

**DEVELOPMENT OF DNA BARCODING FOR
Alpinia galanga (L.) Sw. (MAHA ARATTA) AND RELATED
SPECIES OF FAMILY ZINGIBERACEAE**

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ABSTRACT

Medicinal plants of Family Zingiberaceae; *Alpinia galanga*, *Alpinia calcarata*, *Alpinia malaccensis*, *Alpinia purpurata*, *Hedychium coronarium*, *Hedychium coccineum* are highly used as herbal medicines and are highly potential for the adulteration due to rareness and misidentification of the rhizomes. The authentication of these species is difficult by morphological, organoleptic, or any microscopic characteristics. DNA barcoding provides a fast and effective detection tool for identification of any plants part. The investigation was carried out to develop DNA Barcode for six medicinal plants of Family Zingiberaceae. DNA was extracted and amplified by using universal primers for four genomic regions; ITS1, ITS2, matK and rbcL. PCR protocols were optimized by changing concentrations of template DNA, dNTPs, Mg^{2+} , Taq DNA polymerase, and primers and primer annealing temperatures. DNA was sequenced by Sanger method. High quality unique sequences (e value 0) of short DNA fragments were used to construct DNA Barcodes and Phylogenetic trees. Optimized PCR protocols amplified genomic regions and produced clear and specific short DNA fragments. DNA sequence data showed clean peaks. Unique DNA Barcodes were developed for six medicinal plants. Phylogenetic trees revealed the higher discrimination power at individual genomic regions and all together. These six medicinal plants can be categorized into six species uniquely by this DNA barcoding as a powerful molecular taxonomic technique.

Key Words: Adulteration, DNA Barcoding, DNA extraction, Family Zingiberaceae, PCR optimization, Phylogenetic tree