

基于SSR标记分析小豆及其近缘植物的遗传关系

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Genetic diversity in adzuki bean and its relatives based on SSR markers

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摘要

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摘要 本研究利用87对SSR引物分析了80份栽培小豆(*Vigna angularis*)、22份野生小豆(*V. angularis* var. *nipponensis*)以及10份豇豆属(共7个种)近缘植物,旨在比较豇豆属不同种的遗传多样性,并分析种间的遗传关系。结果显示87对SSR引物在112份小豆及其近缘植物资源中共检测到667个等位变异,其中有75个、71个和82个SSR位点分别在栽培小豆、野生小豆和近缘植物中表现为多态。随机抽样分析发现,平均每SSR位点检测到的等位变异数目为近缘植物>野生小豆>栽培小豆,与多态信息含量(PIC)值一致,说明近缘植物及野生小豆中蕴含着丰富的遗传变异,是栽培小豆育种的重要基因来源。聚类分析显示,栽培小豆、野生小豆和近缘植物间的遗传分化比较明显,分别聚为三大类,其中栽培小豆的遗传背景与其生态环境相对应;近缘植物又可以分为三个亚类,亚类间的遗传距离与其亲缘关系相对应。本研究结果也说明利用SSR标记辅助豇豆属的种间分类是可行的。

关键词: 豇豆属植物 SSR 遗传多样性 遗传关系

Abstract: In order to enhance the use of genetic resources of *Vigna* in breeding of adzuki bean, genetic diversity and relationship were analyzed based on 87 SSR markers. The results showed 667 alleles were detected at these SSR loci among 112 accessions of *Vigna* plants, including 80 cultivated, 22 wild adzuki bean and 10 relative plants. And 75, 71 and 82 were polymorphic in cultivated, wild adzuki bean and relative plants, respectively. Random sampling analysis suggested that the relative plants ranked the first for the average number of alleles per SSR locus, and wild adzuki bean ranked the second, this was agreeable with polymorphism information content (PIC). Cluster analysis divided the cultivated, wild adzuki bean and relative plants into three distinct groups. The genetic background of cultivated adzuki bean basically agreed with their origins. The relative plants could also be divided into three sub-groups, and *V. umbellata* had different genetic background with other wild species. The present study suggested that wild *Vigna* had higher genetic variations than cultivated adzuki bean, and could be used to broadening the gene pool of this crop.

Keywords: adzuki bean *Vigna* genetic diversity SSR

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