

Identification of a QTL for postharvest disease resistance to *Penicillium expansum* in *Malus sieversii*

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Abstract

Blue mold of apple caused by *Penicillium expansum* is one of the most important postharvest rots of apple fruit. Little attention has been devoted to postharvest disease resistance in apple breeding programs due both to a lack of sources of genetic resistance and to the time required for seedlings to produce a sufficient number of fruit to phenotype the trait. *Malus sieversii* PI613981 collected from the wild in Kazakhstan has previously been reported to be resistant to blue mold. The development of genetic markers for this resistance to blue mold would facilitate the marker-assisted selection of this valuable trait in breeding programs. Fruit collected from a 'Royal Gala' × PI613981 mapping population (GMAL4593) in 2011 (145 individuals) and 2012 (115 individuals) were inoculated with *P. expansum* and evaluated for decay. The response of individual progeny to *P. expansum* ranged from highly resistant to highly susceptible, and lesion diameters observed on 101 progeny evaluated both years were significantly correlated. A genetic framework map has been developed for the GMAL4593 population and was used to identify a QTL for blue mold resistance on linkage group (chromosome) 4 and 10. Analysis of the apple genome sequence and functional genomics are currently being used to identify genetic markers derived from putative resistance genes.