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USING THE LOGICAL BASIS OF PHYLOGENETICS AS THE FRAMEWORK FOR TEACHING BIOLOGY

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ABSTRACT

The influence of the evolutionary theory is widespread in modern worldview. Due to its great explanatory power and pervasiveness, the theory of evolution should be used as the organizing theme in biology teaching. For this purpose, the essential concepts of phylogenetic systematics are useful as a didactic instrument. The phylogenetic method was the first objective set of rules to implement in systematics the evolutionary view that the organisms are all connected at some hierarchical level due to common ancestry, as suggested by Darwin and Wallace. Phylogenetic systematics was firstly proposed by the German Entomologist Willi Hennig in 1950 and had considerably importance in the decrease of the role of essentialism and subjectivity in classificatory studies, becoming one of the paradigms in biological systematics. Based on cladograms, a general phylogenetic reference system allows to the depiction and representation of large amounts of biological information in branching diagrams. Besides, the phylogenetic approach sheds light upon typical misconceptions concerning evolution and related concepts that directly affect students' comprehension about the evolutionary process and the hierarchical structure of the living world. The phylogenetic method is also a form of introducing students to some of the philosophical and scientific idiosyncrasies, providing them the ability to understand concepts such as hypothesis, theory, paradigm and falsifiability. The students are incited to use arguments during the process of accepting or denying scientific hypotheses, which overcomes the mere assimilation of knowledge previously elaborated.

KEYWORDS: cladogram, evolution, philosophy of sciences, phylogenetic systematics, science teaching.

INTRODUCTION

One of the greatest scientific endeavors of all times was the idea that all organisms once living on earth, including the extinct species, are the products of descent (with modifications) from common ancestors. This is the central claim of Charles Darwin's (1858, 1859) and Alfred Wallace's (1858) theoretical work. The evolutionary theory was an answer to some questions that worried mankind for centuries (Nelson

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& Platnick, 1981): what is the origin of the natural relationships among organisms? How do we explain the resemblance of say a species of fox, dog and wolf without recurring to supernatural and untestable explanations? The evolutionary theory emphasized that the whole natural world results from materialistic processes acting since the dawn of life on the planet – there is no such a thing as the fixity of species. In biology, everything evolves.

Since the middle of 19th century, evolution has been a pervasive influence for biological sciences. Systematics, dealing directly with the description of natural diversity, was deeply influenced by the evolutionary thought, especially since the Modern synthesis of the 20th century (Mayr, 1982, 2000; Hull, 1988). Nevertheless, despite the efforts of classic taxonomy, until the works of the German entomologist Willi Hennig (1950, 1966) systematics lacked a method that really implemented the concept of common descent. Hennig's pioneering method, known as phylogenetic systematics (latter cladistics), definitively introduced an evolutionary framework to systematics, according to the view that descent with modification was the cause of the group-within-group pattern recognized in the living world. The Hennigian practice of defining and discovering valid biological groups and the relationships within them represented a turning point to biological classifications. It was far-away from the Aristotelian view of species arrangements on the basis of raw similarities, or the practices of classic taxonomy, encumbered with vague notions about adaptation, fitness, the origin of evolutionary novelties, biological species, and natural selection.

Similar to Darwin's unrooted tree presented in his B notebook (http://darwin-online.org.uk/), Hennig (1950, 1966) proposed that relationships within biological groups are in fact genealogical sister-groups relationships. The aim of Hennigian systematics is to hypothesize the sister-group hierarchy, expressing it through branching diagrams called cladograms (for methodological revision, see Kitching *et al.,* 1998, and Schuh, 2000). The only way to compare natural entities is through sister-group relationships, in which two taxa are more closely related to each other than to a third taxon. According to Hennig, the sources of evidences to identify sister-group relationships are synapomorphies, defined as exclusively (modified) features shared by the two sister-groups (inherited from the most recent ancestor) but lacking in the third. The bases for phylogenetic analysis are the phylogenetic homologies, which are features with a common origin in genealogically related groups, but bearing some kind of modification resulted from differentiation through time – or even none modification at all (throughout the paper, the concept of homology will be always considered in its phylogenetic sense opposed to its original essentialist view). Groups recognized on the basis of synapomorphies, containing the common ancestor and all of its descendants are considered to be "natural" or monophyletic (Hennig, 1950, 1966; Kitching *et al.,* 1998, Schuh, 2000).

In order to present a view of the natural world deeply tightened on the theory of descent with modification, the essentials of the Hennigian method can be used as didactic instruments in biology classes – this is the core of our phylogenetic proposal to biology teaching. Such an approach recovers the inherently human impetus for categorizing and organizing things, introducing it into a scientific perspective inside classrooms. The evolutionary framework of phylogenetic systematics can greatly help both teachers and students, inasmuch as the method enables the discussion of characters evolving in time based on the hierarchical organization of biological groups. Apart from being hierarchical syntheses of biological information (from different sources as morphology, behavior, physiology, genetics etc.), cladograms are also hypotheses of relationships resulted from the analysis of biological data. During classes, the analysis of cladograms allows the discussion of philosophical concepts, especially concerning construction, corroboration and refutation of scientific hypotheses, which brings science learners close to the scientific practice (Calor & Santos, 2004).

Teaching biological sciences through phylogenetic systematics does not mean the formal application of the method in primary or secondary biology classes. We do not propose that teachers present how to construct data matrices or how to analyze them in a cladistic context. As pointed by Baum *et al.* (2005), one can interpret trees and use them for organizing knowledge of biodiversity without knowing every detail of phylogenetic methodology. The present paper aims to point out the potential of phylogenetic systematic as a tool to insert evolutionary concepts in biology classes without the mathematical complexity of tree search algorithms but still deeply tied to the logical basis of phylogenetic methodology. The discussion about the reasoning subjacent to phylogenetics extrapolates the mere introduction of technical terminology in biology teaching. The phylogenetic approach is worthwhile since it sheds light upon some typical misconceptions concerning evolution and its outcomes, as will be treated later, and is a form of introducing students to philosophical and scientific terminology, providing them the ability to understand concepts such as "hypothesis", "theory", "paradigm" and "falsifiability". This proposal also follows the recommendations for the future of science teaching made by Antolin and Herbers (2001), who advocate continuous education in scientific methodological principles and practices for teachers, with emphasis on theory of evolution and the debates around it. The intend is not to present a straightforward recipe or a cut-and-dried method valid for any kind of situations a teacher will face in biology classes. The phylogenetic approach is an alternative perspective to face some of the problems related to the teaching and learning of evolution through the consideration of a concrete set of concepts for the organization and treatment of biological contents at different levels of education.

RESULTS AND DISCUSSION

Why is it so important to teach the fundamentals of the evolutionary theory since the first biology classes? As widely known, the evolutionary theory is the current unifying paradigm of biological sciences, and the research program with the greatest explanatory power throughout the biological disciplines (Futuyma, 1999; Mayr, 2000; Gould, 2002; Larson, 2006). In fact, the revolution carried out by Darwin and Wallace held considerable sway beyond biological disciplines and has actually influenced the human thinking in a plethora of areas, from biology to philosophy of science, providing a materialistic view to explain the living world without any kind of supernaturalism. To quote Ernst Mayr (2000), "Almost every component in modern man's belief system is somehow affected by Darwinian principles". Accordingly, it is usual to consider the theory of evolution as the essential pillar of modern biology, and, thus, to use it as the organizing theme in biology teaching. Besides, evolution brings to the school a broader perspective on natural phenomena and the nature of scientific activity (Tidon & Lewontin, 2004).

On the other hand, despite its importance as an integrative theory that relates biology with other areas of knowledge, the contents of evolutionary biology are often presented to the students in just a few class sessions, usually during the last year of their biology courses. Evolution is treated as an independent topic in the scientific curriculum of regular schools, unlinked to other biological disciplines – some textbooks bring the evolutionary theory in a single chapter, without even considering the role of the materialistic process of evolution in modeling the natural world. This is the rule in Brazilian schools (Bizzo, 1994) but the situation is not quite different in North America or other public schools around the world (Scott, 1997; Lerner, 2000; Antolin & Herbers, 2001; Chinsamy & Plagányi, 2008). The fact is that the traditional approach widely adopted in education becomes especially harmful to the understanding of evolution because the theory is removed from its broad natural context (Alles, 2001). Generally, what are kept in mind from such classes are those larger than life figures such as Lamarck and Darwin, and a few oversimplified examples that vulgarize the correctness of the scientific explanations. The split of biology in a subset of disconnected disciplines is a damaging abstraction to biology teaching and prejudices learning.

The results of deficient learning are the permanence and diffusion of a great roll of problematic issues about evolution and correlated subjects (for examples, see Bishop & Anderson, 1990; Aleijandre, 1994; Settlage, 1994; Zuzovsky, 1994; Demastes *et al.,* 1995, 1996; Jensen & Finley, 1996; Ferrari & Chi, 1998; Thomas, 2000; Anderson *et al.,* 2002; and Passmore & Stewart, 2002). Concepts such as temporal dimension and its consequences to the evolutionary process are commonly misinterpreted, as well as the genealogical relationships among men and other animals, whether humans originated through purely natural processes from other forms of life, and the difference between evolutionary changes, evolutionary novelties and progress. This list runs in parallel with several distortions undertaken by general public – for instance, mass media and non-professional commentators – that echo in teaching and learning, thus performing an endless cycle of misinterpretations.

Despite the fact that an insufficient treatment has been given to theory of evolution in Brazilian schools – the difficulties, however, are not exclusive to Brazil, as pointed above –, the National Curricular Parameters (PCN, 2002) of Brazilian Ministry of Education clearly suggest that biological contents should be treated as trans-disciplinary issues based on ecological and evolutionary explanations. There is a theoretical guideline supposed to be followed: biology needs the historical-philosophical dimension given by a broad sense Darwinism and its connections to ecology and other biological areas. In such a sense, the phylogenetic approach herein proposed is advantageous, since it considers each and every aspects of biology education under the view that descent with modification is the unifying concept of life sciences.

The two-step approach

Language is one of the great problems in biology teaching (Rieppel, 2005). Our vocabulary is often limited, and constructed under a non-evolutionary framework, which creates a vast amount of difficulties in communicating evolutionary relationships (*e.g.* bird wings, insect wings, and airplane wings – the same word is used to describe similar structures that have different evolutionary origins, or even none evolutionary origin at all). We grow up thinking in terms of analogy and not homology. To present an evolving natural world, hierarchically organized, the significance of phylogenetic homology needs to be emphasized in science classes since the beginning of formal education. Let's call this the "Phylogenetic homology approach", which is the first step of a broader phylogenetic approach (Figure 1).

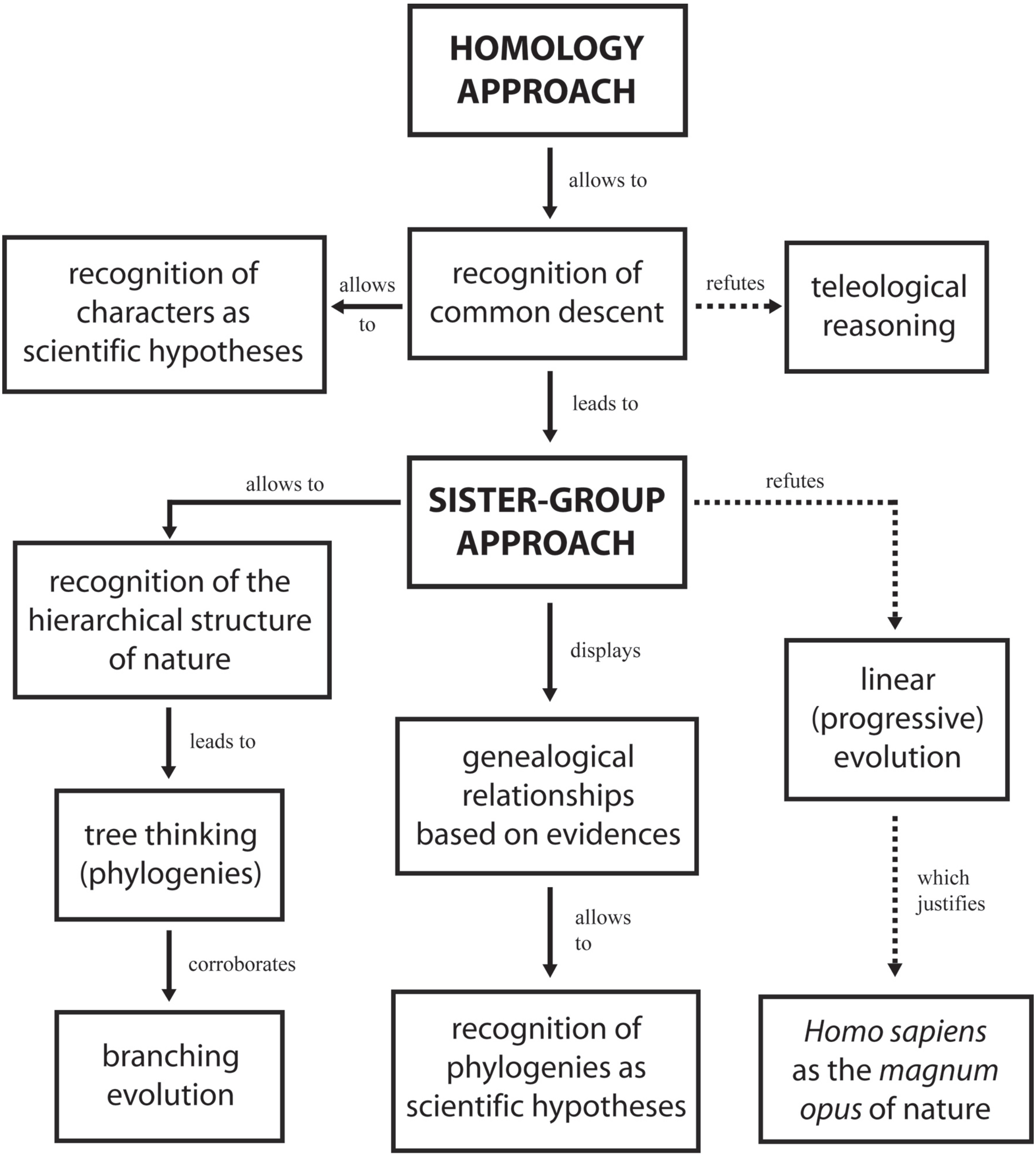

FIGURE 1: Flowchart of the phylogenetic approach for teaching evolution.

The phylogenetic homology approach advocates a non-essentialist view of natural world. Repeatedly during evolution, changes in function precede changes in structure (*i.e.* morphology). Based on this perspective, teachers would be able to present evolution as ongoing modifications of function through time, sometimes followed by modifications of morphology. Such perspective allows us to prevent teleological reasoning (such as the common 'this structure exists *for…*'), because structures may remain morphologically the same, unchangeable, but their related physiological/behavioral nature can modify in time (it should be noted, however, that the form can also change by genetic drift without connection to any known function). This is probably the case of arthropod appendages, for instance. Arthropods such the extinct trilobites had all their legs very similar in structure, but to a great extent variable in function, related to feeding, respiration, reproduction, and locomotion. Yet, the arthropod appendages evolved in greatly different ways, resulting in the enormous morphological and functional variations nowadays presented by the group. In fact, arthropod appendages are all homologous in the different arthropod lineages, despite their remarkable morphological disparity – appendages are the *same* structure, but *differentiated.* How can someone say that the leg exists *for* walking if this structure was not always related to this single function?

The recognition of the biodiversity historical structure logically follows – in fact, it is simultaneous to – the comprehension of what homology means. Every organism is historically connected and has some sort of shared homologous characters. All organisms have cells (bacteria are cells without nucleus). The same way, skin cells are shared by all animals – the epidermis of a jellyfish has the same evolutionary origin of the epidermic layer of a flatworm, an insect, a fish or our own, since epidermis originated in the common ancestor of all Eumetazoa (Nielsen, 2001). Some groups of organisms have bones, and these bones are all modifications of skeletal structures already present in the common ancestor of all the Vertebrata. This means that bones are shared homologous structures among the vertebrates group. In a round-about manner, once we have proposed homology and the origin and diversification of biological features, we can infer the pattern of evolution. After the homology concept is properly understood, how to explain branching evolution? How do we introduce the second step, the "sister-group" approach, mainly based on hierarchical reasoning? To present an evolutionary tree with animals and other living organisms in its terminal branches is not enough – an ulterior elucidation is needed to explain the genealogical reasoning necessary to fully comprehend evolution. At this point, students' previous knowledge about their familiar relationships could be used to illustrate the meaning of genealogy.

With a simple familiar genealogy at hand, the concepts of common ancestor, sister-group, and intrinsic variation can be stated and discussed. Everyone knows that sons are not exactly the same as their parents (they have differences of height, eye or hair color, nose shape, and so on) even though they also bear similarities, which made identifiable the ancestral-descendent relationships. Despite their individual features, two brothers are usually more closely similar to each other than to a third person, as a cousin or a neighbor. What is the cause of brother's closeness? They share the same immediate ancestors, which are not the same ancestors of their neighbors. What about these brothers' sons? They will be closely similar to their parents than to their grandparents. This logical reasoning is helpful to comprehend the hierarchical structure of the natural world but it is necessary to consider that, when dealing with biodiversity and the history of biological lineages, we can hardly observe the co-existence of ancestral forms and their descendants, since the temporal scale related to the origin and diversification of species is broader than that of familiar history. Extrapolating the genealogical scenario to the study of evolution, and associating it to the homology concept, allows the teacher to explain, for instance, why a cat and a lion are more closely related to each other (this sense, they are sister-groups) than to a horse or a fish. As pointed by Gould (2003:23), "The tree of life and the genealogy of each family share the same topology and the same secret of success in blending two apparently contradictory themes of continuity (…), and change".

The base of our approach rests on the phylogenetic homology concept and on the recognition of the hierarchical (genealogical) framework of nature – it is different from a general evolutionary approach since it is totally based on the logic derived from the methodological background of phylogenetic analysis. As soon as the historical perspective of biodiversity has been clearly recognized, the phylogenetic systematics can be introduced as a method for reconstructing the evolutionary hierarchy among biological groups based on the test of hypotheses of homologies. In general, the aim of a phylogenetic analysis is to hypothesize the sister-group hierarchy and express the results in terms of branching diagrams, the so-called cladograms (generally known as phylogenies). The sister-groups are hypothesized through the analysis of characters –

morphological, behavioral, ecological, physiological, molecular – which could be defined as the proposal that certain observed features, in two or more groups, have the same evolutionary origin, *i.e.,* are homologous. Hence, every homologue is a proposal that suggests a particular taxonomic grouping, in such a way that the ultimate purpose of an evolutionary study is to obtain the maximum amount of congruence within its hypotheses of homologies (Farris, 1983).

The Hennigian phylogenetic method distincts between two classes of characters (or character states): (1) the character that occurs in the ancestral is the 'plesiomorphic' (or near the ancestral morphology), while (2) the derived character is the 'apomorphic' (away from the ancestral morphology) (Kitching *et al.,* 1998). Sister-group relationships are discovered only be identifying apomorphic characters inferred to have originated in their most recent common ancestor and shared by its descendants. This way, synapomorphies (shared apomorphies) are proposals of homology (characters states) that were corroborated during the congruence test, in which the sister-groups relationships suggested by all characters are tested simultaneously, and the most parsimonious solution is chosen – the final cladogram is the one in which the hypotheses of independent origin for the characters are minimized (the practice is synthesized in Figure 2). This way, the idiosyncratic nature of science can be explored in two different levels: (1) the dispute among different (congruent or not) characters in the congruence test to infer the cladogram(s), and (2) the confrontation among distinct hypotheses (cladograms) derived from different data sets. According with the education level, the congruent test can be explained using the phylogenetic reasoning of hypotheses comparison without the data matrix.

As said above, a form of representing hierarchies of homologies is a cladogram. Based on cladograms, the whole natural world could be described as an output of the process of descent with modification through time. Every biochemical aspect of life (*e.g.,* the evolution of fermentation, cellular respiration and photosynthesis processes), every animal and botanical morphological feature, every detail in organisms' physiology, in short, every aspects of the living world can be plotted in evolutionary branching schemes, which summarize patterns of character distribution. In the words of Hennig (1966:22), "Making the phylogenetic system the general reference system (…) has the inestimable advantage that the relations to all other conceivable biological systems can be most easily represented through it. This is because the historical development of organisms must necessarily be reflected in some way in all relationships between organisms. Consequently, direct relations extend from the phylogenetic system to all other possible systems, whereas there are often no such direct relations between these other systems". The cladogram is the main tool in the proposal made here, particularly during the establishment of a hierarchical perspective of nature. It orientates teachers before and during classes and helps biology learners to visualize hierarchical patterns in light of an evolutionary point of view. Notwithstanding the pervasiveness of "tree thinking" among professional evolutionary biologists, such concept is not as widely disseminated as it should be in the teaching of evolution (Baum *et al.,* 2005).

It is a fact that the whole tree of life is hardly known (Doolittle, 1999), despite the continuous attempts to solve the sister-group relationships among different kinds of organisms. This is not a problem for the phylogenetic approach herein discussed. The cladograms used in classroom must respect teachers' pedagogical necessities – the guiding phylogenetic hypotheses do not require necessarily a large amount of biological groups with the representation of all sister-group relationships among them. General cladograms displaying representative groups are preferable because they prevent students (and even educators) to miss the point of the class in a confusion of unnecessary species and groups names. The main objective of our proposal is to facilitate the comprehension of biodiversity via an evolutionary framework provided by the phylogenetic reasoning, not to be a compendium of taxon names. The cladograms used in classroom should be derived from previous scientific studies based on supporting evidence, which can be discussed with the students. Such schemes are available in major textbooks (Nielsen, 2001; Brusca & Brusca, 2003; Ruppert *et al.,* 2003; Pough *et al.,* 2004) and specialized reviews (*e.g.,* Zrzavy *et al.,* 1998; Peterson & Eernisse, 2001; Halanych, 2004), as well as in reliable sites such as tree of life project (http://tolweb.org/tree/phylogeny.html) or Berkeley's museum of Paleontology web site (http://www.ucmp.berkeley.edu/index.html).

On the nature of science

According to Davson-Galle (2004:512), "science provides our most generally trusted theoretical picture of the world around us, indeed, of humanity itself. Given this, intellectual users of science should have some educated ideas as to whether that status is deserved. Most general science education is school-based and of course there are limits to what can be done here given that a body of science content is to be acquired by students in a limited curriculum time". Students are first introduced formally to scientific arguments and practices in primary/elementary school. These scientific ideas and procedures are refined in secondary and high schools. However, many biology teachers in primary and secondary schools – this is also valid for physics, chemistry, and other sciences – are often not aware of the criteria used in evaluating scientific hypotheses, and commonly the exposition of broad theories is reduced to superficial or inaccurate discourses. This generates an uncritical and unilluminating approach to science teaching (Martin, 1976). The biology teaching is not a simple repetition

A

Data matrix	Character 1	Character 2	Character 3	Character 4	Character 5	Character 6	Character 7
Taxon A	0	0	0	0	0	0	0
Taxon B	1	1	0	1	1	0	0
Taxon C	0	1	1	1	1	1	1
Taxon D	1	1	1	1	1	1	2
Taxon E	1	1	1	0	1	1	2

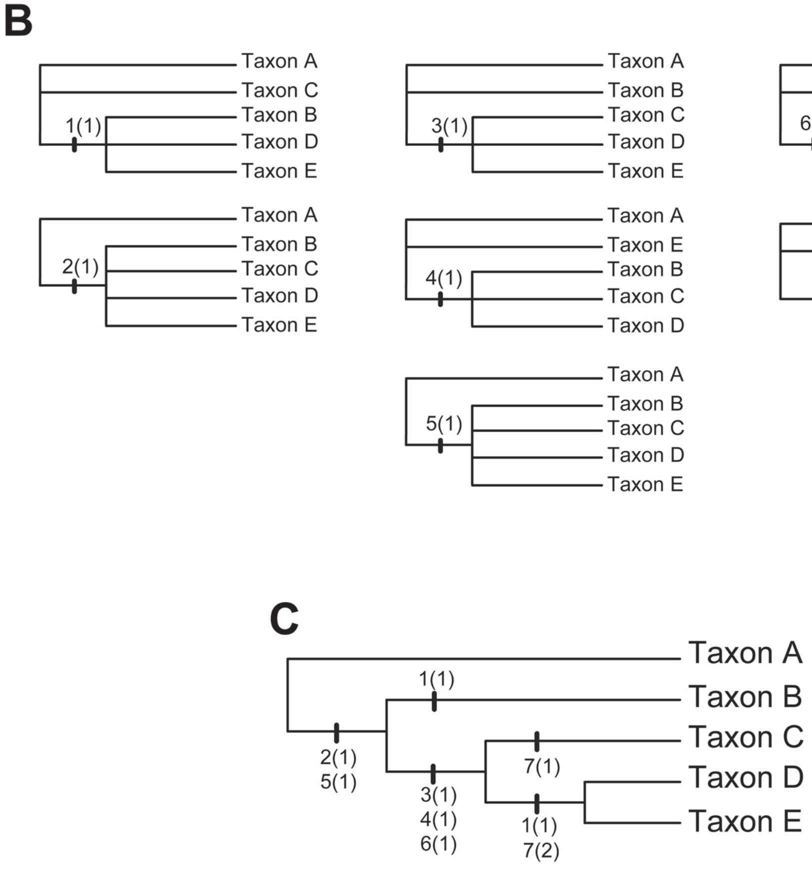

FIGURE 2: Congruence test of characters. A. A simplified data matrix, with 7 characters (6 binary characters and a character with 3 states, called multi-state character) and 5 taxa. B. Using Hennigian argumentation, each character (initially supposed to be a real homology) suggests a certain kind of phylogenetic relationship. C. In the final cladogram all the character states are distributed according to the most parsimonious solution. Here, the character state "0" is proposed as the plesiomorphic condition and the states "1" and "2" as the apomorphic conditions.

of well-established scientific dogmas, but an exercise of evaluation of the explanatory value concerning scientific hypotheses and the evidences used to construct and to support them. Under this perspective, science teaching is tied to philosophy of science, and to the works of philosophers such as Karl Popper, Inri Lakatos and Thomas Kuhn (Gil-Pérez *et al.,* 2002; Calor & Santos, 2004).

As pointed out by Martin (1972, 1976), maximum scientific growth is achieved by working with conflicting scientific theories or research programs (*sensu* Lakatos, 1977). The maximum intellectual growth for students will be reached by treating science as an open field in an endless process of self-construction by the evaluation of many different and conflicting theories or research programs. According to Feyerabend (1962-1963, 1975), plurality of theories must not be considered just as a preliminary step of knowledge which will be substituted by the "true" theory. Theoretical pluralism is an indispensable characteristic of all knowledge that claims to be objective. This is especially applicable in science teaching, since the scientific enterprise is a dynamic activity without canonic proposals or unchangeable statements representing the "real truth". Under the phylogenetic approach, every cladogram is seen as a particular description of the pattern of evolution based on a given data set and not as the final word about the evolution of a group – this kind of doubt may be worked up with students given that evolutionary biology is mainly concerned with the *interpretation* of past events and the depiction of the historical connections among such events. However, a matter of reliability could arise during the substitution of students' "truths" for scientific (possibly transitory) hypotheses but this must be used in teachers' and students' own benefit. To show the apparent uncertainty of scientific reasoning is essential to the depiction of science as a human activity in a continuous process of self-development. In science, there are no definitive "truths".

The cladograms are conjectures about phylogenetic relationships among biological entities resulted from the test of congruence of *prior* statements of homology (de Pinna, 1991). As they are hypothetical, cladograms do not represent unquestionable historical relationships for the groups under inquiry, but (transitory) hypotheses of sister-group relationships based on particular data sets. A cladogram is a hypothesis representing the pattern of relationships among the assumed sample of organisms useful to describe evolutionary scenarios. It is a representation of the largest number of congruent relationships proposed by each of the analyzed characters. Despite some disagreement on the subject, different cladograms derived from different data sources are unfalsifiable according to the Popperian argument (Popper, 1959, 1962). However, when a cladogram is coherent (non-contradictory) with other cladograms – it does not matter the kind of evidences – it means that the hypothesis has a high degree of corroboration. Consequently, as they are scientific hypotheses, cladograms can be tested against data provided by multiple sources. Those cladograms shown to be unsupported (contradictory) are often abandoned, while those that remain well substantiated continue to be used. This context, Popperian philosophy provides the justification for phylogenetic analysis. Hence, conjectures displayed in cladograms represent falsifiable evolutionary hypotheses according to Popperian criteria (Wiley, 1975; Nelson & Platnick, 1981; Farris, 1983; Kluge, 1997; Faith & Trueman, 2001).

The whole phylogenetic method relies on philosophical issues concerning corroboration and refutation of hypotheses of character evolution and on the criteria used to establish valid scientific hypotheses. The method is different, for instance, from classic taxonomy, which is mainly dependent on 'authority' (Hull, 1988, 2001). In presenting phylogenetic schemes, and aware of their philosophical roots, biology teachers will be able to introduce some basic scientific concepts concerning the transitory nature of science and the importance of analyses and criticisms, reinforcing the importance of philosophy of science and critical thinking. This is in accordance with the model of constructivism defended by Bell and Pearson (1992) and Gil-Pérez *et al.* (2002), which considers philosophy of science as a great facilitator of scientific teaching, placing the students in a situation where they produce knowledge and explore alternative reasoning using scientific criteria. The same sense, Matthews (1994) defends that science education has to be relied on methodological issues such as how scientific theories are evaluated and how competing theories are appraised. As synthesized above, the phylogenetic approach suggests to biology teachers a new view about how scientific knowledge is constructed and evaluated, and, to students, it incites the use of arguments and evidences during the process of accepting or denying scientific hypotheses, overcoming the mere acceptation of previously elaborated knowledge. When students think critically, they are evaluating the outcomes of their own thought processes, which make they go far beyond the simple assimilation of new experiences into their preexistent models and instead undergo conceptual change (Kalman, 2002). This perspective of science teaching is defended, in a wide sense, by Furió & Gil (1978) and Gil-Pérez *et al.* (2002), and also by Lerner (2000), to whom a good education in science requires that students understand the central role of theories in scientific methodology.

Solving misconceptions

Despite the inherent value of taking evolution for granted and grounding biology teaching on philosophical criteria, still remains unsolved how to deal with the widespread misinterpretations about the evolutionary theory. As pointed by Kalman (2002), students hold different views from those that will be taught in the classroom. Many factors affect learning, including students prior (mis)conceptions regarding evolutionary issues, scientific epistemology, perception of the biological world, religious beliefs, and so on (Alters & Nelson, 2002). Mistaken assumptions are amplified by the lack of even elementary understanding of evolution by the non-specialized public and mass media, directly affecting students' comprehension of basic concepts.

The phylogenetic approach has the potential to solve some of the common distortions concerning evolution, providing alternative hypothesis to those ones deep-rooted in students' background knowledge. This does not mean to discard students' previous knowledge on the subject. Based on their prior conceptions, students should be allowed to scientifically discuss and analyze their former background (Calor & Santos, 2004). The comparison of scientific knowledge (based on evidences, inquiries and the falsifiability criterion) and pseudo-scientific knowledge (based on general opinions, raised without clear empirical basis or delimited scientific methods) is a form of clarifying the paths that lead to the construction of science itself. It also reinforces the indispensable connection between scientific hypotheses and observable supporting evidences.

Some of the evolutionary misconceptions are so deeply widespread throughout the popular culture that they are often assumed as unequivocal in classrooms – the definitive resolution of such problem in school is a difficult task. The representation of the hominids evolution, led by *Homo sapiens* and started by a little primate resembling a chimpanzee, the *Australopithecus* (or even a proper chimpanzee in some reconstitutions), is an indisputable example of the pervasive influence of mass media in scientific teaching and learning. Almost everyone formally educated would relate this picture to certain aspects of evolution. It is widely disseminated in publicity, television, comic books, cinema, and literature, and actually considered as a reliable representation of the evolutionary theory. In fact, this canonic iconography (Gould, 1989, 1998) hides a great mistreatment of the theory: the idea that evolution means progress through time. The single file is commonly interpreted as the climbing of organic world toward improvement and greater perfection, naturally pushed by the evolutionary process, in a sort of linear upgrade that had been in vogue since Aristotle's concept of *Scala Naturae* (Mayr, 1982; Hull, 1988). From the linear march, people infer the transformation of a most 'primitive' or 'inferior' species in a 'superior' or 'evolved' species. This erroneous interpretation is ordinarily mistaught in biology classes. All teachers must strive to be the most accurate as possible to explain the difference between evolution of species and a deterministic climb toward perfection. Evolution is not the simplistic direct transformation of a 'primitive' lineage into a more complex or derived one (*e.g.,* from a terminal taxon X to other terminal taxon Y), but a natural branching process related to the origin and diversification of species through time, mainly based on common ancestry, random variation, natural selection, neutral genetic changes, and genetic drift. There is no such a thing as a linear chain of organisms going from the primordial bacteria to our species – the great idea brought at light by Darwin (1858, 1859) and Wallace (1858) was the branched aspect of evolution, which is opposite to the traditional viewpoint often mistaught.

The notion of branching evolution, implying the common descent of all living world from a unique origin, is maintained through the display of organisms as terminal taxa in cladograms. As discussed before, the phylogenetic method is a form of expressing sister-group relationships among species raised upon the basic principles of descent with modification, common ancestry and variation through time. The method precludes the proposition of direct ancestors at the nodes of the cladograms, which means that no taxon should be interpreted as the ancestor of another taxon placed above it in the same phylogeny. Therein, in using cladograms as the basis for biology teaching, false interpretations regarding the idea of progress are minimized, since a branching diagram representing sister-group relationships is essentially different from a progressive line of organisms changing toward perfection or species improvement. The arguments that equate biological evolution with progress fall down and become unsupported when biodiversity is phylogeneticaly organized.

All taxa are placed as terminals at the end of branches in cladograms, including fossil species. This sense, the correct interpretation of phylogenetic relationships prevent the inference of direct transformation from a terminal taxa A to a terminal taxon B, whatever species (or more inclusive groups) are analyzed. Considering the hominid lineage and the canonic iconography that intends to represent its evolution, and setting it upon a phylogenetic scheme, a precise explanation of the relationships must clearly states that *Homo sapiens* is not a direct descendant from chimpanzees or some modern ape (neither from *Australopithecus,* since it is also a terminal taxon in the cladogram), but actually a lineage placed in a branch within the whole primate group, more closely related to other species of the genus *Homo (e.g.,* the *H. neanderthalensis)* than either is to species belonging to another hominid genera. The problem of inferring direct ancestors is also common among systematists, especially paleontologists, who usually embed fossil species along the branches of a cladogram in aim to represent the fossils species as true ancestors of apical groups (Donoghue *et al.,* 1989). However, Hennig's method forbids this procedure, since ancestors are always treated as hypothetical entities that could not be directly recognized, inasmuch as they are inferences based on the results of an analytical procedure. Even being obvious that fossils species predates the considered extant species, it is beyond the scientific possibilities to impute the status of ancestral to any species, even fossils. Hence, it is impossible to know whether a fossil actually represents *ipso facto* an ancestor of other recognized taxon or taxa (Schuh, 2000). This is clearly stated in the foreword to the second impression of Hennig's *Phylogenetic Systematics* (1966), by Don Rosen, Gareth Nelson and Colin Patterson: "[With phylogenetic systematics] the idea of organic evolution was thereby changed from a narrative about the history of life to a scientific theory about how nature came to be ordered in its particular hierarchical structure. It also become clear that fossils, long held in some sense to be proof that evolution has occurred, were merely parts of this hierarchy, subject to the same constraints of interpretation as living organisms. This realization marked the beginning of the end of traditional paleontology and its searches for ancestors. Paleontology becomes, in that realization, no longer the keeper of profound evolutionary truths but rather the keeper of extinct parts of nature's hierarchy".

The phylogenetic approach is also a useful tool to obliterate the essentialist notion of unchanging species (for instance, by comparing homologous structures of closely related groups, the teacher will be able to discuss the concepts of temporal change and speciation). Significantly, through a non-creationist and non-essentialist view of the living world connected with a phylogenetic framework organizing the biological knowledge, questions about the position of *Homo sapiens* in evolution are better understood, and the idea that our species is the *magnum opus* of nature is easily refuted (Gould, 1989).

CONCLUSIONS

A scientific theory has consilience when it provides a unifying explanation for a wide range of areas of study (Alles, 2004) – consilience could be considered the main goal of science (NAS, 1998). Nowadays, the scientific inquiry has become an intense search for maximum specialization, often resulting in works mostly based on a rather small amount of evidence or on evidence unconnected with broader facets of the problem. This high-specialized profile of the activity creates a barrier between the current scientific practice and the non-specialized public, among them the science students and even the science teachers. It relies on science educators the task of synthesizing the results of the scientific analysis in a wide and coherent picture of the world (Alles, 2004). Teaching biology by means of phylogenies is a step toward this purpose.

The pedagogical argumentation concerning science education considers students as active participants of the scientific world, not inert listeners. Science learners should be able to criticize theories and hypotheses in light of scientific methodology and concepts, in order to minimize their own misconceptions regarding science, and to make feasible contributions to the scientific learning process. The general aim of our proposal is to present science as a dynamic process toward knowledge, and, accordingly, as a transitory practice that is deeply founded in prior knowledge and delimited methods (Villani, 2001; Laburú *et al.,* 2003; Calor & Santos, 2004). To reach this goal, teachers must be continued educated in scientific reasoning and practices, since the school curriculum under the phylogenetic perspective will be rather different from most part of the traditional textbooks. This could look like a utopia, especially considering underdeveloped nations with few educational resources, but there is a real need of an ongoing training for educators, emphasizing the theory of evolution and the debates around its fundamentals and developments. Only with up-to-dated professors, science courses will be prepared to train students in critical thinking and scientific methodology, which unfortunately is not a widespread praxis of science even among scientists. No scientific theories or laws are learned without their broad context. In scientific manuals, theories are discussed under an observational and empirical basis, and not considered as purely abstractions without evidences (Kuhn, 1962), as is often done in science classes, mainly in primary and secondary schools.

The application of phylogenetics in biology education "contemplates active participation of students in the construction of knowledge and not the simple personal reconstruction of previously elaborated knowledge, provided by the teacher or by the textbook" (Gil-Pérez *et al.,* 2002:561). Despite the fact that cladograms are the final product of phylogenetic analyses, the students are not simple passive listeners in our approach because the comparison of multiple hypotheses is made according to the discussion of the reliability of the proposed homologies and the resultant cladograms. As phylogenetic systematics deals with the evaluation of hypotheses and evolutionary scenarios, the students can compare between alternative ideas (different cladograms) according to established scientific criteria. The aim here is not to take those cladograms as black boxes that should be accepted as the word of authority: the presentation of those final products of the phylogenetic method works as an introduction to epistemological and practical scientific idiosyncrasies, offering to biology learners the ability to understand the scientific practice as a continuous process often characterized by the contraposition of different points-of-view regarding the same subject.

In practice, the use of phylogenetic relationships in school is a form of presenting the entire biology in an evolutionary context. The general aim is to demonstrate a view of evolution different from the traditional Lamarck-Darwin controversy: evolution is a real process, and the theory of descent with modification is the best scientific explanation for the origin and diversification of living organisms on earth. It is important to note that no detailed formalizations on phylogenetic systematics theory and practice are needed to be successful in following the proposed approach. The simple organization of biological diversity in cladograms allows the teacher to work on concepts such as phylogenetic homology, modification through time and common ancestry — the core of evolutionary thinking — with an elegant simplicity. This way, the students keep contact with a new form of analyzing and understanding the nature, far from those endless lists of species names of organisms, structures and systems to be remembered without any consistent framework. If there is a real desire to delimit a new philosophy for biological sciences, utterly grounded on evolution, it is quite important to present it in a real materialistic sense – a process liable for uniting the biodiversity in a great tree of life, in which all the organisms are connected to each other due to common descent. The adoption of a phylogenetic approach in biology teaching intends to show the natural world in all of its greatness and beauty toward an explicit view based on the study of hierarchical patterns within organisms.

RESUMO

A influência da teoria evolutiva é disseminada na visão de mundo moderna. Devido a seu grande poder explanatório e penetração, a teoria da evolução deve ser usada como o tema organizador do ensino de biologia. Para esse propósito, os conceitos essenciais da sistemática filogenética são úteis como instrumentos didáticos. O método filogenético foi o primeiro conjunto objetivo de regras buscando implementar, na sistemática, a perspectiva evolutiva de que todos os organismos estão conectados em algum nível hierárquico devido à ancestralidade comum, como sugerido por Darwin e Wallace. A sistemática filogenética foi proposta inicialmente pelo entomólogo alemão Willi Hennig em 1950 e teve um papel considerável na diminuição da importância do essencialismo e da subjetividade nos estudos classificatórios, tornando-se um dos paradigmas na sistemática biológica. Baseado em cladogramas, um sistema de referências filogenético permite a descrição e a representação de uma grande quantidade de informação biológica em diagramas ramificados. Além disso, a abordagem filogenética lança luz sobre típicas concepções errôneas a respeito da evolução e conceitos relacionados, que afetam diretamente a compreensão dos estudantes sobre o processo evolutivo e sobre a estrutura hierárquica do mundo natural. O método filogenético também é uma maneira de introduzir os estudantes a algumas das idiossincrasias filosóficas e científicas, dando-lhes a habilidade de entender conceitos como hipótese, teoria, paradigma e falseamento. Os estudantes são incitados a usar argumentos durante o processo de aceitação ou refutação de hipóteses científicas, o que extrapola a mera assimilação de conhecimento previamente elaborado.

Palavras-chave: cladograma, ensino de ciências, evolução, filosofia das ciências, sistemática filogenética.

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