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The 21st International Grassland Congress / 8th International Rangeland Congress took place in Hohhot, China from June 29 through July 5, 2008.

Proceedings edited by Organizing Committee of 2008 IGC/IRC Conference

Published by Guangdong People's Publishing House

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Molecular identification of 24 *Cynodon* cultivars using SRAP markers

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Key words : SRAP, *Cynodon* spp., cultivars, molecular identification, UPGMA

Sequence-related amplified polymorphism (SRAP) is a novel molecular marker technique designed to amplify open reading frames (ORFs). The SRAP analytic system was set up and applied to *Cynodon* germplasm identification in this study for the first time. Twenty-four *Cynodon* cultivars were screened by SRAP technique with 90 primer combinations. In the analysis, 30 primer combinations produced stable and reproducible amplification patterns in three repetitive experiments. Among the total 274 amplified fragments, 249 (91%) were polymorphic, with an average of 9 fragments for each primer combination, ranging in size from 100 to 500 bp. The 274 fragments were visually scored one by one and then used to develop a dendrogram with Unweighted Pair-Group Method Arithmetic Average (UPGMA), and the 24 *Cynodon* cultivars were divided into three major groups at the 0.59 similarity level, many of which were in agreement with known pedigrees. From the total 274 fragments, 13 amplified by one primer combinations, Me5-Em7, was able to discriminate between all the 24 bermudagrass cultivars (Figure 1). The DNA fingerprints were then converted into binary codes, with 1 and 0 representing presence and absence of the corresponding amplified fragment, respectively. In the DNA fingerprints, each of the 24 *Cynodon* cultivars has its unique binary code and can be easily distinguished from the others. This is the first report on the development of SRAP technique and its utilization in germplasm identification of *Cynodon* cultivars. The results demonstrated that SRAP is a simple, stable, polymorphic and reproducible molecular marker technique for differentiating bermudagrass genotypes and for determining genetic relationships among them.

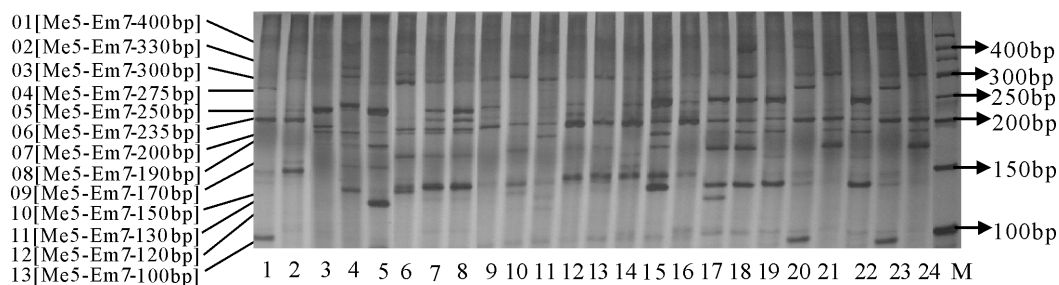


Figure 1 The 13 selected SRAP fragments used for constructing the DNA fingerprints of the 24 *Cynodon* cultivars. Numbers below the figure are the numbered samples of the 24 *Cynodon* cultivars; numbers on the left side of the figure are the sizes (bp) of corresponding fragments of the marker; numbers on the right side of the figure are the fragments that were selected and used for constructing the fingerprints of the 24 *Cynodon* cultivars.; M: DNA marker (50bp, Promega).