

Confirmation of QTLs controlling *Ascochyta fabae* resistance in different generations of faba bean (*Vicia faba* L.)

R. Díaz-Ruiz ^A, Z. Satovic ^B, C. M. Ávila ^C, C. M. Alfaro ^C, M. V. Gutierrez ^C, A. M. Torres ^C and B. Román ^{C D}

^A Colegio de Postgraduados, Campus Puebla. Km 125.5 Carr. Fed. México-Puebla, Santiago Momoxpan, Municipio de San Pedro Cholula, C.P. 72760, Puebla, México.

^B Department of Seed Science and Technology, Faculty of Agriculture, University of Zagreb, 10000 Zagreb, Croatia.

^C IFAPA_CICE. Mejora y Biotecnología. Centro Alameda del Obispo. Avda. Menéndez Pidal s/n. Apdo. 3092 (14080) Córdoba, Spain.

^D Corresponding author. Email: belen.roman.ext@juntadeandalucia.es

Abstract

Ascochyta blight, caused by *Ascochyta fabae* Speg., is a disease of faba bean (*Vicia faba* L.) of worldwide distribution. In this study we have conducted an experiment on *Ascochyta fabae* resistance in 165 recombinant inbred lines (RILs) developed by single-seed descent from the cross between resistant and susceptible lines (Vf6 × Vf136) in which *A. fabae* resistance QTLs (quantitative trait loci) have been previously reported in the original F₂ population. Recombinant inbred lines were inoculated under controlled growth chamber conditions and evaluated for disease severity and infection type index. The linkage map was constructed by MAPMAKER V2.0 and the QTL analysis was carried out using QTL Cartographer. Two hundred and seventy-seven markers (238 RAPDs, 4 isozymes, 5 ESTs, 1 SCAR, 6 SSRs, 2 STSs, and 21 intron-spanning markers) mapped into 21 linkage groups covering 2.856.7 cM, with a mean inter-marker distance of 12.72 cM. Composite interval mapping identified two zones of putative QTL action in the RIL population for DSL (disease severity on leaves) and DSS (disease severity on stems) traits. Putative QTLs (*Af1* and *Af2*) were identified on chromosome 3 and chromosome 2, respectively, and jointly explained 24% of the phenotypic variance of DSL and 16% of DSS. With this study we have (1) confirmed the QTLs for *Ascochyta* blight resistance found in F₃ families in the derived RILs (F₆), (2) re-estimated their position and genetic effects, and (3) assessed the stability of these QTLs in different genetic backgrounds by comparison of the mapping data with a previous QTL study.

Keywords: marker assisted selection, F₂, RILs, QTL evaluation.

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