



Genetic diversity of *Saccharum spontaneum* from geographical regions of China assessed by simple sequence repeats

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ABSTRACT. *Saccharum spontaneum* is the most variable wild relative of sugarcane with potential for use in sugarcane improvement programs. In order to help preserve and exploit this species, 152 accessions from eight major geographical regions in China, including Hainan, Guangdong, Guangxi, Yunnan, Sichuan, Guizhou, Fujian, and Jiangxi provinces, were investigated by analyzing 20 simple sequence repeats (SSRs), including 11 genomic SSRs (gSSRs) and nine SSRs developed from expressed sequence tags (EST-SSRs). A total of 454 alleles were generated by the 20 SSRs, with 295 and 159 alleles detected by gSSRs and EST-SSRs respectively. The Mantel test showed significant correlation between genetic matrixes among the studied accessions revealed by gSSRs versus EST-SSRs, although the average polymorphism of EST-SSRs (17.7) was much lower than that of gSSRs (26.8). Among the eight provinces, collections from Guizhou were the most diverse and those from Guangdong were the most distinct. Clustering analysis and principal component analysis accordantly classified the accessions into four groups, which were “Southwest

group”, “Hainan group”, “Guangdong group”, and “Guangxi group”, based on the geographical origin of the major accessions in each group, demonstrating that geographical factors play an important role in the pattern of genetic structure of Chinese *S. spontaneum*. As two (Guizhou and Yunnan) of the three provinces with highest genetic diversity are located in southwest China, we concluded that southwest China is the region with the highest genetic diversity of *S. spontaneum*.

Key words: *Saccharum spontaneum* L.; China; Genetic diversity; SSR; EST-SSR