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Genetic variability of red clover genotypes on the bases of morphological and microsatellite markers

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Red clover (*Trifolium pratense* L) is one of the most important sources of animal food. Evaluation of the accessions for the extent of genetic diversity is of particular importance for red clover breeding programs as well as for conservation of genetic resources. In the present investigation, 40 diploid and tetraploid red clover genotypes from 17 different countries around the world were screened for their genetic diversity using 13 morphological traits and 15 microsatellite markers. The traits analyzed and investigated were 8 quantitative morphological traits and 5 qualitative traits. Principal component analysis (PCA) and applied GGE biplot model for 8 quantitative character data accounted for 83.7% of the total variation of the standardized data, consisting of 69.2 and 14.5 % of variance attributable to PC1 and PC2 respectively. UPGMA cluster analysis based on the quantitative morpho-agronomic traits allowed the identification of 6 basic groups with genetic distances ranging from 0.56 to 10.35. Spearman correlation coefficient among red clover quantitative traits varied from 0.25 to 0.96. For analyzed qualitative traits Shannon diversity index varied from 3.595 to 3.673 with average value 3.631 and UPGMA cluster analysis based on these type of markers grouped the accessions of red clover into 8 clusters. Microsatellite analysis showed the number of fragments amplified by each SSR primer combination varied from 24 for RCS3681 to 108 for RCS1729 with an average value of 76.4 per primer combination. The similarity coefficients based on 15 SSR markers ranged from 0.50 to 0.90 among the 40 accessions studied. The dendrogram constructed using SSR markers produced ten distinct clusters. The cluster size varied from 1 to 14 genotypes of red clover. Principal coordinates analysis revealed that first (PCoA 1) accounted 5.5% and the second (PCoA 2) accounted for 5% of the total SSR variation. The analyzed red clover accessions showed significant variation in phenotypic and SSR characters, indicating high genetic diversity which could allow development of new cultivars with desired traits through selection and crossing programs.

Biography

Gordana Šurlan Momirović is professor of Genetics at the Faculty of Agriculture University of Belgrade, Department of Genetics and Plant Breeding. Gordana Šurlan Momirović has 202 scientific publications, 5 monographs, 2 textbooks, 20 scientific projects and number of citations at SCI list is 140. For her research use methods in classical and molecular breeding of cereals, comparative genomics of gene families and map-based cloning of resistance genes. She was Visiting Professor at the University of Missouri Columbia, Mo, USA and at Master Academic Study "Environmental Protection" Norwegian University of Life Sciences, Ås, Norway. Gordana Šurlan Momirović is Head of Department for Genetics and Plant Breeding the Faculty of Agriculture University of Belgrade, member of editorial board of Serbian Journal of Scientific Agricultural Research, member of The Genetics Society of Serbia, Vice-President of Fulbright Alumni Association of Serbia, member of Belgrade University Council, member of Accreditation

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