Using Trnh-Psba and Matk to Identify Differences in the Nucleotide Sequences Between Hibiscus Variants

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ABSTRACT

Hibiscus is a flowering plant in the mallow family, Malvaceae. There are about 250 varieties of species found all over the world, growing in sub-tropical and tropical regions. Due to the vast availability of different species around the world, there are bound to be difficulties in distinguishing the *Hibiscus* varieties based on their morphologies alone. Thus, this study aims to use *trnH-psbA* and *matK*, as the DNA barcodes to identify and differentiate between four specific selected *Hibiscus* variants. These variants selected are *Hibiscus rosa-sinensis, Hibiscus taiwanensis* and two unknown but morphologically different *Hibiscus* variants. The Edward's method; with certain modifications, was used to extract the DNA from these plants. DNA was successfully extracted from all but two samples of *Hibiscus taiwanensis*. Then, the successfully extracted DNA was amplified using *trnH-psbA* and *matK* markers separately. All the samples were successfully amplified with *trnH-psbA* but not with *matK*. *matK* failed to amplify *Hibiscus taiwanensis* only. The sequences obtained were processed and analyzed using DNA baser, T-Coffee, Gblocks, BLAST and MEGA5. From the results obtained, it was shown that both markers could not conclusively be used to discriminate among the morphological variants used. *matK* at least showed that one of the unknown variants is not closely related to the others. Thus, alternative markers with higher evolution rates and better ability to discriminate amongst species should be used.