

## ANALYSIS OF MOLECULAR VARIANCE (AMOVA) OF *OROBANCHE CUMANA* POPULATIONS

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The first reports that attest the presence of *Orobanche cumana* Wallr. (broomrape) in sunflower fields date back to 1866 in Russia. Then, due to the expansion of sunflower cultivated area, in 100 years this parasite has spread in Bulgaria, Moldova, Romania, Serbia, Spain, China and in the last 50 years – in the main sunflower producing countries around the world. Until now, eight races of *O. cumana* have been identified, from A to H.

The objective of this research was to study the genetic diversity of 33 *O. cumana* populations originated from 6 countries (Bulgaria, Moldova, Romania, Serbia, China, Turkey) using microsatellite molecular markers like SSR and ISSR. The evaluations were conducted in artificially infected pots in greenhouse conditions. The most highly virulent broomrape races, G and H, was revealed in the majority of studied countries, except of Serbia (race E or less virulent than E). The study of genetic variability of 33 populations was performed based on the analysis of molecular variance method (AMOVA). The results showed for the both marker systems (SSR: within populations 37%, among populations 63%; ISSR: 41% and 59%, respectively), that the most of the total variance was attributed to the differences between populations. At the country level, AMOVA dates for Bulgarian broomrape populations also presented a higher variability among populations while for the populations from Moldova, Serbia, China and Turkey, the molecular variations within populations were a major source of genetic variation. AMOVA results showed that both marker sets, based on molecular data SSR and ISSR, keep the same tendency of distribution of genetic variations.

The molecular differences between identified broomrape races ( $\leq$ E, G, H) very little contributed to the total variability (SSR: among races 10%; ISSR: 11%, respectively). According to the SSR markers (separately for three groups of races) genetic variations within populations are higher for the broomrape populations race H (53%) and lower for those from race G (30%) and  $\leq$ E (36%). In the case of ISSR markers, molecular variations were almost equally divided between intra- and interpopulation diversity, with predominance of diversity between populations for all groups.

In this context, our results indicate that *O. cumana* specie has a very great genetic potential and a high degree of genetic variations which can determine the evolution of more virulent races which is important for creating some sunflower crop breeding strategies and their control.

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**Keywords:** *Orobanche cumana* Wallr., AMOVA, populations, races, genetic diversity.