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彩色棉品系的SSR分子变异研究

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Molecular Variation of the Colored Cotton Lines Based on SSR Markers

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摘要 采用SSR分子标记技术对来自12个组合的62份稳定彩色棉新品系进行分子变异分析。结果表明,从242对SSR中筛选出的29对多态性引物在供试材料中共扩增出198个标记。其中,多态性标记115个,占总标记数的58.1%,这些引物能较好地揭示彩色棉的变异位点。MGHES-6引物扩增的多态性标记最多,其次为BNL2960、CM43和MGHES-66。29对SSR引物的PIC值变化在0.493~0.938之间,平均0.790,说明彩色棉SSR等位基因丰富度较高。基于SSR数据的聚类分析,可将62份新品系分为两大类,一类是由彩色棉种质资源经系统选育获得的材料,另一类是通过杂交选育获得的材料。

关键词: 彩色棉 SSR 分子变异

Abstract: In the study, SSR molecular marker was used to assess the molecular variation of 62 new lines of colored cottons from 12 combinations. The results showed that 29 of 242 pairs of SSR primers could generate polymorphic markers among the tested colored cotton lines. The total number of markers was 195, and the polymorphic markers were 115, accounted for 58.1%. MGHES-6 primer had the most polymorphic markers, followed by BNL2960, CM43 and MGHES-66. These primers could detect the variable SSR sites of the tested cottons very well. The PIC values for SSR primers varied from 0.493~0.938, averaged 0.790. The higher PIC values showed the abundant SSR alleles from the colored cottons. According to the SSR markers, 62 colored cottons were divided into two groups based on UPGMA method. One group included all the lines bred by pedigree selection, the other included the lines bred from hybridization method. The above results laid a foundation for breeding and germplasm utilization of colored cotton.

Keywords: colored cotton SSR molecular variation

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