

大豆叶片性状QTL的定位及Meta分析

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Mapping and Meta-Analysis of QTLs for Leaf Traits in Soybean

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摘要

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摘要 利用Charleston×东农594重组自交系构建SSR遗传图谱, 采用WinQTLCartographer Ver. 2.5软件的CIM和MIM分析方法对2006—2010年(F_{2:14}~F_{2:18})连续5年的大豆叶长、叶宽以及叶柄长数据进行QTL定位, 检测到8个与叶长有关的QTL, 位于染色体Gm01、02、05、11和18上; 9个与叶宽有关的QTL, 位于染色体Gm01、03、05、06、11、12和16上; 8个与有关叶柄长的QTL, 位于染色体Gm01、03、05、06、11、17和18上。2年以上均检测到的叶长QTL为*qLL5a*、*qLL5b*、*qLL1a*和*qLL18*; 叶宽QTL为*qLW5a*、*qLW11a*、*qLW11b*和*qLW12*; 叶柄长QTL为*qLSL11b*。另外, 利用BioMercator2.1的映射功能将国内外常用的大豆图谱上的叶长、叶宽QTL通过公共标记映射整合到大豆公共遗传连锁图谱Soymap2上, 将搜集到的35个叶长QTL、37个叶宽QTL和本研究得到的QTL整合分析, 最终得到5个大豆叶长的“通用”QTL, 位于Gm09、18和19, 其置信区间最小可达5.66 cM; 4个大豆叶宽的“通用”QTL, 位于Gm07、Gm18和Gm19, 其置信区间最小可达5.67 cM, 为今后对大豆叶片性状QTL精细定位, 提供了有利科学信息。

关键词: 大豆 叶片性状 QTL定位 整合分析

Abstract: Leaf length, width and leafstalk length affect the photosynthetic capability of plant and so increasing photosynthetic rate per unit leaf area may improve seed yield in soybean. In this study, we analyzed QTLs data of soybean leaf length, width and leafstalk length from 2006 to 2010 with a F_{2:14}~F_{2:18} of recombination inbred lines (RIL) population derived from a cross between Charleston and Dongnong 594 by mixed linear model approach. Eight QTLs for leaf length (LL) were mapped on the chromosomes Gm01, Gm02, Gm05, Gm11, Gm18 by software WinQTLCartographer Ver. 2.5, nine QTLs were identified for leaf width (LW) on the chromosomes Gm01, Gm03, Gm05, Gm06, Gm11, Gm12, Gm16; eight QTLs were identified for leafstalk length (LSL) on Gm01, Gm03, Gm05, Gm06, Gm11, Gm17, Gm18. *qLL5a*, *qLL5b*, *qLL1a*, and *qLL18* for LL, *qLW5a*, *qLW11a*, *qLW11b*, and *qLW12* for LW, and *qLSL11b* for LSL were identified in more than two years. Furthermore, not only 72 QTLs of leaf traits that have been mapped in many different populations and environments were collected but also QTL mapped by WinQTLCartographer Ver. 2.5 were projected and integrated in the reference map with the software BioMercator2.1. In total, the consensus QTLs of five for leaf length and four for leaf width were obtained in soybean, respectively. The minimum confidence interval of leaf length was shrunk to 5.66 cM. These results would provide a basis for fine mapping QTL and cloning genes in soybean.

Keywords: Soybean [*Glycine max* (L.) Merr.] Leaf traits QTL mapping Meta-analysis

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