

EXPLORING THE GENETIC DIVERSITY OF AN EXTINCT TREE SPECIES IN THE WILD, *FRANKLINIA ALATAMAHA*, USING GENOTYPING-BY-SEQUENCING OF THE SURVIVING CULTIVATED POPULATION

Heather J. Gladfelter^{1,2*}, Lav Yadav², Scott A. Merkle¹ and H. Dayton Wilde²

¹Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA USA;

²Horticulture Department, University of Georgia, Athens, GA USA; [*hjgladf@uga.edu](mailto:hjgladf@uga.edu)

Genetic diversity of an extinct tree species in the tea family (Theaceae), *Franklinia alatamaha*, has been of curious interest since this tree only existed as one remote population when growing in its native habitat on the Georgia Coastal Plain. *F. alatamaha* was first documented by American naturalists John and William Bartram during their travels to Florida in 1765. The only known population of *F. alatamaha* became extinct in the wild by the early 1800s. Fortunately, William Bartram collected seed from this population in 1773 and brought it back to Philadelphia, where he grew plants from the harvested seed, which has allowed *F. alatamaha* to be cultivated as an ornamental for nearly 250 years. All extant *F. alatamaha* trees in the world are derived from that seed collection. The only opportunity to infer the genetic variation that once existed in the original population was to examine the genetic variation in the cultivated population. Leaves from live and herbarium accessions were obtained from 42 sites worldwide. Genotyping-by-sequencing (GBS) was used to determine the genetic diversity and structure of 76 *F. alatamaha* accessions, including a 178-year-old herbarium specimen. STRUCTURE analysis with 9604 high-quality single-nucleotide polymorphisms (SNPs) identified two subpopulations within the cultivated accessions. This result was supported by UPGMA (unweighted pair group method with arithmetic mean) and principal component analyses. F statistics indicated that there was a moderate level of genetic diversity among the cultivated accessions ($F_{ST} = 0.09$), with more genetic diversity among accessions within a subpopulation than between the two subpopulations. The inbreeding coefficient of the cultivated accessions was low ($F_{IS} = -0.4902$), indicating that the sampled trees represent what was once a highly outcrossing population. The genetic differentiation identified in this study may be useful for further development of new horticultural traits such as disease resistance to *Phytophthora* root rot, which inhibits *F. alatamaha* from being cultivated in the region to which it was once native.