INVESTIGATING THE GENETIC BASIS OF VARIATION IN RESISTANCE TO CHESTNUT BLIGHT AMANG CHINESE CHESTNUTS AND INTERSPECIFIC HYBRIDS USING WHOLE-GENOME RESEQUENCING

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Chinese chestnut (*Castanea mollissima* Blume) is the main donor of disease resistance in the breeding program being undertaken by the American Chestnut Foundation (ACF) to restore chestnut forests to the eastern United States. The use of only a few *C. mollissima* resistance donor trees could be a liability for the restoration program if blight resistance in Chinese chestnut is maintained by diverse sets of alleles at blight resistance loci, as is the case in many plant/disease systems. To determine whether Chinese chestnut possesses diverse resistance alleles or a restricted set of "best" resistance alleles, we are using the Chinese chestnut v1.1 draft genome and three blight QTL scaffold sequences (hardwoodgenomics.org) to assemble individual genomes for 24 Chinese chestnuts and interspecific hybrids of variable blight resistance. Currently 14 trees have been sequenced using the Illumina HiSeqplatform, with approximate genome depth between 10 x and 25x, and preliminary analysis has revealed some polymorphisms (SNPs) that appear to segregate strongly between resistant and susceptible trees.

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