

## 籼粳稻杂交后代花时性状的QTL分析

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**摘要:** 研究典型籼稻品种‘七山占’和典型粳稻品种‘秋光’杂交衍生的重组自交系群体及其双亲的花时性状, 并用该群体的分子连锁图谱进行QTL分析, 共检测到6个与水稻花时性状相关的QTL, 包括1个始花时QTL、3个盛花时QTL和2个终花时QTL, 分别位于第1、2、7、8、10和12染色体, 单个QTL的贡献率在7.08%~26.95%之间。有4个增效等位基因来源于粳型亲本‘秋光’, 2个来源于籼型亲本‘七山占’。

**关键词:** 水稻; 数量性状基因座; 花时

## QTL Analysis on Flowering Time in Filial Generations of Cross between Indica and Japonica Rice

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**Abstract:** QTLs for flowering time were identified in the population derived from a cross between typical japonica rice ‘Akihilari’ and indica rice ‘Qishanzhan’. Totally, 6 QTLs for the flowering time of rice were identified and mapped on chromosome 1, 2, 7, 8, 10, and 12, respectively. One putative QTL for flowering-begin-time was located on chromosomes 12. Three putative QTLs for vigorous-flowering-time were located on chromosomes 1, 8 and 10. Two QTLs for flowering-end-time were located on chromosomes 2 and 7. The contribution of single QTL was between 7.08%–26.95%. There were four efficiency alleles from the typical japonica rice ‘Akihilari’ and two efficiency alleles from indica rice ‘Qishanzhan’.

**Key words:** *Oryza sativa*; QTL; flowering time

水稻的“花时”指一天中颖花开放的起始时刻和颖花开放的持续时间。研究表明, 花时的早晚和历时长短是品种的遗传特性, 同时也受环境的影响(王开锡等1990; 田大成1991; 李金军等2007)。一般说来, 籼稻花时早而持续时间长, 粳稻花时晚而持续时间短(王建军等1991; 蒯建敏等1994)。虽然常规水稻花时的早晚对水稻产量没有影响, 但是随着杂交水稻的兴起, 籼粳稻在开花时间上的差异已经严重影响到亚种间杂种优势的直接利用和杂交粳稻的发展。目前对植物成花分子调控机制等已有一些报道(Blázquez等2002; Strayer等2000; Abe等2005; Blázquez和Weigel 2000; Corbesier等2007; Moon等2005; Schmid等2003), 随着分子遗传学及分子生物学的迅速发展, 近年来

在高等植物成花决定过程的基因调控研究方面已取得了很多成就(Achard等2003; 洪薇和曹家树2002; 李林海等2006; Hayama和Coupland 2004), 但上述研究基本集中在花期上, 对水稻花时的遗传规律和相关QTL分析鲜有报道。本研究利用已构建的分子标记连锁图谱与重组自交系(RILs)群体2年花时性状调查数据相结合, 对3个花时性状(始花时、盛花时和终花时)进行QTL分析, 探讨其遗传机理, 为改良水稻花时性状提供科学依据。

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