

MAPPING OF RESISTANCE TO PHYTOPHTHORA CINNAMOMI (PC) IN INTERSPECIFIC AMERICAN/CHINESE AND AMERICAN/JAPANESE CHESTNUT POPULATIONS

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Root rot disease (*Phytophthora cinnamomi*) and chestnut blight (*Cryphonectria parasitica*) are the two most destructive diseases affecting American chestnut *Castanea dentata* (Marsh.) Borkh. Although American chestnut appears not to have any significant resistance to these pathogens, Chinese chestnut, (*C. mollissima*) and Japanese chestnut (*C. crenata*) do have natural resistance. The ability to cross these species with American chestnut provides an avenue to introgress the resistance from these Eastern Asian species into American chestnut. To support introgressive breeding of resistance into American chestnut from these sources, extensive genomic and genetic resources (EST database, physical and transcriptome-based genetic maps) were developed. Three QTLs for resistance to chestnut blight disease (CBD) were detected and delineated on a saturated Chinese chestnut genetic map composed of transcriptome-derived markers. Using a strategy based on sequence-informative markers and a comparative genomics approach with peach and other fully sequenced plant genomes, candidate genes were identified within these genetically marked QTL intervals. Currently these are being tested in transgenic chestnut trees.

For decades, progress in genetic analysis of resistance to *Phytophthora cinnamomi* (*Pc*) the causal pathogen for Phytophthora Root Rot (PRR) was hampered by the lack of a reliable phenotyping system that has been established only recently. Parental Chinese chestnut genotypes transferring *Pc* resistance to later generation Chinese/American hybrid chestnut progenies were selected and verified in small-size progeny tests. An initial genome-wide linkage map was constructed for the BC₁F₁ cross carrying resistance from the Chinese chestnut tree 'Nanking'. In this cross, a QTL was detected and mapped to linkage group E (LG-E). To obtain a more comprehensive understanding of the genetics of *Pc* resistance, we developed 7 additional interspecific hybrid crosses, 6 American/Chinese and 1 American/Japanese. These hybrid families in BC₁F₁, BC₃F₁ and BC₄F₁ configurations represent two Chinese ('Nanking' and 'Mahogany') and one Japanese ('Morrow Mountain') sources of *Pc* resistance. We phenotyped this hybrid material over multiple years and confirmed a QTL signal on LG-E by constructing local LG-E maps composed of transferable EST-SSRs markers from the reference Chinese

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chestnut genetic map. To further saturate these maps with markers and to search for other potential QTL signals, we are exploiting a single-family QTL mapping approach using genome-wide genotyping by sequencing (GBS) for a total of 1576 individuals from crosses phenotyped in 2011-2014. Our current progress in the genetics of *Pc*-resistance in chestnut is reported and discussed in this presentation.