

农学—研究报告

基于EST-SSR的木薯分子标记遗传连锁图谱的构建

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摘要:

此实验以木薯推广品种‘KU50’为母本,‘SC124’为父本通过杂交得到包含240个单株的F1分离群体,利用300对EST-SSR引物,20对SSR和20对SRAP引物组合对亲本和部分群体株系进行多态性分子标记筛选,共获得具有多态性的引物110对。在此基础上,利用这110对多态性引物对该F1群体进行分子标记的多态性分析,共获得269个多态性标记。利用JoinMap 3.0软件对这269个多态性标记进行分组和遗传图谱构建,最后获得了一张包含140个标记的木薯分子遗传连锁图谱,其中EST-SSR标记111个,SSR标记22个,SRAP标记7个;共21个连锁群,其中连锁群1和3(LG1、LG3)上的标记位点最多(15个),LG21标记位点最少(2个)。此遗传连锁图谱的总长度为1314.775 cM,单个连锁群最长为132.904 cM(LG3),最短为0.431 cM(LG19),标记间平均长度9.391 cM。

关键词: 遗传连锁图谱

Based on EST-SSR Construct the Molecular Genetic Linkage Map of Cassava

Abstract:

In this experiment, segregating from an F1 contains 240 separate population of an intraspecific crossed between ‘Ku50’, as female parent, and ‘SC124’ as male parent. We obtained 269 polymorphic markers when used 110 polymorphic primer pairs with the F1 populations, and basing on these 269 polymorphic markers, a genetic linkage map that consisting of 140 molecular markers, including 111 expressed sequence tag (EST)-SSRs, twenty-two simple sequence repeats (SSRs) and 7 sequence-related amplified polymorphisms (SRAPs) was constructed by using Joinmap3.0 software, The genetic map contained 21 linkage groups, and LG1 and LG3 had the most markers, holding 15 markers, however the least linkage group LG21 only had two markers. The genetic map spanned a 1341.775 cM genetic distance, with the longest linkage group LG3 was 132.904 cM, as well as the smallest LG19 was 0.431 cM, and the average marker interval was 9.391 cM.

Keywords: genetic linkage map

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