

INTEGRATED GENOMIC AND GENETIC APPROACH FOR DISCOVERY OF
CANDIDATE GENES ASSOCIATED WITH RESISTANCE TO
PHYTOPHTHORA CINNAMOMI IN CHESTNUT

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Soilborne oomycete *Phytophthora cinnamomi* is one of the most devastating plant pathogens that occurs on all continents of the world except Antarctica and affects several thousand species. Genus *Castanea* is well suited to studying genetics of resistance *Phytophthora cinnamomi* due to availability of resistant Asian and susceptible American and European chestnut species with weak reproductive barriers. We generated and phenotyped for severity of root rot symptoms more than 1,800 individuals derived from interspecific crosses between resistant Chinese chestnut, *Castanea mollissima* ('Mahogany' and 'Nanking' resistance donors), and susceptible American chestnut, *C. dentata* (multiple parents). Saturated genetic linkage maps were constructed with sequence-based markers and used for QTL mapping. Altogether 17 QTLs were detected, and three most consistent QTL intervals were found on the top (qPcE.1), in the middle (qPcE.2) and at the lower end (qPcE.3) of the LG_E. Taking advantage of *C. mollissima* (Vanuxem) v 3.2 genome assembly we re-sequenced five Chinese and five American chestnut accessions and searched for signature of natural selection potentially present in resistant Chinese chestnut genomes coexisting with *P. cinnamomi* in the East Asia. To facilitate candidate gene discovery within QTL intervals, we also initiated a functional genomics study by analyzing gene expression profiles in chestnut roots interacting with *P. cinnamomi* zoospores. In total, 49 regions under selective sweep were detected, and 34 of them were located within QTL intervals on LG_E. Using assembled transcriptome data, we determined if genes within LG_E QTLs were expressed in chestnut roots infected with *Pc* zoospores. As indicated by transcript annotations, genes under selective sweep encode proteins primarily involved in the phenylpropanoid pathway, cell-wall formation, transmembrane transport and signal transduction, and production of reactive oxygen species. Groups of genes either potentially involved in host response to *Pc* or confer plant innate immunity —i.e., glucan endo-1,3-beta-D-glucosidase, patatin-like phospholipase, G-type lectin S-receptor-like serine/threonine-protein kinases, and cysteine-rich receptor-like kinases—were placed on the short list of genes for functional characterization in transgenic American chestnut.