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离子束介导甘蓝全DNA转化拟南芥菜的分子分析

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30 keV的Ar+离子束在1.5×1017 ions/cm2的注入剂量下介导外源甘蓝全DNA导入模式植物拟南芥菜，在94株转化当代植株中，有6株表型产生变异。以其中的一株(T-5)作为研究对象，用80条10碱基随机引物对该株和其子代变异株基因组作随机扩增的多态性DNA分析，引物S176 在T-5和其变异子代T-5-2中扩增出了相同分子量的变异新条带T-5S176-620。T-5S176-620的碱基序列和拟南芥菜基因组序列进行同源比对，结果表明该片段不属于拟南芥菜基因组，Southern杂交实验证明该片段来自供体甘蓝基因组。但是，根据T-5S176-620序列设计的引物不能从甘蓝基因组中扩增出预期长度的DNA片段，结合离子束介导外源全DNA转化的特点和过程，探讨了其中可能的机制。

The total DNA of cabbage was transferred into A. thaliana mediated by Ar+ ion beam with the energy of 30 keV and influence of 1.5×1017 ions/cm2. Among the 94 transferred plants, there were 6 phenotypic variation plants. One of them, marked as T-5, was studied. The genomes of T-5 and its offspring were analyzed by RAPD-PCR with 80 10-base random primers. The result showed that by contrast to the control, a new band, T-5S176-620, was amplified from T-5 and its offspring T-5-2 with random primer S176. Its sequence was aligned with genome of A. thaliana by means of program of homologous alignment. A Southern blot to cabbage genome with T-5S176-620 as probe was carried out. Both of their results indicated that T-5S176-620 was not in A. thaliana but from cabbage. However, the desired length DNA segments could not be amplified from cabbage genome with primers designed with reference to T-5S176-620. In terms of the specialties of total DNA transformation mediated by keV ion beam, the possible reason was analyzed.

关键词

低能Ar+离子介导外源全DNA转化(Total DNA transformation mediated by keV Ar+ ion beam); 拟南芥菜(Arabidopsis thaliana); 随机扩增的多态性DNA(Randomly amplified polymorphic DNA); 同源比对