

STUDIES OF BROOMRAPE POPULATIONS ASSOCIATED WITH INCREASED GENETIC DIVERSITY

Ina BIVOL*, Ana MUTU

Moldova State University, Center of Functional Genetics, Republic of Moldova

E-mail: bivolinga@yahoo.com

In the present investigation an effort was made to identify of broomrape races originating from China and study the level of intra- and interpopulation variability based on the morphometric parameters of the seeds and also the molecular markers.

The racial status of the analyzed populations was established, also two races of broomrape were identified: race G (Ch1 population from Inner Mongolia and Ch3 from Hebei) and race H (Ch2 from Inner Mongolia) using internationally recognized a set of differential *Or* homozygotes lines.

Comparative analyzes on the morphometric characteristics of broomrape seeds performed by descriptive statistical analysis and correlative association revealed significant differences in seed length (Ch1 and Ch3) and length/width ratio (Ch3 and Ch4 from Xianjiang), which is an indication of the moderate level of interpopulation variability. In the case of assess of the intrapopulation variability level, depending on the coefficient of variation of the analyzed parameter, the relatively homogeneous (Ch2, Ch3 and Ch4) and relatively heterogeneous (Ch1) populations were identified.

Genetic variability between and within some broomrape populations from different regions of China was also explored using 15 SSR and 14 ISSR markers. SSR and ISSR markers utility was evaluated by calculating the polymorphism information content, observed and effective number of alleles, *Nei's* and *Shannon* diversity index, number and percentage of polymorphic loci. The high intrapopulation genetic variability was revealed by SSR markers while as for the ISSR primers a high degree of genetic variations was found at the interpopulation level. UPGMA clustering and principal component analysis performed according to ISSR and SSR/ISSR data set allowed to clearly distinguished all the broomrape populations for geographical origin and their racial origin while, in the case of SSR markers did not find this type of correlation.

In conclusion, although the morphological markers were not found better than molecular, after all a combination of both markers would be highly efficient in detecting genetic variability and phylogenetic analysis among different populations of *Orobanche cumana*.

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