

普通野生稻中增产相关QTL的发掘

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摘要 普通野生稻(*Oryza Rufipogon*)是重要的遗传资源, 发掘其优良等位基因将对水稻遗传改良产生重要影响。文章从以珍汕97为轮回亲本, 普通野生稻为供体的BC₂F₁群体中选择一个与珍汕97表型明显不同的单株BC₂F₁-15, 经过连续自交获得回交重组自交系BC₂F₅群体。均匀分布于12条染色体的126个多态性SSR (Simple sequence repeats) 标记基因型分析, 发现BC₂F₁-15单株在30%的标记位点为杂合基因型; 利用该群体共检测到4个抽穗期、3个株高、4个每穗颖花数、2个千粒重和1个单株产量QTL。在第7染色体RM481-RM2区间, 检测到抽穗期、每穗颖花数和产量QTL, 野生稻等位基因表现增效作用; 其他3个每穗颖花数QTL位点, 野生稻等位基因也均具有增效作用。结果表明野生稻携带有增产相关的等位基因, 这些有利等位基因无疑是水稻遗传改良可资利用的新资源。

关键词: 普通野生稻 产量性状 QTL 增效作用

Abstract: Common wild rice (*Oryza rufipogon*) is an important genetic resource. Discovery of desirable alleles in wild rice will make important contributions to rice genetic improvement. In this study, Zhenshan 97 as the recurrent parent and wild rice as the donor parent were used to develop a BC₂F₁ population. One plant BC₂F₁-15 in the population showed distinct phenotype from Zhenshan 97 was selected to produce a population of BC₂F₅ by continuous self-crossing. The genotype assay of the plant BC₂F₁-15 with 126 polymorphic SSR markers evenly distributed on 12 chromosomes showed that it was heterozygous at 30% of the control marker loci. Four, 3, 4, 2, and 1 QTLs were detected for heading date, plant height, spikelets per panicle, grain weight, and single plant yield in the BC₂F₅ population, respectively. One QTL region flanked by the marker interval of RM481-RM2 on chromosome 7 had pleiotropic effects on heading date, spikelets per panicle, and grain yield per plant, and the alleles of wild rice increased phenotypic values. At the other 3 QTLs for spikelets per panicle, common wild rice had positive effects. These results clearly showed that common wild rice carried desirable alleles for yield related traits. The favorable alleles from common wild rice are new valuable genes for rice breeding.

Keywords: common wild rice, yield traits, QTL, positive effects

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