

农学—研究报告

利用ISSR标记分析海南岛五节芒的遗传多样性

吴安迪<sup>1</sup>, 黄小龙<sup>2,2</sup>, 黄东益<sup>3</sup>

- 1. 海南大学农学院
- 2.
- 3. 海南大学

摘要:

对7份来自海南不同地区的五节芒用ISSR标记分析, 采用NTSYS-pc2.10y软件得到相似性系数后, 用UPGMA法进行聚类分析。实验结果显示, 从42条ISSR引物中筛选出了6条合适的ISSR引物, 利用这6条引物对7份五节芒材料进行扩增, 一共扩增出107条带, 不同引物扩增条带数15~22条不等, 平均每条引物产生17.8条带, 其中104条为多态性条带, 占总条带数的97.2%。样品之间的相似系数(GS)在0.4673~0.8318之间, 平均值为0.6816; 遗传距离(GD)在0.1682~0.5327之间, 平均值为0.3184。研究结果表明海南岛的五节芒具有较高的遗传多样性水平, ISSR标记方法适用于五节芒的遗传多样性分析。

关键词: 简单重复序列间区

Genetic Diversity Analysis of Miscanthus floridulus by Using ISSR Marker

Abstract:

7 accessions *Miscanthus floridulus* from different area in Hainan were analyzed by using ISSR markers. The software NTSYS-pc2.10y was used to compute similarity coefficient, and then UPGMA was used for cluster analysis. The results showed that 6 primers were screened from the 42 ISSR primers, and 7 accessions *M. floridulus* were amplified by using the 6 primers. A total of 107 bands were obtained. The number of fragments produced by a primer ranged from 15 to 22, with an average of 17.8. 104 bands were polymorphic, account for 97.2% in all bands. The genetic similarity (GS) was from 0.4673 to 0.8318, with the average of 0.6816. The genetic distance (GD) was from 0.1682 to 0.5327, with the average of 0.3184. The results showed that *M. floridulus* in Hainan Island had a high-level genetic diversity, and the ISSR markers are useful to analyze genetic diversity of *M. floridulus*.

Keywords: ISSR

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通讯作者: 黄东益

作者简介:

作者Email: hdongyi@126.com

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