



## Analysis of genetic diversity among wild bermudagrass germplasm from southwest China using SSR markers

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**ABSTRACT.** Fifty-five wild accessions of bermudagrass (*Cynodon dactylon*) were collected from southwest China (Sichuan, Chongqing, Yunnan, Guizhou, and Tibet), and their genetic diversity was analyzed using simple sequence repeat markers. A total of 267 polymorphic bands were detected with 18 primer combinations. The genetic similarity among the accessions ranged from 0.688 to 0.894 with an average of 0.797. All 55 wild accessions were clustered into 7 eco-geographic groups. Our data showed that the dendrogram was almost in accordance with geographic distribution, and accessions from the same collection sites tended to be clustered into the same group. A genetic differentiation analysis revealed that the percentage of genetic variance was 70.07 and 29.93% within and among groups, respectively. Finally, we discuss the implications of these results for *C. dactylon* in southwest China.

**Key words:** *Cynodon dactylon*; SSR; Genetic diversity; Cluster analysis