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研究报告

中国茶树初选核心种质遗传多样性的RAPD分析

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摘要 以中国茶树初选核心种质中的69份种质为实验材料，采用改良的SDS法提取它们的基因组DNA，并运用优化的RAPD 分析体系对基因组DNA进行分子标记遗传差异研究。从50个随机引物中筛选出32个扩增效果好的引物,对全部试验材料进行了RAPD扩增共得到348条有效带,其中多态性带为328条(占94.3%)，它们之间的遗传距离为0.223～0.723。研究结果表明中国茶树初选核心种质的遗传结构、遗传多样性和遗传距离基本上能较好的代表中国的茶树种质资源。同时，指出结合形态标记和DNA分子标记是构建茶树核心种质较好的选择。

关键词 茶树；核心种质；多样性指数；RAPD

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RAPD Analysis on Genetic Diversity of the Preconcentrated Core Germplasms of Camellia Sinensis in China

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Abstract

The study was to evaluate the genetic diversity of 69 tea cultivars of the preconcentrated core germplasms of Camellia Sinensis in China by the random amplified polymorphic DNA(RAPD).Among 50 arbitrary primers, 32 primers could generate enough amplified bands for all the strains in this study. Among a total of 348 bands observed, 328(94.3%)bands were polymorphic in the 69 cultivars tested except additional 20 cultivars. Genetic distances between the cultivars varied from 0.223 to 0.723. The study indicated that the pre-concentrated core germplasms of Camellia Sinensis in China could well represent the whole collection in respect of genetic structure and genetic diversity and genetic distance. At the same time, it was the best option to establish core collection of Camellia Sinensis in China by combining morphological markers with DNA molecular markers.

Key words Camellia Sinensis；Core collection；Genetic diversity；RAPD

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