

A Tale of Two Crocoducks: Creationist Misuses of Molecular Evolution

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Abstract Although some creationist objections to evolutionary biology are simplistic and thus are easily refuted, when more technical arguments become widespread it is important for science educators to explain the relevant science in a straightforward manner. An interesting case study is provided by misguided allegations about how cytochrome c data pertain to molecular evolution. The most common of these misrepresentations bears a striking similarity to a particularly glaring misunderstanding of what should be expected of a transitional form in a fossil sequence. Although evangelist Kirk Cameron's ridiculous injunction of a hypothetical 'crocoduck' as an example of a potential transitional form is frequently invoked to illustrate the ignorance of many critics of evolutionary science, a strikingly analogous argument was applied to cytochrome c data by biochemist Michael Denton in 1985. The details of this analogy are worth exploring to clarify the fallacy of the widely circulated molecular argument.

1 Introduction

Although creationist arguments are often so rife with fallacies as not to merit scholarly attention, science educators do have a responsibility to address some of them. This is particularly true when invalid conclusions are drawn from a misapplication of relatively complex technical concepts and then widely distributed to uncritical audiences. Careful analysis in such a case stands to inform not only science students but also the creationists who circulate the argument in question. With this goal in mind, the following case study proceeds in several stages. First, I briefly recap the 2007 debate episode in which actor and creationist advocate Kirk Cameron proposed a crocoduck as a viable example of the transitional forms to be expected from the idea that all life is the result of descent from common ancestors. This provides an opportunity to stress the importance of understanding cladistics and 'tree-thinking' when assessing evidence for the history of life. Cameron's

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blunder then can be seen as a particularly egregious example of a more widespread misunderstanding of how phylogenies incorporate both taxonomy and evolutionary relationships. Secondly, I trace the early history of the study of molecular evolution, particularly amino acid sequences for proteins such as cytochrome *c*. This survey provides context for an analysis of the assertions made by intelligent design advocate Michael Denton in his 1985 *Evolution: A Theory in Crisis* (Denton 1985). In particular, Denton claimed that cytochrome *c* amino acid sequence data provide a refutation of common descent because there are no modern cytochrome *c* sequences intermediate between those of prokaryotes and eukaryotes. Although Denton qualified his claim by adding that the common descent hypothesis could be salvaged if the molecular clock of cytochrome *c* runs at a uniform rate in all evolutionary lineages, he dismissed this solution as implausible. His book quickly became a standard citation in anti-evolutionary literature, particularly his cytochrome *c* argument, shorn of Denton's subsequent caveats and qualifications. In spite of numerous refutations that immediately reached print and are still readily accessible, fallacious interpretations of cytochrome *c* data continue to circulate in creationist venues. Denton has been repeatedly referenced or paraphrased approvingly over a period of two decades culminating in Nathaniel Jeanson's recent lectures and online essays for the Institute for Creation Research. After tracing this legacy of Denton's argument, I conclude that science educators can efficiently refute the fallacy in the routinely-cited version of Denton's objection by pointing out the analogy between Cameron's recourse to a mythical crocoduck and the equally incorrect demand for a cytochrome *c* protein intermediate between those of modern eukaryotes and modern prokaryotes. In both cases a fallacious argument gains traction due to the widespread misconception that the evolutionary account of the history of life is a linear progression through fixed stages represented by modern taxa.

2 Kirk Cameron and the Crocoduck

On May 5th 2007 a well-attended debate took place at Calvary Baptist Church in Manhattan, New York (Cameron 2007). At issue was the claim by Kirk Cameron and Ray Comfort, two representatives of a Christian evangelical ministry, The Way of the Master, that they could present a scientific proof for the existence of God. Responses to their arguments came from Brian Sapien and Kelly O' Connor, representatives of the Rational Response Squad, an atheist advocacy group. ABC streamed the debate online and two days later broadcast excerpts for a segment of ABC Nightline Faceoff.

Midway through the debate, Cameron decided to attack evolution due to his perception that it presents an obstacle to theism. He claimed that if evolution has happened there should be an abundance of transitional forms and he then offered examples of what he thought these forms should be. His examples were ridiculous combinations of modern animals such as a bull/frog, a sheep/dog, and, most notoriously, a crocoduck consisting of a crocodile's head affixed to a duck's body. With great aplomb, Cameron announced what he thought was a *reductio* for evolution while brandishing an artist's rendition of the mythical crocoduck.

Science has never found a genuine transitional form, that is, one kind of animal crossing over into another kind, either living or in the fossil record. And there are supposed to be billions of them. Now what I'm about to show you does not exist. These were actually created by our graphic artists. But I want you to keep your eye out for this because this is what evolutionists have been searching for for hundreds of years. All right? And if you find one of these you could become rich and famous. So here's some transitional forms. This is called the crocoduck (Cameron 2007).

Although Cameron's salvo was to some extent delivered tongue-in-cheek, his attempted *reductio* was of course seriously misguided. Modern birds and modern crocodiles are the result of separate lineages that originated from a common ancestor among the Archosaurs of the early Triassic. Early Archosaurs were reptiles distinguished by features such as their socketed teeth and the skull openings in their jaw bones and in front of their eyes; they bore limited similarity to either modern crocodylians or birds, their only extant descendants. Approximately 250 million years ago Archosaurs split into two distinct lineages, each of which constitutes a clade, a collection of all species descended from the same common ancestor. These two lineages are the Pseudosuchia, the clade that includes modern crocodiles, and Avemetatarsalia, the clade that includes dinosaurs and ultimately birds (Nesbitt 2011). Transitional forms would be expected to be found in the fossil record that documents the history of each of these two huge sister taxa, not as a composite of two modern forms. It is ironic that this particular evolutionary divergence is one that has been particularly well-studied and dated by paleontologists.¹

Cameron's most obvious misunderstanding thus pertains to what a viable transitional form should be; a potential candidate for this status would necessarily have to be found in the fossil record, not as a living organism. More specifically, a fossil specimen might be considered a transitional form to the extent that it bore at least some clear characteristics of species coming slightly earlier in the fossil record as well as other characteristics shared by species coming slightly later in the record. One place to look for relevant cases would be in the stem groups that have origins preceding that of a closely related crown group. A relevant candidate for an actual transitional form might be the 150 million year old fossil of *Archaeopteryx* which has some characteristics of earlier theropod dinosaurs and other characteristics of later birds. But that label might with equal merit be assigned to any number of other specimens depending upon which transitional characters are chosen.

Although a full explication of Cameron's confusion would require quite a lengthy treatment, it is important to point out that the transitional form concept that he tries to address is no longer central to modern analysis of the fossil record. Although apparently unknown to Cameron, a shift in emphasis away from transitional forms and direct lineages and toward transitional features became central to evolutionary biology several decades ago. Phylogenetic systematics, or cladistics, was pioneered by Willi Hennig during the 1950s and became widely known through the 1966 English version of his path-breaking book (Hennig 1966). Both taxonomy and phylogeny were revolutionized by Hennig's insight that it is unrealistic to expect all characteristics of an ancestral species to undergo subsequent transitional stages at the same pace. It is much more plausible that various characters would change at rates independent of each other. Some time periods might involve significant changes in one character with other characters remaining relatively stable; during other times the opposite might be the case. Paleontologists thus find it more productive to tabulate the successive modification or acquisition of specific features rather than to try to highlight one form at one point in time as in some sense quintessentially transitional with respect to multiple features. Many individual characters such as tail length or dentition have a quantitative aspect that can be measured for relevant specimens in the fossil record. By focusing on measurable characters, both extant and extinct species can be classified according to the derived traits they share with a common ancestor, traits referred to as synapomorphies. Similarly, the fossil record reveals interesting sequences in which these characters change with respect to quantitative variables. In the context of these sequences, transitional features are commonplace and are easily identified. On the other

¹ Müller and Reisz (2005), Nesbitt et al. (2010), Nesbitt (2011).

hand, any particular organism in its entirety is made up of a great many of these characters and can at best be expected to serve as a good illustration of a transitional state with respect to just some of them.

The construction of cladograms based upon synapomorphies thus does not require prior speculation about direct ancestry through a sequence of individual species (Prothero 2007, pp. 127–141). Instead, cladograms depict the successive acquisition of derived characters and the groups that share them. This approach to systematics became the consensus methodology by the 1990s (Padian and Angielczyk 1999). As paleontologist Kevin Padian commented in a review article in 2001, ‘Cladistics took the focus off direct ancestry and put it on shared ancestry, ...’ (Padian 2001, p. 599). The importance of thinking of evolutionary relationships using the ‘tree thinking’ required by cladograms has received a great deal of attention in both the scientific and science education literature.²

To take an example from the early evolution of birds, consider the following cladogram and caption published in 2003 (Zhou et al. 2003, p. 810) (Fig. 1).

Among theropod dinosaurs, Troodontidae can be distinguished from Compsognathidae due to a retroverted pubis, character 4 in the cladogram. While sharing characters 1–4, *Archaeopteryx* in turn has additional distinguishing characters such as a reversed hallux and asymmetrical flight feathers. In general, the idea that a species or larger taxon is more or less closely related to another is understood in terms of the time that has passed since their divergence from a common ancestor. *Archaeopteryx* thus is more closely related to Troodontidae than to Compsognathidae and this is reflected by its position within the cladogram. The node from which these two lineages diverge, their common ancestor, is not named, nor is any other node. The cladistics approach emphasizes relationships among taxa rather than direct ancestry between species.

It is worth considering in more detail how fossil data contribute to tree-building for the specific example of the gradual descent of birds from maniraptoran theropod dinosaurs, particularly since this example bears upon the issue raised in such a confused manner by Cameron. The fossil record shows that the late Jurassic and early Cretaceous were time periods in which avian features emerged and became correlated so as to constitute a clade distinct from nonavian dinosaurs (Garner et al. 1999; Chiappe 2009). Consider just three characters of obvious interest: teeth, tails and feathers. All three of these characters go through a series of transitions before reaching their eventual condition in modern birds. Teeth gradually become limited and eventually disappear altogether, a loss that apparently happened independently along several different lineages among early birds (Louchart and Viriot 2011, p. 665). There thus is no single sequence of species that represents a unique pathway to the toothless state of modern birds. Instead there are ample examples of various degrees of tooth loss. A relevant set of specimens illustrating this process might include *Archaeopteryx* (complete dentition), *Rapaxavis pani* (partial dentition at premaxillary and rostral dentary), *Sapeornis chaoyangensis* (partial dentition on upper jaw), *Jeholornis prima* (partial dentition on lower jaw), and *Hongshanornis longicresta* or *Confuciusornis* (no teeth). Similarly, tail length decreases gradually as illustrated by long-tailed *Archaeopteryx* and *Jeholornis prima* and short-tailed *Zhongornis haoae*. Tails eventually become short pygostyles made up of fused vertebrae in *Sapeornis chaoyangensis*, *Confuciusornis*, and *Yixianornis grabaui*, the latter being the earliest known bird with the ploughshare-shaped pygostyle found in modern birds (Clarke et al. 2006; Chiappe 2009). Feathers,

² See for example Baum and Offner (2008), Baum and Smith (2013), Catley (2006), Catley et al. (2010), Crisp and Cook (2005), Gregory (2008), Mead (2009), Meisel (2010), Novick et al. (2010, 2011), Padian (2008).

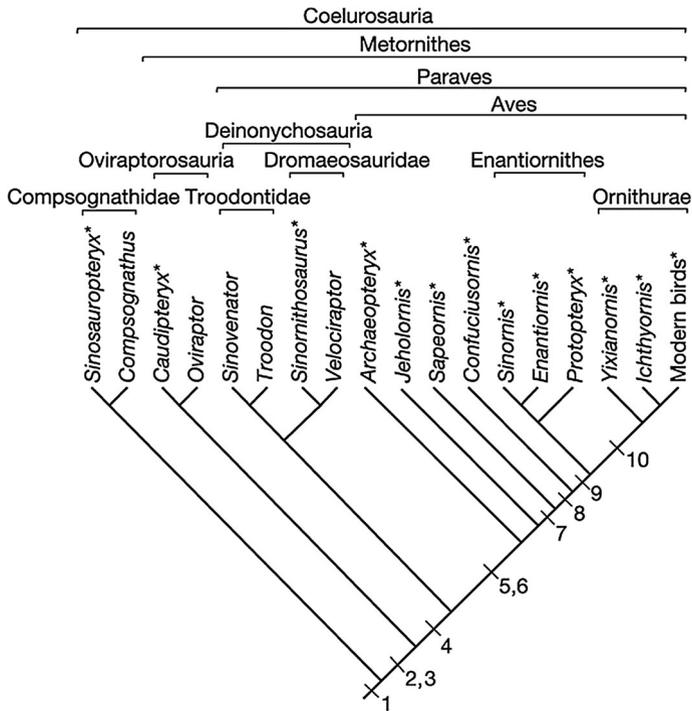


Fig. 1 Cladogram illustrating the relationship of birds with major clades of non-avian coelurosaurian theropods. The numbers at each branching node indicate the first appearance of key morphological characters. 1 unbranched feathers; 2 uncinatate processes on ribs; 3 true branched feathers; 4 retroverted pubis; 5 reversed hallux; 6 asymmetrical flight feathers; 7 pygostyle; 8 horny beak; 9 alula (bastard wing); 10 large, keeled sternum. Taxa indicated with an asterisk are known to have possessed either protofeathers or true feathers. *Source:* Zhou et al. (2003) reprinted by permission from Macmillan Publishers Ltd: *Nature* vol. 421, copyright 2003

perhaps the most commonly recognized characteristic of modern birds, provide a very complex set of data that includes sources from nonavian dinosaurs.³ Filamentous feathers have been found even among nontheropod heterodontosaurs such as *Tianyulong confuciusi* and, more commonly, in Coelurosaurians such as the compsognathid *Sinosauropteryx prima* or the therizinosaur *Beipiaosaurus inexpectus*. Vaned feathers are common among Maniraptorians such as the avialan *Pedopenna daohugouensis*. The asymmetrical vaned feathers used for flight in modern birds are found in the dromaeosaurid *Microraptor* and the well-known *Archaeopteryx*, for example. In each of these cases a character found in modern birds has a history of gradual appearance through many transitional states.

These and a myriad of other more detailed characters have been tabulated and analyzed, resulting in cladograms that depict the statistically best representations of the avian clade and its relatives. Analogous data could be cited for the origins of crocodylians within Pseudosuchia, the sister taxon to Avemetatarsalia, the taxon that includes dinosaurs and birds, both taxa having a source in their common ancestor among the Archosaurs (Nesbitt

³ See for example Chiappe (2009), Garner et al. (1999), Padian (2001), Xu and Guo (2009), Xu et al. (2010).

2011). The modern understanding of evolutionary relationships thus does not attempt to determine lines of direct descent through a series of individual species. Rather, it focuses upon classification based upon shared derived characters. Clades within the resulting nested hierarchy are more or less closely related depending upon their positions with respect to hypothetical common ancestors, each represented as a node at the point in the cladogram where the relevant branches diverge. In recent years representative cladograms often are supplemented with additional information by labeling points at which new characters appear and including illustrative fossils. Padian has referred to these diagrams as ‘evograms’.⁴

This shift in focus from transitional forms to transitional characters is not only of technical value for specialists. It also provides welcome support for a long overdue rejection of the misleading phrase ‘missing link’. The history of this usage goes back to the pre-Darwinian era but unfortunately it is still all too common in both the modern popular press and creationist literature (Kjaergaard 2011). The phrase inappropriately presupposes that a ‘chain’ of direct descent has been established, or at least hypothesized, and that one expected ‘link’ in this chain is unaccounted for. But it was widely recognized even in Darwin’s time that a collection of fossils with ages spread over any particular stretch in time can never with high probability be interpreted as a lineage of direct descent. Most obviously, the problem is that any member of this alleged chain can be expected to have been contemporary with other unknown species, one of which might well be the actual ancestor or descendent of other members of the collection. Although it is tempting to argue for a direct ancestry in some specific cases, the more careful scientific literature avoids this practice in favor of phylogenies. In short, modern evolutionary understanding of the history of life is not based upon alleged transitional forms even though creationists such as Cameron continue to think so.

Briefly put then, Cameron’s errors are of two kinds. First, his understanding of what a transitional form should be is woefully confused in that he expected it to be a composite of two modern species. Secondly, his demand for a transitional form is out of step with more realistic evolutionary expectations for transitional features or characters. Cameron’s ignorance about what should be expected of an evolutionary phylogeny made the mythical crocoduck an immediate sensation and generated extensive internet merriment at Cameron’s expense. The crocoduck in effect became symbolic of the combination of ignorance and arrogance that all too often characterizes those creationists who advance arguments against evolution without even a rudimentary understanding of the relevant science.

While Cameron’s flawed reasoning is easily discredited, an analogous argument originated two decades earlier and still circulates today. The evolving entities in this second case are not crocodiles and ducks but instead are variants of cytochrome c, an important protein found in virtually all extant life. Due to the superficial plausibility and widespread impact of this second argument, it is important that science educators be able to clearly explain how it suffers from some of the same flaws as Cameron’s crocoduck fiasco.

3 Cytochrome c as a Molecular Clock

Comparative analysis of the amino acid sequence of proteins became a topic of intensive research soon after the 1953 discovery of the structure of DNA. For present purposes only a simplified summary of the process of protein synthesis needs to be briefly summarized. The genes for particular proteins are made up of DNA that is transcribed into messenger

⁴ See for example Padian (2001, 2008), Padian and Angielczyk (1999, 2007).

RNA which in turn is translated into a sequence of amino acids constituting each protein. Since each triplet, or codon, of DNA nucleotides codes for a specific amino acid, mutations in DNA can have several different outcomes. Due to redundancies in the genetic code, some mutations result in a new codon that codes for exactly the same amino acid as the initial codon. Other mutations may result in a new amino acid but one that does not impair the function of the resulting protein. These nonsynonymous mutations thus are still neutral with respect to protein function. From an evolutionary perspective it was natural to think that the amino acid sequence in a protein would change over time as these neutral mutations accumulate. Following Frederick Sanger's determination of the amino acid sequence for insulin in 1956, comparison of amino acid sequences for a given protein in different animals soon became feasible. As early as 1958, Francis Crick predicted that the tabulation of a 'protein taxonomy' would yield important evolutionary insights (Crick 1958, p. 142). The expectation that amino acid sequence differences should reflect time since divergence from a common ancestor was developed by Walter Fitch, Emanuel Margoliash, Richard Dickerson, Hans Tuppy, Linus Pauling, Emile Zuckerkandl, Margaret Dayhoff, and many others during the early 1960s.⁵ It was during this period that Pauling and Zuckerkandl started using the phrase 'molecular evolutionary clock' in their analysis of hemoglobin proteins (Zuckerkandl and Pauling 1965b, p. 148).

During these early years in the study of protein evolution cytochrome c became an object of extensive research (Dickerson 1980). In eukaryotes it is an important mitochondrial protein in the respiratory electron transport chain. The ubiquitous presence of closely related cytochromes c in virtually all forms of life and their relatively short sequences of approximately 100–120 amino acids would eventually make comparisons possible between almost any pair of species. Hans Tuppy began sequencing the active site of cytochrome c proteins during the 1950s and in 1961 he collaborated with Emanuel Margoliash, Emil Smith, and Gunther Kreil to publish the full amino acid sequence for horse cytochrome c (Margoliash et al. 1961; Strasser 2010). Other complete cytochrome c sequences soon were available for comparisons. In a 1963 paper Margoliash made some interesting comments about how the sequence varied across species:

...it appears that the number of residue differences between the cytochromes c of any two species is mostly conditioned by the time elapsed since the lines of evolution leading to these two species originally diverged. If this is correct, the cytochromes c of all mammals should be roughly equally different from the cytochromes c of all birds. Since fish diverged from the main stem of vertebrate evolution earlier than either birds or mammals, the cytochromes c of both mammals and birds should be equally different from the cytochromes c of fish. Similarly, all vertebrate cytochromes c should be equally different from the yeast protein." (Margoliash 1963, p. 677).

Margoliash also included the relevant data to confirm these evolutionary predictions. Thus, as early as 1963, research in molecular evolution had demonstrated that cytochrome c amino acid sequences for a wide variety of vertebrates were equally divergent from the corresponding sequence for yeast. This was exactly what is to be expected if there is a juncture in evolutionary history at which all fungi such as yeast diverged from the lineage leading to animals. As Margoliash noted, the data were 'not consistent with a simultaneous formation of all species, which then proceed to accumulate mutations independently. In the latter case all the cytochromes c should be equally different from all others' (Margoliash 1963, p. 677). He reiterated this point in a 1965 publication in which he used other cytochrome c examples.

⁵ For historical accounts see for example Dietrich (1998), Hagen (1999, 2011), Morgan (1998), and for some of the early research see for example Smith and Margoliash 1964, Zuckerkandl and Pauling (1962, 1965a, b).

The line of evolution which later gave rise to both mammals and birds having diverged from that which led to present-day fish at an earlier date than the divergence of the mammalian and avian lines, the cytochromes *c* of various mammals and the chicken are all roughly equally different from the tuna protein. Similar relations are evident for the comparison of all vertebrate cytochromes *c* with the protein from an invertebrate, the moth *Samia Cynthia*, as well as for the comparison of the vertebrate and moth proteins with baker's yeast cytochrome *c*. (Margoliash and Smith 1965, pp. 231–232).

Amino acid sequence data of course can only be extracted from living species. Consequently, all extant species that share a common ancestor have been evolving for the same period of time since their divergence from that ancestor. For example, all mammals have evolved for the same amount of time since the divergence of mammals from their common ancestor with fish and all mammalian cytochrome *c* should be, and is, equally different from that of fish. Although this conformity of the new molecular evidence with earlier phylogenies based upon the fossil record was hardly surprising, it was welcomed by Pauling and Zuckerkandl in a partially tongue-in-cheek passage in the 1965 article in which they first used the phrase 'molecular evolutionary clock'.

Indeed, only the theory of evolution, combined with the realization that events at any supramolecular level are consistent with molecular events, could reasonable account for such a congruence between lines of evidence obtained independently, namely amino acid sequences of homologous polypeptide chains on the one hand, and the findings of organismal taxonomy and paleontology on the other hand. Besides offering an intellectual satisfaction to some, the advertising of such evidence would of course amount to beating a dead horse. Some beating of dead horses may be ethical, when here and there they display unexpected twitches that look like life. (Zuckerkandl and Pauling 1965b, p. 101).

Zuckerkandl's indirect reference to special creationism as a 'dead horse' may have been apt from a scientist's point of view, but the phenomenon was of course alive and well in the broader American culture. The nested hierarchy of similarities displayed by cytochrome *c* data thus served as a welcome support for evolutionary thinking.

1965 was also the year in which research on amino acid sequences up to that point was summarized in the first volume of the *Atlas of Protein Sequence and Structure* (Dayhoff et al. 1965). Primarily due to the efforts of Margaret Dayhoff and Richard Eck, the 1965 *Atlas* included all protein amino acid sequences available at that time (Strasser 2010). For cytochrome *c* these included human, chicken, horse, pig, tuna fish, silkworm moth and rattlesnake as well as cytochrome *c*-551 for the bacterium *Pseudomonas* and cytochrome *c*₂ for the partially sequenced purple photosynthetic bacterium *Rhodospirillum rubrum*. No explicit comparisons were made among these sequences and no effort was made to use the data to construct phylogenies. More extensive subsequent volumes of the *Atlas* made it an increasingly valuable reference work, not only for the data they contained but also for the interpretive essays written by Dayhoff and her colleagues.⁶

The 1966 volume of the *Atlas* included a matrix display comparing the human cytochrome *c* sequence to that of eighteen other species, including several mammals, birds, fish, a moth, and three fungi (Eck and Dayhoff 1966). The *Pseudomonas* sequence was once again included but with only 82 amino acids it was considered to be 'so different that no detailed use of it can yet be made' (Eck and Dayhoff 1966, p. 169). *R. rubrum* was still only partially sequenced at this date. The 1968 volume expanded the discussion of cytochrome *c* data to sequences drawn from a wider range of species that included humans, eight other mammals, birds, reptiles, insects, wheat, and three species of fungus including baker's yeast (Dayhoff and Eck 1968b). The data were again displayed in a matrix showing the number of amino acid differences between any pair of species sequenced. As was to be expected, any member of a set of species had approximately the same number of amino

⁶ Dayhoff (1969b, 1978), Dayhoff and Park (1969), Dayhoff et al. (1978).

acid differences when compared to a species from an outgroup with which they shared the same common ancestor. For example, all vertebrates had between 43 and 49 differences when compared to the wheat sequence and all plants and animal sequences differed from the fungus *Candida krusei* sequence by approximately 50 amino acids. These results were exactly analogous to those Margoliash had predicted and confirmed in 1963 and reiterated in 1965.

The 1966 and 1968 volumes of the *Atlas* also included phylogenetic trees based upon cytochrome c amino acid differences that clearly depicted the divergence points for fungi and plants from insects, fish and the other species sequenced (Dayhoff and Eck 1968a, p. 9). More thorough and highly influential phylogenetic studies based upon cytochrome c comparisons were published by Dayhoff, Margoliash, Walter Fitch, and others throughout the 1960s and early 1970s.⁷ A 1967 Fitch and Margoliash paper was particularly significant; it has been referred to by Francisco Ayala as ‘a paper that may well be considered the founding document of molecular phylogenetics and one that would forever affect the way biologists reconstruct the phylogeny of living species’ (Ayala 2011, p. 5). Cytochrome c data thus was at the very center of the research that became the foundation for the new field of molecular evolution.

The 1972 volume of the *Atlas of Protein Sequence and Structure* presented a more extensive set of cytochrome c data that included the full sequence for the bacterium *R. rubrum*, a data set that would become the basis for many subsequent discussions in creationist literature (Dayhoff 1972, p. D8). The data were once again displayed in a matrix format but now showed percentage differences rather than the number of amino acid differences (Dayhoff 1972, p. D195). The display clearly depicted how the amino acid sequences for all cases of eukaryotic cytochrome c are about 60 % different from the closely related cytochrome c₂ of the bacterium *R. rubrum*. This equidistance was once again as expected from an evolutionary perspective. Since any eukaryote shares the same common ancestor with any bacterium, all eukaryotic cytochrome c amino acid sequences should be equally different from the sequence for any bacterium. Similarly, the sequence for any vertebrate is equally different from that of any insect or any fungus. These and many more cases of ‘equidistance’ were easily recognized due to the matrix display of the data. For example, the percentage differences between any of the listed organisms and the bacterium *R. rubrum* were compiled prominently along the bottom row of the matrix.

The results of these sequence comparisons for cytochrome c were widely publicized in both the scientific and semi-popular literature during the late 1960s and early 1970s. This point is worth emphasizing because some creationists would later claim not only that various examples of equidistance were anomalous but also that they had been overlooked or ignored by the scientific community. For example, in 1973 Dayhoff and Patricia McLaughlin published what they labeled ‘the detailed cytochrome c evolutionary tree’ (McLaughlin and Dayhoff 1973, p. 105) (Fig. 2).

They included 45 species of animals, plants, and fungi, as well as the single celled *Crithidia oncopelti* and the bacterium *R. rubrum*. Their tree clearly showed how the data were in conformity with an early divergence of eukaryotes from bacteria followed by subsequent divergences of plants, animals and fungi with extensive further divergences within these groups. Writing for a broader audience, both Margaret Dayhoff and Richard Dickerson wrote detailed articles on cytochrome c for *Scientific American* (Dayhoff 1969a; Dickerson 1972). Dayhoff used cytochrome c as an example to show how amino acid

⁷ See for example Dickerson (1971), Fitch and Margoliash (1967), Margoliash and Fitch (1968), McLaughlin and Dayhoff (1973), Kimura (1968).

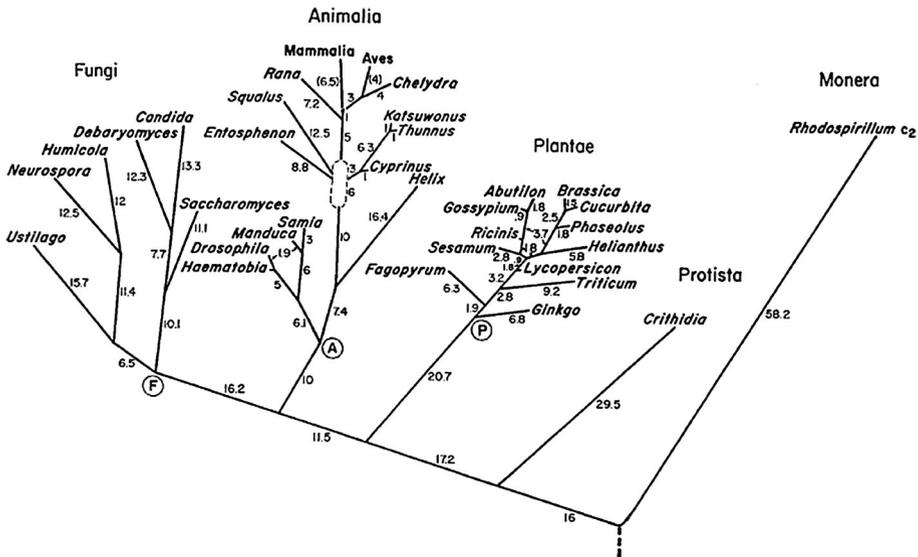


Fig. 2 The detailed cytochrome *c* evolutionary tree. The order of branching for the five kingdoms is the same as configuration 1 Fig. 4. The progression of time is toward the top of the tree. The lengths of the branches are drawn in proportion to the numbers beside the branches, which are PAMs or Accepted Point Mutations estimated to have occurred on these branches. Source: McLaughlin and Dayhoff (1973) with kind permission from Springer Science and Business Media

sequence comparison data are analyzed to construct the most probable phylogeny. Dickerson included a similar discussion both in his *Scientific American* article and in a longer semi-popular publication in 1969 (Dickerson and Geis 1969). The record clearly shows that the numerous cases of sequence equidistance for cytochrome *c* data were recognized as confirmed evolutionary predictions using the molecular clock concept and they were widely publicized as a striking consilience of paleontological and molecular data.

4 Michael Denton's *Evolution: A Theory in Crisis*

In 1985 Michael Denton was not particularly well known in those venues where evolution and creationism are jointly discussed. He had earned his medical degree from Bristol University in 1969 and then completed a PhD in biochemistry in 1974 at King's College London. Between 1973 and 1975 his research resulted in several peer reviewed articles on the biochemistry of red blood cell differentiation. Nevertheless, his 1985 book *Evolution: A Theory in Crisis* quickly became a lightning rod for debates over creation and evolution. Although critics of evolution were gratified that someone with a background in the biological sciences would present arguments that were scientifically far more sophisticated than those usually offered by creationists, most scientists knowledgeable in the relevant disciplines were not favorably impressed and they rejected Denton's arguments as misguided.⁸ For example, both Speith in 1987 and Brauer and Brumbaugh in 2001 concentrated on the most well-known of Denton's biochemical arguments presented in his Chapter 12, 'A Biochemical Echo of

⁸ For example see Brauer and Brumbaugh (2001), Eldredge (1986), Landau (1989), Ridley (1985), Speith (1987).

Typology'. Both critiques were quite harsh and found Denton guilty of badly misrepresenting what data should be expected from the hypothesis of common descent.

Before taking up my own analysis, I should point out that Denton's chapter ran to thirty-three pages and included extensive discussion of the issue of molecular clock rates. He emphasized that interpretations of amino acid sequence data often have been combined with arguments that mutation rates are uniform across species and through time. Denton found these arguments lacking from both selectionist and genetic drift perspectives and he devoted considerable energy to explaining why. The present essay is not the appropriate place to engage the biochemical and statistical complexities of the molecular clock rate issues raised by Denton in the second half of his chapter. They are addressed in an extensive scientific literature that has generated increasingly complex averaging and calibration techniques that are seldom addressed in any detail by creationists.⁹

What is pertinent to the present discussion is Denton's initial claim about cytochrome c data. This is the argument that has been extracted from the broader context of Denton's book and has taken on a life of its own in creationist venues. Just a few pages into his chapter, Denton included an abbreviated version of an amino acid sequence data chart for cytochrome c. His source was the 1972 edition of Margaret Dayhoff's *Atlas*. As had been noted repeatedly between 1972 and 1985, the data show that animals or plants within a closely related group all have approximately the same number of amino acid differences when compared to species outside the group. This was exactly what had been predicted and confirmed from an evolutionary point of view ever since the early days of sequencing in the 1960s. Denton however, presented these data as if they were problematic.

However, the most striking feature of the matrix is that each identifiable subclass of sequences is isolated and distinct. Every sequence can be unambiguously assigned to a particular subclass. No sequence or group of sequences can be designated as intermediate with respect to other groups. (Denton 1985, pp. 278–280).

Denton then focused on a comparison of eukaryotic amino acid sequences to a bacterial sequence.

As far as the bacterium is concerned, all the eucaryotes are equally distant. All the eucaryotic cytochromes are as a class isolated and unique. No intermediate type of cytochrome exists to bridge the discontinuity which divides the living kingdom into these two fundamental types. The bacterial kingdom has no neighbor in any of the fantastically diverse eucaryotic types. The 'missing links' are well and truly missing. (Denton 1985, p. 281).

This is the assertion that would be widely cited in subsequent anti-evolutionary literature. The analogy to Kirk Cameron's later crocoduck rhetoric is striking. Cameron claimed that the notion of common descent implied that there should be a transitional form midway between two extant species, a crocoduck made up of a crocodile's head and a duck's body. Similarly, Denton apparently thought that common descent implies that at the molecular level there should be proteins with amino acid sequences that are intermediate between those for proteins of two extant species. In fact, in their 2001 critique of Denton's book, Brauer and Brumbaugh made exactly this point.

Aside from the fact that Denton's argument is being placed in the domain of molecular biology, it is fundamentally equivalent to the ancient claim that one should expect (if Darwinian evolution is correct) to see animals intermediate in form between, for example, frogs and humans. (Brauer and Brumbaugh 2001, p. 310).

⁹ For access to this enormous topic, see, for example, de Queiroz (2014), Graur and Martin (2004), Lanfear et al. (2010), Lynch (2010), Pulquério and Nichols (2006), Thomas et al. (2006), Welch and Bromham (2005).

Denton was of course far more knowledgeable of relevant science than was Kirk Cameron. He proceeded to explain how the equidistance of all eukaryotic cytochrome c proteins from a bacterium cytochrome c would make sense to him if eukaryotes and bacteria have all had the same stable cytochrome c mutation rates ever since the time of their divergence from a common ancestor. This was the issue that Denton spent most of the remainder of his chapter critiquing. However, as is often the case in anti-evolutionary literature, the subtleties of Denton's exposition generally would be overlooked or ignored. Once Denton's initial argument began to be cited in creationist literature, it took on a life of its own without the caveats that Denton included. To my knowledge Denton has never published any regret over how the preliminary part of his analysis has been used by creationists. This remains the case in spite of his subsequent acknowledgement that he has no objections to the idea of common descent. In fact, in 1998 Denton published a second book in which he argued that the evolutionary process takes place under the constraints and guidance of law-governed design (Denton 1998). In particular, he returned to the topic of cytochrome c data but with quite a different emphasis.

By comparing sequences a curious pattern was observed. For example, in the case of the cytochromes, all the higher organism cytochromes (yeasts, plants, insects, mammals, birds, etc.) exhibit an almost equal degree of sequence divergence from the bacterial cytochrome in *Rhodospirillum*. This means that all their cytochrome genes have changed to about the same degree—in other words, have evolved at a uniform rate. (Denton 1998, p. 290).

Denton now explicitly accepted the idea that the data imply that all cytochrome c genes are evolving at the same uniform rate and he then interpreted this as indirect evidence that “the mutational processes that are changing the DNA sequences of living things over time are indeed being directed by some as yet unknown mechanism, or more likely, mechanisms” (Denton 1998, p. 292). Although still of interest to advocates of intelligent design, Denton's new position no longer conflicted with the concept of universal common ancestry, a particularly sensitive topic for young earth creationists. He made his acceptance of common descent and his rejection of special creationism very explicit in his contribution to a 1999 volume dedicated to Phillip Johnson's impact on the intelligent design movement.

The reason why no current member of the US National Academy of Science is a special creationist is because of the facts, the same facts that in the nineteenth century convinced Darwin and Wallace and all the leading Christian biologists, including Joseph Hooker, Asa Gray, and Charles Lyell, of the reality of descent with modification. (Denton 1999, p. 154).

It is not surprising that many contributors to the anti-evolutionist literature have focused on Denton's initial 1985 discussion rather than his later more nuanced view. Even many of those who include references to more subtle molecular clock issues unreflectively present Denton's initial fallacious argument first and do not point out its flaws (Gish 1993).

5 Cytochrome c in Creationist Literature

The legacy of Denton's 1985 publication is complex. On the one hand, his critiques of evolutionary theory provided inspiration during the period in which Philip Johnson and Michael Behe decided to participate in the initial organizational activity for the intelligent design movement (Forrest and Gross 2007, p. 17). Denton's later clarifications of his position were tolerable to at least some prominent intelligent design advocates and through 2013 he was still listed as a senior fellow of the Center for Science and Culture under the

auspices of the Discovery Institute, the primary intelligent design think-tank. On the other hand, Denton's initial assessment of cytochrome c data generated an extensive lineage of primarily young-earth creationist appropriations of his comments. I will use several examples to demonstrate the wide range of venues in which Denton's argument has appeared. Some of these cases include an appreciation for the additional molecular clock issues Denton noted. Others are less sophisticated and simply repeat the initial argument. I will follow a roughly chronological approach to survey the wide scope of this legacy.

During the 1980s the Foundation for Thought and Ethics developed materials for a creationist textbook designed to supplement high school biology texts. Following the 1987 United States Supreme Court decision against those "balanced treatment" bills that mandated equal treatment of creation science in public school science classes, the initially proposed title of the text was changed to *Of Pandas and People: The Central Question of Biological Origins*, a volume that went through two editions in 1989 and 1993 (Forrest and Gross 2007, pp. 328–330, Scott and Matzke 2007). The authors were listed as Percival Davis and Dean Kenyon, but Michael Behe wrote at least some of the biochemistry section on blood clotting for the 1993 edition (Kitzmiller 2005, Day 10 AM pp. 53–54). Although *Pandas* was purported to advocate intelligent design rather than young earth creationism, the cytochrome c data were marshaled just as they initially had been by Denton. Several examples were cited, including a comparison of insect cytochrome c to that of a variety of vertebrates.

Notice that the cytochrome c of this insect exhibits the same degree of difference from organisms as diverse as human, penguin, snapping turtle, tuna, and lamprey. Considering the enormous variation represented by these organisms, it is astonishing that they all differ from the silkworm moth by almost exactly the same percent. The reason this finding is so surprising is that it contradicts the Darwinian expectation. (Davis and Kenyon 1993, p. 37).

Just as Denton had done in 1985, the authors of *Pandas* asserted that the data contradicted evolutionary predictions when in fact these data were precisely of the type that had been predicted from an evolutionary perspective as early as 1963.

Cell biologist Kenneth Miller made this point assertively when a discussion of *Pandas* arose during his testimony at the Dover Pennsylvania 'intelligent design trial' in 2005. The trial had been instigated by a law suit filed in response to the Dover school board's decision to make students in ninth grade biology classes aware of intelligent design as an alternative to conventional evolutionary theory with copies of *Pandas* available in the school library as a resource (Padian and Matzke 2009). Miller was already quite familiar with *Pandas*, having written a devastating review of the book for the Kansas Citizens for Science website in 1999. In that review he had specifically addressed the cytochrome c issue.

I honestly do not know if the authors of *Pandas* intentionally misrepresented evolutionary predictions or if they simply did not understand them. However, the real story is that the fossil record clearly shows that the entire vertebrate group (including frogs and people) split off from the invertebrates (including worms) many hundreds of millions of years ago. Therefore, the protein sequences of *every animal in that group* should be *equidistant* from *any* single invertebrate. And that is *exactly* what the experimental data show, as the authors of *Pandas* ought to know. The simple fact is that this chapter misrepresents evolutionary predictions on molecular sequences, and thereby covers up the fact that the sequences stand in stunning agreement with evolution. I cannot even imagine a greater misrepresentation of fundamental data to support an incorrect conclusion. (Miller 1999).

Miller thus was already thoroughly familiar with *Pandas* when he participated in the first day of testimony in the Dover case as one of the expert witnesses for the plaintiffs. When asked by American Civil Liberties Union plaintiff attorney Witold Walczak whether the treatment of science and biology in particular in *Pandas* was accurate, Miller responded, 'I

think the treatment of biology by Pandas is inaccurate and in many respects downright false in every section of the book' (Kitzmiller 2005, Day 1 AM p. 112). The first example Miller discussed was the misrepresentation of the cytochrome c data. He even used a diagram from Fitch and Margoliash's (1967) publication to make the point that the correct interpretation of the data had a long history that was ignored in *Pandas*. Several days later, biochemist Michael Behe, one of the defendants' witnesses, was questioned about this example. He defended the *Pandas* account of cytochrome c by pointing out that the initial fallacious argument was supplemented by a brief reference to more subtle molecular clock issues such as the possible variation in mutation rates for species with different generation times (Kitzmiller 2005, Day 11 AM, pp. 49–68). From a pedagogical point of view, this defense is strained. The authors of *Pandas* devoted three pages to Denton's argument, including two illustrations. The additional reference to molecular clock rates consists of two very short paragraphs. Furthermore, the initial fallacious argument is repeated in several illustrated pages of a supplementary chapter entitled 'Biochemical Similarities'. On a subsequent day of his testimony Behe did admit under cross-examination that *Pandas* had incorrectly presented what should be expected from molecular clock data (Kitzmiller 2005, Day 12 PM pp. 32–36).

Throughout the Dover trial many other examples of inaccurate science in *Pandas* were exhaustively discussed in much more detail. Not surprisingly, initial plans for a third edition of *Pandas* were forestalled. Instead, in 2008 the originally planned new edition was thoroughly revised and published as *The Design of Life* by William Dembski and Jonathan Wells (Dembski and Wells 2008). The new chapter on molecular phylogeny did not mention cytochrome c data and instead focused on the alleged unreliability of molecular clock methods to resolve specific details of the history of life, particularly the Cambrian explosion.

Phillip Johnson's *Darwin on Trial*, initially published in 1991, provides a more succinct example, in this case in a book that became a central text for the intelligent design movement of the 1990s (Johnson 1993). Johnson has credited Denton for fostering the skepticism about evolutionary conclusions that inspired *Darwin on Trial* (Stafford 1997). After referring to the usual depiction of cytochrome c data noted by Denton, Johnson concluded:

Judged by cytochrome c comparisons, sesame plants and silkworms are just about as different from bacteria as humans are. In fact, every plant and animal species is approximately the same molecular distance from any bacterial species, and there is no surviving trace of any intermediates that might have filled the "space" between single-celled and multicellular life. If the molecules evolved gradually to their present form, then intermediates must over time have filled that space, but comparing present-day molecules cannot tell us whether these transitional forms ever existed. (Johnson 1993, p. 94).

Although Johnson's statements about the data are tempered compared to the more blunt assertions in *Pandas*, his characteristic lawyerly strategy is designed to inspire doubt about common descent. Amino acid sequence data obviously can only be extracted from living species. By calling attention to the lack of historical data for extinct species, Johnson downplays the fact that the existing data do conform to evolutionary expectations that have been in place since the 1960s.

In 1993, two years after the initial publication of Johnson's *Darwin on Trial* and the same year as the second edition of *Pandas*, Duane Gish devoted considerable attention to amino acid sequence data in his *Creation Scientists Answer Their Critics* (Gish 1993). With his Ph.D. in biochemistry, Gish had been a prominent author and spokesman for the Institute for Creation Research since 1971. In his 1993 volume he dedicated a chapter to

respond to *Scientists Confront Creationism*, a 1983 anthology of critiques of various aspects of creationist science (Godfrey 1983). In particular, Gish responded to the chapter contributed by molecular biologist Thomas Jukes on ‘Molecular Evidence for Evolution’ (Jukes 1983). In the course of a wide ranging discussion, Gish cited Denton’s equidistance argument approvingly. After citing the numerous examples of equidistance noted by Denton, Gish drew the same conclusion.

Since each class at a molecular level is unique, isolated, and unlinked by intermediates, Denton reminds us, then, that molecules, like fossils, have failed to provide the intermediates searched for so intensely by evolutionists ever since Darwin. (Gish 1993, p. 288).

Gish then proceeded to give a relatively thorough discussion of additional issues such as variable mutation rates. As is often the case in creationist literature, however, his arguments are simply compiled for cumulative effect with very little reflection on their specific validity. A more accurate presentation would have pointed out the fallacious nature of Denton’s initial analysis before moving on to other topics.

While Gish’s book and Johnson’s *Darwin on Trial* were published as trade books intended for a general audience, *Pandas* had been commissioned and written amid hopes that it would serve as a supplementary text in public high school biology classes (Homchick 2012). This effort failed in light of the Dover trial testimony and the attendant negative publicity. Meanwhile, young earth creationists had become a growing market for homeschooling teaching materials (Gaither 2009). Science curricula for this market tend to be distinctive since objections to public school science are a major motivation for parents looking for alternatives. Two examples illustrate how Denton’s cytochrome c argument has been uncritically adopted in this venue. Apologia Educational Ministries was founded in 1994 by Jay Wile. Wile had his Ph.D. in nuclear chemistry from the University of Rochester and became interested in homeschooling while teaching at Ball State University. He subsequently wrote or co-authored several Apologia textbooks designed for homeschooling, including *Exploring Creation with Biology*, initially published in 1998 with a second edition in 2005 (Wile and Durnell 1998, 2005). Module #9 in the text is entitled ‘Evolution—Part Scientific Theory, Part Unconfirmed Hypothesis’. Following a lengthy discussion of the distinction between microevolution and macroevolution, Wile devoted several pages to cytochrome c data under the heading ‘Molecular Biology: The Nail in Macroevolution’s Coffin’. As was the case in *Of Pandas and People*, several tables present data resulting from comparisons of various species to one member of an outgroup. In particular, horse, pigeon, tuna, silkworm moth, wheat and yeast are compared to the bacterium *R. rubrum* showing the well-known equidistance of 64–69 % (Wile and Durnell 1998, p. 297). Rather than recognize this as a well-known confirmation of an evolutionary prediction, Wile drew the customary creationist conclusion.

In other words, the data presented in Table 9.2 show none of the evolutionary relationships that should exist if macroevolution really occurred. Instead, this data seems to indicate that the bacterium is just as different from the horse as it is from the yeast! (Wile and Durnell 1998, p. 297)

After mentioning the range of amino acid differences that results when human cytochrome c is compared to that of mammals, fish, plants, yeast and bacteria, Wile claimed that this confirmation of evolutionary expectations is an exception.

This table, or something like it is often presented as strong evidence for macroevolution. There’s only one problem. Much like the evolutionary sequence of the horse, evolutionists know this is a big lie! In order to construct this table, macroevolutionists must *ignore 99 % of the data* from molecular biology and choose only the 1 % of the data that agrees with their hypothesis. Then, they usually

proceed to tell the reader that this kind of data is typical of the data from molecular biology! (Wile and Durnell 1998, pp. 298–299).

The allegation that molecular biologists are forced to lie about their data was a point of emphasis for Wile.

Once again, we see that those who believe in macroevolution are forced to lie in order to make their case look stronger than it is. The data from molecular biology clearly wipes away any hope of being able to relate species in some sort of macroevolutionary framework. Those who really want to believe, however, simply discard the data that disagrees with what they want to believe and concentrate on the tiny subset of data that agrees with their preconceptions. Clearly, this is not real science! (Wile and Durnell 1998, p. 299).

This claim was repeated in a dramatic fashion in a lecture recorded at Monroe Community College in Rochester, New York on March 11, 2005 (Wile 2005). Although the references to lying were dropped for the 2005 s edition of *Exploring Creation with Biology*, very little else from the cytochrome c discussion was changed. A new concluding sentence simply asserted that ‘the data from amino acid sequencing provide strong evidence against macroevolution’ (Wile and Durnell 2005, p. 289). The contrast between Wile’s claims and the actual historical record is of course glaring in its inaccuracy. Cytochrome c data of the type cited by Wile has held a prominent place in the scientific literature for five decades. In June of 2008 Apologia Educational Ministries was purchased by Rachael and Davis Carman along with the copyright to its textbooks which continue to be widely used. Jay Wile remains active in the textbook industry, specializing in science textbooks for elementary school children.

To cite a second example from the home schooling domain, The Parent Company includes in its mission statement the goal ‘to build a Biblical Framework for all of education based on God’s word and God’s relationship with man’. In particular, The Parent Company provides ‘Biblically-based learning materials’, primarily for home schooling (The Parent Company 2003a). These materials include an on-line textbook, *The Creation Explanation*, by Robert E. Kofahl and Kelly L. Segraves, listed as a resource that ‘presents an impressive array of data from the natural world for anyone who seeks a valid alternative to the theory of evolution’ (The Parent Company 2003b). This online edition is a revision of the earlier 1975 publication of the same title (Kofahl and Segraves 1975). Kofahl had earned his Ph.D. in chemistry from Cal Tech in 1954. In 1972, after a teaching and administrative career at Highland College in Pasadena, he became a science coordinator for the reorganized Creation Science Research Center (CSRC) in San Diego (Morris 1984, p. 234). The Center had been created in 1970 through the efforts of Henry Morris, Nell Segraves and her son, the Southern Baptist minister Kelly Segraves (Toumey 1994, pp. 103–112). Although the Segraveses had been early collaborators with Henry Morris to create the CSRC, their disagreement over policy in 1972 led to Morris starting his own much more successful Institute for Creation Research (ICR). Kofahl was recruited by Segraves at that point and they published *The Creation Explanation* soon thereafter. Due to their disparate backgrounds, it can be inferred that Kofahl was responsible for the technical content of their joint publication.

Their book included a brief discussion of cytochrome c data, primarily in response to Richard Dickerson’s 1972 *Scientific American* article (Dickerson 1972). Kofahl argued that a largely invariant section of the cytochrome c amino acid sequence was a result of designed creation rather than natural selection. In 1983 Thomas Jukes wrote a refutation of this argument by pointing out how it would be expected that some amino acids in the sequence could not vary without disrupting protein function (Jukes 1983). Following Denton’s publication in 1985, Kofahl and Segraves dropped most of their earlier criticisms

and concentrated on Denton's argument for their online version of *The Creation Explanation*. Chapter 7 of the online textbook is entitled 'Beliefs and Interpretations of Evidence', and includes a section titled 'Comparative Molecular Structure and the Theory of Molecular Homology and Molecular Evolution'. After stating their opinion that 'Michael Denton has presented the most telling criticism of evolutionary trees based on protein sequence data', Kofahl and Segraves reproduced a version of the relevant data, listed as adapted 'by permission from Denton', and concluded that

... it is evident that the amino acid sequence of the *cytochrome c2* molecules of all of the species in all of the groups of organisms are equally isolated from that of the bacterium *R. rubrum*. Thus there is no basis in this data to indicate that any group is intermediate between other groups. All are equally isolated from all other groups. This data supports the biblical record of creation of each "kind" separate from all other "kinds". (Kofahl and Segraves 2003).

Once again the claim that there should be an 'intermediate' protein between extant forms of cytochrome c is drawn directly from Denton and is strikingly analogous to Cameron's demand for a crocoduck as an intermediate form. There is no indication that Kofahl was familiar with any of the cytochrome c research dating back to the 1950s. Denton's claims about the implications of equidistance were simply repeated and translated into the biblical concept of specially created kinds.

Christian Schwabe, professor of biochemistry and molecular biology at the Medical University of South Carolina, provides an example from a non-creationist perspective. Schwabe is responsible for what he calls the genomic potential hypothesis of evolution (Schwabe 2000). In a 2001 publication he used Denton's argument as evidence that species are not related through common ancestors but have developed independently ever since their pre-biotic chemical origins. 'If one uses bacterial cytochrome as a basis of comparison, it becomes quite obvious that there is no continuous gradient of relatedness from yeast to mammals' (Schwabe 2001, p. 88). Schwabe included a modified version of one of Denton's own diagrams to illustrate their shared interpretation.

Compared to the young earth creationist position, Schwabe's view has not attracted a wide following. Much more influential in this regard would be Jonathan Sarfati, a well-known author and spokesman for Creation Ministries International. His 2002 publication, *Refuting Evolution2*, was written in response to two fairly high profile productions, a 2001 Public Broadcasting Service television series, 'Evolution', and a June 2002 article in *Scientific American* by the editor John Rennie (Rennie 2002). Rennie included a brief discussion of molecular clock evidence for common descent and Sarfati responded by uncritically citing Denton.

Actually, the molecular clock has many problems for the evolutionist. Not only are there the anomalies and common designer arguments I mentioned above, but they actually support a creation of distinct types within ordered groups, not continuous evolution, as non-creationist microbiologist Dr. Michael Denton pointed out in *Evolution: A Theory in Crisis*. For example, when comparing the amino acid sequence of cytochrome C of a bacterium (a prokaryote) with such widely diverse eukaryotes as yeast, wheat, silkworm, pigeon, and horse, all of these have practically the same percentage difference with the bacterium (64–69 %). There is no intermediate cytochrome between prokaryotes and eukaryotes, and no hint that the "higher" organism such as a horse has diverged more than the "lower" organism such as the yeast. (Sarfati 2002, p. 114).

Once again, this example is striking in its close resemblance to Cameron's demand for an 'intermediate' between crocodiles and ducks. Sarfati's references to prokaryotes and eukaryotes of course provide the key to his argument's fallacy. He could safely assume that his intended creationist reading audience would not understand the branching nature of common descent and would think that it involves a linear progression from bacteria

through the sequence of increasingly ‘higher’ eukaryotes he lists. From an evolutionary perspective there are no ‘higher’ or ‘lower’ modern species since all have been evolving for the same period of time. In particular, all the eukaryotes Sarfati mentions have been evolving for the same time since the initial divergence of eukaryotes from bacteria.

One final example follows the same pattern of unreflective citation by a young earth creationist. In 2009 ICR announced that Nathaniel T. Jeanson had joined its staff as a Research Associate after receiving his Ph.D. from Harvard Medical School in cell and developmental biology. According to an ICR biographical summary, Jeanson was home-schooled until high school using an educational curriculum that included ICR materials. He describes himself as a ‘second generation creationist’ who, upon graduation from the University of Wisconsin-Parkside, decided that Harvard Medical School ‘sounded like it would be useful for credentials and evangelism’ (Dao 2009).

On August 16, 2009 Jeanson presented a Boston lecture sponsored by Calvary Chapel in the City. His talk included discussion of cytochrome c data and because this part of the lecture was video-taped, it became a subject of internet discussion. After calling attention to the equidistance of insects to vertebrates together with other similar examples, Jeanson made the truly outlandish comment that ‘We can’t say that we are closer to, let’s say, chimps than we are to yeast, because chimps and humans are equally distant from yeast’ (Jeanson 2009). He then tried to support this amazing *non sequitur* by partially quoting Denton’s 1985 claim that the equidistance of eukaryotes from bacteria ‘must be considered one of the most astonishing findings of modern science’. Several examples of the usual equidistance phenomena were drawn from Denton’s version of the *Atlas* data and cited as anomalies rather than the confirmed evolutionary predictions they actually are. Jeanson followed up on his lecture by writing a series of articles for ICR in their Acts and Facts series. For example, in ‘Molecular Equidistance: The Echo of Discontinuity?’ Jeanson applied the same erroneous interpretation to cytochrome b data:

As demonstrated by the comparisons of yeast to every other creature in the table ..., the yeast *cytochrome b* cannot be arranged in any sort of hierarchy with the other creatures; yeast is *equidistant* from all other creatures. Hence, it appears that yeast *cytochrome b* is isolated, separate, and completely distinct from all other species in the table—it is as close to beetles as it is to humans! In a sense, yeast appears *discontinuous* from the other creatures in the table. This is consistent with the predictions of Genesis 1. (Jeanson 2011).

Jeanson thus takes his place in a long lineage of anti-evolutionary spokesmen reliant upon a misinterpretation traceable back to Denton. The destructive potential of the argument lies in its initial plausibility to anyone not familiar with the relevant science. The argument trades upon a false intuition that modern species represent discrete stages in a linear evolutionary history in which these stages have not changed since their emergence. Calling attention to the close analogy to Cameron’s crocoduck makes the fallacious nature of the molecular argument clear and directs attention to the branching lineages that actually are implied by common descent.

6 Conclusion

It is useful to see how a specific creationist argument originates and diversifies through time. All too often arguments of this nature are encountered shorn of their history. This gives the false impression that they are each based upon a novel discovery of weakness or anomaly in evolutionary theory or data. Instead, these arguments often are simply repeated from prior sources without critical analysis. In the case under discussion, Gish, Jeanson,

Kofahl, Sarfati, Schwabe and Wile, as well as the authors of *Pandas*, all had doctorates in a scientific discipline and were in a position to see the fallacy of Denton's equidistance argument. Of these, only Gish went extensively beyond Denton's initial objection and included discussion of mutation rate issues. Everyone else primarily repeated Denton's misleading call for 'intermediate' amino acid sequences and tried to leave the impression that this was a conclusive refutation of common descent. In this respect the unfortunately insular nature of creationist literature is apparent. Without the benefit of neutral peer review, the habit of uncritically repeating fallacious arguments as long as they have the desired outcome goes unchecked. The publicity of the Dover trial did result in the removal of Denton's argument from subsequent intelligent design literature. Nevertheless, young earth creationists such as Wile and Jeanson continued to repeat the argument in its most simplistic form for years thereafter. The argument was still in circulation when Cameron made his plea for a crocoduck in 2007.

Although one might hope that the argument now will gradually disappear, it is more likely that science educators will continue to encounter it in the future. As has been emphasized in the science education literature, the encouragement of accurate 'tree-thinking' clearly is still needed to derail inappropriate expectations that evolutionary change takes place through a ladder-like progression of fixed stages, either morphological or molecular. Hopefully discussion of the crocoduck fallacy can act as a useful pedagogical prompt in this effort, particularly since both the crocodylian/bird divergence and cytochrome c amino acid sequencing are such high profile scientific topics with such thorough documentation.

The last word should go to Emile Zuckerkandl, one of the first to propose the idea of the molecular clock. Although his comments are directed at proponents of intelligent design, they apply to the young-earth creationists under discussion as well.

As one continues to be faced with the task of sorting out the curses and the blessings of faith, "intelligent design" plays the role of offensive little swarms of insects that more and more fill the air and must be taken care of by spraying biological knowledge before they multiply explosively and threaten civilized life—or its possibility; only its possibility: one must indeed recognize that nobody quite has civilization—apparently because the Great Designer has failed to design humans that, en masse, would do better than produce it in tainted varieties. That is no excuse for losing the measure of civilization we have. (Zuckerkandl 2006, p. 15).

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