

Talk # 2 Geological Record and Phylogenetic Evolutionary Tree

Introduction: Introduce situations or challenges regarding your topic that teachers, chaplains and pastors will be facing in the South Pacific.

The geologic column is the layered stack of rock whose relative sequence is maintained around the world; though the sequence, in its *entirety*, is not present in any *one* place in the world. In much of the column are the fossil remains of once living organisms, many that are different from the organisms alive today. Based on radiometric dating, secular geologists and paleontologists speculate that the significant portion of the column that contains fossil began to be deposited over 540 million years ago, with the ages of the rocks mostly becoming younger and younger as you move up through the column until the “modern age” of deposition. The ages are determined by radiometric dating.

In the early 1800s, Charles Darwin postulated that organisms with very similar features were related. He hypothesized that their *different* characteristics arose over time based on the demands of the environment and competition. He then extrapolated that idea into the theory that *all* organisms evolved from an initial single, simple, universal common ancestor, and that this initial organism, given enough time, random genetic changes, and competition, evolved into the animal forms found in the fossil record and all living diversity and complexity of living organisms that we see on our planet today.

Thus the “evolutionary tree” was brought into existence as the only diagram in Darwin’s book “*On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life*” published in 1859 (Figure 1). Darwin’s original diagram meant to demonstrate “how the degree of similarities between a number of varieties and species is explained by descent from common ancestors” (Overview of Illustrations, Darwin Online).

The tree in Darwin’s book showed how his hypothesis might have played out through time. Darwin’s theory started with a single organism, (though the diagram in his book represents some time after this single organism and contains postulated timelines for at least two different organisms); some organisms branched into different forms with derivations of the original form; some branches ceased, while others continued to grow upward (upward indicates time progressing toward the present, and downward represents times more distant in the past) with a potential of increased complexity. The diagram is Darwin’s hypothesis in *visual* form.

The theory of evolution as an explanation for the origins of living things on earth is nearly the exact opposite of the narrative on the origins of life on this planet as described in the bible. Darwin’s theory gives credit for diversity and specialization to competition and death, while the Bible says that a large number of organisms, with significant diversity in body plan and adaptation to unique environmental niches, were brought in existence in a time frame of only two days though the spoken Word of God, and that death was never a part of the original earth and its biodiversity. The Bible further claims that sometime after creation all organisms with breath in their nostrils were destroyed by a global flood within a time frame of a single year. If

young students are taught to believe in the absolutism of evolution (regardless of its many scientific challenges, some of which are presented below), logic will eventually demand that the young person also give up their belief in God as Creator. Thus the individual will have rejected God's *self-revelation* of this aspect of His divine character and actions, leading the student to completely reject the entirety of the testimony of scripture in favor of naturalism, to their eternal loss. With this in mind, it is part of the privilege of bible-believers to proclaim, along with the first angel, the loud cry that the end of time is coming, judgment will be passed, and *now* is the time to worship God because the biblical narrative is true – God IS *our* creator, as well as the creator of the heaven and earth, the seas and the fountains of water.

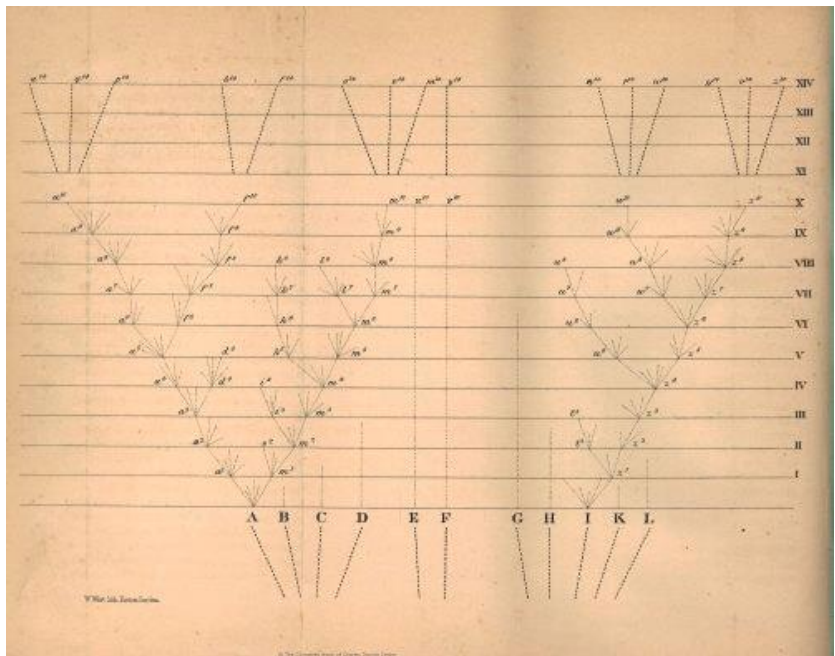


Figure 1. Taken from Darwin, C. R. 1859. *On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life*. London: John Murray. [1st edition]. "The *Origin of species* only had a single illustration, this lithographic diagram by William West demonstrating how the degree of similarities between a number of varieties and species is explained by descent from common ancestors." (Overview of Illustrations, Darwin Online)

Body: Provide the scholarly and technical content which will explore the issues and develop viable solutions and strategies.

Phylogenetic Trees. Through the years, the phylogenetic tree, a visual representation of evolution, has been updated from Darwin's original illustrations in his manuscript. At least some rendition of the "tree of life" can be found in all biology textbooks at nearly every educational level. In the phylogenetic tree below (Figure 2), living organisms are represented, and those thought to be more closely related appear closer together in the diagram (extinct organisms are excluded). For a more detailed explanation of phylogenetic trees, see appendix A.

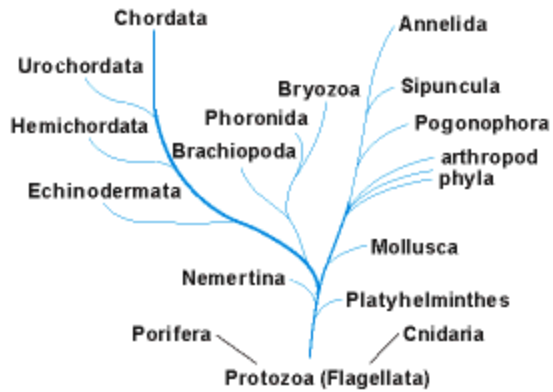


Figure 2 Taken from Valentine & Thomson, *Animal Evolution*, Access Science
 “Phylogenetic tree depicting the possible relations among the animal phyla. The branching pattern is constrained by models of development and of body-plan evolution and by molecular data. Branch length is not drawn to scale.”
 (Valentine & Thomson, *Animal Evolution*, Access Science)

When the evolutionary phylogenetic tree was initially introduced it was a mere hypothesis of Charles Darwin. It was Darwin’s hope that discovery

of more and more paleontological data would support his conclusions, but he did state that, “If numerous species have really started into life at once, the fact would be fatal to the theory of evolution.” (Darwin 1859). The present situation in paleontology is that ongoing and abundant discovery of more and more fossils has *not* supported the Darwinian hypothesis. Instead of evidence for a single, or even a few, organisms at the lowest layers of the geologic column (presumably the very oldest), we find the presence of up to 30 phyla animal phyla suddenly present in the very oldest rocks that contain fossils. This is known as the “Cambrian Explosion” and has been an enigma to evolutionary paleontologists for many, many years (Morris 2006). It is a time “when practically all major animal phyla started appearing in the fossil record” (Wikipedia “Cambrian Explosion”).

“Were Darwin to emerge today from Westminster Abbey no doubt he would be gratified by the progress made. New insights into metazoan phylogenies, radiometric dating and exceptionally preserved fossils have greatly extended, and occasionally refined, our thinking. Progress, therefore, is palpable, but in briefly reviewing this demandingly large area I will suggest that much remains conjectural, some areas of received wisdom may require re-examination, and most significantly a comprehensive explanation for the Cambrian ‘explosion’ eludes us, but not for reasons we might imagine.” Simon Conway Morris, 2006

The Figure 3 below, taken from Dr. Leonard Brand’s book *Faith, Reason, and Earth History* shows the evolutionary prediction versus what is actually found in the fossil record. As you can see, the postulated single organism is not present. Instead, there is the sudden appearance of over many organisms. These organisms are said to appear “suddenly” because there is no fossil evidence of evolutionary ancestors present in the rocks *below* that could be ascribed as ancestors of the organisms found in the Cambrian rocks. Note that biologist currently recognize only about 31 phyla of animals, 14 phyla of plants, and 8 phyla of fungi. So the reality of the presence of 30 phyla of animals represented in the very lowest rock layers is a major challenge to the prediction of evolution and Darwin’s postulated evolutionary tree. I want to be transparent, so I want to note that some of the organisms at those low rock layers are also very simple representatives of the various phyla, at least for the phylum Chordata. Humans are

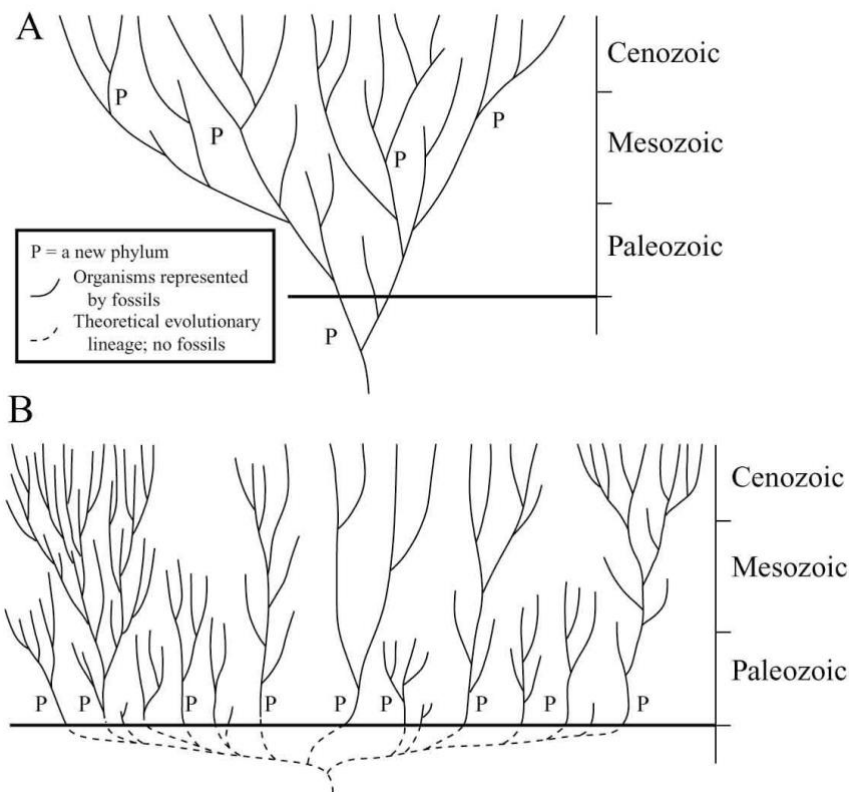


Figure 3. Taken from Brand and Chadwick, 2016 Faith, Reason, and Earth History. “(A) A reasonable expectation for the pattern of evolution, with small changes gradually resulting, through time, in the origin of new phyla. (B) The pattern actually seen in the fossil record, with virtually all phyla present in Early Cambrian sediments. The diversity of phyla is highest at the beginning of the fossil record. This is compatible with independent origins or major groups, followed by speciation within the groups.”

grouped in the phyla “Chordata,” meaning that at minimum, we have a flexible rod supporting our dorsal side. The chordate found in the Cambrian is not a human, or even a reptile, but rather a very small fish-like animal, that doesn’t have vertebrae (At least, not that

paleontologists can tell from the fossil) but indeed appears to have a supportive flexible rod on its dorsal side. Finding this simple example of a chordate in the lowest rock layers can, however, correspond with a flood-like scenario where less intelligent, less motile animals in the very lowest elevations in the oceans were the first to be buried by the oceanic mudslides that likely characterized the initiation of Noah’s flood. Though I will note that finding the simplest representatives of a phylum in the lowest rock layers, is also data utilized by evolutionists to show that the “simple came before the complex” in geologic column and therefore in all phylogenetic trees of life. The point of my noting this is to convey that there is no evolutionary pre-chordate anywhere in the rocks beneath the Cambrian. Nor are there any other organisms that could be ascribed as an evolutionary ancestors to any of the other 29 phyla found in the Cambrian; the animals all suddenly appear which is exactly the situation that Darwin said would negate his theory; and this is exactly the data found in the rock record.

To address the “simple to complex” ideology of the geologic column. The reality is that the organisms that we find at the lowest rock layers are seemingly fully functional and equipped with exquisite cell morphology and function equal to the most complex modern organisms. Take the trilobite as an example



Figure 4 (A) Trilobite (Google Images) (B) Trilobite eye (Taken from Clare Toney, <https://depositsmag.com/2016/11/01/unravelling-the-wonders-of-trilobite-eyes/>)

“Trilobites are a group of extinct marine arthropods that first appeared around 521 million years ago, shortly after the beginning of the Cambrian period, living through the majority of the Palaeozoic Era, for nearly 300 million years” (What are Trilobites, University of Oxford).



Figure 5 Trilobite and other arthropod eyes. https://commons.wikimedia.org/wiki/File:Arthropod_eyes.png

Trilobites are found suddenly and near the base layer of fossil-containing rocks (Cambrian). There is nothing found lower in the rock layers that could be an ancestor of this animal. As you can see from the figure, the trilobite possesses a multi-faceted eye, which compares almost exactly to the modern fly's eye. We know that each facet of a fly's eye has its own lens and its own associated neuron that collects and transmits information from that particular facet to a processing center in the fly's brain. Neurons are the most complex of *any* living cell, and here we find them at the earliest layers of the geologic column, fully formed and presumably fully functional as these animals are pervasive in rock layers evolutionarily estimated from 521 to ~200 millions years ago (this translates to a creationists perspectives as a THICK layer of sediment. There appear to have been millions and millions of trilobites killed during the flood – they were a very common animal!) Additionally, fossils of trilobites are found around the world (What are Trilobites, Oxford University), so we can assume that in order for this animal to be so prevalent, they most likely had functional eyes. The point of my noting this is to convey that the most complicated cells known to modern science are found in the lowest layers of the fossil record – which does not support the “simple to complex” evolutionary model.



Figure 6 (Top) the author's children in early 2023. (Bottom) the author's son and husband in early 2022.



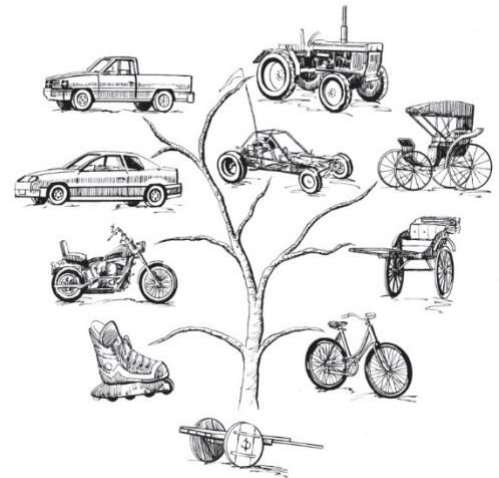
Comparing sequences from different species. The act of comparing DNA or protein sequences of different species is the very basis of phylogenetic tree generation. The updated evolutionary theory claims that DNA sequence similarities between similar looking and acting organisms, and the large portions of DNA that appear to be unused in higher level animals, are evidence of evolutionary history. That is to say, from an evolutionary perspective, in almost every case where there is *similarity*, there is the assumption of *relatedness*. This is different from a creationist's perspective, where we do not feel that it is necessary to assume relatedness just because of similarity (e.g. My children are related to each other, the fact that they LOOK alike supports this reality. The fact that my children *look* like my husband supports the fact that he is indeed their father. The point of my noting this is to convey that it is also true

that two people can look very much alike, but also not be related at all.) Evolution essentially claims that similar looking organisms must be related, except when they are not.* *This usually happens when two very similar looking organism actually turn out to have very different genomic sequences. So the “rule” of “relatedness-based-on-similarity” that is applied to fossil remains turns out to be applied only *most* of the time; remembering that we thus far have not gotten DNA sequences for fossils, so relatedness-based-on-similarity is the only rule ever applied to these animals.

When we begin to compare sequences, either DNA or protein, between different species there actually are a lot of areas that are more supportive of a creationist worldview rather than an evolutionary worldview. The main point they consider is that similarity in sequence or form denotes relatedness. In response to this, and based on how we see intelligent *human* engineers work, the creationist says that similarity in sequence or form denotes the necessity of similar

function, and doesn't have to imply relatedness, using an example we actually see in real life (empirical evidence) we can compare wheeled vehicles and see how they have changed through time. One could logically make a phylogenetic tree (Figure 7 Brand 2006) of these forms and rightly see how they have changed over time. But in our experience, we know that these are not related, but improvements made on a *common functional theme* by intelligent human engineers. Could animals not be the same, regardless of the fact that they can reproduce, while vehicles cannot? Below are some data that creationists can consider as we look for evidences of creation in the human genome and in sequence comparisons.

Figure 7



1. Different DNA/protein sequence comparisons give different phylogenetic trees. For example, when comparing rRNA sequences for a group of organisms you might get a different phylogenetic tree than when comparing glucose transporter genes for the same group of organisms. So the phylogenetic tree (and supposed most closely related organisms) generated from sequences of a specific protein might not match a phylogenetic tree based on a different protein, or a cladogram based on *structural* similarities.

In my own research I generate and look at phylogenetic trees all the time. The trees are very helpful. But my reason for generating the trees is different than an evolutionary biologist; the point of generating and studying phylogenetic trees is based on a *functional* premise. When we are seeking similarity in sequence, or three dimensional configuration (the similarity in *theme* as discussed below), we are looking for similarity in *function*. Much molecular biology is wrapped up in trying to figure out the puzzle that is the cell, tissue, organ, and organismal function: What is the *function* of the structures and proteins that we find in each system. If some other researcher has already extensively studied a protein very similar to what I am researching, there is a very high probability that what they have discovered about their protein also applies to the protein I am studying – saving me hundreds of thousands of dollars and potentially years of research. Instead, I can generate a phylogenetic tree, establish which proteins are most like the one I am studying, then look up the published papers on those proteins to discover what is already known about their functions. Of course, most researchers also assume relatedness when they are studying phylogenetic trees, but the reality is that the data merely shows similar sequences, and says nothing about whether the organisms are related or not. Creationists traditionally have concluded that living things on this planet share *structural* and *sequence* similarities because of the need to have similar *functions*, and that these similarities point to a *common shared Creator* of us all who

cares for us; a Creator who also placed humans and the animals in similar environments in which to live, thus necessitating the need for similar *functions*. For additional comments on phylogenetic trees varying when different sequences are used, see appendix B.

2. DNA sequences are very similar between very disparate organisms (ie “humans share 60% similarity with banana trees,” we are also 60% similar to fruit flies; see Figure 6). Evolutionists and creationists agree this is because of the need for *similarity in function of the cell*. Every living cell must carry out a certain number of functions to maintain its life, whether that is a plant cell, a human cell, or a fruit fly cell. Similar functional requirements yields similar DNA sequences!

“Sequence similarity” is a nuanced phrase because often you are considering genomes of different sizes, or only comparing coding regions. Take a look at the sentences below:

“If it doesn’t have a tail it’s not a monkey, it’s an ape.”

“If it doesn’t have a tale it’s not a story, it’s a quote.”

“If the prose fails to convey a moral, is it anything more than random words?”

Imagine that the sentences above are DNA sequences. Clearly the first two sentences are most similar, with the same numbers of words, many identical words, even though they don’t have the same total number of letters. In the computer program algorithms that generate phylograms, these sequences would be grouped closely together. You can see that the last sentence is longer, with divergent numbers of words and letters. Yet the last sentences deals with a similar *theme* as the second sentence. In computer algorithms that groups together *functional* domains, it is likely that the last two sentences would be grouped more closely together. All of these types of nuances need to be competently considered when comparing sequences. And these differences are very like what you might find when comparing DNA sequences of different species. So when we say something is 90% similar, or 40% similar, the real meaning can be much more nuanced than what a first glance might suggest.

Note the lower right hand corner of Figure 8, “It’s important to note that genes make up just 2% of DNA. Therefore, something that is 50% genetically similar to you may only share a fraction of your DNA.” This statement indicates that when the words “Chimpanzees are 98% similar to Humans” are stated, that they are only comparing the *coding* sequences of our DNA. The coding sequences (genes) are the specific areas in the long string of DNA that are the templates (codes) for building something else, like a protein, or functional RNA strand. We will consider the other 98% of DNA in humans that are *not* genes further below.

How Genetically Similar

Are We To Other Life Forms?

Of the 3 billion genetic building blocks that make us living things, only a handful are uniquely ours. **Humans are 99.9% genetically similar to one another, but what about other non-human life forms?**

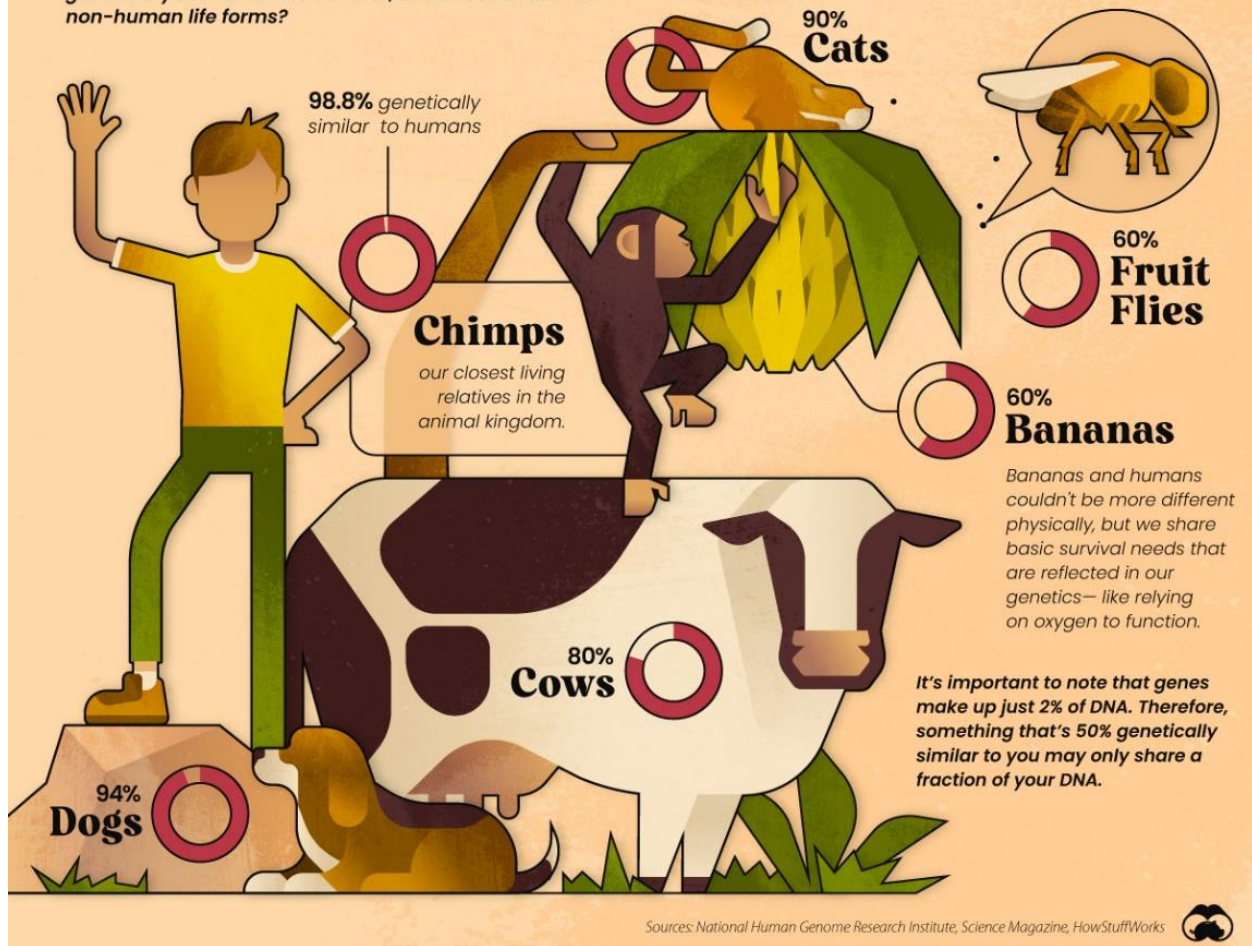


Figure 8 (taken from Ang, Visual Capitalist, 2021)

I want to take a tangent here and mention a very, very significant point regarding chimpanzee and human genetics. The genomes of humans and chimps are said to be 98% similar, and our common ancestor is said to have lived 5 million years ago. However, there is a significant point that is never included in this story that was discovered in 2010: while human and chimpanzee *somatic* chromosomes (non-sex; anything other than the X and Y chromosome) *do* appear to be very similar, the Y-chromosome of chimpanzees and humans are so very different that the researchers doing the work were astounded. In fact, they indicate that if only the Y-Chromosomes were compared, humans and chimpanzees are as *diverse* (or *only as related*, per

evolution) as a human and a chicken (Hughes et. al., 2010), which is fairly astounding as evolutionists believe chickens are the living descendants of theropod dinosaurs! So take a moment to think through the implications of such a reality. According to evolutionary theory, humans and chimpanzees shared a common ancestor only 5 million years ago. Our genes are very similar (though we will talk about non-coding regions below), but the male Y-chromosomes between humans and chimpanzees are so different that sequence comparisons would never would suggest evolutionary relatedness! So if the Y-chromosome is so dissimilar, then that throws the entire “relatedness” argument into serious doubt. In Figure 7 you can see a linear, 1:1, comparison of human and chimpanzee Y-chromosomes; beside it you can visualize a linear 1:1 comparison of the human and chimpanzee Chromosome 21 sequence indicating very similar sequence and congregation of the genes on the 21st chromosome. There is hardly any similarity in the human and chimpanzee Y-Chromosomes. In response to this publication, it was suggested that the Y-Chromosome might be especially subject to mutation, which might be able to explain away the variability between chimps and humans. However, a study in 2000 had already shown that the exact opposite is true. The human Y-chromosome is actually specially *protected* from mutation and shows a much lower variability between human males than would be predicted based on variations found between the other portions of the male genome (Underhill et. al., 2000). Therefore the reality of the human and chimpanzee Y-chromosomes being completely divergent from each other throws the entirety of evolutionary suggestion of a shared common ancestor into doubt.

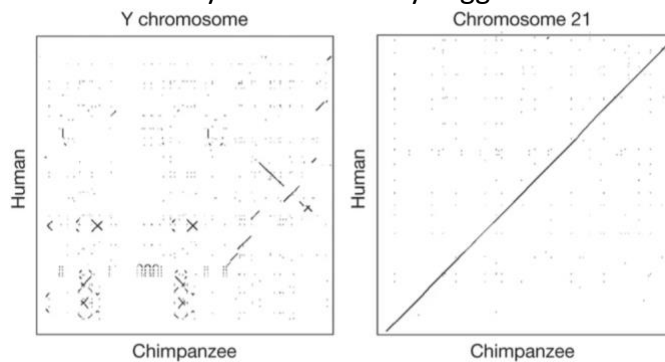


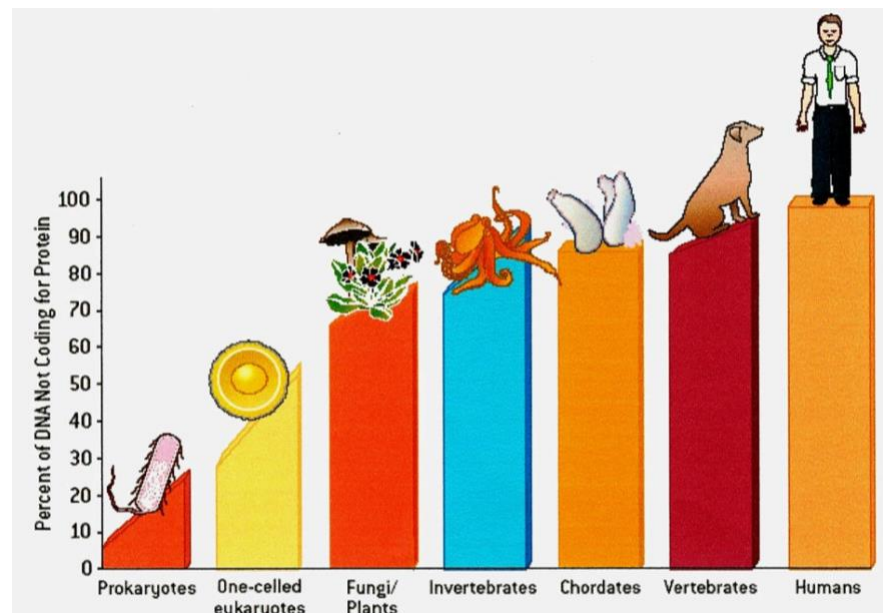
Figure 9 taken from Hughes et. al. 2010 “Dot plots of DNA sequence Identity between chimpanzee and human Y chromosomes and chromosomes 21.”

3. Much of the human genome does not actually code for a protein, instead over 98% of the human genome is “non-coding.” These non-coding regions have been referred to as “junk” DNA (some portions are also “pseudogenes.”) Since its discovery, non-coding DNA has been touted as a very strong evidence for evolution, and has been explained as 1) remnants of once-functional genes that have mutated away from functionality and have become artifacts of human’s own ancient evolutionary past, but 2) can now serve as source material for new mutations that will generate new adaptations that one day will move the species *Homo sapiens* to its next evolutionary step. This realization fueled evolutionists to increased mockery of creationists and unfortunately has caused many creation believers to lose their faith over the years.

So let's first apply a tiny bit of common sense to this argument – do you really think 98% of your DNA is junk? Would you be willing to remove and throw away 98% of your DNA? If most of our DNA was unneeded, and in fact increased mutations might lead us more quickly to improved evolutionary gains, why do humans currently go to such great lengths to protect our DNA? (Sunscreen? Not-smoking? Avoiding carcinogens like radiation, tobacco, alcohol, radon, asbestos, benzene, formaldehyde, alcohol, processed meat, etc.) Would these precautions need to be so rigid if only 2% of your DNA was important?

Let's move from a mere logical approach to the suggestion that most of our DNA is junk to actual research on the subject: The Encyclopedia of DNA Elements (ENCODE) is a public research project launched by the US national human genome research institute in September 2003, (including over 400 scientists). In 2012 they published multiple peer-reviewed articles in a single issue of the highly prestigious biological journal, *Nature*. One main finding of this research was that 80% of the human genome was "associated with at least one biochemical function" (Nature, 2012). Really the human genome has very little "junk" at all. Instead, much of the functional non-coding DNA is involved in the *regulation* of the expression of coding regions. Furthermore the expression of each coding region is controlled by multiple regulatory sites located both near and distant from the gene. These results demonstrate that gene regulation is far more complex than was previously believed, and that in fact the human genome is *not* mainly composed of non-functional DNA. We now know that organisms with higher and higher intelligence also have higher and higher percentages of non-coding DNA (Mattick, 2004) Figure 10 below illustrates the amount of non-coding DNA found in different organisms.

Figure 10 Figure created by L. Brand based on Mattick 2004. "Non-coding sequences make up only a small fraction of the DNA of prokaryotes. Amount Eukaryotes, as their complexity increases, generally so, too, does the proportion of their DNA that does not code for protein. The noncoding sequences have been considered junk, but perhaps it helps to explain organisms' complexity."



4. I want to say just a little bit about genetic entropy. John Sanford, a reputed Cornell University geneticist has calculated the generational mutation rate of humans at about 100 mutations in his book "Genetic Entropy," (Sanford & Baumgardner, 2014) which is undisputed by secular geneticists. That means, you are bringing with you 100 new mutations from your grandfather, another 100 new mutations from your father, and your child will have 100 new mutations compared to you. Your child has 400 more mutations than his great grandfather. This is the falling apart of our genome: genetic entropy. Because these mutations are "near neutral" they actually are not selected against by natural selection. Even secular geneticists agree that the vast majority of mutations are deleterious (Keightly & Lynch, 2003) and unfortunately, this rate of mutation the future for humanity cannot look good, neither can our past be as long as evolution claims. We simply could not retain humanness at this mutation rate for the last 5 million years. For a well written review of this subject, please see Paul Price, 2020.

Conclusion: Provide practical strategies, applications and solutions regarding your topic that can be used by teachers, chaplains and pastors in the South Pacific.

In this paper we explored the theories and implications of phylogenetic trees. We highlighted evidence from the geologic column that supports the biblical model of species and genera origin. We saw that the record of dead organisms does not support the theory that there was a single common ancestor, instead most phyla of animals appeared suddenly in the rock record. Also the suggestion of a "simple" to "complex" phylogeny by evolutionary theory is in doubt when we recognize the extremely complex cells present in the beginning of the geologic column when comparing modern fly and fossil trilobite eyes. We also found that some of the basic tenets of evolutionary theory lack evidential support as demonstrated by investigations into genomics from the Encode Consortium project, human and chimpanzee Y chromosome comparisons, and genetic entropy.

When I approach these subjects with students, I often will say that the theory of evolution is merely a guess at this earth's origins if someone is coming from a perspective of "there is no God." And how can I blame anyone for trying to comprehend where we came from and what our purpose is? I never degrade evolutionists. But it is ok to point out that evolutionary theory fails in so many ways to account for what we actually find in nature, and therefore as a theory, it needs to be replaced. Additionally, the theory requires so much more faith than Christianity to merely get over the initial hurdle of entropy and the laws of thermodynamics and biochemistry that must be broken for life to begin in a purely naturalistic model. Also, there is every human's university knowledge that information comes from intelligent beings, and things don't "fall upwards into complexity, but fall downwards into ruin." But that Christians don't need to blindly make guesses about our origins, instead the bible tells us how things happened, and what took place. The evidence that we find in nature universally testifies that this narrative of historic events as recorded in the bible is true. I talk to my students about the great controversy, the originally created "good" on this earth, and how that is still so visible and

discoverable, but that the fall of humans into sin separated humanity from the tree of life, and sin brought degradation and death, not to mention a literally curse on the ground, animals, and plants. That this curse is also clearly evident in the natural world; and measureable scientifically.

As part of discussing the failures of evolution to account for the things we see in the natural world, I think it is important that students realize that much of the “evidences” given for evolution in text books, are instead *theories* about how things could have happened in the past, but for which there isn’t actually any data to support the theories. Most explanations are truly mere conjecture. Albeit, conjecture from a point of intelligence and ingenuity, but conjectures none-the-less. If the conjectures were actually reproducible in a laboratory in the modern age, absolutely those experiments would have been done and published, and touted (loudly)! Instead, at present, every text book only recites the one experiment done in 1950 by Miller and Urey which shows a few amino acids can be made from fundamental chemicals. But the other things that are simultaneously made during this experiment themselves testify that life could not have evolved from natural processes.

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Appendix A:

“Phylogenetic tree” is a term that includes both “cladogram” and “phylogram.” Both are tree-like diagrams that group organisms together based on physical similarities, including anatomical and genetic similarities. Cladograms do not try to show mathematical variances between groups, nor do they try show the (presumed) evolutionary process that took place, whereas phylograms often indicate an evolutionary time span between branches of the trees (Boudreau, Visible Body Online). The “time span” is a calculated number based on the sequence differences between the protein, or DNA, that is being compared. The calculation of the timespan between branches of a phylogenetic tree is based on 1) the number of variances (mutations) between the sequences, and 2) the estimated time it takes for a single point mutation to become fixed in a population. The result of this calculation is an “evolutionary” date for how long ago the two sequences were identical (or the time since there was a common ancestor). So the functional outcome of the differences between cladograms and phylograms, is that phylograms are more often built on protein or DNA sequences where variances between sequences can be mathematically measured, and assumptions about the time it takes to generate such changes can be applied, and therefore a numerical time frame generated (with presumed evolutionary consequences) based on the sequences variabilities between organisms. Conversely, relationships (presumed evolutionary relatedness) for *extinct* organisms can only be built on anatomical/morphological, or assumed behavioral characteristics, because, presumably, the DNA or protein sequences of these animals are unavailable due to the very old nature of the samples. Cladograms do not have a mathematical component attached to estimate the time it took for the anatomical structure to arise by evolution and therefore it is typically a cladogram that is used to represent evolutionary relationships between *extinct* animals as opposed to phylograms that are more often used on animals for which DNA or protein sequences are available (living organisms). When you find a tree with numbers at the branch points, those number represent the number of times (out of 100 or out of 1000) where the sequences aligned together. The computer program that analyzes the sequences compares them to each other either 100 or 1000 times, depending on what the user had requested. Therefore if you see a branch with a very high number like 94 or 967, then you know that those sequences are very similar, because 94% or 96.7% of the time, the sequences are more similar to each other than the other sequences in the group you are comparing.

Appendix B:

The point of my noting this is to convey that the phylogenetic trees I generate for the proteins I am studying are based on specific proteins and might be different if I based the tree on some *other* protein sequence or a DNA sequence. For example, I study the protein Aer2 in the bacterium *Pseudomonas aeruginosa*. I can gather the sequences of similar Aer2 proteins from *Vibrio cholera*, *Vibrio parahaemolyticus*, and *Methylomicrobium*; and I can gather the sequences for a similar protein (Aer) from *Escherichia coli*, *Salmonella*, *Shigella*, and many other organisms, and compare all of those sequences. The resulting tree probably will look different than the phylogenetic tree generated from the rRNA of all the same organisms. (Hypothetically, the tree based on Aer sequences might say that *Methylomicrobium* is more closely related to *Vibrio*, where the tree based on rRNA might say that *Methylomicrobium* is more closely related to *Pseudomonas*. Please note, I have not generated these trees, I am speaking hypothetically.) In *microorganisms*, this variance can be attributed to “lateral (or “horizontal”) gene transfer,” because microorganisms can transmit small numbers of genes between different species via conjugation, transfection, or merely by picking up new genes when they encounter DNA in their environment and incorporate it into their own genome! (that is, some microorganisms can get new DNA from some other source besides their parent) But in higher organisms, this *does not* happen. Variant phylogenetic trees from different proteins or DNA sequences between different organisms are acceptable to a creationist (because we do not assume relatedness) and an evolutionist model, but should only be acceptable to evolutionists when we are talking about *microorganisms*, but is not at all acceptable to the evolutionary model for *higher* organisms. If the organisms really are related, then they are related across their entire genomes, and they will not look related in only some portions of their genome, because that is how genetics works universally for all organisms that cannot carry out lateral gene transfer. But we DO find these types of variations in phylogenetic trees in high organisms – one of particular importance below. This reality is inexplicable in an evolutionary model.

