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Sommario

Brown Rot disease (BR) caused by the necrotrophic fungus Monilinia spp. is a major problem for the peach fruit market, causing significant losses at post-harvest level. Previous work demonstrated the possibility of discriminating between susceptible and tolerant peach genotypes, suggesting a quantitative nature of the BR resistance. In order to uncover genomic regions associated with this trait and identify molecular markers for marker assisted selection (MAS), an F1 segregating population from the intra-specific Contender (tolerant cultivar) x Elegant Lady (susceptible cultivar) peach cross has been chosen for QTL analysis. Phenotypic analysis was performed over two harvest seasons, using an artificial infection procedure that measured skin and flesh resistance to a M. fructigena field isolate. Significant correlations were found between the data obtained in the two years and between the two traits. Maturity date (MD) was also highly correlated with resistance traits. Genotyping 110 CxEL individuals allowed the construction of a linkage map (CxEL map), containing 78 SSR, covering a total genetic distance of 317.7 cM, and having an average marker density of 4.7 cM/marker. Both parametric (interval mapping) and non-parametric (Kruskal-Wallis analysis) QTL analysis using genotypic and phenotypic data from CxEL revealed two QTL clusters: a QTL underlying skin resistance located on LG CxEL-2 (explaining a 15% - 22% of the total phenotypic variability), and a QTL associated with flesh resistance

(explaining a 30% - 35.2% of the total phenotypic variability), collocating with a major MD QTL on LG CxEL-4. These results suggest that resistance to BR has at least two main components: the first related to avoidance of fungal penetration, and a second earliness-associated factor associated with fungal spread after penetration. Furthermore, markers M1a (CxEL-2) and UDAp-439 (CxEL-4) may provide useful tools for MAS for BR-resistance breeding programmes.

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