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ISSR and SSR markers in assessing genetic diversity of *Orobanche cumana*

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Among molecular markers, Inter Simple Sequence Repeats (ISSR) and Simple Sequence Repeats (SSR) have been successfully used in population genetic studies. In present research 13 ISSR and 12 SSR markers were employed in order to determine the genetic diversity and relationships among 39 broomrape populations, collected from different regions of Republic of Moldova (Northern – N, Central – C and Southern – S) and belonging to different races (E, F, G and H). The level of genetic polymorphism, obtained with two types of markers where convergent, demonstrating that the combination of methods are important for establishment of genetic variation among *O. cumana* populations and races differentiation. Thus, the comparative analysis of PIC index revealed the values ranging from 0.27 to 0.77 with a mean value 0.57 and 0.23 to 0.48 with mean value 0.40, for SSR and ISSR markers respectively. The Mantel test showed higher values of correlation coefficients between the races E and G (0.731), G and H (0.622), E and H (0.575) in case of SSR analysis and, respectively, 0.702; 0.670; 0.669 in case of ISSR analysis. The multiple correlation coefficients (*Pearson*) for broomrape populations with distinct geographic origin were quasi similar for both markers: (N:C) = 0.395 (SSR) and 0.409 (ISSR); (N:S) = 0.427 (SSR) and 0.396 (ISSR); (C:S) = 0.673 (SSR) and 0.631 (ISSR). The data obtained as a result of analysis using SSR and ISSR markers demonstrate a higher degree of genetic similarity of *O. cumana* populations from the Central and Southern regions of the country and of the race E of broomrape with G and H.

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