

研究论文

以湖南和湖北大豆 [*Glycine max* (L.) Merr.] 为例分析影响遗传多样性评价的因素

关媛¹, 鄂文弟^{1,3}, 王丽侠¹, 关荣霞¹, 刘章雄¹, 常汝镇¹, 曲延英², 邱丽娟^{1,*}

1,*

¹中国农业科学院作物科学研究所, 国家农作物基因资源与遗传改良重大科学工程/农业部作物种质资源与生物技术重点开放实验室, 北京 100081 ²新疆农业大学, 新疆乌鲁木齐 830052 ³东北农业大学, 教育部大豆生物学重点实验室, 黑龙江哈尔滨 150030

收稿日期 2006-1-26 修回日期 网络版发布日期 接受日期 2006-7-16

摘要 以不同来源大豆种质为材料进行基因组SSR分析, 探讨大豆遗传多样性研究方法, 旨在为科学评价大豆种质资源提供参考。当取样比例相同时, 湖北大豆的遗传丰富度显著高于湖南大豆, 但两省大豆遗传多样性指数之间没有显著差异。当取样量相同时, 利用随机取样法比较, 湖南大豆的遗传多样性显著高于湖北, 而利用聚类取样比较, 两省大豆的遗传多样性没有显著差异。在遗传多样性指数相同情况下, 湖北大豆的遗传丰富度显著高于湖南大豆。取样数与三个遗传多样性评价参数(等位变异数、Shannon指数、He)之间均达到显著和极显著相关。以湖南大豆为例, 估算出在大豆SSR遗传多样性分析中, 至少需要50~60个样本, 即占总体9.0%~10.8%的取样比例, 才能代表总体的遗传变异。提出在评价大豆遗传多样性时, 应用大豆样本数对其遗传多样性指数计算公式进行修正, 建议将Shannon指数计算公式改为 $H = -\ln N \sum P_i \ln P_i$ (N为样本数)。根据修正公式分析, 结果表明, 湖北大豆的遗传多样性高于湖南大豆。

关键词 大豆 遗传多样性 SSR标记 Shannon指数 期望杂合度 等位变异数 取样量

分类号

Analysis of Factors Influencing the Genetic Diversity Evaluation Using Two Soybean [*Glycine max* (L.) Merr.] Collections from Hunan and Hubei

GUAN Yuan¹, E Wen-Di^{1,3}, WANG Li-Xia¹, GUAN Rong-Xia¹, LIU Zhang-Xiong¹, CHANG Ru-Zhen¹, QU Yan-Ying², QIU Li-Juan^{1,*}

¹ National Key Facility of Crop Gene Resources and Genetic Improvement / Key Laboratory of Crop Germplasm & Biotechnology, Ministry of Agriculture / Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081; ² Xinjiang Agricultural University, Urumchi 830052, Xinjiang; ³ North east Agricultural University, Key Laboratory of Soybean biology. Ministry of Education, Harbin 150030, Heilongjiang, China

Abstract Accessions from Hunan and Hubei provinces in the Chinese soybean pre-core collection were analyzed with SSR markers to determine an optimal strategy in genetic diversity evaluation. The results showed that when analyzed with the same sampling ratio, the number of alleles in accessions from Hubei province was higher than those from Hunan province, however the difference was not up to significant level in genetic diversity index. When analyzed with same sample size by random sampling, accessions from Hunan province were higher both in number of alleles and diversity index than those from Hubei, while there was no significant difference between them as sampled based on cluster. Accessions from Hubei were larger in number of alleles than those from Hunan when sampled by the same genetic diversity index. Genetic diversity index was influenced by sample size as we concluded, and we deduced that in genetic diversity analysis, a minimum of 50 - 60 accessions (9.0% - 10.8% percent of total accessions) was required to represent most of genetic variation, so that it could explain the total genetic variation. An adjustment of the formula for Shannon index was also proposed after a set of analyses based on accessions from Hunan and Hubei. And with it, accessions from Hubei showed higher genetic diversity than those from Hunan province.

Key words Soybean Genetic diversity SSR Markers Shannon index He Number of alleles Sample size

DOI:

扩展功能

本文信息

- ▶ [Supporting info](#)
- ▶ [PDF\(640KB\)](#)
- ▶ [\[HTML全文\]\(0KB\)](#)
- ▶ [参考文献](#)

服务与反馈

- ▶ [把本文推荐给朋友](#)
- ▶ [加入我的书架](#)
- ▶ [加入引用管理器](#)
- ▶ [复制索引](#)
- ▶ [Email Alert](#)
- ▶ [文章反馈](#)
- ▶ [浏览反馈信息](#)

相关信息

- ▶ [本刊中 包含“大豆”的 相关文章](#)
- ▶ [本文作者相关文章](#)

- [关媛](#)
- [鄂文弟](#)
- [王丽侠](#)
- [关荣霞](#)
- [刘章雄](#)
- [常汝镇](#)
- [曲延英](#)
- [邱丽娟](#)

