CHAPTER

23

Integrative Taxonomy - A Novel Approach to Biological Studies

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Taxonomy is the discipline of Biology that identifies, names and classifies organisms according to certain rules. Taxonomists are scientists who study classifying and taxon (taxa-plural) is a category into which related organisms are placed. Aristotle was the first taxonomist dividing organisms into land, sea and air dwellers and Linnaeus introduced the binomial nomenclature (Genus and species) where the genus is always capitalized followed by species in lower case. Taxonomy is central to exploring and understanding biodiversity. Alpha taxonomy deals with the species category, beta taxonomy with higher categories. The need for good alpha taxonomy is further increased by the biodiversity crisis both for assisting conservation programs and documenting diversity before it is lost.

Reasons to Classify

- Shows evolutionary relationships
- Accurately & uniformly names organisms
- Prevents misnomers such as starfish & jellyfish that aren't really fish
- Uses same language (Latin) for all names
- Prevents duplicated names because all names must be approved by International Naming Congresses (International Zoological Congress)
- Naming rules are followed called the International Code for Binomial Nomenclature

Integrative Taxonomy

A multisource approach that takes advantage of complementarity among disciplines, i.e., fields of study, has been called combined, mul-tidisciplinary, multidimensional, collaborative, or integrative taxonomy mainly focusing on the species level. Integrative taxonomy does not replace traditional taxonomy. Rather, it compresses the traditional but slow taxonomic routine of visiting a taxonomic problem repeatedly into one procedure by coordinating the findings of different disciplines under the procedure. By doing so, integrative taxonomy improves rigor, more confidence in taxonomic information and consequently provides taxonomic stability.

DNA barcoding, a new method for the quick identification of any species based on extracting a DNA sequence from a tiny tissue sample of any organism, is now being applied to taxa across the tree of life. As a research tool for taxonomists, DNA barcoding assists in identifi cation by expanding the ability to diagnose species by including all life history stages of an organism. As a biodiversity discovery tool, DNA barcoding helps to flag species that are potentially new to science. As a biological

tool, DNA barcoding is being used to address fundamental ecological and evolutionary questions, such as how species in plant communities are assembled. The process of DNA barcoding entails two basic steps: (1) building the DNA barcode library of known species and (2) matching the barcode sequence of the unknown sample against the barcode library for identification. Although DNA barcoding as a methodology has been in use for less than a decade, it has grown exponentially in terms of the number of sequences generated as barcodes as well as its applications. Detailed species and larval level identification forms the pre-requisite for the proper conservation and management of the declining deep water shrimp resource of the country. DNA barcoding has been successfully used for species identification and discovery of new species, utilizing 650 base pair fragment of the mitochondrial gene, cytochrome oxidase subunit I (COI). COI was effectively used for the discrimination of closely related species and detection of cryptic species as well as for the identification of fish products. Mitochondrial DNA (Mt-DNA) sequence information has been used as an accurate and automated species identification tool for carrying out studies in a wide range of animal taxa, due to the presence of a significant amount of information.

Materials and methods

2.1. Sample collection

(a) Proper disposable or easily sterilized tools. (b) Proper individual storage containers for the organisms and tissues. (c) Data collection tools to handle specimens, tissues. (d) Photo documentation materials (digital camera with appropriate lens(es), memory cards, backup hard drives).

2.2. Storage buffers

(a) Dry ice and cooler. (b) Salt solution. (c) EtOH—95% (nondenatured). (d) Formalin or other voucher specimen preservation solution(s)

2.3. Extraction components

(a) Lysis buffer for extraction method. (b) Proper plates, tubes or storage vessels. (c) When possible, on-site portable DNA extractor.

2.4. PCR components

(a) PCR reaction ingredients and primers . (b) Positive control 16S or 18S and COI

2.5. Sequencing, data QC, and analysis.

Data analysis

Molecular sequences were checked and confirmed using ABI SeqEditor v.1.0. Protein coding gene sequences (COI and Cytb) were translated into amino acids using Transeq (EMBOSS online tool) to avoid the inclusion of pseudogenes. All the sequences were blasted to report GenBank data to verify the potential contamination and the nucleotide sequences were aligned using the Clustal W algorithm. The aligned data was edited using bioedit V.7.0.5.2, gaps of sequences treated as missing data. All the sequences were submitted to GenBank. The pairwise genetic distance was calculated using MEGA 6.0.

Morphological analysis

In case of deepsea penaeid shrimps ancestral state reconstruction (ASR) was used to evaluate character evolutions. Fifty-two morphological characters (24 binary, 27 multistate and one non-informative) were chosen and considered for phylogenetic analyses based on the original taxonomic works of Ramadan (1938), *Crosnier (1978; 1985), Pérez-Farfante (1997) and Dall (1999). All these major characters were re-examined carefully. The data matrix was analyzed with maximum parsimony using combinations of programs: Mesquite v.3.01 (*Maddison and Maddison 2015) *and* PAUP v.4.0 (Swofford 2002). These characters were given equal weightage and unordered, the code given for each state (i.e., 0, 1, 2, 3, and 4). Branch support was assessed using 1000 bootstrap replicates without any outgroups. Results acquired from both morphological and molecular tools was combinedly assessed before deriving to any conclusion of a particular species, which is nothing but integrative taxonomy.

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