



Assessment of genetic diversity of cucumber cultivars in China based on simple sequence repeats and fruit traits

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ABSTRACT. The cucumber (*Cucumis sativus* L.) is an important crop grown worldwide. In this study, the genetic diversity of 42 cucumber cultivars in China was analyzed using 51 pairs of simple sequence repeat (SSR) primers. These primers identified 129 polymorphic loci, 95.6% of which were polymorphic. The mean effective number of alleles, mean Nei's gene diversity, and mean Shannon's information index were 0.36, 0.16, and 0.21, respectively. A cluster analysis demonstrated that the 42 cultivars could be divided into three groups, a result that was largely consistent with those of a principal component analysis (PCA). The PCA indicated that the three groups displayed significant variation in fruit traits. The cultivars of group 1 tended to have longer fruits (>30 cm), longer fruit ends (>4 cm), larger fruit diameters (>5 cm), a sharp strigose fruit spine, and the same fruit end shape. The basal color of the fruit in group 2 was dark green. Group 3 cultivars have no wax or mottling on the fruit surface. Our study

demonstrates the value of our SSR primers for assessing genetic diversity in cucumber.

Key words: Cucumber; *Cucumis sativus* L.; Simple sequence repeat; Fruit traits; Genetic diversity