

论文

应用SRAP标记分析黑芝麻核心种质遗传多样性

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摘要:

利用SRAP分子标记技术对中国芝麻资源核心收集品中的黑芝麻种质进行遗传多样性分析。结果表明, 13对引物组合对100份黑芝麻核心种质共扩增出稳定清晰的条带182条, 其中多态性条带126条, 占69.2%, 每对引物组合的条带数和多态性带数分别为14.0个和9.7个; 供试材料间成对遗传相似系数介于0.469~0.986, 平均为0.726, 通过UPGMA法, 在遗传相似系数为0.68处可将供试材料聚为5个类群, 表明黑芝麻核心种质具有较丰富的遗传多样性, 聚类结果与地理分布没有明显的关系; 遗传多样性指数是南方黑芝麻核心种质(0.3557) > 中部种质(0.3415) > 北方种质(0.2986)。本研究结果较全面反映了中国保存的黑芝麻种质资源遗传多样性特点, 为我国黑芝麻资源进一步考察收集和引进, 以及优异黑芝麻基因资源挖掘和育种利用提供了理论依据。

关键词: 黑芝麻 核心种质 SRAP 遗传多样性

Genetic Diversity Analysis of Black Sesame(*Sesamum indicum* DC) Core Collection of China Using SRAP Markers

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Abstract:

China has a long history and rich germplasm resources for growing black sesame. Black sesame is well used because of its nutrition superior to black rice and black soybean. However, Research on black sesame is relatively less than that on other crops. In the paper, genetic diversity of black sesame core collection of China was analyzed using SRAP (sequence-related amplified polymorphism) markers. The results showed that 13 SRAP primer combinations were employed to evaluate the genetic diversity of 100 black sesame accessions, a total of 182 amplified fragments were detected and 126 of them were polymorphic, the polymorphism percentage was 69.2%, the number of amplified fragments and polymorphic fragments of each primer combination were 14.0 and 9.7, respectively. The 100 accessions were grouped into five clusters at genetic similarity of 0.68, indicating the genetic diversity of these accessions was abundant. As regards geographic regions, Shannon's information index of black sesame accessions in south China (0.3557) was the highest, the followings were that in central regions of China (0.3415) and north China (0.2986). The characteristics of genetic diversity of black sesame core collection of China were fully revealed in this study, which provided the theoretical foundations for further exploring, collecting and introducing black sesame germplasm as well as mining and utilizing excellent black sesame germplasm in the future.

Keywords: Black sesame Core collection SRAP Genetic diversity

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