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Delineation Of QTLs For Resistance To Fire Blight In *Malus* 'Robusta 5' Accessions

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Breeding of fire blight resistant scions and rootstocks is a goal of several international apple breeding programmes, as options are limited for management of this destructive disease of caused by the bacterial pathogen *Erwinia amylovora*. Genetic mapping of quantitative trait loci (QTLs) for resistance has been a first step towards enabling marker assisted selection for fire blight resistance. A large effect QTL for fire blight resistance has been previously reported on Linkage Group

(LG) 3 of *Malus 'Robusta 5'* (Peil et al. 2007, 2008). In this study, we first re-considered the quantification of the complex disease phenotype in two 'Robusta 5' mapping populations used in previous studies and then employed both composite interval mapping (CIM) for analysis of single QTLs and the additional QTL mapping (addqtl) function of R/qtl software. CIM enabled the resolution of individual QTLs at distinct locations in the two populations with peaks located 6 cM apart. The upper of these two QTL co-located with a leucine-rich repeat receptor-like protein (*MxdRLP1*) candidate resistance gene. Subsequent analysis with addqtl enabled the detection of an additional QTL in one of the mapping populations where a single QTL had previously been mapped. The additional QTL was in a similar location to the upper of the two QTL detected by CIM. Allelotypic differences within LG3 that were detected between the 'Robusta 5' clones used in the study are believed to underlie the differential effects in the two mapping populations.