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 ‘Protzoa’. It was editorially heralded with the statement ‘After decades of radical reform, protistan systematics has reached a consensus’. If consensus means that data provide congruent insights and that most researchers agree on what the insight is, then consensus has not arrived on either front. The article mentions 54 supramolecular 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 Protzoa. Am Nat 154, 580–594). 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 (Purify & others, 2000). Evaluating support for the current classification of eukaryotic diversity PLoS in press). The remaining supergroup, the opisthokhons, 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 at taxa or by the need to continually redefine the concepts (as with Lobozoa or the now-lapsed Anchozoa), is evidence of premature action. 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 cilary – 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 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, Protzoa, 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.

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 megaglyphic research and better taxon sampling, but disagree with numerous other judgments. I do not use algae, bikonts, unikonts, opisthokhons, chromalveolates, cabozoa, corticates as taxa, nor do I reject Sporozoa. Fun and Plantae in my sense since 1981 are actually usually 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 accepted as mono/holophyletic taxa, not rejected. Heliozoa as I define them 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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