MOLECULAR CHARACTERIZATION OF THE MAJOR RESISTANCE GENE *Or7* CONTROLLING RESISTANCE TO *OROBANCHE CUMANA* IN SUNFLOWER

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Abstract

Resistant cultivars play an important role to control sunflower broomrape (*O. cumana*) in fields. Some of them carry the *Or7* locus, a major resistance gene that confers resistance to *O. cumana* race F, the main race in South of Spain. We used a combined approach to map the locus to the chromosome 7 by GWAs on 55 lines and by using a segregating population of 355 RILs. *In silico* analyses and genetic data located the *Or7* gene in a genomic region of 850kb. We then restricted the genomic region of the *Or7* gene by genotyping a large segregating population of 14,000 F2 plants and by identifying 271 F2 recombinant plants between the two markers surrounding the 850 kb genomic region. After selfing each of the 271 F2 plants, almost all F3 families were phenotyped in field, the corresponding F4 families were phenotyped in the same field, and in controlled conditions to confirm the F3 families phenotype. Finally the *Or7* gene was located in a window of around 55 kb, containing 2 predicted genes coding for Leucine Rich Repeat proteins. To obtain the parental genomic sequences, we created and screened two BAC libraries from the susceptible and resistant lines. The comparison of both genomic sequences showed a high level of divergence with large structural variations, suggesting a wild origin of the *Or7* gene. We performed a molecular diversity analysis of the region, in a panel of 170 accessions of wild relatives, wild and cultivated sunflower. Only one haplotype was found on *Or7*+ lines for a gene close to the 55 kb window. A transcriptomic analysis is underway to better understand the role of the *Or7* gene during the interaction.

Keywords: *Or7*, resistance, cloning, LRR protein, wild relatives