Barcoding Biological Diversity: A New Microgenomic Identification Approach

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Abstract

Morphology-based taxonomy suffers from its inherent limitations, even though most of biological research depends on reliable identifications of species. A recent microgenomic identification approach, which is now being called the "DNA-barcoding," presents a promising potential of developing into a real-time, on site tool for identification of organisms, especially animals and of providing an added insight into evolutionary history. For animals, the DNA-barcode seems to have been found in the mitochondrial genome and researchers are in quest of developing similar microgenomic DNA-barcoding systems for other domains of biological diversity. This article discusses the DNA-barcoding technique and considers some of the implications of this approach.

Key words: DNA-barcode, cytochrome *c* oxidase subunit I (COI), mitochondrial DNA

Taxonomy is hard

Reliable on-site, real-time identification of species has always been a burden for biologists, as well as for conservationists, environmentalists, collectors, tourists, farmers, law enforcement, security and customs officials, nature enthusiasts and so on. All these groups of people with different interests have the same need when it comes to species identifications. To mention just a few, for example, farmers want to know what insects have been infesting their crop without losing much time, whereas homeland security or customs officials need to know whether a particular organism is bringing any threat to the well-being of country. Moreover, it can be a great tool for law enforcement when the rarest one of the two closely-related species differing in their conservation status (such as CITES) was illegally harvested, but perpetrators argue otherwise. Therefore, the ability of correctly identifying species has far-reaching implications not only in ecology and biodiversity research, but also in many aspects of environmental management and policy.

Unfortunately, the morphology-based taxonomy has always had its limitations. First of all, traditional dichotomous taxonomic identification keys always require high level of expertise. In many cases they are not easily understood by users due to their specialized jargons (Hebert *et al.*, 2003b). Even with the help of glossary of the taxon-specific terms, it is hard to know what the key is describing unless one is an expert in that field. Let us for a minute imagine that you needed to identify an insect specimen using identification keys which reads as "forewings membranous, hind wings forming halteres and tarsi three-segmented." There are people who are sufficiently literate in the field to understand what this means. But majority of people, even majority of biologists, would have no idea what this sentence is describing.

Second, taxonomic keys are effective only for a certain sex or developmental stage of a life cycle. Take an example of birds. Even though birds are the most well-known class of organisms, imagine trying to classify young nestlings of leaf-warblers (genus *Phylloscopus*) into species. It is next to impossible because they all look the same. Take another example, crane flies (family Tipulidae) in this case. Taxonomic keys for this group are mostly based on adult male crane flies. Therefore, you would run into a trouble if you have a crane fly larva (leatherjacket e.g.) or an adult female specimen.

Third, cryptic species and highly variable species are not very uncommon in nature (Knowlton, 1993) and in such cases morphology-based identification is useless. And finally, it is impossible to use a single