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研究报告

鸭茅种质资源遗传多样性的ISSR研究

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摘要

采用ISSR分子标记技术对来自国内及亚洲、欧洲、美洲9个国家共50份鸭茅品种(系)进行遗传多样性研究。12个引物共扩增出多态性带101条，平均每个引物扩增的多态带数为8.41条，多态性条带比率(PPB)为86.3%，材料间遗传相似系数范围在0.6116到0.9290间。这说明鸭茅具有较丰富的遗传多样性。根据研究结果进行了聚类分析和主成分分析，可将50份鸭茅材料分为5大类，来自于相同洲的鸭茅能聚在一类，中国和美国的鸭茅品种(系)能分别聚在同一类，呈现出一定的地域性分布规律。并对鸭茅种质资源的收集保存提出建议。

关键词 鸭茅 种质资源 ISSR 遗传多样性

分类号 Q943

Genetic Diversity of *Dactylis glomerata* Germplasm Resources De-tected by Inter-simple Sequence Repeats (ISSRs) Molecular Markers

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Abstract

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<P>Inter-simple Sequence Repeat (ISSR) molecular markers were used to detect the
genetic diversity among 50 materials of <EM>Dactylis glomerata</EM> collected from China
and other countries. Twelve primers produced 101 polymorphic bands, averaged
8.41 bands each primer pair. The average percentage of polymorpgic bands was
86.3.8%, and the range of GS (define) was 0.6116—0.9290, indicating a rich genetic diversity of<EM> D. glomerata</EM>. Based on the cluster
and principal component analyses on the genetic characteristics,<EM> D. glomerata</EM>
could be divided into 5 groups according to the nearest phylogenetic
relationship. In most cases, accessions from the same continent were classified
into the same group, the accessions from China and the United States belong
to the different groups, respectively, indicating the geographical distribution of
genetic diversity of <EM>D. glomerata</EM>. The present paper also discussed collection
and conservation of germplasm resources in <EM>D. glomerata</EM>.</P>

Key words Dactylis glomerata germplasm resources ISSR genetic diversity

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