

研究论文

不同生长环境下水稻结实率数量性状位点的检测

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摘要 以籼稻密阳23与粳稻吉冷1号配制所获得的F2:3群体200个家系作为作图群体, 在北京、昆明、三亚、公主岭和韩国春川等5个点进行水稻结实率的鉴定, 并利用SSR标记对水稻结实率数量性状位点进行检测。结果表明, 水稻结实率表型值及其在F3家系群中的分布以及所检测到的QTL数目因生长环境不同而有较大差异, 说明QTL与环境有明显的互作效应。水稻结实率在F3家系群中呈接近正态或偏态的连续分布, 是多个基因所控制的数量性状。共检测到与水稻结实率相关的QTL 14个, 分布于第1、2、3、4、6、7、8、10和12染色体上, 对表型变异的贡献率为4.9%~15.3%。分别位于第1、2、6和12染色体RM1~RM259、RM263~RM6、RM340~RM30、RM270~RM17区间的qSSR1、qSSR2、qSSR6和qSSR12至少在2种生长环境下均检测到, 对表型变异的贡献率分别为4.9%~8.4%、4.8%~7.2%、7.6%~10.7%和7.4%~10.4%。以上多数QTL增效等位基因均来自吉冷1号, 基因作用方式主要为部分显性或显性或超显性。

关键词 水稻 结实率 不同生长环境 数量性状位点 微卫星标记

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Identification of QTLs for Seed Setting Rate in Rice under Different Growing Environments

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Abstract The quantitative trait loci (QTLs) for seed setting rate were identified using F2:3 population including 200 lines derived from a cross of indica and japonica “Milyang 23/Jileng 1” with microsatellite markers. The evaluation of seed setting rate was conducted in Beijing, Kunming, Sanya, Gongzhuling of China and Chuncheon of Korea, respectively. The value of seed setting rate and its distribution in F3 lines and the number of detected QTL were significantly different due to different growing environments, indicating the interaction between QTL and environment significantly. The seed setting rate showed near normal or partial continuous distributions, suggesting that it was quantitative trait controlled by many genes. Fourteen QTLs were detected on chromosome 1, 2, 3, 4, 6, 7, 8, 10 and 12, which explained the observed phenotypic variance from 4.9% to 15.3%. qSSR1, qSSR2, qSSR6 and qSSR12 which were found in more than two growing environments were detected in RM1 – RM259 on chromosome 1, RM263 – RM6 on chromosome 2, RM340 – RM30 on chromosome 6 and RM270 – RM17 on chromosome 12, respectively, and explained 4.9% – 8.4%, 4.8% – 7.2%, 7.6% – 10.7% and 7.4% – 10.4% of observed phenotypic variation, respectively. The allelic genes of QTLs mostly coming from Jileng 1 were partial dominance or dominance or over dominance to these of Milyang 23.

Key words [Rice](#) [Seed setting rate](#) [Different growing environment](#) [Quantitative trait loci \(QTL\)](#) [Microsatellite marker](#)

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