Development of Species Level DNA Barcodes to Identify Cultivated Edible Mushrooms

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The majority of edible mushrooms belong to *Basidiomycetes* and these mushrooms have become more important in recent times for their medicinal and nutritional properties. For many years, species of this phylum have been mainly classified by their phenotypic traits, however, taxonomic identification based solely on morphological features can be misleading and unreliable. In contrast, DNA based identification provides a powerful and reliable method for taxonomic discrimination of fungi, it can be performed at any growth stages using parts of the fruit body, mono-and dikaryotic mycelia, or any other organic fungal. In the current study, two different molecular markers including Internal Transcribed Spacer (ITS) I and II and Intergenic Spacer (IGS) I were developed to identify the common cultivated edible mushroom species. Phylogenetic trees could clearly distinguish the analysed species by showing distinct clades. Species differentiations were re-confirmed by AMOVA analysis, nucleotide divergence, haplotyping and Pvalues. Moreover, the designed primers could be employed in phylogenetic studies of other *Basidiomycetes*. Polymorphism occurred throughout the regions of interest due to insertion-deletion and point mutations, and differentiated the analysed families as well as genera. This study proved that the two developed molecular markers can be used for taxonomic identification of the common cultivated edible mushrooms in *Basidiomycetes*.

Basidiomycetes, ITS, IGS, DNA Barcode, Taxonomic Identification

Introduction

Malaysia possesses a great diversity of edible mushrooms (Vikineswary et al., 2007) and a climate that is suitable for growing them throughout the year. Current research activities in Malaysia are particularly focused on discovering new wild mushroom varieties with nutritious potential and/or medical properties for commercial exploitation (Vikineswary et al., 2007). Though a variety of edible mushrooms can be found in Malaysia, almost all varieties cultivated are not native to Malaysia. Identification and introduction of new wild edible mushrooms and production of new high yield hybrids could improve the market, reduce the costs of cultivating, and increase the farmers' revenue. However, in Malaysia, there has been limited research on the identification and phylogenetic relationships of edible *Basidiomycetes* using molecular techniques.

For many years, *Basidiomycetes* species have been mainly classified by their common phenotypic traits, including fruit body shape and size, days to maturation, yield, and body colour patterns (Gonzalez and