

Analysis of Genetic Polymorphic SSR Markers in Germplasm Resources of the Natural Colored Cotton

WANG Ju-qin¹, LI Fu-zhen¹, QIU Xin-mian¹, BAO Li-sheng¹, LU Yan-ting²

(1. *Central of Crop Molecular Breeding, Institute of Crop and Nucleonic Technology Utilization, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China*; 2. *Technical Popularization Station of Economic Specialty, Jinhua, Zhejiang 321017, China*)

Short sequence repeats (microsatellite, SSR) and expressed sequence tags-SSR (EST-SSR) markers were employed to analyze the genetic diversity of natural colored cotton varieties. About 490 pairs of SSR markers spanning the 26 chromosomes were selected from the cotton microsatellite database, they were composed of the NAU, BNL, MUSS, and CIR markers, and there was one marker every 5 cM on average. Eighteen natural brown and 4 green fiber cotton varieties were used to analyze the genetic diversity and evolution, including 5 *Gossypium arboreum* (A genome), 12 *G. hirsutum* (AD genome) and 5 *G. barbadense* (AD genome) subspecies. The genetic polymorphism analysis showed that 201 pairs of SSR primer were polymorphic among the 22 varieties tested, and the polymorphism ratio of primers was 45.2%. In total, 243 polymorphic bands were obtained, and the average polymorphic loci were 1.2 per SSR marker. These results demonstrated that EST-SSR and SSR markers had high polymorphism in the tested natural colored cotton varieties. Based on cluster and similarity analysis, the genetic distance was ranged from 0.11 to 0.42 among the tested 22 varieties. Twenty-two varieties were clustered into 3 main groups. The phylogenetic relationships of the natural brown and green fiber cottons are closer in the same species than the subspecies. But the polymorphic ratio was 5% higher in the green than in the 8 brown fiber cotton varieties in *G. hirsutum*. Furthermore, there was a remarkable difference of the genetic diversity among the Longlümian 3, Yuancaimian 3, and Zhecaimian 3, the natural green fiber cotton varieties. These differences probably came from the different original germplasms in natural colored cotton breeding parents. These fundamental polymorphic SSR databases at the genome level help us to further understand the genetic evolution relationships and to use the right breeding programs to improve the natural colored fiber quality.

Key words: natural colored cotton; germplasm; genetic diversity; genetic evolution; simple sequence repeat (microsatellite, SSR)