



Genetic variation and comparison of orchardgrass (*Dactylis glomerata* L.) cultivars and wild accessions as revealed by SSR markers

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ABSTRACT. Orchardgrass is a highly variable, perennial forage grass that is cultivated throughout temperate and subtropical regions of the world. Despite its economic importance, the genetic relationship and distance among and within cultivars are largely unknown but would be of great interest for breeding programs. We investigated the molecular variation and structure of cultivar populations, compared the level of genetic diversity among cultivars (Baoxing, Anba, Bote, and Kaimo), subspecies (*Dactylis glomerata* ssp *Woronowii*) and advanced breeding line (YA02-116) to determine whether there is still sufficient genetic diversity within presently used cultivars for future breeding progress in China. Twenty individuals were analyzed from each of six accessions using SSR markers; 114 easily scored bands were generated from 15 SSR primer pairs, with an average of 7.6 alleles per locus. The polymorphic rate was 100% among the 120 individuals, reflecting a high degree of genetic diversity. Among the six accessions, the highest genetic diversity was observed in Kaimo ($H = 0.2518$; $I = 0.3916$; $P = 87.3\%$) and 02-116 had a lower level of genetic diversity ($H = 0.1806$; $I = 0.2788$; $P = 58.73\%$) compared with other cultivars tested. An analysis

of molecular variance revealed a much larger genetic variation within accessions (65%) than between them (35%). This observation suggests that these cultivars have potential for providing rich genetic resource for further breeding program. Furthermore, the study also indicated that Chinese orchardgrass breeding has involved strong selection for adaptation to forage production, which may result in restricted genetic base of orchardgrass cultivar.

Key words: *Dactylis glomerata* L.; Cultivar; Simple sequence repeats; AMOVA