

论文

花生栽培种SSR遗传图谱的构建

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摘要:

花生栽培种品种间分子多态性相对缺乏,至今未构建出较完整的分子遗传图谱。本研究以粤油13和阜95-5为亲本,通过杂交构建包含184个F₆重组自交系的遗传作图群体。采用652对genomic-SSR引物和392对EST-SSR引物对亲本进行多态性检测,从中筛选出121对多态性引物,在亲本中共检测到123个多态性位点。利用作图群体对多态性SSR位点进行遗传连锁分析,获得包含108个SSR标记(102个genomic-SSR标记和6个EST-SSR标记),涉及20个连锁群,总长568 cM,平均图距为6.45 cM的花生栽培种遗传图谱。与前人构建的花生野生种(*A. duranensis* × *A. stenosperma*, AA genome)SSR遗传图谱比较,初步确定本研究构建的遗传图谱中有11个连锁群与野生种遗传图谱的6个连锁群存在同源关系。

关键词: 花生;SSR;遗传图谱

Construction of Genetic Linkage Map in Peanut (*Arachis hypogaea* L.) Cultivars

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Abstract:

Molecular genetic map is a fundamental organizational tool for genomic research. However, a comprehensive genetic linkage map for peanut cultivars has not yet been developed due to extremely low levels of DNA polymorphisms in cultivated peanut. In this study, 184 recombinant inbred lines (RIL), derived from a cross between two Spanish type peanut cultivars (Yueyou 13 × Fu95-5), were used as mapping population. A total of 652 pairs of genomic-SSR primers and 392 pairs of EST-SSR primers were used to detect the polymorphisms between the parental cultivars. Of them, 121 SSR primer pairs amplified 123 segregating loci and were selected to analyze the RIL population. A genetic linkage map consisting of 108 SSR loci (102 genomic-SSR and 6 EST-SSR) in 20 linkage groups and covers 568 cM with an average distance of 6.45 cM of intermarker was constructed. By comparing the SSR genetic map of *Arachis* (*A. duranensis* × *A. stenosperma*) with AA genome, 11 linkage groups in the linkage map constructed in this study were confirmed to have homology with 6 linkage groups of wild peanut species.

Keywords: Peanut (*Arachis hypogaea* L.); SSR; Genetic linkage map

收稿日期 2008-05-16 修回日期 2008-09-11 网络版发布日期 2009-01-15

DOI: 10.3724/SP.J.1006.2009.00395

基金项目:

本研究由国家高技术研究发展计划(863计划)项目(2006AA10Z156),广东省自然科学基金项目(06025389,07117967)资助

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