

应用分子标记研究氮素胁迫条件下水稻叶片叶绿素含量差异的遗传背景

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摘要 在氮素限制供应条件下, 籼稻品种IR42与广亲合粳稻品种Palawan剑叶及下位叶的平均叶绿素含量差异显著。叶绿素含量在Palawan/IR42杂交F2代中呈正态分布。104个分布与12条染色体的RFLP标记基因型之间表型平均值方差分析与区间作图分析结果表明, 分别位于染色体2、4、7上的3个QTL位于RZ58/RG102、RG143/RG329和RG634/RG650之间。与RG143及RG102连锁的QTL具有显著加性效应, 与RG102连锁的QTL显示显著的显性效应。单个QTL效应对群体变异贡献为5%以上。各标记位点不同基因型平均数比较表明, RG143和RG102位点表现为隐性基因效应, IR42与Palawan基因型平均数差异显著超过群体平均数10%以上, RG634位点IR42与杂合基因型之间平均数差异也超过群体平均数10%以上。非等位基因互作效应分析表明, 染色体10与9上的RZ625与RG667位点之间具有显著的显著×显性交互效应, 该效应可解释群体变异的7%以上。本研究首次报道水稻不同基因型在氮素限制供应条件下与叶绿素含量变异相关的数量性状位点 (QTLs) 及基因效应分析, 用不同的研究材料及在不同的氮素条件下研究比较本研究结果是必要的。

关键词 [水稻](#) [叶绿素含量](#) [数量性状位点](#)

分类号

Investigation on Genetic Background of Leaf Chlorophyll Content Variation in Rice Under Nitrogen Stressed Condition via Molecular Markers

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Abstract

Significant difference of chlorophyll content in completely extended flag and the second leaves under nitrogen stressed condition was found between two rice varieties, IR42, an indica variety and Palawan, a Japonica wide compatibility variety. The average amounts of chlorophyll content were normally segregated in the F2 population derived from a cross of Palawan/IR42. One hundred and four RFLP markers mapped on 12 chromosomes were used to identify putative QTLs underlying the variation in chlorophyll content. Orthogonal contrasts and interval mapping analysis indicated that three QTLs, located on chromosome 2, 4 and 7, were flanked by RZ58/ RG102, RG143/RG329, and RG634/ RG650 respectively. Additive gene action was predominant at RG143 and RG102 loci, but dominant effect was significant at RG634 locus. The detected single QTL could explain more than 5% of variation in chlorophyll content in the population. Mean comparisons for genotypic classes of markers closely linked to the detected QTLs indicated that the marker loci RG143 and RG102 showed recessive gene action and the phenotypic differences between IR42 and Palawan genotypes at the two marker loci exceeded 10% of the population mean. The phenotypic difference between IR-42 genotype and heterozygote at GR634 locus also exceed 10% of the population mean. Non-allelic interaction effect was detected between marker loci RZ625 and RG667 on chromosome 10 and 9 with significant ($P < 0.01$) dominant X dominant gene action which could explain more than 7% of the whole population variation in chlorophyll content. This is the first time to report the QTLs underlying chlorophyll content variation in rice under nitrogen stressed condition. It is necessary to confirm the results by using different mapping populations under different nitrogen supply conditions.

Key words [Oryza sativa L.](#) [Chlorophyll content QTLs](#)

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