

# IDENTIFICATION OF DIFFERENT *JASMINUM* SPECIES BY USING COMBINATION OF *matK* AND *rbcL* AS THE DNA BARCODE

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## ABSTRACT

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Jasmines, is the largest genus in the family Oleaceae. It has potential economic value, which makes identification of valuable species and genetic variants important. This leads to the research on *Jasmine* species identification with the use of DNA barcode. DNA barcode is the short DNA sequences based on the genes of plants, and is distinct in every single species of the plant. *rbcL* and *matK* are the DNA barcodes used in this research to identify and classify *Jasmine multiflorum*, *Jasmine nitidum*, *Jasmine sambac* and *Jasmine angulare*. An organic based method which involves the use of Edward buffer was applied for the DNA isolation of different types of Jasmine. The quantitative result of the extracted DNA from all plant samples was not satisfactory. However, the qualitative result of genomic DNA and PCR products from all plant samples shown satisfactory results in which all can be amplified and gave intense bands in the gel electrophoresis. The *rbcL* and *matK* PCR products were sequenced, and compared with sequences on BOLD and GenBank. As a conclusion, *Jasmine sambac1* was identified at both the species and genus level with the maximum identity of 100%. However, in other sample *Jasmine multiflorum1*, *Jasmine multiflorum2*, *Jasmine nitidum*, *Jasmine sambac2* and *Jasmine angulare* species level identification was not consistent with the morphologically identified species.