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Host resistance to *Erwinia amylovora* – germplasm, breeding, genetics

Andreas Peil¹, Klaus Richter², Annette Wensing³, Ofere Emeriewen^{1,4}, Pierre-Marie LeRoux⁵, Thomas Wöhner¹, Andrzej Kilian⁶, Andrea Patocchi⁵, Magda-Viola Hanke¹, Henryk Flachowsky¹, Mickael Malnoy⁴

¹Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Horticultural and Fruit Crops, Pillnitzer Platz 3a, 01326 Pillnitz, Dresden, Germany; ²Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Resistance Research and Stress Tolerance, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany; ³Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Plant Protection in Fruit Crops and Viticulture, Schwabenheimer Str. 101, 69221 Dossenheim, Germany; ⁴IASMA Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach, 1 – 38010 San Michele all'Adige (Trento), Italy; ⁵Research Station Agroscope Changins-Wädenswil ACW, Department of Plant Protection and Fruit and Vegetable Extension, Schloss 1, 8820 Wädenswil, Switzerland; ⁶Triticarte P/L, PO Box 7141, Yarralumla, Canberra, ACT 2600, Australia

The most important bacterial disease affecting pome fruit is fire blight caused by *Erwinia amylovora*. It can cause devastating economic losses and is reliably controlled only by the application of antibiotics, which are banned in many European countries due to environmental, sustainable and consumer friendly issues. One solution could be the utilization of fire blight resistant cultivars in apple production.

In 2003, we started an approach at Dresden-Pillnitz to detect different mechanisms conferring resistance to fire blight aimed at their combination in new cultivars. Four segregating populations were established to map QTLs for fire blight resistance. The donors used were three wild species accessions *Malus baccata* (MALD0004), *M. fusca* (MALD0045), *M. × robusta* 5 and the Pillnitz cultivar Rewena. The susceptible parent in each case was Idared. Grafted scions of each progeny were inoculated with *E. amylovora* strain Ea 222_JKI in at least for two years. Average percent lesion length (PLL) of all progenies was determined. Genetic linkage maps were established using DArT-, SCAR-, SNP-, and SSR-markers. Whereas in Rewena no QTL could be determined, major QTLs were detected in *M. baccata* on linkage group 12, in *M. fusca* on linkage group 10, and in *M. × robusta* 5 on linkage group 3 explaining up to around 50, 85 and 85% of the phenotypic variance, respectively. The case that all resistance QTLs are located on different linkage groups enhances the chance that different mechanisms are acting in the donors.

Additionally, trees of the Idared by *M. × robusta* 5 population were planted in an orchard and flowers were inoculated in two consecutive years. The QTL on linkage group 3 could be confirmed after mapping.