

## 大豆开花盛期快速叶绿素荧光参数的QTL分析

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### QTL Mapping for Fast Chlorophyll Fluorescence Parameters in Soybean

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**摘要** 【目的】定位大豆R2时期（开花盛期）快速叶绿素荧光参数（JIP参数）QTL，分析不同参数间的遗传关系，比较参数在R2和R6时期（鼓粒盛期）遗传基础的异同。【方法】以大豆品种科丰1号和南农1138-2及其杂交衍生的184份重组自交系为材料，在盆栽条件下测定R2时期JIP参数，检测其QTL。【结果】检测到16个JIP参数QTL，分布在连锁群A1、C2、D2、I、M、N和O上，单个QTL的LOD值为2.40—5.65，贡献率为4.40%—20.06%；检测到3个同时控制多个参数的染色体区间，分别是连锁群C2上标记区间Satt286—Satt316、连锁群I上标记区间Sat\_418—Satt650和连锁群O上标记区间Sat\_231—Sat\_196。【结论】不同JIP参数间既有共同的控制基因（QTL），也有各自独特的控制基因；JIP参数多数QTL不能在R2和R6时期重复检测到，控制其表达的遗传机制较为复杂；连锁群O上标记区间Sat\_231—Sat\_196在大豆R2和R6时期均检测到，该区间可能存在稳定表达的控制光合器官内禀结构和功能的基因，具有一定的育种价值。

**关键词：** 大豆 快速叶绿素荧光参数(JIP参数) 重组自交系 QTL定位

**Abstract:** 【Objective】The present study is aimed to identify QTL associated with fast chlorophyll fluorescence parameters (JIP parameters), examine the genetic relationships among different parameters, and compare the genetic base underlying the parameters between the two growth stages of R2 and R6 in soybean. 【Method】A pot experiment was carried out to evaluate five JIP parameters at R2 growth stage using 184 recombinant inbred lines (RILs) derived from a cross between two varieties of Kefeng 1 and Nannong 1138-2, and then the QTL of above parameters were detected and mapped. 【Result】A total of 16 QTL, located on linkage groups (LGs) A1, C2, D2, I, M, N and O, respectively, were identified, and explained phenotypic variation ranging from 4.40% to 20.06% with the LOD score from 2.40 to 5.65. Three major genomic regions were detected to be associated with several parameters simultaneously, which were between markers Satt286 and Satt316 on LG C2, marker Sat\_418 and Satt650 on LG I, and marker Sat\_231 and sat\_196 on LG O, respectively. 【Conclusion】Different JIP parameters might be controlled by the same or different genes. Most of the QTL associated with JIP parameters were not detected consistently at R2 and R6 growth stage, indicating that the genetic mechanism underlying the JIP parameters is relatively complicated. The marker interval between Sat\_231 and Sat\_196 on LG O was detected at both R2 and R6 growth stage, and this genomic region may contain stably expressing genes underlying the intrinsic features of the photosynthetic apparatus and be useful in the breeding practice of soybean.

**Key words:** [soybean](#) [fast chlorophyll fluorescence parameters \(JIP parameters\)](#) [recombinant inbred line \(RIL\)](#)  
[QTL mapping](#)

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