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Principle of Conservatism of Cellular Structures as the Basis for Construction of the Multikingdom System of the Organic Word

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Abstract

This chapter describes the history of megasystematics (taxonomy of higher taxons) from Karl Linnaeus till the present day. Nowadays, the Whittaker's five-kingdom system of cellular organisms is the best known. This system has made monophyletic the kingdoms of plants, fungi, and animals but increased the heterogeneity of the kingdom Protoctista. There is one of the qualitative peculiarities of the subcellular level of the organization of living systems, which has been named "the principle of conservatism." We offer the multikingdom system of cellular organisms, based on this principle. In many ways, it can be done based on intuition. We promote the concept of three branches of cellular organisms that is accepted in megasystematics. It is proposed to give these branches of organic word the rank of domains Archaea, Bacteria, and Eucarya. The Empire Cellulata is divided into three domains, which, in turn, are divided into several kingdoms. Our system contains 26 kingdoms.

Keywords: history of megasystematics, multikingdom phylema, the most primitive eukaryotes

1. Introduction

The history of megasystematics (taxonomy of higher taxons) dates back to the eighteenth century when a classification system of the living beings was created by the father of systematics (or taxonomy) Karl Linnaeus, which comprised two kingdoms—Vegetabilia and Animalia

(**Figure 1**). In the nineteenth century, the kingdom of fungi (Mycetoideum), on the one hand, and the kingdom of Protista or Protoctista, on the other, uniting unicellular or most of the lower organisms, were erected; however, most biologists continued adhering to the two-kingdom system.

The system of R.H. Whittaker is the most frequently adopted. He recognizes in his later work [1–4] the prokaryote as a kingdom Monera and divides the eukaryotes into three kingdoms—higher kingdoms of plants, fungi, and animals, which as three stocks were transferred by him from the lower kingdom of Protista (**Figure 2**).

In that classification scheme, red and brown algae were placed near the base of the stock of plants, green algae were placed both in the protist kingdom (apparently, unicellular forms) and at the base of the plant kingdom, whereas myxomycetes were positioned near the base of the stock of fungi. This system is the most popular and in common use till date. The frequently adopted is Whittaker's five-kingdom system of cellular organisms modified by Lynn Margulis [5–8]. She thus made monophyletic the kingdoms of plants, fungi, and animals but increased the heterogeneity of the kingdom Protoctista. L. Margulis herself frankly admitted that “the

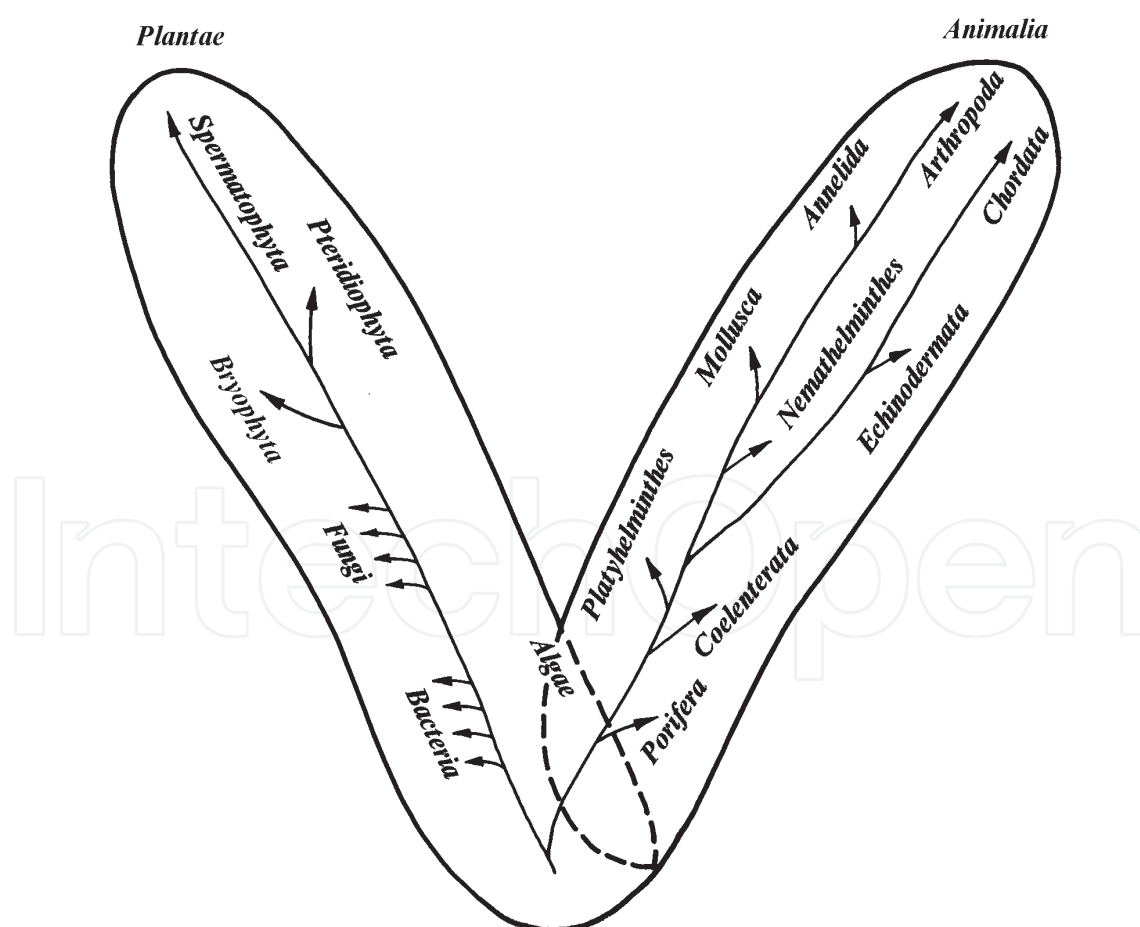


Figure 1. Two kingdoms of K. Linnaeus system (from Drozdov [5]).

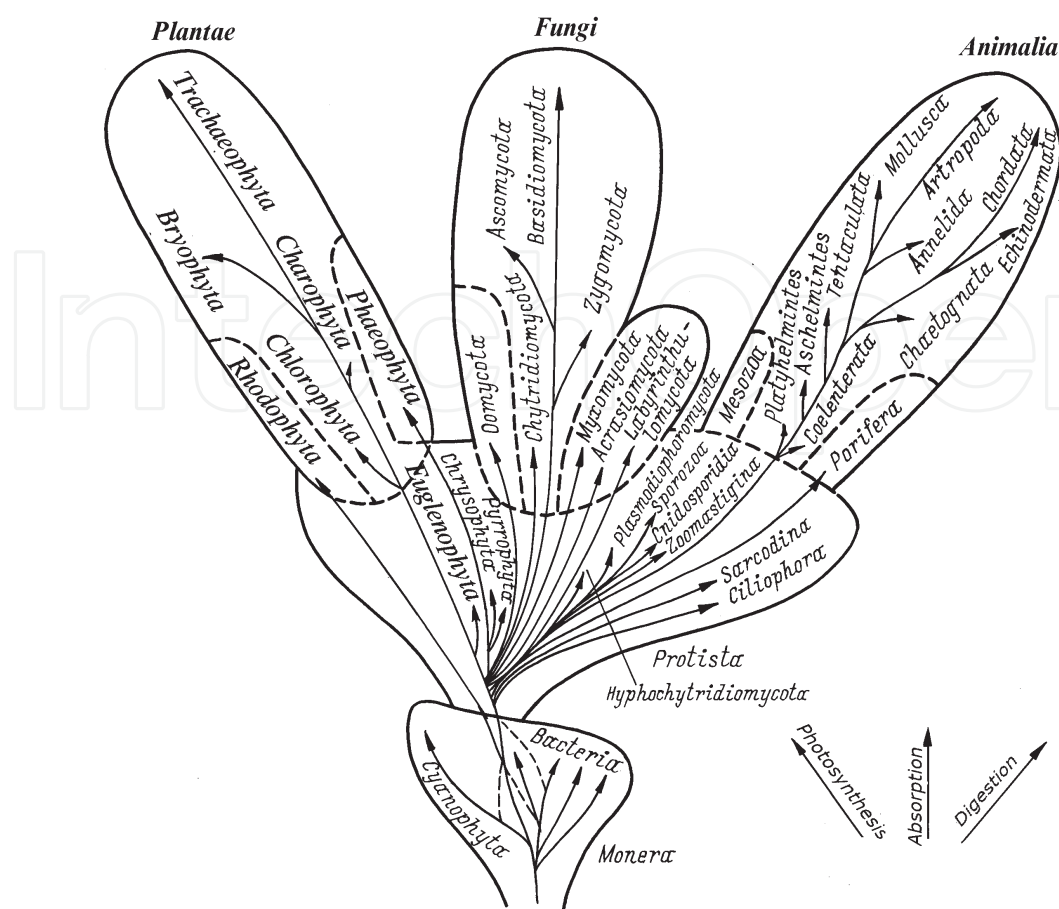


Figure 2. Five kingdoms of R. Whittaker system (from Drozdov [5]).

protocist kingdom becomes looking as if it were a dump." From these words of L. Margulis, it unambiguously follows that all schemes with few eukaryotic kingdoms (1–4) will err toward inadmissible polyphyly, as is confirmed by contemporary cytological and, especially, molecular biology data.

2. History of megasystematics

Whittaker's scheme was one of the last systems where adaptive features are interwoven with truly phylogenetic characteristics, that is, convergent similarity is claimed to be affinity. Being an ecologist, R.H. Whittaker himself pointed to the adaptive character of evolution of three higher kingdoms, which are connected with their feeding mode: plants are generally autotrophs, fungi feed by absorption, whereas animals are characterized by holozoic nutrition and digestion. R.H. Whittaker indicated this main trend in evolution with three arrows near each of the three higher kingdoms. As regards higher plants (development of the root, conductive system, orifices, reduction of gametophyte, and then loss of flagellate stage, appearance of seed and fruit), true fungi (loss of flagella),

and higher vertebrates (appearance of amnion, egg enclosed by membranes, or viviparity), their progressive evolution is not related to feeding, but rather it is connected with adaptation for life on land and with the abandonment of whatever, even temporary, residence in the aquatic environment. It is no occasion that both the botanist Zernov [9] and the ecologist Odum [10, 11] considered Whittaker's scheme to be a functional, i.e. (*id est*), ecological, rather than a taxonomic one, and Y. Odum emphasized that his kingdoms, which are "functional kingdoms," should not be confused with taxonomic ones, although there are some parallels. It is therefore natural that L. Margulis, when revising Whittaker's system, replaced these arrows with another ones, indicating haplo-diploid nature of plants, diploid nature of animals, dikaryoid nature of fungi, and haploid nature of algae.

Other systems have been considered by us in details [12, 13]. In them [14–19], the eukaryotes are subdivided into 6–18 kingdoms. Thus, Edwards [16] proposed to distribute plants among seven kingdoms belonging to two subkingdoms of Prokaryota (kingdom of blue-green algae) and eukaryotic plants with six kingdoms: Erythrobionta with one division Rhodophyta, Chlorobionta embracing four divisions (Chlorophyta, Bryophyta, Tracheophyta, and Euglenophyta), Ochrobionta comprising four divisions (Phaeophyta, Chrysophyta, Cryptophyta, and Pyrrophyta), Myxobionta with four divisions (Myxogastriomycota, Dictyosteliomycota, Acrasiomycota, and Protosteliomycota), Fungi 1 with four divisions (Zygomycota, Ascomycota, Basidiomycota, and Chytridiomycota), and Fungi 2 comprising three divisions (Labyrinthulomycota, Hyphochytridiomycota, and Oomycota). One can concur with most of Edwards' kingdoms. Division of fungi into two kingdoms is well-grounded. All divisions of Fungi 2 are now assigned to the same kingdom as Ochrobionta. Only Myxobionta are now removed from plants and distributed among two kingdoms.

After K. Linnaeus, the author of system, as well as J. Cuvie, who introduced the high-rank category of phylum, which also proved very useful, was the first case. The category of domain was set forth later.

It has become absolutely clear that the major high-rank taxonomic categories of Linnaeus are insufficient and new ones are needed. The simplest way is using additional categories such as subphylum, subkingdom, and superkingdom. Many scientists went this way, but, in doing so, they were compelled to introduce more categories such as "Überreich," "Oberreich," "Unterreich" [19] or "Superkingdom," "Subphylum," "Infraphylum," and "Parvikingdom" [20–24].

Vorontsov [26–28] was the first who introduced into scientific usage a major taxonomic category higher in rank than kingdom, the empire. He recognized two empires: of precellular organisms in which he placed a single kingdom, that of viruses, and the empire of cellular organisms embracing two subempires: subempire of prenucleate organisms comprising bacteria and blue-green algae and the subempire of nucleate organisms (or eukaryotes). The introduction of such high-level taxonomic category as the empire is of much importance for taxonomy and quite a bold suggestion.

3. Principle of conservatism of subcellular structures

The multikingdom system of the organic world was advanced by us [11, 12, 28–30]. It was based on the principle of conservatism of cellular structures formulated by Mashansky and Drozdov [31, 32]. There is a biological paradox: the subcellular structures are highly conservative.

While discussing the structural foundations of biological systems, we should not limit our attention by fixing it only to the correlation of various levels of the organization of living matter, to what we are used to call the problem of integration. We have to realize that every single level is unique in its qualitative specificity and particular features.

There is an enormous variety of cells. They differ in their morphology, functions, and their chemical structure. However, when we proceed to the next, the so-called subcellular level, we are confronted with the fact that the principal structure of basic cellular organelles, such as membranes, mitochondria, centrioles, filaments, ribosomes, endoplasmic reticulum, and Golgi apparatus, remains unchanged in a wide variety of objects. In the hierarchical sequence of the organizational levels of biological systems, it is the subcellular level, and that merits ever greater attention for its most remarkable characteristic feature, namely its membranous structure—its supermolecular system of proteins, lipids, and polysaccharides of several types. We can be certain to expect some new properties to be discovered typical of the structure and functions of cellular organelles on account of the peculiarities of their level of organization.

There are only two variants of the ultrastructure of biological membranes (lipid bilayer in Eubacteria and Eukaryotes and single layer in Archaeobacteria), two variants of ribosomes, six variants of ultrastructural organization of plastids, three variants of organization of mitochondria, three variants of organization of nuclear apparatus, and three variants of organization of kinetic apparatus.

A suitable object for a comparative morphological analysis is presented by mitochondria. For identifying of mitochondria can be taken the typical organization of their membranes. The lipoprotein nature of mitochondrial membranes does not cause any doubt, neither does the similarity of these membranes to the ones belonging to other organelles. Yet, there are data on the mitochondrial membrane testifying to its structural as well as functional uniqueness.

Mitochondria are remarkable for the great variety of their organizations. There are lamellar or tubular crysts that can exist singly or densely packed, or they can be either scattered or highly organized. There can be several small mitochondria in a cell, or a single one spreading over a large number of shoots: there can be one mitochondrion in a cell, or quite a number of them densely packed together. Despite such great variety, the general pattern of the structure of mitochondria invariably repeats itself—it is one and the same in mushrooms, algae, multicellular animals, and plants. There are four types of structures of the crysts of mitochondria—the lamellar, the tubular, the tubularly vesicular, and discoid one. The nature of mechanisms determining the morphology of mitochondrial crysts is unknown yet. Nevertheless, the func-

tional peculiarities of the cells are of considerable significance. Thus, in the cells synthesizing steroid hormones, we find mitochondria with tubularly vesicular crysts. However, an injection of steroid hormones to lower invertebrate allows to transform the mitochondria of the neurons with typically lamellar crysts into those with tubularly vesicular ones [31].

Mitochondria can cardinaly change their ultrastructure under the impact of alternating factors or training. This signifies high liability in mitochondria, the ultrastructure of which is determined by the function of the cells irrespective of the systematic position of the object. On the basis of presently available material on the ultrastructure of mitochondria of the cells of a great variety of tissues as well as the specificity of their responses to various alternating factors, it is possible to state that there are no convincing facts which might permit to fix any correlations between the level of phylogenetic position, or ontogeny and the ultrastructure of mitochondria in investigated species belonging to different realms of living organisms. All the observed differences in the ultrastructure of mitochondria can be accounted for by their functional peculiarities, their loads during a certain period of activity. There, evidently, lies one of the qualitative peculiarities of the subcellular level of the organization of living systems, which has been named "the principle of conservatism" [31, 32].

These facts demonstrating the lack of changes in cellular organelles, such as rather intricate in their organization mitochondria, during the long process of their evolution give a reason to conclude that already at the early stages of evolution, the structural as well as chemical organization of living systems was rather complicated and well developed. This fact calls for a discussion of the problems of the early stages of evolution, beginning with the appearance of life on Earth, which is currently widely discussed on various levels, and extreme views are being stated.

The uniformity of the structure of cellular organelles, such as mitochondria and, perhaps, even those of a more intricate organization, namely filaments, gives grounds to view them as structures formed on one single occasion. The structure of nucleic acids has a common origin in all living systems. This conclusion is prompted by the widely known uniformity of the code formed on four bases.

The above-mentioned conception should explain why mitochondria have a genetic code that differs very slightly from that of the nucleus as well as that of the prokaryotes. In fact, the code of mitochondria differs very little from the universal one. Only five codons have different meaning: methionine, isoleucine, tryptophan, and, also, a changed terminator. While analyzing these divergences, it is possible to see that the code of mitochondria is nearer to the quasidouble "ideal" one. This may testify the fact that the code of mitochondria is more ancient than the universal one. Possibly, there was a time when all cells had a code similar to that of present-day mitochondria. Then, some changes occurred in the general code, but in mitochondria, the code proved to be more stable. The reason for this may lie in the small size of the genome of mitochondria and so every mutation brought about such changes in the characteristics that proved lethal.

There is another important problem, namely, why the mitochondrial genetic system, once formed, survived in the evolution practically unchanged, and how could it preserve its independence in the cell. Mahler and coauthors [33] suggested the opinion that, as polypeptides

coded by DNA and belonging to mitochondrial complexes are rather hydrophobic, they must be synthesized somewhere near the place of their inclusion into the mitochondrial membrane and cannot be transported through the cell. Probably, the preservation of mt-DNA throughout the evolution was due to it serving as a supplier of the functionally indispensable elements to mitochondria.

We believe that the most topical, fruitful, and perspective objective of megasystematics is the elaboration of multikingdom system consisting of monophyletic taxa, and we are aware of all difficulties of this task. One of the main difficulties is that now in a boiling cauldron of new information, one can hardly make a whatever stable system. There are many reasons for this. The ultrastructure of many protists has not yet been studied; the structure of many organisms is either very peculiar or unclear so that they cannot be classified with the existing taxa of even high rank; the degree of conservatism of cellular structures is being elucidated; and the techniques for demonstrating relatedness are being improved. It is, therefore, no accident that different authors recognize different number of kingdoms, and the authors themselves sometimes remake their systems too hastily. Thus, Cavalier-Smith [34] delineates seven kingdoms among the eukaryotes; 3 years later, he already recognized nine kingdoms, and later he reduced the number of kingdoms to six [21–24, 35–39].

4. Multikingdom systems of the organic world

Nevertheless, the adherents of monophyletic system have made tremendous progress. The kingdom Ochrobiontes (Chromobionta or Chromista) is distinctly delineated; along with a number of divisions of chlorophyll C-containing algae, it embraces some groups from the kingdoms Fungi and Protozoa. The kingdom Viridiplantae comprises all green algae Chlorophyta s. lato, bryophytes, and higher plants but no more; the kingdom Metazoa (but not Animalia!) is also monophyletic. Some kingdoms are not as clearly delineated as Euglenobiontes, Alveolates, Cryptobiontes, Prymnesiobiontes, etc. are. However, some groups, among them Foraminifera, Radiolaria s. lato, and others, have not yet been placed properly. Instead of being squeezed, without due grounds, into the existing kingdoms, these groups should rather be regarded as groups incertae sedis, as is done by many taxonomists.

When analyzing the old system, in which features of adaptive similarity and phylogenetic relatedness turned out to be intermingled, there is an increasing criticism from various investigators that many taxa are not monophyletic but rather ecomorphological notions. Shafranova [40] addressed this problem in her paper "Plant as a Life Form." Mirabdullaev [41, 42] correctly points out that the former system of protists was primarily the system of life forms (ecomorphs) rather than phylogenetic taxa and that similar structural patterns can arise convergently. Many foreign scientists are now coming to analogous conclusions. Here, the question arises: what should be done with out-dated, traditional notions that serve no longer as taxa, namely plants, protists, animals, heliozoans, flagellates, sporozoans, etc. To avoid extremely troublesome and even unnecessary rejection of old terminology, many researchers

began using them not as taxa but as designations of ecomorphs or life forms [43, 44]. This does not necessarily imply that the existing terminology should be changed radically. Up to now, in botanical institutions, mycologists have successfully worked hand in hand with algologists, and both prokaryotic bacteria and eukaryotic fungi have been applied in microbiological industry.

Moreover, it has turned out that these terms can and must be used in the ecomorphological system or the system of life forms, which has long been a necessity. Teofrast's system was one of early attempts at constructing such a system. To date, a variety of such systems have been created at different levels. Unfortunately, the ecomorphological system was elaborated independently of the taxonomic one, which was thought of as if being something stable, and its terms were little used. The adoption and use of the terms that are well established in taxonomy were not appropriate for the new system. Thus, in his ecomorphological system, which is one of the better developed, for high-rank taxa, he retains the names "Kingdom," "Division," "Phylum," and "Class," which can cause only confusion. Barr's viewpoint seems to be more correct [44]. Only for fungi, he proposed two systems: a phylogenetic one, where fungi were distributed among three kingdoms—Eumycota, Chromista, and Protozoa—and an ecological one, in which fungi in the old sense constitute union 1 of Fungi.

The idea is to create, on the basis of the old system in which the genetic and ecomorphological criteria were intermingled, two parallel systems—the phylema or phylogenetic, taxonomic system and the ecomorphological system. The elaboration of the ecomorphological system is a very complicated task, although much has been done in this respect. Without doubt, many descriptive terms of traditional systematics will find their place in the new system.

At present a lot of biologists study the problems of megasystematics. Close with our megasystem was build up the system by Leontiev and Akulov [45]. But most of new systems limit themselves to study the sequence of nucleotide in ribosomal RNA. The molecular biologists studying rRNA work at different countries—in USA, Canada, Belgium, Japan, and different European countries like Russia. There are a few sites in Internet, where the phylogenetic trees are represented. A lot of such trees were published last years. Attention should be paid to the discussion of their systems as variant of five-kingdom system. Nevertheless, Cavalier-Smith [20–24, 34–39] already published the six to nine kingdoms systems. He comprises two empires—Prokaryota and Eukaryota.

Since the end of year 1970, the concept of three branches of cellular organisms is accepted in megasystematics [46]. It is proposed to give these branches of organic word the rank of domains Archaea, Bacteria, and Eucarya [47–51]. Therefore, the empire Cellulata is divided to three domains, which, in turn, are divided into several kingdoms [25, 39] (**Figures 3–7**).

The scheme reflects the great diversity of life forms of bacteria adapted to living in almost all ecological niches. Some of them such as *Ancalochloris* (1), *Aquaspirillum* (2), and *Chromatin* (3) live in water, whereas *Aquaspirillum* can use a chain of magnetized particles to find sediments, rich in nutrient agents. *Haloarcula* (4) are distributed in the saline marshes. *Pyrodictium* (5) prefers hot places; *Rhizobium* (6) settles in the roots of plants and produces nitrogen available to the host tissue form. Type of bacteria: *Escherichia* (7), *Streptococcus* (8),

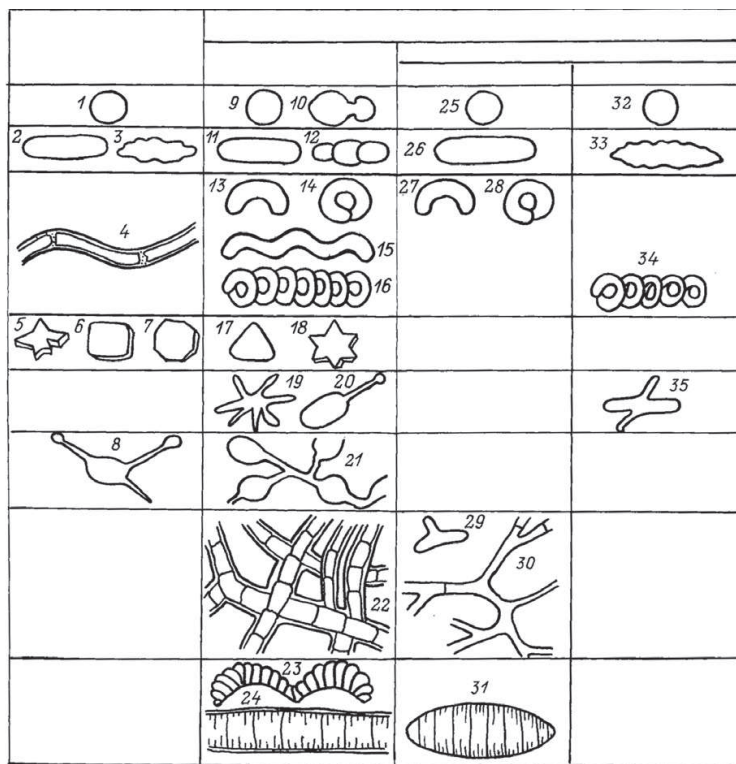


Figure 3. The main bacteria morphotypes (from Kussakin, Drozdov [11]). Archaeobacteria: 1, *Methanococcus*; 2, *Methanobacterium*, *Halobacterium*; 3, *Thermoplasma*; 4, *Methanospirillum*; 5, *Haloarcula*; 6, square bacteria; 7, *Sulfolobus*; 8, *Pyrodictium*. Gram-negative bacteria (Gracilicutes): 9, *Neisseria*, *Veillonella*; 10, *Gemmiger*; 11, *Escherichia*; 12, *Seliberia*; 13, *Vibrio*, *Bdellovibrio*; 14, *Mycrocycilus*; 15, *Spirillum*; 16, *Spirochaeta*; 17, *Angulomicrobium*; 18, *Stella*; 19, *Prosthecomicrobium*; 20, *Caulobacter*; 21, *Hyphomicrobium*, *Rhodomicrobium*; 22, *Mastigocoleus*; 23, *Simonsiella*; 24, *Oscillochloris*, *Oscillatoria*. Gram-positive bacteria (Firmicutes): 25, *Micrococcus*; 26, *Bacillus*, *Erysipelothrix*; 27 and 28, *Desulfotomaculum*, *Clostridium*; 29, *Mycobacterium*; 30, *Streptomyces*; 31, *Caryophanon*, *Oscillospira*. Mycoplasma (Tenericutes): 32, 33, and 35, *Mycoplasma*; 34, *Spiroplasma*.

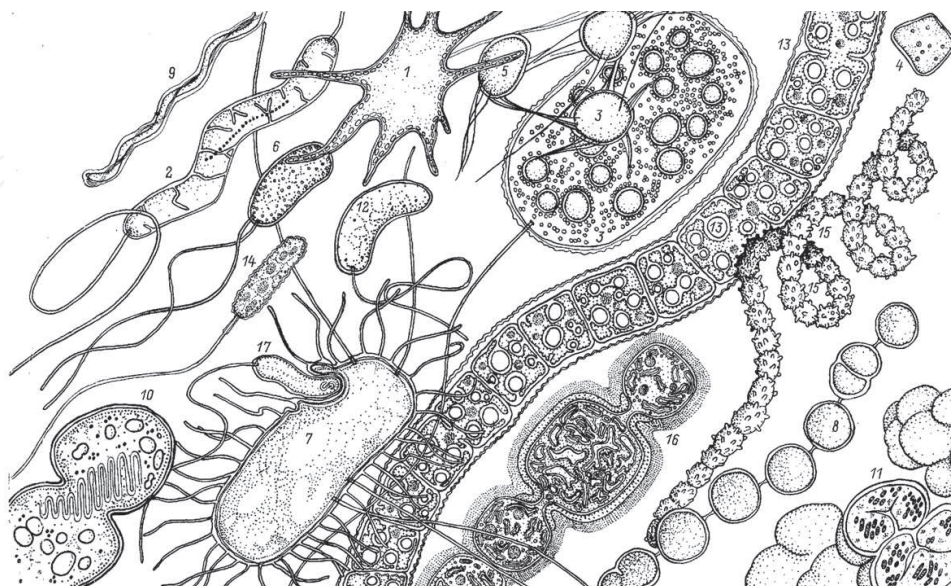


Figure 4. The different forms of Eubacteria (from Drozdov [5]).

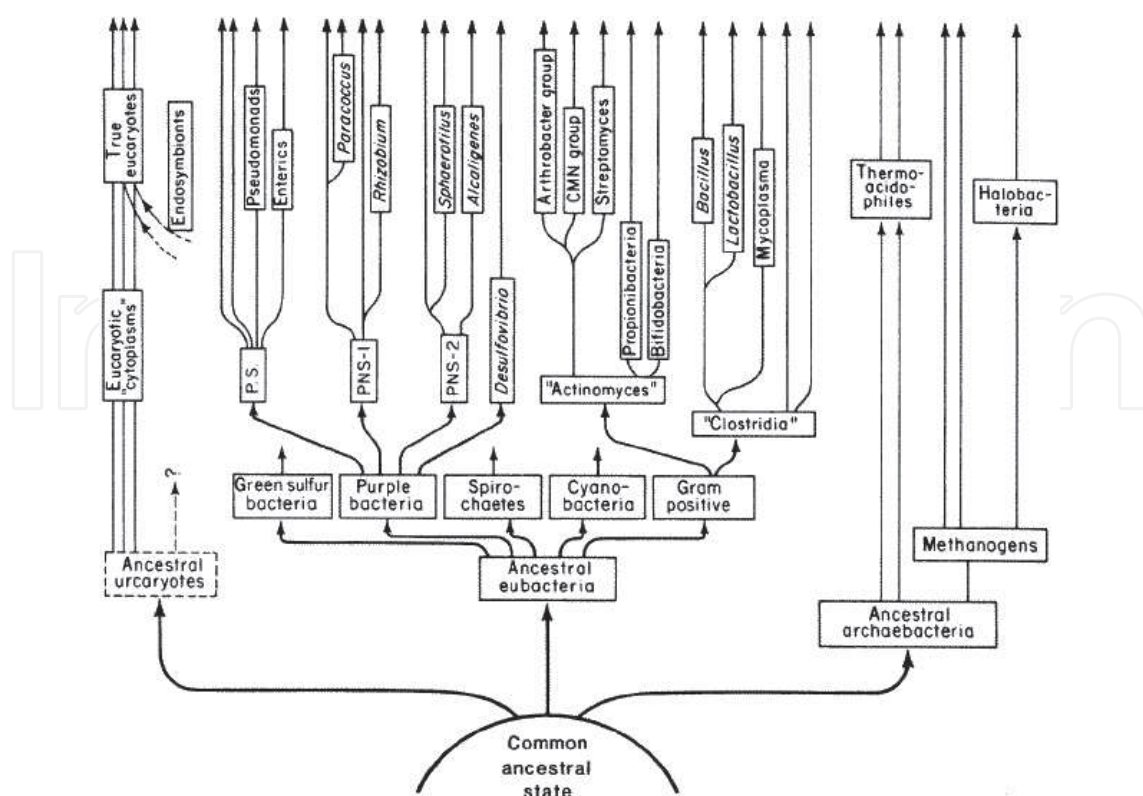


Figure 5. Schematic representation of the major lines of prokaryotic descent (after Fox et al. [46]).

and *Treponema* (9) cause various diseases in humans. The metabolism requirements can combine incompatible species of bacteria: aerobic methane consumer *Methylococcus* (10)

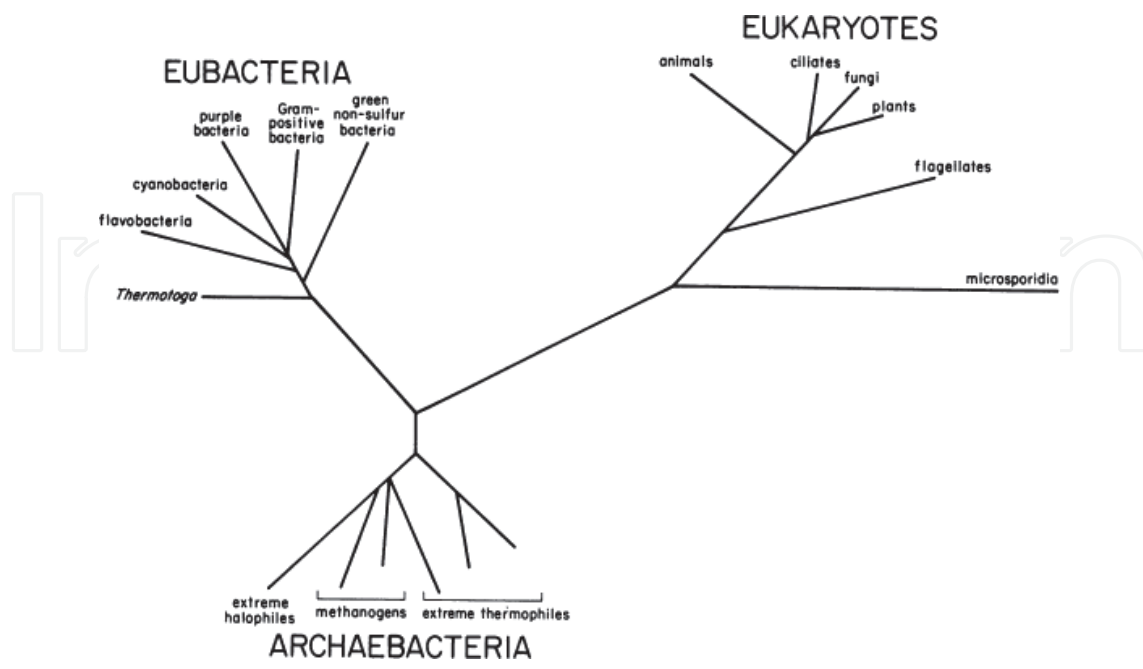


Figure 6. Unrooted tree shows the three branch of organic world (after Woese [49]).

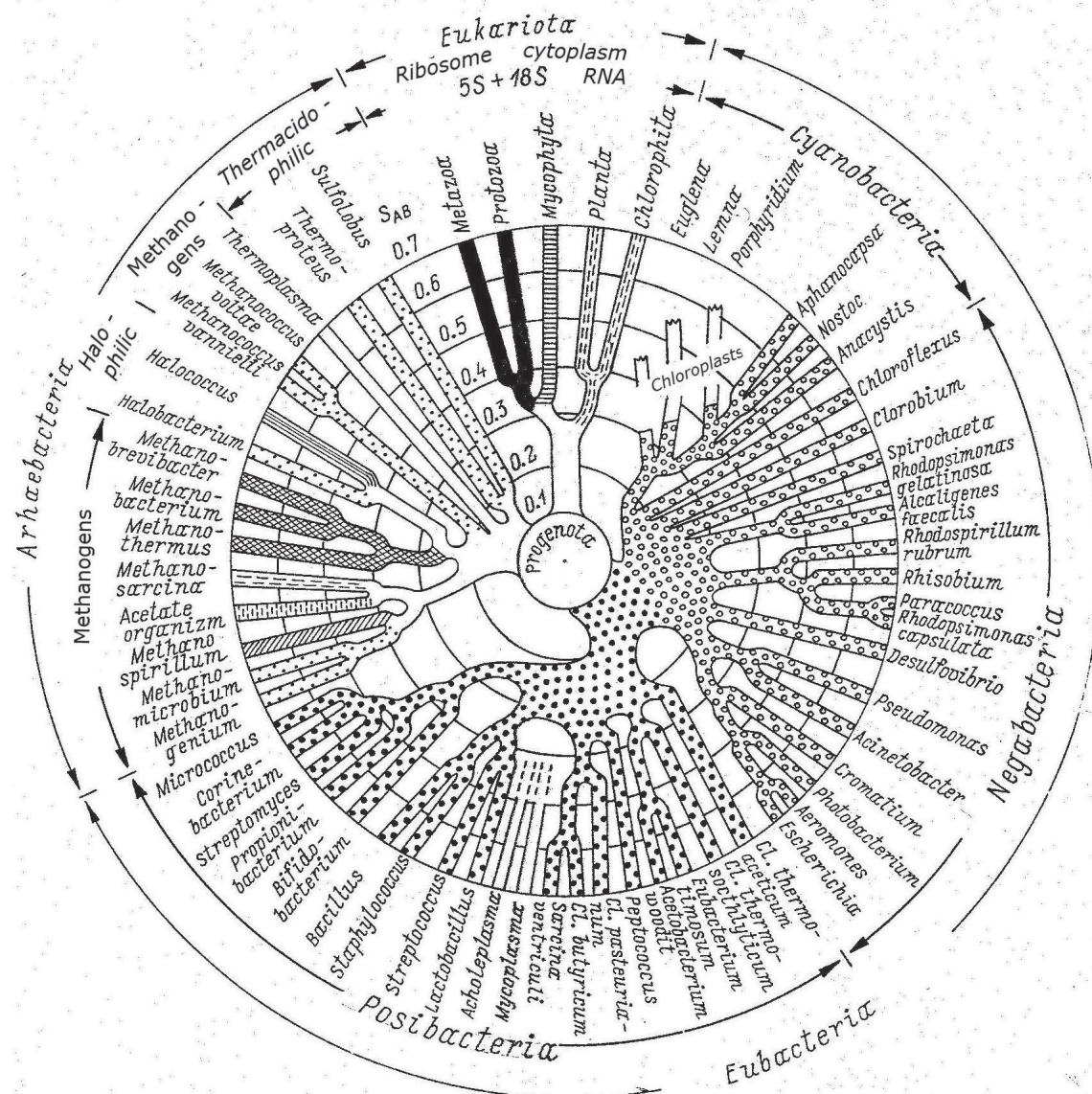


Figure 7. Kandler ring. The phylogenetic unrooted tree constructed on base of analysis rRNA and cell wall (for prokaryotes) (after Kandler [52]).

draws *Methanosarcina* (11), and anaerobic producing methane *Desulfovibrio* (12), producing hydrogen sulfide—*Ancalochloris* (1), *Beggiatoa* (13), and *Chromatium* (3)—requires hydrogen sulfide. Another group of bacteria, consuming hydrogen sulfide, *Thiobacillus* (14), is used for extraction of metals from ore. *Streptomyces* (15) secrete antibiotics. *Anabaena* (16) produces oxygen from water in the process of photosynthesis, whereas *Bdellovibrio* attacks many other bacteria (17).

We support this idea and propose to distinguish 4 kingdoms in Archaeobacteria, 7 kingdoms in Eubacteria, and 15 kingdoms in Eukaryotes. Our system we represent as scheme (Figure 8) and as the table (Table 2). In Table 1, we propose the next ends for word of designations of taxa on levels kingdom, phylum, class and order.

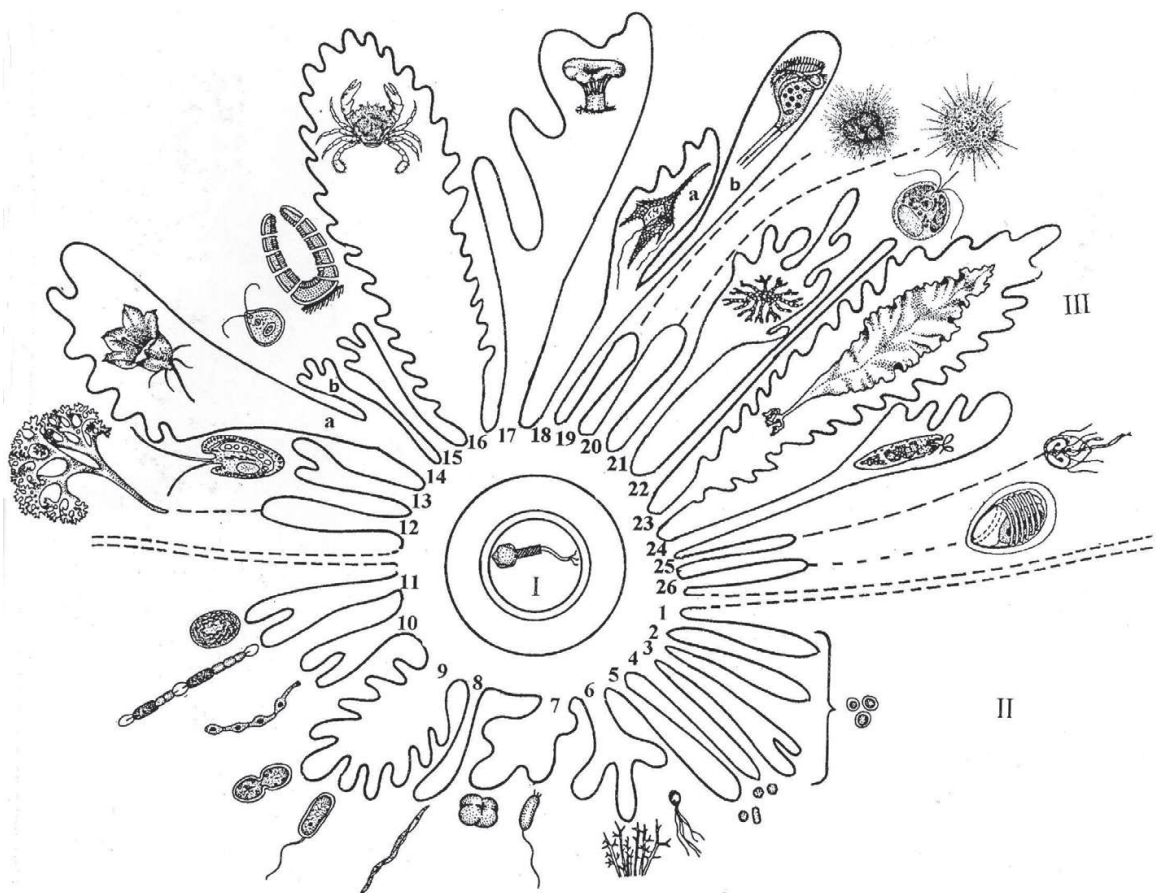


Figure 8. The multikingdom phylogenetic unrooted tree constructed on base of principle of conservatism (after Drozdov [5]). I, Virae; II, Prokaryotes: 1, Methanobacteriobiontes; 2, Halobacteriobiontes; 3, Thermoacidobacteriobiontes; 4, Archaeotenericutobacteriobiontes; 5, Tenericutobacteriobiontes; 6, Actinobacteriobiontes; 7, Firmicutobacteriobiontes; 8, Spirochaetobacteriobiontes; 9, Scotobacteriobiontes; 10, Anoxyphotobacteriobiontes; 11, Oxyphotobacteriobiontes; III, Eukaryotes: 12, Rhodobiontes; 13, Cryptobiontes; 14, Chlorobiontes (a, Thallobionti; b, Embryobionti); 15, Parazoobiontes; 16, Metazoobiontes; 17, Mycobiontes; 18, Alveolatobiontes (a, Peridiniobionti; b, Parameciobionti); 19, Foraminiferobiontes; 20, Radiolariobiontes; 21, Myxobiontes; 22, Prymnesiobiontes; 23, Heterokontobiontes; 24, Euglenobiontes; 25, Archaeomonadobiontes; 26, Microsporobiontes.

Category	Applicable ends	Category	Applicable ends
Superkingdom	-obiontoi	Superclassis	-idees
Kingdom	-obiontes	Classis	--indes
Subkingdom	-obiontoi	Subclassis	-iones
Superphylum	-ophylaces	Superorder	-iformi
Phylum	-ophylea	Order	-iformes
Subphylum	-ophylinea	Suborder	-oidei

Table 1. Applicable ends for word of designations of taxa on kingdom, phylum, classis, and order taxonomic rank.

Imperia Cellulata

Dominion Archaeobacteria

I. Kingdom Thermoacidobacteriobiontes

1. Phylum Sulfolobophyles
2. Phylum Thermoproteophyles

II. Kingdom Archaeotenericutobacteriobiontes

3. Phylum Thermoplasmophyles

III. Kingdom Halobacteriobiontes

4. Phylum Halobacteriophyles
5. Phylum Halococcophyles

IV. Kingdom Methanobacteriobiontes

6. Phylum Methanobacteriophyles

Dominion Eubacteria

Superkingdom Gracilicutobiontoi

V. Kingdom Cyanobiontes (Oxyphotobacteriobiontes)

7. Phylum Nostocophyles
8. Phylum Prochlorophyles

VI. Kingdom Anoxyphotobacteriobiontes

9. Phylum Rhodospirillophyles
10. Phylum Chlorobiophyles

VII. Kingdom Scotobacteriobiontes

11. Phylum Thiobacillophyles
12. Phylum Desulfovibriophyles
13. Phylum Azotobacteriophyles
14. Phylum Pseudomonadophyles
15. Phylum Enterobacteriophyles
16. Phylum Bacteroidophyles
17. Phylum Caulobacteriophyles
18. Phylum Myxobacteriophyles
19. Phylum Cytophagophyles
20. Phylum Rickettsiophyles
21. Phylum Chlamydiophyles

VIII. Kingdom Spirochaetobacteriobiontes

22. Phylum Spirochaetophyles

Superkingdom Firmicutobiontoi

IX. Kingdom Actinobacteriobiontes

23. Phylum Mycobacteriophyles

24. Phylum Corynebacteriophyles

25. Phylum Actinomycetophyles

X. Kingdom Eufirmicutobiontes

26. Phylum Clostridiophyles

27. Phylum Bacillophyles

28. Phylum Lactobacillophyles

29. Phylum Micrococcophyles

XI. Kingdom Tenericutobiontes

30. Phylum Mycoplasmophyles

Dominion Eukaryota

XII. Kingdom Microsporobiontes

31. Phylum Microsporidiophyles

XIII. Kingdom Archemonadobiontes

Superphylum Archamoebophylacei

32. Phylum Pelomyxophyles

Class Pelornyxiodes

Class Mastigamoeboides

Superphylum Metamonadophylacei

33. Phylum Retortomonadophyles

34. Phylum Hexamitophyles

35. Phylum Oxymonadophyles

Superphylum Parabasaliophylacei

36. Phylum Trichomonadophyles

Class Trichonymphiodes

XIV. Kingdom Euglenobiontes

Subkingdom Percolobionti

37. Phylum Acrasiophyles

Class Vahlkampfioides

Class Acrasilodes

Class Percolomonadiodes

Class Lyromonadioides

Subkingdom Euglenobionti

38. Phylum Stephanopogonophyles

39. Phylum Diplonemophyles

40. Phylum Bodonophyles

41. Phylum Euglenophyles

XV. Kingdom Myxobiontes

Subkingdom Myxomycetobionti

42. Phylum Cercomonadophyles

43. Phylum Dictyosteliophyles

44. Phylum Physarophyles

Subkingdom Myxozoobionti

45. Phylum Entamoebophyles

46. Phylum Haplosporophyles

47. Phylum Pararnyxiophyles

48. Phylum Myxidiophyles

XVI. Kingdom Rhodobiontes

49. Phylum Bangiophyles

XVII. Kingdom Alveolatobiontes

Subkingdom Peridiniobionti

Superphylum Peridiniophylacei

50. Phylum Peridiniophyles

Superphylum Apicomplexophylacei

51. Phylum Perkinsophyles

Class Colpodelliodes

Class Perkinsiodes

52. Phylum Gregarinophyles

Subkingdom Parameciobionti

53. Phylum Hemimastigophyles

54. Phylum Parameciophyles

XVIII. Kingdom Heterokontobiontes

55. Phylum Bicosoecophyles

56. Phylum Labyrinthulophyles

57. Phylum Saprolegniophyles

58. Phylum Hyphochytriophyles

59. Phylum Diatomophyles

60. Phylum Triboneroatophyles

61. Phylum Fucophyles

62. Phylum Eustigmatophyles

63. Phylum Synurophyles

64. Phylum Chrysococcophyles

65. Phylum Raphidomonadophyles

66. Phylum Dictyochophyles

67. Phylum Pedinellophyles

Class Pedinelliodes

Class Actinophryiodes

Class Clathruliniodes

Addition to Kingdom Heterokontobiontes

Class Pelagomonadiodes

XIX. Kingdom Foraminiferobiontes

68. Phylum Psamminidophyles (=Xenophyophora)

69. Phylum Foraminiferophyles

70. Phylum Plasmodiophoreophyles

XX. Kingdom Radiolariobiontes

71. Phylum Sphaerozoioophyles (=Polycystinea)

72. Phylum Phaeodiniophyles

73. Phylum Acanthometriophyles

74. Phylum Sticholoncheiophyles

XXI. Kingdom Prymnesiobiontes (=Haptophyta)

75. Phylum Prymnesiophyles (=Haptophyles)

XXII. Kingdom Cryptobiontes

76. Тип Cryptomonadophyles (Cryptophycota)

77. Тип Centrochelidophyles (Acanthocystidae)

XXIII. Kingdom Chlorobiontes (=Viridiplantae)

Subkingdom Thallobionti

78. Phylum (Division) Prasinophyles

79. Phylum (Division) Chlorophyles

80. Phylum (Division) Charophyles

Subkingdom Embryobionti (= Cormobionti)

81. Phylum (Division) Bryophyles

82. Phylum (Division) Rhyniophyles (= Psilophyles)

83. Phylum (Division) Psilotophyles

84. Phylum (Division) Lycopodiophyles

85. Phylum (Division) Equisetophyles (Sphenophyles)

86. Phylum (Division) Polypodiophyles (= Filicophyles)

87. Phylum (Division) Pinophyles (= Gymnospermae)

88. Phylum (Division) Magnoliophyles (= Angiospermae)

XXIV. Kingdom Mycobiontes (= Fungi)

Subkingdom Opistomastigomycotobionti

89. Phylum (Division) Chytridiomycotophyles

Subkingdom Amastigomycotobionti (= Eufungi=Eumycota)

90. Phylum (Division) Mucoromycotaphyles (= Zygomycota)

91. Phylum (Division) Trichomycotaphyles

92. Phylum (Division) Ascomycotaphyles

93. Phylum (Division) Basidiomycotaphyles

XXV. Kingdom Parazoobiontes

94. Phylum Choanoflagellata (= Craspedomonadia)

95. Phylum Spongia (= Porifera)

XXVI. Kingdom Metazoobiontes

96. Phylum Placozoa

97. Phylum Cnidaria

98. Phylum Ctenophora

99. Phylum Platyhelminthes

100. Phylum Orthonectida

101. Phylum Nemertini

102. Phylum Entoprocta (= Kamptozoa)

103. Phylum Sipuncula

104. Phylum Mollusca

105. Phylum Echiurida

106. Phylum Annelida

107. Phylum Pogonophora

- 108. Phylum Vestimentifera
- 109. Phylum Tardigrada
- 110. Phylum Pentastomida
- 111. Phylum Onychophora
- 112. Phylum Arthropoda
- 113. Phylum Rotifera
- 114. Phylum Cycliophora
- 115. Phylum Acanthocephala
- 116. Phylum Dicyemataria (= Rhombozoa)
- 117. Phylum Nemathelminthes
- 118. Phylum Loricifera
- 119. Phylum Gastrotricha
- 120. Phylum Nematomorpha
- 121. Phylum Priapulida
- 122. Phylum Kinorhyncha
- 123. Phylum Chaetognatha
- 124. Phylum Phoronida
- 125. Phylum Bryozoa
- 126. Phylum Brachiopoda
- 127. Phylum Hemichordata
- 128. Phylum Echinodermata
- 129. Phylum Chordata

Incertae sedis: Genera *Gyromitus*; Genera *Discocelis*; Genera *Jacoba*.

Table 2. Multikingdom system of the cellular living beings.

5. The root phylogenetic tree

The construction of a root phylogenetic tree based on the principle of conservatism is not simple. It is necessary to analyze the structure of the six systems of cellular organelles in each Protista group: surface apparatus (membranome), genetic apparatus (karyome), synthetic apparatus (syndetome), mitochondria, plastids, and kinetic apparatus (kinetome). In many ways, it can be done based on intuition. Of course, now the study of the building of phylema of the organic world focuses mainly on the genomic level. Nevertheless, we tried to present phylema of the organic world in a tree, where the kingdom is placed as the complexity of the systems of cellular organelles (**Figure 8**). The main complication is the allocation

of the core group in the structure of the tree. It may seem that the problem is simple—the most primitive group includes cells of the simplest arrangement structure. Certainly, the simplest organisms are Microsporobiontes—eukaryotic unicellular intracellular parasites. They have only plasmatic membrane, nucleus, and ribosome. Moreover, their ribosome is closer to 70S-prokaryotic ribosome than to 80S-eukaryotic ribosome. The first molecular studies of ribosomal RNA sequence suggest that Microsporidia are extremely ancient eukaryotes [35, 53]. Later, biochemists discovered that phylogenomics supports Microsporidia as the earliest diverging clade of sequenced fungi [54–59]. Therefore, Microsporidia are secondarily simplified, during adaptation to intracellular anaerobic existence.

The second candidate for the most primitive Eukaryota is the Kingdom Archemonadobiontes with Pelomyxophyles, Retortomonadophyles, Hexamitophyles, Oxymonadophyles, and Trichomonadophyles. They are anaerobic organisms without mitochondria but have from two to numerous flagella. The problem is: had they originally no primary mitochondria or they lost them during adaptation to anaerobic environment? Most professionals concerned with megasystematics are inclined to consider anaerobic eukaryotes as the result of their secondary simplification: they have lost their mitochondria, adapting to obligate anaerobic metabolism.

Rhodobiontes (red algae) had no flagella originally or they have lost them? This is a problem, because they are marine algae only and flagella are necessary organelles in water environment.

6. Conclusion

Euglenoids that have all organelles (membrane with special cell wall, nucleus, 80S ribosome, mitochondria with discoid crista, plastids, and flagella), may be considered as most primitive Eukaryota. According to our system [12], Kingdom Euglenobiontes Leedale, 1974 (from the Greek eu -, in English “good,” in compound words it means “well-developed,” “authentic,” consistent with the ideal and glene—the pupil of the eye) combines the heterotrophic or autotrophic green, usually unicellular monad often amoeboid, but usually with a monadic form in the cycle, rarely colonial organisms. They have and mitochondria with cristae that are usually flattened, rounded with a tapered base—discoid, rarely vesicular, or even less often ribbon-like tube; usually single-nucleus; mitosis in a closed intranuclear ortomitosis; reproduction by a longitudinal division; sexual process is unknown. This kingdom includes two subkingdoms: Euglenobionti and Percolobionti. Although acrasia and heterolobosea amoebas are combined into one common taxon usually called Heterolobosea, we prefer to give it the name from the type genus Acrasia-Acrasiophyles.

With this assumption, understanding of phylogenetics of Eukaryota has no problem. Eukaryota are divided into two branches: Tubulicristata (with mitochondria with tubular crista) and Lamellicristata (with mitochondria with lamellar crista). Cryptomonads occupy an intermediate position with riblike crista and nukleomorf in plastids (**Figure 9** and **Table 2**).

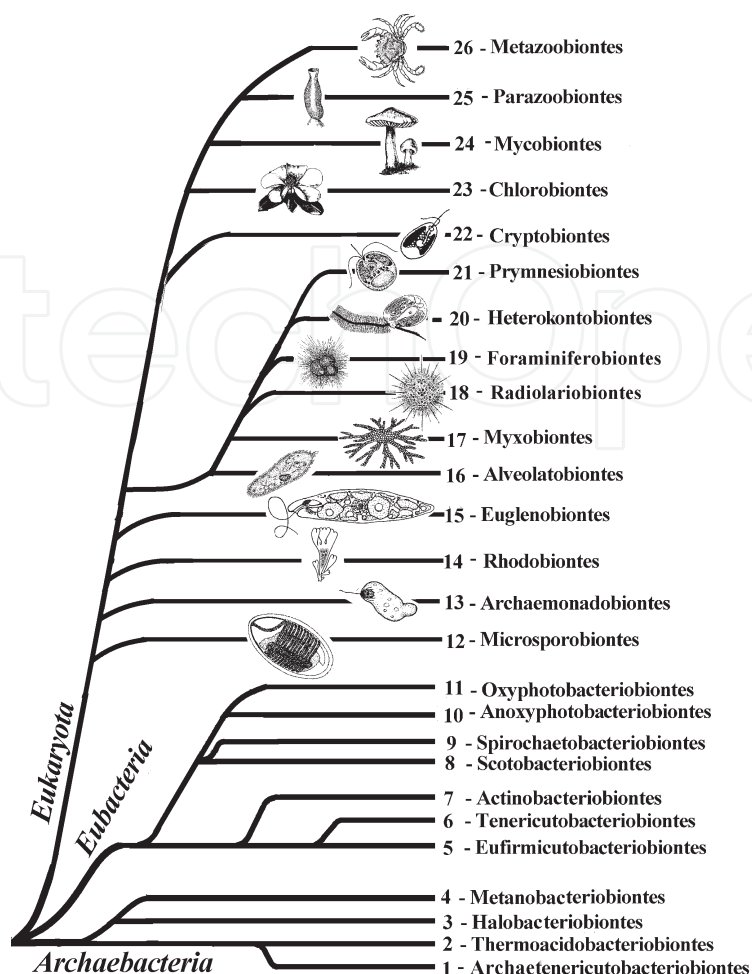


Figure 9. The multikingdom phylogenetic hierarchical tree constructed on base of principle of conservatism (after Drozdov [5]).

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