研究论文

RAPD和AFLP标记分析中国马铃薯主要品种的遗传多样性

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摘要 采用RAPD 和AFLP两种方法分析71份中国各地马铃薯主要品种,均可将其完全区分,并可对其进行分子鉴定;证明中国马铃薯主要品种遗传组成上差异小,遗传多样性差。由于标记方法的原理差异和栽培马铃薯遗传组成复杂性,用2种方法分类的结果有所差异。AFLP标记检测获得的Shannon-weaver指数和Simpson指数均高于RAPD标记检测的结果,AFLP标记检测多态性的能力远高于RAPD标记。AFLP标记平均每个引物组合检测到100.1个位点,其中54.9条为多态性位点,而RAPD标记的相应数据分别为12.5和9.8个。不同的标记方法在马铃薯遗传多样性研究中存在差异,聚类结果从分子水平反映了中国现有主要马铃薯品种遗传基础的狭窄。 关键词 <u>马铃薯</u> RAPD AFLP 遗传多样性 分类号 S532

Genetic Diversity Analysis of Chinese Main Potato Cultivars by RAPD and AFLP Makers

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Abstract Cultivated Potato(*Solanum tuberosum subsp. Tuberosum*) is planted widely in China. The origin of germplasms is varying complicated and disordered at present. Many researches have paid their attention to potato genetic diversity by s hape and biochemistry analysis, while studies on molecular genetic diversity were few in China. Using RAPD and AFLP methods, the genetic diversity of 71 Chinese main potato cultivars was analyzed. Comparing with the amplified results of RAPD and AFLP markers, each primer combination of AFLP identified 100.1 loci averagely, among which 54.9 were poly morphic(Table 3), while each RAPD primer only detected 12.5 loci, of which 9.8 were polymorphic(Table 2). The Shanno n-weaver index and Simpson index from AFLP were all higher than those from RAPD indicating the genetic diversity identified by AFLP was higher than that by RAPD(Table 4). There were differences between the two methods in genetic diversities, due to different principles of AFLP and RAPD, and some cultivars were clustered into different groups. However the re sults showed that both of the two methods could identify the 71 potato cultivars, which were clustered into 3 to 4 group s(Fig.1, Fig.2). Analysis of average genetic distance by AFLP and RAPD suggested that the kinship is close among 71 Chine ese main potato cultivars, which indicate that the genetic basis of potato germplasm in China is narrow. The relationships of cultivars showed by the results were identical to the family tree basically. Due to the simple technique and low cost, RAP D is more suitable to distinguish cultivars and seed potato purity. In genetic diversity analysis, more methods should be use d to conform one another to draw correct conclutions.

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