

## Comparing *matK* and *rbcL* Sequences among *Jasminum sambac*, *Jasminum grandiflorum* and *Jasminum nitidum*

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### ABSTRACT

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DNA barcodes are used to assign samples of unknown origin to specific taxonomic groups i.e., short DNA sequences (600-800bp) of a standard segment for species identification. In my study, I used the *matK* and *rbcL* barcode sequences to identify the *Jasminum grandiflorum*, *Jasminum sambac* and *Jasminum nitidum*. In these species, Edwards's method was able to provide of sufficient quality and quantity of DNA for PCR. In my results, the *matK* gene showed ease of amplification compared to *rbcL* gene. The second trial of *matK* with diluted DNA samples show higher success rate. For species discrimination, the neighbor-joining tree was used to construct phylogenetic trees based on T92 model as it was the best fit sequence model based on *matK* and *rbcL* gene. Based on the *matK* gene, *J. grandiflorum* is more closely related to *J. sambac* (Distance= 0.010) then *J. nitidum* (Distance= 0.020); while based on the *rbcL* gene, *J. sambac* is more closely related to *J. nitidum* (Distance= 0.007) then *J. grandiflorum* (Distance= 0.018). Although the tree topology based on *matK* and *rbcL* genes were different, the individuals of the three species grouped together. Hence, *J. sambac*, *J. grandiflorum* and *J. nitidum* can be identified using *matK* and *rbcL* gene. Further research to identify and compare with other *Jasminum* species is needed.