

研究报告

不同生长环境下水稻最上节间长度QTL定位研究

乔保建^{1,2}, 王盈盈¹, 朱晓彪¹, 洪德林¹

1. 南京农业大学作物遗传与种质创新国家重点实验室, 南京 210095

2. 河南省平顶山市农业科学研究所, 平顶山 467000

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摘要

利用由98个家系组成的 Nipponbare/Kasalath//Nipponbare 回交重组自交系 (backcross inbred lines, BIL) 作图群体 (BC1F12和BC1F13) 和复合区间作图方法 (CIM), 在3种不同的生长环境下对水稻最上节间长度进行了 QTL 分析。结果表明, 3种不同的生长环境共检测到 13 个 QTL, 分布于第 1, 2, 3, 5, 6, 8, 10, 11 染色体上, 解释性状变异的 3.97%~15.21%。其中qUIL-6在3种不同生长环境中均检测到, qUIL-1a, qUIL-3a, qUIL-3b和 qUIL-10a 等4个位点在两种不同生长环境中均被检测到, 说明这些 QTL 位点受环境影响较小, 表达较为稳定。

关键词 [水稻; 最上节间长度; 不同生长环境; 数量性状基因座定位; 复合区间作图法](#)

分类号

QTL analysis of the uppermost internode length in rice under different growing environments

QIAO Bao-Jian^{1,2}, WANG Ying-Ying¹, ZHU Xiao-Biao¹, HONG De-Lin¹

1. State Key Laboratory of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Nanjing 210095, China;

2. Institute of Pingdingshan Agricultural Sciences, Pingdingshan 467000, China

Abstract

<P>A mapping population of 98 backcross inbred lines (BC1F12 and BC1F13), derived from a backcross of Nipponbare (japonica) / Kasalath (indica) // Nipponbare by the single seed descent methods, was employed to map quantitative trait loci (QTL) of the uppermost internode length in rice under different growing environments by composite interval mapping method. The results showed that 13 QTLs relating to the uppermost internode length were detected under three different growing environments, and these QTLs were located on chromosome 1, 2, 3, 5, 6, 8, 10 and 11, explained 3.97% - 15.21% of observed phenotypic variance,

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respectively. The locus of qUIL-6 was detected in three growing environments,
and qUIL-1a, qUIL-3a, qUIL-3b and qUIL-10a were detected in two growing environments, indicating that these QTLs were stable and little affected by the environment.
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Key words [rice](#) [the uppermost internode length](#) [different growing environments](#) [quantitative trait locus mapping](#) [composite interval mapping method](#)

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通讯作者 洪德林 pbts@njau.edu.cn