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Molecular characterization of bermudagrass germplasm using sequence-related amplified polymorphism markers

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Bermudagrass [*Cynodon dactylon* (L.) Pers.] germplasm has a broad resource of genetic diversity that can be used for turfgrass forage and conservation. Bermudagrass is widely distributed in world, but genetic information is lacking on DNA molecular variation in geographically disparate forms. Accordingly, this study was conducted to assess molecular genetic variation and genetic relatedness among thirty-five *C. dactylon* var. *dactylon* accessions and twenty-one public cultivars originating from 4 countries (China, Australia, USA and India). The objectives of this study were to use sequence-related amplified polymorphism (SRAP) markers in the evaluation of genetic diversity in a diverse collection of 56 bermudagrass germplasms. Thirty SRAP primer combinations were used. It is the first report of home and abroad bermudagrass germplasm resources relationship by using SRAP markers. Cluster analysis by the unweighted pair-group method with arithmetic averages (UPGMA) based on 268 (in total of 274) polymorphic bands indicated that there were six clusters (Figure 1). The coefficients of genetic distance among the genotypes ranged from 0.57 up to 0.97 and averaged 0.77. The genetic diversity estimate, H_e , average 0.27. Both Principal Coordinate Analysis (PCA) and UPGMA analysis indicated the similar results that the ecological varieties were clustered in different groups. The Australia cultivars, some USA cultivars, Xinjiang cultivars, and so on, were distinctly differentiated. This shows there is a wide genetic diversity among genotypes within *C. dactylon*. Ferriol et al. (2003) reported that the information obtained from SRAP markers was more concordant with the morphological variations and the evolutionary history of the morphotypes than that found with AFLP markers. The use of PCR-based technologies such as SRAP is an effective tool for estimating genetic diversity, identifying unique genotypes as new sources of alleles for enhancing turf characteristics, and for analyzing the evolutionary and historical development of cultivars at the genomic level in a bermudagrass breeding program.

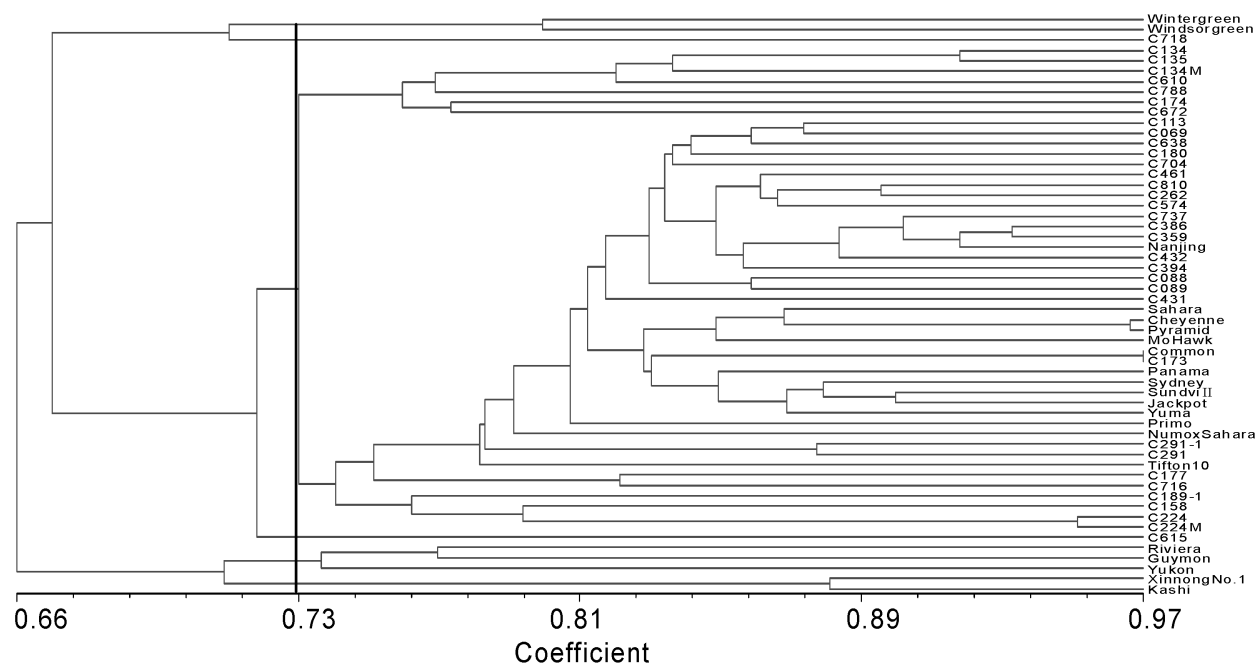


Figure 1 Dendrogram of 56 *Cynodon dactylon* (L.) Pers. produced by UPGMA clustering method based on the genetic similarity matrix derived from 268 SRAP markers.

Reference

Ferriol M, Pico B, Nuez F (2003). Genetic diversity of a germplasm collection of *Cucurbita pepo* using SRAP and AFLP markers. *Theor Appl Genet*, 107, 271-282.