

研究论文

中国黄淮和南方夏大豆 (Glycine max L.) SSR标记的遗传多样性及分化研究

李林海, 邱丽娟, 常汝镇, 贺学礼

中国农业科学院作物科学研究所, 农业部作物种质资源与生物技术重点开放实验室, 北京 100081

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摘要 以黄淮和南方两种类型共288份夏大豆为实验材料, 用60个SSR位点进行多个遗传多样性指标的分析, 旨在明确黄淮夏大豆 (HHS) 和南方夏大豆 (SS) 品种资源的遗传分化, 为夏大豆品种资源的利用提供依据。结果表明, 在夏大豆中共检测到808个等位变异, 每个SSR位点等位变异变化于2~38个, 平均13.47个, 其中HHS的等位变异数 (725个) 和特异等位变异数 (141个) 低于SS (729个和145个), 且特异等位变异的位点不同, 但差异不显著; HHS的平均数遗传多样性指数显著高于SS, 而相似系数显著低于SS, 但两种夏大豆之间的相似系数 (0.103~0.209) 显著低于类型内的相似系数 (0.161~0.307)。两种夏大豆类型之间的分化系数为8.72%, 相比之下, 各夏大豆类型内的分化更明显。这些结果表明, HHS和SS内部的遗传变异丰富, 但两者之间存在明显差异, 这为大豆的育种亲本选配及多起源学说提供了依据。

关键词 [夏大豆](#) [遗传多样性](#) [分化](#) [SSR标记](#)

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Differentiation and Genetic Diversity of SSR Molecular Markers for Huanghuai and Southern Summer Sowing Soybean in China

LI Lin-Hai, QIU Li-Juan, CHANG Ru-Zhen, HE Xue-Li

Key Laboratory of Crop Germplasm & Biotechnology, the Ministry of Agriculture, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081

Abstract China owns the most soybean germplasm resources in the world, and is the origin of the soybean too. There are 11207 accessions of summer sowing soybean, accounting for 49% in Chinese soybean germplasm resources. Chinese Summer sowing soybean is divided into 2 different ecotypes: Huanghuai summer sowing soybean (HHS) and Southern summer sowing soybean (SS). It will provide valuable information for broadening genetic base of modern cultivars and deducing the evolution of cultivated soybean by using the genetic diversity existed in it. In this experiment, 142 HHS and 146 SS accessions sampled from the primary core collection, which was established by Qiu et al. (2003) [1] based on the total of HHS (4711) and SS (6496) (Table 1), were analyzed at 60 SSR loci for their genetic diversities. The aim was to illustrate the genetic similarities and diversities in order to provide the evidence for study and utilization of summer sowing soybean germplasm resources. The results indicated that there were total of 808 alleles at 60 loci with average 13.47 alleles per locus. The HHS had 725 alleles and 141 unique alleles, which were lower than those of SS (729 and 145), and the loci for unique alleles were different between two types of summer sowing soybeans, though there was no significant difference. Comparing genetic diversities being represented Simpson index (SI), the HHS was higher than SS, and SI (0.76) of HHS was significantly different from that of SS (0.73). Though there was obvious differentiation (8.72%) between two types of summer sowing soybean, the differentiation within each of them was even higher (Table 3). By comparison of pairwise similarities between or within each types of summer sowing soybeans, similarity coefficients within HHS ranged 0.161—0.285, which was lower than that within SS (0.191—0.307), but they were relatively higher than those (0.103—0.209) between two types of summer sowing soybeans (Fig.3, Table 6). These parameters indicated that both HHS and SS had abundant genetic diversities and differentiation as compared with those between them. It provides molecular evidence for multiple origins of soybean and parent selection in soybean improvement.

Key words [Summer sowing soybean](#) [Genetic diversity](#) [Differentiation](#) [SSR marker](#)

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