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Efficiency of microsatellite markers in genotyping of *Orobanche cumana* populations

Microsatellites or simple sequence repeats (SSRs) markers are widely dispersed across the genome, have a codominant and multiallelic nature, high variability and informativeness, and a specific chromosomal location. For this reason, they are playing a significant role in different fundamental and applicable fields, including genetic studies at the individual, population, species levels, and molecular breeding programs. In this study, the utility of 15 microsatellite markers in discrimination of 33 *Orobanche cumana* (broomrape) populations from different geographical locations was assessed: Republic of Moldova (11 populations), Romania (1), Bulgaria (4), Serbia (7), Turkey (7) and China (3). The PCR amplification products obtained showed differences by number and size depending on the markers used (3 and 16 alleles). A total of 110 alleles with fragment sizes ranged from 76-343 bp were determined. The evaluation of the genetic polymorphism of SSR markers was performed by the *effective number of alleles per locus* (Ne) with an average of 5.31, *Polymorphic Information Content* index (PIC) – 0.75, *Nei's genetic diversity* index (H) – 0.78 and, *Resolving Power* index (Rp) – 5.79. High values of all indices revealed the significant informative capacity and effectiveness of markers studied. At the same time, most markers showed PIC values higher than 0.5, indicating a high polymorphism in *O. cumana* populations. Seven microsatellite markers (Ocum-052, Ocum-059, Ocum-074, Ocum-081, Ocum-087, Ocum-196, Ocum-197) were selected based on the analyzed statistical parameters, suggesting that these markers can efficiently measure genetic diversity in broomrape. Based on the Rp index and PIC values of these 15 SSR markers, genetic diversity of Turkish (Rp: 4.774; PIC: 0,722) and Moldavian (Rp: 4.394; PIC: 0,716) *Orobanche cumana* populations was higher than in other populations. However, the studied microsatellite (SSR) markers system characterized very well the genetic structure of all *O. cumana* populations included in this study. Selected markers could eventually be useful for breeders and sunflower seed producers to improve their control strategies for this parasitic plant.

Key words: SSR markers, genetic polymorphism, genotyping, population, *Orobanche cumana*