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Biblical History and the Y Chromosome

By Matthew L. Welborn

Traced: Human DNA's Big Surprise (2022) is the most recent book by Dr. Nathaniel Jeanson.¹ Jeanson holds a PhD in cell and developmental biology from Harvard University and also has a BS degree in molecular biology and bioinformatics from the University of Wisconsin.

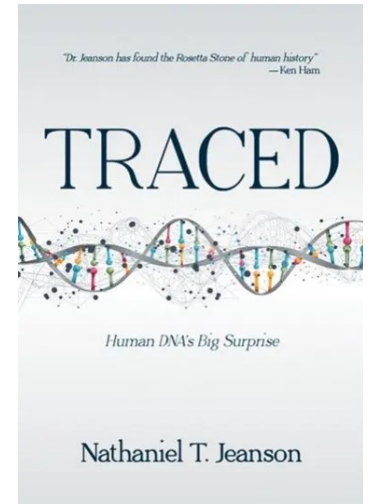
Jeanson holds to the young earth, biblical perspective on human origins and recently has also completed a series of videos available on YouTube produced with Ken Ham from the Answers in Genesis ministry. This video series also presents many of the ideas from *Traced* and is entitled "A new history of the Human Race." Jeanson has published a number of research papers and a book over the last 10 years describing his recent research in genetics and, in particular, how DNA sequences change over time across generations of animals and in humans.

In this new book, Jeanson presents his hypotheses about specific connections between recent discoveries in the sequences of the human DNA and specific events and periods in human history as recorded in the book of Genesis and other historical records. In this review, I will draw primarily from the book itself, *Traced*, as well as some of Jeanson's previous papers that explain more details of his work. In addition, I reference another book review written by Robert Carter, PhD. Carter is also a geneticist and creation scientist and provides a very insightful review that highlights the strength of the book as well as potential areas for future work.

Jeanson begins his book in Part 1 with a few chapters of background information about recent developments in genetics. In these chapters, he makes several key points that help set the stage for the rest of the book. In chapters 1 and 2, Jeanson describes several common misconceptions we have about the human family both today and throughout history. Two of these new insights that Jeanson explains are that the human family in the ancient world

was "smaller than we think" and that we today are therefore "more connected than we think."

To illustrate these points, for example, he presents in chapter 1 a discussion of historical population densities across the ancient world. In particular, he discusses how the population of the ancient world was much smaller and how it changed rapidly over time. For example, when King David was on the throne in about 1000 BC, the world population was only about 50 million people. One thousand years later, the world population had tripled to 170 million people (about three times larger). From AD 1 to AD 1000, the population grew more slowly—reaching 260 million people in AD 1000 and around 350 million people in AD 1400. In contrast to this slow, steady growth, the world population grew by a factor of 20 to nearly 8 billion people over the next 600 years. This explosion in human population has been largely due to modern medicine and improvements in agriculture and technology. As a result of this unprecedented growth, the world we live in now is unique in human history. Jeanson uses this insight about human history to help the reader understand human population growth over history during the last 4500 years and to also begin to understand how these changes and human population migrations can be related to specific evidence that has been found through the study of human DNA. As a result, in chapter 2 Jeanson uses this insight about the much smaller human population sizes in historical times to show how human groups and families could easily share and descend from



¹ Jeanson NT (2021) *Traced: Human DNA's Big Surprise*, Master Books, Green Forest, AR.

common ancestors over the course of hundreds or a few thousand years.

In chapter 3, Jeanson makes one further introductory point, and that is that the mixing together of our ancestors' genetic information through intermarriage between families and people groups has been faster than we typically assume. Genetic calculations show that the physical human features such as ethnic and group differences can rapidly mix and change over the course of just a few generations. Such blending and changes between groups does not require long periods of time; and differences we sometimes consider important, such as ethnic or national identities, change quickly by historical measures and are not as central to who we are as a human family.

In Part 2 of *Traced* (chapters 5–12) Jeanson relies heavily on recent research based on the sequencing of the human male Y chromosome over the past few decades. For this reason, it is worth spending some time to understand why this chromosome tells us not just about how humans are designed by their Creator and how we each live and grow today, but it also provides unique insight into the history of the human race. As human DNA is passed down from generation to generation, the information stored in the DNA from both the mother and the father is mixed and passed on to the different children that they have together. Each child gets a different mix of the parents' DNA through recombination. The Y chromosome is unique, however. The Y chromosome is only present in men—not in women. Women have an XX pair while each male has a single copy of the Y chromosome in their XY pair. So, as the Y chromosome is passed down, from fathers to sons; no parental mixing occurs within this portion of the DNA as it does with the other chromosomes shared by men and women. This unique property allows scientists to reconstruct history by looking at the Y chromosome through inferences about the occurrences and spreading of mutations in the Y chromosome among human populations.

As DNA is copied inside of cells during replication, occasionally there are “copy errors” or mutations. One primary type of mutation is a single point mutation, also known as a single nucleotide polymorphism or SNP. If such a mutation occurs in the Y chromosome of the cell that fertilizes to the mother's egg, the mutation will continue to be passed down to all male descendants in

subsequent generations. As a result, such mutations allow scientists to reconstruct a *phylogenetic tree* of the different ancestor Y chromosome sequences going back in history. In this tree, the occurrence of a mutation in a Y chromosome in the past becomes a branch point. All males descending from such a point in the tree possess that same specific mutation, whereas those in other branches do not. By carefully analyzing the DNA from many living males, the constructed tree shows the relationships between men alive today and how closely they are related through common ancestors. Figure 1 shows a representation of such a tree for the Y chromosome that was created by the Simons Genome Diversity Project (SGDP) and referenced by Carter to provide in his review² context for results shown by Jeanson in *Traced*.

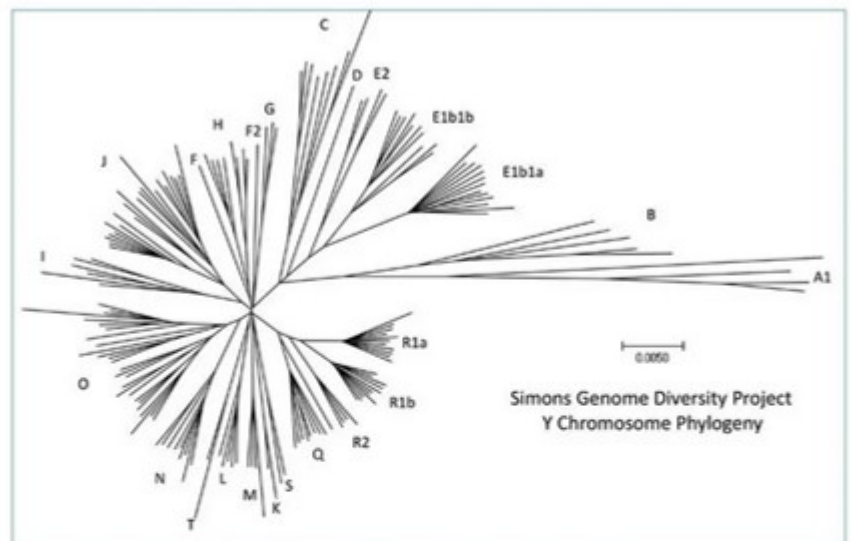


Figure 1: An unrooted tree that shows the relationships between the different human Y chromosome sequences based on the Simons Genome Diversity Project (SGDP), as shown in Carter.² Carter describes how a biblical interpretation would likely conclude that the “root” of the tree is near the center of the “starburst,” whereas a typical evolutionary interpretation would assume the root to be somewhere along the A1 branch (to the right of the branching point to branch B). Branch lengths are proportional to mutation difference counts.

One of the main results that Jeanson presents in *Traced* is a specific version of the Y chromosome phylogenetic tree that he uses to connect specific branches of the Y chromosome tree (known as haplogroups) to specific people groups, events, and even individuals that we know from history. Before we look at the more detailed results presented by Jeanson, however, it is helpful to better understand some of the assumptions that will need to be made to begin to connect the evidence from Y chromosome sequence data to specific historical groups and events.

² Carter R (2022) The promises and pitfalls of correlating Y chromosome genetics to human history, *J Creation* 36(2):34–39

In the example phylogenetic tree cited from the literature and shown in Figure 1 (taken from Carter's review²), there are no assumptions about time durations or specific events or people. That tree simply shows inferred relationships between modern groups by the graph that shows branching from a single central point to the distinct clusters and end points that represent sequences taken from men living today. This tree also has no "root"—an assumed oldest starting point that reflects a single sequence that is ancestral to all of the others. This unrooted tree only shows relationships based on sequence differences, and even these relationships are sometimes only estimates or "best guesses" based on statistical analysis of often noisy genetic sequence data that can itself contain errors or inconsistencies. In general, the location of the actual tree root is not known—it must be inferred through analysis, and it's important to understand that scientists disagree about the location of this root in the actual historical Y chromosome tree.

In *Traced*, Jeanson presents a very different phylogenetic tree (Fig. 2). This specific rooted tree incorporates his assumptions about how the Y chromosome tree maps into human history. In particular, *Traced* contains two specific sets of assumptions that allow Jeanson to reach his specific conclusions that we will discuss below. Firstly, Jeanson proposes one specific point in the tree as the "root" of the tree. In Figure 2, this point that appears near the center of the tree in Figure 1 now becomes the starting point (in time), and so the graph is redrawn to show a tree where the left side is the beginning and where time and genetic descent are shown flowing to the right.

The second key assumption that Jeanson makes is about *how often* these mutations occur in time, that is, assumptions about the *mutation rate*. In general, the analysis of mutations in Y chromosome sequences allows the construction of the basic tree (as in Figure 1) that would typically have differences or branch lengths that are just based on the number of mutations (differences) between the sequences that correspond to the nodes. To understand *how long in time* this mutation process has taken, it would be necessary to estimate or assume how long each mutation or series of mutations takes to occur, typically measured in years or generations.

Suffice to say, there is significant disagreement among scientists about what the mutation rate is for the Y chromosome sequences. This determination of mutation rates is an active and quite controversial area of research. In Jeanson's case, his previous work has led to a result of three to five mutations per generation in the human male Y chromosome.³ Evolutionists on the other hand have

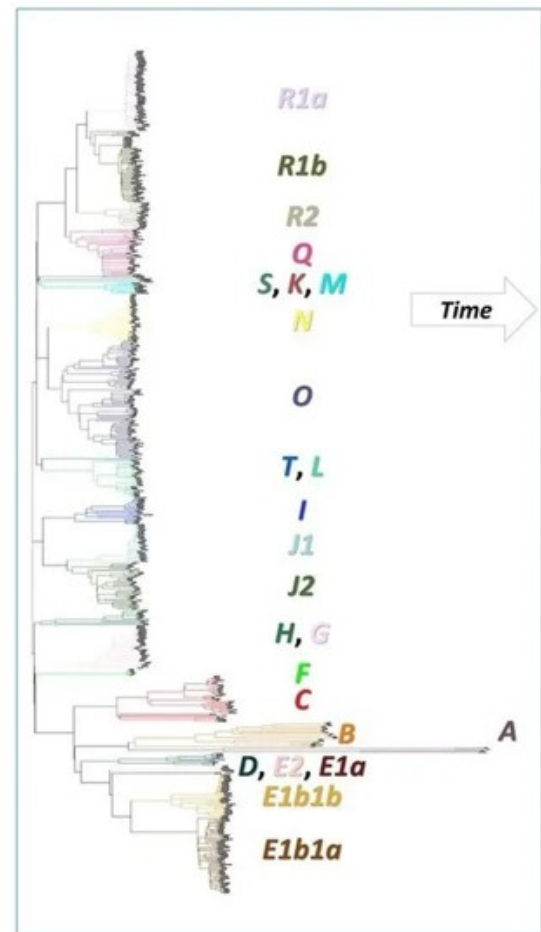


Figure 2. Jeanson's phylogenetic tree for the human Y chromosome. Here the root of the tree (Noah) is shown at the left edge and the different groups of genetic descendants flow to the right. Note that by choosing one specific node in the tree to be the root, Jeanson is concluding that that one node is the oldest ancestor of all the other nodes. Note also that one result of this choice for Jeanson is that some of the branch groups extend much longer to the right because the branch lengths are drawn to maintain a length that is proportional to the mutation count relative to the root sequence.

arrived at much lower mutation rates that end up producing much longer periods of time for human history. Although it is beyond the scope of the book or this review, one critique of some of these longer results (lower mutation rates) is that they incorporate specific assumptions about evolutionary age of the human race and genetic relationships to other species.³ Essentially, the critique is that they assume that humans have been alive for hundreds of thousands of years and therefore the mutation rate must be much lower. Carter points out that determining the mutation rate is extremely challenging since the specific mutations points that are found depend significantly on the noisiness of the sequence data and the assumptions that an individual researcher makes in the analysis.²

³ Jeanson NT, Holland AD (2019) Evidence for a human Y chromosome molecular clock: pedigree-based mutation

rates suggest a 4,500-year history for human paternal inheritance. *Answers Res J* 12:393–404

Returning to *Traced*, Jeanson uses his previous results and assumptions about human Y chromosome mutation rates to establish specific dates and points in the tree that correspond to specific time ranges in human history. To describe these genetic-to-historical connections, Jeanson spends a large part of *Traced* working through the different branches of the tree based on the collected sequence data from different parts of the world today.

Chapters 5 through 12 of *Traced* comprise Part 2 of this book. In this part, Jeanson steps through different geographic areas of the world: from Africa to Europe, the Middle East, South Asia, East Asia, the Far East, and the Pacific regions. For each of these regions, Jeanson describes the different distributions of Y chromosome groups in each of these regions based on DNA collected from men in the different people groups that live in those areas today. Part 2 of the book has significant amounts of detail and many color illustrations that detail the sequences from different branches of the tree (the Y chromosome haplogroups) and how they are distributed around the world today in different populations. Chapter 5 is a good example of how Jeanson presents this information for one particular area of the world. In this case, the analysis presents data from different populations in the continent of Africa. Jeanson analyzes these distributions along with other data, such as the distribution of languages over time and geography, to draw conclusions about how humans first arrived in Africa through Egypt and spread to the different parts of Africa over time. One unique aspect of Jeanson's analysis is that he combines his assumptions about mutation rates to put specific dates in historical time frames with the different spreads of human populations seen in the Y chromosome data.

In the rest of Part 2 of his book (chapters 7–12), Jeanson repeats this analysis for other parts of the world starting with Europe and the Middle East. He links together historical periods and kingdoms with different groups and branches of the Y chromosome tree. He then continues to trace the spread of the human race through the Far East, into the Pacific, and over into the American continent. Jeanson's work is acknowledged by Carter to be significant as it represents a first attempt to connect genetic information entries with a biblical model of human history. This is made possible by providing specific ranges of dates for when the different branches of the tree split off during the migration of human peoples from the Middle East to other parts of the world.

In Part 3 of the book, the final chapters, Jeanson looks back into the most ancient branches of the Y chromosome tree. It is here that he works to connect different branches of the tree with the biblical record of human history as recorded in Genesis in chapters 10 and 11. In particular, after Noah's flood, all of humans descended from Noah, his three sons and their wives. Jeanson describes his own


theory and how he reached his conclusions about where Noah and his sons occur in the Y chromosome tree. After that, he also traces the different descendants of Noah's sons as recorded in the table of nations. Jeanson presents a specific theory that the branches of the Y chromosome tree represent the branches of the human family descended from Noah and his sons as the human race spread throughout the world after the Genesis flood.

Finally, in his analysis in Part 3, Jeanson presents his own theory about the branch of the Y chromosome tree that contains the likely lineage of the Jewish nation, Abraham and Isaac and Jacob and their descendants. Based on discussion in the review by Carter, it is clear that there may be some disagreement about which branch contains the Jewish people.

In the review by Carter, there are several other important points made that are worth repeating here. One subject of interest in modern genetic research is that of "Ancient DNA": sequences of DNA extracted from people that are no longer living. Over the last few decades, scientists have come to understand that they can recover DNA samples from bones or bodies of people that have been dead for quite some time, including people in known history or even going back to other human groups such as the Neanderthals or another group more recently discovered known as the Denisovans. The analysis of this new genetic data—from Y chromosome or other sources—is still in very early stages, and Carter believes it could bring some important insights into the study of human history from a genetic perspective. Carter also believes that the analysis and use of ancient DNA data is important in the discussion of creation science.

Another point of caution from Carter's review of *Traced* is that the initial assumptions about constant mutation rates for DNA made by Jeanson in *Traced* are likely premature. In ongoing research, scientists are describing reasons why mutation rates in human DNA are likely not constant over time and across different branches of the human genetic tree. These could include many factors such as the environment, medical problems with individual people or groups, and even things such as the age of a man when they become fathers. Jeanson's work was based on assumptions that mutation rates were fairly constant over different branches of the tree—it seems likely that future work still needs to be done in this area.

Carter and Jeanson do agree in many areas and on one key point in particular: the evolutionist position that human DNA records hundreds of thousands of years of human history and eventually leads back to common ancestors with apes and chimpanzees is rejected by both men. There is a huge literature in this active research area and many challenges for evolutionists to explain. *Traced* is a fascinating book as it begins the work to unite modern genetic research on the Y chromosome phylogenetic tree

and the wealth of knowledge that we have about human history from the Bible and other sources. 

COMING EVENTS

TASC Zoom Meeting, October 13, 7:00 pm EST

“Biblical History and the Human Y Chromosome” will be presented by Matt Welborn, PhD in electrical engineering from Massachusetts Institute of Technology. The talk will present a recent review of the book *Traced: Human DNA’s Big Surprise* by Dr Nathaniel Jeanson, a Harvard graduate with a PhD in cell and developmental biology. The talk will present the major ideas from Jeanson’s book about connections between recent discoveries in the sequences of the human DNA and specific events and periods in human history as recorded in the book of Genesis and other historical records. We will also provide some additional background on the study of the Y chromosomes and the implications of mutation rates in human DNA.

Join Zoom Meeting

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