ICZN UPDATE

Several issues now confronting the zoological community make desirable the development of a 5th edition of the International Code of Zoological Nomenclature (Code). Prime among them are:

1) Electronic publication
2) Registration of names
3) Typification of newly discovered rare and endangered species.

http://iczn.org/content/5th-edition-web

Outline - Modernization of alpha taxonomy

1. Tools - digital imaging, databases
2. Dissemination – WWW, e.g. Zookeys
3. Tools - Molecular data, species demarcation, phylogeography

Prognosis

Some numbers on the decline of alpha taxonomy...

Authors of 6 + plant taxa - 1999: 44% deceased or emeritus
50% of curators of Diptera lost since mid-1970’s C. Thompson

The Problem

Taxonomy “old fashioned”

Tower of Babel : each taxon has its own language (terminology)
No single, on-line, depository of species names
No accurate compilation of all described species
2,300 new beetle species named per year
“Taxonomic impediment” or “Bottleneck”

Loss of traditional skills
The Problem

Types

Catalogs

of types:

Nicrophorus -

Location

unknown

For types

of 67 of

236 names.

Modernization of alpha taxonomy

Tools - digital imaging, databases

- The “toolbox” of the alpha taxonomist grows with the advances of technology
  - Printing press, c.1450 AD
  - Microscope, c.1590 AD

- Photography, color images, audio recordings…
- Scanning Electron Microscopy

Modernization of alpha taxonomy

Recall that alpha taxonomy seeks unique character states to diagnose taxa

“Is this population/species/genus unique? Is it diagnosable? How can one identify this species? What is different about it from all other species?”

Phylogenetics seeks shared character states to infer relationships among taxa

Modernization of alpha taxonomy

Phenotypic data management

- morphology
- behavior
- pheromones
- songs
  etc.

Identification keys, guides - more & more online (e.g. lab web exercise)

Modernization of alpha taxonomy

Digitization of phenotypic data

- Databases of biogeographic data
- export “material examined”

- Morphology: SEM, Auto-montage songs etc.
  - identification keys
  - multi-entry keys
    e.g. Scarab key
Multi-entry keys offer many advantages over dichotomous keys.
Modernization of alpha taxonomy

Mitochondrial genome - circular

13 protein coding genes
2 rRNA genes
22 tRNA genes

DNA Sequence data

e.g. mtDNA - COII gene

N. americanus    ATGATAACATGAAAAACACTTATATCACCAGATAGAGCTTCACCATTAATAGAACAATTAT
N. concolor      ATGATAACATGAAAAACATTAATGTCTCCTGACAGTGCCTCTCCATTGATAGAACAACTTA

61 base-pairs (nucleotides) - each site is a character

Advantages - some:
1. All living organisms have DNA
2. Sequence is most basic level of biological information
3. We understand much about the processes of sequence evolution

Problems - some
1. Sample size issues - costly to obtain large sample sizes
2. Lack of information or too much information (+misinformation) [same problem for morphology]
3. Multiple substitutions at one site “overwrite” prior substitutions

Haplotype: A set of closely linked alleles (genes or DNA polymorphisms) inherited as a unit. A contraction of the phrase “haploid genotype.” Different combinations of polymorphisms are known as haplotypes.
Species demarcation


- Identification of “species” is challenging because
  1) differences of opinion on whether species are “real”
  2) differences of opinion on what concept to use
- Conservation biologists require reliable, unambiguous classifications
- Legal protection of “species”
- Used fish, Leatherside chub, - approached species question as a testable hypothesis

Species demarcation


- Was classified as 1 species, Gila copei
- Genetic data suggested there might be 2 species
- Used data applicable to 3 different species concepts:
  - Phylogenetic
  - Phenotypic similarity
  - Ecological

Phylogeography

Johnson et al. 2005. Leatherside chub

Head Shape

Johnson et al. 2005. Leatherside chub

Ecology

Johnson et al. 2005. Leatherside chub
Examined taxonomic boundaries with 3 species concepts:

1) phylogenetic - reciprocal monophyly & fixed diagnostic character states (mtDNA & nDNA)
2) Similarity - statistical differences in cranial shape
3) Ecology - local adaptation in growth & foraging rates

Conclusion: there are 2 species

Modernization of alpha taxonomy

New tools in the taxonomist’s toolbox:

For phenotypic, traditional data
- digitization
- databases
- web dissemination

For molecular data
- phylogeography & species demarcations
- DNA sequence data

Terms - from lecture & readings

Taxonomic impediment / bottleneck
Uncorrected sequence difference
Base-pairs

Phenotypic data
Character state
Character
Molecular data
Proteins, Isozymes
Cytogenetics
Karyotyping
RFLPs
PCR
Primers
TAQ polymerase

You should be able to

Describe the taxonomic impediment - what are some key problems? What are some solutions?

Be able to list different aspects of the new digitized alpha taxonomy, e.g. web databases, on-line multi-access identification keys etc. (& what are some advantages of multi-entry keys)

Be able to briefly describe how PCR works

Be able to describe pros & cons of DNA data for alpha taxonomy (including DNA bar-coding).

Describe what steps you think are best to identify a new species (data types, methods, etc.).