

利用极端材料定位水稻粒形性状数量基因位点

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Identification of QTLs for Grain Traits in Rice Using Extreme Materials in Grain Size

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摘要

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摘要 利用极端大粒材料GSL156(千粒重71.9 g)与特小粒材料川七(千粒重12.1 g, 轮回亲本)杂交、回交获得的BC₂F₂ 216个个体作为图群体, 在北京进行稻谷粒长、粒宽、粒厚、长宽比、千粒重等粒形性状的鉴定。采用单标记分析和复合区间作图法, 利用SSR标记对粒形性状进行数量性状基因座检测。结果表明, 上述粒形性状在BC₂F₂群体均呈正态连续分布, 表现为由多基因控制的数量性状; 共检测到与粒形性状相关的QTL 28个, 分布于第1、2、3、4、5、6和12染色体上。其中*qGL3-2*、*qGL3-3*、*qGT12-1*、*qGT2-1*、*qGT5-1*、*qGW1-1*、*qGW12-1*、*qGW2-1*、*qGW5-1*、*qRLW3-1*、*qTGW12-1*、*qTGW2-1*、*qTGW3-3*和*qTGW5-1*对表型变异的贡献率分别为13.70%、52.51%、21.13%、18.79%、20.92%、14.59%、18.33%、30.03%、20.05%、24.53%、13.47%、11.43%、21.30%和15.68%, 为主效QTL。其中, 第3染色体上检测出来的QTL最多。在所有检测到的28个QTL中, 6个QTL的增效等位基因来源于小粒亲本川七, 而其余QTL的增效等位基因均来源于大粒亲本GSL156, 基因作用方式主要表现为加性或部分显性。第3染色体RM7580~RM8208区间是分别与粒宽、长宽比和千粒重相关的3个主效QTL的共同标记区间, 第2染色体的RM7636~RM5812区间、第5染色体的RM3351~RM26区间和第12号染色体的RM1103~RM17区间是分别与粒宽、粒厚和千粒重相关的3个主效QTL的共同标记区间, 这些区间对粒形贡献率较大, 为进一步精细定位或克隆这些新的粒重或粒形QTL奠定了基础。同时大粒亲本对稻谷粒长、粒宽、粒厚和千粒重等性状的增效作用显著。

关键词: 水稻 粒形性状 微卫星标记 数量性状基因座

Abstract: The grain length (GL), grain width (GW), grain thickness (GT), ratio of grain length to width (RLW), and 1000-grain weight (TGW) were evaluated in Beijing. Using a BC₂F₂ population including 216 lines derived from a backcross combination between GSL156 with large grain (71.9 g) and Chuanqi with small grain (12.1 g). The quantitative trait loci (QTLs) for above five grain traits were identified by composite interval mapping using SSR markers. The results showed that the five grain traits exhibited a normal continuous distribution in BC₂F₂ population, indicating that they were quantitative traits controlled by multiple genes. A total of 28 QTLs conferring the five grain traits were detected on chromosomes 1, 2, 3, 4, 5, 6, and 12, respectively. Fourteen QTLs, namely *qGL3-2*, *qGL3-3*, *qGT12-1*, *qGT2-1*, *qGT5-1*, *qGW1-1*, *qGW12-1*, *qGW2-1*, *qGW5-1*, *qRLW3-1*, *qTGW12-1*, *qTGW2-1*, *qTGW3-3*, and *qTGW5-1*, were main-effect QTLs and explained 13.70%, 52.51%, 21.13%, 18.79%, 20.92%, 14.59%, 18.33%, 30.03%, 20.05%, 24.53%, 13.47%, 11.43%, 21.30%, and 15.68% of the observed phenotypic variance, respectively. Among them, most QTLs were mapped on chromosome 3. Six QTLs had the alleles contributing to positive effect which were derived from small grain parent Chuanqi while the other 22 QTLs alleles from large grain parent GSL156. The modes of gene action were mainly additive or partial dominance. The marker interval RM7580 - RM8208 on chromosome 3 was common to the three QTLs for GW, RLW, and TGW, respectively. The marker interval, RM7636 - RM5812 on chromosome 2, RM3351 - RM26 on chromosome 5, and RM1103 - RM17 on chromosome 12, were common to the three major QTLs, which were associated with GW, GT and TGW, respectively. The eight SSR markers used in this study would be useful in molecular breeding in rice. The alleles from parent with larger grain were showed significant effects on GL, GW, GT, and TGW.

Keywords: Rice Grain trait SSR marker Quantitative trait locus

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