

Thesis Title	Identification of Tea Varieties Collected from Northern of Thailand Using DNA Barcodes
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ABSTRACT

Tea plant (*Camellia sinensis* (L.) O. Kuntze) is an economically important crop in Thailand. Their leaves are frequently used as the primary ingredients in a variety of tea preparation. There are no reports on barcode analysis of wild tea plants in Thailand. Thus, the aimed of this study was to create a DNA barcode of 135 wild tea plants using the *matK*, and *psbA-trnH* genes. Both DNA barcodes were 100% successfully amplified and sequenced. The *matK* gene showed a good result in identification efficiency, accurately demonstrating 100% identity to the expected species, *C. sinensis* in 64 tea plants. Some tea plants displayed 100% identification with the other *Camellia* species, whereas the remaining tea plants displayed 99.10% to 99.89% identity with *C. sinensis*. In *psbA-trnH* just only one tea plant was detected 100% identity to *C. sinensis* and the remaining showed 97.24% - 99.80%. Based on the blast results, all of the tea plants in this study were identified as *C. sinensis*. According to sequence alignment, *matK* detected 12 SNPs in 72 tea plants, which is more than *psbA-trnH* did (7 SNPS in 72 tea plants). The *psbA-trnH* showed the highest genetic distance (0.0131), which might be caused by indels. Phylogenetic trees clearly separated all wild tea plants into numerous groups. This demonstrated that tea plant with the same SNP position and

pattern of SNPs are likely to be classified into the same cluster, though this was not entirely consistent with the morphological tree. As a results, DNA barcoding is a practical technique for identifying plant species, and the *matK* gene was thought to be a barcode for wild tea plants.

Keywords: *C. sinensis*, DNA Barcoding, *matK*, *psbA-trnH*, Tea Plant

