

TOWARDS AN UNIVERSAL SET OF DIFFERENTIAL SUNFLOWER GENOTYPES FOR PRECISE BROOMRAPE RACE IDENTIFICATION

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Abstract

Sunflower broomrape (*Orobanche cumana* Wallr.) is a holoparasitic weed that infects roots of sunflower in large areas of Europe and Asia, and it has been identified recently in North Africa. The parasitic interaction between sunflower and *O. cumana* generally follows a gene for gene model. It has been reported the existence of five pathogenic races of *O. cumana* named as A to E, controlled by resistance genes *Or1* to *Or5*. New populations overcoming *Or5* resistance and named as race F were identified from the middle 1990's in most of the areas infested by sunflower broomrape. Nowadays, increasingly virulent populations classified as races G and H are becoming predominant in countries around the Black Sea and Spain. However, there are doubts about the racial status in sunflower broomrape and research community needs imperiously of a common set of differentials to determine precisely the races present in specific countries. To clarify this situation and propose a new system of differentials we have evaluated 24 broomrape populations from different countries in which sunflower is facing broomrape. These populations were evaluated on eight inbred lines and four hybrids carrying different resistance genes, including lines used in previous studies like B117, NR5 and P96, for instance, and hybrids extensively used along Europe. The results showed that broomrape racial situation is more complex than it has been proposed before and that it is needed to include several differentials to be able to discriminate different races of what has been named before as race F, G and H. A new set of differentials will be proposed preliminarily to understand this variability and discussed with scientific community.

Keywords: broomrape, *Helianthus annuus* L., race, sunflower, virulence