

Mapping Resistance to *Phytophthora cinnamomi* in Chestnut (*Castanea* sp.)

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Abstract

Phytophthora cinnamomi (Phytophthora crown and root rot, or ink disease) is now known to infect several hundred plant species in the world and is especially linked to the widespread death of mature chestnut (*Castanea*) and evergreen oak (*Quercus ilex* L.) trees in southeast United States. With an expanding geographical distribution of *P. cinnamomi* in Northern America, and coupled with the chestnut blight disease (caused by *Cryphonectria parasitica*) that initially decimated the 4 billion-strong American chestnut population (about 30 percent of trees in the Appalachian mountains), *P. cinnamomi* is becoming a crucial limiting factor in natural regeneration and reforestation due to the high susceptibility of both young seedlings and mature trees. In this preliminary study, we report the use of various genomic resources for identifying quantitative trait loci (QTLs) and candidate genes (CGs) underlying resistance to root rot disease. The strategy involved the use of single nucleotide polymorphism (SNP) markers and a small segregating population (48 progenies) for the construction of a transcriptome-based map and identification of root rot disease resistance QTLs. Using a resistant Chinese chestnut and susceptible American chestnut parents, two major QTLs were detected on the chestnut linkage group E (64.8 cM map length) at a logarithm of the odds (LOD) of 4.42 and 5.39. These QTLs spanned 3 cM (12-15 cM) and 16 cM (42-62 cM), respectively and explained 34.6 ± 11 percent and 40.4 ± 10.9 percent of the total phenotypic variance, respectively. Following the alignment of this low resolution map (211 mapped SNP markers) against the high density consensus chestnut map, additional expressed sequence tag (EST)-based markers provided better marker saturation of the QTLs. Two of these EST-based markers within the QTLs reveal two plausible CGs that include CCR1 (Cinnamoyl CoA Reductase 1) and BAG1 (BCL-2-Associated Athanogene 1). Additionally, comparative analysis with the peach genome using the chestnut physical map revealed that the chestnut QTL regions correspond to homologous segments of the peach genome on chromosome 3 and 4. The homologous regions in peach identified three plausible CGs including RPH1 (resistance to *Phytophthora*), NPR3/NPR4 (non-expresser of pathogenesis-related genes 3/4) and BAG4 (BCL-2-Associated Athanogene 4). Following Southern hybridization on chestnut bacterial artificial chromosome (BAC) filters using overgo probes, the co-localization of the CGs with the QTLs was confirmed. For further validation based on gene expression, a larger mapping population, or an association mapping panel, is required. These results can provide functional markers for precise and accurate marker-assisted breeding for introgression of resistance genes into the American chestnut. Transgenic trees are currently also been developed in parallel based on cloned CGs.

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