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Genetic diversity among soybean genotypes assessed by molecular markers

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Soybean (Glycine max (L.) Merr.) is one of the oldest crop in the world, with a history of growing over 4000 years. At the same time it is the most important legume in the global world production. Simple Sequence Repeat (SSR) markers are widely used for estimation of genetic diversity within different species, due to their reproducibility, co-dominant and multi-allelic nature. Molecular characterization among soybean genotypes was done with 36 SSR markers, with at least one primer from each linkage group, to determine the genetic diversity. Twenty soybean accessions and varieties obtained from Maize Reasearch Institute, Zemun Polje were analyzed. A total number of detected alleles was 116 and number of alleles varied between two to six, with an average of 3.22 alleles per marker. Thirteen unique alleles were obtained from eleven SSR loci in nine genotypes. Molecular analysis revealed a high polymorphism of SSR loci. Pairwise coefficients of genetic similarity calculated by Dice ranged from 0.14 to 0.74. Genetic similarity matrix was used to construct dendrogram by UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method in NTSYSpc2 program package. This clustering method distinguished 20 soybean genotypes in two subclusters and one branch.

Biography

Danijela Ristic completed her under-graduation and PhD studies on Belgrade Faculty of Biology, University of Belgrade. She is scientific associate at Laboratory of Molecular Genetics and Physiology at Maize Research Institute "Zemun Polje". Her main researches are genetic characterization and evaluation of maize and soyabean, as well as genetic diversity of a forest trees.

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