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DNA Barcoding: A New Tool with Wide Array of Applications

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DNA barcoding is a new term introduced in to scientific literatures by Hebert and coworkers almost a decade ago (1). The concept of barcoding alone is well-known to the public: a series of black bars printed on many commercial products (1-3) (Universal Product Code), which are used to distinguish different products. Advances made in molecular biology and molecular techniques late 20th century e.g. sequencing technologies, has inspired scientists to apply barcoding concept to all domains of life by using the unique nature of DNA for each single species, in order to generate a comprehensive library of living organisms on the planet earth (2, 6). Such an ambitious initiative would result in a global DNA barcode database which will be valuable for biological scientists, medical, governmental and legal agencies as a mean of identification (1). The first initiative for DNA barcoding was funded in Canada and later on several DNA barcoding campaigns came in to the scene. The International Barcode of Life consortium (http://ibol.org/) was established in 2004. It is an international initiative devoted to develop DNA barcoding as a global standard for the identification of biological species. The Consortium for the Barcode of Life (CBOL), an international consortium coordinated from Smithsonian Institute in Washington (USA), was established to promote DNA barcoding, coordinate efforts and generally oversee the standardization process (6). DNA barcoding is a technique for discriminating species through analysis of sequence data, i. e. short sequences of genetic material in the genome that are unique to that organism are used to identify species mainly through PCR amplification by using primers for the broadest-possible target taxonomic group (1-3, 5-6). The usefulness of DNA barcodes for proper discrimination of species was first demonstrated in animals. A 648 nucleotide base pair length region from the mitochondrial cytochrome c oxidase 1 (CoI) gene was used to identify different animal species; such that, this short sequence has emerged as the standard barcode region for higher animals (3, 7). The important criteria for barcode loci are effective species-level identification– chieved when inter specific variation exceeds intraspecific, universality, good sequence quality and coverage. Several global DNA barcoding campaigns have been established to target specific taxonomic groups such as plants, fungi, protists, bacteria and different entities of the kingdom animal including fishes, brides, insects, nematodes, mammals etc (1, 6). In most cases in animals, CoI provides adequate resolution. However, in plants, fungi the substitution rates of this gene are much slower, and scientists are actively searching for barcode genes (6). For example the nuclear ribosomal Internal Transcribed Spacer (ITS) region has been proposed as universal DNA barcode marker for Fungi by the Fungal Barcoding Consortium published. However, in certain groups of fungi the ITS region fail to discrimination species; such that, secondary barcode loci will be needed for the proper delineation of species in question (5).

One of the most important issues in DNA barcoding is standardization. A DNA barcode is not the same as a DNA sequence. For a barcode, the sequence should stem from a voucher specimen with the voucher being accessible in public collections and the trace files on which the sequences are based should be publically available (1, 4). The quality and uniformity of data in databases is very crucial for the success of DNA barcodes as a universal molecular identification key. To achieve this goal, a set of guidelines and protocols should be set from collecting species to storing molecular data. The final goal of DNA barcoding project is to create a barcode reference library, where sequence data must be integrated with well characterized taxonomic units (1, 4, 6). Reference sequences are the core component of the DNA barcoding initiative i. e. the reliability of library depends on the quality of the voucher specimens from which reference sequences are obtained. When the voucher specimens are characterized and verified

by expert taxonomists; then, newly generated sequences can be easily compared to the library (1, 6). Eventually, a compiled public library of sequences linked to named specimens together with faster and cheaper sequencing will make DNA barcoding increasingly useful.

The primary aim of DNA barcoding technique is to provide a reliable, cost-effective and accessible solution to the problem of species identification in order to obtain a better taxonomic resolution compare to morphological approaches, by allowing even non-specialists to identify species in question. With the aid of DNA barcode, a species can be identified based on a little amount of DNA extracted from any biological material (tiny amount of tissue, blood, from seeds, or from sterile, juvenile or fragmentary materials) when morphological identification is difficult or even impossible (1, 5, 6). This technique will be useful in many ways: rapid and accurate identification of harmful microorganisms for human in medical, governmental and legal agencies, studying extinct species, discriminating possible cryptic species, identifying immature specimens and resolving adult and larval stages within the same species and even controlling the identity of food of animal and/or vegetal origin, e.g. fishes for sale in supermarkets (1, 6).

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