

籼稻稻米碾磨与外观品质性状的QTL定位

梅德勇, 朱玉君, 樊叶杨

中国水稻研究所, 国家水稻改良中心/水稻生物学国家重点实验室, 杭州 310006

MEI De-Yong, ZHU Yu-Jun, FAN Ye-Yang

Chinese National Center for Rice Improvement/State Key Laboratory of Rice Biology, China National Rice Research Institute, Hang-zhou 310006, China

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摘要 文章利用籼稻交组合特青/IRBB衍生的重组自交系群体, 在2个环境下对稻米碾磨品质和外观品质进行QTL定位。共计检测到控制稻米碾磨品质的QTL 12个和控制外观品质的QTL 18个, 包括糙米率8个、精米率2个、整精米率2个、粒长7个、粒宽5个和长宽比6个, 这些QTL分布于除第4和12染色体外的其他10条染色体上。其中, 第3染色体涵盖粒形基因GS3的区域对粒长、长宽比、糙米率和整精米率具有较大效应, 其贡献率分别为56.71%、42.23%、10.05%和4.91%; 第5染色体涵盖粒宽基因GW5的区域对粒宽、长宽比、糙米率和精米率具有较大效应, 表型变异贡献率分别为59.51%、36.68%、19.51%和4.56%。此外, 第6染色体涵盖直链淀粉含量基因Wx的区域对糙米率和精米率具有较小效应。GS3和GW5对糙米率和粒形具有重要作用。

关键词: 碾磨品质 粒形 数量性状座位 籼稻

Abstract: Quantitative trait loci (QTL) controlling six milling and appearance quality traits were analyzed over 2 years using recombinant inbred lines derived from two *indica* rice Teqing and IRBB. A total of 30 QTL for these traits were detected, of which eight were for brown rice rate (BRR), two for milled rice recovery (MRR), two for head rice recovery (HRR), seven for grain length (GL), five for grain width (GW), and six for length/width ratio (LWR). The QTL were distributed on all chromosomes except for chromosomes 4 and 12. A QTL cluster with major effects on GL, LWR, BRR, and HRR was located in the RM15139-RM15303 interval on chromosome 3, which includes the GS3 gene for grain size. The phenotypic variances explained by the QTL were 59.51%, 36.68%, 19.51%, and 4.56%, respectively. QTL affecting GW, LWR, BRR, and MRR were clustered in the RM437-RM18038 region of chromosome 5, which covers the GW5 gene for grain width, and contributed 59.51%, 36.68%, 19.51%, and 4.56% to the total variance. QTL with minor effects on BRR and MRR were mapped to the RM190-RM587 interval covering the Wx gene for amylase content on chromosome 6. These results suggest that GS3 and GW5 may play a major roles in the genetic control of BRR and grain shape.

Keywords:

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通讯作者 樊叶杨 Email: fanyeyang@hotmail.com

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