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摘要: The BIL (backcross inbred line) population derived from the cross between Koshihikari (good eating and cooking quality, japonica) and Kasalath (poor quality, indica) was used to analyze the QTLs for amylose content (AC), gelatinization temperature (GT), gel consistency (GC) and protein content (PC). Eight main-effect QTLs including 2 for AC, 3 for GT, 2 for GC and 1 for PC were identified. Moreover, 27 epistatic QTL pairs including 7 for AC, 5 for GT, 4 for GC and 11 for PC were also detected while for AC and GT, one main-effect QTL with a major gene was detected, respectively. Therefore, the main-effect QTL might be more responsible for the current variation than the epistatic QTL. The result indicated that the main-effect QTL is the primary genetic basis for those traits. However, for PC, the epistatic QTL explained a much greater portion of the total variation than main-effect QTL, suggesting that epistatic loci are the primary genetic basis for such trait. In the experiment, chromosome segment substitution lines (CSSLs) were used to confirm reliabilities of the main effect QTLs detected in BIL population. Of the 8 main-effect QTLs for 4 traits in BIL analysis, 6 were confirmed and 2 remained unconfirmed by CSSLs analysis.

关键词: rice quality; quantitative trait locus; molecular marker; chromosome segment substitution lines  
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