



### 陆地棉吐絮铃数及吐絮率的QTL定位

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### Quantitative Trait Locus Mapping of Number and Percentage of Cracked and Open Bolls in *Gossypium* L.

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摘要

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**摘要** 采用复合区间作图法, 对陆地棉sGK9708 × 0-153组合的重组近交系(RI)及永久F<sub>2</sub>群体在曲周(2009年)、安阳(2009, 2010年)3个环境条件下的吐絮铃数和吐絮率进行QTL检测, 共获得18个QTLs。其中, 7个与吐絮铃数相关, 加性效应在-0.46~0.33之间, 可解释的表型变异为5.86%~11.28%; 11个与吐絮率相关, 加性效应在-3.64%~3.20%之间, 可解释的表型变异4.68%~9.84%。这些QTLs主要分布在25号(吐絮铃数/吐絮率: 3个/6个, 下同)、16号(2个/2个)、18号(1个/2个)染色体和LG49(1个/1个)上。这18个QTLs中, qPOB-16-2在RI群体中的3个环境下被稳定检测到, qCOB-16-1、qPOB-25-3和qPOB-25-4在RI中的两个环境下被稳定检测到。这些QTLs可以应用于吐絮铃数和吐絮率的分子标记辅助选择。

**关键词:** 陆地棉 永久F<sub>2</sub>群体 重组近交系 吐絮铃数 吐絮率 QTL

**Abstract:** The recombinant inbred lines(RI) and immortalized F<sub>2</sub> (IF<sub>2</sub>) populations derived from the cross between *Gossypium hirsutum* L. lines sGK9708×0-153 were used to detect quantitative trait loci(QTLs) underlying the number of cracked and open bolls (COP) and percentage of open bolls (POB). Field experiments were conducted in Quzhou, Heilongjiang Province in 2009 and in Anyang, Henan Province, in 2009 and 2010. QTL analysis was conducted by the CIM method. Seven and 11 QTLs, which explained 5.86%~11.28% and 4.68%~9.84% of the phenotypic variation of COB and POB respectively. Three, two, one, and one QTLs related to COB were located on chromosomes 25, 16, 18, and LG49, respectively; while six, two, two, and one QTLs related to POB were on chromosomes 25, 16, 18, and LG49, respectively. However, no common QTLs were detected in the RI and F<sub>2</sub> populations. qPOB-16-2 was detected in the population in three environments, and qCOB-16-1, qPOB-25-3, and qPOB-25-4 were detected in two environments. The stable QTLs might be useful for molecular-assisted selection in future cotton breeding programs.

**Keywords:** upland cotton(*Gossypium hirsutum* L.) immortalized F<sub>2</sub> population recombinant inbred lines cracked and open bolls percentage of open bolls QTL

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