QTL MAPPING BLIGHT RESISTANCE IN CHINESE X AMERICAN CHESTNUT HYBRID FAMILIES

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Chestnut blight (caused by *Cryphonectria parasitica*, *Cp*) and Phytophthora root rot (caused by *Phytophthora cinnomomi*, *Pc*) have nearly extirpated American chestnut throughout its native range in eastern North America. We have mapped QTLs for resistance to both pathogens using several control-pollinated hybrid families (American and Chinese chestnuts) scored in artificial inoculation experiments. Results for *Pc* resistance will be discussed in a separate presentation. For *Cp* we implemented a genome wide association (GWAS) analysis using multiple backcross families and one F_2 family that were derived from three unrelated Chinese chestnut donor trees. Adding to the complexity of the genetic materials, the inoculation experiments were run in different years, such that years were confounded, but with standard protocols and the same two pathogen isolates across years. Standardizing resistance phenotypic data for each isolate and each inoculation experiment enabled an across-families GWAS. Results from the GWAS identified several resistance-associated QTLs. All but one of these QTL (on LG_B) were isolate specific. Thus it appears that *Cp* resistance is relatively complex due in part to important interactions with pathogen isolates. We recommend that breeding programs consider this apparent pathogenic variability in their screening and deployment activities.