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REVIEW ARTICLE

DNA Barcoding and its Application in Fish Biodiversity Identification: A Review

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ABSTRACT

This article includes concept of DNA barcoding, requirement in animals and plants, methods of barcoding, its use and significance with/over taxonomy. Article also includes descriptions of fish DNA barcoding concept, its efficiency to detect the degree of genetic divergence between species and on intra species level, online data systems and their use.

Key words: Barcoding, taxonomy, species, genetic, divergence.

1. INTRODUCTION

Till now, biological specimens were recognizedby means of morphological features like the shape, size and color of body parts. In certain cases a trained technician could mark routine identifications using morphological "keys" (step-by-step directions of what to look for), but in most cases,skilled professional taxonomist is needed. If a specimen is smashed or is in an immature stage of development, even specialists may be unable to make identifications. Barcoding solves these complications because even non-specialists can obtain barcodes from smallquantities of tissue. This is not to say that traditional taxonomy has become less important. Rather, DNA barcoding can help a dual purpose as a new tool in the taxonomist toolbox improving their knowledge as well as being an innovative device for non-experts who need to make a quick identification [M S Bloch *et al.*, 2014].

In 2003, Paul Hebert, researcher at the University of Guelph in Ontario, Canada, proposed "DNA barcoding" as a technique to identify species. Barcoding practices a very short genetic sequence from a standard part of the genome. A short DNA sequence of 600 base-pair in the mitochondrial gene for cytochrome *c* oxidase subunit 1 (CO1) [Herbert *et al.*, 2003 a] has been accepted as a practical, standardized species-level barcode for animals.

Conceptually, any reliable, nonzero sequence variation that differentiates two species should work as a DNA barcode. Additionally, DNA barcodes do not involve any demonstration of the homology of mutations as would be desired in a phylogenetic marker. In other words, low levels of divergence may be enough to distinguish among species even if not suitable to estimate phylogenetic interactions.

1.1- REQUIREMENTS FOR DNA BARCODES:

The gene region that is being used as the standard barcode for almost all animal groups is a 648 base-pair region in the mitochondrial cytochrome c oxidase 1 gene ("CO1"). COI is proving highly operative in recognizing birds, butterflies, fish, flies and many other animal groups. COI is not an effective barcode region in plants because it evolves too slowly, but two gene regions in the chloroplast, matK and rbcL, have been approved as the barcode regions for plants.To be practical as a DNA barcode a gene region must satisfy three criteria:

- *(i)* comprisemajor species-level genetic variability and divergence,
- *(ii)* keepconserved bordering sites for developing universal PCR primers for wide taxonomic application, and
- *(iii)* Have a shortsequence length so as to enable currentskills of DNA extraction andamplification.

Immense on-line digital library of barcodes will serve as a standard to which the DNA barcode sequence of an unidentified specimen from the

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forest, garden, or market can be matched. Like to genomics, which has augmented the process of recognizing novel genes and comparing gene utility, DNA barcoding will allow users to efficiently recognize known species and speed the discovery of species yet to be found in nature. DNA barcoding aims to use the information of one or a few gene regions to identify all species of life.

1.2- Fish DNA Barcoding

DNA barcode is an efficient technique for species level identification using an array of species specific molecular tags derived from 59 region of the mitochondrial Cytochrome c oxidase I (COI) gene [Herbert *et al.,* 2003 b]. Phylogenetic systems, in combination with conservation genetics, provide a critical framework for understanding diversity[Jean Pierrey, 2002]and predict helplessness to exploitation of tropical reef fishes[Simon *et al.,* 1999]. Efficiency of this method centers on the degree of genetic divergence between species and intra species level identifications [Ward *et al.,* 2005]. Hence, DNA bar coding is to recognize and to increase the number of unfamiliar taxa in biological conservation and biodiversity surveys, based on sequence diversity [Herbert *et al.,* 2003 b; Marshall 2005].

The Fish Barcode of Life Initiative (FISH-BOL) is a global effort to coordinate an assembly of a standardized reference sequence library for all fish species, one that is derived from voucher specimens with authoritative taxonomic identifications. The benefits of barcoding fishes include enabling species identification for all probable users, including taxonomists; highlighting specimens that characterize a seriesdevelopment of identified species; flagging previously unrecognized species; and perhaps most importantly, enabling identifications where traditional methods are not appropriate.Over the last 7 years the Fish Barcode of Life effort has been creating aappreciatedcommunal resource in the form of an electronic database containing DNA barcodes, images, and geospatial coordinates of studied specimens. The database contains associations to voucher specimens, information on species spreading, nomenclature, confident taxonomic information, collateral natural history information and literature citations. FISH-BOL thus supplements and boostspresent information resources, including the Catalog of Fishes, FishBase and various genomics databases.

FISH-BOL.org is the initial site of an ongoing effort to bring the information gathered through this initiative to the both its participants and the broader community. It functions as a portal to BOLD (Barcode of Life Datasystems), and as an information resource for the community at large.

The DNA barcoding technique could overcome the difficulty faced in morphological identification and reduces the misidentification of commercially important fishes in all stages[Sachithanandam*et al.,* 2012].

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