MAPPING QTLS FOR BLIGHT RESISTANCE AND MORPHOLOGICAL TRAITS WITH COMPLEX CHESTNUT FAMILIES

Shenghua Fan[1,2], Laura L. Georgi[3], Frederick V. Hebard[4], Jiali Yu[5], Albert G. Abbott[6], C. Dana Nelson[7,8]

[1] Research associate, Forest Health Research and Education Center, University of Kentucky, Lexington, KY, USA
[2] Research associate, Department of Horticulture, University of Kentucky, Lexington, KY 40546
[3] Research scientist, Forest Health Research and Education Center, Damascus, VA, USA
[4] Chief Scientist Emeritus, The American Chestnut Foundation, Meadowview, VA, USA
[5] Graduate research assistant, UT-ORNL Graduate School of Genome Science and Technology, Knoxville, TN 37996
[6] Bioscience team leader, Forest Health Research and Education Center, University of Kentucky, Lexington, KY, USA
[7] Co-Director, Forest Health Research and Education Center, USDA Forest Service, Southern Research Station, Lexington, KY, USA
[8] Project leader, Southern Institute of Forest Genetics, USDA Forest Service, Southern Research Station, Saucier, MS, USA

Chestnut blight (caused by *Cryphonectria parasitica, Cp*), together with Phytophthora root rot, has nearly extirpated American chestnut (*Castanea dentata*). In contrast to the susceptibility of American chestnut, many Chinese chestnut (*C. mollissima*) genotypes are resistant to blight. In this research, we performed a series of GWAS studies for blight resistance originating from three unrelated Chinese chestnut trees (Mahogany, Nanking and M16) and a QTL study on a Mahogany-derived F2 family. We evaluated trees for resistance to blight after artificial inoculation and scored nine morphological traits that are the hallmarks of species differentiation between American and Chinese chestnuts. Blight resistance and morphological trait QTLs that were identified in the GWAS and F2 mapping studies were compared. Results support a moderately complex genetic architecture for blight resistance, as 13 QTLs were found on 11 chromosomes across all studies, including two previously identified QTLs (Cbr1 and Cbr3). Additionally, blight resistance QTLs overlapped with 9 of 15 morphological trait loci indicating that it will be challenging, but still possible, to eliminate Chinese chestnut alleles for these distinguishing traits while still achieving high blight resistance in the backcross hybrid chestnuts. Finally, comparison between QTL intervals for blight resistance and those previously published for root rot resistance, revealed common disease resistance loci on chromosome A, E, and K.