Identification of *Uvaria* sp by barcoding coupled with high-resolution melting analysis (Bar-HRM)

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ABSTRACT. DNA barcoding, which was developed about a decade ago, relies on short, standardized regions of the genome to identify plant and animal species. This method can be used to not only identify known species but also to discover novel ones. Numerous sequences are stored in online databases worldwide. One of the ways to save cost and time (by omitting the sequencing step) in species identification is to use available barcode data to design optimized primers for further analysis, such as high-resolution melting analysis (HRM). This study aimed to determine the effectiveness of the hybrid method Bar-HRM (DNA barcoding combined with HRM) to identify species that share similar external morphological features, rather than conduct traditional taxonomic identification that
require major parts (leaf, flower, fruit) of the specimens. The specimens used for testing were those, which could not be identified at the species level and could either be *Uvaria longipes* or *Uvaria wrayias*, indicated by morphological identification. Primer pairs derived from chloroplast regions (*matK, psbA-trnH, rbcL, and trnL*) were used in the Bar-HRM. The results obtained from *psbA-trnH* primers were good enough to help in identifying the specimen while the rest were not. Bar-HRM analysis was proven to be a fast and cost-effective method for plant species identification.

**Key words:** Barcoding; High-resolution melting; Species identification; *Uvaria* sp; Chloroplast genes