VARIASI SEKUENS DNA YANG DIAMPLIFIKASI MENGGUNAKAN PRIMER atpBrbcL PADA BEBERAPA KULTIVAR KACANG TANAH

VARIASI SEKUENS DNA YANG DIAMPLIFIKASI MENGGUNAKAN PRIMER atpB-rbcL PADA BEBERAPA KULTIVAR KACANG TANAH
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Peanut is one of food crops commonly consumed in Indonesia. This species comprises several cultivars such as Kancil, Bison, Jerapah, Talam, and Tuban, each of which has its individual advantages and disadvantages. The vast variation among peanut cultivars leads to the need of study on genetic diversity and relationship among them using particular molecular marker. This study aims to see whether variation on DNA sequences among some peanut cultivars based on the amplicon sequences. The method involves some sequential steps, i.e. genomic DNA isolation using CTAB protocol, amplification of DNA sequences were edited manually using Bioedit version 7.0.4.1. Sequence alignment was performed using ClustalW, which is also implemented in Bioedit version 7.0.4.1. Arlequin 2.0 was used to calculate nucleotide diversity p. Phylogenetic analysis was performed using Maximum Parsimony in MEGA 5.0. The results showed that considerably high variation in DNA sequences of some peanut cultivars amplified with atpB-rbcL primers are observed. On the other hands, very close genetic relationship among cultivars is found.
Fakultas Biologi Universitas Jenderal Soedirman
2017-03-01
2017
DOI: 10.20884/1.sb.2017.4.1.377
Scripta Biologica
Vol 4, No 1 (2017)
11–14
https://journal.bio.unsoed.ac.id/index.php/scribio/article/view/377/pdf