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Investigating how undergraduate Biological Sciences students understand tree-thinking: results from two Brazilian institutions

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Abstract

Phylogenetic Systematics (PS) is a biological field that investigates how organisms relate to one another, being phylogenetic trees the most direct visual representations of evolution. Currently, PS plays a central position in evolutionary studies. However, there is still a limited comprehension of such subject by people in general and scientists; that limitation is not only related to its own interpretation, but also to its meaning. Skills to visualize evolutionary kinship in a phylogenetic tree abstraction are collectively called 'tree-thinking', which is still a critical educational component. Biological Sciences undergraduate students from two Brazilian institutions were asked to evaluate PS, and we could verify that students were already able to recognize common ancestry and point out features of organisms from the tree. Students have shown greater difficulty, though, in recognizing kinship degrees amongst *taxa*, perceiving similar trees with different node rotations, and mapping time. Participants have demonstrated the acquisition of these skills as PS is taught in introductory curricular subjects. Such acquisition was not the same with both groups, as very different profiles, including formal knowledge of phylogeny and evolution contents, have been noted.

Keywords: Tree-Thinking; Philogenetic Systematics; Undergratuated Biology Students

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1. Introduction

Even though evolution is recognized as a central axis and the unifying subject in modern biology (Dobzhansky, 1973; Futuyma, 2002), its comprehension is still far from being properly diffused. Brazilian researchers, for instance, have pointed out the influence of media (magazines, papers, television, comic books, internet and others) disseminating information that is not scientifically accurate (Santos and Calor, 2008). Thus, the presence of misconceptions is one of the major challenges in biological education.

Furthermore, the miscomprehension of evolution is not a recent concern. Many scientists have interpreted the history of life after *On the Origin of Species* had been published as a teleological and progressive process. One classic example is the first interpretation of the Burgess Shale's animals, found in 1909 by Charles Doolittle Walcott, which were seen as ancestors of the current living organisms that lived after the Cambrian explosion. Some years later, though, they were actually classified as an entire different new *Phylum* (Gould, 1990). Gould, in his book *Wonderful Life: The Burgess Shale and the Nature of History*, proposed that this means a new conception of life, which cannot be seen as a progressive line. The experimentation, extinction, and contingency are important patterns in evolution.

Phylogenetic trees are the most direct and disseminated graphic representations of evolutionary processes. Phylogenetic Systematics is the science that studies and re-builds such trees, aiming to suggest kinship amongst various organisms of a group (Hennig, 1965). The term 'tree-thinking' was coined to describe the ability of visualizing evolutionary relationships in a phylogenetic tree abstraction (Meisel, 2010), and its comprehension is extremely important to properly understand evolution. Even though Phylogenetic Systematics is a current field, Darwin already had the idea of ramification and described the metaphor of the tree of life in his "Natural Selection" chapter, not only the branching of evolutionary lineages but also the broken branches and the importance of extinction in the evolutionary process (Darwin, 1859).

Therefore, tree-thinking can be a useful pedagogical tool. Hobbs and collaborators (2013) mentioned that several authors noted the difficulty of undergraduate students to build, interpret, and make comparisons among phylogenetic trees. The acquisition of phylogenetic thinking skills is still a challenge and a critical educational component (Gregory, 2008). Tree-thinking should be understood not in a way of teaching the specific systematic terminology and the complex ability of reconstructing evolutionary trees. The major interest is to read and to interpret those trees, being able to comprehend what they communicate.

In such context, the present paper aims to: a) diagnose previous abilities regarding tree-thinking by undergraduate Biological Sciences students in two Brazilian institutions, which had not learned Phylogenetic Systematics previously; and, b) verify how such skills were developed with the formal teaching of Phylogenetic Systematics.

2. Methods

We surveyed students with questionnaires to diagnose their knowledge and skills regarding tree-thinking. Participants were freshmen or second-semester students in 2015 attending Biological Sciences at two public institutions in Sao Paulo State, Brazil (Institution A and Institution B). In both institutions, Phylogenetic Systematics is taught in introductory curricular courses, during which questionnaires were applied.

Two questionnaires were applied in each group: in the beginning (before students could have any formal education in Phylogenetic Systematics), and after the course completion (during which specific topics on Phylogenetic Systematics were taught). Questionnaires consisted of two main parts: I) Data of participants' profiles (age, gender, previous studies of evolution or systematics, and type of high school – public or private); II) Four interpretative questions of phylogenetic trees, all of them based on "The Tree Thinking Challenge", by Baum *et al.* (2005) and an additional question based on Meir *et al.* (2007). Each question aimed to assess a specific skill regarding tree-thinking and to survey possible interpretative mistakes commonly found in phylogenies (Table 1). Even though questions were different in initial and final questionnaires, skills to be verified were corresponding. Statistical analyses and comparisons were deployed to check students' performance in both questionnaires in each one of the abilities individually, thus we could verify if some interpretation aspects had improved. In this analysis we used qui-square tests, and we analysed each question in terms of right or wrong answers.

Table 1. Skills of tree-thinking involved in each question. Categories were defined by the authors.

Question	Skill
1	To recognize kinship amongst *taxa*.
2	To identify common ancestors.
3	To interpret trees with different topologies, although with the same meaning.
4	To point out group features based upon phylogenetic trees and recognize evolutionary novelties.
5	To map time.

Meir *et al.* (2007) also identified some skills for correctly interpreting evolutionary trees. We have in common only the skill regarding reading traits from the tree (number 4, in our questionnaire). They also related skills as deducing ancestral traits given some terminal *taxa* traits, which is related to our first question. Another skill is to be able to reconstruct trees given a small set of extant species. Even though it is important to biologists, and so it is important to undergraduate biology students, we were interested only in the interpretative tree-thinking aspects.

Initially, we analysed each question individually. We also analysed if the number of right and wrong answers changed between the first and the second questionnaires, and which of the alternatives were mostly chosen by the participants. In a further moment, participants were graded from zero to five (one point for each right answer), and average grades of each group were calculated. We, then, analysed both the average grades and the variation between students, using a one way ANOVA test to verify a general improvement of tree-thinking knowledge.

3. Results and Discussion

A total of 245 questionnaires were applied. At the Institution A, 86 and 81 participants answered initial and final questionnaires, respectively. At the Institution B, 41 and 37 participants answered initial and final questionnaires, respectively. In table 2, it is possible to see all right and wrong answers, which were used to calculate the qui-square (Table 3). In the same table, the percentage of right answers is represented for a better data visualisation.

Table 2. Results of both questionnaires (I-initial and F-final) in all participants groups (based on researched data).

		Institution A (diurnal)			**Institution A (nocturnal)**			**Institution B**		
Question		**Right Answers**	**Wrong Answers**	**(%)**	**Right Answers**	**Wrong Answers**	**Percentage**	**Right Answers**	**Wrong Answers**	**(%)**
1	**I**	4	43	**8.5**	12	27	**30.8**	6	32	**15.80**
	F	27	14	**65.9**	18	23	**43.9**	6	31	**16.20**
2	**I**	44	3	**93.6**	30	5	**76.9**	33	6	**84.60**
	F	31	9	**77.5**	35	6	**85.4**	23	7	**76.70**
3	**I**	22	23	**46.8**	12	26	**30.8**	11	25	**30.60**
	F	35	6	**85.4**	30	8	**78.9**	10	23	**30.30**
4	**I**	37	10	**78.7**	29	10	**74.4**	21	19	**52.50**
	F	6	40	**90.2**	9	27	**90.2**	19	16	**54.30**
5	**I**	6	40	**12.8**	9	27	**25.0**	0	34	**0.00**
	F	35	6	**85.4**	34	6	**85.0**	21	11	**65.60**

Table 3. Statistical Analyses carried out with software based on researched data.

		1	**2**	**3**	**4**	**5**
Institution A (diurnal)	Qui square	31.557	4.721	12.772	2.172	45.506
	Degrees of freedom	1	1	1	1	1
	Probabilty	**<0.00001**	**0.0298**	**0.00035**	**0.14054**	**<0.00001**
Institution **A (nocturnal)**	Qui square	1.471	0.002	17.224	3.493	27.765
	Degrees of freedom	1	1	1	1	1
	Probabilty	**0.225**	**0.964**	**0.00003**	**0.06163**	**<0.00001**
Institution B	Qui square	0.003	0.701	0.001	0.024	32.725
	Degrees of freedom	1	1	1	1	1
	Probabilty	**0.956**	**0.402**	**0.975**	**0,877**	**<0.0001**

At the Institution A, we noticed a meaningful change of interpreting kinship amongst species (Ability 1 – $P < 0.00001$) represented in a phylogeny. Likewise, there were significant changes on how to perceive that nodes might be rotated (Ability 3 – $P < 0.00035$), as well as mapping time correctly in a cladogram (Ability 5 – $P < 0.00001$). The difference found in the second question, in which students' right answers choice decreased, was due to the level of difficulty. Even though in both initial and final questions they needed to recognize the common ancestor, the latter was more difficult because instead of saying which node represented the most recent common ancestor, they needed to draw a new branch in the cladogram, in the same clade as the closest group. At the Institution B, the percentage of right and wrong answers was very similar between both questionnaires; a meaningful difference was found only in relation to time mapping (right answers rose from zero to 65.6%).

Two questions (the only ones that did not improve at the Institution A) were answered correctly in all groups by most of the undergraduate students in both questionnaires, thus showing that skills to recognize common ancestry and to map characteristics of organisms are more intuitive and more easily comprehended than the others.

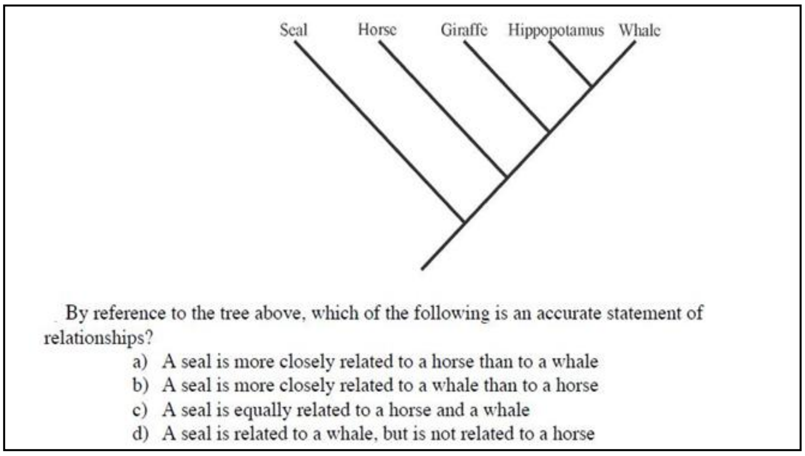
At the Institution A, the initial average grade of the diurnal group was 2.38, and the final one, 4.02 (Table 4); the initial average grade of the nocturnal group was 2.33, and the final one, 3.76. There was a difference between treatments "before" and "after" in both groups by testing with ANOVA ($F = 32.79$, $P < 0.0001$, Degrees of Freedom = 3). On the other hand, the rise from 1.73 to 2.13 in the average grade at the Institution B was not significant ($F = 1.068$, $P = 0.36$, Degrees of Freedom = 3).

Table 4. Initial and final average grades.

	Initial average grade	Final average grade
Institution A (diurnal group)	2.38	4.02
Institution A(nocturnal group)	2.33	3.76
Institution B	1.73	2.13

Results have evidenced a pattern of similar answer in each question, with interpretative mistakes commonly found in phylogenetic trees. Regarding kinships, the most accepted alternative that participants chose was the one representing the mistake of reading across the tips. Such perspective considers groups placed in closer sites more related to each other.

Both number of wrong answers in question 1 and question 5 in the initial questions demonstrated the same misconception, defined by Meisel (2010) and Gregory (2008) as **reading across the tips**. Students could have interpreted the relatedness among the *taxa* depending if they are represented in nearby positions. In other words, they could have incorrectly read meaning into the relative order of the groups represented on terminal nodes. This view could be also related to a ladderized misinterpretation of the evolutionary process which is, according to Meisel (2010), a symptom of a teleological conception in which “primitive species give rise to advanced species”. This could also explain some of the responses for question number 5 and is also related with a progressive view of evolution. Figure 1 represents a question related with the ability number one (recognizing kinship among *taxa*). The right answer is “the seal is equally related to both a horse and a whale” because they share the exact same ancestor. However, many students answered, especially in the first questionnaire, that “seal is more closely related to a horse than to a whale”, showing that they were either reading across the tips or counting the nodes (between seals and horses, two nodes, and between seals and whales, four nodes).



By reference to the tree above, which of the following is an accurate statement of relationships?

a) A seal is more closely related to a horse than to a whale
b) A seal is more closely related to a whale than to a horse
c) A seal is equally related to a horse and a whale
d) A seal is related to a whale, but is not related to a horse

Figure 1. Example of questions related to the ability of recognizing relationships among taxa. Based on: The Tree Thinking Challenge (Baum *et al.*, 2005).

Participants also demonstrated the misconception of incorrectly mapping time. Figure 2 shows one of the evolutionary trees in which participants should draw an arrow representing the direction of time. Few students had this tree-thinking ability from the beginning. The most common representation of time in the initial questionnaire was a horizontal arrow that crossed over from one organism to the other, thus implying that living organisms could be ancestors of other organisms, independently of branching patterns and more recent common ancestry. The incorrect mapping of time is a mistaken interpretation that is directly associated with a linear view of evolution, leading to the thinking that extant species are ancestors of other living ones. This was also observed by Meir *et al.* (2007) in a study about college misconceptions. Other misconceptions found in the above study were: “node counting”, “straight line equals no change”, and “tip proximity indicates relationship", already mentioned before. The correct answer of figure 2 is a vertical arrow, from the root (N) to the tips.

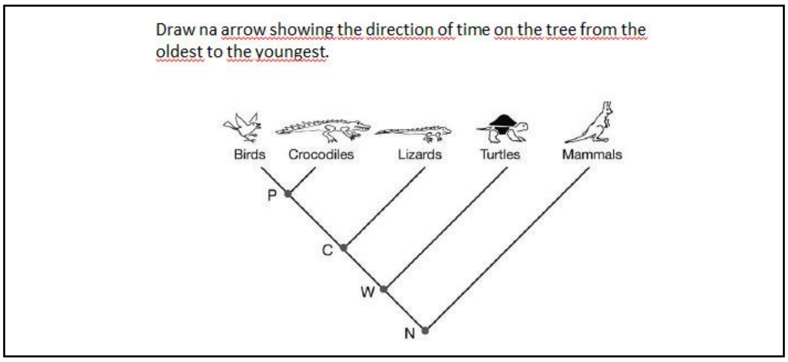

Draw na arrow showing the direction of time on the tree from the oldest to the youngest.

Figure 2. Example of questions related to the ability of mapping time. Based on Meir *et al*. (2007).

Finally, a huge difference in profiles between the two institutions could explain some of the differences found in our results. Besides differences of age and schooling type, there was a big difference regarding the fact whether students had had or not previous classes on evolution and phylogenetic systematics (Table 5). At the Institution B, the group of students was heterogeneous in terms of age, and more students apparently had not studied such subjects prior to attending Biological Sciences classes.

Table 5. Data of participants' profile based on research information.

Categories	**Variables**	**Institution A (diurnal)**	**Institution A (nocturnal)**	**Institution B**
Age	18 or younger	61.15%	24.9%	22.05%
	From 19 to 21	34.25%	53.45%	23.5%
	From 22 to 25	3.5%	16.15%	14.15%
	Older than 25	1.05%	2.55%	38.9%
Gender	Female	68.2%	45.6%	55.25%
	Male	31.8%	54.4%	44.75%
Type of High School	Public	37.45%	63.75%	77.95%
	Private	63.05%	36.25%	22.05%
Preparatory courses	Yes	60.1%	58.8%	42.4%
	No	39.9%	40.2%	57.6%
Previous studies of evolution	Yes	87%	82.1%	63.2%
	No	13%	17.9%	36.8%
Previous studies of Phylogenetic Systematics	Yes	68.9%	52.6%	12.8%
	No	31.1%	47.4%	87.2%

We would also like to emphasize an aspect revealed by table 5. Some biology undergraduate students had never studied evolution before at both institutions, thus showing us that the teaching of evolution needs to be more disseminated in Brazil. This fact is very concerning because of the biological importance of evolution *per se*, as previously stated here, and because the Brazilian Curricular Parameters (PCN) includes evolution not as a content, but as a way of studying biodiversity in an ecological and evolutionary perspective (Brazil, 2000, p. 18). Therefore, Phylogenetic Systematics is an effective tool to achieve such perspective.

4. Conclusions

In all of the study groups, participants have demonstrated skills in tree-thinking related to common ancestors of a certain group, as well as in mapping features in a cladogram. However, critical abilities found in all initial questionnaires included: 1) recognition of evolutionary kinship degree amongst the represented groups; 2) perception of the importance of tree-branching patterns (which leads to understand that nodes might be rotated without changing phylogeny direction); and, 3) time mapping. In relation to the Institution A, there was a significant conceptual change and improvement of already mentioned skills after activities and classes focused on Phylogenetic Systematics had been applied. At the Institution B, we could not verify the same change between initial and final questionnaires, except the ability of mapping time.

In short, the interpretation of phylogenetic trees, representations often used by media and textbooks, is not intuitive and various interpretative mistakes are present in common sense. Some skills of tree-thinking have demonstrated to be less present *a priori,* and their acquisition may demand a specific pedagogical interference. We could also verify, by analysing data, that such interference may not be enough to an accurate comprehension of phylogenetic trees, thus influencing participants' context and profile. One should pay more attention to tree-thinking in Biology, integrating it to the teaching of biological evolution, and using it when studying biodiversity as a visual and pedagogical tool explorer.

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