DEVELOPMENT OF KNOWLEDGE OF THE TAXONOMY AND PHYLOGENY OF LIVING ORGANISMS FOR FUTURE BIOLOGY TEACHERS

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Abstract. The science does not operate with the only recognized scheme representing the taxonomy of living organisms. Each version of it is temporary employed. We offer the school-level curriculum to include the system of two domains (Prokaryotes and Eukaryotes) and seven kingdoms (Viruses, Bacteria, Archaea, Protista, Plants, Fungi, Animals). Further research can be focused on the improvement of the scheme of living organisms due to the recent advances in the molecular branches of eukaryotes on the phylogenetic tree (Amoebozoa, Opisthokonta, Archaeplastida, Excavata, supergroup SAR); evolution factors (horizontal gene transfer and symbiogenesis). It should also take into account the school-level curricula, pupils’ age and tutor’s teaching skills.

Keywords: training biology teachers, phylogeny, taxonomy, phylogenetic trees and cladistics methods.

Introduction

The strategy of scientific and academic support for the transition to the sustainable development requires a teacher to understand the natural and scientific world view, explain the organic evolution and biodiversity classification. Publications of recent decades (V. Aloshyn, L. Vorobeva, K. Voze, I. Dovgal, S. Edl, T.Kavalje-Smit, S. Karpov, M. Kovbljuk, Je. Kunin, O. Kusakin, I. Pavlinov, S. Rudyshyn V. Samilyk, A.Shatalkin et al.) have shown that: 1) natural and scientific world view as well as the taxonomy of living organisms is disputable and temporary concerted (voluntary agreement) by scientists in their arguing objective and systematized knowledge; the only universally accepted taxonomy of living organisms does not exist; 2) the molecular phylogeny newly views phylogenetic relationships and taxonomy; 3) the number of species of cultivated plants and farm animals is negligible compared with the total number of species. Setting the place of a type in the system will help foreseeing its properties, including useful to humans, which is important in the connection with the development of genetic engineering. 4) School biology textbooks reflect the old paradigm of the taxonomy of living organisms, which does not take into account current scientific trends in the molecular phylogeny.

The existence of distinguishing scientific perspectives is always positive since methodologically valuable knowledge emerges at the intersection of competing views on the issue. We believe that the transition to the new taxonomy concern all (scientists, training experts and teachers) lack of arguments to reject traditional and familiar. To teach academic discussions about creating a new taxonomy is difficult but advisable for developing critical thinking abilities by students (pupils). It is not correct to teach according to the pragmatic principle and deliver that, for example, fungi are organisms explored by mycologists and microbiology is the science about the study of all living creatures that can be seen under a microscope. Thus, the problem of scientific understanding the taxonomy and phylogenetic relationships exist, and biology teachers require scientific guidance which can be further explained to students. Children not yet burdened with outdated knowledge will perceive new information in a way they will be taught.

Results

It is appropriate to consider the history of morphological classifications. First, Aristotle distinguished two major taxa – plants and animals later added with fungi. Traditional system of organisms was built from the top to bottom because the upper levels of the phylogenetic tree have the most essential differences in their characteristics strongly influencing lower levels of the hierarchy.
The founder of the scientific taxonomy (the science that deals with the classification of living organisms and family relationships between them), is Carl Linnaeus (1707-1778). In 1735, he published his major work «Systema Naturae» and proposed a binary classification of plants and animals. Linnaeus grouped plants into 24 classes according to the external signs of their flowers; described 4200 species of animals divided into six classes: mammals, birds, amphibians, fish, worms and insects. The amphibians included reptiles and the worms consisted of all known at the time invertebrates except insects. The taxonomy of plants and animals by Karl Linnaeus enabled biology to develop. However, it did not take into account microscopic organisms (this group was called “chaos” by Linnaeus).

The microscope allowed seeing many different small organisms (microbes) that originally were added to whether animals or plants. Then, distinguishing nature of microbes was found and they were isolated and added to other kingdoms. The forceful scheme dividing the world of organisms into prokaryotes and eukaryotes declared the division of organisms by the most significant differences and has been still widely used.

Consider historical approaches to the classification of the organic world (Table 1).

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E. Haeckel described three kingdoms – Plants, Animals and Protista including diatom algae, amoebae, sponges and some other organisms. As for fungi and bacteria, they belonged to the lower-level plants and some of them – to protista.

The taxonomy by Utteker R. (1969) counted five kingdoms: 1) Monera (bacteria, cyanea); 2) Protista (protozoa, chrysophyceae, euglenoza, hypholydrides, plasmodiaphora); 3) Plants (green algae, brown algae, red, mosses and vascular plants); 4) Fungi (slugs, oomycota, hydrides, fungi themselves); 5) Animals (multicellular). This scheme was heuristic, since half a century Protista being relatives of plants, animals and fungi have been looked for.

The biochemical methods including DNA sequencing (determining the nucleotide sequence of a plot) enforced the development of the molecular phylogenetics focused on determining the degree of relationships between the taxa based on the similarity of conserved genes. By employing these facts, Vyoze K. (1990) built a system of three domains (bacteria, archaea, eukaryotes).

Thomas Cavalier-Smith, a prominent British evolutionist, proposed taxonomic system in which eukaryotic organisms are divided into two monophyletic super kingdoms (two phyla) - Unikonta and Bikonta. The first super kingdom consists of unicellular and multacellular organisms (their unicellular forms have the only one flagellum (Opisthokonta); these are multacellular animals and fungi which are organisms of amoeboform without flagella (Amoebozoa). Bikonta includes eukaryotic organisms (plants etc.), unicellular forms of which have two flagella. The organic world was divided by T. Cavalier-Smith into 6 kingdoms – bacteria, protozoa, chromista consisting of organisms that have two eukaryotic cells, one of which is contained within another and has chloroplast; early, this polyphyletic group was a part of protista), plants, fungi and animals. The need of distinguishing phyla for living organisms with one and two flagella has been still discussed.

Therefore, all taxonomies describe the relationships among taxa and provide understanding the history of all living organisms (phylogenesis). Visual representation of evolutionary relationships between organisms is done by means of graphs, called “phylogenetic tree” or “tree of life” (TL).
The concept of the tree of life was introduced for the first time by Charles Darwin in 1837. In particular, he wrote on the 36th page of his notepad «B» that he had already thought about his first evolutionary tree (Fig.1). Then, Darwin depicted it as the illustrations for his “The Origin of Species”.

![Image of the first evolutionary tree by Charles Darwin, 1837](image-url)

Fig. 1. The first evolutionary tree by Charles Darwin, 1837

The history of science justifies that the idea of picturing genetic relationships in the form of a tree is not owned by Charles Darwin. Trees were used for centuries to depict ancestry, for example of royal families. However, Charles Darwin (1859) suggested that the whole history of life can be represented as a giant tree. Herewith, green branches with buds match existing species and previous branches show extinct forms. Such a link between new and old branches of the tree was an attempt to integrate all modern and extinct species via the common ancestor, which created a classification.

For the time Charles Darwin lived, it was the very ambitious assumption because there was no hard evidence for the existence of a common ancestor of all life forms (Dovgal, 2009). A few years after the publication of “The Origin of Species”, Ernst Haeckel populated the Darwin’s abstract tree by real life forms (Fig. 2). Since that time, the tree of life became the central element of the evolutionary biology.

For a long time, the traditional phylogenetic study has contributed the concept of the tree of life by Darwin-Haeckel on the basis of comparison of morphological (animals’ skeleton, the structure of plants’ flowers) and embryological features of organisms. The unicellular eukaryotes (Protista) and bacteria (Monera) were placed at the root of the tree. Thus, the tree of life described the only evolution of eukaryotes. However, this concept did not cover all the cellular forms of life.

Darwin saw the evolution as the basis of phylogenetic concept. The hierarchy was stipulated by independent divergent changes of modified descendants of the common ancestor. Intermediate forms went towards extinction. Nevertheless, he stressed that the natural selection was not the only driving force of the evolution and drew attention to the limited supply of random and uncertain changes. He also considered signs which were acquired through the correlation with adaptive features important. Hence, all distinctive features must have been considered. This approach was called phenetic in the taxonomy of the organic world.
Fig. 2. The tree of life by Ernst Haeckel, 1866
With the development of paleontological research, the phenetics “took a back seat”. It was replaced by cladistics based on the principles of phylogenetic taxonomy (evolutionary history) by the German entomologist B. Hennig (50s of the 20th century). The approach was to distinguish monophyletic branches and establish the position of the ancestral form of the studied group of organisms. The phylogenetic conclusions were made based on the sequence of apomorphic signs (observable only within the same taxonomic group); however, functional significance of signs was not taken into account. Thus, the cladistics does not allow distinguishing all existing apomorphies delineating groups.

The evolutionists did not recognize the need of comparing molecular base of the gene evolution exposed to the natural selection since the adaptivity paradigm in the evolutionary biology and the hypothesis by one of the founders of synthetic theory of the evolution (STE) Ernst Mayr suggested that genes of taxonomically different organisms were significantly different between them (given phenotype differences between organisms).

In the early 60s of the 20th century, the genetic analysis of different life forms progressed to the extent that it became apparent that the genomes of bacteriophages (viruses) and bacteria evolve as well as the genomes of eukaryotes. The synthetic theory of the evolution again did not take these facts into account as viruses and bacteria significantly varied on key factors of creation of plants and animals (peculiarities of sexual reproduction and reproductive isolation).

Scientists began to viewed prokaryotes from the evolutionary perspective after the revolutionary work by Charles Woese released in 1987. K. Woese (1928-2012) is the founder of the phylogeny and the first who defined archaea. K. Woese found that: 1) the nucleotide pRNA sequence of all forms of life is conservative; 2) such universal conservative molecule evolves at a constant rate similar to the so-called “molecular clock” model. Through a comparative analysis of pRNA for different groups of bacteria, the domain Archaea was discovered (this group had the qualitative differences compared to other bacteria and eukaryotes). Further studies of conservative proteins (ribosomal proteins, translation factors, subunits of the DNA-dependent RNA polymerase and membrane ATP) allowed making the important discovery of the late twentieth century, that is the tree of life with three domains (super kingdoms) – Bacteria, Archaea and Eukaryotes. The pRNA evolutionary tree of three domains has become synonymous with hypothetical tree of life by Charles Darwin.

K. Woese and his followers compared the pRNA phylogenetic tree of three domains with the tree of life by Darwin and Haeckel. By agreement, scientists assumed that the tree of life originates from the so-called "last universal common ancestor» (last universal common ancestor, LUCA) – the closet hypothetical common ancestor of all living organisms that now exist on the Earth. This probiont lived approximately 3,6-4,1 billion years ago. Its ribosome structure and the cell membrane evolved and developed.

Assume that the problem of the systematics may be addressed by means of the following decision. We will employ approaches to the taxonomy of living organisms given the needs of education and practice offered by scientists and trainers. We suggest using the system of 7 kingdoms (Viruses Archaea, Bacteria, Protista, Plants, Fungi and Animals) – Fig. 3. It is understandable for teachers and students, because nobody canceled: 1) categories of the taxonomy (kingdom, type, class, order, family, genus, species); 2) the subject and objects of the botany (plants), zoology (animals), microbiology (bacteria, protista), mycology (fungi) and virology (viruses).

Traditions play an important role in science. For example, the term “vitamin” = vita (life) + amine (containing nitrogen), which is vital substance containing a chemical element N. The vitamin C does not contain nitrogen; however, none of the scientists would decide on changing the name of the “ascorbic acid”.

The kingdom of Viruses comprises non-cellular forms of life that are autonomous genetic systems (parasites at the genetic level). The classification of viruses take into account the size, availability of the super capsid, the type of nucleic acid, polarity and virulence etc.

The kingdom of Bacteria includes small prokaryotic organisms with cellular structure. They inhabit different environments: water, soil, hot springs and polar regions. Also, they may be contained in the air, inside and on the body of living organisms. They play a significant role in the biosphere since they decompose and mineralize organic remains of dead organisms, destroy the rocks and contribute to the soil formation.

The kingdom of Archaea (Archaebacteria) contains representatives living in various conditions (some – without oxygen, while others – in brine; others – at 90-100 °C et al.). They have a specific structure of the cell wall and intracellular structures. Earlier, archaea and bacteria were combined in the kingdom of Monera, but
now this classification is considered obsolete. Archaea have an independent history of evolution and are different from other types by genetic and biochemical characteristics. Some signs (e.g. organization of ribosomes) show that archaea are closer to eukaryotes rather than to prokaryotes.

![Diagram of the systematics of the main taxa of living organisms]

Fig. 3. The systematics of the main taxa of living organisms

The kingdom of Protista consists of different in structure and way of life nuclear organisms (over 150 thousand species) not having tissue differentiation. This group includes unicellular eukaryotes.

Eukaryotic organisms with photoautotrophic nutrition form the kingdom of Plants. They have different structure and size. There are plants of conditional lower and higher levels. The kingdom of Fungi includes both unicellular and multicellular organisms with heterotrophic type of nutrition. They have no chlorophyll and thus, in modern phylogenetic system, fungi are relatives of animals. That is, fungi should correctly classified as “mycobiota” rather than “flora”. Certain types of fungi may exist in symbiosis with algae (lichen) and higher plants. The kingdom of Animals includes multicellular eukaryotic organisms and choanoflagellate that are heterotrophic and capable of active movement.

As a result of molecular phylogeny, scientists try to divide eukaryotes not into kingdoms but into the branches of the phylogenetic tree (Fig. 4).

Thus, animals, fungi, unicellular and colonial choanoflagellate (collar flagellate) belong to the Opisthokonta branch; higher plants, green, red and stoneworts – to the second – Archaeplastida. The remaining branches are occupied by protozoa and algae, which are named quite unusual: Amoebozoa, Excavata, integrated group SAR (Stramenopiles + Alveolata + Rhizaria) – the derivative of Stramenopiles (synonyms: Heterokonta, Chrysomona – golden and brown algae), Alveolata (combines ciliates, spores and dinoflagellate), Rhizaria (foraminifera, radiolarians, Apusozoa and others). This scheme can be taken as a working hypothesis. It is not relevant for schools because it did not stand a long time.

The main problems of phylogeny (justification of family ties) and the origin of makrotaxa are caused by the lack of information about the organisms basing phylogenetic branches of eukaryotes. Then, it is advisable to study the flagellum protista.

Discussion

The phylogeny and taxonomy currently put questions without answers; have many hypotheses and unreliable methods for isolating old taxa into new ones. There are many constraints in describing protista and prokaryotes in terms of epidemiology and phylogeography. There is no widely recognized systematics of living organisms; each of its modern scientific versions is imperfect and temporary (for ease of scientists). We recommend to use the system of 7 kingdoms (Viruses, Bacteria, Archaea, Protista, Plants, Fungi, Animals) at schools, which is understandable for teachers and students, because nobody canceled: 1) categories of
taxonomy (kingdom, type, class, order, family, genus, species); 2) the subject and objects of the botany (plants), zoology (animals), microbiology (bacteria, protista), mycology (fungi) and virology (viruses).

Fig. 4. New (2012) phylogenetic tree of Eucaryota

Branches of the tree: Amoebozoa (amoeba, slugs); Opisthokonta (multicellular animals, fungi, choanoflagellate); Archaeplastida (higher plants, algae, green, red, stoneworts); Excavata (euglena, trichomonas and other protozoa parasites); super group SAR : (Stramenopiles + Alveolata + Rhizaria), where Stramenopiles (synonyms: Heterokonta, Chrysomonada – gold and brown algae), Alveolata (ciliates, spores and dinoflagellate), Rhizaria (contains foraminifera, radiolarians and others.)

We consider that further investigations will be focused on changing the classification of living organisms given: 1) the latest advances in the molecular phylogeny on branches of eukaryotes (Amoebozoa, Opisthokonta, Archaeplastida, Excavata, supergroup SAR); horizontal gene transfer as a factor of the prokaryotes evolution; symbiotic scenario of the eukaryotes origin; 2) peculiarities of the school curriculum, pupils’ age and teachers’ pedagogical skills. All these aspects are important for biology teachers in terms of the teaching principles of scientific, clear and visible learning.

The main problems of phylogeny (justification of family ties) and the origin of makrotaxa are caused by the lack of information about the organisms basing phylogenetic branches of eukaryotes. Then, it is advisable to study the flagellum protista. In turn, branches basing the tree of life require certain genes to be researched so that their affiliation to the main groups can be proved.

References