

植物遗传学

# 水稻生物学产量及其构成性状的QTL定位

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### 摘要

QTL的加性效应、加性×加性上位性效应及它们与环境的互作效应是数量性状的重要遗传分量。利用IR64/Azucena的125个DH品系为群体, 分析了水稻生物学产量及其两个构成性状干草产量和谷粒产量的遗传组成。用基于混合模型的复合区间作图(MCIM)方法进行QTL定位。检测到12个位点有加性主效应, 27个位点涉及双位点互作, 18个位点存在环境互作。结果表明水稻生物学产量和它的两个构成性状普遍存在上位性效应和QE互作效应。此外, 还探讨了性状间相关的遗传基础。发现4个QTLs和一对上位性QTLs可能与生物学产量与干草产量之间的正相关有关。3个QTL可能与干草产量与谷粒产量之间的负相关有关。这些结果可能部分地解释了这3个性状相关的遗传原因。通过对水稻生物学产量及其两个构成性状所定位QTL的分析, 加深了对数量性状QTL的认识。首先, QTL的上位性效应和QE互作效应是普遍存在的; 其次, QTL的多效性或紧密连锁可能是遗传相关的原因, 当QTL对两个性状作用的方向相同时可导致正向遗传相关, 反之则为负向遗传相关, 当有些QTL表现为同向作用而另一些QTL表现为反向作用时, 则可削弱性状间的遗传相关性; 第三, 复合性状的QTL效应可分解为其组成性状的QTL效应, 如果QTL对各组成性状的效应方向相反而相互抵消, 可使复合性状的QTL效应不易被检测; 第四, 加性效应的QTL常参预构成上位性效应, 而具有上位性效应的QTL并非都有加性主效应, 表明忽略上位性的QTL定位方法会降低检测QTL的功效; 最后, 鉴别不同类型的QTL效应有利于指导育种实践, 选择主效QTL适用于多环境, QE互作QTL适用于特定环境, 对上位性QTL应强调选择基因组合而非单个基因。

### 关键词

数量性状位点; 生物学产量; 干草产量; 谷粒产量; 上位性; 水稻

### 分类号

## Mapping QTL for Biomass Yield and Its Components in Rice (*Oryza sativa* L.)

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### Abstract

<P>Additive effects, additive by additive epistatic effects, and their environmental interactions of QTLs are important genetic components of quantitative traits. Genetic architecture underlying rice biomass yield and its two component traits (straw yield and grain yield) were analyzed for a population of 125 DH lines from an inter-subspecific cross of IR64/Azucena. The mixed-model based composite interval mapping approach

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(MCIM) was used to detect QTLs, There were 12 QTLs detected with additive main effects, 27 QTLs involved in digenic interaction with aa and/or aae effects, and 18 QTLs affected by environments with ae and/or aae effects. It was revealed that epistatic effects and QE interaction effects existed on biomass yield and its component traits in rice. In addition, the genetic basis of relationships among these traits were investigated. Four QTLs and one pair of epistatic QTLs were detected to be responsible for the positive correlation between biomass yield and straw yield. Three QTLs might be responsible for the negative correlation between straw yield and grain yield. This result could partially explain the genetic basis of correlation among the three traits, and provide useful information for genetic improvement of these traits by marker-assisted selection.

**Key words**

[quantitative trait locus \(QTL\); biomass yield; straw yield; grain yield; epistasis; rice \(Oryza sativa L.\)](#)

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