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CONSTRUCTION OF APPLE MOLECULAR MAPS IN THE 'GOLDEN DELICIOUS' X 'FREEDOM' PROGENY AND QTL ANALYSIS FOR SCAB RESISTANCE

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AFLP and SSR markers were used to construct two apple genetic linkage maps using the double pseudotestcross population 'Golden Delicious' x 'Freedom'. 'Freedom' is a cultivar derived from two different scab resistance sources: the male parent is heterozygous for the V_f gene (inherited from *Malus floribunda* 821), while the female parent is derived from an "Antonovka" type of resistance. The presence of at least two genes controlling scab resistance in 'Freedom' was postulated to explain the segregation observed in its crosses with a scab-susceptible cultivar.

Fifty-three SSR primer pairs were used to build the frame of the map that was implemented by using 15 AFLP primer combinations, that produced a total of 542 segregating AFLP markers.

The 'Golden Delicious' map comprised 238 markers (196 AFLPs and 42 SSRs) divided in 19 linkage group. The total map length was 883 cM with a marker density of 3,7 cM. The 'Freedom' map consisted of 283 markers (241 AFLPs and 42 SSR) mapped on 19 linkage groups and spanning 1066 cM. The average distance between two markers was 3,8 cM.

All F_1 seedlings were inoculated in greenhouse with a local strain of *Venturia.inaequalis*. Resistance and susceptibility of each seedling was assessed at 14 and 21 days after the inoculation by using a type of symptoms and sporulation severity scales. Two significant QTLs for scab resistance were identified in the 'Freedom' genetic map.