



## Assessing genetic diversity of cotton cultivars using genomic and newly developed expressed sequence tag-derived microsatellite markers

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**ABSTRACT.** Estimations of genetic diversity and of relationships between varieties are crucial for cotton breeding. The genetic diversity of 59 core cotton cultivars, most of which were collected from China's main cotton-growing areas, was analyzed based on genomic and newly developed expressed sequence tag-derived microsatellite markers, using total DNA extracted from fresh leaf tissue. Three hundred and two fragments were detected, of which 255 were polymorphic. The number of amplification products generated by each primer varied from 2 to 14, with a mean of 5.08 bands/primer. The polymorphism information content was 0.50 to 0.90, with a mean of 0.80. The genetic similarity coefficients were calculated and dendrograms were constructed by the unweighted pair group with arithmetic mean method; the resulting distance matrix gave a dendrogram with four main clusters. Some cultivars with similar pedigrees could be clustered. For example, Zhong206 and Shanmian4, both derived from Deltapine15, were clustered. The genetic similarity coefficient of the 59 core cultivars ranged from 0.53 to 0.99, with a mean of 0.72, indicating that there was a relatively high level of genetic variation.

**Key words:** *Gossypium hirsutum*; EST-SSRs; Genomic-SSRs; Genetic diversity