

研究论文

# 水稻永久F2群体抽穗期QTL的上位性及其与环境互作效应的分析

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**摘要** 利用源于杂交水稻汕优63的重组近交系(RI), 进行系间随机交配构建了水稻永久F2(IF2)群体。采用QTL作图软件QTL Mapper 2.0对IF2群体的抽穗期性状进行了分析, 共发现了21个QTLs, 分布于10条染色体上。对抽穗期QTL的加性效应, 显性效应, 加×加、加×显、和显×显上位性效应进行了估计, 对遗传主效应与环境的互作效应做了预测。结果表明, 鉴别出的QTL中, 加×加上位性显著程度最高, 其次是加性效应。加×加上位性与环境的互作效应以及加性与环境的互作效应预测值, 显著性程度相对较高; 加×显上位性与环境的互作效应预测值均不显著; 显性、显×显上位性与环境的互作效应预测值只有很少达到显著。本文讨论了构建IF2群体的困难及其对QTL作图可能产生的影响。

**关键词** [水稻](#) [永久性F2群体](#) [抽穗期](#) [QTL](#) [上位性](#) [QTL×环境互作](#)

**分类号** [S511](#)

## Use of Permanent F2 Population to Analyze Epistasis and Their Interaction Effects with Environments for QTLs Controlling Heading Date in Rice

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**Abstract** Immortalized F2 population in rice was constructed by random mating among recombinant inbred (RI) lines derived from a famous elite hybrid rice, Shanyou 63. Analysis on heading date of permanent F2 population was conducted through QTL Mapper 2.0, a software for QTL mapping. A total of 21 QTLs which distributed on 10 chromosomes were identified. Additive effects, dominance effects, epistatic effects of additive × additive, additive × dominance, and dominance × dominance of QTLs for heading date were estimated, the interaction effects between main genetic effects and environments were predicted. The results showed that a few of single effects for identified QTLs were up to the significance of 0.05, among which epistatic effects of additive × additive were most significant, next were additive effects. The interaction effects of additive and epistasis of additive × additive with environments presented higher significance; no significant interaction effect of additive × dominance with environments was found; only few of interaction effects of dominance and dominance × dominance with environments were observed. The difficulty for constructing IF2 population and the possible influence on QTL mapping were discussed also.

**Key words** [Rice](#) [Immortalized F2 population](#) [Heading date](#) [QTL](#) [Epistasis](#) [QTL×environment](#)

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