

DNA Barcoding Hibiscus Plant Species using RBCL Gene and TRNH – PSBA Intergenic Spacer Region

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ABSTRACT

Plants have enabled humans to advance by providing us with food, medicine and raw materials for producing goods. In order to gain those benefits from plants, we need to be able to accurately identify and differentiate those plants at a species level. DNA barcoding uses particular regions of the DNA to identify species, for plants *rbcL* and *matK* are the standard genes for barcoding. The objective of the thesis was to test the *rbcL* and *trnH-psbA* combination on *Hibiscus*, a genus of medicinal and culinary importance. Leaf samples were collected from *Hibiscus schizopetalus*, *Hibiscus esculentus* and *Hibiscus sabdariffa*. DNA was extracted from the leaf samples; *rbcL* and *trnH-psbA* were amplified via PCR. 9 samples were successfully amplified and sequenced. The results revealed *trnH-psbA* gave identification similar to morphological identification unlike, *rbcL* which is a relatively easier loci to successfully perform PCR on compared to *trnH-psbA*. Other DNA barcode combination should be tested on *Hibiscus* species.