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Species Identification from DNA Barcoding Technology

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Abstract:

DNA barcoding is a taxonomic method that identify the species in fast and accurate way. It is the method that uses the short DNA fragment, generated from the standard region of genome for the individualization. It works as a new biological tool in organismal biology to increase the understanding about natural world. DNA barcode technique is used in all prokaryotic and eukaryotic plants and animals. Different types of barcode has been discovered that are used for the species identification. In animal, cytochrome oxidase I (COI) is used while in plant different types of barcodes such as rbcL, matK, trnHpsbA, ITS2 and so on. These barcodes have the limits as they are used for the particular species. In this technology, BLAST (Basic Local Alignment Search Tool), and BOLD (Barcode of Life Database) are used to maintain the data of museum and herbarium species and used as a standard for the comparison purpose. In this review study, the main objective is to find out the ability of DNA barcoding for the species identification.

Keywords: *Barcoding, Species, BLAST, BOLD*

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Introduction

For the species level identification, DNA barcoding concept is very popular. It is a taxonomic method used to identifying the organism and its species. In DNA Barcoding, a short genetic marker is used to identify DNA of an organism because of the specific variation between short DNA sequences from a uniform locality of genome. Unknown sample in the pre-existing classification is identified by the help of DNA barcoding and also determines whether unknown species in sample is separated or combined. Different barcode region are used: segment of mitochondrial gene cytochrome oxidase I (COI) contain 600 base pairs, a barcode region is used in case of animal. It is also used in plant to identifying the leaves because of the absence of flowers and fruits. A portion of plastid gene rbcL codes for the larger unit of Ribulose-1, 5-bisphosphate carboxylase (RuBisCO) and Maturase K gene (matK), Standard DNA barcode with the additional regions can be used for the plant, proposed by Plant Working Group, CBOL in 2009. But rbcL gene reported as low discriminating power. Now, a huge number of reference DNA barcode sequences have been generated from taxonomically authenticated species. Hence, the identification of species from any unstructured plant part can be made from the similarity search with reference database (Sarvananda, 2018; Mahadani and Ghosh, 2013).

DNA Barcoding Method

Two basic steps are required for the process of DNA barcoding.

1. **Make a barcode library of known species**- A taxonomic expertise is required in selecting one or several individuals per species to serve as reference samples. First, DNA barcodes for texa already housed in museum collection and herbaria should be generated by all taxonomists in their monographs. A voucher is made, used as a permanent record to connect the DNA barcode with a particular species of plant, fungus or animal.

2. **Unknown sample' barcode sequence is matched against the barcode library for identification-** Once the barcode library is generated. Then, unidentified sample's DNA barcode is compared to the known sample's barcode using some type of matching algorithm. A matching tool, Basic Local Alignment Search Tool is provided by Genbank that search the relation between a questioned sequence and a sequence library.

The process is ended with the identification of unknown sample. While for the answering of biological questions, barcodes can also be used as tools (Kress, 3).

Applications of DNA Barcoding

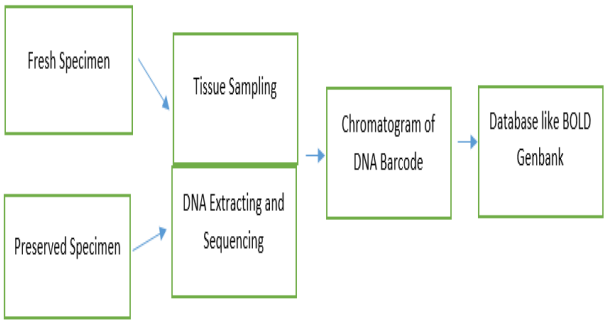

Figure 1: DNA Barcoding Method

1. **Agriculture Pest Control**: The identification of pest in any stage of life can be done by DNA barcoding and make easy to control them. The management of fruit flies is contributed by barcoding with the identification and stop them at border.

2. **Disease Vectors Identification:** The identification of vector species that can cause severe infective diseases to organism and curing by DNA barcoding.

3. **Sustaining Natural Resources**: Illegal trade of products made of natural resources (Hardwood Trees) are monitored by natural resource managers using DNA barcoding.

4. **Endangered Species Protection:** DNA barcoding is used by law enforcement to protect the endangered species.

5. **Monitoring Water Quality:** The health of species, living in the lakes, ponds and streams can be measured by DNA barcoding. It can improve the determination of quality and create better policies to ensure safe supply of drinking water.

6. Natural health Products Authentication

7. Identification of plant leaves when flowers or fruits are not present

8. Medicinal Plant Identification (Kaur, 2015).

Review of Literature

Sahare and Srinivasu (2012), DNA barcodes allows the identification of species from even a small

processed material. For the identification of medicinal plants at the molecular level ITS region barcode sequencing has been used. Eco RV with Each of the plant specific ITS region gives unique digestion that can be again used for identification.

Ghosh, Mahadani and Sharma (2013) researched on Rauvolfioideae (family of Apocynaceae) medicinal plant and found matK sequence information (DNA barcode) is helpful in correcting the species identification for medicinal plants of Rauvolfioideae and also help in providing diagnostics for the identification of mal species forensics in herbal formulation.

Techen, *et al.* (2013), the increasing demand for herbal remedies, authentication of medical plant material is important. For easy identification, it is important to provide a sole, extensive database with DNA data. The Barcode of Life Plant Working Group recommends the genomic regions rbcL, matK for barcoding, but other genomic regions could be more useful for medicinal material identification. Furthermore, depending on the material analyzed, one or the combination of up to three genomic regions was necessary to provide the required information for identification.

According to Duan *et al.* (2014) DNA barcoding have some problems in the identification of plant species as universal DNA barcode in plants is very difficult to obtain because of the widespread hybridization in the plants. Some DNA barcodes have poor universality. The barcode is based on traditional taxonomy due to which the accuracy of experimental materials is critical. Hence, barcode and the combination of barcode's ability for identification should be compared and evaluated by plant taxonomy, molecular biology, bioinformatics and other methods.

Aziz, Ahmad and Naim (2015) studied identification of medicinal plants. He used three DNA Barcode for his study ITS2, rpoC1, and trnH-psbA and gave a conclusion that trnH-psbA is the best marker for the differentiating 12 medicinal plant used by Malay traditional healers. Before, this study there was no record of these plants species in the Genbank.

Hubert and Hanner (2015) proposed that the linkage of DNA world with traditional approach of taxonomy, DNA barcoding has been settled as new standard for data quality, accessibility and reproducibility which make the use of DNA sequences in others field of biology more sustainable. The DNA sequencing is not only helpful in objective methods for species delineation as well as new tools for species identification but significantly challenged the manner of collection and creating biodiversity knowledge publicly available and paved the way more sustainable practices in taxonomy.

Raja *et al.* (2017) tried to find out identification of fungal samples by ITS barcoding marker and concluded that dietary companies can validate the accuracy of ingredient in dietary supplements. Barcoding methods can give the guaranty of industry's product reliability, consumer safety and product integrity. In their study, they showed the pros and cons of ITS barcode marker in the fungi.

Enan *et al.* (2017) compared the herbarium plant with the fresh plants using matK, rbcL, and rpoC1 barcode marker. They concluded that fresh samples are better amplified compare to herbarium samples, and neither matK nor rpoC1 are sufficient to identify the plant species while rbcL regions has real prospective to distinguish the plant species into suitable family and genus.

Braukmann *et al.* (2017) studied on Canadian Flora. The efficiency of DNA barcoding was tested across a diverse set of communities in Canadian flora. Three standard barcode markers (rbcL, matK, ITS2) were used in this study and concluded as three barcodes are efficient separately (>90%). matK showed the high resolution while ITS2 showed slightly lower performance. according this paper, ITS2 has two major advantages short length makes it fit for HTS based application and it can be recovered from diverse taxa as well as form vascular plants and fungi.

Future Perspective of DNA barcoding

A new perspective of DNA barcoding is "purpose-driven barcode" which is suitable for multi levels such as identification of living organisms, reconstructing community phylogenies, detecting environmental biodiversity information and exploring ecological network structure. Mega phylogenies in face of the post genomic era would be generated by developing new integrative sequencing strategies. For land integrating genetic, morphological and environmental information, intelligent identification systems or online server platforms will established to make DNA based plant identification more precise, convenient and interesting. For commercial authentication and endangered plant taxa against the illegal international trade, national-level DNA barcode sequence libraries of economically valuable tree species will be constructed (Pei, Chen and Kress, 2017).

Conclusion

DNA barcoding is fast and accurate method for the species identification in which different types of barcode are used. But these different barcodes are not

applicable to all plant species as the large number of plant species are present in the universe. One barcode works for the many types of species so it is difficult to determine the species on the basis of one barcode. It gives the reliability and integrity of the products and ensure the safety of consumer as in the dietary products. From this review study, we concluded in the end as more than one genomic region should be examined for the identification of species**.**

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