

An Overview of the DNA Barcoding of Plants

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ABSTRACT

DNA barcoding makes use of nucleotide sequence variations in small, agreed upon and standardized regions from nuclear and/or cytoplasmic genome(s) to provide unique identification tags (DNA barcodes) to species. DNA barcodes could be from coding or non-coding regions of either of the genome. The concept was proposed in 2003, on the basis of successful use of a 658 base pair long region in mitochondrial cytochrome c oxidase 1 gene (*COI*), towards its 5' end for the discrimination of 200 closely allied lepidopteran species. After extending this successfully to other animals, this region was projected as the universal barcode for all eukaryotes. However, this locus was not found to be suitable for plants, except a few macroalgae due to low nucleotide substitution rate in their mitochondrial genome. Therefore, initial focus in the DNA barcoding of plants was to identify locus/loci which could provide a suitable barcode for plants akin to *COI* for animals. The investigations conducted since 2005, when the first substantial paper on DNA barcoding of plants appeared, have led to the conclusion that no single locus whether from the chloroplast or nuclear genome could provide a universal barcode for plants. Even among the different combinations of loci proposed and tested as possible barcode, none provides 100 % species identification across the plant kingdom. The best option appears to be a three-locus barcode comprising *maturase K* (*matK*) and Rubisco Large Sub-unit (*rbcL*), both from the chloroplast genome, and Nuclear Ribosomal Internal Transcribed Spacer (nrITS). However, even the use of complete chloroplast genome has been proposed as a possible barcode. The present paper aims to introduce readers to the concept of DNA barcoding for species level identification and is an overview of the current state of DNA barcoding in plants and its possible and realized applications.

Key words: *COI*, DNA barcoding, ITS, *matK*, plants, *rbcL*, universal barcode

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