

# BOTTLENECKS IN DNA BARCODING OF FUNGI

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## ABSTRACT

The aim of this short review is to discuss the current status of marker selection in DNA barcoding of fungi and controversies which restrict the universal standardization of single marker. Identification of fungi at the DNA level is known as DNA barcoding. This leads to shifting of the fungi identification from phenotypic to molecular taxonomy. Besides that, the bottleneck is known as part of the whole process in a chain. Hence, the bottleneck is responsible for the capacity reduction of the whole process due to its restricted potential. The mitochondrial gene cytochrome c oxidase I (COI) is a typical DNA barcode marker that is mostly used for animals. However, it is not suitable for identification of fungi due to the introns hurdle and insufficient determination. Thus, the usage of COI in other taxa is not possible which averts its universal application. The DNA sequences derived from internal transcribed spacer (ITS) region has been accepted as the best marker for the fungal barcode. Although ITS sequence has been an utmost tool for identifying fungi, the establishment of an elevated standard sequence database is also vital for creating a network.

**Keywords:** Phylogenetic analysis; mitochondrial gene cytochrome c oxidase I (COI); Internal Transcribed Spacer (ITS); Mushroom.

## INTRODUCTION

DNA barcoding allows rapid and easy identification of species using short and standardised nucleotide sequences [1,2]. This is particularly useful for cryptic group organisms such as bacteria and fungi when the universal genomic region in target lineages have been

employed [3]. The mitochondrial cytochrome oxidase I (COI) locus appears to be the satisfied region for most of the taxonomic group [4]. However, COI is not appropriate to be used for fungal identification. Besides, ITS is adopted as the primary DNA barcode marker for fungi even though limited studies have been conducted on this region [5,6,7]. At the same time, there is a