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TASC

TASC's mission is to rebuild and strengthen the foundation of the Christian faith by increasing awareness of the scientific evidence supporting the literal Biblical account of creation and refuting evolution.

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Review of *Replacing Darwin: The New Origin of Species* by Nathaniel T. Jeanson

By Dan W. Reynolds

Dr. Nathaniel Jeanson's new book *Replacing Darwin: The New Origin of Species*[1] was released in October of 2017. Jeanson holds a doctorate in cell and developmental biology from Harvard (2009). He joined the staff at the Institute for Creation Research (ICR) in 2009 but has since moved to Answers in Genesis (AIG) where he is a research biologist, author, and speaker. Jeanson has written numerous lay articles, book chapters, and technical papers in secular and creationist journals.[2] He has also debated several evolutionists.[3]

In *Replacing Darwin*, Jeanson shows how the known data and principles of genetics fit biblical history as understood by young earth creationists (YECs). He develops a testable model of speciation consistent with Genesis and makes predictions. Jeason provides sufficient backgrounds in basic biochemistry and genetics for non-specialists to grasp his arguments. He has uncovered interesting relationships between speciation and time for several biological families.

The book includes copious endnotes and graphical illustrations, references, a glossary, but no index.

The following review will cover the book chapter by chapter.

Chapter 1: Inevitable

Two paradigm shifts in biology were inevitable. At the time of Darwin, fewer species were known than today. Each species appeared well adapted to its particular habitat, as though designed that way. This led some to the ideas of fixity of species in adaptations and locations. Darwin said these ideas were wrong. He provided evidence for descent with modification in related species and for species migration. This appeared to overturn the teachings of many creationists of Darwin's day. Darwin speculated that all species could be explained by descent with modification from a universal common ancestor. Since the time of Darwin, science has learned of genetics and has a much broader and deeper knowledge of biology in general—knowledge that will lead to the next paradigm shift. Jeanson focuses on speciation: how it works, what affects the rate, etc.

Chapter 2: The Secret of Life

The question of the origin of species concerns the origin of traits. Mendel was the first to elucidate the principles of inheritance. Mendel found concerning traits: they remained distinct (did not blend), appeared and disappeared in family trees, came in dominant and recessive types, that maternal/paternal traits remained distinct, and the instructions for different traits are sorted independently. Mendel did not show why traits behaved the way they did. Darwin was apparently unaware of Mendel's work.

Insofar as cellular reproduction is concerned, we now know that somatic cells (non-sex cells) undergo mitosis to produce cells with a diploid chromosome number (two sets of chromosomes) while sex cells undergo meiosis to produce cells with a haploid number (single set) of chromosomes. We also know that chromosomes contain the information for traits.

Historically, scientists had to figure out if the information for traits was stored in proteins or nucleic acids. Since proteins consist of 20 types of amino acids and nucleic acids of a mere four nucleotides, many suspected DNA was a simple substrate that carried proteins where the information for traits resided. However, experiments were conducted that showed DNA did indeed carry the information for traits. Watson and Crick figured out the structure of DNA in the 1950s.

Chapter 3: Cracking the Code

We now know that DNA controls traits. In the cell, ATP is the energy currency, proteins are the workhorses, and DNA carries the blueprints. DNA is a polymer of monomer units strung together. Each monomer unit consists of ribose (a sugar), a phosphate group, and a base (purine or pyrimidine). A single monomer unit is called a nucleotide. There are four basic monomer units; they are represented

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[1] Jeanson NT (2017) *Replacing Darwin: The New Origin of Species*. Master Books, Green Forest, AK.

[2] Dr. Nathaniel T. Jeanson, <https://answersingenesis.org/bios/nathaniel-jeanson/> Accessed 2018 Jan 04

[3] See <http://tasc-creationscience.org/article/current-science-and-creation> for a summary of a debate with Dennis Venema of Biologos that took place in April of 2017.

by the letters A, C, G, and T (adenine, cytosine, guanine, and thymine, respectively). The sequence of monomers in DNA codes for amino acids in proteins using the *genetic code*. Every three contiguous monomer units in DNA (called a "codon") corresponds to a particular amino acid. In the cell nucleus, DNA is read and converted (transcribed) into a messenger RNA (mRNA), a close representation of a section of DNA. The mRNA is transported to a cellular machine called the ribosome where it is translated into a sequence of amino acids to form a protein.

A gene is a section of DNA that codes for proteins that have specific functions in the cell. There are both mitochondrial DNA (mtDNA) and nuclear DNA (nucDNA). Mitochondrial DNA was sequenced in humans before nuclear DNA.

Genomes of several organisms have been sequenced. It has been learned that only a small portion of the human genome is used to code for proteins. What does the remaining "non-coding" DNA do? Some said it was inactive, redundant, or left over from the evolutionary process. It is possible that some genes are activated by environmental conditions and not typically expressed. Scientists perform "knock-out" experiments to determine the function of DNA in non-human species. In other words, sections of DNA are removed from the genome of an organism to see what effect its removal will have. In this way the functions of sections of DNA can be determined. Comprehensive knock-out experiments for a mammal have yet to be performed, so it is premature to make the claim that the majority of non-coding DNA is non-functional ("junk"). The ENCODE project examined 1% of the non-coding DNA of the human genome for possible function. They found that at least 80% of the non-coding DNA was transcribed into RNA, suggesting function. It has been found that the non-coding regions of genomes correlate with biological complexity better than the protein coding regions, suggesting that the non-coding regions do indeed carry significant information, probably for regulatory activity. ENCODE did not look at the portions of the genome involved exclusively in development; such DNA would only have function then. The trajectory of discovery favors genome-wide functionality.

Non-coding DNA is probably involved in regulatory functions (when and how fast to make specific proteins), embryonic development, the timings of protein manufacture, stagings of proteins for construction of molecular machines, switches, etc. Some non-coding DNA is transcribed into short chain micro-RNA that binds to specific sites in DNA thereby regulating transcription of those sites. Some RNA is involved in the splicing of mRNA before it is translated in the ribosome. We are just beginning to understand the development process, how coding and non-coding DNA coordinate when, where, and how structures are sequentially put in place to produce a fully functional organism.

Chapter 4: The Riddle of Geography

Darwin used inductive reasoning when writing the *Origin of Species*. He gathered facts, then tested hypotheses against the facts to see which best fit the data. Today species are isolated globally by oceans, deserts, and mountains. In the past, animals may have migrated by land bridges no longer in existence such as between Russia and Alaska or between modern Australia and Southeast Asia. An ice age would have removed water from the oceans and exposed land bridges. Recession of the ice sheets would have covered the land bridges once more.

Descent with modification from a common ancestor can explain the global patterns of distribution. In this scenario, a common ancestor wandered to various locations. These locations then became isolated. Microevolution then produced location-specific species. Through his observations, Darwin was able to eliminate the then creationist ideas of fixity of species and location.[4]

Chapter 5: The Riddle of Ancestry

Jeanson describes the Linnaean classification system: species, genus, family, order, class, phylum, kingdom. More organisms are included in each level of classification as one goes from species to kingdom. The higher the classification group, the more diverse the organisms; organisms in a family are more diverse than those in a genus. Darwin looked at similarities and differences between organisms and assumed they were the result of descent with modification. Similar structures were said to be homologous.[5] He noted how the patterns of similarities among organisms could be grouped into nested hierarchies. He assumed the pattern was the result of what we call macroevolution, molecules to man evolution.

When selecting a hypothesis among competing hypotheses, one has to keep in mind that better hypotheses may not have yet been formulated. Jeanson shows how man-made vehicles can be arranged into nested hierarchies. Hence a nested hierarchical pattern is consistent with descent with modification from a common ancestor *and* designed objects. Hence the observation of nested hierarchies is equivocal on the origin of species and can't distinguish between evolution and design. Interestingly, the original Linnaean system was based on function, not alleged evolutionary relationships. Darwin's explanations did not eliminate the design hypothesis.

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[4] Of course, today creationists acknowledge variation within kinds, which Darwin got right, but reject macroevolution, which Darwin mistakenly embraced.

[5] However, some similarities between organisms are believed to be a result of "convergent evolution," not common ancestry. See <http://tasc-creationscience.org/article/can-nature-perform-same-miracle-multipletimes-problems-convergent-evolution>

The poor design and vestigial organ ideas from evolutionists were argued from ignorance, not rigorous research. It was thought that some organs were poorly designed and hence could not have been the work of an omnipotent and omniscient creator. It turned out that the organs in question were merely poorly *understood* and not poorly designed. The "backwards" wiring of the human eye is a good example of this.[6] Likewise, "vestigial" organs thought to be useless leftovers from evolution have function after all. Jeanson mentions the appendix, coccyx, and "whale legs" as examples here. Jeanson predicts future criticisms of design will come from the least studied areas in biology.

Jeanson discusses breeds and species. Breeds have resulted from human domestication while species are a result of natural selection in the wild. For most mammals and birds, there are usually many more breeds than species. This is because humans can deliberately select desired traits through controlled mating and isolation in a relatively efficient manner.

As stated previously, the old ideas of fixity of species and locations were falsified by the evidence. Creationists had the wrong understanding. But this did not prove universal common ancestry (macroevolution) as Darwin supposed. The Hebrew word for created kind is *min*. Jeanson says that a *min* is defined by organisms that can hybridize, probably grouped at the level of family or order. Modern creationists acknowledge descent with modification within created kinds and the potential roles of migration and isolation in speciation. Our current understanding of the variation and distribution of kinds is consistent with creationist views. Jeanson says the current evidence does not distinguish between universal common ancestry and design.

Chapter 6: A Stitch in Time

Most evolutionists put the origin of breeds back to about 12,000 years ago. There are hundreds of horse and donkey breeds, but only seven equid species in the wild. The same pattern is seen for cattle, sheep, antelope, pigs, rabbits, camels, llamas, dogs, wolves, cats, chickens, ducks, etc. Jeanson thinks it is unreasonable to assert that it only took a few thousand years for humans to produce hundreds of breeds but nature millions of years to produce a handful of species. Jeanson says it probably does not take long for nature to produce species.

There are living today 5400 mammal species, 1300 genera, and 200 families. If most vertebrate species (70,000) arose in the last 12,000 years, it would mean that 98.4% of extant vertebrate diversity arose recently. The rate at which we discover new species is much greater than the rate of speciation so that we currently do not have enough data to say if rapid speciation has occurred. The experiments that would demonstrate if rapid speciation has occurred have not been done.

Chapter 7: Turning the (time) Tables

Genetic research has shown there are DNA sequence differences due to mutations between generations of organisms. Mutations come in many forms: single nucleotide polymorphisms (SNPs), insertions, deletions, translocations, etc. The mutation rate per generation can be measured. We can get the time of origin of a mutation by comparing DNA differences between organisms and extrapolating backwards with the known mutation rate.

Many organisms have nuclear DNA and mitochondrial DNA. At present we have 6800 curated animal mtDNA sequences, 880 from mammals. We have a combined total 50,000 curated and uncurated vertebrate mtDNA sequences. We can get nested hierarchies from comparison of mtDNA sequences between different families. This result fits the expectations of both evolutionary and design models. Jeanson's model holds that variations in mtDNA sequences *within* families are functionally neutral and are simply a result of descent with modification from common ancestors. However, the differences found in mtDNA sequences *between* families he believes will show functional differences since the families don't share a common ancestor but a common designer. The evolution model, on the other hand, predicts that all mtDNA differences are functionally neutral, being due to genetic drift, not design. The potential multiple functions for proteins coded for by mtDNA have not been studied; future experiments may address this.

Jeanson examines the mtDNA mutation rate in humans. The human mtDNA mutation rate is one mutation for every five to eight generations. Evolutionists say humans emerged 200,000 years ago. Evolutionist usually hold to uniformatarianism, the idea that natural rates remain the same over time.

Creationists have performed experiments and made observations consistent with accelerated rates of change in nuclear decay, tectonic plate movements, deposition rates, and other geological processes. In other words, there are evidences that support a recent creation of the earth.

Jeanson builds his arguments assuming constant mtDNA mutation rates. Evolutionists often infer a mutation rate by considering differences in DNA sequences of extant organisms and the alleged date of speciation or lineage splitting based on standard geological dating. Few actually measure the mutation rate directly (in real time). According to evolution, *homo* diverged from chimpanzees 4.5 to 17 million years ago. We know that the human mtDNA mutation rate, measured directly, is one mutation every five to eight generations. A generation occurs every 15 to 50 years. Hence, we would expect one mutation eve-

[6] Sarfati JD (2008) Fibre optics in eye demolish atheistic 'bad design' argument. *Creation* 31(1):45–47, <https://creation.com/fibre-optics-in-eye-demolish-atheistic-bad-design-argument> Accessed 2018 Jan 04

ry 76 to 419 years. Based on the evolutionary timescale then, there should be 21,480 to 447,368 differences in the mtDNA between humans and extant chimpanzees,[7] but there are only 1483. There are approximately 17,000 base pairs in mtDNA. If evolutionists are correct about the timescale, the human mtDNA would be "mutationally saturated" or completely scrambled relative to the chimpanzee mtDNA, but there is only a 9% difference. The same problem is encountered in the mtDNA differences between Neanderthal and extant humans and between Africans and non-Africans. Consistently, actual mutation rates applied over alleged evolutionary time overestimate the actual number of mutations observed. Clearly, the results suggest either a different mutation rate or much shorter timescale. The measured mutation rates and known differences in mtDNA align well with the biblical creation hypothesis of a 6000-year-old earth.

There is evidence that African mtDNA has mutated faster than non-African mtDNA. One possible cause is that African women marry earlier. Also, there is evidence that African nucDNA mutates faster than non-African nucDNA.

It has been known for years that human mtDNA differences divide into three major groups designated L, M, and N. L, M, and N are known as halogroups.

There is evidence that the earth was once underwater. There are marine fossils on mountains and in land-locked areas far from the sea. Some sedimentary rock layers extend over entire continents or even farther. The deposition of those layers must have been catastrophic, or there would not have been much fossilization. There are fossils of animals giving birth, of fish being eaten, etc., suggesting sudden and rapid burial. The eruption at Mount St. Helens demonstrated that sedimentary layers hundreds of feet thick could be laid down in hours to days, that canyons can be formed rapidly, how multiple fossilized forests could form as the result of a single volcanic eruption, and possibly how coal seams could be produced quickly. Recent discoveries of dinosaur soft tissue in association with intact biomolecules suggest the dinosaurs have been extinct for only thousands of years, not millions. All these observations are in accord with the Flood of Noah covering the entire earth a few thousand years ago.

Amazingly, genetics match predictions of the Flood model. Mitochondrial DNA is inherited exclusively from mothers. There were three young married women on the Ark who would have repopulated the earth after the Flood 4500 years ago. There are three major types of human mtDNA in the world! Also consistent is the Babel dispersion where one would expect sudden formation of several variants in human mtDNA due to rapid separation and isolation of various groups of people. This is what is actually observed!

There was about 1650 years from Adam to Noah's sons, 2000 years from Adam to Abraham, and 2500 years from the Flood to Jesus. From Adam to the Flood was 1700 years and from the Flood until now was 4500 years. There were probably about 10 generations between Adam and the Flood. On the mtDNA map[8] of humanity, the three major halogroups are joined by relatively short line segments, indicating there is not much difference between them. This is consistent with the three young women on the Ark, in that they came from a world where only a few generations had lived before them. From these three nodes emanate dozens of other mtDNA variants, each at a relatively greater distance than the three major halogroups. This is consistent with the dispersion at Babel where there would have been rapid dispersion and isolation of dozens of groups. Since Babel, there have been many generations accounting for the relatively larger distances between the dozens of mtDNA variants we see today and the three major halogroups from which they emerged. Incredible! The history of humanity is in our genome. What we know about the mtDNA of humans fits the 6000-year biblical timescale, explains the three halotypes, and the relative differences between pre- and post-Flood humanity.

There are some animals where the mtDNA data does not seem to fit the creation or evolutionary timescales. Examples are mice, chickens, and penguins. However, only one study has been done for each of these animals. It took several studies to get an accurate human mtDNA mutation rate.

On the other hand, the mtDNA data for roundworms, fruit flies, water fleas, and baker's yeast do fit the 6000-year timescale when divergence of genera, not families, is considered.

Hence genetics suggest a very short (6000-year) timespan for life on earth and not hundreds of millions of years. The young earth creation framework makes genetic predictions that have fit real data across very diverse organisms (six species, two kingdoms, three phyla).

Chapter 8: A Pre-existing Answer

Nuclear DNA differences are more difficult to compare across species. The nested hierarchies seen in the nucDNA

[7] Jeanson assumes the mtDNA mutation rate of chimpanzees is the same as for humans. The mtDNA mutation rate for chimpanzees has not been determined. However, the chimpanzee nucDNA mutation rate is within 12% of human nucDNA mutation rate, so the assumption is reasonable.

[8] Jeanson NT (2016 Apr 27) On the origin of human mitochondrial DNA differences, new generation time data both suggest a unified young-earth creation model and challenge the evolutionary out-of-Africa model. <https://assets.answersingenesis.org/doc/articles/arj/v9/out-of-africa/figure-1.pdf> Accessed 2018 Jan 04

are consistent with both evolution and creation models. The functions of DNA may discriminate between the two views. For the evolution model, all differences in nucDNA are due to mutations. In the creation model, differences in mtDNA sequences are due to design and mutations. When comparing DNA sequences in similar genes in different families, evolution says all differences are due to mutations, while creation says the differences were designed with distinct functionality. Another prediction involves the non-coding DNA regions: evolution says there will be much non-functionality, while creation predicts functionality for most of the genome. Results from the ENCODE project have suggested that at least 80% of the human genome is functional. These results are preliminary, but the trajectory is clear: most non-coding DNA in the human genome is functional and serves in a regulatory capacity. However, only systematic knockout experiments can fully demonstrate this.

Evolutionists say that shared pseudogenes[9] point to common ancestry. However, many alleged genetic "mistakes" have proved otherwise. One example is the alleged fusion of human chromosome 2.[10] Presumably, since most apes have 24 chromosomes and humans have 23, there must have been a chromosome fusion event in the past (since we allegedly share a common ancestor). However, the alleged region of fusion is not a scar but has been found to be fully functional.[10] The alleged fusion event was based on ignorance, not rigorous research.

The measured human and chimp nucDNA mutation rates are the same: 78 base pairs per generation. According to evolution, the human/chimp split occurred between 4.5 and 7 million years ago. The evolutionary model predicts only half of the actual differences. Hence the evolutionary model and timescale over predicted the actual mtDNA differences and under predicted the actual nucDNA differences. Whatever mechanism evolutionists invoke to explain the mtDNA results (natural selection, slower mutation rate in the past, etc.), another mechanism will be needed to explain the nucDNA results. Some have said the homo/chimp split occurred 11 to 17 million years ago, but this would make the mtDNA discrepancy even worse.

The known human nucDNA mutation rate applied to the last 200,000 years (alleged time of the emergence of *homo sapiens*) greatly underestimates the actual number of mutations between humans in Africa (515,000 predicted; 4.31 million observed).

Human chromosomes differ by millions of single nucleotide polymorphisms (SNPs) between and within individuals. When DNA sequences in a chromosome pair are identical, they are said to be homozygous. When they differ, even by one base pair, they are said to be heterozygous. Inheritance, and not mutations, is the main cause of heterozygosity within individuals.

Plant inbreeding experiments showed that the nucDNA mutation decreased as the heterozygosity decreased. This same phenomenon has been observed in humans and chimps. And as the nucDNA becomes more homozygous, it becomes less probable that recombination and gene conversion will generate novel combinations of genes.

Creationists explain the mtDNA data by mutations and the nucDNA differences as pre-existing in Adam and Eve (greater than 99% of all differences were already in Adam and Eve) when they were created. The same ideas would apply to all vertebrates.

The YEC model envisions three bottlenecks: Adam and Eve, the Flood, and the Babel dispersion. Each bottleneck was followed by exponential population growth. A population bottleneck need not be a genetic bottleneck, provided there is rapid growth following the population bottleneck. A rapid population expansion results in a large number of mutations that are rare in frequency. The current nucDNA differences among humans look like the result of a recent and rapid population expansion. Both evolutionary and creation models can explain this. However, the YEC model makes testable models about the history of civilization assuming a 6000-year timescale and that all common variants trace back to Adam and Eve. The Y-chromosome (from men only) and mtDNA (from women only) can serve as molecular clocks; they can be used to look at historical migrations.

Jeanson speculates that most nucDNA differences in other species were also built-in at creation and hence will prove to have unique functionality. In contrast, evolution would predict that these differences are due to mutations only and are functionally neutral.

Chapter 9: From DNA to Visible Traits

There are 70,000 vertebrate species in 1100 families. How could tens of thousands of species form in just a few thousand years? Answer: there are an enormous number of chromosome combinations possible from a pair of heterozygous parents. All extant human chromosomes are very diverse and scrambled. For example, human chromosome #1 comes in many varieties. Mutations alone can't account for this diversity in 6000 years starting from a homozygous pair. We would expect only 15,400 mutations in humans over 6000 years. In the creation model, we can assume Adam and Eve started with roughly 40,000 heterozygous sites per chromosome.

In forming sex cells, chromosomes undergo recombination and gene conversion. In recombination, chunks of DNA are swapped between pairs of the same chromosome to generate a new combination of genes and hence traits. Gene conversion is similar but only tiny amounts of

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[9] Evolutionists believe that pseudogenes are non-functional remnants of once functional genes.

[10] Reynolds D (2015 Apr) On the origin of humans. <http://tasc-creationscience.org/article/origin-humans> Accessed 2018 Jan 04

DNA are involved. Each chromosome usually goes though a recombination event per generation while only every other chromosome undergoes gene conversion per generation. Without mutations, the DNA sequences in genes remain the same; it is the combination of genes that changes. All base pairs in a given chromosome are said to be linked. Recombination and gene conversion disrupt this linkage. In the 6000 years of biblical history, there could have been between 6200 and 39,600 linkage disruption events, assuming generational time of 15 to 50 years, in a single lineage. Hence there would have been between 135 and 498 linkage-breaking events per chromosome in the last 6000 years for a single lineage. Since there have been many lineages, the number of possible versions of a given chromosomes is huge. If each chromosome today existed in 100 versions (a conservative estimate), there would be 10^{85} number of possible chromosome combinations. In other words, if you have heterozygous ancestors, an almost limitless variety of combinations of chromosomes, genes, and traits are possible. This same thinking applies to other species.

How do some traits get isolated and become a new species? Speciation can occur when a new combination of traits confers an advantage that facilitates having more offspring relative to others or by migration and isolation of a subpopulation. Can migrations in the wild isolate populations quickly enough to produce tens of thousands of new species in 6000 years? We know breeding can do this easily. Human breeders have produced 850 horse breeds that have five to six million nucDNA differences. There are between 10 and 28 million differences in nucDNA sequences in horses in the wild. Hence, if human breeders can create so many species starting with relatively little genetic diversity, then natural selection should be able to generate a few species (seven in the case of equids) starting with relatively greater genetic potential (heterozygosity). Starting with a large diversity, many different combinations of chromosomes can be generated rapidly. Migration events can isolate subpopulations. The isolated subpopulations would become more homozygous because of inbreeding. DNA variety can be lost due to chance, infertility, small numbers of offspring, some individuals never mate, etc. The more homozygous a population becomes, the less it resembles the original population. Speciation can occur when a subpopulation has become isolated and moves towards homozygosity. The speciation process involves three steps: (1) formation of genetic distinctiveness, (2) isolation of distinct individuals, and (3) regrowth of new populations. Steps 1 and 2 may occur in any order. We have data for 300 to 400 mammal species representing 23 mammal orders concerning their gestation times, age of sexual maturity, litter sizes, and lifespans of parents. Provided that the founder couples had significant heterozygosity, generating tens of thousands of new vertebrate species in 4500 years (since the Flood) from 1100 pairs of vertebrate ancestors is feasible mathematically.

For evolutionists, the ultimate cause of genetic change is mutation. Since the mutation rates are slow and the number of differences in extant organisms are large, much time would be required to explain the current diversity. For creationists, heterozygosity (millions of differences in DNA sequences of chromosome pairs) was built into organisms from the beginning by the Creator, so long periods are not required for the production of new species. Starting with heterozygous organisms, visible distinctiveness in offspring would soon be apparent. In the creation model, recombination and gene conversion would provide many new varieties of combinations of traits quickly since the differences are already built-in. In contrast, the differences needed for speciation in the evolution model come slowly and sequentially through a mutation/natural selection process.

The 6000-year speciation model is necessary to explain the origin of the observed mtDNA differences in light of the measured mutation rate, the origin of nucDNA differences (built-in at creation), and the combination of heterozygous ancestors needed to explain the number of species within families.

Chapter 10: On the Origin of New Species

A small heterozygous population will tend towards homozygosity. When this happens, some recessive traits will be revealed. The creation and evolution models agree that all species within families share a common ancestor. They also agree that mtDNA differences result from mutations although mutation rates are disputed. We can use mtDNA differences to construct branching ancestral trees, much like a human family tree.

Consider the Bovidae family (cattle, sheep, antelope). There are hundreds of species in this family for which there is ample nucDNA and mtDNA information for analysis. There are only a few thousand mtDNA differences separating any two species within this family. We can draw a branching tree from these data. The tree shows splitting (speciation events). The distances between the splitting events (branch points) to new species are reflective of the number of mtDNA differences. A plot of the number of species (y-axis) versus the number of mtDNA differences from the tree's root (x-axis) forms a straight line with a positive slope. Assuming a constant mtDNA mutation rate, the plot shows the number of species as a function of time. Straight-line plots of this nature can be drawn for the species within many mammal families (Old World monkeys, weasel, deer, cat, dolphin, dog). What these plots suggest is that there is a constant mtDNA mutation rate *within families* and the mtDNA mutation rate *per species* decreases as homozygosity increases. For nucDNA, speciation decreases heterozygosity and hence the potential for speciation.

Most nucDNA differences between equids are homozygous within the equid species. Of the 26 million nucDNA differences between the imperial zebra and the domestic

horse, just two million are heterozygous within the domestic horse. Other species display the same pattern.

There are 16,000 species of mammals in the fossil record, but only 5400 are living today. There are 550 mammal families in the fossil record, but only 150 living now. Extinction accounts for the differences. Most families today are species-poor. Early extinction events would remove heterozygosity and hence speciation potential. This could explain why there are so many species-poor families today.

Jeanson speculates there may be a linkage between nucDNA heterozygosity and the mtDNA mutation rate.

Jeanson's work facilitates a few predictions. He predicts that the linear relationship between number of species and time discussed above will be observed in more families and that these plots coupled with measured mutation rates will reveal correct rates of speciation. Also expected is that most non-coding DNA will be functional. Differences in mtDNA sequences between families are expected to reflect functional differences and not just be due to neutral mutations. Measured mtDNA mutation rates and known mtDNA differences within families are expected to fit the creation timescale assuming a constant mutation rate and created kinds started with no mtDNA mutations.

Jeanson's book is a good example of original creationist research. He shows how operational science produces results in harmony with biblical history. He makes testable predictions. Time will tell if his model can explain new data as it comes.

ANOTHER REASON TO BELIEVE A BIBLICAL AGE OF THE EARTH

Zircons often contain a large amount of helium produced by a large amount of radioactive decay. However, these small, inert helium atoms would be expected to have diffused out of the zircon crystals long ago based on evolutionary models. Instead, the data indicate that the helium was produced recently (no more than 6000 years ago) by accelerated radioactive day.

COMING EVENTS

TASC will not be meeting in January but will resume our normal meeting schedule in February. Instead, we wish to encourage you to attend the showing of the film *Alien Intrusion* produced by Creation Ministries International. The film will show one time only on Thursday, January 11 at 7:00 PM in several theaters in the Raleigh area. For more information, go to http://www.alienintrusion.com.