

# Carol Loopstra

Associate Professor

Office: WFES 306

Email: [c-loopstra@tamu.edu](mailto:c-loopstra@tamu.edu)

Phone: (979) 862-2200

## Undergraduate Education

B.S. Forest Management, Oregon State University

## Graduate Education

M.S. Forest Science, Oregon State University

Ph.D. Genetics and Forestry, North Carolina State University

## Pronouns

she/her/hers

## Professional Summary

Carol Loopstra is an associate professor in the Department of Ecology and Conservation Biology with teaching and research interests in the biological aspects of Forestry. She teaches “Forest Trees of North America” and “Tree Improvement and Regeneration”. Her research has evolved over time from molecular biology of forest trees focusing on wood development and drought resistance to conifer genomics focusing on drought resistance. Her latest project is funded by the USDA and is a collaboration with the Western Gulf Forest Tree Improvement Program. This project is an attempt to take earlier work and use WGFTIP progeny tests to develop molecular markers and biomarkers that can be used to assist with selection of and breeding for trees with increased water-use efficiency and drought resistance while at the same time increasing photosynthetic efficiency and growth.

## Research Interests and Specializations

Forest Tree Genomics and Molecular Biology, Drought tolerance

## Recent Publications

Caballero M, Lauer E, Bennett J, Zaman S, McEvoy S, Acosta J, Jackson C, Townsend L, Eckert A, Whetten RW, **Loopstra C**, Holliday J, Mandal M, Wegrzyn J, Isik R Towards genomic selection in *Pinus taeda* (Pinaceae): Integrating resources to support array design in a complex conifer genome. Applications in Plant Sciences. In Press.

Li J, West JB, Hart A, Wegrzyn JL, Smith MA, Domec J-C, **Loopstra CA**, Casola C. Extensive variation in drought-induced gene expression changes between loblolly pine genotypes. *Frontiers*

in Genetics. In Press.

Lu M, Krutovsky KV, **Loopstra CA** (2019) Predicting adaptive genetic variation of loblolly pine (*Pinus taeda* L.) populations under projected future climates based on multivariate models. *J of Heredity* 110 (7)

Lu M, **Loopstra CA**, Krutovsky KV (2019) Detecting the genetic basis of local adaptation in loblolly pine (*Pinus taeda* L.) using whole exome-wide genotyping and an integrative landscape genomics analysis approach. *Ecology and Evolution* 9(4)

Lu M, Seeve CM, **Loopstra CA**, Krutovsky KV (2018) Exploring the genetic basis of gene transcript abundance and metabolite levels in loblolly pine (*Pinus taeda* L.) using association mapping and network construction. *BMC Genetics* 19:100