A New Perspective on Human Evolution

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Abstract

This paper reviews past Bahá'í scholarship on evolution, identifies a gap in this scholarship in light of current evolutionary biology, and uses cladistics—a modern approach to biological classification—to reconsider certain perceived tensions between current concepts in evolutionary biology and certain statements of 'Abdu'l-Bahá. A summary of taxonomy and phylogenetic tree construction is given, with special emphasis placed on cladistics, a methodology not available in 'Abdu'l-Bahá's day, and heretofore not mentioned in Bahá'í-authored publications related to evolution. This paper concludes with examples of how cladograms may aid in conceptualizing some of the evolution-related statements of 'Abdu'l-Bahá, (for example, His statement that "man is not an animal"). In using this approach, the intention of the author is not to re-interpret 'Abdu'l-Bahá's statements, nor to "prove" any particular interpretation thereof, but rather to bring modern concepts of evolutionary biology into Bahá'í discourse on evolution.

Resumen

Este artículo examina la pasada erudición Bahá'í sobre la evolución, identifica una brecha entre esta erudición a la luz de la actual biología evolucionaría, y utiliza la cladística-una metodología moderna para la clasificación biológica-para reconsiderar ciertas tensiones percibidas entre los actuales conceptos en biología evolucionaría y ciertas declaraciones de 'Abdu'l-Bahá. Se presenta un resumen de la taxonomía y la construcción del árbol filogenético con especial énfasis en la cladística, una metodología no disponible en el tiempo de 'Abdu'l-Bahá y hasta ahora no mencionada en la publicaciones Bahá'ís relacionadas con la evolución. El artículo concluye con ejemplos de cómo cladogramas podrían ayudar en la conceptualización de algunas declaraciones de 'Abdu'l-Bahá relacionadas con la evolución, (por ejemplo, Su declaración que "el hombre no es animal"). En el uso de esta metodología, la intención del autor no es reinterpretar la declaración de 'Abdu'l-Bahá, tampoco "probar" una interpretación particular relacionada, sino, traer conceptos modernos de la biología evolucionaría al discurso Bahá'í sobre la evolución.

Résumé

Dans le présent article, l'auteur passe en revue les études bahá'íes sur l'évolution, y relève une lacune à la lumière de la biologie évolutive actuelle et utilise la cladistique – une approche moderne de la classification biologique – pour réexaminer certaines divergences perçues entre des concepts actuels de la biologie évolutive et certaines déclarations de 'Abdu'l-Bahá. Il présente une synthèse de la taxonomie et de la construction d'arbres phylogénétiques, en accordant une attention particulière à la cladistique, une méthodologie qui n'existait pas à l'époque de 'Abdu'l-Bahá et qui n'a pas été mentionnée jusqu'à présent dans les publications bahá'íes relatives à l'évolution. L'article se termine par des exemples illustrant comment les cladogrammes pourraient aider à

conceptualiser certaines déclarations de ‘Abdu’l-Bahá sur l’évolution (par exemple, sa déclaration selon laquelle « l’homme n’est pas un animal »). En utilisant cette approche, l’auteur n’a pas l’intention de réinterpréter les déclarations de ‘Abdu’l-Bahá, ni de « prouver » une interprétation particulière de celles-ci, mais plutôt d’introduire des concepts modernes de la biologie évolutive dans le discours bahá’í sur l’évolution.

Introduction

Between 1904 and 1905, ‘Abdu’l-Bahá gave a series of table talks on a number of subjects, published in 1908 as *Some Answered Questions*. From 1910 to 1913, He traveled to Europe and North America, and gave many public talks on a wide range of issues. Again, many of these addresses were collected and published as *The Promulgation of Universal Peace*. One subject that He addressed in a number of these talks was human evolution. In these talks, He challenged some of the notions that were current at the time, most notably that because man[1] had descended directly from an ancestor of other primates, the human being was, therefore, merely an animal like any other (Haeckel 6). ‘Abdu’l-Bahá states that man holds a distinct station in the chain of life, and that this distinction is spiritual rather than merely physical (*Promulgation* 262).

‘Abdu’l-Bahá’s statements on the topic of evolution have been the subject of some scrutiny—mostly by Bahá’ís themselves, who have tended to either read these as an endorsement of a position that seems to be at odds with established scientific consensus, or as requiring careful interpretation in order to show that they are, in fact, compatible with that consensus. In this paper, I offer a different approach by drawing on relatively recent developments in the methods used within evolutionary biology itself. When viewed through the lens of cladistics, the apparent tension between ‘Abdu’l-Bahá’s statements and scientific truth reveals itself to be more a matter of perspective than a fundamental disjuncture in need of reconciliation.

Situating the Contribution

Prior Scholarship

On the subject of evolution, much has been written by Bahá’í scholars over the years.

In *The Purpose of Physical Reality*, John S. Hatcher asserts that “the Bahá’í teachings reject the views of both the creationists and the evolutionists as their theories are commonly presented.” Creation as a whole is eternal, and evolution (cosmological, geological, and biological) is the unfolding of that creation (48–52). Further, in *Close Connections*, Hatcher deduces from ‘Abdu’l-Bahá’s comments that the transformation of human evolution “occurs solely within a species or state,

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[1] ‘Abdu’l-Bahá uses this term, as others did at the time, to indicate humanity in general.

even though these stages of transformation may be radically different in appearance" (122).

Anjam Khursheed, in *Science and Religion: Towards the Restoration of an Ancient Harmony*, asserts that the Bahá'í writings affirm evolution, but that this evolution is divinely directed and not the outcome of blind chance (88–92).

In an article published in the *Journal of Bahá'í Studies*, Craig Loehle presents the view that humans did not evolve accidentally, but according to God's purpose, as "the unfolding of God's Plan" (51). However, this planned unfolding is not to be perceived in a Creationist sense as literally a step-by-step intervention by God, but rather as a gradual actualization of potentialities mediated by an evolutionary process according to natural law. He also develops the concept of human beings as a "special creation" (i.e., transcending other life forms) and yet emerging with other life forms through biological evolution.

William S. Hatcher offers a cogent argument for the increased "complexification" of evolution as proof of the existence of God ("A Scientific Proof"). He starts with an analogy. The directedness of a falling object, which theoretically is free to move in any random direction, but which only moves in one direction—down—offers proof that there is an "invisible force"—gravity—acting on the object. Similarly, evolution is generated by the random actions of mutation and natural selection, yet it, too, only moves in one "direction"—towards greater complexity—implying the action of an invisible force. Moreover, this force must possess the properties of life itself, including the higher consciousness of humans. From this, Hatcher concludes that this force must be divine.

Following the thought of this earlier article, Hatcher held neo-Darwinian theory to be based on the complete randomness of both mutations and natural selection (a position no longer held in modern evolutionary biology).[2] Resting on this assumption of total randomness, Hatcher attests that neo-Darwinian theory is incapable of explaining the "complexification" of evolution (*Epilogue*). As in his article of fifteen years prior, he argues for the existence of an "evolutionary force," divine in origin.

Such a position verges on "intelligent design," the theistic position that life holds evidence of purposeful creation that cannot be based on chance alone. However, as noted, Hatcher's fundamental premise, that of the complete randomness of both mutation and natural selection, is disputed by current research in evolutionary

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[2] Modern evolutionary biology asserts that mutations, broadly speaking, are not entirely random in the statistical sense, but are shaped by adjacent probabilities—for example, the location of the mutating base pair in a nucleotide sequence. As a rough analogy, the outcome of the role of a die is not completely random in the statistical sense, but is limited or shaped by the number of sides of the die. This has important implications for the apparent directionality of evolution.

biology (Martincorena and Luscombe; Gregory, “Understanding Natural Selection”).

In his 1993 book, *The Challenge of Bahá’u’lláh*, Gary Matthews seeks to reconcile the apparent contradiction between biological human evolution (as it was then understood) and ‘Abdu’l-Bahá’s statements on the uniqueness of the human station by arguing that the contradiction is semantic: the emergence of the soul constitutes a new “species” in a general, not biological, sense. He adds that further research “may someday settle this issue” (109).

Paul Lample, the compiler of *Bahá’u’lláh’s Teachings on Spiritual Reality*, states that the Bahá’í teachings support the scientific concept of evolution while rejecting that evolution operates solely by chance; evolution is essentially purposeful (101). He also asserts that ‘Abdu’l-Bahá’s statements regarding the uniqueness of the human station should not be interpreted to mean that humans emerged through a separate, parallel evolutionary pathway.

In 2001, Keven Brown and Eberhard von Kitzing produced a monograph, *Evolution and Bahá’í Belief*, that systematically surveys the philosophical (as opposed to strictly scientific) concepts of evolution, both in Western (i.e., European) and Eastern (i.e., Islamic) traditions leading up to, and current with, the time when ‘Abdu’l-Bahá made His major comments related to evolution.

In 2003, Courosh Mehanian and Stephen Friberg published an article that gathered the main statements of ‘Abdu’l-Bahá regarding evolution, and analyzed them in light of general evolutionary concepts. They concluded that, although humans are biologically part of evolution, “man is much more than an animal,” being endowed with a spiritual reality not shared with animals.

In a conference paper published in *Lights of Irfán*, Ian Kluge makes no attempt to reconcile ‘Abdu’l-Bahá’s statements on evolution with current scientific thought; on the contrary, he holds that they should be accepted as stated, while waiting for scientific research and thinking to catch up. This position, however, precludes any nuanced interpretation of ‘Abdu’l-Bahá’s statements.

In his master’s thesis, Salman Oskooi takes the position that ‘Abdu’l-Bahá’s statements on evolution must be taken simply at face value, and that, since they are at odds with current evolutionary science, ‘Abdu’l-Bahá’s comments are simply wrong. Oskooi does assert the infallibility of ‘Abdu’l-Bahá on spiritual matters, but claims that this infallibility does not extend to scientific or other subjects. However, Oskooi’s position is founded on a letter written on behalf of Shoghi Effendi regarding his own infallibility as being confined to matters relating to the Cause, which Oskooi extends to apply to ‘Abdu’l-Bahá as well. In contradiction to this position, a letter on behalf of the Universal House of Justice to an individual believer states that this limitation of infallibility does not apply to ‘Abdu’l-Bahá (Universal House of Justice, *Messages* 545–46).

In 2023, Bryan Donaldson published a monograph, *On the Originality of Species*, which propounds that ‘Abdu’l-Bahá’s statement, “man is not animal” (‘Abdu’l-Bahá, *Promulgation* 359) should be taken as literally true in a biological sense, and proposes that this can be explained by a “parallel evolution” by which humans evolved separately from animals (including primates). Criticism of this position can be found elsewhere (Perry).

Bahman Nadimi’s article “Bahá’í View on Biological Evolution” posits that the evolution of humans did not start at the inception of life on Earth but rather began with some unknown, specialized biological structure at a later stage, suggesting that humans and animals evolved on completely separate paths. There is no scientific evidence for this conjecture.

The Gap in Bahá’í Scholarship on Evolution

For all the valuable perspectives found in this prior scholarship, these contributions all come from the perspective of the *philosophy* of evolution, not the *science* of evolutionary biology. Moreover, this discussion has been confined to Darwinian and neo-Darwinian concepts, which are rooted in the nineteenth and twentieth centuries, and limited by the knowledge and understanding of those times. As we are now well into the twenty-first century, the time has come to bring modern evolutionary biology into dialogue with ‘Abdu’l-Bahá’s statements on evolution. There are many ways to accomplish this. I choose to approach this subject through the path of phylogenetics and cladistics, which have been foundational to evolutionary biology since the 1960s (Henning), and have since been well substantiated by research as explained further in this paper.

In taking this new approach, my intention is *not* to re-interpret the statements of ‘Abdu’l-Bahá, nor to “prove” any particular interpretation of His statements, but rather to demonstrate how incorporating current evolutionary science enriches the discourse on this subject, which is at the nexus of any discussion of one of the central tenets of the Bahá’í Faith, that of the harmony between science and religion.

Premises

The premises of this paper are derived from the overarching themes expounded by ‘Abdu’l-Bahá in His science- and evolution-related talks, as identified by Friberg and Mehanian. These premises are:

1. In terms of biological evolution, humans have progressively evolved from a simpler form (‘Abdu’l-Bahá, *Some Answered Questions* 210). This is consistent with current evolutionary theory.
2. The essential nature of humans has always existed in potentiality, regardless of the outward organismic form at any point of

evolution (223). This declaration challenges the very concept, implicit in the mainstream scientific discourse since Darwin, that what it means to be human can be described in strictly taxonomic (i.e. biological classification) terms.

3. The feature that distinguishes humans from animals is not the biological organism, but the human spirit, also referred to as the rational soul (241). This does not deny that genus *Homo* can properly be viewed as a taxon[3] in tribe *Hominini*, family *Hominidae*, and order *Primates*, but it challenges the notion that this classification fully explains what a human being is. In other words, the human is, but not *simply*, a primate.

A Developing Discussion

Within the Bahá’í community at large, the questions and discussions regarding human evolution are not settled, nor must they be, nor even should they be. The intersections of science and religion will always be dynamic because they are subject to both changes in scientific theory and in human understanding of scripture; in other words, the questions and discussions unfold as our comprehension of reality evolves.

Some of ‘Abdu’l-Bahá’s comments on evolution have been seen as enigmatic, initiating attempts—as the earlier literature review shows—at resolution. For example, I draw the reader’s attention to one statement by ‘Abdu’l-Bahá that seems so directly literal in meaning that some feel challenged to understand it in light of evolutionary theory. Specifically:

> The lost link of Darwinian theory is itself a proof that man is not an animal. How is it possible to have all the links present and that important link absent? Its absence is an indication that *man has never been an animal*. It will never be found. (*Promulgation* 355; emphasis added)

In his book, *On the Originality of Species*, Bryan Donaldson holds the position that this statement must be taken in its most literal sense, and therefore posits that human evolution was parallel to, not colinear with, primate evolution. This goes against overwhelming scientific evidence (White et al.), and, although Donaldson makes a valiant effort to reinterpret these findings, his effort ultimately fails not only on evidence but on first principles: the concept that humans have always been human throughout evolutionary history by reason of latent potential cannot be explained by parallel evolution because the problem of instantiation—when and how humans became human—remains. The theory of parallel human evolution merely pushes the problem

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[3] Taxon (plural taxa) is a general term for any group of organisms that biologists classify together based on shared characteristics such as types of locomotion or reproduction. Species, genera, families, and higher classifications are all examples of taxa.

of instantiation back to an earlier, and entirely speculative, time in evolutionary history (Perry).

For any ongoing discussion on the subject of human evolution, the following excerpt from a letter written on behalf of the Universal House of Justice can be regarded as a grounding statement:

> The Bahá'í view of evolution is more complex and nuanced than that put forward today by those who present evolution and creation in dichotomous terms. Evolution may be understood as the means set in motion by God through which life changes and unfolds. A Bahá'í can strive to reconcile contemporary scientific views with the published statements of 'Abdu'l-Bahá, which need not be understood to imply a kind of parallel evolution. Rather, 'Abdu'l-Bahá has explained that human life came into existence when the appropriate conditions were established. (5 July 2010)

In the spirit of this statement, I seek to take a holistic approach towards human evolution by viewing it through a different lens (as will be explained in this article) than has heretofore been used in Bahá'í discussions of evolution, one that may help us see 'Abdu'l-Bahá's explanations as harmonious with mainstream scientific consensus.

Ways of Understanding Evolutionary Relationships

There are several ways of viewing evolution, all of which are scientifically valid within the limits of the scope and quality of the underlying data they draw from and the inherent restrictions of the analytic methods on which they are based. It is important to understand that these different presentations of evolutionary data are not contradictory; rather, they view the same phenomena from different perspectives, and, therefore, are complementary. With the exception of the naturalistic tree model commonly used in popular culture, all methods mentioned in this paper are fully accepted within the scientific community. Different methods are chosen for varied reasons. The fact that each of these is simply a distinct perspective that does not contradict other perspectives is evidenced by occasional variations in the terminology by which they are invoked in the literature. A dendrogram, for example, may be referred to as a phylogenetic tree because it really *is* a phylogenetic tree viewed from a different perspective. While variable terminology can occasionally be problematic for the outside inquirer, it does not interfere with a crucial point of this paper, which is that the findings of modern evolutionary biology have a reciprocity and complementarity with 'Abdu'l-Bahá's statements on evolution.

What follows, then, is a brief discussion of phylogenetics—the broad discipline concerned with the evolutionary relationships between organisms—in order to frame an exploration of two distinct ways of presenting those relationships. The technical details in this section are given to provide context for the overall point that two equally valid and accurate ways of looking at evolution can each highlight aspects of this phenomenon that the other obscures.

PHYLOGENETICS

The discipline of phylogenetics (from the Greek *phylon* for “race” or “tribe” and *geneia* for “origin”) is the study of the evolutionary relationships that form the basis of taxonomic[4] classification (Haque). First emerging in the mid-twentieth century, phylogenetics now forms the core of evolutionary biology (Losos et al.).

A phylogenetic tree (figure 1) is the diagrammatic representation of these relationships. By common convention, the beginning of the tree represents the last common universal ancestor (LUCA) for all subsequent forms of life. Consistent with its descriptive designation, a phylogenetic tree arborizes according to divergent evolution, with the point of divergence (called the node) being the most recent common ancestor (MRCA). The tree in figure 1, for instance, depicts the three taxonomic domains (a domain being the highest level category of classification of life): Bacteria, Archaea, and Eukaryota (or Eukarya). Each domain contains a number of kingdoms—the domain Eukaryota, for instance, contains the kingdoms Protista (a term now being used less formally), Fungi, Plantae, and Animalia.

While the first systematic efforts at taxonomy, beginning with Linneus, relied on visual appraisal of shared and different characteristics— bats and birds, for example, both have wings with homologous bone structures, but have completely different modes of reproduction, and so we conclude that bats are flying mammals rather than birds—modern phylogenetics has a wider range of ways to assess how organisms are related. In addition to *phenetic* (i.e., morphological) data (Panchen 132–68)—physical traits such as limbs, gills, and feathers—a phylogenetic tree can be generated using genomic (i.e. molecular) data (Fuellen)—DNA, RNA, and protein sequence

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[4] *Taxonomy* (from the Greek *taxis* for “order” and *nomos* for “law”) is the discipline of naming life forms based on evolutionary relationships. The naming of organisms is as old as language itself, but the systematization of biological naming began with Carl Linnaeus in the eighteenth century. Taxonomic hierarchies are based on the range of evolutionary commonalities (i.e. biological characteristics), with *species* being the unit with the greatest specificity for these characteristics. The progression from most specific (the least commonality) to most general (the greatest commonality) is species → genus → family → order → class → phylum → kingdom → domain. This hierarchical system makes taxonomy more than “a glorified form of filing”; the taxonomic classification of an organism expresses our current understanding (or theory) about its relationship to all other life (Gould 98).

homologies; behavioral data (MacLean et al.)—migration, mating, etc.; and statistical analysis (Gavryushkina et al.)—Bayesian inference, maximum likelihood. The phylogenetic tree is a true and accurate representation of currently available scientific data bearing on evolutionary relationships. However, it is only a qualitative (or at best semi-quantitative) representation, and new data can sometimes lead to changes in the tree.[5]

Before proceeding, it is worth noting that the contention that a number of perspectives on evolutionary relationships are equally valid does not mean that *any* method of visualizing those relationships is valid. For example, in contrast to phylogenetic trees, and to cladograms that we will review later, the common image of a naturalistic tree to represent evolution is misleading in important respects (figure 2). The innate appeal of using a naturalistic tree to describe evolution is understandable. The "tree of life" concept predates Darwin, and a contemporary of Darwin, Ernst Haeckel, used a naturalistic tree to describe evolution as it was then understood. It has remained a popular image ever since, and is what is commonly envisioned when thinking of evolution. However, this representation is not used in the scientific community. The naturalistic

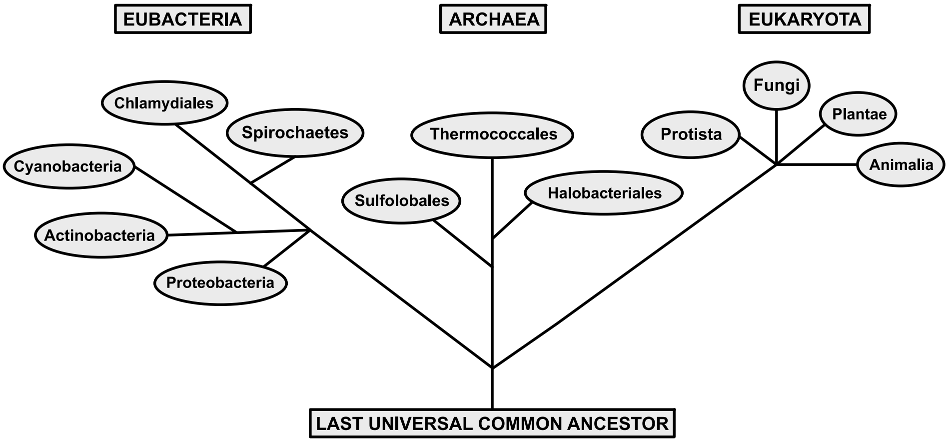

Figure 1. Phylogenetic Tree of Life (after https://www.greennature.ca/tree-of-life/)

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[5] For example, it was long disputed whether the giant panda is most closely related to raccoons or bears, due to its sharing morphological characteristics with both. Only once genomic data was available was it determined that the giant panda is, in fact, a true bear. Interestingly, genomic data also showed that the red panda was not in fact a close relative of the giant panda, despite their geographical proximity and several shared morphological features (O'Brien et al.).

tree image obscures and misrepresents actual evolutionary features and relationships in ways that a true phylogenetic tree does not. For example, in figure 2, the placement of Protista at the roots of the tree is problematic. To the layperson, this placement would seem to suggest that all other life evolved from Protista, when in actuality all modern members of Protista share a common ancestor (LUCA) with the rest of living organisms. The figure gives no position for LUCA, but if it did, it would have to be at some point of the thick trunk—which would further confuse the layperson, for whom the tree image intuitively suggests a linear progression from roots to trunk to branches. The use of a literal tree image presents further difficulties. For one, the trunk's ramification into thinner and thinner branches—in the manner of a natural tree—falsely implies some kind of diminution, as of biological information or complexity, when in fact the opposite is true. It also falsely implies derivation, as if a later form of life is merely derived from an earlier form, when in fact new forms of life can emerge with novel properties. Finally, the naturalistic tree shown in figure 2 obscures the true evolutionary pathways of, and relationships between, taxa.

The use of a naturalistic tree to present scientific findings is a good example of how the *way* we represent data can profoundly influence—and in this case, impair—what we can *perceive* about the data.

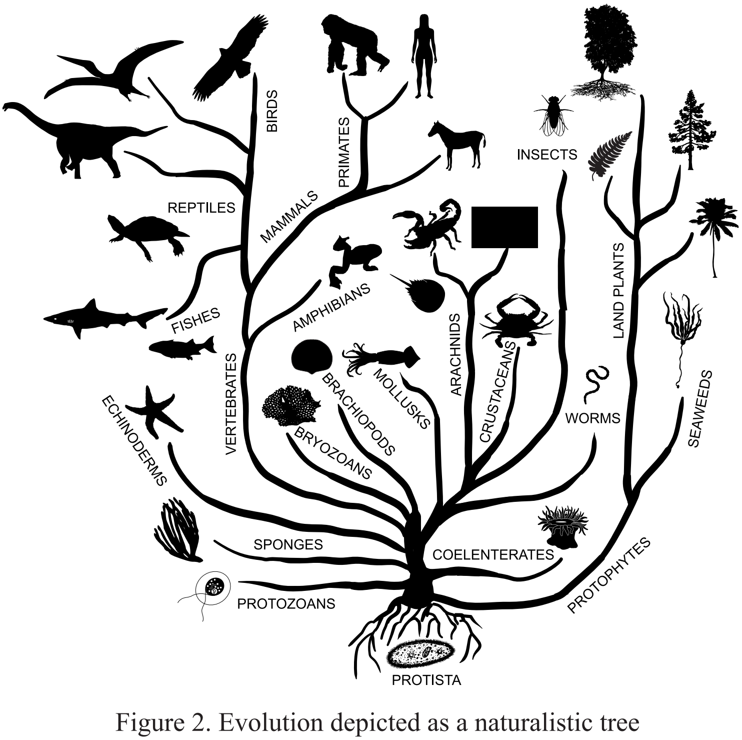

Figure 2. Evolution depicted as a naturalistic tree
(after https://earthsky.org/earth/new-tree-of-life-doesnt-look-as-youd-imagine/)

Dendrograms

Returning to actual scientific practice, phylogenetic trees can be represented in diagrammatic form as dendrograms to visualize evolutionary relationships more easily. In figure 3, taxa belonging to the phylum Chordata are mapped according to their evolutionary relationships using data, both quantitative (genomic information, carbon dating to determine the age of fossils, etc.) and qualitative (observed phenetic similarities and differences, etc.). The horizontal axis loosely represents evolutionary time, meaning that nodes further towards the left of the dendrogram represent a branching-off between lineages that occurred earlier in time than those further to the right. Thus, the most recent common ancestor of agnathans (jawless vertebrates) and Gnathostomata (jawed vertebrates) lived before the most recent common ancestor of marsupial and placental mammals. The vertical axis loosely represents evolutionary "distance." Thus, marsupial and placental mammals are more closely related to each other than either is to frogs.

The Problem of Evolutionary "Progress"

Dendrograms, if constructed faithfully to a sound underlying data set, are one valid way of visualizing evolutionary relationships, and are useful for a number of purposes. If they are the only lens we use for this purpose,

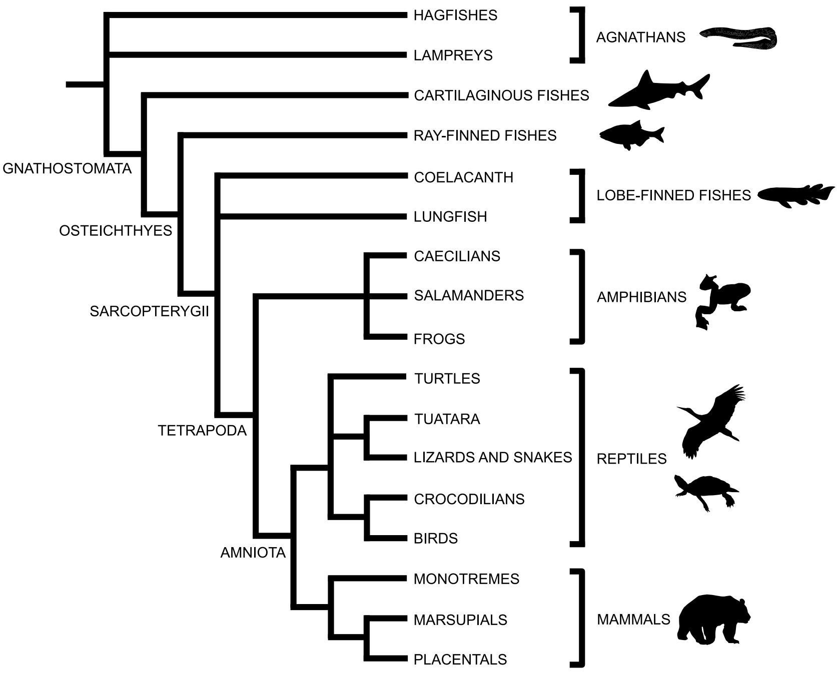

Figure 3. Simple evolutionary dendrogram
(after https://www.instituteofcaninebiology.org/how-to-read-a-dendrogram.html)

however, we may draw inferences from the underlying data that a different visualization would not lead us to, or fail to draw inferences that another (different but equally valid) visualization might suggest. Consider one of the recurring themes in the statements of ‘Abdu’l-Bahá: the directionality and hierarchy of evolution from simpler to more complex organisms, from “lower” to “higher” forms of life, and especially the station of human beings in the order of life; see, for example, “Evolution and the Existence of Man” (*Some Answered Questions* 220–27). This is contrary to the received opinion of most evolutionary biologists now active in the field. Thus, any exploration of ‘Abdu’l-Bahá’s statements on evolution must address this issue.

Although scientifically correct and useful for charting evolutionary pathways, dendrograms, like most evolutionary tree models, tend to obscure one important aspect of evolution: the progressive emergence of higher orders of life, and the evolutionary relationships based on this emergence. The current dogma holds that, because much (but not all) evolution occurs by chance mutation and natural selection, it must be purposeless, and, therefore, directionless. By extension of this position, a popular tenet is that biological evolution does not advance, it merely changes.[6] Increasing biological complexity, though not denied, is simply dismissed as a byproduct of mindless adaptation. However, there is no scientific basis for this tenet. It is what Richard DeWitt refers to as a philosophical/conceptual “fact” as opposed to an empirical fact; the former are commonly mistaken for the latter even by scientists (31–35).

Because of this position, *teleology* and *progress* are terms effectively banned from the literature in evolutionary biology (Kadykalo). Yet it is undeniable that life has evolved from simplicity to higher and higher orders of complexity in both functionality and capacity (Lipps et al.). This progressive complexity is, of course, captured in the underlying data upon which evolutionary trees are based; however, the *way* these data are presented minimizes or even obscures this phenomenon. For example, dendrograms generally only show evolutionary relationships; information about organismal form and function is entirely missing. A dendrogram is, of course, not incorrect because of this omission; it simply focuses on only one aspect of evolution. A mathematical equivalent of this operation is to plot the 1-dimensional scalar of a 3-dimensional vector. The scalar can only reflect one aspect of the vector, thereby concealing the deeper, richer information of the vector itself. In a comparable manner, this dendrogram shows no increasing complexity; indeed, no “progress” at all.

Every map or model, of course, must simplify the reality that it seeks to explain. A political map of the globe omits topographical features; if we want to know where the high and

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[6] I personally have heard a professor of evolutionary biology proclaim, “Humans are no more advanced than amoebas, they just occupy different niches.”

low points of the earth are found, we need a topographical map. This paper therefore now turns to a different kind of "map" of evolutionary relationships: modern cladistics, which can be used to visualize the statements of 'Abdu'l-Bahá regarding biological hierarchy, and thus help to reconcile (though not re-interpret) His statements with a modern scientific perspective.

CLADISTICS

To bring twenty-first century evolutionary biology into dialogue with 'Abdu'l-Bahá's statements on evolution, we turn to the field of cladistics, which did not exist in 'Abdu'l-Bahá's day. The term was coined in the 1950s and cladistics was established as a subdiscipline of biology by the 1960s.

Cladistics offers a different way of viewing evolution (Williams and Ebach), and can be described as a method of systematic classification within phylogenetics. It operates by arranging taxa into groups, called clades. A clade consists of all taxa that share particular features in common, to the exclusion of all other taxa. For example, Gnathostomes are jawed fish (and their descendants) that diverged from Agnatha, which are jawless chordates such as lampreys. All subsequently evolved creatures with jaws, including all tetrapods (vertebrates with four limbs), are grouped into the clade Gnathostomata, while Agnatha are excluded from this clade. (The shared features that constitute clades—jaws in this example—are called *synapomorphies*, a term that we will return to later).

Though traditionally based on phenetics (observable similarities), which is a relatively simple methodology, the apparent evolutionary relationships identified by cladistics can be verified with molecular data (Mavrodiev and Madorsky), fossil records (Cracraft), ethological studies (Fentress), and by advanced statistical (Huelsenbeck, Ronquist, et al.) and computational (Brooks et al.) methods. Data acquired by separate, complementary methods allow clades to be defined with increasing rigor (Faith and Cranston).

As with all scientific methodologies, cladistics has strengths and weaknesses. While these are summarized in Appendix A, for our purposes one particular strength stands out: cladistics is particularly good at visualizing evolutionary history in terms of phenetics and evolutionary development (Harrison). In other words, it helps us identify when something new has appeared through the processes of evolution.

CLADOGRAMS

Cladograms are visual representations of cladistics. They are diagrams that map clades, primarily on evolutionary morphogenesis.

The diagrammatic structure of the cladogram represents both the evolutionary lineage and relatedness of taxa (figure 4). The "root" represents the most recent common ancestor for all the taxa included in a particular cladogram. As we follow the diagram up from the root, we find “internal nodes”—bifurcations that represent speciation events and common ancestors for subsequent (i.e. above the node) divergent evolutionary lines. Taxa—which can represent individual species or larger taxonomic groups (i.e., clades)—are represented by “terminal nodes” (such as the letters A through F in figure 4). The evolutionary lineage of a given taxon is thus represented by the straight lines connecting a terminal node back to the root. Taxa sharing the same most recent common ancestor are identified as sister taxa. An outgroup is a species or group of species that is closely related to, but not part of, the other taxa being studied (the ingroup). The function of the outgroup is to serve as a reference point for determining the evolutionary relationships of the ingroup (Huelsenbeck, Bollback, et al.).

To see how cladograms can visualize evolutionary relationships, consider figure 5. Here, the root is the most recent common ancestor for all the taxa shown in the figure, from lampreys (Petromyzon) to lizards (Lacertillia). Internal nodes indicate the last common ancestor for subgroups of taxa; for example, the rightmost internal node represents the last common ancestor for lizards and birds (Aves). The taxa (terminal nodes) in this diagram are all clades representing many species. This cladogram allows us to see that birds are more closely related to lizards than to lampreys. The validity of any cladogram to depict these relationships is, of course, dependent on the data used to construct the cladogram.

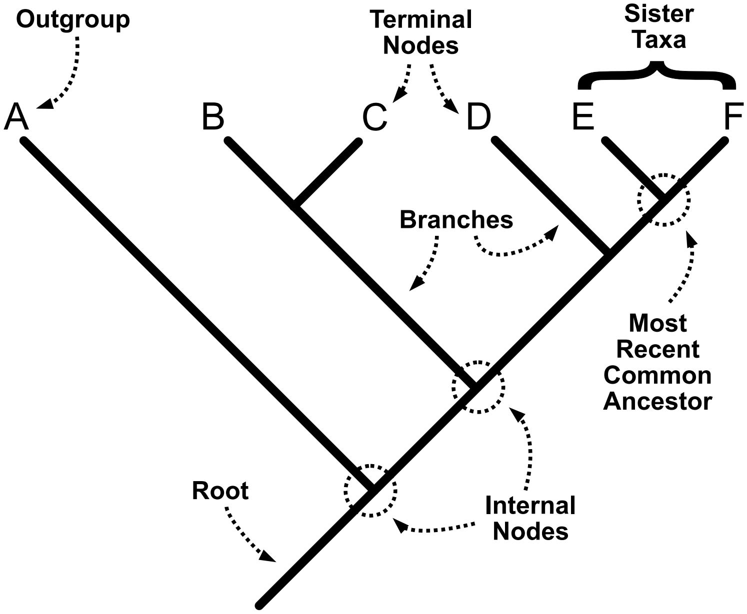

Figure 4. Basic cladogram structure

Before proceeding further, it is important to take in some cautionary considerations for using cladograms as representational tools of evolution (Gregory, "Understanding Evolutionary Trees"). First, it is most important to understand cladogram topology. Any internal node can be rotated 180° without changing the topology of the cladogram. For example, in Figure 6, the cladogram on the left (figure 6A) is equivalent to the cladogram on the right (figure 6B). Visually, the internal node for sister taxa E and F (EF) and taxon D, which we will call clade D(EF), has been rotated 180° about its vertical axis. The left-to-right order of the taxa was changed from A-B-C-D-E-F (figure 6A) to A-B-C-F-E-D (figure 6B). This gives the appearance that the evolutionary relationships of the taxa have changed, but they have not: when traced in the cladogram, the evolutionary pathways and divergent nodes are still the same.

What's important to note here is that the long "main line" of the cladogram represents the direct evolutionary path for whichever particular taxon is found at the rightmost terminal node. It is quite natural for the viewer to consider this node, and its taxon, the ultimate "destination" and focus of the cladogram. However, because nodes can be rotated about their vertical axis without changing the topology of the cladogram, there is *no* singular main line; the choice of which taxon is situated on the main line is made by whoever creates the cladogram. The cladogram can be rearranged such that any of the included taxa can be the terminus of the main line. This is demonstrated in figure 6, where taxon F is the terminus of the main line in figure 6A, and taxon D is the terminus of the main line in figure 6B.

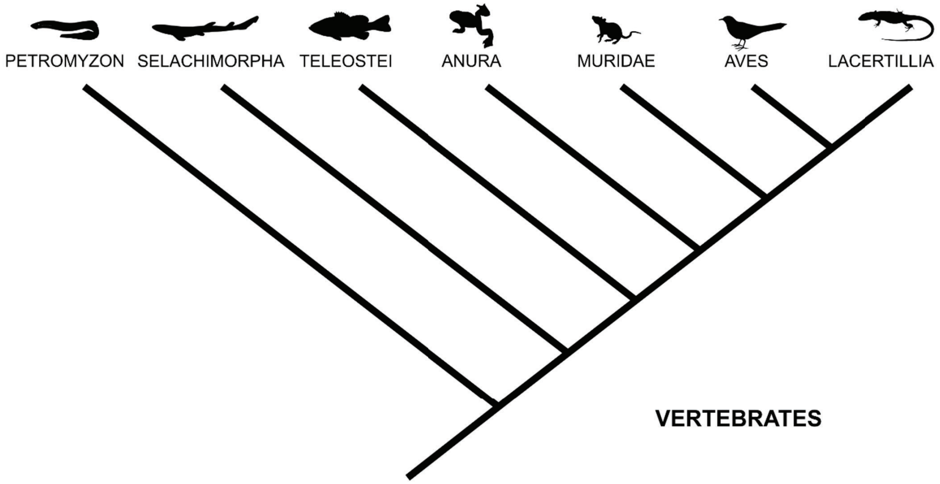

Figure 5. Simple cladogram of vertebrates
(after https://biologydictionary.net/cladogram/)

This is not an inherent weakness of the cladogram as a representational model; on the contrary, it shows the ability of the model to represent the underlying data more clearly, depending on subject focus. Indeed, while the same evolutionary pathways depicted in cladograms are also present in dendrograms and other phylogenetic trees, they can be obscured by the visual arborization, the structural complexity, of these models. In cladograms, not only are these pathways readily apparent, but by transposing taxa along the vertical axis at the proper nodes, the direct lineage of any taxon of interest can be easily visualized. Again, these manipulations do not modify the underlying scientific empirical facts in any way, any more than looking at a sculpture from different angles changes the sculpture itself. However, the viewer needs to be aware of this "polymorphic" property, or they could be misled into thinking that the main line is an immutable backbone.

Having been introduced to the structure and properties of cladograms, we can now explore their applications in biology by expanding our understanding of clades. Clades are defined by particular identifying features (synapomorphies) that taxa have in common. For example, as shown in the cladogram in figure 7, the embryos of fish, lizards, rabbits, and humans develop within amniotic sacs (a synapomorphy), and thus belong to the clade Amniota. All of these creatures have a vertebral column (another synapomorphy), as do lancelets and lampreys; thus, all belong to the clade Vertebrata. However, lancelets and lampreys do not have amniotic sacs, and so are excluded from the clade Amniota. Note also that the clade Amniota is nested in the clade Vertebrata, i.e., all members of clade Amniota are also members of clade Vertebrata, but not all vertebrates are amniotes.

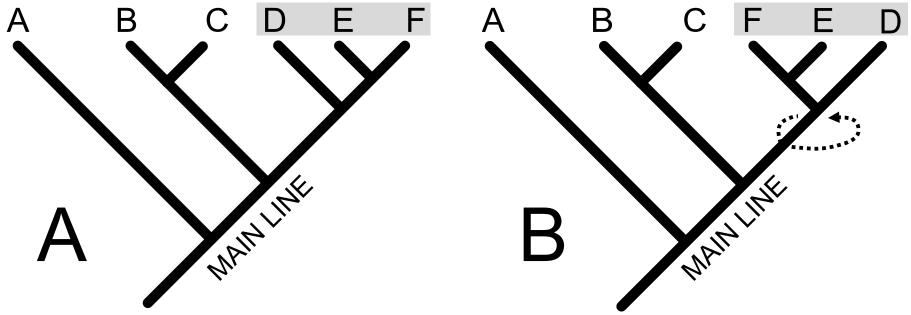

Figure 6. Cladogram equivalence. In panel B, taxa D-E-F have been rotated 180° to appear as F-E-D, yet the topology—and, therefore, the evolutionary relationship it represents, is unchanged.

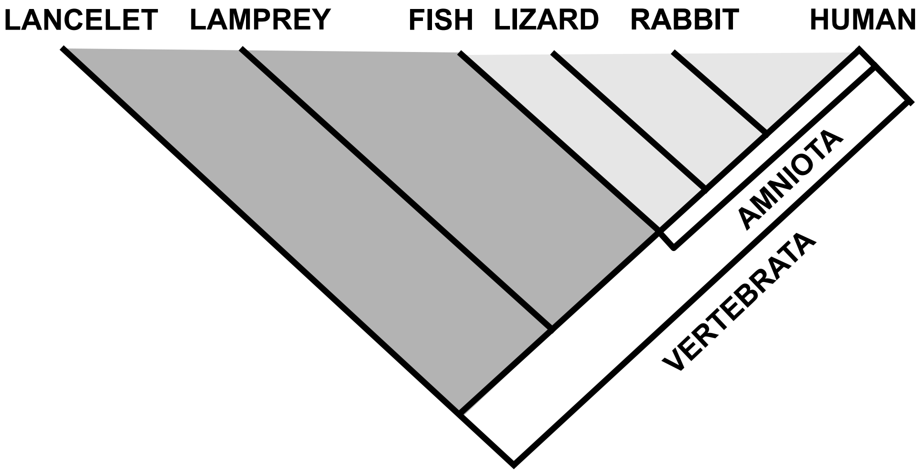

Figure 7. Cladogram with two clades
(after https://bio.libretexts.org/workbench/general_ecology_ecology/chapter_7%3a_the_history_of_life_systematics_and_phylogeny/7.7%3a_phylogeny_and_cladistics)

Figure 8 depicts a wider spectrum cladogram with more examples of synapomorphies and clades. It demonstrates several notable characteristics of cladograms in general: 1) By convention, evolution (the development of taxa with new adaptive features) is depicted as proceeding from left to right. 2) The main line has a positive slope to indicate, vaguely at least, the passage of evolutionary time. 3) The horizontal distance between taxa qualitatively reflects their evolutionary distance (biological difference). 4) The emergence of synapomorphies gives rise to new clades. 5) As evolution continues, specialization and complexity tend to increase and, therefore, the resulting clades generally become more focused, having smaller numbers of taxa included. However, there are many exceptions to this, and this characteristic should be taken as phenomenological. 6) The main line shows the direct evolutionary line for a particular taxon, the selection of which depends on how the cladogram is configured.

This last characteristic is perhaps the most important for the purposes of this paper, which deals with human evolution. Recall that what appears to be the main line is entirely dependent on how we “rotate” the taxa and clades in a cladogram, the topology of which is determined by true evolutionary relationships based on scientific data, and remains unchanged in that cladogram no matter how we view it. This is a subtle but profound distinction that will be developed in the rest of this paper.

The representative value of cladograms is that, because they are based on the appearance of evolving features, evolutionary progress in complexity and functionality can be easily seen. This property can evoke consternation among systematic biologists who hold

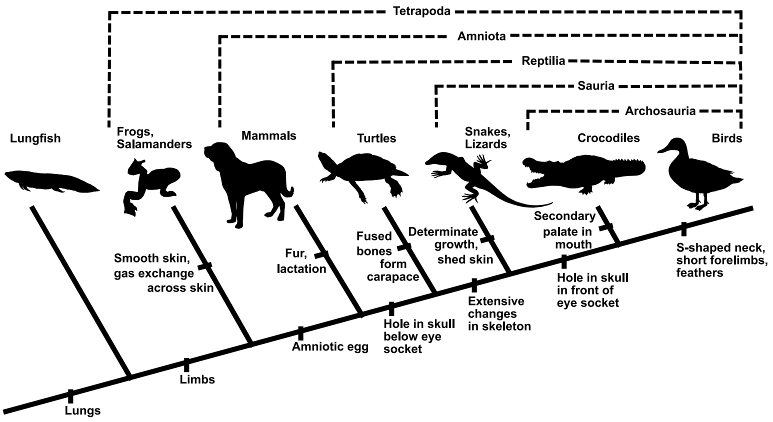

Figure 8. Broad spectrum cladogram withlabeled synapomorphies and clades (after https://srsscience.weebly.com/cladograms--dichotomous-key.html)

what has become a central dogma in evolutionary biology: that evolution has no purpose, no direction, and, therefore, no progression. The corollary of this viewpoint is that one form of life is not more "evolved" than another form of life. Taken to its logical extreme, paramecia are just as "advanced" as humans. Thus, any cladogram that purports to show evolutionary progress is considered to be anthropocentric (Sandvik). Yet, undeniably, evolutionary progress *does* occur, in the form of emerging biocomplexity (Zhang). One need not invoke any kind of teleology to accept this fact; it is due to entirely natural, evolutionary mechanisms (Lenski et al.).

To give an example of how cladograms can clearly reveal the emergence of increasing biocomplexity in evolution, we can examine a cladogram of land plants (figure 9). This cladogram shows some of the evolutionary steps leading to the emergence of angiosperms from a green algal evolutionary ancestor. Angiosperms exhibit greater biocomplexity than their green algal ancestors by having specialized multicellular structures such as roots, stems, leaves, and flowers, which enable advanced nutrient transport, reproduction, and environmental adaptation. They also possess advanced genetic regulation and co-evolutionary relationships with pollinators, reflecting increased ecological integration and evolutionary innovation. In this cladogram, each evolutionary step is a synapomorphy that demarcates a clade. For example, the evolution of multicellular embryos, a synapomorphy that is the hallmark of land plants, places plants ranging from liverworts to angiosperms in the clade Embryophyta (Lecointre and Le Guyader 175). In a similar manner, evolution of vascular tissue led to plants belonging to the clade Vasculata, and the evolution of seeds gave rise to the clade Spermatophyta. In this cladogram, the evolutionary "progress" of plants from simple green algae to biologically advanced angiosperms can be easily seen.

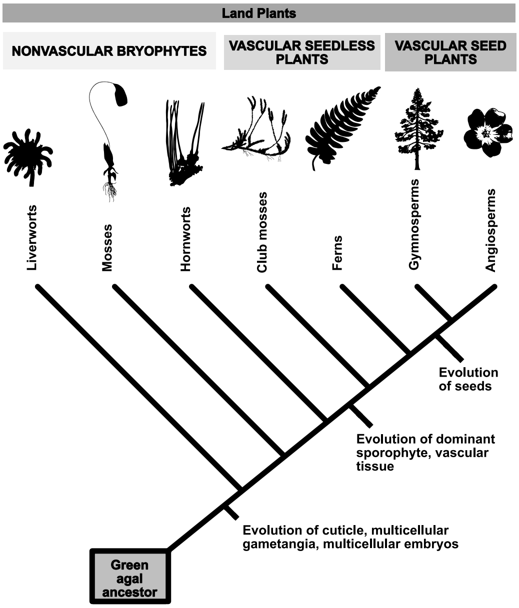

Figure 9. Cladogram of plant evolution (after https://www.bartleby.com/solution-answer/chapter-27-problem-15tyu-biology-mindtap-course-list-11th-edition/9781337392938/evaluate-and-synthesize-15-interpret-data-according-to-the-cladogram-in-figure-27-5-which-plants/f02fcaab-560e-11e9-8385-02ee952b546e)

Using Cladograms to Understand Human Evolution

As a representational tool, cladograms offer a different—and, as far as I can tell from my review of the Bahá'í-related literature, heretofore unexplored—way of visualizing 'Abdu'l-Bahá's statements on evolution. I emphasize here that viewing these statements through a cladistic lens is *not* re-interpreting scientific facts, *not* proposing a new theory of evolution, *not* discarding other representations of evolution such as phylogenetic trees, and above all, *not* re-interpreting the statements of 'Abdu'l-Bahá. Viewing human evolution by means of cladograms is simply using a well-accepted method to perceive evolutionary phenomena (pathways and emergence) that are less apparent with other methods (Ashlock). Although it can be argued that there is an inherent anthropocentricism in the use of cladograms, nevertheless we can apply this method of viewing of human evolution if we keep the proper use of cladograms, described above, in mind.

We begin with figure 10, which shows a cladogram of human-related synapomorphies (indicated by dotted lines). In this figure, the term *pleisomorphies* refers to ancestral traits not shared with humans; *synapomorphies* refers to those traits shared with humans. The more primitive synapomorphies are lower in the cladogram. Taxa sharing the same synapomorphy are in the same clade. For example, the kangaroo, mouse, and human all have hair, placing them in the “Hair” clade Mammalia; the kangaroo, however, though possessing a choriovitelline placenta, lacks the more developed chorioallantoic placenta (Themes), and thus does not belong to the “Placenta” clade Placentae. Although the cladogram shown in figure 10 is extremely simplified—indeed, simplistic, showing only a few evolutionary steps—the main line of this cladogram clearly shows the direct evolutionary path for acquiring more characteristics of the current human species, *Homo sapiens*.

Focusing on the order Primates, the cladogram in figure 11 shows the development of humans within this order. Some synapomorphies, from opposable thumbs to bipedalism, that distinguish primate taxa into smaller and smaller clades are labeled, but many more synapomorphies are not identified. In customary practice, cladograms are simplified for the sake of visualizing general evolutionary relationships. Also not shown are the taxa that evolved after the advent of bipedalism (e.g. *H. erectus* and *H. heidelbergensis*) which belong in the genus *Homo* along with *H. sapiens*. These taxa, including modern humans, constitute their own clade. We will explore the implications of this in the concluding remarks.

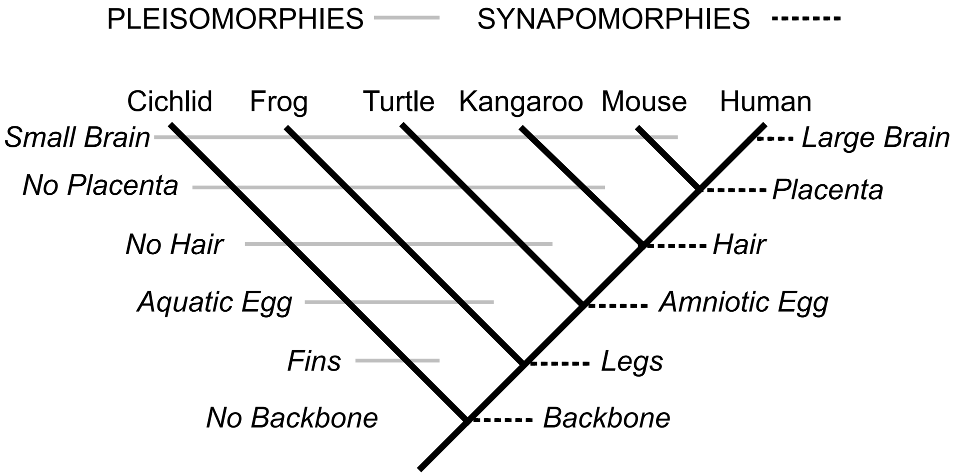

Figure 10. Cladogram showing synapomorphies
(after https://rainbow.ldeo.columbia.edu/courses/v1001/cladogram1.html)

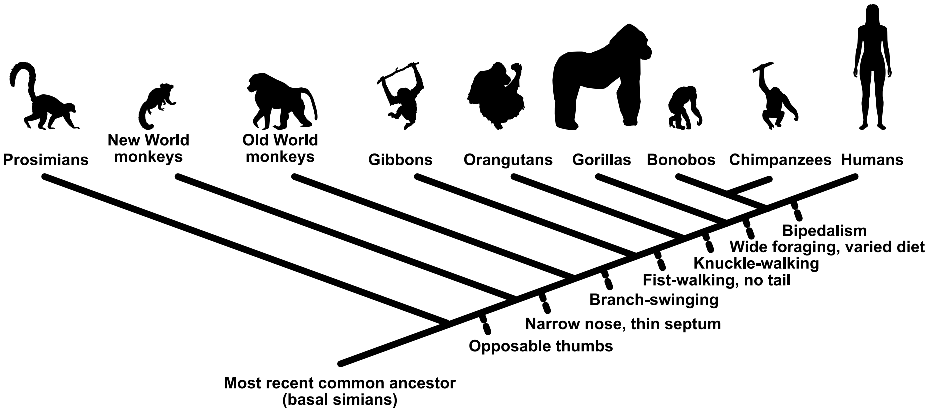

Figure 11. Primate cladogram
(after https://www.pinterest.com/pin/leventozgul1970-adl-kullancnn-evolution-panosundaki-pin--623678248370219145/)

Understanding 'Abdu'l-Bahá's Statements in Light of Cladistics

Using the cladogram as a visualization tool—not to prove anything, but to better comprehend evolutionary relationships—we can now turn to some of the statements made by 'Abdu'l-Bahá about human evolution. In so doing, the intention is not to advance a new interpretation of His statements, but rather to stimulate the reader to revisit and deepen their own understanding of these statements.

Statement One

> The human spirit, which distinguishes man from the animal, is the rational soul, and these two terms—the human spirit and the rational soul—designate one and the same thing. This spirit, which in the terminology of the philosophers is called the rational soul, encompasses all things and as far as human capacity permits, discovers their realities and becomes aware of the properties and effects, the characteristics and conditions of earthly things. (*Some Answered Questions* 241)

In approaching human evolution from a Bahá'í perspective, the fundamental tenet is: humans are separate from animals by reason of having rational souls. 'Abdu'l-Bahá declares that

> [T]he foremost degree of comprehension in the world of nature is that of the rational soul. This power and comprehension is shared in common by all men, whether they be heedless or aware, wayward or faithful. In the creation of God, the rational soul of man encompasses and is distinguished above all other created things: It is by virtue

> of its nobility and distinction that it encompasses them all. (*Some Answered Questions* 250)

The defining feature of the human being—the human essence, in the sense that ‘Abdu’l-Bahá discusses it—is spiritual, not physical. This should be borne in mind: while a cladogram can clarify the nature of human beings’ biological relationship to animals in a way that helps us view some of ‘Abdu’l-Bahá’s statements on evolution in a new light—as I hope to demonstrate here—it does not directly speak to the core of ‘Abdu’l-Bahá’s argument, which focuses on the spiritual essence of the human being.

Statement Two

> The forms assumed by the human embryo in its successive changes do not prove that it is animal in its essential character. . . . Realizing this we may acknowledge the fact that at one time man was an inmate of the sea, at another period an invertebrate, then a vertebrate and finally a human being standing erect. Though we admit these changes, we cannot say man is an animal . . . (*Promulgation* 359)

The straightforward meaning of this statement can be easily visualized by the main line depicting human evolution in figures 10, 11, and 12. I re-emphasize that this direct lineage is also evidenced in phylogenetic trees and other representations of human evolution, but that it is obscured by the structures of those models. The cladogram helps us see more clearly when specific synapomorphies appeared in human ancestors—including those synapomorphies alluded to in this statement by ‘Abdu’l-Bahá, namely the vertebral structure, the development of four limbs with bony digits that characterizes tetrapods and enabled vertebrates to live on land, and bipedalism. As a distinct clade in these cladograms, the question of whether the human being is an animal becomes essentially semantic. Consider that from a certain perspective, we can call all tetrapods—all amphibians, reptiles, mammals, and birds—fish, since their last common ancestor with modern fish was a creature we would categorize as a fish or fish-like creature. However, the development of the defining tetrapod synapomorphy, and the further development of the synapomorphies that characterize each of those animal groups, make it more meaningful in most contexts to call a reptile a reptile, a mammal a mammal, etc., rather than thinking of them as “fish.” It is similarly reasonable to argue that humans are both within Animalia and yet defined by distinguishing features that set them apart. And while some of these are synapomorphies of the kind considered by evolutionary biology (morphological features such as bipedalism and large brain size), the most distinguishing “synapomorphy” from a Bahá’í perspective is the actualization and appearance of the human spirit. We will examine this more closely in the concluding remarks.

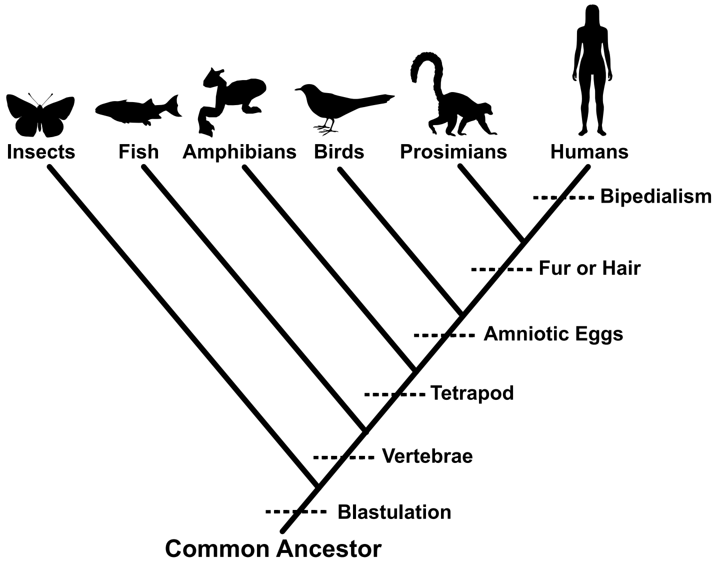

Figure 12. Human evolutionary line from anancestor common to other life forms (after https://www.pinterest.com/pin/189573465546096403/)

Statement Three

> The lost link of Darwinian theory is itself a proof that man is not an animal. How is it possible to have all the links present and that important link absent? Its absence is an indication that man has never been an animal. It will never be found. (*Promulgation* 359).

Figure 13 is a simplified primate cladogram showing the evolutionary relationships between humans and other primates. The bifurcations along the backbone indicate the points at which other primates diverged from the human evolutionary line. Each node of these bifurcations represents the most recent common ancestor (MRCA) of all clades above the node. The cladogram clearly shows that, indeed, there is no “missing link” in the sense held in ‘Abdu’l-Bahá’s time. A missing link would imply *direct* descent from the other primates: chimpanzees, gorillas, etc. Rather than a missing link, humans shared a MRCA at earlier points in evolutionary history with each of the other primates shown in figure 13. This is a subtle but profound distinction. Rather than “direct descent” as it was understood in ‘Abdu’l-Bahá’s time, what really occurred was successive divergence: the splitting off of preceeding taxa over time. The notion of a “missing link” has been dismissed in modern evolutionary biology (Williams and Ebach 1), just as ‘Abdu’l-Bahá predicted that it would be.

Now, what of the evolutionary line prior to each of the MRCAs shown in figure 13? We may consider some of these evolutionary predecessors as having the potential of evolving into higher organisms, even though in actual form and function these predecessors possessed none of the outward characteristics of the higher organisms. This potentiality is indicated ipso facto by the subsequent emergence of more advanced species. A mystery of the phenomenon of emergence is that the properties of an emergent entity, whether physical (e.g., a mineral) or biological (e.g., a species) are not found in its predecessor entities; in other words, the predecessors will not themselves display the newly emergent properties. To use a physicochemical example, a molecule of water, H_2O, is composed of two atoms of hydrogen and one atom of oxygen, yet neither elemental hydrogen nor oxygen have any of the physical properties of water: its fluidity, viscosity, boiling point, etc. The potential characteristics of water are only realized when water "emerges" from the chemical combination of hydrogen and oxygen.

This concept can be applied to the emergence of humans, although in this case the emergence is more gradual and, therefore, not as obvious at any given step. This potential for emergence existed in the evolutionary line preceding the MRCAs of humans, chimpanzees, and other primates. 'Abdu'l-Bahá alludes to this emergence when He states, "from the beginning the embryo possesses all perfections, such as the spirit, the mind, sight, smell, and taste—in a word, all the powers—but they are invisible and become apparent only gradually" (*Some Answered Questions* 229). The gradual emergence of the human line with the successive divergence of each subsequent MRCA supports the concept of the potentiality of humans in evolutionary deep time.

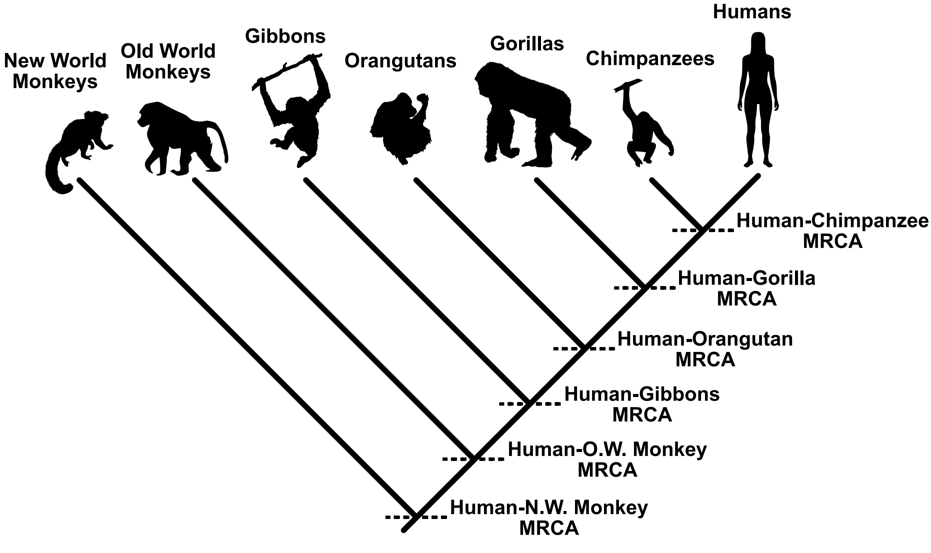

Figure 13. Simplified primate cladogram
(after https://www.researchgate.net/figure/cladogram-depicting-the-phylogenetic-relations-among-seven-primates-adapted-from_fig1_279854352)

There is, of course, a point in evolutionary history when early humans (in biology, hominins) physically appeared on the earth. This appearance may be considered an inflection point between human "potentiality" and human "actuality" in the evolutionary sense used here. This biological emergence conceivably could have been after the divergence of the last primate/human MRCA. This would be in accord with a statement of 'Abdu'l-Bahá that "…it is possible that man simply came into existence after the animal" (*Some Answered Questions* 221). This concept is developed further in Statement Four.

STATEMENT FOUR

> [T]he antecedence of animals to man is not a proof that the essence of the human species was altered or transformed or that man came from the animal kingdom. For so long as it is acknowledged that these different beings have appeared in time, it is possible that man simply came into existence after the animal. Thus we observe in the vegetable kingdom that the fruits of different trees do not appear all at once; on the contrary, some appear earlier in the season and others later. This priority is not a proof that the later fruit of one tree was produced from the earlier fruit of another. (*Some Answered Questions* 221)

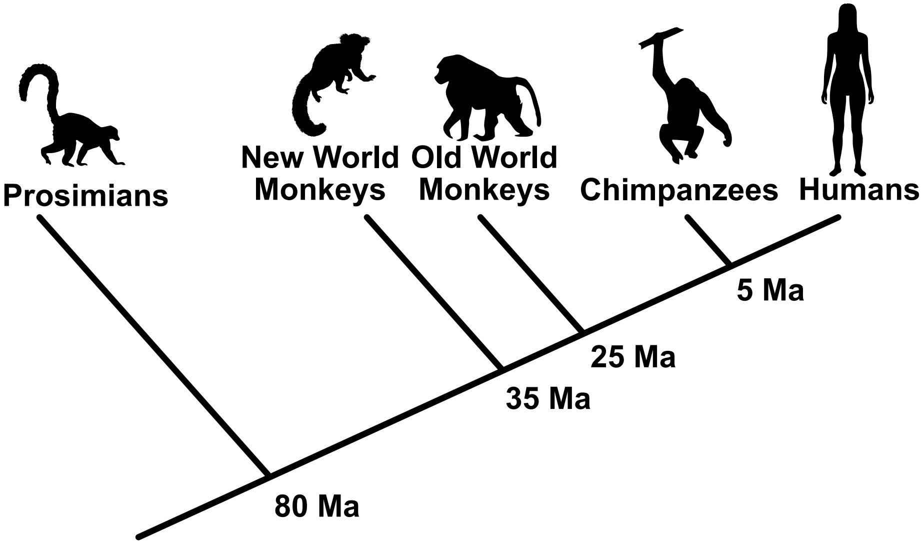

Figure 14. Cladogram showing evolutionary divergence between humans and other primates (Ma = megaannum = millions of years ago) (after https://www.researchgate.net/figure/phylogenetic-tree-of-primates-cladogram-showing-the-evolutionary-divergence-between_fig1_336892351)

The cladograms shown in figures 11, 12, 13, and 14 express this phenomenon. To see this, it is important to note that each of the non-human groups (chimpanzees, gorillas, etc.) did not appear at the evolutionary time of the related MRCA; these groups gradually evolved into their present state just as humans did. (This is why, for example, it is incorrect to say that "humans descended from chimpanzees"; rather, both chimpanzees and humans evolved from a MRCA.) Thus, the topmost horizontal row of each cladogram represents the "fruits" of the different evolutionary "trees" (i.e., the different evolutionary pathways shown in the cladograms). For example, the cladogram in Figure 14 clearly shows that prosimians represent an "earlier fruit" appearing earlier in the evolutionary "season" from a "different tree."(The cladogram in Figure 14 may appear as a single tree, but this is only because each evolutionary pathway for chimpanzees, gorillas, etc. is simplified to a single line; if mapped at a higher resolution that included more evolutionary ancestors and their taxonomic branches, each line in Figure 14 would appear as a tree in its own right.) Alternatively, 'Abdu'l-Bahá's statement makes sense if we consider the "main line" of Figure 14 to be like the soil from which a number of trees (portrayed as simple lines in the cladogram) grew, with each species in those trees being "fruits." This in no way contradicts, or is contradicted by, other statements in the Writings that all of creation is essentially one—clearly, all past and present existing entities in the physical creation are "fruits" of the one "tree" of creation—and consonant with Statement Four, the prior appearance of these "fruits" is not a proof that the later fruit of one tree was produced from the earlier fruit of another: humans did not directly descend from chimpanzees, monkeys, or prosimians.

Statement Five

> Let us suppose that man once bore a resemblance to the animal and that he has since evolved and transformed. Accepting this statement does not prove the transformation of species, but could instead be likened to the changes and transformations that the human embryo undergoes before reaching its full development and maturity, as was earlier mentioned. To be more explicit, let us suppose that man once walked on all fours or had a tail: This change and transformation is similar to that of the fetus in the womb of the mother. Even though the fetus develops and evolves in every possible way before it reaches its full development, from the beginning it belongs to a distinct species. (*Some Answered Questions* 223)

Here, 'Abdu'l-Bahá draws a parallel between human embryogenesis, wherein "ontogeny recapitulates phylogeny"[7] and human phylogenesis. In

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[7] The concept that "ontogeny

the long evolutionary history leading to the appearance of species *Homo sapiens*, humans have always been human in potentiality. A human embryo is always human regardless of how it may transiently appear *in utero*. It takes time for the embryo to develop into a baby to enter the extrauterine world. In similar fashion, it took time for human form and capacity to be realized in the natural world, allowing the human spirit, the rational soul, to manifest.

The MRCA of humans and any other species—be it chimpanzee, gorilla, or shark—gave rise to divergent lineages through its offspring, one eventually leading to humans and the other to another species. While this ancestor was not human in the taxonomic sense, it can be metaphorically viewed as an embryonic stage in humanity's development, representing a form oriented toward the eventual emergence of human-specific traits. This perspective rejects the notion of a separate, non-animal lineage evolving into humans, and instead affirms that the human form arose from a continuous line of "proto-human" ancestors—traceable along the backbone of a cladogram—culminating in a biological structure capable of manifesting the human spirit or rational soul.

CONCLUDING REMARKS: ARE HUMANS A SEPARATE CLADE?

Stepping back from all interpretations and speculations on the meaning of 'Abdu'l-Bahá's statements on human evolution, there is, I believe, a fundamental grounding principle, formulated by William Whewell and quoted by Darwin himself in the preface page of *On the Origin of Species*, that we must keep in mind:

> But with regard to the material world, we can at least go so far as this—we can perceive that events are brought about not by insulated interpositions of Divine power, exerted in each particular case, but by the establishment of general laws.

Bahá'ís are in full agreement with this statement. The fundamental position in Bahá'í belief is that the natural universe, together with its underlying physical laws, were created by God ('Abdu'l-Bahá, *Promulgation* 462–63). They believe that the natural world and its laws are the manifestations of God's creative power, and that nature reflects God's will. Moreover, Bahá'ís understand that physical reality is not a fixed and static creation, but a dynamic and ongoing emanation from God, who sustains it by His will: God the Creator is God the Creating (J. Hatcher, *Purpose* 48). Furthermore,

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recapitulates phylogeny" was first formulated by Étienne Serres in the 1820s, based on the work of Johann Friedrich Meckel, and is known as the Meckel-Serres Law (Dupont). Championed by Ernst Haeckel in his *General Morphology of Organisms* in 1866, it was widely accepted up through the time of 'Abdu'l-Bahá's statements. Since then, this concept has been largely discredited (Linhard). However, the point that 'Abdu'l-Bahá was making still applies.

Bahá’ís accept that evolution operates according to consistent and universal natural laws that never deviate from their course; science can therefore investigate these universal laws without need of invoking divine “tinkering” in a mechanistic sense. Based on these premises, we can infer that human evolution is coherent and compatible with scientific investigation—it can be fully explained by natural mechanisms, both deterministic and stochastic—and yet still is purposeful and progressive, and reveals the signs of God. Yet the central dogma of current biology is that evolution is purposeless and directionless, that progressive evolution is an illusion, that there is no hierarchical order to life, and—especially—that humankind occupies no special station in life (Kadykalo). Cladograms cannot disprove this belief—or any philosophical interpretation of evolution, theistic or atheistic. Indeed, in spite of their having been criticized as being inherently anthropocentric, introducing an unintended bias in their presentation (Sandvik), we have seen that a cladogram can be arranged so as to give to the unwary reader the appearance that any species—from the human to the hagfish—was the main driving purpose of evolution. So what *can* cladograms do, and why have I suggested that they can help reveal that the apparent tension between some of ‘Abdu’l-Bahá’s statements on evolution and contemporary science is illusory?

Remembering that every model or map has a particular function, and draws out a particular, partial truth about the thing that it represents, we can say that when given the necessary data and when properly applied, cladograms can clearly reveal emergent biocomplexity and the evolutionary pathways of any species, genus, family, order, etc., efflorescing into the majestic diversity of life—including *Homo sapiens*.

Returning to the definition of a clade: a group of taxa that 1) share a common ancestor, and, therefore, 2) have an exclusive evolutionary history; and 3) possess one or more synapomorphies composed of characteristics, traits, and functional capabilities from molecular to organismal levels. Clades are established by genetics and other molecular studies, paleontology and paleobiology, systematic morphology, and ethology. Thus, cladistics is grounded in scientific research that is current, rigorous, and well accepted. This grounding allows us to use cladistics as a valid technique to help us consider human evolution in light of ‘Abdu’l-Bahá’s statements on the subject.

Archaic species of genus *Homo* that evolved after the advent of bipedalism include *H. habilis*, *H. erectus*, *H. heidelbergensis*, *H. neanderthalensis*, and *H. floresiensis*. Along with *H. sapiens*, these taxa are assigned to the tribe Hominini, which includes chimpanzees and bonobos. Archaic and modern humans are further classified in subtribe Hominina, and chimpanzees and bonobos are classified in subtribe Panina, genus *Pan*. The last common ancestor between *Pan* and *Homo* lived at least five, and perhaps as early as seven, million years ago (Tocheri et al.).

Within this taxonomic structure, genus Homo could be assigned to its own clade based on these established synapomorphies: bipedalism (Leutenegger), genetic homology (Coleman), a significantly larger cranial capacity (Stanyon et al.), complex linguistics (Tattersall; Corballis), and culture formation employing fire, tools, and art (Lake). Current scientific evidence suggests that differences in mental abilities between apes and humans are gradual (Penny). This is consistent with evolutionary development as a whole: ethological studies repeatedly demonstrate rudimentary thought and feeling in lower mammals, suggesting that this distinction is in degree, not kind. Others, however, such as the biological anthropologist and linguist Terrence Deacon, see this in a different light. In Deacon's words, "Biologically, we are just another ape. Mentally, we are a new phylum of organisms" (23). In biological taxonomy, Phylum is a classification rank positioned just below Kingdom, representing a significantly different evolutionary category (Williams and Ebach 31).

For humans, therefore, perhaps a more exclusive clade could be derived based on the one "synapomorphy" that is unique, 'Abdu'l-Bahá attests, among the entire range of life: the rational soul, which He describes as possessing moral will and a consciousness capable of transcending nature and perceiving the Light of God (*Some Answered Questions* 250). An appropriate designation for this clade might be: *Rationalis*.

Appendix A – Strengths and Weaknesses of Cladistics

Some advantages of cladistics include (Ashlock):

1. It is grounded in evolutionary theory and is complementary to, not incompatible with, other methodologies in phylogenetics.
2. It is based on empirical data with diverse properties, obtained from separate methods and sources, which improves classification validity.
3. It is quite useful for studying evolutionary relationships in all the major specialties of biology from botany to zoology.
4. It is particularly good at visualizing evolutionary history in terms of phenetics and evolutionary development (Harrison).

Taken collectively, these advantages make cladistics an ideal approach to understanding evolution in general and, for our interests, human evolution in particular. More importantly, this approach offers a platform for higher discourse with wider communities, lay and scientific alike.

David Williams and Malte Ebach, co-authors of the standard textbook on cladistics have said, "*cladistics is classification*" (403, original emphasis). In biology, classification in general can be problematic for several reasons that apply to cladistics:

1. Cladistics isn't well suited to accommodate reticulate evolution (Sneath), i.e., evolution that occurs from the lateral exchange of genetic information by horizontal gene transfer, etc. (Belal and Heath). Horizontal gene transfer can occur in bacteria, for example, by generalized transduction from viral infection (Arnold et al.).
2. Cladistics is better at incorporating some types of data than others. For example, it is not an ideal classification system for fossil records that are incomplete and lacking information about evolutionary relationships (Grantham).
3. Cladistics can be restrictive, limiting the inclusion of subtly diverse taxa (Christoffersen). This is a criticism of taxonomy in general.

Cladistics is focused on the classification of known taxa rather than the discovery of unknown taxa (Williams and Ebach 396). This is not a disadvantage *per se*, it merely reflects the focus of any classification methodology.

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