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北疆早熟陆地棉品种的遗传多样性分析

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Analysis of Genetic Diversity of Early Maturing Upland Cotton Varieties in Northern Xinjiang

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摘要 从SSR水平分析北疆早熟陆地棉品种的遗传多样性，为该棉区种质资源的创新和新品种选育提供依据。利用38个SSR引物对北疆33个早熟陆地棉品种进行遗传多样性分析，通过NTSYS-pc2.11软件计算品种之间的相似系数，并进行聚类和系谱追溯。38个引物在33个品种中共扩增出126个条带，平均每个引物为3.32个。共检测出160个等位基因，等位基因变异的多态信息含量（PIC）在0.1690～0.8503。33个品种间的遗传相似系数在0.4120～0.9560，遗传相似系数在0.57～0.61可将33个棉花品种分为2类。其中，第Ⅰ类包含17个品种，第Ⅱ类包含16个品种。在第Ⅰ类中以贝尔斯诺血统为主，第Ⅱ类中以中棉所17和新陆早16号血统为主。SSR标记分析与系谱分析的结果对北疆棉花品种间的遗传多样性分析结论基本一致。本研究表明北疆棉花品种的遗传基础狭窄。

关键词： 棉花 北疆 SSR标记 遗传多样性 聚类分析

Abstract： We analyzed genetic diversity of cotton in order to provide information for evaluation of germplasm resources and breeding in our local region. Thirty-eight pairs of SSR primers were used to analyze the genetic diversity of early maturing upland cotton varieties in northern Xinjiang. The genetic similarity(GS) coefficient, the category, and information on the genealogy of accessions were calculated using NTSYS-pc 2.11 software. We detected 126 bands among 33 varieties. The primers had 160 alleles, with a mean of 3.32; and the polymorphic information content (PIC) was around 0.1690 to 0.8503. The genetic similarity coefficient of 48 accessions ranged from 0.4120 to 0.9560. The germplasm resources of GS ranged from 0.57 to 0.61 and could be categorized into two major groups. The consanguinity of the first group including 17 varieties was Belshinuo; for the other group including 16 varieties, the main consanguinities were CCRI 17 and Xinluzao 16. The results of SSR markers were in accordance with the analysis of genetic diversity, indicating that the cotton varieties we tested possess little genetic diversity.

Keywords： cotton northern Xinjiang SSR genetic diversity cluster analysis

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