

ET-ISJ标记的开发及陆地棉遗传图谱构建

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Development of Exon-Targeted Intron-Exon Splicing Conjunction (ET-ISJ) Marker and Establishment of Upland Cotton Genetic Map

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摘要

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摘要 根据植物结构基因外显子拼接位点的保守序列, 设计扩增外显子的ET-ISJ (exon targeted intron-exon splice junction) 标记引物。利用1 280对ET-ISJ引物组合, 在陆地棉品种渝棉1号和T586中, 筛选获得69对多态性引物组合, 占引物组合的5.4%。用多态性ET-ISJ引物组合检测(渝棉1号×T586) $F_{2:7}$ 重组近交系群体, 得到70个位点。以70个ET-ISJ标记位点与523个SSR、59个IT-ISJ、29个SRAP和8个形态标记进行连锁分析, 构建的遗传连锁图谱包括59个连锁群和673个位点(68个ET-ISJ、510个SSR、58个IT-ISJ、29个SRAP和8个形态标记)。连锁图覆盖3 216.7 cM, 占棉花基因组的72.3%, 标记间平均长度为4.8 cM。68个ET-ISJ标记分布于20条染色体。研究表明ET-ISJ标记多态性较高、稳定性好, 可有效用于棉花与其他植物遗传连锁图谱构建。

关键词: 陆地棉 外显子定靶内含子-外显子剪接位点标记 遗传图谱

Abstract: Cotton is the leading fiber crop in the world, and upland cotton contributes over 95% of cotton production. The genetic map of upland cotton is far from saturated, so it is necessary to develop new markers for it. ET-ISJ (exon targeted intron-exon splice conjunctions) maker primers were designed according to the conserved intron-exon splicing junction sequences. A total of 1 280 ET-ISJ primer combinations were used to screen polymorphism between upland cotton cultivar Yumian 1 and T586, and 69 of which showed polymorphism, accounting for 5.4% of total primer combinations. The 69 polymorphic ET-ISJ primer combinations were used to detect (Yumian 1 × T586) $F_{2:7}$ recombinant inbred line population, and 70 ET-ISJ loci were obtained. Linkage analysis was conducted on 70 ET-ISJ loci, 523 SSR, 59 IT-ISJ, 29 SRAP and 8 morphological loci, and a linkage map including 59 linkage groups and 673 loci (68 ET-ISJ, 510 SSR, 58 IT-ISJ, 29 SRAP and 8 morphological loci) was established. The linkage map covered 3 216.7 cM, accounting for 72.3% of cotton genome, with an average interval of 4.8 cM between two markers. Sixty-eight ET-ISJ loci were located on 20 chromosomes. The present study demonstrated that ET-ISJ markers are stable, relatively-high polymorphic, and able to be effectively applied in genetic map construction of cotton and other plant's.

Keywords: Upland cotton (*Gossypium hirsutum* L.) ET-ISJ Genetic map

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