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Evidence of a major QTL for fire blight resistance in the apple wild species *Malus fusca*

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Fire blight is a common and very destructive disease affecting apple (*Malus x domestica*) and pear (*Pyrus communis*) productions. Caused by the bacteria *Erwinia amylovora*, its devastating economic effects ranges from losses in yield to severe damage or death of trees in the orchard, and in extreme cases loss of a whole orchard. The only reliable and effective management measure available to producers is the use of antibiotics. However, dependence on antibiotics treatment is not sustainable given such risks as the rapid selection of antibiotic-resistant populations and environmental-associated risks, which have led to their application being forbidden in many countries. Therefore the planting of fire blight-resistant cultivars seems to be the most probable strategy since it is eco-friendly. However until now, there is no fire blight resistant apple variety produced for the global market. Host resistance to fire blight in *Malus* is thought to be quantitatively controlled. Thus, several quantitative trait loci for resistance have been identified in some accessions of *Malus* spp. 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'. F₁ progenies used for mapping were artificially inoculated with *E. amylovora* strain Ea 222_JKI at a concentration of 10⁹ cfu/ml in 3 different years. Highest value of average percent lesion length (PLL) of all progenies was 23.1% in 2006 with 9.0 % as lowest in 2012. The averages of 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 two DArT markers (971000 and 970840) with the highest significance. The blast results of the sequences of both markers on the 'Golden Delicious' reference genome revealed their localisation on LG10. SSR markers were designed from the 'Golden Delicious' genome to replace these DArT markers and to determine the QTL region. Interval mapping revealed a strong QTL on LG10 explaining about 65% of the phenotypic variation. This is the first report on a fire blight resistance QTL of *M. fusca* and the only one located on LG10.