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黄瓜果实相关性状QTL定位分析

苗晗, 顾兴芳, 张圣平, 张忠华, 黄三文, 王焯, 程周超, 张若纬, 穆生奇, 李曼, 张振贤, 方智远

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Mapping QTLs for Fruit-Associated Traits in Cucumis sativus L.

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- 摘要
- 参考文献
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摘要 【目的】果实性状对黄瓜的商品性及产量具有重要影响, 对黄瓜果实性状进行QTL定位分析将有助于了解其遗传机制, 为黄瓜果实性状改良以及高产、稳产育种提供有益参考和帮助, 同时也可对基因的精细定位及克隆奠定基础。【方法】利用华北保护地类型黄瓜材料9930和欧洲温室类型黄瓜材料9110Gt为亲本构建的遗传图谱, 结合不同年份、不同季节4次表型鉴定数据, 采用MapQTL4.0软件对12个黄瓜果实相关性状进行多座位QTL模型(MQM)检测。【结果】检测到与8个商品瓜性状相关的QTLs 18个: 瓜长Fl (3个)、把长Fsl (1个)、瓜粗Fd (1个)、瓜长/把长Lsr (5个)、瓜长/瓜粗Ldr (1个)、刺色Fsc (4个)、刺密度Fsd (1个)、果瘤大小Fws (2个); 与4个种瓜性状(种瓜长Sfl、种瓜粗Sfd、种瓜重Sfw、种瓜果皮颜色Sfc)相关的QTLs 14个。其中表型贡献率≥10.0%的主效QTL有27个, 占QTL总数的84.4%, 这些QTL大都分布在Chr.5和Chr.6上。各QTLs的LOD值在3.53—42.21, 可解释8.4%—73.1%的表型变异。【结论】本研究检测到与12个黄瓜果实性状相关的QTL共32个, 其中刺色和果瘤大小2个性状在2006—2009年春季两季均检测到主效QTL位点, 并获得紧密连锁的特异标记(SSR02697、SSR19256、SSR15818、SSR06003、SSR00116、SSR05321、SSR00004、SSR02309), 可用于基因精细定位研究。

关键词: 黄瓜(*Cucumis sativus* L.) 果实性状 数量性状座位QTL 重组自交系RIL 微卫星标记

Abstract: 【Objective】As one of the important fruit vegetables, cucumber (*Cucumis sativus* L.) owns the characters of fructification which to be major focused in the study of breeding. Generally, the characters of fructification can be classified into two categories: related characters of production and fruit quality. These two major characters have a significant influence on the production and commercial production of cucumber. QTL mapping and analysis were conducted for fructification characters of cucumber in this study. While these results will be beneficial for understanding the genetic mechanism of fructification characters, they also can provide helpful information for molecular marker assisted selection of cucumber breeding for high yield, gene fine mapping and gene cloning. 【Method】A SSR linkage map of cucumber was constructed using 148 F9 recombinant inbred lines (RILs) which originated from a narrow-cross between 9110Gt and 9930 in an experiment. Phenotypic data were investigated four times in various seasons. In this study, the multiple QTL model (MQM) method of software package MapQTL version 4.0 was used to map and analyze QTLs. 【Result】Eighteen QTLs were detected for 8 commercial fruit characters: 3 for fruit lengths(Fl), 1 for fruit stalk lengths(Fsl), 1 for fruit diameter(Fd), 1 for fruit length / diameter ratio(Ldr), 5 for fruit length / stalk ratio(Lsr), 4 for fruit spine color (Fsc), 1 for fruit spine density (Fsd), 2 for fruit warts size(Fws), 14 QTLs were detected for 4 traits of mature fruit for seed harvest (length, diameter, weight and color). These QTLs were practically mapped on chromosome 5 and 6, respectively. Twenty-four QTLs explained phenotypic variation more than 10%. Their LOD values varied between 3.53 and 42.21, which explained 8.4%-73.1% of the phenotypic variation.

【Conclusion】A total of 32 QTLs were detected for 14 character of fructification. Fsc and Fws were found to be expressed consistently under four cropping seasons in a greenhouse cultivation environment. The tight linkage markers (SSR02697, SSR19256, SSR15818, SSR06003, SSR00116, SSR05321, SSR00004, SSR02309) can be used in gene fine mapping in cucumber.

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Key words: cucumber(*Cucumis sativus* L.) fruit-associated traits quantitative trait locus (QTL) recombinant inbred lines (RILs) SSR marker

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