



The November issue of *Microbiology Today* on a Systematics theme was very well received. The articles also provoked some interesting debate. The following items have been selected for publication.

Classifying protists

The November 2006 issue included a commentary on our understanding of the diversity of 'Protozoa'. It was editorially heralded with the statement 'After decades of radical reform, protozoan systematics has reached a consensus'. If consensus means that data provide congruent insights and/or that most researchers agree on what the insight is, then consensus has not arrived on either front.

The article mentions 54 suprafamilial taxa. We have assigned these to broad categories (Table 1). The qualifications for placing each taxon in a column are precluded because of space.

Over half of what is referred to as part of the 'settling down' of the consensus remains in debate. There is consensus, but it is with the taxa established by the end of the 20th century on the basis of anatomical studies (Patterson, 1999, The diversity of eukaryotes. *Am Nat* 154, S96–S124). The lack of consensus at higher levels is remarkable given that the logic for using comparative sequence analyses to infer phylogenies seems unassailable. We have shown, through meta-analysis of a large number of molecular surveys, that the monophyly of emergent supergroups 'Amoebozoa', 'Chromalveolates', 'Excavates', 'Plantae' and 'Rhizaria' is contra-indicated by many comparative molecular studies (Parfrey & others, 2006, Evaluating support for the current classification of eukaryotic diversity. *PLoS* in press). The remaining supergroup, the opisthokonts, lacks a clear identity. In the sense of a group that brings together animals and true fungi, it is very frequently

supported, but not sufficiently as to silence dissenters who regard plants as forming the sister group to the animals. The deep elements of the tree of eukaryotes are difficult to resolve for a diversity of reasons. The heterogeneous rates of evolution present problems to the algorithms that are designed to reconstruct phylogeny. This problem is compounded by lateral gene transfer, excessive paralogy, and, we believe, – most significantly – by taxonomic undersampling.

Uncertainty arises from other areas as well. There is an over-readiness to use hypothetical synapomorphies as bases for new taxonomies before adequate

opportunity has been provided to test the hypotheses. The instability of many taxa, whether indicated by their short life as taxa or by the need to continually redefine the concepts (as with Loukozoa or the now lapsed Archezoa), is evidence of premature actions. As an example, the distinction between unikonts and bikonts is weak because the argument depends on features of flagellar (in the article referred to as ciliary – revealing a further absence of consensus) transformations, a process that has been studied in too few microbial eukaryotes for us to be confident of patterns. Instability also emerges from a lack of nomenclatural discipline. Many terms

Table 1. Categorization of suprafamilial taxa reflecting degrees of 'consensus'

Widely accepted	In use but ambiguous	In use but consensus lacking	Widely rejected as monophyletic taxa
Alveolata	Apusozoa	Amoebozoa	Algae
Animals	Cercozoa	Bikonts	Amoebae*
Ants	Chrysomonads	Cabozoa	Heliozoa
Apicomplexa	Choanozoa	Corticates	Flagellates*
Choanoflagellates	Dinozoa	Chromalveolates	Fungi
Chlorarachnean algae	Glaucophyta	Chromista	Plantae
Ciliates	Heterokonta	Diphyllatea	Protozoa
Cryptista	Foraminifera	Discicristata	Sporozoa*
Dinoflagellates	Jakobea	Excavata	
Euglenoids	Malawimonadea	Loukozoa	
Euglenozoa	Opisthokonta	Metamonads	
Haptophyta	Percolozoa	Radiozoa	
Mastigamoebae	Rhizaria	Retaria	
Microsporidia	Thecamonadea	Unikonts	
Myxozoa			
Rhodophyta			
Suctoria			
Viridiaeplantae			

*Taxa rejected in the *Microbiology Today* article.

are not defined when they are used or familiar terms are 'hijacked' and used to badge different assemblages of organisms. As a result, Amoebozoa, Plants, Protozoa, Heliozoa, and Fungi all have more than one meaning and their use in dialogue about eukaryotic evolution remains confusing.

The resolution of the early and main branches of the tree of eukaryotes is not yet in consensus. There is a continuing need for investment in the exploration and resolution of deep branches of the eukaryotic tree of life. Within the US, several major studies within the *NSF Assembling the Tree of Life* programme embrace the microbial eukaryotes. We remain optimistic that increasing taxon sampling combined with dispassionate evaluation of all available evidence will bring more robust understanding of the origin and diversification of eukaryotic life. But not for a few more years at least.

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Tom Cavalier-Smith replies:

This letter mixes sense, over-simplification, tendentiousness, quibbles and misleading error. I entirely agree over the difficulty of resolving basal eukaryotic branches and the need for much more megaphylogenetic research and better taxon sampling, but disagree with numerous other judgements.

I do not use algae, bikonts, unikonts, opisthokonts, chromalveolates, cabozoa, corticates as taxa; nor do I reject Sporozoa. Fungi and Plantae in my sense since 1981 are actually widely accepted as mono/holophyletic taxa, not rejected. Heliozoa as I use it refers only to Centrohelea (holophyletic), plus perhaps a microheliozoan (needs more research). No taxon in column 2 is ambiguous as I define them, but some changed circumscription historically, which is only natural, and is also true of many in column 1, and partly why some taxa are in columns 3–4. Glaucophyta is totally unambiguous; Cercozoa is too, despite crazily erratic misuse by some.

Nobody claims that Protozoa is a holophyletic taxon, but it is a perfectly respectable paraphyletic one (see Cavalier-Smith, 1998, A revised six-kingdom system of life. *Biol Rev* 73, 203–266.).

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The species concept

It was good to read the interesting articles on systematics in the November issue of *Microbiology Today*. The admirable discussions on the species concept, however, suffer from a fundamental misconception that is seen in almost all contributions to this topic in microbiology in recent years. This is the advocacy of a single molecular measure to define species.

The term 'species' was taken from Latin by the early botanists and zoologists in the sense of the smallest distinct groups of individual organisms, that is, the members of a group were not only very similar to each other, but the group was also distinct from nearby groups.

The earliest usage did not prescribe in what manner groups were distinct, though it was usually based on some form of overall morphological similarity. The groups thus corresponded to primary clusters. These were the smallest clusters that were clearly distinct from others. The same can hold good today for groups from molecular sequence or other data. At this taxonomic level it is scarcely material whether the computer analyses are phenetic or phylogenetic.

The concept of primary distinct clusters has been retained by botanists and zoologists to this day, though sometimes qualified by additional criteria. Thus, in plants an extremely homogeneous group, whose members are scarcely distinguishable, is a 'microspecies'. In zoology two groups that do not interbreed but are otherwise scarcely distinguishable are 'sibling species'.

As was noted in these discussions, the concept of a 'biological species' as a group that does not interbreed with others cannot be used in bacteria. But the corollary, that now we can measure molecular relationship a species should be defined by some single chosen level of similarity, is unsound. This cannot accommodate both variable and homogeneous primary clusters. It is ironic that, having found an objective measure of relationship, it should be advocated in this manner for the taxonomic category to which it is least applicable.

Under the definition of a species as a primary cluster, only a single strain (the type strain) is needed to anchor it unambiguously in the system. One may have to work with more strains to find the similarities between them all, and so to obtain primary clusters, but it gives a sounder taxonomy. Taxonomy is an information system. Primary clusters are indispensable for this, both for information retrieval and nomenclature.

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