

研究论文

水、旱栽培条件下稻谷粒型和粒重的相关分析及其QTL定位

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收稿日期 2006-1-9 修回日期 网络版发布日期 2006-12-18 接受日期 2006-7-2

摘要 为了解水、旱栽培条件下水稻粒形和粒重的表型及QTL变化, 以陆稻品种IRAT109和水稻品种越富构建的双单倍体群体为材料, 系统分析了稻谷粒长、粒宽、粒重及长宽比在水、旱栽培条件下的相关性, 并进行了数量性状基因位点的比较定位。结果表明, 水、旱条件下, 粒长与长宽比和粒重均呈极显著正相关; 粒宽与长宽比呈极显著负相关, 与粒重极显著正相关, 4个性状在水、旱条件间相关性都达极显著正相关。其中粒长的相关系数最高, 达0.817, 粒宽的相关系数最低, 为0.457。表明粒长受水分影响最小而粒宽受水分影响较大。粒重、长宽比介于二者之间。两种条件下共检测到14个QTLs, 分布于水稻1、5、6、7、10和12染色体上, 其中控制粒长的5个, LOD值为1.93~5.11, 贡献率为5.97%~28.85%; 控制粒宽的1个, LOD值为2.39, 贡献率为12.76%; 控制长宽比的3个, LOD值为2.08~4.6, 贡献率为7.78%~21.89%; 控制粒重的5个, LOD值为2.68~9.45, 贡献率为4.1%~14.8%。其中控制粒长的qGL-5及控制粒重的qGWt-1a和qGWt-1b在水、旱条件下均能检测到, 在抗旱育种中可用于分子标记辅助选择籽粒性状。QTL分析的结果进一步验证了表型分析结果, 粒宽相对易受土壤水分影响, 粒长、粒重和长宽比, 受水分胁迫影响较小, 遗传比较稳定。

关键词 [水稻](#) [粒型](#) [粒重](#) [加倍单倍体群体 \(DH系\)](#) [数量性状基因座位 \(QTL\)](#) [水、旱栽培](#)

分类号

Correlation Analysis and QTL Mapping of Grain Shape and Grain Weight in Rice under Upland and Lowland Environments

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Abstract Grain length (GL), grain width (GW), length width ratio (LWR) and grain weight (GWt) are most important apparent quality traits in rice, which are positively correlated with the commercial value of rice especially in international market. Moreover, grain shape is also a vital factor related to rice yield and milling quality. Compared with GL, GW and LWR, grain weight is one of the most important components related to rice yield. Several studies reported that GL, GW, LWR and GWt were controlled by some QTLs were detected under lowland condition. There have been no reports about QTLs for grain shape and grain weight under both upland and lowland conditions. Therefore, it is necessary to analyze the correlation and inheritance of grain shape and grain weight between under upland and under lowland conditions, especially to find QTLs under upland condition.

A doubled haploid (DH) population consisting of 116 DH lines developed through anther culture of the F1 hybrid between an upland rice cultivar 'IRAT109' and a lowland rice cultivar 'Yuefu' was used in this study. The parents and the 116 DH lines were planted under water- and dry-cultivation conditions, on the experiment farm of China Agricultural University in 2002. Seeds of parents and 116 DH lines were harvested at maturity, and used to measure grain length, grain width, length width ratio and grain weight. QTLs analysis was conducted with QTL Mapper version 1.0 and the constructed molecular linkage map consisting of 165 molecular markers, which covered 1 535 cM in length with an average distance of 9.3 cM between adjacent markers. A threshold probability of $P < 0.005$ was used to declare the existence of additive QTLs. Correlation analysis between grain shape and grain weight was conducted using the software of SPSS.

Positively significant correlations between GL and LWR and between GL and GWt in both upland and lowland environments were observed. Negatively significant correlations between GW and LWR and positively significant correlations between GW and GWt under the two environments were also detected. This result indicated that GL, GW, LWR and GWt had closely genetic background. All the four traits in upland environment were significantly correlated with those in lowland environment respectively, with the biggest correlation coefficient of 0.817 for GL and the smallest coefficient of 0.457 for GW. Therefore, compared to GW, GL was less affected by water stress (upland condition).

A total of 14 QTLs were detected for GL, GW, LWR and GWt, which located on chromosome 1, 5, 6, 7, 10 and 12. Ten Q

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TLs had high general contribution with explained variance of over 10%. For GL, one QTLs under upland condition and four QTLs under lowland condition were detected respectively. These QTLs explained 5.97% – 28.85% of phenotypic variance. The LOD score was 1.93 – 5.11. For GW, only one QTLs was detected under upland condition. The LOD score and general contribution was 2.39 and 12.76% respectively. For LWR, one QTLs under upland condition and two QTLs under lowland condition was detected respectively. These QTLs explained 7.78% – 21.89% of phenotypic variance. The LOD score was 2.08 – 4.60. For GWt, there were two additive QTLs under upland condition and three additive QTLs under lowland condition respectively. They explained 4.1% – 14.8% of phenotypic variance. The LOD score was 2.68 – 9.45. Three QTLs qGL-5, qGWt-1a and qGWt-1b were both detected under upland and lowland environments (common QTL). Two co-localized QTLs (qGL-1a and qGWt-1a, and qGL-1b and qGWt-1b) controlling GL and GW were detected. These QTLs would be helpful in MAS of grain shape breeding.

Key words [Rice](#) [Grain shape](#) [Grain weight](#) [Doubled haploid population](#) [Quantitative trait loci](#)

DOI:

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