

GENETIC DIVERSITY OF *OROBANCHE CUMANA* POPULATIONS USING ISSR MARKERS

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Abstract

The parasitic plant *Orobanche cumana* Wallr. has become a limiting factor for sunflower crops. The genetic diversity of broomrape from the Republic of Moldova is still grossly under-studied. This not only leads to unclear status of taxonomically problematic species and their local intraspecific taxa, but also hampers the assessment of their relevance as actual or potential treats for agricultural.

The aim of this study was to evaluate the inter-population variability of the phytopathogen *Orobanche cumana* Wallr. in the Republic of Moldova. The study of genetic polymorphism was carried out in 39 populations of *O. cumana* through the application of 14 ISSR markers.

The assessed have demonstrated different levels of genetic variability, depending on primers. The genomic-molecular analysis has shown that populations belonged from the Central and Southern region of the Republic of Moldova are characterized by the presence of the high number of alleles and are more polymorphic comparative with those from the North. Some populations in the South region (in particular, Carabetovca, Alexanderfeld, Ştefan-Vodă and Slobozia Mare) showed the major differences in the obtained profiles and a high level of genetic variability.

Taking into account the results regarding the genetic distance, the clustering analysis and the molecular profiles, we can conclude that the populations of *Orobanche cumana* in the Republic of Moldova have major differences at the molecular level.

Keywords: *Orobanche cumana*, ISSR, genetic distance, population variability