

**GENETIC CHARACTERIZATION OF THE INTERACTION BETWEEN
SUNFLOWER AND OROBANCHE CUMANA.**

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ABSTRACT

Orobanche cumana is a major disease in cultivated areas around the black sea and in Spain. The pathogen spread recently to several other countries (France, China ...). During the last ten years, several new *O. cumana* races have emerged but very few efficient methods were available to control their development. Genetic resistance was the more efficient and introgression of major resistance loci was successfully used to produce new resistant sunflower varieties. With the recent emergence of new virulent races, novel resistance loci need to be mapped and characterized. A recombinant inbred line population, derived from the cross between the lines HA89 and LR1, was used to map QTLs controlling quantitative resistance to race F. The phenotyping has been conducted on the 107 lines of the population at different stages of the interaction. We evaluated each line for (i) the capacity of their root exudate to induce germination of *O. cumana* seeds, (ii) their ability to induce incompatible attachment, (iii) the number of broomrape tubercles in growth chamber, and (iv) the number of broomrape emergences in the field. Different response profiles were observed at these 4 stages of development, indicating several resistance mechanisms in sunflower. Interestingly, even if the two parental lines showed a close resistant phenotype, we observed a large diversity of the resistance level in the population. Combined with this detailed phenotyping analysis, we performed the genotyping of the sunflower recombinant inbred lines using an AXIOM array of 586 985 SNPs. QTLs will be mapped for the different traits.

Key Words : *Orobanche cumana*, sunflower, QTL, resistance