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植物遗传学

我国陆地棉基础种质遗传多样性的SSR分子标记分析

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摘要

利用398对BNL、JESPR 、TMB等SSR引物，对不同亲本来源、不同选育时期、不同种植生态区的43份陆地棉基础种质进行了遗传多样性的SSR分子标记分析。扩增产物用8%的非变性聚丙烯酰胺凝胶检测,银染观察并照相。遗传多样性带型分析按位点多态信息量（PIC），Shannon-weaver多样性指数（H’）等方法，利用NTSYSpc2.1软件计算品种间的遗传相似系数（Jaccard系数），并用类平均法（UPGMA）进行聚类。结果表明所选择多态性引物分布在棉花基因组的第3、4、5、8、9、10、16、18、20、23号等染色体上，36对多态性引物在基础种质中扩增等位基因130个，其中多态性等位基因占80%,每个引物扩增等位基因2～8个，平均3.6个，PIC为0.278～0.865，平均0.62，基因型多样性（H’）为0.451～2.039，平均1.102，基础种质间SSR遗传相似系数平均为0.610，变幅为0.409～0.865，这说明所选基础种质基因组水平的多样性较丰富，变化范围大、代表性强。按品种不同选育时期来讲，第一、二、三期基础种质的SSR分子标记平均遗传相似系数分别是0.587、0.630、0.630，说明现代基础种质比早期基础种质在基因组水平的差异呈下降的趋势，可能是由于育种者偏重于使用优质高产性状的亲本品种，致使我国棉花的育种基础逐渐变窄。不同棉区基础种质SSR标记性状差异大，北部特早熟棉区基础种质间的SSR标记的多样性大于黄河、长江棉区，主要原因是长江、黄河棉区的育种过分强调高产、优质品种选育，品种间的差异变小；基础种质中的国内品种SSR相似系数（0.624）比引进品种（0.585）高，说明国内品种在遗传多样性上目前还没有超越国外品种。总之，我国棉花现代基础种质比早期基础种质的遗传多样性呈下降的趋势，黄河、长江主产棉区基础种质的遗传多样性还没有超过国外基础种质，品种间的遗传背景较为狭窄，还必须采用多种途径丰富我国棉花种质资源的遗传多样性。

关键词

基础种质；SSR；遗传多样性

分类号

Genetic Diversity of Source Germplasm of Upland Cotton in China as Determined by SSR Marker Analysis

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Abstract

<P>The genetic diversity of 43 sources of Upland cotton germplasm with different parental origins, breeding periods, and ecological growing areas in China were studied on the basis of simple sequence repeat (SSR) markers. A total of 130 gene alleles with 80% polymorphism were detected from 36 SSR primers. The number of alleles per primer ranged from two to eight with an average of 3.6. The polymorphism information content (PIC) range was 0.278-0.865, with an average of 0.62. The average genotype diversity index (H') was 1.102, the highest was 2.039 and the lowest was 0.451. The average coefficient of the genetic similarity of SSR markers among source germplasm was 0.610, ranging from 0.409 to 0.865. These indicated that the genetic diversity at the genomic level of the selected source germplasm was rich, and was representative of the diversity of the germplasms, in general. The diversity at the genome level of the base germplasm from the second and third breeding periods was decreased compared to that of the first period, indicating that the cotton genetic background in China became narrow gradually.

The diversity of SSR markers among the base germplasm from early maturity cotton growing areas in the north was higher than those from the Huanghe and Yangtze growing areas. The molecular marker genetic similarity index of the domestic varieties was higher than that in the introduced varieties, which indicates that the genetic diversity in domestic cultivars was lower than that in the introduced varieties. This study gives an overview of the genetic diversity of the cotton germplasm base in China, and provides a guide for breeders to develop new cultivars efficiently.</P>

Key words

source germplasm；SSR；genetic diversity

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