Human DNA Variation Linked to Biblical Event Timeline

by Jeffrey Tomkins, Ph.D.
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Each person is different, and each, except an identical twin, has unique DNA differences. These differences can be traced across global populations and ethnic groups. Furthermore, recent research provides interesting insight about the approximate time that these DNA differences entered the human race.

A new study reported in the journal *Science* has advanced our knowledge of rare DNA variation associated with gene regions in the human genome.[1] By applying a demographics-based model to the data, researchers discovered that the human genome began to rapidly diversify about 5,000 years ago. Remarkably, this data coincides closely with biblical models of rapid diversification of humans after the global flood.

The vast majority of DNA base sequences between any two humans are nearly identical, so the few differences are traceable among people groups. The human genome project has continued to analyze thousands of humans throughout the world for variation in their DNA sequence. Researchers link this variation with many human traits and heritable diseases.[2]

Typically, this variation is evaluated using single DNA base differences or single nucleotide polymorphisms (SNPs) between individuals and populations. Because of the type of standardized "gene chip" technology commonly used, most SNP analyses evaluate only the most variable parts of the human genome and, therefore, exclude the much less variable protein-coding regions.

The recent *Science* study analyzed the DNA sequences of 15,585 protein-coding gene regions in the human genome for 1,351 European Americans and 1,088 African Americans.

The data proved ideal for examining the course of human genetic variation over time, partly because protein-coding regions are less tolerant of sequence variation than other parts of the genome; these regions record more reliable, or less "noisy" historical genetic information.

Typically, evolutionary scientists incorporate *hypothetical* deep time scales taken from paleontology or just borrowed from other authors to develop and calibrate models of genetic change over time.[3] In contrast this *Science* study used demographic models of human populations over known historical time and known geographical space. The resulting data showed a very recent, massive burst of human genetic diversification.

The authors wrote, "The maximum likelihood time for accelerated growth was 5,115 years ago." Old-earth proponents now have a new challenge: to explain why…

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