

## THE CHINESE CHESTNUT GENOME: A REFERENCE FOR SPECIES RESTORATION

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The American chestnut (*C. dentata*) is one of the most well-known and studied examples of near total mortality of a forest tree across its native range due to exotic diseases. It is one of the few species with large-scale genomics-enabled breeding programs, which rely on introgression of resistance genes from Asian chestnut species. To support the efforts to restore American chestnut, we assembled a chromosome-scale reference genome from the Chinese chestnut (*C. mollissima*) cultivar ‘Vanuxem’. Comparative genomics with peach (*Prunus persica*) and oak (*Quercus robur*) reveal largely conserved genome organization, including across key quantitative trait loci (QTLs), but also significant expansion and contraction of particular gene families. Resequencing of 5 *C. dentata* and 5 *C. mollissima* genotypes enabled analysis of signatures of selection, providing insights into the evolution of resistance to chestnut blight (*Cryphonectria parasitica*) and new candidate resistance genes. With this genomic resource as well as additional upcoming resources, chestnut is becoming a promising platform for forest tree genotype-to-phenotype research and for leveraging genomics in species restoration.