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两种供氮水平下水稻成熟期相关性状的QTL定位

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摘要 以特青为母本与Lemont杂交, 然后用特青为轮回亲本回交, 建立特青背景下的染色体片段置换系(CSSL)群体。在正常和低氮条件下分别在生长后期对株高(PH)、单株穗数(PN)、叶绿素含量(CC)、地上部干物重(SDW)和单株籽粒产量(YD)等性状进行了QTL分析, 共检测到31个QTL。其中在正常供氮水平下控制PH、PN、CC、SDW和YD的QTL数目均为3个; 在低氮水平下检测到5、4、5和2个影响PH、PN、CC和SDW的QTL, 在低氮水平下没有检测到控制YD的位点。大部分QTL集中在第2、3、7、11和12染色体上, 影响不同性状或在两种供氮水平下影响同一性状的QTL在染色体上成串或成簇分布。其中第6、7、12染色体上RM30-RM439、RM18-RM478、RM309-RM270、RM235-RM17等区域同时检测到控制多个性状的QTL, 表现出明显的一因多效现象。推测仅在低氮水平下检测到的QTL可能跟水稻对低氮胁迫耐性有一定的关联。

关键词 [水稻, 氮肥, 数量性状座位, 染色体片段置换系, 基因定位](#)

分类号

Identification of related genes at ripening stage in rice under two N levels

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Abstract

QTL underlying related traits at the maturity stage under two different N applied levels were investigated by using a population of chromosome segment substitution lines (CSSLs) derived from a cross between Teqing and Lemont. A total of 31 QTLs referring 5 traits [(Plant height(PH), Pancile number per plant(PN), Chlorophyll content(CC), Shoot dry weight(SDW) and Grain yield per plant(YD)] in rice were detected. Under normal N level, three QTLs were detected in each trait, while under low N level, 5, 4, 5 and 2 QTLs were detected for PH, PN, CC and SDW respectively. Most of the QTLs were located on chromosome 2, 3, 7, 11 and 12. QTLs controlling different traits or the same trait under different N levels were mapped on the same or adjacent intervals, forming several clusters in rice chromosomes. More than two traits were detected on four intervals (RM30-RM439, RM18-RM478, RM309-RM270, RM235-RM17), suggesting existed of some pleiotropic effects. It was supposed that some QTLs only detected at low N level might be related with the ability to tolerate the low N stress in rice.

Key words [Oryza sativa L.](#) [nitrogen fertilization](#) [quantitative trait loci](#) [chromosome segment substitution lines](#) [gene mapping](#)

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