The Identification of Nucleotide Sequence Polymorphisms and Gene Resources for Cinnamomum osmophloeum Kaneh. Inferred from ITS2 and Chloroplast DNA Loci.

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ABSTRACT

The present study attempts to identify the gene resources of Cinnamomum osmophloeum Kaneh. (CO) by analyzing the nucleotide sequences of the partial non-coding internal transcribed spacer 2 (pITS2) of the ribosomal DNA and the trnL-trnF chloroplast genome. Seventy-three geographical strains of CO, preserved in the Lien Hua-Chin Research Center of the Forestry Research Institute and the Hua-Lin Forestry Center of Chinese Culture University, were collected and analyzed by PCR amplification and DNA sequencing to study the genetic diversity and nucleotide sequence polymorphisms of the tested specimens. Our results allowed us to accurately identify the lineage of CO and to conclude that the strains belonging to the Lien Hua-Chin Research Center had much higher genetic diversity than those preserved in the Hua-Lin Forestry Center. Multiple sequence alignments demonstrated that the variability of the nucleotide sequence polymorphisms for the pITS2 region was higher than those of the trnL intron and trnL-trnF IGS regions among the 73 tested specimens of CO. Cluster analyses, using the neighbor-joining and maximum parsimony methods, for the 73 tested geographical strains of CO and species of Cinnamomum registered in the GenBank and EMBL databases were performed to demonstrate the genus and species distribution of the samples. Here, we describe the use of pITS2 polymorphisms as a genetic classifier and report the establishment of a DNA sequence database for CO gene resource identification. The sequence database described in this study can be used to identify CO specimens at the inter- or intra-species level using pITS2 DNA sequences, which illustrates its value in gene resource identification.

Keywords: Cinnamomum osmophloeum Kaneh.; gene resource; SNP; Molecular Systematics

REFERENCES


