

## What is a species, a genus, a family...?

Many BBS members probably noticed last autumn's BRYONET debate regarding species concepts and classification. Is this debate important to us? Well, if traditional species are man-made constructs rather than 'real biological entities' they are no longer comparable. Consequently, they are not equal in conservation contexts, in ecological hypothesis building, or in their contributions to ecosystem diversity and function. The implications of this debate are therefore fundamental to all biologists.

Traditionally, species were recognized based on morphological similarity and dissimilarity, or on various biological characteristics. Species were classified into genera, genera into families, and so on. We still base our ideas about relationships on morphology and biologically relevant features, but in addition we now have molecular data (DNA). One type of information often resolves specific relationships; DNA from the cell nucleus may reveal different relationships than chloroplast DNA, and morphology sometimes resolves other relationships. DNA data are so important nowadays because the amount of molecular information has increased so rapidly, and not because its quality is better than morphology per se.

Recent advances in systematic research have revealed that the biological world is not as rigidly organized as implied by earlier ideas of classification. Instead, it seems as if we find everything from 'completely similar' individuals to various levels of dissimilarity. So, why do we not observe such a continuum in morphology, but instead experience more or less distinct entities as species, genera, etc.? These perceived entities are what remain after individuals or lineages (branches in the phylogenetic tree) have become extinct through evolutionary history, combined with stabilizing evolution (not all combinations of features are viable). Molecular patterns may parallel morphology, or the two are incongruent. Even if our brains want to recognize morphological units, accumulating molecular evidence suggests that 'species', as they are usually understood, are as artificial as higher taxonomic categories. Molecular patterns show much more clearly than morphology that there is really a continuum from similar to dissimilar lineages at

different levels that are isolated or exchange genetic material with varying frequencies. We can look at this as a tree where some branches anastomose (i.e. join), most frequently among short distal twigs that recently diverged from each other.

Many systematic biologists attempt to combine a phylogenetic understanding of the organic world with the old way of classifying organisms. This approach accepts only monophyletic groups, i.e. groups that include all descendants of a single ancestor. Unfortunately, there are not enough hierarchical levels in the old system, and in the real world many morphologically or biologically relevant groups do not include all descendants of an ancestor; this leads to so-called paraphyletic groups.

A striking species-level illustration of these problems is *Scorpidium cossonii*, which is paraphyletic when *S. scorpioides* is recognized. Synonymizing the latter with the first means a great loss of biologically significant information. On the other hand, if we protect *S. scorpioides* in addition to the molecularly similar *S. cossonii*, we preserve much less of total diversity than if we conserve the molecularly very different *S. revolvens*. Traditional 'species' are simply not comparable to each other in numerous contexts, including ecology and species history, and a different way of considering the biological relevance of organisms is required. Similar dilemmas appear at all levels of relationships.

Some biologists strive to resolve the problems of naming entities by looking at the biological world completely in terms of phylogenetic patterns, by naming branches in the tree of life. This 'PhyloCode' approach ([www.ohiou.edu/phylocode/](http://www.ohiou.edu/phylocode/)), which is still under development, provides great flexibility; all units can be named if they are meaningful rather than because of their morphological circumscriptions. There is no need to fit everything into the rigid and far too few traditional hierarchical levels. Every lineage can be named if this is relevant for a purpose, and the smallest recognized monophyletic units could be called species. We can expect more debates before everyone becomes satisfied with the PhyloCode, but it seems to be the way forward.

Lars Hedenäs  
(e [lars.hedenas@nrm.se](mailto:lars.hedenas@nrm.se))