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两种供氮水平下水稻生长后期相关性状的QTL定位

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摘要

以明恢63为母本Lemont为父本构成的杂交组合,通过两个供氮水平的田间试验,在后期相关性状上检测到6个QTL,分别位于第1、3、5、6、9和12号染色体上。其中,控制株高(PH)、穗长(PL)、单穗粒数(PN)、千粒重(TGW)和单穗稻产量(PW)等性状的位于第5、6号染色体上的QTL,其贡献率分别为9%、9%、12%、13%和9%,其贡献率大于其他性状,表明这几个性状在遗传上相关性较大。其中6号染色体上的QTL,以及分别位于第1、3、5、12号染色体上的QTL,分别控制穗长、单穗粒数和千粒重,表明这些性状一致性较高。表明这些性状在水平下相关性较大,这些性状的QTL,分别位于第1、3、5、12号染色体上。

关键词

水稻 , 氮肥 , 5a-dihydro , hydrolase , gene , 5a1 , QTLs , phenotypic , genetic , adaptation , Tian , 江苏省 , gene , mapping

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Identification of Related QTLs at Late Developmental Stage in Rice (Oryza sativa L.) Under Two Nitrogen Levels

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Abstract

Two QTL underlying related traits at the late developmental stage under two different nitrogen levels were investigated in rice using a population of chromosome segment substitution lines (CSSL) derived from a cross between Teqing and Lemont. A total of 6 QTLs collecting 5 traits, rise in, plant height (PH), panicle number per plant (PN), other-ear/spit weight (OE), other-ear/spit weight (OE), and grain yield per plant (YB), were detected. Under normal N level, 3 QTLs were detected for each trait, while under low N level, 5, 4, 5 and 2 QTLs were detected for PH, PN, OE and 50W 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 chromosome. More than two traits were controlled by QTLs on one of four chromosomes (RM16,RM18, RM18,RM270, RM250,RM273, and RM18,RM273), suggesting that there were some pleiotropic effects. It was supposed that some QTLs only detected at low N level might be associated with the ability to tolerate the low N stress in rice.

Key words

Oryza , sativa , L., chromosome , substitution , population , trait , loci , QTLs , phenotypic , genetic , adaptation , Tian , 江苏省 , gene , mapping

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