Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Genetic variation of *Kaempferia* (Zingiberaceae) in Thailand based on chloroplast DNA (*psbA-trnH* and *petA-psbJ*) sequences

J. Techaprasan[1], S. Klinbunga[1], C. Ngamriabsakul[2] and T. Jenjittikul[3]

[1]National Center for Genetic Engineering and Biotechnology, Klong Luang, Pathum Thani, Thailand
[2]School of Science, Walailak University, Nakhon Si Thammarat, Thailand
[3]Department of Plant Science, Faculty of Science, Mahidol University, Bangkok, Thailand

Corresponding author: J. Techaprasan
E-mail: jiranan@biotec.or.th

Genet. Mol. Res. 9 (4): 1957-1973 (2010)
Received May 9, 2010
Accepted July 18, 2010
Published October 5, 2010
DOI 10.4238/vol9-4gmr873

ABSTRACT. Genetic variation and species authentication of 71 *Kaempferia* accessions (representing 15 recognized, six new, and four unidentified species) found indigenously in Thailand were examined by determining chloroplast *psbA-trnH* and partial *petA-psbJ* spacer sequences. Ten closely related species (*Boesenbergia rotunda*, *Gagnepainia godefroyi*, *G. thoreliana*, *Globba substrigosa*, *Smithatris myanmarensis*, *S. supraneanae*, *Scaphochlamys biloba*, *S. minutiflora*, *S. rubescens*, and *Stahlianthus* sp) were also included. After sequence alignments, 1010 and 865 bp in length were obtained for the respective chloroplast DNA sequences. Intraspecific sequence variation was not observed in *Kaempferia candida*, *K. angustifolia*, *K. laotica*, *K. galanga*, *K. pardi* sp nov., *K. bambusetorum* sp nov., *K. albomaculata* sp nov., *K. minuta* sp nov., *Kaempferia* sp nov. 1, and *G. thoreliana*, for which more than one specimen was available. In contrast, intraspecific sequence polymorphisms were observed in various populations of *K. fallax*, *K. filifolia*, *K. elegans*, *K. pulchra*, *K. rotunda*, *K. marginata*, *K. parviflora*, *K. larsenii*, *K. roscoeana*, *K. siamensis*, and *G. godefroyi*.

A strict consensus tree based on combined *psbA-trnH* and partial *petA-psbJ* sequences revealed four major groups of *Kaempferia* species. We suggest that the genus *Kaempferia* is a polyphyletic group, as *K. candida* was distantly related and did not group with other *Kaempferia* species. Polymorphic sites and indels of *psbA-trnH* and *petA-psbJ* can be used as DNA barcodes for species diagnosis of most *Kaempferia* and outgroup species. Nuclear DNA polymorphism should be examined to determine if there has been interspecific hybridization and chloroplast DNA introgression in these taxa.

Key words: *Kaempferia*; Chloroplast DNA; *psbA-trnH*; *petA-psbJ*;
DNA barcode
