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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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HOW OLD IS HUMANITY?

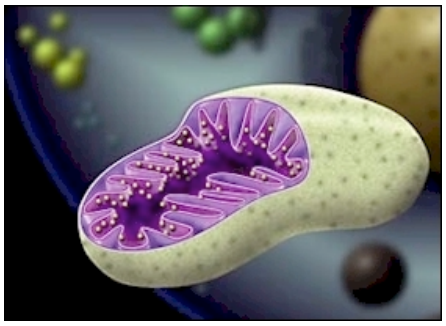
By David A. Plaisted, PhD

There are a number of evidences that the human race is very young. For example, in an article in *Science*[1], the age of the human race is is estimated to be 1,000 to 10,000 generations: "…1000 to 10,000 generations old, which is roughly the age of the human population,…"

We review some evidence for the youth of the human race, including recent findings concerning mitochondrial DNA mutation rates that give even a much younger age than 1,000 generations.

Age estimates are obtained by observing differences between the DNA of different individuals and are calculated using estimates of mutation rates. Mitochondrial DNA is often used for this; it is separate from the bulk of the human DNA, which is found in the cell nucleus. Mitochondrial DNA has about 16,000 base pairs and mutates, apparently, much faster than the nuclear DNA. Human mitochondrial DNA has been completely mapped, and all the coding regions are known, and the proteins or RNA for which they code. Some of the mitochondrial DNA does not code for anything and is known as a control region. This region appears to mutate faster than any other region, because the variation among humans is greatest here.

Recently, mitochondrial DNA mutation rates were measured directly.[2] The mutation rate in a segment of the control region of mitochondrial DNA was directly measured by comparing mitochondrial DNA from siblings and from parents and their offspring. Mitochondrial DNA was found to mutate about 20 times faster than previously thought, at a rate of one mutation (substitution) every 33 generations, approximately. In this section of the control region, which has about 610 base pairs, humans typically differ from one another by about 18 mutations. By simple mathematics, it follows that the human race is about 300 generations old. If one assumes a typical generation is about 20 years, this gives an age of about 6000 years.



The rapid mutation rate of mitochondrial DNA can be used to determine the age of a species.

This calculation is done in the following way. Let us consider two randomly chosen human beings, assuming all human beings initially have identical mitochondrial DNA. After 33 generations, two such random humans will probably differ by two mutations, since there will be two separate lines of inheritance and probably one mutation along each line. After 66 generations, two randomly chosen humans will differ by about four mutations. After 100 generations, they will differ by about six mutations. After 300 generations, they will differ by about 18 mutations, which is about the observed value.

We see that the mathematics is extremely simple. However, this timetable would revolutionize the history of humanity from a scientific standpoint, so biologists attempt to explain away the data. They do this in the following way: They assume that in this control region, most of the mutations are harmful. This means that individuals having more mutations are more likely to die, so that among surviving individuals, the number of mutations increases more slowly.

However, this explanation is implausible for the following reasons. First, we know that the control region does

[1] Collins, F., Guyer M., Chakravarti A. (1997) Variations on a theme: human DNA sequence variation. *Science* 278:1580-1581

[2] Parsons, T.J., Muniec D.S., Sullivan K., Woodyatt N., Alliston-Greiner R., Wilson M.R., Berry D.L., Holland K.A., Weedn V.W., Gill P., Holland M.M. (1997) A high observed substitution rate in the human mitochondrial DNA control region. *Nat. Gen.* 15:363-367

not code for any protein or RNA, so it is unlikely that mutations there would be harmful. Second, the fact that there is a lot of variation between individuals in this region suggests that mutations there do not have a harmful effect. Finally, one study noted that humans evolve (that is, accumulate mutations) 1.8 times faster in the control region than in silent sites in the mitochondrial DNA.[3] Silent sites do not affect the amino acid coded for, and so they generally do not have much of an effect. The fact that the control region evolves 1.8 times faster (that is, mutations accumulate 1.8 times faster) indicates that the control region has even less of an influence than the silent sites, also making it unlikely that mutations in the control region are harmful. A similar result was found for ducks, in which the control region evolves 4.4 times faster than the mitochondrial DNA in general.[4] This is additional evidence that the control region is not constrained much and that mutations there are not very harmful.

Despite the sensational impact of this calculation on the chronology of the human race, we see that the most reasonable interpretation of the data is to assume that the human race is in fact about 6000 years old. It is possible that the mutation rate has changed to some extent throughout history, but it is hard to imagine this making much of a difference in the end result. Since mitochondria in all organisms are quite similar today, it is reasonable to infer that they were also similar in the past and had a similar mutation rate. Furthermore, because of the high intrinsic mutation rate of mitochondrial DNA, any environmental effect would be very small by comparison. Any environmental agent that would increase the mitochondrial DNA mutation rate by 10 percent would wreak havoc with the nuclear DNA because the nuclear mutation rate is so much smaller and the nuclear DNA is so much larger.

Another piece of data indicating a young humanity is the striking uniformity among human males in the Y chromosome.[5] This has been used to give an age estimate of about 40,000 years or less for the human race.[6] It is now known that mutations accumulate much faster in males than in females. This means that the Y chromosome will tend to mutate twice as fast as other chromosomes, since it is always in the male line, which might reduce this estimate of about 40,000 years to about 20,000 years. See Gibbons[7] for more recent discussion in which the author gives older ages. These older ages could be a result of a higher nuclear DNA mutation rate in the past, due to a higher intensity of radiation during the Flood. Such an increase in radiation would not have much effect on the mutation rate of mitochondrial DNA because it mutates so much faster.

Yet another piece of evidence is the tremendous uniformity found among humans in a 50 kb segment of an ALU region of the nuclear DNA.[8] Only one difference was found between humans in this region, also implying a very young age for the human race.

It will be interesting to see the results of similar studies on other organisms. Probably the only reason that the human race seems so young compared to other species is that it has been studied more. When mutation rates are measured for other species, probably revealing significantly greater rates than in humans, similar young ages will probably be obtained.

In fact, there is already some evidence in this direction, based also on mitochondrial DNA. Since mitochondria are similar in all organisms, it is reasonable to assume that mitochondrial DNA mutates at about the same rate in all organisms. Also, all organisms that are roughly the same size as humans should have roughly the same number of cell divisions per generation in the female line. For humans, this is 24 divisions. Therefore, it is reasonable to assume that all organisms whose size is in the range mouse-to-elephant probably have about the same rate of mitochondrial DNA mutation per generation as humans. One biologist informed me that these assumptions are reasonable.

Now, in a portion of the control region that has about 600 base pairs, human mitochondrial DNA mutates about once every 33 generations. This translates to about one percent divergence between two random individuals every 100 generations. In another portion of the control region, humans appear to mutate a little slower, at about one percent every 150 generations. (This follows because typical humans differ by about 8 mutations in a region of about 400 base pairs that was used to study Neanderthal DNA. This amounts to a difference of about

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[3] Horai, S., Hayasaka, K., Kondo, R., Tsugane, K., Takahata, N. (1995) Recent African origin of modern humans revealed by complete sequences of hominoid mitochondrial DNAs. *Proc Natl Acad Sci USA* 92(2):532-536

[4] Sorenson, M.D., Fleischer R.C. (1996) Multiple independent transpositions of mitochondrial DNA control region sequences to the nucleus. *Proc Natl Acad Sci USA* 93:15239-15243

[5] Dorit, R.L., Akashi, H., Gilbert, W. (1995) Absence of polymorphism at the ZFY locus on the human Y chromosome. *Science* 268:1183-1185

[6] Whitfield L.S., Sulston, J.E., Goodfellow P.N., (1995) Sequence variation of the human Y chromosome. *Nature* 378:379-380

[7] Gibbons, A. (1997) Y chromosome shows that Adam was an African. *Science* 278(5339):804-805

[8] Knight, A., Batzer, M.A., Stoneking, M., Tiwari, H.K., Scheer, W.D., Herrera, R.J., Deininger, P.L. (1996) DNA sequences of Alu elements indicate a recent replacement of the human autosomal genetic complement. *Proc Natl Acad Sci USA* 93(9):4360-4364

two percent.) Therefore, it is also reasonable to suggest that other species in the mouse-to-elephant range will diverge at about one percent every 100 to 150 generations in the mitochondrial DNA control region.

In this regard, it is interesting to see what the typical differences are between individuals in different species. For example, in the control region, wolves and coyotes differ by about 7.5 percent.[9] By our previous calculations, it would take about 750 to 1000 generations to achieve this divergence. With a generation time of a few years, this would imply a separation time of a few thousand years ago. Wolves differ from each other by about two percent in the control region.[10] This implies an origin about 200-300 generations ago. With a few years generation time, this would be a thousand years or so ago. This low figure might be explained because the whole control region changes somewhat more slowly than the parts considered earlier. The same reference states that dogs also differ by about two percent, leading to a similar time of origin. Most dog species differ within themselves by about one percent, implying a more recent origin.

The mitochondrial DNA of seven species of diving ducks has been studied.[11] The control region divergence was less than 17 percent. This translates to 1700-2500 generations, which, at a few years per generation, is also in the several thousands of years range. Closely related species of birds have also been studied.[12] The difference in total mitochodrial DNA was about five percent or less. This probably translates to about 20 percent in the control region, and thus about 2000 to 3000 generations. With two or three years per generation, this again translates to a separation time of a few thousand years ago.

We can also obtain similar young ages for bacteria and Drosophila based on nuclear DNA mutation rates. The generation time for E. coli is about 20 minutes, or about 50 generations per day and 15,000 generations per year. In 6,000 years there would be about 100 million generations. The mutation rate per base pair per generation is about 10^{-9} in bacteria.[13] Thus in 100 million generations, there would be about a 10 percent change in the non-functional DNA and a 20 percent difference between two random individuals. The actual difference observed for E. coli is about 5 percent.[14] This low figure might be explained by a lower mutation rate and by the fact that a considerable portion of the bacterial DNA is functional.

For Drosophila, the generation time is about two weeks. This leads to 25 generations per year, and about 150,000 generations in 6,000 years. The mutation rate for Drosophila is about 2×10^{-8} per nucleotide per generation or even twice as high or more.[15] This rate may also be computed from the fact that Drosophila has about 20,000 genes, each gene has about 1,000 base pairs, and there appears to be about one slightly harmful mutation per zygote per generation in Drosophila.[16] In 150,000 generations, there would be a change of about 3×10^{-3} in non-functional DNA, and about a 0.6 percent difference between two random individuals. Since the mutation rate is likely twice as high, this difference could be as high as 1.2 percent. The observed value is about 1.5 percent. The increase could be due to a slightly higher mutation rate, a slightly smaller generation time, mutational hot-spots, differences at the Creation, or an origin slightly longer than 6,000 years ago.

This is undoubtedly just the tip of the iceberg, and many similar results will undoubtedly soon be reported. We hope that these results will cause biologists to give more serious consideration to the possibility that the Biblical record of a recent creation is historically accurate.

COMING EVENTS

Thursday, June 8, 7:00 P.M., Providence Baptist Church, 6339 Glenwood Ave., Raleigh

"Tour the Galapagos Islands and Determine for Yourself if Darwin Really Saw 'Evolution in Action' There" will be the title of the talk by Mark Stephens, MCS, for the June 8 TASC meeting. Mark will share pictures that he took on his trip to the Galapagos Islands with the Institute of Creation Research scientists and portions of a video to make you feel you have toured the islands yourself! It will be the closest you may come to actually touring for yourself and coming to meaningful conclusions based on the ICR scientists' assessments and scientific evidences seen while on the tour versus naturalistic evolutionary dogma espoused by Darwin and others about the islands. Please come and bring a guest to this meeting that should interest you and strengthen your faith in God, our Creator.

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[9] Morell, V. (1997) The origin of dogs: running with the wolves. *Science* 276(5319):1647

[10] Vila, C., Savolainen, P., Maldonado, J.E., Amorim, I. R., Rice, J.E., Honeycutt, R.L., Crandall, K.A., Lundeberg, J., Wayne, R.K. (1997) Multiple and ancient origins of the domestic dog. *Science* 276(5319):1687-1689

[11] Sorenson, M.D., Fleischer, R.C. (1996) Multiple independent transpositions of mitochondrial DNA control region sequences to the nucleus. *Proc Natl Acad Sci USA* 93(26):15239-15243

[12] Klicka, J., Zink, R.M. (1997) The importance of recent ice ages in speciation: a failed paradigm. *Science* 277(5332): 1666

[13] Spetner, L. (1997) *Not by Chance*, Judaica Press, Brooklyn, NY, 92

[14] Moreel, V. (1997) Bacteria diversify through warfare. *Science* 278(5338):575

[15] Kondrashev, A.S. (1988) Deleterious mutations and the origin of sexual reproduction. *Nature* 336:435-440

[16] Crow, J.F. (1997) The high spontaneous mutation rate: is it a health risk? *Proc Natl Acad Sci USA* 94:8380-8386

Thursday, July 13, 7:00 P.M., Providence Baptist Church, 6339 Glenwood Ave., Raleigh
Phillip G. Johnson. Topic to be announced.

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