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Development Of Molecular Markers For Fire Blight Resistance (*Erwinia amylovora*) In *Malus* (Apple) By A Candidate Gene Approach

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Fire blight, caused by the bacterial pathogen *Erwinia amylovora*, is a destructive disease of apple and pear. The goal of this project is to use genomic approaches to identify molecular markers for use in marker-assisted breeding for fire blight resistance. Genes differentially expressed in apple in response to fire blight were identified by transcript profiling and then ranked for their potential impact on resistance based on bioinformatics and inferences drawn from the scientific literature. Single nucleotide polymorphism (SNP) and simple sequence repeat (SSR) markers derived from highly ranked ESTs (candidate genes) were mapped in families segregating for fire blight resistance. Candidate gene markers that co-localized with known QTLs for fire blight resistance were then selected for further analysis and marker evaluation. This approach was successful in identifying two markers derived from a leucine rich repeat receptor-like protein (LRR-RLP) and a class III peroxidase (Prx) that were associated with the fire blight resistance QTL on linkage group 3 of *Malus* 'Robusta 5'. The LRR-RLP is predicted to localize to the outside of the cell and contains a conserved 24 amino acid consensus motif associated with extracytoplasmic plant resistance gene LRRs. Prx genes are ascribed a wide variety of functional roles including defense against bacterial pathogens. This approach is now being applied to other sources of fire blight resistance in *M. x domestica* and *M. sieversii*. The results demonstrate the utility of combining functional genomics and a candidate gene approach to identify molecular markers for complex biological traits.

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