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用 ISSR 标记分析红麻种质资源的遗传多样性

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摘 要:为明确红麻种质资源的遗传多样性和亲缘关系,以 20 个国家的 32 份红麻(*Hibiscus cannabinus* L.)种质资源为材料,从 90 个 ISSR 引物中筛选出 22 个多态性引物对供试材料进行 PCR 扩增,最终选用条带最清晰、多态性明显的 13 个引物的扩增数据进行统计分析。结果表明:(1)13 条 ISSR 多态性引物共扩增出谱带总数 59 条,多态性条带总数为 47 条,多态性条带比率达 79.66%,其遗传多样性较丰富;(2)在切割线 L_1 取值为 0.73 时,可将供试材料分为一个由 22 份栽培品种构成的 L_{1-1} 大类群,以及由 8 份野生材料和 2 份古老地方品种构成的 3 个独立的个类和 3 个不同小类群。(3)当切割线 L_2 取值为 0.77 时,又可将第 1 个大类群 L_{1-1} 中 22 份栽培品种根据其亲缘关系,重新划分为 I_1、I_2、I_3、I_4 4 个不同的亚类群,各亚类群表现出明显的地域性特点。(4)聚类结果显示,红麻多数栽培品种之间的遗传差异较小,亲缘关系较近,其遗传多样性比野生材料明显狭窄。

关键词:红麻;种质资源;ISSR;遗传多样性;聚类分析

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The Analysis of Genetic Diversity of Kenaf Germplasm Based on Inter-simple Sequence Repeats

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Abstract: In order to probe the relationship and genetic diversity of the kenaf (*Hibiscus cannabinus*) germplasm, 32 kenaf varieties from 20 countries were studied, and 22 primers screened from 90 ISSR primers were used to amplify the DNA, from which 13 primers with polymorphic and clear bands were analysized. The results were as follows: (1) 59 bands were amplified based on 13 primers, among which 47 bands were polymorphic, and the percentage of polymorphic bands was 79.66%, which indicated the genetic diversity was correspondingly rich. (2) The 32 kenaf accessions could be classified into two groups at the level of D = 0.73; one large group named L_{1-1} constituted of 22 cultivars, there antique kinds and there subgroup including 8 wild varieties and 2 antique local species. (3) The 22 cultivars in the first group L_{1-1} could be divided into 4 subclasses (I_1, I_2, I_3, I_4) at the level of D = 0.77, which had visible regional character. (4) The cluster result indicated that most of the cultivars had small genetic diversity and relationship. It was obvious that the basis of the inheritance of kenaf cultivars were comparatively narrower than the wild species.

Key words: Kenaf (*Hibiscus cannabinus* L.); Germplasm; ISSR; Genetic diversity; Cluster analysis

红麻(*Hibiscus cannabinus* L.,kenaf)为锦葵科木槿属一年生韧皮纤维作物,是麻纺与造纸的优质原料,具有生长速度快、丰产性高、适应性广、抗逆性强等特性。红麻公认起源于非洲[1],1908 年引入我国种植,已有百年的历史。1980 年以来,我国红麻种质资源搜集、保存、鉴定和育种利用研究工作取得了较大的进展[1],使我国红麻育种和单产居国际领先水平[2]。随着生物技术的发展,进一步深化红麻种质资源遗传多样性及有利基因的发掘与利用研究,是育种取得突破性进展的关键。我国学者程舟[3,4]、郭安平[5,6]、祁建民[7-9]、陶爱芬[10]等虽利用 RAPD、ISSR、AFLP 分子标记技术已作了一些初步的研究。但总体上,我国黄红麻类种质资源的遗传多样性及亲缘关系的分子标记研究仍比较滞后[2]。已

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