

研究报告

野生鸭茅种质遗传多样性的AFLP分析

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摘要 本文应用扩增片段长度多态性(AFLP)技术,从64个引物对中筛选出9个,分别对37份鸭茅种质进行扩增,共得到400条清晰条带。其中多态性带336条,平均多态位点水平为84.0%,表现出较高的多态性。利用NTSYS-pc软件计算种质间的遗传距离,变化范围为0.0692~0.4214。用UPGMA方法进行聚类分析,在遗传相似系数为0.81水平上37份鸭茅种质可分为8个类群。用EIGEN方法进行主坐标分析,建立种质间相互关系的二维图。各种质在二维图中的分布与UPGMA聚类基本吻合。从分子水平分析,鸭茅遗传变异与染色体倍性和地理分布密切相关。

关键词

[鸭茅](#); [种质](#); [遗传多样性](#); [AFLP](#)

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AFLP Analysis on Genetic Diversities of Natural *Dactylis glomerata* L. Germplasm Resources

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Abstract

37 accessions of natural *Dactylis glomerata* L. were collected and applied for genetic diversity assessment by the method of Amplified Fragment Length Polymorphism (AFLP). 9 primer combinations were selected from 64 preparations and then applied to analyze these accessions; and a total of 400 DNA fragments were amplified, among which 336 were polymorphic averagely rating 84.0%. Genetic distance from 0.0692~0.4214 among the accessions was calculated by the NTSYS-pc software. The dendrogram was constructed by UPGMA on the basis of genetic distance matrix. Meanwhile, 9 clusters were defined at the genetic similarity of 0.81. A two-dimensional PCO plot was also produced by EIGEN so as to reveal similar relationships among accessions, and it presented the same distribution pattern as that from the cluster analysis. These results demonstrated that genetic variation in *D. glomerata* L. germplasm is closely correlated with their karyotype and geographical distributions.

Key words

[Dactylis glomerata L.](#) [AFLP](#) [germplasm resources](#) [genetic diversity](#)

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