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MULTIVARIATE STATISTICAL METHODS IN ANALYSIS OF BROOMRAPE GENETIC DIVERSITY

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Genetic diversity is the variation of heritable characteristics in a population, which can results from evolution, mutation, migration, domestication, natural selection and plant breeding. For the genetic diversity analysis are widely used the multivariate data from multiple measurements at morphological, biochemical and molecular level on each investigated individual. The cluster analysis, principal component analysis (PCA), principal coordinate analysis (PCoA) and multidimensional scaling (MDS) are most commonly employed and appear particularly useful.

The aim of these investigations was to evaluate the efficiency of multivariate statistical algorithms in the analysis of genetic relationships among 39 broomrape (*Orobanche cumana* Wallr) populations from three regions (Nord, Centre and South) of Republic of Moldova. The clustering (AHC, UPGMA) and multivariate methods (PCoA, PCA) have been tested with different data distributions (quantitative and binary) of various type of variables (the length, width of seeds and their ratio, molecular data obtained via simple sequence repeats and inter simple sequence repeats markers).

The applying of different approaches for data analysis led to a different ranking of the genetic and environmental factors, which are important in identification of race composition and distribution of broomrape on the territory of the Republic of Moldova. So, the results achieved by cluster (UPMGA) and PCo analyses on the molecular data, highlight the geographic origin of populations, while the cluster analysis (AHC) of morphological data revealed the contribution of different climatic conditions for geographical distribution of parasite.

Since each of these data sets and different methods of analyses provide different types of information, the choice of analytical methods depends on the objectives of the experiment and the available technological resources. With increases in the sample size of accessions, the identification of genetic variability and the classification of biological material have considerable significance. Knowledge about genetic diversity and relationships among individuals may be an invaluable aid in plant conservation and breeding.

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