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## Genetic Diversity of Wild *Cynodon dactylon* Germplasm Detected by SRAP Markers

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**Presenter Information**

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## Genetic diversity of wild *Cynodon dactylon* germplasm detected by SRAP markers

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**Key words:** *Cynodon dactylon*, SRAP, genetic diversity, cluster analysis, group

**Introduction** Bermuda grass is one of the most important and widely utilized turfgrasses in south China, owing to its good capability of adaptation to hot or drought conditions. In this study, sequence-related, amplified polymorphism (SRAP) molecular markers were used to detect the genetic diversity of thirty-two wild accessions of *Cynodon dactylon* collected from Sichuan, Chongqing, Guizhou and Tibet, China.

**Materials and methods** Total DNA was extracted from approximately 0.5g of leaf tissue using a modified CTAB method. Fourteen primer pairs were selected for the SRAP analysis based on what could produce reproducible and clear bands. PCR amplification reactions were carried out in 20 $\mu$ l volume, containing 10 $\times$  PCR Buffer 2 $\mu$ L, MgCl<sub>2</sub> 2 $\mu$ L (25mm/L), dNTP 1.6 $\mu$ L (2.5mm/L), 1 $\mu$ L (10 $\mu$ M/ $\mu$ L) primers, 0.2 $\mu$ L (5U/ $\mu$ L) Taq DNA polymerase and 40 ng of template DNA. PCR amplification was performed as follows: initial 5 min at 94 $^{\circ}$ C; 5 cycles of 1 min at 94 $^{\circ}$ C, 1 min at 35 $^{\circ}$ C, 1 min at 72 $^{\circ}$ C; 35 cycles of 1 min at 94 $^{\circ}$ C, 1 min at 50 $^{\circ}$ C, 1 min at 72 $^{\circ}$ C; a final 10 min extension at 72 $^{\circ}$ C. Only bands that could be unambiguously scored across all the sampled populations were used. SRAP amplified fragments, with the same mobility according to the molecular weight (bp), were scored manually for band presence (1) or absence (0). The resulting presence/absence data matrix was analyzed using POPGENE and NTSYS-pc, version 2.10.

**Results** The following results were obtained: (1) Fourteen primer pairs produced 132 polymorphic bands, the percentage of polymorphic bands in average was 79.8%. The Nei's genetic similarity coefficient of the tested accessions ranged from 0.591 to 0.957. These results suggested that there was rich genetic diversity among the wild resources of *C. dactylon* tested. (2) Thirty-two wild accessions were clustered into four groups. Moreover, the accessions from the same origin frequently clustered into one group. The findings implied that a correlation among the wild resources, geographical and ecological environment. (3) Genetic differentiation between and within six eco-geographical groups of *C. dactylon* was estimated by Shannon's diversity index, which showed that 65.56% genetic variance existed within group, and 34.44% genetic variance was among groups.

**Conclusions** The average percentage of polymorphic bands in the study was 79.8%, higher than the study of genetic analyses of Chinese *Cynodon* accessions by AFLP markers (61.1%, Wu *et al.*, 2006). It can be seen that SRAP could be a simple and effective method to the study of genetic diversity of wild *C. dactylon* germplasm. Fully sampling the genetic diversity of *Cynodon* in China will require more comprehensive collection throughout its distribution.

### Reference

Wu YQ, Taliaferro CM, Bai GH, Martin DL, Anderson JA, Anderson MP, Edwards RM. Genetic analyses of Chinese *Cynodon* accessions by flow cytometry and AFLP markers. *Crop Sci*, 2006, 46: 917-926.

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