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农学—研究报告

不同遗传背景下陆地棉衣分和子指性状QTL定位

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摘要:

为陆地棉产量性状有关的分子标记辅助育种奠定理论基础，以高品质中长绒棉品种‘新陆早24号’为父本，转基因抗虫棉常规品种‘鲁棉研28号’和高产、优质棉花新品种‘冀棉516’为母本，构建F2和F2:3分离群体；利用7638对SSR引物对‘鲁棉研28号’和‘新陆早24号’进行多态性进行筛选，共获得225对多态性引物，对238个F2单株DNA扩增获得238个多态性标记位点，其中185个构建了包括44个连锁群，总长为1509.38 cM的遗传连锁图谱，标记间的平均距离为8.16 cM，覆盖棉花总基因组的33.91%。根据已有图谱的定位结果，40个连锁群与染色体建立联系。利用复合区间作图法定位‘鲁棉研28号’与‘新陆早24号’分离群体F2单株和F2:3家系的衣分和子指性状QTL，其中得到3个衣分和5个子指的QTL；根据定位结果，选择了14对SSR引物，分析‘冀棉516’与‘新陆早24号’的多态性，其中6个标记构建了两个连锁群。1个衣分和1个子指的QTL在两个群体中均检测到，这些共同QTLs为分子标记辅助育种奠定了基础。

关键词: QTL

QTL Mapping for Lint Percentage and Seed Index in Upland Cotton (Gossypium hirsutum L.) of Different Genetic Backgrounds

Abstract:

In order to establish theoretical basis on the molecular marker assisted selection for upland cotton, two F2 populations and their corresponding F2:3 family lines were constructed, which included common male parent with high fiber quality, ‘Xinluzao24’, one of female parent with commercial transgenic variety, ‘Lumian28’, and the other with high-yield traits, ‘Jimian516’. 7638 pairs of SSR primer were used to screen the polymorphism between ‘Lumianyan28’ and ‘Xinluzao24’, finally 225 pairs of polymorphic primer were obtained for genotyping its F2 population, which produced 238 polymorphic loci. A genetic linkage map with 185 loci was constructed, which comprised of 44 linkage groups covering 1509.38 cM with an average distance of 8.16 cM between the two neighbor markers, and approximately 33.91% of the cotton genome. 40 linkage groups were assigned to the corresponding chromosome. Three QTLs for lint percentage and five for seed index were identified with Composite Interval Mapping (CIM) method in the population related to ‘Lumianyan28’ and ‘Xinluzao24’. According to the QTL mapping results, 14 pairs of SSR primer were selected to screen the polymorphism between ‘Jimian516’ and ‘Xinluzao24’ and its F2 population, so two linkage groups with six loci were constructed. One QTL for lint percentage and one for seed index were detected in the two genetic populations. These stable QTLs might be useful in the molecular marker assisted selection (MAS) breeding programs.

Keywords: QTL

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