

GENETIC MAPPING AND FUNCTIONAL GENOMICS ANALYSES OF THE RESISTANCE/SUSCEPTIBLE RESPONSE IN CHESTNUT SEEDLINGS TO *PHYTOPHTHORA CINNAMOMI* INFECTION

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Due to availability of resistant Asian and susceptible American and European chestnut species, *Castanea* is ideally suited for studying plant-*Phytophthora cinnamomi* (*Pc*) interactions. We employed a genetic approach to map resistance to *Pc* in interspecific crosses using resistant Chinese chestnut, *Castanea mollissima* (“Mahogany” and “Nanking” resistance donors) and susceptible American chestnut *C. dentata* (multiple parents). Five BC1, BC3 and F2 populations (1,435 individuals in total) were phenotyped multiple years for root rot severity and genotyped by reduced genome-representative sequencing. Using extensive sets of markers anchored to the *C. mollissima* genome v1.0 assembly, we constructed genetic maps and identified genomic regions underlying resistance to *Pc* in multiple crosses. The most consistent QTL signals in crosses with both Mahogany and Nanking backgrounds were detected in the lower part of LG E. Based on performance in years 2015 and 2016, we selected Nanking-derived F₂ reciprocal crosses NK5 and NK6 segregating for healthy:unhealthy:dead trees in a ratio 1:1:1 ($P < 0.05$) for further studies of plant-*Pc* interaction using transcriptomics and metabolomics approaches. In a pilot experiment we challenged 1-year old NK5 progeny with *Pc* and harvested root tissue at 7 time-points (0, 1, 2, 3, 5, 7 and 14 days) post inoculation. Non-inoculated plants were used as controls along with inoculated Chinese and American chestnut seedlings. Inoculated plants were monitored for progression of root rot symptoms and the three most resistant and three most susceptible plants were chosen for RNAseq analysis and metabolite profiling. Results of these experiments and the initial mapping experiments will be presented.

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