

研究论文

SSR分子标记检测出的花生类型内遗传变异

唐荣华^{1, 2}, 高国庆², 贺梁琼¹, 韩柱强¹, 单世华³, 钟瑞春¹, 周翠球¹, 蒋菁¹, 李杨瑞², 庄伟建⁴

1. 广西农科院经济作物研究所, 南宁530007;
2. 广西作物遗传改良生物技术重点开放实验室, 南宁530007;
3. 山东省花生研究所, 青岛266100;
4. 福建农林大学作物科学学院, 福州350002

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摘要

花生是我国重要的食用油和蛋白质来源作物, 鉴定其DNA分子多态性对品种改良和资源评价具有重要的意义。从已公布的花生Genomic-SSR和EST-SSR引物中筛选出34对引物, 用来分别鉴定花生4大类型各24份共96份品种资源的分子变异, 其中龙生型资源全部来自广西, 普通型资源中有11份从国外引进, 有13份来自广西和国内其他省市, 多粒型资源只有两份来自中国, 其他22份分别来自印度、美国和非洲等地, 珍珠豆型资源中有22份是来自中国各地的育成品种或农家品种, 有2份来自国外。研究结果为: 分别有10 ~ 16对SSR引物能在4大类型花生资源中扩增出多态性DNA片段; 这些多态性SSR引物都具有多位点特性; 首次为SSR分子标记设立了一个新的评价指标——区别指数, 多态性SSR引物的区别指数最高达0.992; 资源间的平均遗传距离, 多粒型为0.59, 普通型为0.48, 珍珠豆型为0.38, 龙生型为0.17。根据遗传距离采用最长距离法对4大类型花生资源分别进行了聚类分析, 构建了资源间的遗传关系图, 花生4大类型可进一步分成不同类群, 资源间的亲缘关系与其来源相关。观察到PM15和PMc297的扩增产物具有类型特异性, PM15能在龙生型、普通型和多粒型花生资源中扩增出多态性条带, 而在珍珠豆型花生中扩增条带完全相同, PMc297也有相似的扩增结果。由于在多粒型花生资源中检测出的遗传多样性最丰富, 研究结果支持西班牙专家Krapovickas 1994年公布的花生栽培种分类系统。总之在花生4大类型内资源中能检测出丰富的SSR分子标记, 开发出更多的SSR分子标记将能充分揭示花生分子水平的变异, 从而使花生遗传图谱构建、分子标记辅助育种成为可能。

关键词 [花生; SSR; 遗传多样性; 区别指数](#)

分类号

Genetic Diversity in Cultivated Groundnut Based on SSR Markers

Ronghua Tang^{1, 2}, Guoqing Gao², Liangqiong He¹, Zhuqiang Han¹, Shihua Shan³, Ruichun Zhong¹, Cuiqiu Zhou¹, Jing Jiang¹, Yangrui Li, Weijian Zhuang^{4, ①}

1. Cash Crops Research Institute, Guangxi Academy of Agricultural Sciences, Nanning 530007, China;
2. Guangxi Crop Genetic Improvement and Biotechnology Lab, Nanning 530007, China;
3. Shangdong Peanut Research Institute, Qingdao 266100, China;
4. Department of Crop Science, Fujian Agriculture and Forestry University, Fuzhou 350002, China

Abstract

<P> Peanut (*Arachis hypogaea* L.) is an important source crop for edible oil and protein. It is important to identify the genetic diversity of peanut genetic resources for cultivar development and evaluation of peanut accessions. Thirty-four SSR markers were used to assess the genetic variation of four sets of twenty-four accessions each from the four botanical varieties of the cultivated peanut. Among the tested accessions, ten to sixteen pairs of SSR primers showed polymorphisms. The maximum differentiation index, which was defined as the degree of genetic differentiation, was as high as 0.992 in the tested accessions. Each accession could be discriminated by a specific set of polymorphic SSR primers, and the intra-variety genetic distance was determined among accessions, with an average of 0.59 in var. *fastigiata*, 0.46 in var. *hypogaea*, 0.38 in var. *vulgaris*, and 0.17 in var. *hirsuta*. Dendro-grams based on genetic distances were constructed for the four botanical varieties, which revealed the

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existence of different clusters. It was concluded that there was abundant intra-variety SSR polymorphism, and with more and more SSR markers being developed, the intrinsic genetic diversity would be detected and the development of genetic map and marker-assisted selection for cultivated peanut would be feasible. </P>

Key words [Arachis hypogaea](#) [SSR](#) [genetic diversity](#) [differentiation index](#)

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通讯作者 唐荣华 ronghua@163.com