



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QTL Analysis of Ascochyta Blight Resistance in Chickpea

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Abstract: Recent advances in quantitative trait loci (QTL) analysis have facilitated studies on Ascochyta blight, caused by *Ascochyta rabiei* Pass (Lab.), resistance in chickpea (*Cicer arietinum* L.). Using a recombinant inbred line (RIL) population derived from an interspecific cross between *C. arietinum* and *C. reticulatum*, the same 2 QTLs conferring resistance to Ascochyta blight were identified at 2 locations by interval mapping. Genotype X environment (G x E) interaction was significant both between years at the same location and between locations. The effect of QTL-1 on linkage group 8 (LG-8) was greater than that of QTL-2 on LG-4 at Pullman while the effect of QTL-2 was higher than that of QTL-1 at Eskişehir. Dissection of QTLs with molecular markers provides a better understanding of resistance to Ascochyta blight in chickpea. Validation of both QTLs in a second environment promises the application of marker-assisted selection (MAS) for this trait. Changes in magnitudes of the QTL's effect in 2 locations indicate possible differences in pathogen populations and environmental interactions.

Key Words: Chickpea, Ascochyta blight, quantitative trait locus, recombinant inbred line, molecular markers

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