

WHOLE-GENOME SEQUENCING OF CHESTNUTS (*CASTANEA*) REVEALS INTER- AND INTRASPECIFIC GENETIC VARIATION IN REGIONS ASSOCIATED WITH RESISTANCE TO CHESTNUT BLIGHT AND PREDICTED DISEASE RESISTANCE GENES

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Uncovering the genetic basis of chestnut blight resistance is critical to transferring blight resistance into susceptible American chestnut (*Castanea dentata*). Three major blight resistance QTL have been discovered, but the genes underlying the QTL are not known. Furthermore, it is likely that genes entirely outside these three QTL regions play a role in blight resistance. Using the draft Chinese chestnut (*Castanea mollissima*) genome assembly and whole-genome sequences from 24 individual chestnuts, including highly resistant *C. mollissima*, moderately susceptible *C. mollissima*, highly susceptible *C. dentata*, hybrids, and “Clapper,” one of the resistance donors from the TACF breeding program, we carried out association tests to identify SNPs associated with blight resistance. The vast majority of associated SNPs were localized to 15 distinct regions on 9 of 12 linkage groups. Three of these regions appear to correspond to previously identified blight resistance QTL. Of the predicted genes that contain associated SNPs, many are similar to known resistance genes in other plants. Patterns of heterozygosity and nucleotide divergence in the predicted gene sequences indicate that while many are essentially “fixed” with one highly homozygous genotype in *C. mollissima* and a divergent one in *C. dentata*, genes that differentiate the most resistant *C. mollissima* from more susceptible *C. mollissima* show elevated nucleotide diversity and heterozygosity in resistant trees.

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