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植物遗传学

利用重组自交系和SSR标记进行陆地棉株型QTL的鉴定和定位

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摘要

通过中棉所12与8891的杂交及多代自交，获得由180个家系构成的重组自交系F8、F9群体。重组自交系群体，两亲本及F1于2002、2003两年种植；对株型性状进行了研究。两年共调查了10个株型形状，利用该重组自交系群体，采用SSR为主体的分子标记构建了遗传连锁图，并对株型性状进行了单位点和双位点水平的QTL定位。结果表明，QTL加性效应和上位性互作效应作为棉花重组自交系株型性状的遗传基础起着重要作用， 中棉所12与8891间多态性位点偏少，而表型差异较大且其杂交种潜杂棉二号有很强的杂种优势，QTL互作可部分解释这一现象。结合对产量品质性状的研究结果，认为上位性可能是潜杂棉二号杂种优势的重要遗传基础。

关键词

株型，加性效应，上位性效应，数量性状位点

分类号

QTL Mapping for Plant Architecture Traits in Upland Cotton Using RILs and SSR Markers

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Abstract

<P> Xiangzamian 2 (XZM2) is the most widely cultivated cotton hybrid in China. By crossing two parents Zhongmiansuo12 and 8891 and upon subsequent selfings, we got F8 and F9 populations having 180 recombinant inbred lines. Ten plant architecture traits were investigated in two years with this population. A genetic map was constructed mainly with SSR markers. Quantitative trait loci (QTL) conditioning plant architecture traits were determined at the single-locus and double-locus levels. The results showed that epistastic effects as well as additive effects of QTL played an important role as the genetic basis of cotton plant architecture. The QTL detected in our research might provide new information on improving plant architecture traits. The polymorphism of molecular markers between ZM512 and 8891 were quite limited, while significant differences between their phenotypes were found and the hybrid XZM2 expressed high heterosis in yaild. All these could be partly explained by the effect of epistatic QTL. </P>

Key words

plant architecture; additive effect; epistatic effect; QTL

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