



亚洲棉种质资源的SSR遗传多样性分析

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Study on Genetic Diversity of *Gossypium arboreum* L. Germplasm Resources with SSR Markers

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摘要

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摘要 对我国棉花中期库保存的200份不同地理来源的亚洲棉代表性样本进行了SSR遗传多样性分析, 结果表明: 亚洲棉分子水平的遗传多样性较高。83个多态性位点共检测到368个等位基因变异, 其中多态性的等位基因数为329个, 平均每个SSR位点3.964个。位点多态性信息量(PIC)变幅为0.010~0.882, 平均0.578, PIC值大于0.7的标记有33个(占39.8%)。基因多样性(H')变幅为0.031~2.163, 有效等位基因数(Ne)变幅为1.010~8.496。华南棉区基因遗传多样性最高, 其次为长江流域棉区、黄河流域棉区, 从理论上支持被广泛接受的亚洲棉在我国的传播路线是由南到北, 华南棉区是中棉种系的遗传多样性富集中心。利用软件NYSTS-pc2.20, 采用类平均法(UPGMA)进行聚类分析, 种质间SSR相似系数变幅为0.58~0.997, 平均0.745, 在阈值0.73处200份亚洲棉聚为8个类群, 贵池小子棉白子单独聚为一群, 与其他种质遗传距离较远。遗传距离和地理距离没有必然联系, 但种质间亲缘关系处于极端远或极端近时, 则地理距离一般也趋于较远或较近。

关键词: 亚洲棉 遗传多样性 SSR标记

Abstract: In this study, we used SSR markers to analyze the genetic diversity of 200 accessions of geographically varied *Gossypium arboreum* cultivars in the National Medium-term Gene Bank of Cotton in China. Abundant genetic diversity was uncovered. Using 83 SSR primers, we detected 368 alleles, 329 of which were polymorphic. The mean number of polymorphic alleles per locus was 3.964. PIC values ranged from 0.010 to 0.882(average = 0.578); 33 loci (39.8% of the 83 SSRs) were identified as possessing high information content($PIC > 0.7$). The Shannon-Weaver diversity index(H') ranged from 0.031 to 2.163, and the effective number of alleles(Ne) varied from 1.010 to 8.496. With respect to molecular genetic diversity, the three main cotton-growing areas of China were ordered from highest to lowest as follows: South China, the Yangtze River region, and the Yellow River region. This ranking is consistent with the widely accepted theory that *G. arboreum* cultivation in China spread from south to north, and the fact that South China is the most germplasm-rich region for the *G. arboreum* landrace 'Sinense'. A UPGMA cluster analysis was performed on the genetic distance matrix using NYSTS-pc2.20 software. Similarity coefficients among the 200 *G. arboreum* accessions ranged from 0.58 to 0.997(average = 0.745), with the accessions clustering into eight groups at a genetic distance of 0.73. The cultivar 'Guichi Xiaozimianbaizi' was genetically distant from the other accessions, showing specific genetic variation. No significant correlation was observed between genetic and geographic distance, although genetic distance was generally consistent with degree of geographical separation.

Keywords: *Gossypium arboreum* L. genetic diversity SSR markers

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