

## HIGH-DENSITY LINKAGE MAPPING AND GENETIC DISSECTION OF RESISTANCE TO BROOMRAPE (*OROBANCHE CRENATA* FORSK.) IN PEA (*PISUM SATIVUM* L.)

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Pea (*Pisum sativum* L.) is a widely cultivated legume of major importance for global food security and agricultural sustainability. Crenate broomrape (*Orobanche crenata* Forsk.) (Oc) is a parasitic weed severely affecting legumes, including pea, in the Mediterranean Basin and the Middle East. Previously, the identification of the pea line 'ROR12', displaying resistance to Oc, was reported. Two-year field trials on a segregant population of 148 F7 recombinant inbred lines (RILs), originating from a cross between 'ROR12' and the susceptible cultivar 'Sprinter', revealed high heritability (0.84) of the 'ROR12' resistance source. Genotyping-by-sequencing (GBS) on the same RIL population allowed the construction of a high-density pea linkage map, which was compared with the pea reference genome and used for quantitative trait loci (QTL) mapping. Three QTLs associated with the response to Oc infection, named *PsOcr-1*, *PsOcr-2* and *PsOcr-3*, were identified, with *PsOcr-1* explaining 69.3% of the genotypic variance. Evaluation of the effects of different genotypic combinations indicated additivity between *PsOcr-1* and *PsOcr-2*, and between *PsOcr-1* and *PsOcr-3*, and epistasis between *PsOcr-2* and *PsOcr-3*. Finally, three

Kompetitive Allele Specific PCR (KASP) marker assays were designed on the single nucleotide polymorphisms (SNPs) associated with the QTL significance peaks. Besides contributing to the development of pea genomic resources, this work lays the foundation for the obtainment of pea cultivars resistant to Oc and the identification of genes involved in resistance to parasitic Orobanchaceae.