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小扁豆种质资源SSR标记遗传多样性及群体结构分析

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摘要:

从145对SSR引物中筛选到14对多态性引物,对选取国家种质库的440份小扁豆种质资源进行SSR标记遗传多样性 分析, 共检测出87个等位变异, 平均每个SSR位点6.2143个; 平均Shannon-Weaver指数(I)为1.1869。16个不 同地理来源群体间表现出显著的遗传多样性差异,国外群体的遗传多样性水平(0.9837)远高于国内群体(0.3485)。 PCA、UPGMA法聚类分析和Structure群体结构分析结果相互间完全吻合。440份参试材料从遗传结构上可划分为8 ▶加入引用管理器 个组群,揭示国外群体遗传分化大,群体间的亲缘关系较远,国内群体与之相反。研究结果显示,山西、宁夏和甘 肃省是我国小扁豆资源遗传多样性最丰富、遗传关系较复杂的地区,应对该区域小扁豆资源进一步搜集、保护和研 究。同时,应继续加强小扁豆资源的国外引种与交流,做进一步系统研究和开发利用。

关键词: 小扁豆 种质资源 SSR标记 遗传多样性 群体结构

Analysis of Genetic Diversity and Population Structure in Lentil (Lens culinaris Medik.) Germplasm by SSR Markers

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Abstract:

A total of 440 lentil accessions, randomly chosen from the National Gene Bank, were employed in the experiment. Fourteen polymorphic SSR markers was screened from a total of 145 SSR primer pairs, detected a total of 87 allelic variations. High level of diversity has been detected, with an average allele number of 6.2143 and an average Shannon-Weaver index (I) of 1.1869 by 14 SSR primer pairs. The results indicated significant differentiations among the 16 groups of lentil resources in genetic diversity from diversed geographic origins. The genetic diversity within alien accessions was obviously higher than that within Chinese resources. Population structure within the subcollection of 440 individuals was defined, and 8 clusters were identified based on SSR markers by using Structure 2.2 software. The results of PCA, UPGMA cluster and population structure analyses revealed that the genetic structure was multiplex; the genetic distance was broader among foreign populations than that among Chinese populations. More survey and collecting trips, conservation and study should be made for the lentil genetic resources in Shanxi, Ningxia, and Gansu provinces, where the highest genetic diversity level existed in China. Furthermore, international exchange and introduction of lentil genetic resources should be enhanced, for more systematic studies and exploitation.

Keywords: Lentil Genetic resources SSR markers Genetic diversity Population structure

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