

QTL MAPPING FOR BROOMRAPE (*OROBANCHE CUMANA* WALLR.) RESISTANCE IN SUNFLOWER

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ABSTRACT

Broomrape (*Orobancha cumana* Wallr.) is one of the most important biotic factors *causes* reduction in sunflower *yield*. *Although breeding for* broomrape resistance is most effective method to control the disease, development of cultivars resistant to broomrape is not easy due to quantitative nature of the resistance. Although few QTLs were identified for broomrape race F resistance, none of the QTLs is suitable for marker assisted selection (MAS) due to small effect. In the present study three major QTLs were identified on LG7, LG11 and LG12 for broomrape race F resistance in sunflower by using high density SNP map constructed by *genotyping by sequencing (GBS) approach*. Total phenotypic variation (PVE) explained by the identified QTLs was 82%. This is the first report of *QTL mapping for* broomrape race F resistance *using a high density SNP map*. QTLs identified in this study will be valuable molecular genetics tools for broomrape resistance.

Key Words : *Helianthus annuus*, molecular breeding, genotyping by sequencing (GBS), broomrape race F