#33

Characterization of Resistance to Fire Blight (*Erwinia amylovora*) and Blue Mold *(Penicillium expansum)* in Exotic and Domesticated *Malus* (apple) germplasm

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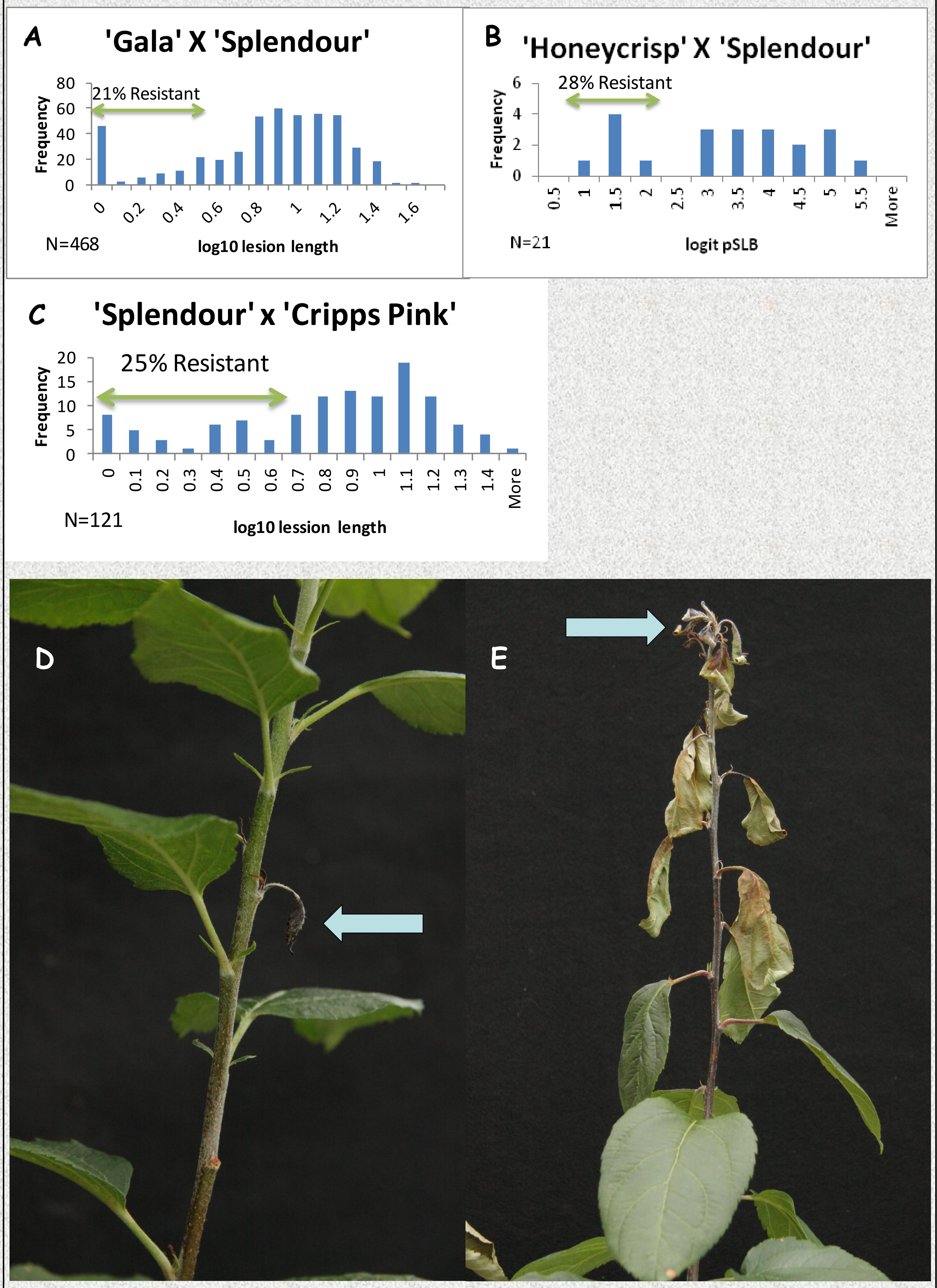
Fire Blight Resistance in 'Splendour'

'Splendour' is a commercial apple cultivar from New Zealand with excellent flavor that has been observed to be fire blight resistant under conditions of natural infection. To evaluate 'Splendour' as a potential donor of fire blight resistance, three 'Splendour' populations were evaluated for their resistance to fire blight and found to be segregating **1 Resistant:3 Susceptible (Fig 1**).

To facilitate QTL analysis, 100 individuals from the 'Gala' X 'Splendour' mapping population (Fig 1a) are being genotyped. If QTLs for fire blight resistance are identified (2 predicted from the segregation ratio), the 'Splendour' X 'Cripps Pink' (Pink Lady) and WSU 'Honeycrisp' X 'Splendour' populations will be used to validate molecular markers identified for the QTLs.

Figure 1. ***Segregation of resistance to fire blight*** in the progeny of **A**: 'Gala' X 'Splendour', **B**: WSU 'Honeycrisp' X 'Splendour' (HxSp), and **C**: 'Splendour' X 'Cripps Pink' populations. **D**: Resistant and **E**: susceptible response to inoculation with the fire blight pathogen in the HxSp 21 days after inoculation. Arrows point to the site of inoculation.



Abstract

The overall goal of this project is to develop the genetic resources and information necessary to incorporate the selection of resistance to fire blight and blue mold into U.S. apple breeding programs. Genetic improvement of host resistance has been identified by the U.S. apple industry as a desired method to mitigate production risks associated with economically important diseases such as fire blight and blue mold.

Fire blight: Several fire blight resistance QTLs have been described in *Malus*, however most come from exotic germplasm of poor fruit quality. Three bi-parental populations derived from 'Splendour' apple, which has excellent flavor and is resistant to fire blight, were found to segregate for resistance to fire blight (1R:3S) when challenged with *Erwinia amylovora*. These populations are being genotyped to identify the genetic basis of this resistance. (see left panel)

Blue Mold: Although there is no known resistance to blue mold in *M. ×domestica*, *M. sieversii* PI613981 collected from the wild in Kazakhstan is resistant. Fruit collected from a 'Royal Gala' X PI613981 mapping population (GMAL4593) were inoculated with *P. expansum* and evaluated for decay over a three year period. A genetic framework map has been developed for the GMAL4593 population and was used to identify QTLs for blue mold resistance on linkage groups 4 and 10. (see right panel)

Another approach to identify marker trait associations for fire blight resistance within domesticated *Malus* cultivars is to utilize the pedigree-linked germplasm of the RosBREED project. (see below)

Fire Blight Resistance in RosBREED *Malus* Crop Reference Set

The RosBREED project has developed a set of pedigree-linked apple breeding germplasm that spans multiple generations and it has successfully used pedigree-based analytical software to simultaneously enable QTL discovery and validation within the reference set. Although fire blight resistance is not a trait currently targeted by the project, determining the fire blight resistance/susceptibility of the reference set may allow us to leverage the accomplishments of the RosBREED project to enable marker-assisted breeding of fire blight resistance in existing seedlings and selections of U.S. apple breeding programs. The *Malus* Crop Reference and Washington State University (WSU) Breeder Pedigree Sets were propagated and a replicated research orchard will be established at WSU, Wenatchee, WA in spring 2015 and used to determine the resistance of this germplasm to fire blight.

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Blue Mold Resistance in *Malus sieversii*

Malus sieversii PI6139Blue mold of apple, caused by *Penicillium expansum,* is one of the most important postharvest rots of apple fruit worldwide. *P. expansum* is also of great concern to fruit processing industries (juices, baby food, ready to eat slices, etc.) due to its production of patulin, a highly toxic mycotoxin. Little attention has been devoted to postharvest disease resistance in apple breeding programs due both to a lack of sources of genetic resistance and the current prohibitive cost of waiting to evaluate fruit resistance. The development of genetic markers for resistance to blue mold would facilitate marker-assisted selection of this valuable trait.

81 has previously been reported to be resistant to blue mold (Janisiewicz et al. 2008 HortScience 43:420). Fruit was collected from a 'Royal Gala' X PI613981 genetic mapping population (GMAL4593) in 2011-2013, inoculated with *P. expansum* and evaluated for decay **(Fig. 2).** Two QTLs for blue mold resistance were identified on LG04 and LG10 based upon the mean lesion diameter 7 days after inoculation in 2011 and 2012 fruit samples **(Fig. 3)**.

Figure 2: Segregation of resistance to blue mold in mature fruit harvested from individual progeny of the GMAL4593 genetic mapping population ('Royal Gala' X *M. sieversii* PI613981) and evaluated for resistance to blue mold following controlled inoculation with *Penicillium expansum*. Two representative progeny showing **A:** susceptible and **B:** resistant disease responses 7 days post inoculation (dpi). **C:** Eleven replicate fruit of each accession were inoculated and evaluated 5 and 7 days post inoculation.

Figure 3: QTLs for resistance to blue mold (*Penicillium expansum*) on LG04 and LG10 of GMAL4593 ('Royal Gala' X *Malus sieversii* PI613981) mapping population. The QTL on LG10 co-locates with the polygalacturonase (*Md-PG1*)/fruit firmness QTL (Costa et al. 2010 J Exp Bot 61:3029). Software = MapQTL6 Kyazma,,Method = MQM multiple-QTL model, Algorithm = regression model.