



III International Symposium on Molecular Markers in Horticulture



Riva del Garda (Trento)

Italy,



Under the Auspices of the
Autonomous Province of Trento

**DArT and SSR markers are linked with a strong QTL for resistance to fire blight in the apple wild species
*Malus fusca***

Authors: ofere4real@yahoo.co.uk

Name	Surname	Institution	Address	Country
<u>Ofere</u>	<u>Emeriewen</u>	Research and Innovation Centre, Fondazione Edmund Mach	Via E. Mach, 1 – 38010 San Michele all'Adige (Trento)	Italy
Andrzej	Kilian	Diversity Arrays Technology	Triticarte P/L, PO Box 7141, Yarralumla, Canberra, ACT 2600	Australia
Klaus	Richter	Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Resistance Research and Stress Tolerance	Erwin-Baur-Str. 27, 06484 Quedlinburg	Germany
Andreas	Peil	Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Horticultural Fruit Crops	Pillnitzer Platz 3a, 01326 Dresden	Germany
Mickael	Malnoy	Research and Innovation Centre, Fondazione Edmund Mach	Via E. Mach, 1 – 38010 San Michele all'Adige (Trento)	Italy

Abstract: The most important bacterial disease affecting pome fruit is fire blight caused by *Erwinia amylovora*. Antibiotics treatment is the only reliable control measure for this devastating disease, yet their use is strictly regulated if not completely banned in many European countries due to environmental and sustainable issues. Since resistance can be genetically determined, planting of fire blight-resistant cultivars seems to be a highly probable approach. In this study, we explored a segregating population derived from a cross between the apple wild species *Malus fusca* and the *Malus x domestica* cultivar 'Idared'. The mapping population was artificially inoculated with *Erwinia amylovora* strain Ea222_JKI at a concentration of 10⁹ cfu/ml in 3 different years. A new library of DArT clones was constructed using the complexity reduction method that identified 1080 DArT markers after images were processed using DArTsoft. SSR markers were sourced from literature and used to genotype the population. The averages of percentage lesion length (PLL) of all replicates of each genotype were used as numerical traits for statistical analysis. A Kruskal-Wallis analysis, used to determine marker-phenotype association revealed one linkage group containing DArT markers significantly linked to fire blight resistance. To determine the corresponding linkage group, the DArT markers were sequenced and sequences aligned to the 'Golden Delicious' reference genome. SSR markers were developed from the 'Golden Delicious' genome to replace highly significant DArT markers and to determine the QTL region. Interval mapping revealed a strong QTL on LG10 explaining about 65% of the phenotypic variation. Through genome walking approach aimed at determining the resistance region, additional SSR markers have been developed and mapped.

Keywords: *Erwinia amylovora*, Fire blight, DArT markers, SSR markers, QTL

Type of presentation: [Oral](#)

Topics:

- Molecular mapping and marker development