DNA barcodes show gaps between species and support recent common bottleneck

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A recent publication by Stoeckle and Thaler in *Human Evolution* challenges biologists to reconsider the history of life on earth.[1] The paper, entitled *Why Should Mitochondria Define Species?*, is based on analyses of DNA barcoding data accumulated over a decade. The authors concluded that 1) there are large gaps between genetic sequences of animal species; 2) all animal species expanded from small founding populations "within the last one to several hundred thousand years". The paper has drawn some comments in popular media. How do we view these findings from a creationist perspective?

Is the gene representative?

The data used consisted of relatively short DNA sequences, and were originally not intended for studying phylogenetic relationships between species but for DNA barcoding (the identification of species), i.e. similar to the forensic analysis carried out to identify individuals. However, as millions of sequences have been deposited, Stoeckle and Thaler were able to mine the data for phylogenetic insight.

DNA barcoding in animals is most often accomplished by analyzing the mitochondrial cytochrome oxidase subunit I (COI). COI is a molecule that directly works with oxygen gas to burn food. It is located in subcellular structures called mitochondria. While most DNA in animal cells resides in the nucleus, a small fraction is found in mitochondria (figure 1). Compared to nuclear genes, small mitochondrial DNA (mtDNA) molecules are inherited via the maternal line only. They are also more stable and more similar among species, which is why they are conveniently used for DNA barcoding. This homologous nature of mtDNA lends itself well to phylogenetic analyses, which is why Stoeckle and Thaler described it as 'commeasurable'. Although the COI gene constitutes only 5% of the mitochondrial genome, and less than a millionth of the total genome of a human, phylogenetic trees based on this gene are congruent with trees based on the entire mitochondrial genome. Clustering of the COI sequences also corresponds well with holistic classifications produced by taxonomical experts, and creationist Nathaniel Jeanson finds mtDNA trees accurate and useful.[2]

All animal species experienced a recent bottleneck?

One surprising finding of the paper is that variation of the COI gene within humans and among different animal species (intraspecific variance) are similar, with average pairwise differences between 0.0% and 0.5% (0.1% for humans). Variations within species are due to mutations. Stoeckle and Thaler argued that these mutations do not affect reproductive fitness (i.e. they are neutral mutations) and are free to accumulate over time. Indeed, mutations in mitochondrial genes are more likely to be neutral compared to those in nuclear genes because the mitochondrial gene reading system is simpler and less nuanced than the nuclear system (i.e. there are fewer isoacceptor tRNAs and there is no alternative splicing). Whether the mutations are completely neutral or near neutral, natural selection is unlikely to stop their accumulation.[3]

Accumulation of random mutations can serve as a molecular clock. Even though mutation rates may vary throughout history and across species, the number of mutations is nonetheless a reflection of time. The fact that all animals have accumulated similar numbers of mutations strongly indicates that their populations grew during the same time period. Thus, Stoeckle and Thaler concluded:

> "Namely that the extant population, no matter what its current size or similarity to fossils of any age has expanded from mitochondrial uniformity within the past 200,000 years."

Stoeckle and Thaler proposed "bottlenecks, founder effects, lineage sorting, and gene sweeps" to explain mitochondrial uniformity. By lineage sorting, they meant one form of mitochondrial genome takes over other forms due to random drifting (like random loss of family names in a population), while gene sweep refers to a genetic takeover by strong positive selection. "Lineage sorting is most efficient when the population is small", and genome sweep requires that "the entire population's mitochondrial genome must re-originate from a single mother".

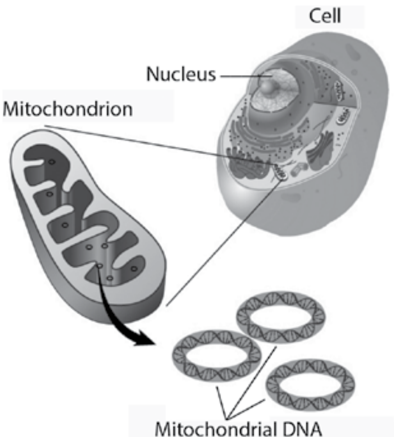

Figure 1. The cell, mitochondria, and mitochondrial DNA

Then the authors commented:

> "Not certain is whether different processes have led to a similar result throughout the animal kingdom or if a single process operates throughout. Occam's razor, the principle of parsimony, suggests that a single explanation should be considered."

Just a few years ago, the same authors were still arguing against this idea:

> "If bottlenecks limit variation, then a universal low ceiling implies recent population crashes for all species. This appears unlikely– almost a Noah's Ark hypothesis– although perhaps long-term climate cycles might cause widespread periodic bottlenecks."[4]

So, they named the elephant in the room! The data neatly fit with a young creation and a global Flood, although it is difficult to distinguish between the founder effect of creation and the bottleneck effect of the Flood, since the two events are not separated by a very long period.

Is the clock accurate?

It is impossible to determine how fast the mitochondrial clock ticked in the past, or if it always ticks at a constant rate, but we can evaluate the timeframe given in the paper based on how the clock was calibrated. Since humans and animals originated at about the same time, Stoeckle and Thaler dated animal species according to accepted human history, which is based on "full genome sequence analysis of thousands of individuals and tens of thousands of mitochondria, paleontology, anthropology, history and linguistics". Fossils played a significant part in the ultimate calibration.[5,6] Jeanson, on the other hand, estimated the age of human mitochondria solely based on observed mutation rates (5–8 mutations per generation) and found that variations of the human mitogenome agree more with a biblical timeframe of ~6,000 years than the generally accepted 200,000 years.[7,8]

Linnaeus versus Darwin

A key finding in the paper is the genetic discontinuity between species. In contrast to the low variance between individuals of the same species, the sequence differences between species are much larger. Stoeckle and Thaler wrote:

> "The clustering of barcodes has two equally important features: 1) the variance within clusters is low, and 2) the sequence gap among clusters is empty, i.e. intermediates are not found."

This is not surprising since a barcode is designed to distinguish between species. The COI gene would not have been successful in bar coding if there were significant sequence overlaps among species. However, Stoeckle and Thaler have a good reason to emphasize this discontinuity. Molecular phylogeny was designed to quantify similarities and differences between organisms, and the nature of the data has always given the impression that differences between taxa are only quantitative. (It is much harder to visualize qualitative differences in DNA and protein sequences than in whole animals.) Since many phylogenetic trees today derive from DNA sequences, molecular evolutionary studies have greatly relied upon them despite their conflicts with paleontology and other inherent discordances arising from their use.[9] However, as DNA barcodes of individual organisms accumulated, Stoeckle and Thaler were able to see that mitochondrial genomic variances are "constrained within narrow parameters".

They correctly went back to Linnaeus and Darwin as they quoted a paper by Aves *et al.*:

> "In a founding document of phylogeography, Avise and colleagues noted the long-standing divide in biology between the intellectual lineages of Linnaeus for whom species are discrete entities and those of Darwin who emphasize incremental change within species leading to new species."[10]

Starting with the *Scala Naturae* (Great Chain of Being) handed down since the days of Aristotle, Carl Linnaeus (1707–1778) wrote his *Systema Naturae*, in which he introduced biological classification and binomial nomenclature. To counteract Linnaeus' conception of discontinuity between taxa, Comte de Buffon (1707–1788) wrote *Histoire Naturelle*, advocating "imperceptible gradations" in nature.[11] The debate between organic continuity and discontinuity continues until today, as Stoekle and Thaler point out:

> "The tight clustering of barcodes within species and unfilled sequence space among them are key facts of animal life that evolutionary theory must explain."

They even proposed a hypothesis for it:

> "The variable distance between the most closely related living species presumably reflects differing numbers of *extinct intermediate sequences* [emphasis added]."

A new evolutionary law?

To Stoeckle and Thaler, extinction is an explanation of the gaps. They mentioned "a new evolutionary law" proposed by Van Valen in 1973.[12] Dubbed the Law of Extinction, it states: "All groups for which data exist go extinct at a rate that is constant for a given group."

The 'law' was mainly derived from fossil records. According to Van Valen, the extinctions were primarily due to ecological interactions between species, so the probability of extinction is independent of the age of the species. Like most others, Van Valen also believed in constant generation of species.

If no species survive long ages, all species at any point in history should appear new. However, since the law postulates that different taxa go extinct at different rates, it cannot explain why all extant animal species have comparable mitochondrial ages.

Interestingly, the Law of Extinction has gained support from contemporary biology. In his book, *Genetic Entropy*, John Sanford proposes that all species have a finite lifespan, and not due to extrinsic factors but due to random genetic mutations eroding the genome. Without constant generation of new life-forms, Sanford's theory argues against a long history of life.

More is coming?

Stoeckle and Thaler pointed out that there were still 23 phyla of small invertebrate animals where clustering of DNA barcodes was not clear, and they expect better illumination of their history as more barcoding is performed in the future.

Creationists have been trying to define the biblical concept of 'created kinds' (baramins), from which all species—extinct and extant—descended. While Stoekle and Thaler showed gaps between species of various genera, they also gave examples where interspecific variances are relatively low, such as the bear (*Ursus*) genus, which is explainable with evidences of hybridization of derivatives from one created kind. It seems that DNA barcoding data may also help further development of baraminology.

Conclusion

Stoeckle and Thaler courageously challenge Darwinian gradualism. Although the absolute ages of animal species are questionable, the consistently young mitochondrial ages are consistent with either a recent creation, or a genetic bottleneck conferred by the Genesis Flood. Not only does the paper exclude the possibility of long evolutionary ages, the findings of molecular discontinuity provide additional evidence against the classical concept of gradualistic genetic transitions promoted by evolutionists.

References

1. Stoeckle, S.M. and Thaler, D.S., Why should mitochondria define species? *Human Evolution* **33**(1–2):1–30, 2018. 10.14673/HE2018121037.
2. Jeanson, N., *Replacing Darwin: The new origin of species*, Master Books, Green Forest, AR, pp. 248–249, 2017.
3. Sanford, J.C., *Genetic Entropy and the Mystery of the Genome*, FMS Publications, Waterloo, NY, pp. 45–68, 2008.
4. Stoeckle, M.Y. and Thaler, D.S., DNA barcoding works in practice but not in (neutral) theory, *PLOS ONE* **9**:7e100755, 2014.
5. Cann, R.L., Stoneking, M., and Wilson, A.C., Mitochondrial DNA and human evolution, *Nature* **325**(6099):31–36, 1987.
6. Stringer, C., The origin and evolution of *Homo sapiens*, *Philosophical Transactions of the Royal Society B: Biological Sciences* **371**(1698):20150237, 2016.
7. Jeanson, ref. 2, pp. 182–186, 2017.
8. For a recent summary of molecular genetic evidence towards a young creation see: Tomkins, J., Empirical genetic clocks give biblical timelines, *J. Creation* **29**(2):3–5, 2015.
9. Tomkins, J. and Bergman, J., Evolutionary molecular genetic clocks—a perpetual exercise in futility and failure, *J. Creation* **29**:26–35, 2015.
10. Avise, J.C. Neigel, J.E., and Arnold, J., Demographic influences on mitochondrial DNA lineage survivorship in animal populations, *J. Molecular Evolution* **20**:99–105, 1984.
11. Sloan, P.R., The Buffon–Linnaeus controversy, *Isis* **67**(3):356–375, 1976.
12. Van Valen, L., A new evolutionary law, *Evolutionary Theory* **1**(1):1–30, 1973.