Empirical genetic clocks give biblical timelines

Jeffrey P. Tomkins

The idea of an evolutionary molecular genetic clock has significantly impacted and influenced modern biology. The technique employs biological sequence comparisons between taxa to estimate rates of evolution and is routinely calibrated with deep-time estimates taken from paleontology. In addition to this evolutionary bias, the following problems also plague its use:

1) different genes/sequences give widely different evolutionary rates,
2) different taxa exhibit different rates for homologous sequences, and
3) divergence dates commonly disagree with paleontology despite being calibrated by it.

Furthermore, because the molecular clock idea is directly tied to the neutral model theory of evolution, recent discoveries in full codon utility and pervasive genome-wide biochemical functionality utterly negate its foundational premises.[1]

What would happen if the assumption of evolution and deep time were not used to calibrate the molecular clock models? Would DNA sequence variation provide usable information to help test creationist predictions about origins? Interestingly, we have a variety cases from both secular scientists and studies done by creationist researchers where DNA clocks were measured empirically within single taxa and without deep-time calibrations and only yielded ages of 5 to 10 thousand years, not millions. Each of these different test cases will be discussed in turn below, but first let us visit the idea of genetic entropy which is closely connected.

Genomic entropy and genetic clocks

When mutational events occur during meiosis, they can be inherited and passed on to the next generation and when these are empirically measured within a pedigree, an estimate of the mutation rate can be achieved. In fact, scientists have actually measured this rate in the genome of humans in multiple studies and found it to be between 75 and 175 mutations per generation.[2–9] Using this known data about mutation rates, a variety of research groups have been able to model the accumulation of mutations in the human genome over time using complex computer simulations incorporating the standard restraints of population genetics theory.[10–16] They found that over 90% of deleterious mutations fail to be selected away even with intense natural selection. Because of this, the buildup of mutations would eventually reach a critical level and become so severe that humans would eventually go extinct at a point called *error castastrophe*.[17,18] This process of genome degradation over time and successive generations is called *genetic entropy*.[17,18] And remarkably, the process of human genome degradation is closely mirrored by the biblically documented trend of declining human lifespan, particularly in the last approximately 4,300 years since the Flood.[15,18–20] In addition to these extensive simulation studies, largely performed by intelligent design theorists, prominent evolutionists have also shown that the problem of mutation accumulation in the human genome is accompanied by the inability of selection to alleviate it.[5,21]

After the experimental results of genetic entropy in the human genome via computational simulation were published in multiple papers (cited above), their conclusions were spectacularly confirmed by two high-profile genetic studies based on empirical data that essentially provided the same results, and also within a timeframe that paralleled biblical events.[5,6] Both secular studies involved sequencing the protein-coding regions (exons) of the human genome, called the exome.[22,23] The projects examined the preponderance of rare single nucleotide variants that occur in human exomes—one study analyzed 2,440 individuals and the other 6,515. Over 80% of the single nucleotide variants in protein-coding exons were considered to be deleterious or harmful (associated with heritable disease) and researchers attributed the unexpected presence of these harmful mutations to 'weak purifying selection'. This essentially means that the alleged ability of natural selection to remove these harmful variants from human populations was powerless to do so, a finding also observed in the computer simulation models discussed above.[11,14–16]

A major analytical benefit of this type of rare variant data in the exome is due to the fact that protein-coding regions are less tolerant of mutation than other parts of the genome, providing more reliable historical genetic information about human populations. In addition, this type of data can be conveniently integrated into demographic models over known historical time and geographical space. When the researchers did this, they discovered a very recent massive burst of human genetic diversification, primarily associated with genetic entropy. One of the research papers stated: "The maximum likelihood time for accelerated growth was 5,115 years ago."[22] The other paper uncovered a similar timeline, which places the beginning of human genetic diversification close to the Genesis Flood and subsequent dispersion of people groups at the Tower of Babel. Importantly, this recent explosion of rare genetic variants clearly associated with genetic entropy also follows the same pattern of human life expectancy

rapidly declining after the Flood as mentioned above.[18,20]

Mitochondrial DNA variability and genetic clocks

One other important realm of molecular clock research demonstrating a recent creation comes from creation scientist Nathaniel Jeanson, who has been examining mutation rates in mitochondrial genomes.[24] The mitochondrial DNA molecule is typically inherited maternally and its mutation rates can accurately be measured in pedigrees to produce a lineage-specific clock. When these clocks are also not calibrated by evolutionary timescales, but by using the organism's generation time, a more realistic and unbiased estimate of that creature's genetic life history can be obtained. By comparing the empirical mitochondrial clock rates in fruit flies, round worms, water fleas, and humans, Jeanson demonstrated that a creation event for all of these organisms (including humans) occurred not more than 10,000 years ago (figure 1).

Creationist scientists Sanford and Carter have also conducted independent study into human mtDNA variation in which they statistically analyzed over 800 different sequences, and reconstructed a very close approximation of Eve's original mitochondrial genome.[18,25] They found that "the average human being is only about 22 mutations removed from the Eve sequence although some individuals are as much as 100 mutations removed from Eve".[18] The most recent empirical estimate of the mutation rate in human mitochondria is about 0.5 per generation.[26] Based on this rate, even for the most mutated mitochondrial sequences, Sanford and Carter determined that "it would only require 200 generations (less than 6,000 years) to accumulate 100 mutations".[18]

Surprisingly, evolutionists were actually the first to note these biblically supportive timeframes. Buried within

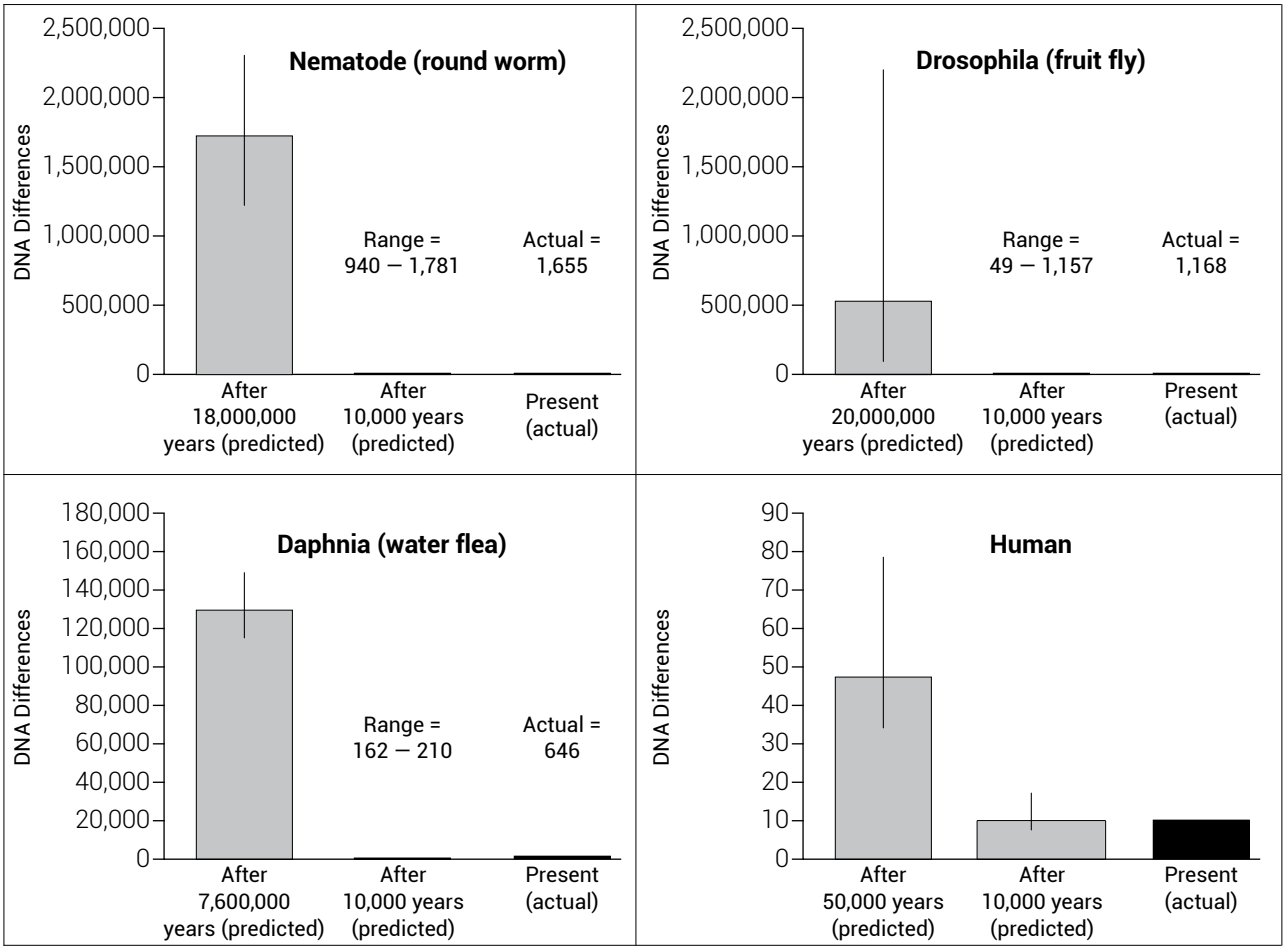

Figure 1. Graphs showing the recent origin of mitochondrial DNA diversity. The first, second and third bars show the evolutionary predicted diversity (based on deep time), the amount predicted after only 10,000 years, and the amount actually found in the sequence, respectively. Black bars represent a 95% confidence interval. In all four cases, the empirical data fits a predicted biblical timeframe of 10,000 years or less. Data is calculated using average generation time and the empirical mutation rate. This image was created from data published in reference 16 by permission of the author.

a secular research paper in 1997, the same trends recently observed by creationists regarding human mtDNA mutation rates were first reported, but received little attention in the evolutionary community.[27] The authors of the paper state:

> "Using our empirical rate to calibrate the mtDNA molecular clock would result in an age of the mtDNA MRCA [most recent common ancestor or the first human woman] of only ~6,500 years."

One year later, another secular researcher remarked about this study stating:

> "Regardless of the cause, evolutionists are most concerned about the effect of a faster mutation rate. For example, researchers have calculated that 'mitochondrial Eve'—the woman whose mtDNA was ancestral to that in all living people—lived 100,000 to 200,000 years ago in Africa. *Using the new clock, she would be a mere 6000 years old* [emphasis added]."[28]

The article continues to note that the new findings of faster mutation rates that point to mitochondrial Eve about 6,000 years ago, have even contributed to the development of new mtDNA research guidelines used in forensic investigations adopted by the FBI. Now, over 17 years later, and using even more mtDNA data, Jeanson, Carter, and Sanford are spectacularly confirming this previous unheralded discovery.

In addition to the mtDNA data, Sanford and Carter have also analyzed the Y chromosomes of modern men which they found to be only about 300 mutations on average different than the consensus sequence of a Y chromosome Adam.[18] As a result, they state:

> "Even if we assume a normal mutation rate for the Y chromosome (about 1 mutation per chromosome per generation), we would only need 300 generations (about six thousand years), to get 300 mutations."

As with their previous mtDNA work, this is the most straightforward application of the DNA clock concept and provides data perfectly in accord with a biblical timeframe for the origins of man.

Conclusion

In contrast to the flawed evolutionary paradigm of a molecular clock that assumes evolution on a grand scale and incorporates deep-time calibrations, a straightforward empirical approach constricted to analyses within a single taxa, typically yields dates of not more than about 5,000 to 10,000 years. Thus, when the hypothetical evolutionary constraints are removed, and the data is analyzed empirically, biblical timelines are achieved.

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