Eukaryotes: an update

Eukaryotic Taxonomy

I added 8 taxons: *Colponema*, *Fonticula*, *Telonema*, Katablepharidae, Haplosporidia, Paramyxia, Ellobiopsida, and Hemimastigota, and split Celestina and Heterolobosa, making 51 taxons. I also added 17 characteristics and excluded 6 (because of errors), making 331. The added ones were:

320. posteriorly-directed flagella with fold
321. tripartite mastigonemes
322. myzocytosis
323. nuclear dualism
324. haplosporosomes
325. cell-within-cell division
326. pellicular plates with 2-fold rotationl symmetry
327. metaboly
328. trailing flagellum circumferential
329. ameboid streaming
330. siliceous skeleton 0 - 1+ 2 opaline
331. rpl36 plastid gene
332. flagellar apparatus with 2 concentric microtubular arrays
333. telonemasome-K body
334. ejectisome-R body
335. dodecagonal axonemal microtubular pattern
336. celestite (strontium sulfate)

The TNT format for the data set (starts with 0) was kept.

PAUP (Swofford, 2018), Wagner, and ACCTRAN were used. There were no topological constraints, and there was no weighting. There were 12 optimal trees, 14.67 mln. rearrangements, 1247 steps, and 278 parsimony-informative characteristics. The score of the best tree or trees was 1122, the CI was .35, and the RI was .45.

The new PAUP version is better as it recognizes the largest clade, so Eukaryota shows up, but the percentage of optimal trees it appears in and the resampling values for it are not given; presumably the MPT percentage is 100 and the resampling values are high.

In the majority consensus Histonia again appears in all optimal trees, but the probabilty values also continue to be under 50. Cercobiota, Excavata, Nuclearidae-*Fonticula,* and Pelomyxida-Myxobiota appeared in all optimal trees, but not Cellulosa, Filosa, Chromista, Euchromista, nor Taxopoda-Eulobosa. And there was still no Alveolata nor Dinociliata nor Miobiota (Myzobiota). It should be noted, in regards to Myzozoa, that myzocytosis is considered characteristic of this group, but it occurs as well in Euglenaria, e.g., *Peranema* and *Diplonema*. Since Alveolata and Miobiota are not corroborated by classical evidence they should not be considered monophyletic. Hemimastigota fails to group with Euglenaria and is regarded as a supraregnal lineage in one molecular taxonomy (Lax et al, 2018).

In the probability tree (Table 1) the juxtaposition of several groups hints at possible clades: Chromista (including *Telonema* and Katablephidae), Cercomyxa, *Fonticula*-Nuclearida, and Excavata (including *Colponema*, Hemimastigota, and Euglenaria), as these have synapomorphies.

Heterolobosa are divided into 2 subphyla, Tetramitia and Pharyngomonada (1 genus), based on 18S rRNA analysis (Harding et al, 2013), with the 17-1 helix as the molecular synapomorphy and loss of the R1-C fiber system as the phenotypic synapomorphy for the former, but this arrangement is still

tentative, as it has not been subjected to a cladistic analysis. A new family in Heterolobosa, Psalterimonadidae (9 species in 5 genera, *Psalterimonas, Sawyeria, Monopylocystis, Harpagon,* and *Pseudoharpagon*) has been identified genotypically and corresponds to the phenotype (Panek et al, 2014), as it is anaerobic, amitochondriate, and has a harp-like structure composed of the microfibrillar bundle and rootlet 2, and a fibrous sheet underlying the basal bodies, however, these features also occur in *Percolomonas* and *Lyromonas*. Seven of the Vahlkampfidae genera are quadriflagellate (*Tetramastigameba, Tetramitus, Willaertia*, *Monopylocystis, Harpagon, Pharyngomonas,* and *Percolomonas)*, like some polymastigotes and some green algae; *Psalterimonas* has 4 sets of 4 flagella each. Ten genera have been added to Vahlkampfidae in the last several years and 3 to Gruberellidae, making a total of 29. Vahlkampfidae and Schizopyrenida are regarded as polyphyletic, but there needs to be a cladistic analysis based on classical evidence to confirm them as such.

A new algal group, Chromales (erroneously called Chromida), comprising *Chromera* and *Vitrella,* has been discovered (by Moore et al in 2008) and is possibly related to Telosporidia (Apicomplexa), a group considered to be formerly phototrophic, and both groups have red algal plastids (Moreira and Lopez-Garcia, 2014; Linares et al, 2014). The non-photosynthetic apicoplast of Telosporidia, which has 4 membranes, like Chromista, and the putative kinship with Chromales are regarded as an indication of loss of chloroplasts, with a subsequent change to a parasitic life style.

The traditional classification for Sporozoa, established by Leuckart in 1879, contained subclasses Telosporidia (orders Gregarinida, Coccidia, and Hemosporidia), Acnidosporidia (orders Sarcosporidia and Haplosporidia), and Cnidosporidia (orders Myxosporidia, Actinomyxidia, Microsporidia, and Helicosporidia). Helicosporidia (1 genus) turned out to be a green alga, and Sarcosporidia was placed in Coccidia as a family, and as microsporidians and myxozoans (myxosporidians) go to Fungi and Animalia, respectively, the name Telosporidia is synonymous with Apicomplexa and is designated as such by Margulis and Schwartz (1998).

Table 1. Probability Tree for Eukaryotes.

		bootstrap		jackknife
Hypothetical Ancestor				
Eukaryota				
Cyanidioschyzon				
Metakaryota		75		77
Cyanidiobiota	69		72	
Neokaryota		81		79
Glaucobiota				
Rhodobiota		85		81
Stylonematales				
Rhodellae				
Porphyridiales				
Eurhodobiota				
Plasmodiophorae				
Spongomonada				
Plantae				
Telonema				
Katablepharidae				
Chlorarachnia				
Cryptomonada				
Haptomonada				
Heterokonta				
Cercomonada				

Myxobiota				
Metacercobiota	73		69	
Opisthokonta	71		63	
Ascetospora		70		70
Marinamebae		68		63
Foraminifera				
Actinopoda		57		62
Heliocelestina		94		95
Desmoth.-Centrohel.	83		77	
Celestina		95		90
Pheodaria				
Taxopoda				
Dinoflagellata				
Ciliophora				
Apicomplexa				
Fonticula				
Nuclearida				
Vampyrellida				
Gromida				
Euglyphida				
Colponema				
Jakomastigota		88		79
Heterolobosa		97		99
Hemimastigota				
Euglenaria				
Pelomyxida				
Eulobosa				

The results were again disappointing, as the homoplasy was high (but this would be expected because of the large matrix), and the probability tree convincingly supported only 13 clades out of a possible 41, which is only about a quarter. However, Celestina Heterolobosa, were robustly confirmed, and the confidence for Opisthokonta and Foramaxia (Retaria is not a good name as actinopods do not have reticulate pseudopods) were substantially higher.

The rpl36 gene, which unites Hacrobia (Haptomonada, Picorhodobiota, *Telonema*, Cryptomonada-Katablepharidae, Centrohelida), was included in the analysis, but the group was not at all recovered.

Prerhodophyceae+Rhodobiota is often recovered in genotypic taxonomies, however, the sampling is limited in most. Red algae most likely evolved their plastids from Cyanobacteria which has chlorophyll a only and phycobilins, while plant plastids probably evolved from Chloroxybacteria which has chlorophyll a and b and no phycobilins. There were at least 4 secondary plastid symbiogeneses: chlorophyll c in chromistans (from a red alga), chlorophyll b in chlorarachnians (from a green alga), chlorophyll b in euglenoids (also from a green alga), chlorophyll c in dinoflagellates (from a heterokont, hence the 4 fucoxanthins, which occur in heterokonts, found also in dinoflagellates, and the symbiote is still recognizable), and possibly in Telosporidia (from a red alga).

Red algae as basal is supported by molecular evidence (Hori and Osawa, 1987; Hori et al, 1990; Luttke, 1991; Nozaki et al, 2007) and Archeoplastida as polyphyletic is also supported by molecular evidence (Hori and Osawa, 1987; Hori et al, 1990; Luttke, 1991; Olsen, 1994; Bhattacharya, 1995; Nozaki et al, 2007; Yoon et al, 2008; Kim and Graham, 2008; Tekle et al, 2008; Parfrey et al, 2010; etc.) as well as previous classical evidence (Lipscomb, 1985, 1989, 1991). Red algae as the most

primitive eukaryotes was agreed to also by Pascher (1931), Copeland (1947, 1956), Vada (1952), Chadefaud (1960), Jeffrey (1971), Leedale (1974), Margulis (1974), Edwards (1976), Taylor (1978), Cavalier-Smith (1978), Parker (1982), Takhtadzhyan (1983), Möhn (1984), and Starobogatov (1986, who, as well, separated *Cyanidium* as phylum Cyanidiophyta). They are considered as the most primitive eukaryotic plants (in the widest sense, so more primitive than funguses) in Moreau (1960) and Caratini (1971) and considered as isolated in the former. Van Den Hoek and colleagues (1995) have glaucophytes as the earliest eukaryotic algae, with red algae next.

And Archeoplastida as polyphyletic is also supported by molecular evidence (Hori and Osawa, 1987; Hori et al, 1990; Luttke, 1991; Olsen, 1994; Bhattacharya, 1995; Nozaki et al, 2007; Yoon et al, 2008; Kim and Graham, 2008; Tekle et al, 2008; Parfrey et al, 2010; etc.) as well Lipscomb (1985, 1989, 1991).

Pueschel remarked in 1990, "Being an ancient lineage, the red algae have undergone a broad range of modifications in cellular organization. Even the spectrum of morphological possibilities, from unicellular forms . . . to complex . . . parenchymatous thalli, fails to convey the degree of cellular diversity" (Saunders and Hommersand, 2004). As noted in Saunders and Hommersand, the morphological and fine structural diversity of red algae is as striking as their genetic variation revealed in molecular studies. There are at least 3 patterns of Golgi association, 3 methods by which cells achieve multinuclearity in development, several methods of establishing intercellular connections through cellular fusions and pit-plug formation, 5 distinct patterns of mitosis, 3 patterns of cytokinesis, and 3 patterns by which the various reproductive structures are formed.

Van Den Hoek et al (1995) remark that a comparison of evolutionary distances based on 5S rRNA (Hori and Osawa, 1987) between genera within various groups show that in red algae they are higher overall than those between genera of other algae, higher plants, and animals, which attests to rhodobiotes' great antiquity and that this agrees with the fossil record. Red algae have 22-56, green algae <.02-45, and brown algae 1-5. Mammals have 0.

The fossil record corroborates red algae as the ancestral eukaryotes (Table 7-5) since the oldest undisputed eukaryotic fossil identified as a member of a modern group is *Bangiomorpha* Butterfield 2000 (Rhodobiota s.s.) from 1.2 bya in the Middle Proterobiotic found in the Hunting Formation on Somerset Island in Nunavut, Canada (Javaux, 2007). There are no fossils of *Cyanidioschyzon*, nor of the other 2 Prerhodophyceae genera, but, as it is basal among the known forms, it would probably be about 2 bln. yrs. old, since the oldest eukaryote is an acritarch (*Valeria* Horsfield, 1829) at 1.8 bya (Javaux, 2007). Acritarchs are spherical, organic-walled microfossils, named by Wm. Evitt (1963), a geologist at Stanford, from the Greek *acrit* for uncertain or confused and *arch* for origin. There are about 400 genera (Corliss, 1984).

Dinoflagellate chemical markers have been reported from several Proterobiotic and even Archeobiotic units as old as the 2.5-2.8-bln.-yr.-old Mount Bruce Supergroup, Pilbara Craton, Australia (Porter, 2006), but, given its age, the Archeobiotic occurrence is attributed to an independent (non-dinoflagellate) origin and the Proterobiotic occurrences have been interpreted as either possible contaminants or dinosteroid precursors that do not by themselves indicate dinoflagellates were present. Interestingly, the Paleobiotic record of dinosteroid abundance correlates well with that of acritarch diversity, suggesting that many acritarchs may represent dinoflagellate cysts. Many modern dinoflagellate cysts lack diagnostic characteristics, and would probably be grouped with the acritarchs if found as fossils. Several research papers have suggested certain Proterobiotic acritarchs might be dinoflagellate cysts, which showed that some Ediacaran acanthomorphic acritarchs have chemical and fine-structural traits consistent with a dinoflagellate affinity, although this is contested by others.

However, the acritarchs lack a characteristic dinoflagellate feature, the archaeopyle or excyst pore through which the dinoflagellate exits the cyst; they also lack the cingulum groove, which is characteristic of many dinoflagellates. Various other algae can form cysts that are superficially similar. It is not clear what the acritarchs were. They probably included a number of eukaryotic algal clades,

and are therefore a "form taxon", including all those spore-shaped fossils that have not been conclusively assigned to another group.

Porter adds that because the taxonomic distribution of these traits is not well documented, it is impossible to know whether their occurrence in both fossil and modern groups is due to homology or convergence, and, if due to homology, whether their occurrence reflects an apomorphic or plesiomorphic state. The earliest phagotrophs known are arcellinids (lobose testate amebas) dated at 742 mya (in the Neoproterobiotic), found in the Chuar Formation, Grand Canyon (Porter et al, 2003).

Green algae are sometimes said to be the oldest eukaryotes at 1.5 bln. yrs. (Emiliani, 1995), and Loeblich placed the origin at 900 or 1000 mya (at the beginning of the Late Proterozoic), but these are disputed and UCMP states fossils superficially resembling green algae date back to the Precambrian. MicrobeWorld.Org says they go back 500-600 mln. yrs. Prasinophycean phycomas are readily fossilizable and their distinctive morphologies have permitted their recognition in rocks as old as Precambrian age (Margulis et al, 1990). The calcified Dasycladales fossils are the second oldest of the green algae, dating back to the Precambrian (Margulis et al, 1990).

The fossil record has an abundance of autotrophs in the Precambrian and a paucity of heterotrophs in that same eon, which indicates autotrophs are the most primitive eukaryotes, contrary to the prevailing and probably erroneous opinion.

Porter says heterotrophs are necessarily the earliest eukaryotes but does not substantiate this extraordinary claim. Presumably she is refering to molecular phylogenies and therefore sees them as foolproof, which they are definitely not. She offers 2 possible explanations for the absence of heterotrophs in the Precambrian. One is that heterotrophic diversity may have been low due to limited primary productivity in Mesoproterozoic oceans. Evidence for this is primarily hypothetical, and empirical evidence is even more uncertain. The other is, according to her, more likely and is taphonomic (fossilization) bias due to algae having organic walls which make them more preservable, while these are supposedly rare in heterotrophs, and mineralized eukaryotes from the Precambrian are rare. But organic walls are not rare in funguses and Fungi is a very large group, so the argument is invalid. Of course, the most probable explanation is that autotrophs are the earliest eukaryotes, and prerhodophyceans are the most primitive eukaryotes we know of.

My phylogenies are mostly in accord with the fossil record as only 3 taxons out of 10 (Foramaxia counted as 1), Heterokonta, Eulobosa, and Haptomonada, are not in agreement with it, appearing earlier in the fossil record (the first 2) or later (the 3rd) than indicated in the phylogenies, and it's possible the disagreements are because of dating error (see later). In the typical molecular taxonomies 6 of 10 are in disagreement with the fossil record: Rhodophyceae, Heterokonta, Plantae, Eulobosa, Animalia, and Fungi, the first 3 later than they should be and the second 3 earlier than they should be.

Molecular supergroups are usually touted as certain or probable but most are only moderately, ambiguously, or weakly supported. Philippe et al (2000) state that only opisthokonts, archeoplastids, and alveolates are unambiguously recognized by molecular taxonomists, but it is only the first of these that is strongly supported.

Here is a summary from the review/survey of genotypic analyses by Parfrey et al (2006) (the 1st column is the number of studies the taxon occurs in, the 2nd is the number of studies including the taxon, and the 3rd is the percentage; figures include both nuclear and plastid genes):

Opisthokonta	43	51	84.3
Rhizaria	19	29	65.5
Amebozoa	20	42	47.6
Archeoplastida	26	61	42.6
Chromalveolata	16	60	26.6
Excavata	9	39	23

Alveolates, chromistans, unikonts, bikonts, and retarians were not included, but apparently, chromistans are not usually recovered, and alveolates are probably not either or are weakly supported. Chromalveolates, like archeoplastidans, are recovered with plastid genes but not nuclear ones.

Baldauf et al (2000) present an analysis of various proteins, single, pairwise, 3-way, and all-4, in 15 categories. The 4 proteins are EF-1alpha, actin, alpha-tubulin, and beta-tubulin. Of the 18 groups included, bootstrap values showed moderate (50-74) to strong (75-100) support, except for Chromalveolata (Heterokonta+Ciliata-Apicomplexa), Archeoplastida (plants, red algae, and glauophycans), Plantae+Rhodobiota, Miozoa (ciliophores and apicomplexans), and Excavata. Conosa was not included, however, Amebozoa (Eulobosa-Myxobiota) was. Bikonta and Chromista were not included either. The following is a summary of the 8 supergroups included (figures include both nuclear and plastid genes).

	strongly supported	moderately supported	total	%
Opisthokonta	11	2	15	80
Amebozoa	3	0	4	75
Unikonta	6	5	15	57
Miozoa	4	2	15	33
Discicristata	4	0	15	27
Chromalveolata	1	2	8	25
Plantae+Rhodobiota	0	1	8	6
Archeoplastida	0	0	8	0

The percentage I calculated from the score--2 points for strongly supported, 1 for moderately supported, and 0 for weakly supported--out of the total possible score. The following are the score percentages including also other proteins and rRNA (SSU, LSU, and combined) for resampling support presented in the article from other analyses:

Amebozoa	87.5
Opisthokonta	62
Miozoa	50
Unikonta	33
Chromalveolata	27.5
Discicristata	27
Plantae+Rhodophyceae	21
Archeoplastida s.l.	12

Combining Baldauf et al with Parfrey et al we get the following averages:

Opisthokonta	73
Amebozoa	68
Archeoplastida	27
Chromalveolata	25
Excavata	25

Parfrey et al (2010) say that their analysis demonstrates that supergroup taxonomies are unstable and that support for them varies tremendously, indicating the currently accepted classification for eukaryotes is likely premature, yet it is touted as certain by most molecular taxonomists, and it is not

likely premature, it is certainly and egregiously in error.

They also point out that Archeoplastida support comes primarily from phylogenomic analyses and these may be picking up misleading EGT (endosymbiotic gene transfer) signal of genes independently transfered from the plastid to the host nucleus in the 3 archeoplastid clades.

Stiller and Harrell (2005) emphasize that the "clade" can be explained by "short-branch exclusion" and "subtle and easily overlooked biases can dominate the overall results of molecular phylogenetic analyses of ancient eukaryotic relationships. Sources of potential phylogenetic artifact should be investigated routinely, not just when obvious 'long-branch attraction' is encountered." Tekle et al (2009) point out that red and green algae have different rubisco protein complexes and light-harvesting compounds and state that support for the monophyly of Archeoplastida host genomes is generally high in analyses of large data sets (phylogenomics) with *limited taxon sampling,* and reanalysis of Rodriguez-Ezpeleta and colleagues' data, including additional taxons of interest and with removal of fast-evolving sites, which may produce spurious relationships, did not support the monophyly of the group, and that their (Tekle et al's) *taxon-rich* analyses of the 4 most-sampled markers (SSU, actin, alpha-tubulin, and beta-tubulin) similarly failed to recover it. They also state that these results suggest incongruence due to the conflicting signals of the host and the plastid genomes, but they also show that a cause of the artifact is limited taxon sampling.

Archeoplastida are not supported in my analysis, as expected, as they have no synapomorphies, are weakly supported genotypically, and are contradicted by Lipscomb's classical analysis, by 35 molecular analyses, and by Goloboff et al's combined analysis.

Foramaxia, combining actinopods and forams, which receive a high confidence value of nearly 80 in TNT, are partly corroborated in several molecular studies.

Rhizaria are also not recovered, not surprisingly, as the group is ill-defined and only moderately supported in molecular phylogenies (Parfrey et al, 2007), statistical support for it is inconsistent in multigene genealogies with larger taxon sampling (Yoon et al, 2008), it is ambiguously supported in Goloboff et al (2009), and is an obviously artificial group.

So, in other words, those who consider molecular taxonomy as foolproof or superior not only disregard the phenotypic evidence that doesn't agree with it, but also the molecular evidence that goes against their clearly erroneous view of eukaryotic phylogeny.

Possible Mini-Kingdoms

Pawlowski (2013) identifies 8 eukaryotic "micro-kingdoms" ("micro-kingdom" is a rank) which are Apusomonadidae-Ancyromonadidae, Collodictyonidae-Rigidifilida, Katablepharidae-Cryptophyta, Glaucophyta-Picobiliphyta, Centrohelida, rappemonads, Haptophyta, and Telonemia. Most or all, however, may well be related to larger groups.

Apusomonada branches robustly with Thaumatomonada in my classification, and Ancyromonada have affinities with either cercomonads or euglenarians as *Ancyromonas* Kent, 1880 is considered by some as a junior synonym for *Bodo,* which is in Kinetoplastida, and Mylnikoff, writing in 1990, treats it as *Heteromita,* which is in Cercomonada (Patterson & Zölffel, 1991). Contrary to Pawlowski, Ancyromonadidae do not form a clade with Apusomonada in molecular classifications (Atkins et al, 2000). *Collodictyon* Carter, 1865 is probably the same as *Tetramitus* (Patterson & Zölffel, 1991), which is in Vahlkampfidae.

Centrohelida robustly branches with most other actinopods in my analyses.

Little is known about the newly discovered rappemonads (named for Michael Rappé of the U. of Hawaii), but they branch with haptomonads and cryptomonads in molecular taxonomy and have 1 or 2 bilobed chloroplasts, like haptomonads tend to have (Kim et al, 2011).

Breviata is another group considered of uncertain position, but *Mastigamoeba balamuthi* (formerly known as *Phreatamoeba balamuthi*), which is a pelobiote that was isolated from a well in

Gambia by Chávez et al in 1986, is now studied under the name of *Breviata* Walker et al, 2006 (Mastigameba - bms.ed.co.uk).

'Picobiliphytes' were at first thought to be phototrophic but later were found to be heterotrophic, without plastids and without photosynthesis (Seenivasan et al, 2013; Moreira and Lopez-Garcia, 2014). They branched with Cryptomonada-Katablepharidae in Not et al in 2007 and Cuvelier et al in 2008, but with less than 60% bootstrap support; with *Telonema* with 80-90% confidence and indirectly with Haptomonada, Cryptomonada-Katablepharidae, and Glaucobiota in Yoon et al in 2011; and with Glaucobiota in Burki et al in 2012 with less than 60% support (Moreira and Lopez-Garcia, 2014).

The picozoan cell is divided into 2 parts, one containing the nucleus, mitochondrion, dictyosome, and flagellar apparatus, and the other containing a cytostome, food vaculoes, and vesicles, divided by a vacuolar cisterna of unknown function. And it has an atypical, cyclical 'jump, drag, and skedaddle' motion. (Moreira and Lopez-Garcia, 2014).

Supplementary Information

For the phylogenetic classsification of Plantae, the names of the 2 basic divisions should be Cruciata (or Cruciophyta) and Unilaterala (or Unilaterophyta), but Protochlorophyta and Neochlorophyta could also be used.

The added and split taxons are included in the habitats table and the stats for them are the following:

		ords.	fams.	gen.	sp.
Polycystina		2	17	61	?
Acantharia		4	20	50	150
Schizopyrenida		1	2	14	?
Ellobiopsida		1	1	5	?
Haplosporidia	1	2	3	31	
Paramyxia		1	1	3	6
Hemimastigota		1	1	3	?
Acrasida		1	1	2	?
Katablepharaceae		1	1	2	?
Colponemia		1	1	1	?
Telonemia		1	1	1	?

Table 3. Taxons Listed by Habitats (++ = predominant)

	oceanic	neritic	inttdl	brksh	frshwtr	terrestrial
Eukaryotes						
Myxobiota						+
Acrasia						+
Plasmodiophorae						+
Fonticula						+
Desmothoracida				+		
Prerhodophyceae				+		+
Hemimastigota				+		+
Cormophyta		+	+	+		++

Amastigomycota		+	+	+	+	++
Euglyphida		+	+	+	++	++
Chytridiomycota		+			++	++
Metazoa	+	+	+	+	+	++
Gromida		+	+	+	+	+
Eulobosa		+	+		+	+
Katablepharidae		+	+		+	
Jakobida		+			+	+
Schizopyrenida		+			+	+
Vampyrellida		+			+	+
Polymastigota		+			+	+
Apicomplexa		+				++
Cercomonada				+	+	+
Euglenoida		+	+	+	++	+
Green Algae	+	+	+	+	++	+
Heterokonta		++	++	+	++	+
Rhodobiota		++	++	+	+	+
Cryptomonada	+	+	+	+	+	
Haptomonada	+	+	+	+	+	
Dinoflagellata	+	++	+	+	+	
Haplosporidia		+		+	+	
Ellobiopsales		+			+	
Spongomonada				+		
Glaucobiota				+		
Chlorarachnia		+	+	+		
Pelomyxida		+		+		
Nuclearida		+		+		
Heliozoans		+		+		
Choanoflagellata		++		+		
Ciliata	+	+		+		
Forams	+	+				
Pheodarea	+	+				
Polycystina	+	+				
Acantharia	+	+				
Paramyxea	+?	+				
Telonema	+?	+				
Colponema	+?	+				

(Data mostly from Margulis et al, van den Hoek et al, Lee et al, Holt et al, and Parker).

Plasmodiophorae, Haplosporidia, Paramyxea, Apicomplexa, and Polymastigota are entirely or almost entirely parasitic, the first in land plants and the latter 4 in animals; they are designated here according to the habitat of the host. And epizoic or epiphytic forms are designated according to the organism they live on, e.g., *Cryptochlora*, a chlorarachnian, was found on green algae in the supralittoral zone so is terrestrial.

Convenience Classification

And as molecular phylogenies also fail to support a clear taxonomy, showing manifestly artificial

groups such as Prerhodophyeae, Archeoplastida, and Rhizaria, and misplacing Metabacteria, Opisthokonta, and the protozoan Amebae (all of which are derived instead of primitive) because of LBA (long-branch attraction), and some others that have substance have also weak support like Chromalveolata and Chromista or Euchromista, as the fossil record will remain incomplete, and as missing information continues, it appears an accurate phylogenetic classification at the super-group level is unattainable in any near future and may never be. In such a situation, convenience classification becomes even more important and is what we should use more than evolutionary taxonomies at the super-group level (Figure 1, Table 1).

A 4-kingdom arrangement without a protistan kingdom is more useful and informative, unlike most modern alternative systems, which had a protistan kingdom of some sort. This particular taxon, maintained by gradists as monophyletic and phylogenetic, is especially artificial even by convenience standards.

The 4 kingdoms are Bacteria (prokaryotic, mostly osmotrophic, and with typically a murein wall), Phyta (usually autotrophic, producing, and with a typically cellulose wall), Mycota (osmotrophic, decomposing, mostly with a chitinous wall), and Zoa (phagotrophic, consuming, with no wall). Phyta, Mycota, and Zoa can also be called Autotropha, Osmotropha, and Phagotropha. The 2 superkingdoms are Prokaryota and Eukaryota. The walled, eukaryotic kingdoms are placed side by side. It is biaxial so horizontal lines separate cristal types and vertical lines separate trophic modes (a double line separates nuclear type). Terrestrial and usually multicellular forms are placed higher, and acquatic, usually unicellular ones lower. Related or similar groups in the same subkingdom are placed close together and those across kingdoms are placed on the same line. The bases are, then, trophic mode/functional community, wall composition, presence or absence of a wall, cristal shape, chlorophyll type, number of chloroplast envelopes, ecology, and nuclear type. The table places together the phylogenetically related taxons across kingdoms.

Exceptions are Acantharia with lamellar cristas (sometimes said to be flattened tubular like Cryptomonada); Mesozoa and water snakes (in Animalia), *Aphelidium* (in Fungi), trypanosomes (in Kinetoplastida), and several jakobids with tubular cristas (trypanosomes also have discoid cristas in their life cycle and *Aphelidium* also have lamellar cristas in theirs); Mycetozoa has phagotrophic stage; Vampyrellae vesicular cristae; several schizopyrenids have a walled (cyst) stage.

Similar taxonomies were Takhtadzhan's, but ochrophyceans were lumped with green algae, and blue bacteria were separated from eubacteria, and Leedale's pteropod scheme, and the internal arrangement for the component kingdoms is different from theirs.

In Heterogracilicutes, Neganaerobia are parasitic (except for Desulfobacteria) and unpigmented (except for Enterobacteria), while Negaerobia are free-living (except for a few in Pseudomonada and Flavobacteria) and pigmented (except for Planctobacteria and Caulobacteria). In Autogracilicutes, the exceptions are Chloroflexi and Rhodobacteria, which are heterotrophic. Clatabacteria are the chemolithotrophic g roups. In Metabacteria, the 3 major groups each have both auto- and heterotrophic representatives.

Euglenophyceae is Euglenales (the Euglenida of Busse and Preisfeld), and it contains all the phototrophic genera of Euglenaria, Aphagea contains its osmotrophic genera, and Euglenozoa all the phagotrophic ones (Kinetoplasta, Diplonemia, Petalomonada, and Peranemia, except *Cryptobia*, in Kinetoplasta, which is osmotrophic; the Trypanosomes, in Kinetoplasta, may be osmotrophic, as they are parasitic). Dinophyceae contain the phototrophic species and there are 7 orders (Prorocentrales, Dinotrichales, Phytodinales, Thoracospherales, and Gonyaulacales; 2, Dinophysiales and Gymnodiniales, have members that are either phototrophic or phagotrophic), while Dinozoa are phagotrophic and contain 5 orders (Blastodiniales, Oxyrrhinales, Noctilucales, Syndiniales, and Dinamebidales). Telascetospora have a proteinaceous-walled, mostly oocyst, stage, are sporulating, and are osmotrophic, so they are placed in Mycota; they include Telosporidia and Ascetospora (Haplosporidia+Paramyxia). Heteroflagellata contains Opalinata-Proteromonada, Bicosecidales, and

Pseudodendromonadales. Pseudofungi and Hydromyxa make up Heteromycota.

Figure 1. Convenience Classification.

Table 2. Tabulated Convenience Classification.

spk. Prokaryota
kgdm. Bacteria
sbk. Eubacteria
spph. Togabacteria
spph. Gracilicutes
phyl. Heterogracilicutes tax. nov.
cl. Neganaerobia tax. nov.
cl. Negaerobia tax. nov.
phyl. Autogracilicutes tax. nov.
cl. Clatabacteria tax. nov.
cl. Photobacteria
spph. Mollicutes (Tenericutes)
spph. Firmicutes
phyl. Endospora
phyl. Actinobacteria
sbk. Metabacteria (Mendosicutes)
spk. Eukaryota
kgdm. Phyta
sbk. Rhodophyta (Prerhodophycota, Rhodophycota, Glaucophycota)
sbk. Chlorophyta
spph. Chlorophycota (Prasinophyceae, Euchlorophyceae, Charophyceae)
spph. Cormophyta
phyl. Bryophyta
phyl. Pteridophyta
phyl. Spermophyta
sbk. Euglenophyta
sbk. Tubuliphyta
spph. Chlorarachnia
spph. Chromophyta
phyl. Ochrophyta
phyl. Dinophyta
kgdm. Mycota
sbk. Fungi
hpph. Chytridiomycota
hpph. Amastigomycota
spph. Zygomycota
spph. Diplokaryomycota
phyl. Microsporidia
phyl. Ascomycota
phyl. Basidiomycota
sbk. Tubulimycota
phyl. Plasmodiophorae
phyl. Myxomycota
phyl. Telascetospora
sbph. Ascetospora
sbph. Telosporidia (Apicomplexa)
kgdm. Zoa

sbk. Animalia
infk. PrimiAnimalia (Spheroformazoa, Cadherozoa [Filasterozoa, Choanozoa])
infk. Metazoa
hpph. Diploblastica (Parazoa, Placozoa, Mesozoa, Myxozoa, Actinozoa)
hpph. Triploblastica
spph. Protostomia (Helminthes, Arthropoda, Mollusca)
spph. Deuterostomia (Lophophorata, Echinodermata, Chordata)
sbk. Discozoa
phyl. Pseudociliata
phyl. Heterolobosa
phyl. Nucleariidae
sbk. Tubulizoa
phyl. Marinozoa (actinopods, forams)
phyl. Ciliata
phyl. Flagellata
cl. Spongomonada
cl. Colponemia
cl. Hemimastigota
cl. Jakomastigota
phyl. Amebae
sbph. Lobosa
cl. Pelomyxida (ameboflagellates)
cl. Eulobosa
sbph. Filosa
cl. Cercomonada (ameboflagellates)
cl. Vampyrellae
cl. Testafilosa

Geology

Concerning the geology chapter, Chapter 19, Written in Tablets of Stone, it should be added that radioactive decay rates have been found to be unstable, by David Alburger and colleagues at Brookhaven, contrary to the conventional view of a constant rate, as they may be subject to seasonal changes caused by the Sun (Solar ghosts may haunt Earth's radioactive atoms, 2009, New Scientist.Com). This could have important implications for geological time.

In Cremo and Thompson's Hidden Archeology book there is evidence presented, for example, of anatomically-modern, human skeletons 60 mln. yrs. old and cultural artifacts 2 bln. yrs. old, which can make sense only if the dating methods are in error.

Also, soft tissue and biomolecules in dinosaurs have been found surprisingly preserved by Mary Schweitzer and colleagues in 2005 (Soft-tissue vessels and cellular preservation in *T. rex*, Science), yet such preservation (68 mln. years) is ruled out by current paleontological models, as DNA is supposed to last only about 100,000 yrs. (at a constant 10° C) and protein a few million years (at a constant 10° C) (San Antonio et al, 2011 (Dinosaur peptides suggest mechanisms of protein survival, Plos One). This would mean the Earth is actually young, so evolutionary processes would be much faster than we would have thought.

However, possible explanations of how such preservation could occur have been put forward by San Antonio et al in 2011 (loc. cit.) and Schweitzer herself in 2014 (A role for iron and oxygen chemistry in preserving soft tissue, cells, and molecules from deep time). But they are unconvincing.

Whatever the case, many studies have demonstrated speciation happens far more quickly than

Darwin ever imagined, in the space of decades, which biologists call rapid evolution. Human influence has been invoked as a cause, but not all cases can be so explained, and there is no reason to suppose rapid evolution has not occured before humans and that there can't be other causes, such as earthquakes, volcanic eruptions, and extreme weather. Also, in some of the fish specimens in the Santana Formation in Brazil, fossilization was so rapid that detailed cellular structure may be seen with microscopic examination (Flickr.Com). So, biologically speaking, there may be nothing surprising about a young Earth.

Furthermore, it may be that the rate of geological processes has been similarily overestimated. For instance, gold can form in only 55,000 yrs. instead of the 100s of 1000s or mlns. in conventional thinking (Gold Mine Deposited Rapidly, GeoTimes.Org).

And there are other facts that suggest a young earth:

The total concentration of uranium salts in the oceans (estimated at less than 1E+17 grams) could be accumulated in less than 1 million years.

The atmospheric content of helium-4 (the most abundant isotope of helium) is only 1/30 that of the amount it should be if the Earth were 4 bln. yrs. old. The current content indicates an age of only 133 mln. yrs.

There would be over 50 feet of meteoritic dust all over the surface of the Earth if the Earth was 5 bln. years old.

If humanity is really about 2.5 million years old, using cautious population estimates (2.4 children per family, average generation, and life span of 43 years) the world population would have grown from a single family to 10 to the 2700th power over one million years.

Some geologists find it difficult to understand how the great pressures found in some oil wells could be retained over millions of years.

Since the amount of C14 is now increasing in the atmosphere, it may be assumed that its quantity was even lower in the past. This condition would lead to abnormally low C14/C12 ratios for older fossils. So the age of the atmosphere might be less than 20,000 years old.

But, as Stansfield (1977, pp. 80-84) says, all these factors are questionable because they assume constant rates, when the rates are likely to have fluctuated widely over Earth history, but he admits that, for lead 206 and uranium 238, each assumption is a potential variable, the magnitude of which can seldom be ascertained. And he also admits,

"It is obvious that radiometric techniques may not be the absolute dating methods that they are claimed to be. Age estimates on a given geological stratum by different radiometric methods are often quite different (sometimes by hundreds of millions of years). There is no absolutely reliable long-term radiological 'clock.'"

In other words, we can't claim to know the age of the Earth with any degree of accuracy or certainty, but the figures proposed by the Chaldeans (Holmes, 1913) and ancient Chinese (Drake, 2007), of 2.15 mln. years and 88 mln. years, respectively, which I mention in the same chapter, appear to be more realistic, especially the latter.

Below is a speculative exercise based on the Chinese figure. We can assume the age for heterokonts is overestimated, as they branch later than plants. And possibly the age for haptomonads

and eulobosans is also erroneous, as they branch earlier and later, respectively, than the ages estimated for them.

Table 4. Taxons Indicated by Geological Time (according to the fossil record) and Trophic Mode (the start years are given for each period in mya).

		autotrophic	osmotrophic	phagotrophic
Cretaceous	1.3			
	2.8			Pheodaria
Jurassic	2.88			
Triassic	4.2			
	4.4	Dinoflagellata		
Permian	5			
Carboniferous	5.7			
	6	Haptomonada		Ciliophora
Devonian	7.2			
Ordovician	8.8			
	10	Euglenoida		
Cambrian	10.1			
Late Proterobiotic	10.86			
	11			Polycistina
	11.6			Forams
	12		Fungi	
	14			Animalia
	15	Plantae		Eulobosa
Middle Proterobiotic	18			
	20	Heterokonta		
	24	Rhodobiota		
Early Proterobiotic	36	acritarchs		
	72	Cyanobacteria		

Errata:

On page 248 Haplosporidia are said to be diplokaryotic but they apparently are not. They are binucleate like typical Fungi, Microsporidia, Ciliophora, Paramyxea, and some forams, and there is confusion over the terms 'dikaryotic" and "diplokaryotic", as they are used interchangeably or synonymously, for Fungi and Microsporidia, but are also defined differently, the latter often as a pair of diploid nuclei, and the former as mycelium containing pairs of closely associated nuclei typically of different mating types (genetically different). Haplosporidia, Paramyxea, and Ciliophora are said to have nuclear dualism or nuclear dimorphism, but are not usually considered di- or diplokaryotic. There is also heterokaryosis, which is defined in the same way as the dikaryon and as nuclear dimorphism, but is said to occur in funguses but also ciliates and forams!

On page 230 ebrids are said to possess a dinokaryon (permanently condensed chromosomes), which has been affirmed as recently as 2000 in Lee et al, but in the last few years it apparently has been found that they do not.

Pseudociliata (=*Stephanopogon* Entz, 1884) probably goes with Heterolobosa instead of Euglenaria because of similarities in fine structure and molecular biology with *Percolomonas*

(Vahlkampfidae) in particular (Yubuki & Leander, 2008). In Margulis and Chapman's Kingdoms and Domains from 2009, the group includes 4 genera: *Stephanopogon, Percolomonas, Psalterimonas, and Pernina.*

In Table 15-6 of Empire Biota a node is missing between Sauropsida and Anapsida, so it should be:

Amniota
Sauropdsida
Mesosauridae
Eureptilia
Anapsida
Diapsida

And on p. 214 the gross misrepresentation in phonetic transcripton of certain French vowels, which I discuss in my book The Tree of Language, includes also the short u (ʌ in the IPA) as in the English 'fun', usually written as 'o', as in *vote* or *chopine,* which is misrepresented as a long 'a' (ɔ in the IPA)(this does occur, however, in the combination 'or'), and since recently the final 'e' (œ in the IPA), which is misrepresented as the schwa (neutral vowel)(ə in the IPA). The sounds are not dialectical, they occur universally, as much in Québec as in France and elsewhere. I asked 4 linguists why this practice exists, but they did not answer the question, probably out of embarassment.

We can guess the puzzling practice is political (and obviously nonsensical), as so often happens in orthodox science, which is not very rational, so for all its bizarreness and seeming inexplicability, there might be method to the madness. It seems to be a policy of accomodating the Anglophone accent, whereby the short 'a' of French (æ in the IPA) is gratuitously pronounced long (for unknown reasons), so the medial 'a' (a in the IPA) is used to approximate it, and the short 'i' (ɪ in the IPA) is pronounced as a long 'e' (e in the IPA) in the final position because there's no such sound in English in that position (and it's carried over into the initial and middle positions), which is exactly how it's transcribed, and the final 'e' is pronounced as a schwa, which is exactly how it's transcribed, and the short 'u' is pronounced as a long 'a', which is exactly how it's transcribed, too. And many Francophones like it because they don't like to admit there are vowel sounds in their language that are also in English, and many Spanish and Italians like it because the medial 'a' and the long 'e' are common sounds of their languages. So there is a convergence of interests in the policy of misrepresentation in the phonetic transcription for those vowels and not in the others. Whatever the explanation, the convention is an embarassment to science.

They were doing much the same to Portuguese but have recently abandoned it just as suddenly and mysteriously as they had adopted it, perhaps because they realized it was serving them no purpose.

Besides the mispronunciation of the 'a', the strange Anglophone accent mysteriously and gratuitously pronounces the French 'ss' as 'z', when it is always pronounced as 's' and in English usually so, and the 's' between vowels is mysteriously and gratuitously now pronounced as an 's', at least at the end of a name, when it is always pronounced as a 'z' in French and usually so in English, as in 'enterprise', 'amuse', 'refuse', 'accuse', 'please', 'tease', all except the last being loans from French.

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