**Protist research (cont.)**

***From He et al., (2014):***

Phylogenetic study of Eukaryote tree using 37 ‘euBac’ mitochondrial proteins (universal eukaryote genes of bacterial origin).

Finds the eukaryote root between the excavates and ‘Neozoa’ – i.e. the rest of the eukaryote taxa (SAR, Archaeaplastida etc.).

Strong support for the monophyly of both these groups found in all models tested.

No Metamonads represented in analysis!

Concedes that there are still many missing taxa in dataset, which ‘may be found to branch deep to Discoba, or between Discoba and Neozoa.’

Accepts that root of the eukaryote tree could be within the excavate taxa (paraphyletic excavates). However, the Metamonads are necessarily absent from this analysis as they are all amitochondriate (see Roger et al., 2017) (presumably their MROs lack the protein homologs used in this analysis). Absence of *Malawimonas*, with normal mitochondria, is not explained.

‘Extensive similarities have been identified between Neozoa and *Naegleria*, the only fully sequenced free-living discobid. However, *Naegleria* is still only a single data point in the vast stretch of evolutionary time…’

***From Yabuki et al., (2018):***

*Ophirina* = deep-branching discobid but bears some morpho. Similarity to non-jakobid and non-discobid excavate taxa.

“One hypothesis suggests root may lie near or within Discoba” 🡪 He et al. (2014).

Possesses ventral groove.

*Ophirina* recovered as sister taxon to Jakobids in 156-gene phylogeny, strongly supported. Discoba = sister group to Metamonads, but not strongly supported. No excavates appear to be deeply-branching in analysis, although *Ophirina* is basal with respect to the Discoba.

Presence of two vanes on posterior flagellum in Ophirina is atypical of Discobids.

Presence of perpendicular striations of material in these vanes is ‘evidence against the vanes being a convergent character’ (???)

(some) Stramenopiles and Alveolates also possess these vanes. But they lack the obvious striated electron-dense material.

‘Vanes of Metamonads, Malawimonads and Discobids (inc. *O. amphinema*) resemble each other far more than they do any other comparable (non-excavate) structures.’

***From Vesteg et al., (2019):***

Up to date review of Euglenozoa phylogenetics, including recently discovered group, the Symbiontids.

The three main branches of Euglenozoa are Kinetoplastida (parasites), Diplonemida, and the Euglenida. Most of the Euglenida are free-living phagotrophs or *osmotrophs*. A minority, the Euglenales and Eutreptiales, are photosynthetic.

Origin of phototrophy is thought by many to have occurred from the secondary endosymbiosis of a prasinophyte green alga and a phagotrophic, eukaryovorous euglenid.

Jakobid mitochondrial genome contains highest number of genes among eukaryotes – evidence that it is most similar to the mitochondrial genome of LECA. Why is this necessarily the case???

***From Keeling and Burki (2019):***

Review of Eukarote evolution. Describes the excavate taxa as previously being regarded as a supergroup (along with Malawimonads) but being mostly unsupported in molecular phylogenies.

Reiterates possibility of ancestral excavate hypothesis: ‘similar feeding groove has been found in protists clearly branching in other supergroups, suggesting that the excavate condition might be ancestral to most or even all eukaryotes and not an indication of relatedness in one subgroup.’

Interesting side note on eukaryote diversity discovered via eDNA sampling: potentially very biased against parasites and other symbionts which won’t be detected from within their animal hosts. Seems likely that eDNA sampling is missing a great deal of protist diversity!

Lopsided trees (i.e. huge diversity on one side of a node, only a few spp. on the other) are not uncommon in eukaryote phylogenomic analyses. What is the reason? Lack of sampling on the sparse side? Or a genuine lack of diversity (less successful lineaege)? If the latter is true, as has been shown to be the case in multicellular lineages, then these ‘lone-branch’ taxa, e.g. *Telonema*, *Ancyrocysta*, *Palpitomonas* etc. could be massively informative for studying the evolution of major eukaryote lineages.