



**Biotica
Research
Today**
Vol 4:8
2022

606
608

Application of DNA Barcode for Cultivar Identification in Tuber Crops

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Open Access

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Keywords

Barcode, cpDNA, Species identification, Tuber crops

Article History

Received on: 23rd August 2022

Revised on: 26th August 2022

Accepted on: 27th August 2022

E-mail: bioticapublications@gmail.com

How to cite this article?

Jena *et al.*, 2022. Application of DNA Barcode for Cultivar Identification in Tuber Crops. *Biotica Research Today* 4(8):606-608.

Abstract

For precise species identification, DNA barcoding depends on sequence variation within a condensed and defined section of the genome known as a “barcode.” This strategy is based on the analysis of variation within a typical DNA barcode area, which is helpful in determining taxonomic relationships. The number of studies involving identification, taxonomic decisions and the discovery of cryptic species has grown rapidly. Recently, tuber crops have gained more popularity as when compared to other staples. They come in a variety of species and variants that have either developed naturally or as a result of human intervention. In order to properly characterise them and research their variety, which may ultimately result in the genetic development of these crops, it is imperative to utilise DNA barcodes to identify them.

Introduction

According to the studies conducted over year, there are around 8.7 million species of plants and animals in existence. However, only around 1.2 million species have been identified and described so far, most of which are insects. Without any proper and reliable identification tool it is very tough for any biologist and taxonomist to discriminate and identify different living species. Identification of organisms has recently gained more importance taking in account the species conservation that are in threatened position because of the changing global condition and rapid loss of natural habitat (Fernandez *et al.*, 2021). As a modern and faster approach, DNA barcoding has emerged as an efficient technique for species identification or varieties identification as well as for documenting of bioresources. It is a molecular marker based method which uses highly conserved regions of nuclear, mitochondria or chloroplast DNA for identification at genetic level. The term DNA Barcode was first used by Paul Hebert of University of Guelph. It uses ~ 650 bp region of mitochondrial COI in animals and various conserved chloroplast regions (*rpoC*, *rpoB*, *matK*, *atpF-atpH*, *rbcl*, *psbK-psbI*, *trnH-psbA*) in plants (Kress and Erickson, 2008).

Table 1: List of different Barcode markers

Organism group	Barcode marker gene/ locus
Animals	COI, Cytb, 12S, 16S
Plants	matK, rbcl, psbA-trnH, ITS
Bacteria	COI, rpoB, 16S, cpn60, tuf, RIF, gnd
Fungi	ITS, TEF1 α , RPB1, RPB2, 18S, 28S
Protozoa	ITS, COI, rbcl, 18S, 28S, 23S

Application of DNA Barcoding

There are applications in areas, like testimony of the important and endangered ethno medicinal plant bioresource, correct species identification and decrypting of the indigenous as well as conventional knowledge of these plant usage and promoting them through bioprospecting (Figure 1). Recent advancements have led to the use of DNA barcoding in Plant variety and cultivar identification.

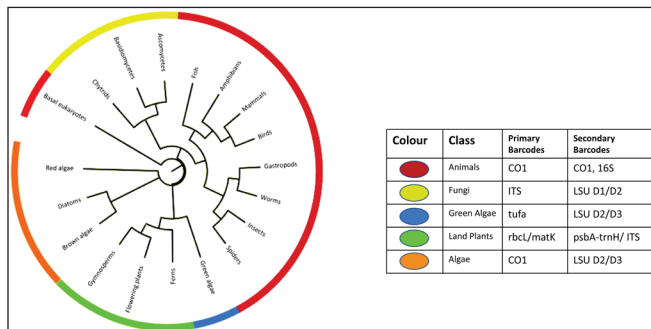


Figure 1: Primary and secondary barcodes for different organisms

Plant Variety and Cultivar Identification

Plant variety and cultivar identification is one of the most important aspects in agricultural systems. The large number of varieties or landraces among crop plants has made it difficult to identify and characterize varieties solely on the basis of morphological characters because they are non-stable and originate due to environmental and climatic conditions, and therefore phenotypic plasticity is an outcome of adaptation. To mitigate this, scientists have developed and employed molecular markers, statistical tests and software to identify and characterize the required plant cultivars or varieties for cultivation, breeding programs as well as for cultivar-right-protection (Figure 2). The establishment of genome and transcriptome sequencing projects for many crops has led to generation of a huge wealth of sequence

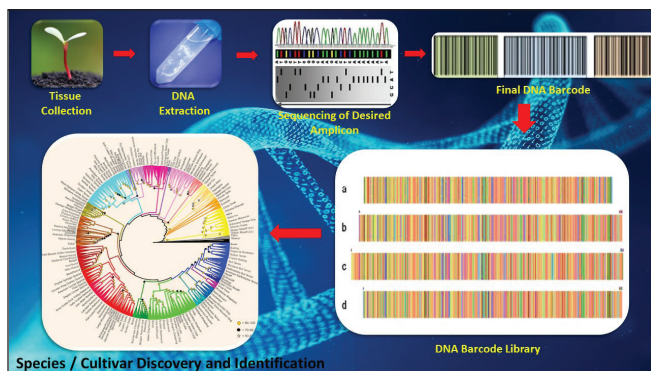


Figure 2: Steps followed for species or cultivar identification using DNA Barcode markers

information that could find much use in identification of plants and their varieties. On reviewing the current status of plant variety and cultivar identification, DNA barcoding has emerged as a most promising tools. A single SNP (Single nucleotide Polymorphism)/ InDels (Insertion or Deletion) can differ the two varieties in a conserved nucleotide environment.

Uses of DNA Barcode in Tuber Crops

Tuber crops constitute a considerable part of the world's food supply and are a valuable source of animal feed. Recently, they have gained more popularity as when compared to other staples, tuber crops are sources of relatively larger amounts of energy and nutrition with some cultivars contributing significant iron, zinc, calcium, and vitamins A and C to diets. In addition to the main role as an energy contributor, they provide a number of desirable nutritional and health benefits such as antioxidative, hypoglycemic, hypocholesterolemic, antimicrobial, and immunomodulatory activities. There are lots of tuber crops such as sweet potato, taro, yam, yam bean in the frontline along with cassava, greater yam, arrowroot which still left to be widely used in our regular diet. They have a vast species diversity as well as different varieties that have either evolved naturally or by human interference. It is essential to identify them for proper characterization and diversity study which can later on lead to genetic improvement of these crops. At present, crops like taro, sweet potato and yam have been identified using DNA barcodes using the matK and rbcL region of Chloroplast DNA (cpDNA) in Nigeria, Indonesia and Brazil (Ude et al., 2019; Syamsurizal et al., 2021). Hence it has opened the possibility of using DNA Barcodes in other tuber crops for species as well as cultivar identification.

Limitations to DNA Barcode

DNA barcoding is currently a widely used and effective tool that enables rapid and accurate identification of plant species (Jena et al., 2019); however, none of the available loci work across all species. Because single-locus DNA barcodes lack adequate variations in closely related taxa, recent barcoding studies have placed high emphasis on the use of whole-chloroplast genome sequences which are now more readily available as a consequence of improving sequencing technologies. While chloroplast genome sequencing can already deliver a reliable barcode for accurate plant identification it is not yet resource-effective and does not yet offer the speed of analysis provided by single-locus barcodes to unspecialized laboratory facilities. Here, we review the development of candidate barcodes and discuss the feasibility of using the chloroplast genome as a super-barcode. We advocate a new approach for DNA barcoding that, for selected groups of taxa, combines the best use of single-locus barcodes and super-barcodes for efficient plant identification. Specific barcodes might enhance our ability to distinguish closely related plants at a much precise scale.

Conclusion

In conclusion, barcode markers work well at species and cultivar identification and new discovery. Though after all the studies, the exact method or algorithm to be used in searching the barcode database has not been thoroughly investigated nor debated, particularly as regards a multilocus DNA barcode. Clearly, DNA barcoding has great potential for enhancing ecological and evolutionary investigations if the right genetic markers are selected. The selection of a plant DNA barcode based on a comparative and quantitative analysis can lead to better species identification as well as cultivar identification in the tuber crops.

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