

Improved GWAS Methods Refine the Model of Multi-Genic Blight Resistance in Hybrid Chestnut

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The American chestnut (*Castanea dentata*) once spanned the Appalachian region of North America before chestnut blight (*Cryphonectria parasitica*) led to the tree's functional extinction. The chestnut blight fungus persists in the environment throughout the American chestnut's historical range. The potential to resurrect the American chestnut through interspecific hybridization and backcross breeding with Chinese chestnut (*Castanea mollissima*) holds promise but largely depends on the underlying genetics of the Chinese chestnut's resistance to chestnut blight. To expand our understanding of the genetics of blight resistance, we used improved GWAS techniques to analyze data combining blight inoculation phenotypes across several families of hybrid origin. Our analysis identified twenty peak QTNs, eleven with well-defined QTL regions. When analyzed jointly, these QTNs and QTL regions account for roughly 2.8 to 5% of the genome, while explaining 13 to 23% of the phenotypic variation in canker size, the standard measure of blight resistance. Several QTN candidate genes are directly related to the regulation of reactive oxygen species and, more broadly, to a pathogen defensive response. These results suggest that several genes across the chestnut genome contribute to blight resistance but that the trait is not quantitative in the traditional sense, where hundreds or thousands of genes contribute equally to the observed phenotype.