Curriculum vitae-Vidya Vuruputoor (vidya.vuruputoor@uconn.edu)

As a Conservation Genomics Scientist, I specialize in leveraging advanced genomic technologies to investigate long-term population dynamics through the study of long-lived organisms, particularly gymnosperms. My expertise spans both theoretical and applied aspects of plant genetics, supported by a Master's degree in Plant Biotechnology, specialized in Molecular Plant Breeding and Phytopathology. Currently, I am spearheading a conservation project focused on the Eastern Hemlock, integrating host-pest interaction studies with conservation genomics. My research portfolio extends to investigating genome evolution and meiotic processes, utilizing moss species as model organisms due to their unique haploid-dominant life cycles. This work provides valuable insights into transcriptome dynamics following whole genome duplication events. Additionally, I contribute to the rapidly evolving field of bioinformatics, with a particular focus on genome annotation of non-model plant species, addressing critical gaps in our understanding of plant genomics.

EDUCATION

University of Connecticut	Ph.D. student	2020-Present
Wageningen University	MS in Plant Biotechnology	2019
Vellore Institute of Technology	B.tech in Biotechnology	2017

PUBLICATIONS

Castellano, K. R., Neitzey, M. L., Starovoitov, A., Barrett, G. A., Reid, N. M., **Vuruputoor, VS,** Webster, C.N., Storer, J.M., Pauloski, N.R., Ameral, N.J. and McEvoy, S.L., McManus C, Puritz J.B., Wegrzyn JL, O'Neill, R. J. (2025). Genome assembly of a living fossil, the Atlantic horseshoe crab Limulus polyphemus, reveals lineage-specific whole genome duplications, transposable element-based centromeres and a ZW sex chromosome system. *Molecular Biology and Evolution*, msaf021.

Vuruputoor VS, Starovoitov A, Cai Y, Liu Y, Rahmatpour N, Hedderson TA, Wilding N, Wegrzyn JL, Goffinet B. Crossroads of assembling a moss genome: navigating contaminants and horizontal gene transfer in the moss *Physcomitrellopsis africana.* G3: Genes, Genomes, Genetics. 2024 Jul;14(7):jkae104.

Vuruputoor, V.S., Monyak, D., Fetter, K.C., Webster, C., Bhattarai, A., Shrestha, B., Zaman, S., Bennett, J., McEvoy, S.L., Caballero, M. and Wegrzyn, J.L., 2023. Welcome to the big leaves: Best practices for improving genome annotation in non-model plant genomes. Applications in Plant Sciences, 11(4), p.e11533.

Singh, G., **Vuruputoor, V. S.**, & Kalaichelvan, C. (2018). A Nutrition Dense Additive for Processed food items. Research Journal of Pharmacy and Technology, 11(6), 2229-2234.

Vuruputoor, VS., Adak S. and Kalaichelvan, C. (2017) Allergens and Molecular Diagnosis. Research Journal of Pharmaceutical, Biological, and Chemical Sciences. 8. 37-48.

Vuruputoor, VS., & Kalaichelvan, C. (2015). View of Role of nutrition in cancer. Research Journal of Pharmacology and Toxicology. 6. 58-63.

Karuppasamy, Ramanathan & Shreenidhi, R & **Vidya, VS** & Veerappapillai, Shanthi. (2015). Statistical Analysis of State-Wise Dengue Data in India. Research Journal of Pharmaceutical, Biological, and Chemical Sciences. 6. 1557-1567

POSTER PRESENTATIONS

- **Vuruputoor VS,** Fetter KC, Myles MN, Stephens C, Kannan NS, Nodeh HR, Wang D, BenJeddi S, Baukus D, Chaganti T, Glendening A, Perkins C, Stuart J, Provatas A, Butnor J, Nelson D, Smith B, Johnson S, Kersten R, Cernak TA, Wegrzyn JL (Feb 2025) "From needles to reads: Utilizing'omics' technologies to inform conservation of the eastern hemlock" [Poster presentation]. Graduate Student Symposium, Department of Ecology and Evolutionary Biology, University of Connecticut, 2025.

- **Vuruputoor VS,** Fetter KC, Myles MN, Stephens C, Kannan NS, Nodeh HR, Wang D, BenJeddi S, Baukus D, Chaganti T, Glendening A, Perkins C, Stuart J, Provatas A, Butnor J, Nelson D, Smith B, Johnson S, Kersten R, Cernak TA, Wegrzyn JL (Jan 2025) "From needles to reads: Utilizing'omics' technologies to inform conservation of the eastern hemlock" [Poster presentation]. A GIFT SEED, North Carolina State University, 2025.
- **Vuruputoor VS,** Fetter KC, Myles MN, Stephens C, Kannan NS, Nodeh HR, Wang D, BenJeddi S, Baukus D, Chaganti T, Glendening A, Perkins C, Stuart J, Provatas A, Butnor J, Nelson D, Smith B, Johnson S, Kersten R, Cernak TA, Wegrzyn JL (Sept 2024) "From needles to reads: Utilizing'omics' technologies to inform conservation of the eastern hemlock" [Poster presentation]. Institute of System Genomics (ISG) Networking event, University of Connecticut, 2024.
- **Vuruputoor VS,** Fetter KC, BenJeddi S, Baukus D, Heileman K, Perkins C, Stuart J, Provatas A, Butnor J, Nelson D, Wegrzyn. (Jul 2024) "Tale of the terpenes: analysis of molecular mechanisms across hemlock species" [Poster presentation]. North American Forest Genetics Society, 2024.
- Glendening A, **Vuruputoor VS**, Fetter KC, Cernak T, Smith BC and Wegrzyn JL. (Jan 2024) "Shearing the Wool(ly): An Adelges tsugae Genome for Hemlock Conservation" [Poster presentation]. Plant and Animal Genomes Conference, 2024.
- Webster CN, Hart A, **Vuruputoor VS**, Chinta V, Zaman S, Bhattarai A, Fetter KC and Wegrzyn JL. (Jan 2024) "EnTAP: Rapid, Accurate, and Scalable Functional Annotation for the Transcriptomes and Genes of Non-Model Eukaryotes" [Poster presentation]. Plant and Animal Genomes Conference, 2024.
- **Vuruputoor VS,** Wegrzyn J, Fetter K, Nelson CD, Abbott A, Schmutz J, and Leebens-Mack JH. (May 2021) "Conserving hemlocks: Utilizing Genomic resources" [Poster presentation]. Forest Genetics 2021.
- **Vuruputoor VS**, Patel N, Wegrzyn J, Goffinet B. (Aug 2021) "Assembly of the first allopolyploid moss genome based on Physcomitrium sp. from North America" [Poster presentation]. Bryophytes, lichens, and northern ecosystems in a changing world (BL2021).
- **Vuruputoor VS**, Wegrzyn J, Fetter K, Nelson CD, Abbott A, Schmutz J and Leebens-Mack JH. (Aug 2021) "Assessing genetic differences related to differential resistance in hemlocks (Tsuga sp.) through comparative transcriptomics" [Poster presentation]. Botany 2021.

ORAL PRESENTATIONS

- **Vuruputoor VS**, Starovoitov A, Cai Y, Liu Y, Rahmatpour N, Hedderson T, Wilding N, Wegrzyn JL and Goffinet B. (2024) "Crossroads of Assembling a Moss Genome: Navigating Contaminants and Horizontal Gene Transfer in the Moss Physcomitrellopsis africana". Plant and Animal Genome Conference, San Diego, CA.
- **Vuruputoor VS**, Fetter KC, Myles M, Kannan NS, Nodeh HR, Smith BC, Johnson S, Kirsten R, Cernak T and Wegrzyn JL. (2024) "The Ongoing Impact of Hemlock Woolly Adelgid on Eastern Hemlocks: Longitudinal Study Results". Plant and Animal Genome Conference, San Diego, CA.
- Webster CN, Alex Hart, **Vuruputoor VS**, Chinta V, Zaman S, Bhattarai A, Fetter KC and Wegrzyn JL. (2024) "EnTAP: Rapid, Accurate, and Scalable Functional Annotation for the Transcriptomes and Genes of Non-Model Eukaryotes". Plant and Animal Genome Conference, San Diego, CA.
- Neitzey M, Castellano K, Starovoitov A, Gabriel Barrett, Noah Reid, Webster CN, **Vuruputoor VS**, Puritz J, Wegrzyn JW and O'Neill R (2024). "New Findings from a Living Fossil: Limulus polyphemus Genome and Insights into Horseshoe Crabs". Plant and Animal Genome Conference, San Diego, CA.
- **Vuruputoor VS**, Starovoitov A, Cai Y, Liu Y, Rahmatpour N, Hedderson T, Wilding N, Wegrzyn JL and Goffinet B. (2023) "Crossroads of Assembling a Moss Genome: Navigating

Contaminants and Horizontal Gene Transfer in the Moss *Physcomitrellopsis africana*". Biodiversity Genomics.
- Fetter KC, Webster CN, Hart A, **Vuruputoor VS**, Chinta V, Zaman S, Bhattarai A, and Wegrzyn JL. (2023) "EASEL (Efficient, Accurate, Scalable Eukaryotic modeLs), a tool for the improvement of eukaryotic structural and functional genome annotation". Evolution, Albuquerque, NM.
- **Vuruputoor VS**, BenJeddi S, Fetter KC, Wegrzyn JL. (2023), "Transcriptomics and Metabolomics Approaches to Investigate Hemlock (Tsuga sp.) Resistance Mechanisms". Plant and Animal Genome Conference, San Diego, CA.
- **Vuruputoor VS**. (2023), "Assessing molecular mechanisms of hemlock resistance (Tsuga sp.) through comparative transcriptomics and metabolomics". Plant and Animal Genome Conference, San Diego, CA.
- **Vuruputoor VS**. (2022), "Assessing genetic differences in hemlock resistance (Tsuga sp.) through comparative transcriptomics and metabolomics". Botany, Anchorage, AK.
- **Vuruputoor VS**. (2022), "Debugging the hemlock: Utilizing genomic resources to conserve the eastern hemlock". National Forest Genetics Society, Asilomar, CA.
- **Vuruputoor VS**. (2022), "Debugging the hemlock: Utilizing genomic resources to conserve the eastern hemlock". Plant Genomes Online.
- **Vuruputoor VS**. (2022), "Debugging the hemlock: Utilizing genomic resources to conserve the eastern hemlock". Graduate Student Symposium, University of Connecticut, CT.

INVITED SEMINAR TALKS

- **Vuruputoor VS,** Fetter KC, Myles MN, Stephens C, Kannan NS, Nodeh HR, Wang D, BenJeddi S, Baukus D, Chaganti T, Glendening A, Perkins C, Stuart J, Provatas A, Butnor J, Nelson D, Smith B, Johnson S, Kersten R, Cernak TA, Wegrzyn JL (Mar 2025) "From needles to reads: Utilizing'omics' technologies to inform conservation of the eastern hemlock", Harvard Forest, Massachusetts, USA.
- **Vuruputoor VS,** Fetter KC, Myles MN, Stephens C, Kannan NS, Nodeh HR, Wang D, BenJeddi S, Baukus D, Chaganti T, Glendening A, Perkins C, Stuart J, Provatas A, Butnor J, Nelson D, Smith B, Johnson S, Kersten R, Cernak TA, Wegrzyn JL (Sept 2024) "From needles to reads: Utilizing'omics' technologies to inform conservation of the eastern hemlock", Arnold Arboretum, Massachusetts, USA.

GRANTS

American Conifer Society(2021)- $600 towards generating the first reference genome of *Tsuga canadensis*

Ronald Bamford Grant (2021)- $1500 towards assessing transcriptomes across hemlock species to assess the molecular mechanisms underlying genetic defense to stressors.

Ronald Bamford Grant (2022)- $1500 towards additional sequencing for the *Tsuga canadensis* reference genome

Conference Participation Award (2023)- $700 towards participating in conferences during the Summer of 2023

Ronald Bamford Grant (2023)- $1500 towards participating in the Plant and Animal Genomes conference held in January of 2024.

Sargant Award (2024)- $8500 towards generating the first reference genome of *Tsuga canadensis* and assessing transcriptomes across hemlock species to assess the molecular mechanisms underlying genetic defense to stressors.

New England Botanical Society Award (2024)- $1500 towards assessing transcriptomes across hemlock species to assess the molecular mechanisms underlying genetic defense to stressors.

Rednalis Award (2024)- $6000 towards assessing transcriptomes across hemlock species to assess the molecular mechanisms underlying genetic defense to stressors.

Ronald Bamford Grant (2024)- $1500 towards participating in the North American Forest Genetics Society conference in July of 2024.

MENTORSHIP

Daniel Monyak (2021)- Dan contributed immensely to the paper on benchmarking non-model plant genomes (Vuruputoor et al, 2022). He was a high-school student at the time and was introduced to Linux and shell programming, as well as current tools and techniques in genome annotation software.

Sophia BenJeddi (2022)- Sophia generated six hemlock transcriptomes during her semester as an intern at the Plant Computational Genomics lab. As an undergraduate major in ecology, it was her first experience in bioinformatics, and she learned a great chunk of bioinformatic tools related to RNA-seq analysis in her time here.

Victoria Burton (2023)- Victoria is an undergraduate major in ecology and evolutionary biology, and she is helping me in setting up the first few pilot trials in generating eastern hemlock seedlings. As we try out various germination protocols, she is also introduced to field sampling techniques with liquid nitrogen, as well as future LCMS and GCMS analysis techniques.

Meghan Myles (2023)- Meghan is a graduate student enrolled in the Data Science program at the University of Connecticut. She has been introduced to field sampling techniques with liquid nitrogen and is aiding in analyzing the raw data of terpenoid profiles because of GCMS analysis.

Adam Glendening (2023)- Adam is a RAMP scholar at the Plant Computational Genomics lab and has been enthusiastically leading the generation of the hemlock woolly adelgid genome. They will be assessing the genome for factors that allow the hemlock woolly adelgid to be so successful in infecting susceptible hemlocks. They will be submitting their manuscript on this genome in November of 2024.

Vikesh Chinta (2023)- Vikesh has contributed immensely to the development of the genome annotation pipeline currently under development in the lab, EASEL. He has also developed user-friendly reports as an addition to the latest EnTAP release.

David Baukus (2024)- David has helped graciously in volunteering for sampling every month for the eastern hemlock conservation project. He is now interested in delving into the pathways that are significant in the interaction between the eastern hemlock and the hemlock woolly adelgid. He has also aided in RNA extractions.

Airianna McGuire (2024)- Airianna is a RAMP scholar at the Plant Computational Genomics lab and has been enthusiastically following tutorials to get acquainted with bioinformatics. She is now being introduced to genome assembly tools, and is working on assembling the Mink genome, assessing SNP variants in beech genomes, and assembling a haplotype-level resolution of the Arctic Grayling, and will soon join the Plant Computational Genomics Lab!