatician/Faculty Research Associate 03/2017 - 08/2018
Forest Ecosystems & Society, Dr. Glenn Howe

- Provided bioinformatic support to faculty and the Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC).
- Assembled a transcriptome for Western white pine and called variants.
- Assisted with the creation of transcriptome-based genotyping array for Douglas-fir.
- Wrote scripts and modified in-house software using R, Perl, C#, and Java.

TEACHING EXPERIENCE

University of Connecticut, Teaching Assistant 01/2019 - 12/2019

- Responsible for leading laboratory lecture and activities for introductory Biology

PROFESSIONAL EXPERIENCE

University of Oregon, Software Developer/Research Assistant 04/2014 - 03/2017
Center on Teaching and Learning

- Designed and developed data-driven web applications and tablet-based instruction tools on behalf of education researchers for the purpose of assessing student learning and the effectiveness of curricular programs.
- Independently developed custom applications using JavaScript-based frameworks and libraries such as AngularJS, EmberJS, NodeJS and Bootstrap, and MySQL databases.
- Participated in agile, team-based development of a large Zend Framework (PHP OOP) application with a PostgreSQL database. Refactored legacy code and adding new features and bug fixes.
- Used standard developer tools such as Git, Jira, and Confluence, and developed in Linux virtual machines.

Oregon State University, Web Manager/Analyst Programmer 3 10/2010 - 04/2014,
OSU Libraries & University Press 08/2006 - 05/2009

- Responsible for the web presence of OSU Libraries and Press, including web applications related to resource discovery and access, instruction, digital collections, and supplementary sites for OSU Press publications.
- Primarily worked in Drupal, JavaScript, some Ruby on Rails, and with proprietary and open-source library systems.

Oregon State University, Interim Department Head 05/2009 - 10/2010
OSU Libraries & University Press, Emerging Technologies & Services

- Managed system administrators, programmers, and desktop support staff to meet the organizational technology-related goals.
- Served on the management team and participated in strategic planning.

TRAINING

Bioinformatics Analysis for Conservation Genomics 2023
Smithsonian-Mason School of Conservation, 10-day residential course

AWARDS

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

University of Connecticut, Ecology and Evolutionary Biology-Museum of Natural History Botany Award (\$6000)	2019-2022
The Arnold Arboretum of Harvard University Sequencing Award (\$9127)	2021
Botanical Society of America, Bill Dahl Graduate Student Research Award Bill Dahl Graduate Student Research Award (\$1500)	2020
University of Connecticut Institute for Systems Genomics Linda D. Strausbaugh Fellowship in Genetics and Genomics (\$1600)	2019

PUBLICATIONS

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

McEvoy, S. L., Meyer, R. S., Hasenstab-Lehman, K. E., Williams, C. M. (in review). The reference genome of an endangered Asteraceae, *Deinandra increscens* subsp. *villosa*, endemic to the Central Coast of California. 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. (2023). Welcome to the big leaves: best practices for improving genome annotation in non-model plant genomes. *Applications in Plant Sciences*, e11533.

McEvoy, S. L., Lustenhouwer, N., Melen, M. K., Nguyen, Oanh, Marimutha, M. P. A., 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*, esad033.

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

SELECTED ORAL PRESENTATIONS (5 of 9)

Botany, "Conservation genomics of an endangered Asteraceae native to the Central Coast of California." 2023

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

Botany, "Genomic characterization and comparison of two maples highlights genes involved in the stress response to acidic soils." 2021

Forest Genetics Student and Postdoc Symposium, "Genomic characterization of two maples highlights genes involved in the stress response to acidic soils across seasons", 2021

Plant & Animal Genomes, "Sweet Genomes: Assembling, Annotating and Comparing Three Maples." 2020