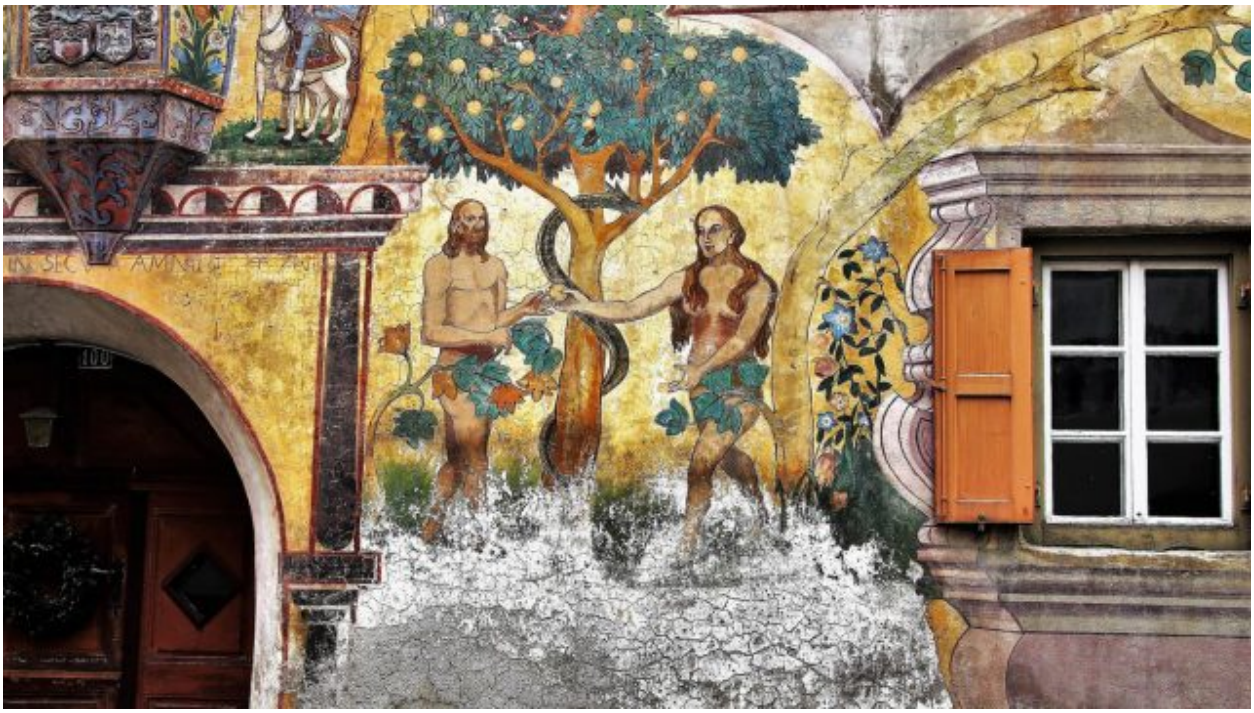

Article

Does Genetics Point to a Single Primal Couple?

- By **Dennis Venema**
- and **Darrel Falk**

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- Adam & Eve
- Evolution

A Single Primal Couple?

Most Christians who have grappled with the science of genomics (the branch of biology that compares the DNA sequences of different organisms to one another) have done so with the question of *common ancestry* in mind: do humans share an ancestor with other forms of life, such as chimpanzees?

Here the evidence is very compelling, and reasonably accessible to non-specialists. For example, the human genome has numerous defective genes embedded it, and the vast majority of these defective genes are also present in the chimpanzee genome in the same relative positions with identical mutations. This sort of evidence is easily understood due to its qualitative nature.

A second question, and one that is less frequently explored even by Christians who accept common ancestry, is the issue of human/hominid *population sizes* during our evolutionary history. Specifically, is the human race descended from one ancestral pair in the recent past? Are we, as C.S. Lewis puts it in his *Chronicles of Narnia*, the "sons of Adam and daughters of Eve"? Is there genomic evidence to suggest that the human race is genetically derived from a primal pair? Here the evidence is more difficult for non-specialists to appreciate, because it is quantitative in nature.

Genomics can be used as an estimate of population sizes in the past by measuring genetic variation in the present. Genes come in different forms, or alleles: for example, the human ABO blood types are determined by three alleles of one gene. Some genes in human populations exist in hundreds of forms.

The catch, however, is that any individual person can only carry at most two different varieties of any one gene: one from mom, the other from dad. It therefore follows that a large population can pass on a large number of gene forms (alleles), but a population that passes through a population "bottleneck"—where only a small number individuals survive—will fail to pass on most of its genetic variation to future generations.

Attempting to square the Genesis account and common ancestry by positing a literal Adam and Eve who were the progenitors of the entire human race is, biologically speaking, looking for the most extreme population bottleneck a sexually reproducing species can experience: a reduction to one breeding pair.

Is there evidence that such a bottleneck has ever occurred? Dr. Peter Enns has been exploring whether this is even the right question to be asking from a biblical perspective (here, here, here, and here). Here we explore three independent ways of answering the question, this time from a biological point of view.

Method I:

The genetic consequences of a bottleneck required by a literal reading of Genesis 2-3 would be severe: at maximum, four gene-forms (two from each parent) would be passed on by Adam and Eve. Interbreeding in the (necessarily very small) population after the bottleneck would result in the further loss of some alleles due

to chance alone. In short, the genetic impact of such an event would leave a stamp on the genome of that species that would persist for tens of thousands of generations as mutations slowly generated genetic diversity.

We can use this information, then, to estimate the minimum number of people that could have existed at any point in time. First we ask how many different alleles there are for a number of genes within the current population. Correcting for the rate at which we know new forms of genes appear (mutation), we can calculate the minimum number of people needed to generate the current amount of diversity. Numerous studies analyzing many different genes all point to a bottleneck. However, these studies are all clear: during the bottleneck, there were several thousand individuals, not two.

Method II:

In earlier posts, we have discussed the fact that DNA segments known as Alu repeats, can insert themselves at various locations in the genome. It turns out that the Alu sequence comes in various forms, like different makes of cars—Fords, Toyota, etc. There are several thousand families of Alu.

Consider just one family, which we will call Ya5. Members of this family have been inserted into human chromosomes at 57 mapped locations. If all humans descended from a single pair of individuals, all humans would have each of the 57 elements in pretty much the same locations, since individual members of the family almost never move. However, the human population consists of groups of people who share some insertion points but not others. The multiple shared categories make it clear that although a human population bottleneck occurred, it was definitely never as small as two. In fact, this line of evidence also indicates that there were at least several thousand people when the population was at its smallest.

This method is much different than Method I since it does not depend upon mutation rate, but the answer is similar.

Method III:

A third independent estimate makes use of a concerted research effort called the HapMap project. Humans have 3 billion bits of information in their genomes. (The official term for one bit is a “nucleotide.”) The bits between any two individuals differ at many sites, which is, of course, why we don’t all look the same.

In the HapMap project, one million of these differences have been analyzed by examining something called linkage disequilibrium The technical details are beyond the scope of our discussion, but to give you a feeling for how it works, imagine that you have a gene for blue eyes and a gene for a bent finger, both of which you

inherited from your dad. Assume these genes reside in the same “neighborhood” on chromosome 2. Because these genes are close to one another, chances are that if your brother got the blue eye allele from your dad, he would have received the bent finger allele as well. After all they are neighboring genes, both on chromosome 2. Why? Blocks of genes in the same neighborhood on a chromosome are usually inherited together. Alleles that are *very* close together on chromosomes tend to stay together for many generations before they are “mixed and matched” through a process called recombination.

Now pretend that someone analyzes both your DNA and that of your brother in a double blind experiment. The investigator would, upon examining the results, be able to say, “I’ll bet these two people are related to each other.” And he would be right.

Now picture being able to do this, not for two differences, but for a million differences all at once and not just for two people, but for many people from all over the world. Using this approach, it is possible to tell how many people gave rise to all the prevalent combinations of differences. In short, we can tell if everyone came from just two people at any time in the last 200,000 years. So did we?

No.

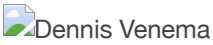
This third independent method tells us that everyone alive today is related, but not to a single pair of people. We are related to a population that consisted of several thousand people with their several thousand combinations of these million genetic differences.

Here’s the real point of this. When you have one way of doing a calculation and you get a certain answer, perhaps you are justified in being a little skeptical. Perhaps you made a mathematical mistake, or maybe you made a faulty assumption. However, when you do your calculation using two totally different approaches, using methods with completely different assumptions, and each method gives you the same answer, you become convinced it is correct. Three, of course is just icing on the cake.

So that’s the situation we are in with regard to the human population size in ancient history. There was a bottleneck. There were likely fewer people alive during that time than the number of fans attending a typical NHL hockey game. (We don’t know if they were all together in one village, of course, but the total was small.) However, it was not two people. Our species diverged as a population. The data are absolutely clear about that.

Notes & References

About the Authors



Dennis Venema

Dennis Venema is professor of biology at Trinity Western University in Langley, British Columbia. He holds a B.Sc. (with Honors) from the University of British Columbia (1996), and received his Ph.D. from the University of British Columbia in 2003. His research is focused on the genetics of pattern formation and signaling using the common fruit fly Drosophila melanogaster as a model organism. Dennis is a gifted thinker and writer on matters of science and faith, but also an award-winning biology teacher—he won the 2008 College Biology Teaching Award from the National Association of Biology Teachers. He and his family enjoy numerous outdoor activities that the Canadian Pacific coast region has to offer.

Darrel Falk

Darrel Falk is the author of *Coming to Peace with Science: Bridging the Worlds Between Faith and Biology* and speaks frequently on the relationship between science and faith at universities and seminaries. From 2010 to 2012, he served as president of BioLogos. Under his leadership, the BioLogos website and daily blog grew to thousands of readers and hundreds of authors, the Biology by the Sea workshop trained Christian biology teachers, and private workshops in New York were a forum for conversation and worship with top evangelical leaders. As president, he brought BioLogos into conversation with Southern Baptist leaders and with Reasons to Believe, and today he continues to be a key member of those dialogues. Falk received his B.Sc. (with Honors) from Simon Fraser University, and earned his Ph.D. from the University of Alberta. He did postdoctoral work at The University of British Columbia and the University of California, Irvine before accepting a faculty position at Syracuse University in New York. Darrel's early research focused on Drosophila molecular and developmental genetics with funding from the National Institutes of Health and the National Science Foundation. In 1988 he transitioned into Christian higher education in the biology department at Point Loma Nazarene University in San Diego, where he is now Emeritus Professor of Biology.

He is a member of the American Association for the Advancement of Science, the Genetics Society of America, and the American Scientific Affiliation.

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