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BARCODE USAGE POTENTIAL IN SEPARATION OF SPECIES FROM EACH OTHER

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ABSTRACT: DNA sequencing, in which key sequences serve as barcode, has recently attracted attention as an important technology in identifying species. It is also known that with the use of this technique, the separation of living species from each other is faster. In order to distinguish the living species of taxa from each other, especially the mitochondial cytochrome C subunit 1 gene has been used as a DNA marker. It is also seen that the separation of living species in taxa from each other can be solved with this technology. In addition, barcoding has achieved considerable success in matching species with potentially encrypted and adult samples to immature ones among living species. Morever, It appears to be an important molecular-based tool for identifying and differentiating DNA barcode-living species and for differentiating them. This review examines the progress, potential of DNA barcoding in living species.

KEY WORDS: DNA barcoding, taxonomy, separation of species

Identification of living species, their distinction from each other and their characterization are very important for biological life. To date, much data has been learned about the relationship between these living creatures within themselves and among other living species by studying behavior and morphological differences (Stoeckle, 2003; Blaxter, 2003). The world is suggested to contain between 10 and 100 million eukaryotic living species (May, 1988). Identification of living species numbers in this given range was carried out by taxonomists using current methods. In addition, In addition, the phenotypic plasticity and genotypic variation used to identify living species can lead to their identification errors (Comstock et al., 2002; Whitfield, 2003). These issues also affect people working in other disciplines such as endangered species, monitoring fisheries, exposing and controlling the spread of harmful species or diseases, and researching the movement of biological species in the World (Baker & Palumbi, 1994; Baker et al., 2003; Besansky et al., 2003; Lambert et al., 2005). From this point of view, it is clearly seen that more simple and practical methods are needed to distinguish living species from each other (Baker et al., 2003; Besansky et al., 2003). Rapid advances in DNA sequencing methods have brought along the possibility of using variations in short sequences of DNA as specific tags for species in a process known as DNA barcoding. This approach of tagging this barcode-based species as gene sequences has also been widely accepted among those working with species belonging to different living groups with morphological identification difficulties such as viruses (Mayo & Horzinek, 1998), bacteria (Woese, 1987), protists (Unwin & Maiden, 2003), and Rhodophyta (Cavalier-Smith, 2004; Saunders, 2005). The techniques studied according to the morphological features used to distinguish species from each other are difficult to

reach or apply without any training. So, it has been demonstrated that a system of species identification is required more quickly for all taxa. this requirement has led to the establishment of the life barcode consortium (CBOL), which aims to provide such a DNA barcode for each species in the World (Barcode of Life, 2006).

TECHNICAL APPROACH TO DNA BARCODE

The DNA-barcoding process

A DNA barcode is a short nucleotide sequence determined from the genome of that species used to identify an organism at the species level. Inraspecific variation in these short nucleotide sequences realizes the differentiation tools of species. Although DNA is not part of taxonomy, it is not an instrument for reconstruction of phylogenetics. it only provides an important way to relate species directly to taxonomic information. The basis of DNA bar coding is the selection of a suitable DNA sequence within the genome of the species to be distinguished. Mitochondrial DNA (mtDNA) can give different positive approaches than nuclear DNA (Herbert et al., 2003a). According to Drake's observation, the rate of mutation to occur in DNA is directly proportional to the size of the genome. Based on this, mitochondrial DNA is known to have a more conserved genome structure in which it mutates less in the evolutionary process (Drake et al., 1998). It consists of a single pair of circular genetic structures that contain mitochondria, 13 proteins, two ribosomal genes, several t-RNA encoding gene regions in animal cells (Research Collaboratory for Structural Bioinformatics (RCSB) Protein Databank (PDB), 2006). Cytochrome c oxidase is a large membrane protein found in mitochondria which is highly conserved among the species that use the oxidative phosphorylation pathway to carry out its metabolism (Cytochrome c oxidase homepage, 2006). This protein contains several subunits synthesized in the nuclear nucleus and three subunits synthesized in the mitochondria. The cytochrome c oxidase enzyme consists of two subunits. The mitochondrial subunits of this enzyme are called I, II and III, while the catalytic subunit of the same enzyme is known as (COI). The nucleotides of the gene encoding the catalytic subunit (COI) of the enzyme provide sufficient variation to distinguish between species. In recent studies of barcodes using CBOL, it has been stated that a 648 bp nucleotide sequence of the COI gene should be selected to produce a generally suitable barcode (Blaxter, 2004; Barcode of Life, 2006).

The effect value of DNA barcoding

In most studies to date, it has been demonstrated that the DNA barcode is created using the COI gene (Hebert et al., 2004a; Saunders, 2005), and this helps to resolve taxonomic uncertainty (Whiteman et al., 2004; Greenstone et al., 2005) or to clarify the taxonomic definition. In some studies (Paquin & Hedin, 2004; Ward et al., 2005), a DNA barcode was used to resolve species in problematic taxonomic groups or to identify higher taxa than large animal populations (Brown et al., 2003). In studies on DNA barcode, similar protocols are applied with minor differences. DNA extracted from the tissue samples belonging to the species is applied by using PCR method using common primers that accept international acceptance and sequence analyzes are made from the samples obtained. Sequence profiles obtained from species are compared both between species and between high taxa (Remigio & Hebert, 2003).

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Discrimination of species

In most of the review articles investigated, it has been observed that it provides a great taxonomic distinction with the application of DNA barcode technique (> 95%) (Hebert et al., 2003b; Whiteman et al., 2004; Lorenz et al., 2005).

While the cross-species variation is generally known to be less than 1%, the mean cross-species conflict is determined as 11.3%. This difference between intra and interspecific differences at COI were detemined in arachnid (Paquin & Hedin, 2004; Barrett & Hebert, 2005), lepidopter (Hebert et al., 2003a; Hebert et al., 2004a; Hajibabaei et al., 2006), dipter (Smith et al., 2006), bird (Hebert et al., 2004b), fish (Ward et al., 2005) and collembolan species (Hogg & Hebert, 2004). In another study, COI barcoding enabled to identify arachnids and carbides of different life stages, including eggs, larvae or nymphs and pupae (Greenstone et al., 2005). In addition, potentially encoded species were identified using DNA barcoding among butterflies (Hebert et al., 2004a), flies (Smith et al., 2006), birds (Hebert et al., 2004b), arachnids (Barrett & Hebert, 2005) species. The effectiveness of DNA barcoding in the detection of scrambled species has also been demonstrated in three parasitic worm studies (Hu et al., 2002a; Ngarmamonpirat et al., 2005). In another study, by analyzing COI fragments, it found high inraspecific COI variation between tapeworm and hookworm species (Hu et al., 2002b).

RESULTS

Currently, there are some problems with anthropogenic origin that have been recognized, with regard to the demonstration of biodiversity. environmental problems and unconscious consumption of nature are known to pose the danger of extinction of many species (Shearer et al., 2002). The idea that some of the eukaryotes are not known to science led taxonomists to define them. In the identification studies of some of the eukaryotes, DNA barcoding is considered as a tool that can be an auxiliary solution. Although it helps to differentiate between species by DNA barcoding technique, it does not suggest neither the place of taxonomy nor the reconstruction of phylogenies (Nielsen & Matz, 2006). However, the DNA barcode technique is also thought to be a useful tool for taxonomists and some other institutions and individuals interested in species identification (Lipscomb et al., 2003). In addition, Based on the studies carried out, it has been revealed that DNA barcoding in general, separation of problematic species and an important tool in detecting new species. In addition, taxa, which are under the influence of rapid speciation, demonstrate the power of discrimination between species, as they show little COI deviation between species within (Ebach & Holdrege, 2005). Therefore, the COI barcode is a molecular diagnostic tool for identifying animal species and cannot be expected to act as a stand-alone character for deeper phylogenetic reconstruction. Morever, given the current level of accuracy, it has been suggested that COI barcoding has proven to be sufficiently discriminatory in studies to demonstrate considerable utility as a tool for species differentiation and species distinction (Hebert & Gregory, 2005).

DISCUSSION

DNA barcoding is thought to be an important potential as a tool for users to link the samples of the species they are researching to taxonomic information databases, as well as for identifying species that do not have any data yet.

Although barcoding method does not provide a detailed taxonomic explanation and it is not entirely a tool in the phylogenetic restructuring. However, it has been suggested to help speed up the development of taxonomic studies on species. To date, the data obtained from the studies, this effectiveness of the barcode system has been revealed. It is suggested that the success of DNA barcoding will reach an even more advanced position by introducing different new types of identification programs. It is also necessary to solve problems associated with species that are resistant to identification by COI gene sequences in barcoding. Some new tools may be needed to make more detailed taxonomic evaluations of problematic or resistant species. An example of such tools is the Tree of Life (ToL) project, which provides a framework for electronically publishing taxonomic information in a searchable database. It is suggested that DNA barcodes can mediate to quickly link samples to ToL information and contribute to the growing database of species identification and separation. Nevertheless, ToL, on the other hand, can provide taxonomic information about species according to the information provided by DNA barcodes. By means of barcoding and connecting the data obtained from it to the ToL network, the type identification process can be facilitated and it can also enable the use of ToL information that cannot be considered yet. Thus, it is thought that both scientific approaches can increase the value of modern taxonomy [44,45,46,47]. (Schindel & Miller, 2005; Smith, 2005; The Global Biodiversity Information Facility, 2006; Tree of Life, 2006).

In this review article we prepared, it has been determined that studies based on taxonomic studies and molecular level have made the most contribution at the molecular level. Morever, with barcode applications, it has been observed that it contributes to phylogenic studies such as the identification of new species, the relationship of the species with its class, and the relationships between the species. the most important contribution value here is that it enables the establishment of a scientifically based link between the morphological features and genetic material of the species.

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