

GENETIC DIFFERENTIATION AND RELATIONSHIPS OF *OROBANCHE CUMANA* POPULATIONS FROM DIFFERENT SUNFLOWER PRODUCING COUNTRIES

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Orobanche cumana Wallr. is an important species of obligate parasitic weed, naturally distributed from central Asia to south-eastern Europe, where it parasitizes wild *Asteraceae*. Until now, broomrape was recorded in more than 60 countries around the world, causing significant economic damage in crop production especially in Central and Eastern Europe, Spain, Turkey, Israel, Iran, Kazakhstan, and China.

Accelerating rate of parasite evolution and distribution could rapidly diminish the effectiveness of control measures and strategies related to the deployment of resistance genes. Therefore, knowledge about the population structure of parasite are critical to the design of appropriate resistance breeding programs and effective weed control.

Thus, the present study focused on the assessment of the genetic diversity among and within 33 broomrape populations belonging to different sunflower producing countries (Moldova, Romania, Bulgaria, Serbia, China, Turkey) and races (E, G, H) employing microsatellite molecular markers (SSR). The structure of populations was analyzed using different methods (AMOVA, Nei statistics, PCA), based on GenAlEx 6.503 and XLSTAT 2014.5.03 software.

The genetic differentiation (Φ_{ST}) between pairs of *O. cumana* populations with different origins indicate values between 0.170 and 0.686 ($p < 0.001$), revealing a strong and very strong differentiation between the populations from different countries. The highest differences were found between populations from China and other countries, indicating that geographic distance is a substantial barrier to gene exchange between populations. AMOVA analysis showed significant genetic differences between groups (countries), as well as between populations within groups and individuals within populations. So, 36% of total genetic diversity was attributable to divergence between groups, 30% to population differentiation within groups and 34% to individual differences within populations. The first 2 components from a PCA explained about 41% of the total variation in the data. Cluster analysis showed that the majority of populations from the Republic of Moldova, Romania and Bulgaria, which are geographically close, were included in one group, Serbian populations formed a separate subcluster, and populations from Turkey and China grouped together. As a result, new data of broomrape population structure were accumulated.

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Keywords: *Orobanche cumana* Wallr., genetic diversity, molecular markers SSR, races, population genetic structure.