CONSERVATION AND POPULATION GENETICS OF THE FEDERALLY ENDANGERED TORREYA TAXIFOLIA (TAXACEAE)

Lauren A. Eserman¹, Ashlynn Smith², Laurie Blackmore³, Juliet Rynear⁴, Lilly Anderson-Messec⁵, Jim Leebens-Mack⁶, Chazz Jordan⁷, Emily E. D. Coffey⁸

¹ Research Scientist, Conservation & Research Department, Atlanta Botanical Garden, Atlanta, GA, USA 30309 (leserman@atlantabg.org);
² Gulf Coast Coordinator, Research Scientist, Conservation & Research Department, Atlanta Botanical Garden, Atlanta, GA, USA 30309;
³ Conservation & Research Manager, Conservation & Research Department, Atlanta Botanical Garden, Atlanta, GA, USA 30309;
⁴ Executive Director, Florida Native Plant Society, Melbourne, FL, USA 32902-0278;
⁵ TorreyaKeepers Project Director, Florida Native Plant Society, Melbourne, FL, USA 32902;
⁶ Professor and Interim Curator of the University of Georgia Herbarium, Plant Biology Department, University of Georgia, Athens, GA, USA 30602;
⁷ Graduate Student, Dept of Plant Biology, University of Georgia, Athens, GA, USA 30602;
⁸ Vice President for Conservation and Research, Conservation & Research Department, Atlanta Botanical

Garden, Atlanta, GA, USA 30309.

Florida torreya, or Torreya taxifolia (Taxaceae), is one of the most endangered conifers in North America and is endemic to the ravines east of the Apalachicola river in the Florida panhandle. In the last century, populations have declined from nearly 700,000 trees in the early 1900s to around 700 trees today. This dramatic decline is the result of an invasive fungal pathogen, Fusarium torrevae. For the last 30 years, staff at the Atlanta Botanical Garden have been collecting cuttings for safeguarding, caging trees to prevent deer browsing, and tagging and monitoring wild trees in Torreya State Park and the Nature Conservancy's Apalachicola Bluffs and Ravines Preserve. Recently, partnership with the Florida Native Plant Society has allowed outreach to private landowners to locate, tag, and collect cuttings of trees on private lands. Using the collection of trees from across its range, we are performing conservation genetic studies of *Torreva taxifolia* using target gene capture to assess the level of genetic diversity and population structure remaining in the wild. Conifers are notorious for having extremely large and highly repetitive nuclear genomes, making typical population genomic techniques such as Genotype-by-Sequencing (GBS), restriction site-associated DNA sequencing (RADseq), and genome skimming unfeasible. Gene capture, in contrast, allows for targeted sequencing of specific loci in the genome and allows us to overcome the problem of the large, repetitive genome structure. This method is a cost-effective way to obtain DNA sequence variation necessary to distinguish among closely related populations. Together, these projects will advance conservation efforts for this critically imperiled conifer.