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A Computer Model of Mutation Accumulation on Y Chromosomes Suggests Events Recorded in Genesis Produced Common Variants

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Abstract

Genetic variation on Y chromosomes is due to mutations accumulated as men have descended from Noah. Many of the Y chromosome common variants found today were produced by historical events causing large demographic changes when the world population was small. To gain understanding of how the ancient events described in Genesis following the Flood may have produced these common variants, a computer model was built. Output from this model suggests that this common variant pattern is the result of tragic demographic events, including the Babel dispersion and the Ice Age, resulting in population collapse and opportunistic male reproduction. High mutation rates in long-lived patriarchs may also have contributed to increasing common variants on Y chromosomes. The model most closely matches the common variant pattern when parameters are adjusted to reflect the historic record of Genesis. The population expands rapidly with few deaths until 560 men with their families disperse from Babel. The model further suggests that patriarch profiles of mutations might be found on the Y chromosomes of all men today.

Introduction

It is generally understood that the Y chromosome bears a unique record of human history (Ponzik et al., 2016). Phylogenetic trees made from Y chromosome variant data display a deep-node structure indicating the unique phylogeny of the human Y chromosome (Bergstrom et al., 2020). Evolutionists assume that mutations producing this record have accumulated on Y chromosomes over several 100,000 years of population stasis in Africa during the Pleistocene epoch (Harpending et al., 1998) followed by rapid expansion of lineages as humans migrated out of Africa, commensurate with technological developments, about 50,000 years ago (Ponzik et al., 2016). Creationists attribute the characteristic variant pattern to historical events recorded in Genesis

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during and after the time of the Babel dispersion about 4300 years ago (Carter, 2009). Both sides agree that the rapid expansion of male lineages displayed in the Y chromosome phylogenetic tree is consistent with rapid population growth during recorded history. Rapid population growth, with associated growth in the number of male lineages, leads to the large numbers of rare variants found in Y chromosome databases. However, common variants are produced by long periods of population stasis, or by episodes of population collapse and recovery (Harpending et al., 1998). The challenge for creationists is to explain how the common variant pattern and deep-node structure was produced in a much shorter period of time, following the Flood during the early stages of rapid population growth. An answer may be found by computer modeling. Numerical simulation and computer modeling can help determine the demographic events that would cause the accumulated mutations to assume the pattern seen in the Y chromosome databases. Parameters of a model can be adjusted to produce output which can be compared to the real data, providing insight into real historical events. In this way, an explanation of the cause of the complex genetic pattern may be discerned where direct mathematic analysis is not possible (Baumgardner et al., 2008).

Here a computer model of Y chromosome mutation accumulation is presented to show that the characteristic common variant pattern found on Y chromosomes today could have been caused by a series of population collapses, or bottlenecks, corresponding to historical events recorded in Genesis. In this paper, the common variant pattern from the Y chromosome file of the 1000 Genome database is described. Based on the biology of Y chromosome inheritance and the initial conditions derived from Genesis, a computer model of mutation accumulation is presented and its parameters adjusted to produce output resembling the real data. A discussion of the model's assumptions, main functions and justification of these functions then follows. Lastly, consideration is given to predictions regarding future discoveries from analysis of genomic databases.

The 1000 Genome Data

Large databases of Y chromosome genomic sequences are available to the public on the internet. The 1000 Genomes Project (1000G) (1000 Genomes Project Consortium, 2015) and the Human Genome Diversity Project (Bergstrom et al., 2020) provide genetic sequences of Y chromosomes from around the world.

The 1000G database contains the mutations (variants) found on the Y chromosomes of 1,233 men of 26 populations from the Americas, Europe, Africa, and Asia. These mutations are listed in a file in the "variant call format" (VCF). This VCF file was downloaded from the International Genome Sample Resource website and the allele frequencies (AF) of all the variants were extracted with a Python script. Figure 1 shows the minor allele frequency distribution for these variants which lie within the 10.4 million bases (MB) of Y chromosome sequence where most of the variant data in the file is found (Ponzik et al., 2016). The vast majority of variants are rare (AF<0.5%) and would fall in the first bin, which has been reduced from 57,329 variants so that the other bins would appear on the plot. These rare variants are an indication of recent, rapid population expansion, well documented in historical records (Jeanson, 2019). All mutations enter the population as rare variants, each arising in a single person (Sanford et al., 2018, pp. 200–216). So

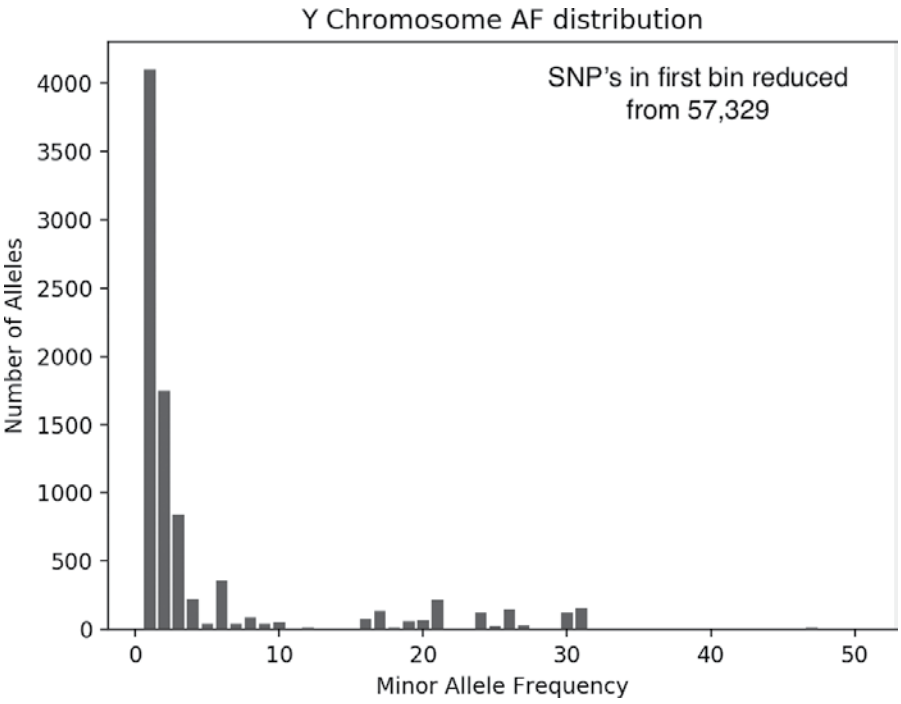

Figure 1. The minor allele frequency distribution for the variants of the 1000G data for the Y chromosome. The majority of the mutations, single nucleotide polymorphisms (SNP), in the first bin (57,329) are not shown.

rapid population expansion is characterized by accumulation of large numbers of rare variants. Since this study is concerned with ancient demographic events that produce common variants, these rare variants can be ignored as they are not the main concern of this paper.

Figure 2 shows only the common variants of Figure 1, those variants between AF 5% and 50%. On Figure 2 there are very few variants above AF 32%, but many variants are found between AF 16% and 32%. The largest bin, at AF 21%, has over 200 variants. Between AF 16% and 32% there are 10 bins with 10 variants or more. A total of 861 variants in the file have AF in this range. As will be seen in the description of Y chromosome inheritance below, these variants between AF 16% and 32% are mysterious because common variants in this range challenge the notion of simple clonal inheritance, yet they are the source of the deep-node structure of the phylogenetic tree. These are the variants that must be explained in a manner consistent with the record of Genesis and descent of all men from Noah.

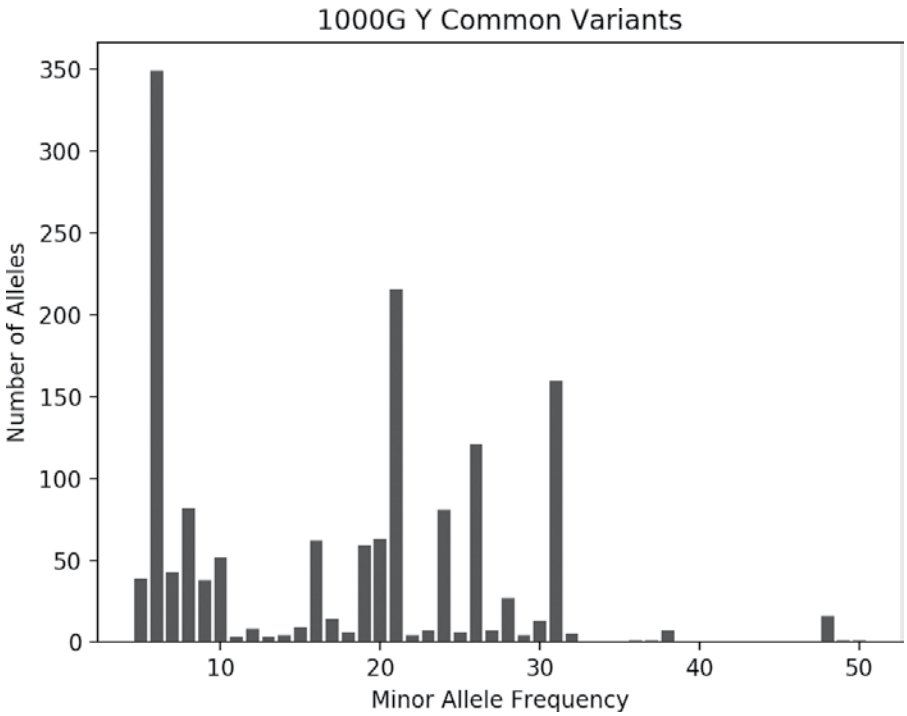

Figure 2. The allele frequency distribution of the common Y chromosome variants of the 1000G project. Minor allele frequency axis runs from 5% to 50%.

Y Chromosome Inheritance

Of the 46 human nuclear chromosomes, the Y presents the easiest case for modeling due to the fact that it is passed from father to son without chromosomal crossing over and without admixture from the maternal genome (Carter et al., 2018, pp. 133–151). As such, the Y chromosome, and any mutations in its sequence, is inherited in a clonal fashion. Today, the men of the world are more than 99.9% identical in their Y chromosome sequences, each man carrying only about 600–800 variants in the 10.4 MB part from which most of the variant data of the 1000G is obtained (Jordan, 2020). For these reasons, the model needs only to follow the accumulating mutations as the generations descend. The pedigree-based Y chromosome mutation rate has been measured to be about 3 mutations per man per generation (Jeanson and Holland, 2019). Thus, today, every male has about 3 more mutations on his Y chromosome than his father, 6 more than his grandfather, and 9 more than his great grandfather. His son will have about 3 more mutations on the Y chromosome than he has. In this way, the mutations are seen, today, to be accumulating in a clock-like fashion (Jeanson, 2020). Based on the average number of mutations found on Y chromosomes today this clock indicates that all men have descended from a last common male ancestor who lived about 200 generations ago. This would be Noah, who gave his Y chromosome to his three sons, presumably with unique mutations to each. Based on these considerations, each Y chromosome should have a genetic record of descent according to its lineage from one of Noah's three sons, assuming they each received a unique set of mutations on their Y chromosome.

The Computer Model

Written in Python, the finished model (Y_sim_Pdrive.py) can be found at "github.com/marshalljordanmd/Y-simulations."

The model has three main functions, "Growth," "Mutation," and "Famine." The Growth function gives each male a number of sons in the next generation. Each son receives the unique Y chromosome mutations of his father. Once the males of the next generations are produced, the previous generation of males is allowed to die without producing any more sons. The first two generations are hard coded in the model. The first generation, "Gen_0," consists of three men representing Shem, Ham and Japheth. "Gen_1" consists of the 16 grandsons of Noah listed in Genesis 10 (5 sons of Shem, 4 sons of Ham, and 7 sons of Japheth). Subsequent generations grow at a rate set according to a parameter which randomly varies from 4 to 7 sons.

The Mutation function supplies new mutations to each of the males in the next generation. All these mutations are sequentially numbered so they can be followed and AF for each mutation computed at the end of each run of the program. To account for "patriarchal drive," where the long-lived patriarchs described in Genesis are thought to have supplied many mutations to the Y chromosomes of their sons, a variable mutation rate function was devised based on the computer simulations of Carter (2019). Figure 9 of that paper shows the average number of new mutations per Y chromosome per year for 2000 simulated years following the Flood. The initial decay of this curve resembles a negative exponential out to 1000 simulation years, with the average number of new mutations decreasing from a maximum of 30 to 3. An equation was fitted to this simulation plot, and then converted from time in years to time in generations, with a generation assumed to be 30 years, resulting in Equation 1.

$$u(g) = C\, e^{-0.09g} \qquad \text{Equation 1}$$

Here "u(g)" is the number of new mutations per Y chromosome in generation "g." The constant "C" is the "Patriarchal Drive Coefficient." In the program, the number of new mutations was caused to randomly vary up or down within 2 standard deviations of a Gaussian distribution with mean of u(g) mutations, providing realism by mirroring the stochastic process of mutation. Equation 1 provides a maximum number of mutations to Noah's sons and falls to 3 per male per generation at 25 generations post-Flood. With this equation in the mutation function, the mutation rate is very high initially, reflecting patriarchal drive, and then decreases to the modern level as life spans decrease as recorded in Genesis.

When the populations grow to exceed the maximum, the Famine function culls the populations back to the specified maximum by randomly eliminating men (and their unique mutations) from the population. Without this function, the populations rapidly expand to the point of overwhelming the computer's memory. This function acts like a carrying capacity for each of the three subpopulations. The maximum populations were set to 400, 500, and 600 for the lineages of Shem, Ham and Japheth, respectively. These maximums were chosen based on assumptions of the relative numbers of these lineages in the 1000G data and to make the final population size to be about 1,200 men, which is the sample size of the 1000G data.

With these initial three main functions, the program was run for 25 generations. The AFs were computed for all mutations and common AF bins plotted, producing the common variant distribution in Figure 3, which differed substantially from the 1000G common variant distribution in Figure 2. The simulation had only three common variant peaks, representing the three patriarch mutation profiles, above AF 16%, whereas the 1000G plot, Figure 2, has a dozen common variant peaks above AF 16%. To mimic the 1000G data, the model had to be improved to produce more common variants between AF 16% and 32%.

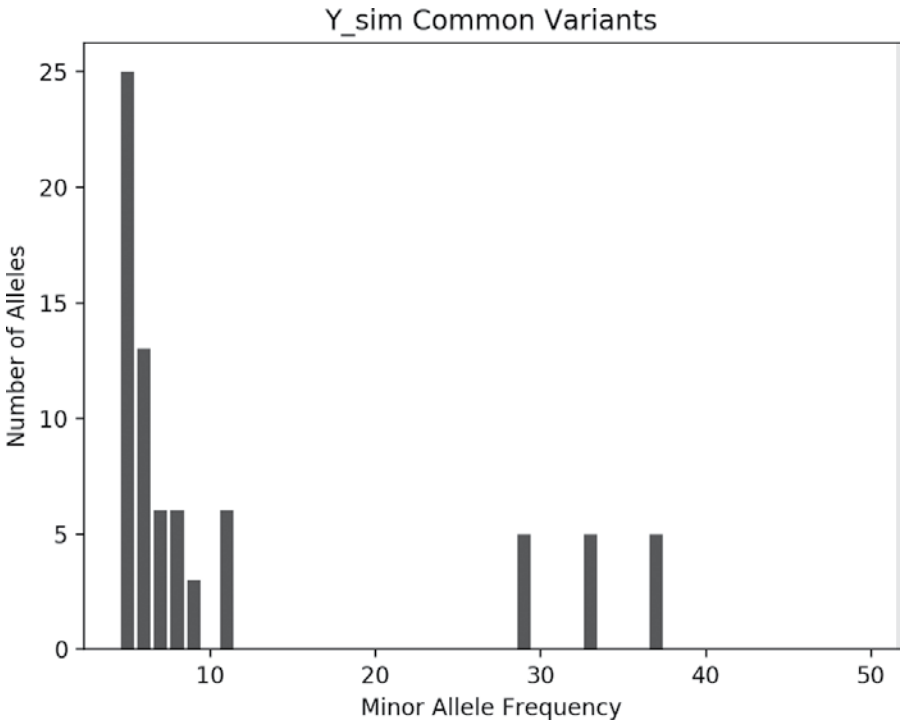

Figure 3. The allele frequency distribution of a run of the model Y_sim.py for 25 generations with no bottlenecks, no GK sons, and no patriarchal drive mutations.

A moment's consideration supplies an answer for how to improve the model. Consider the case of generation zero (Gen_0) where Noah's three sons each have one mutation on the Y chromosome inherited from their father. The AF of these Gen_0 mutations would be 1/3, or 33% in Gen_0. When passed to their sons in Gen_1, these patriarch mutations (patriarch signatures or pro-

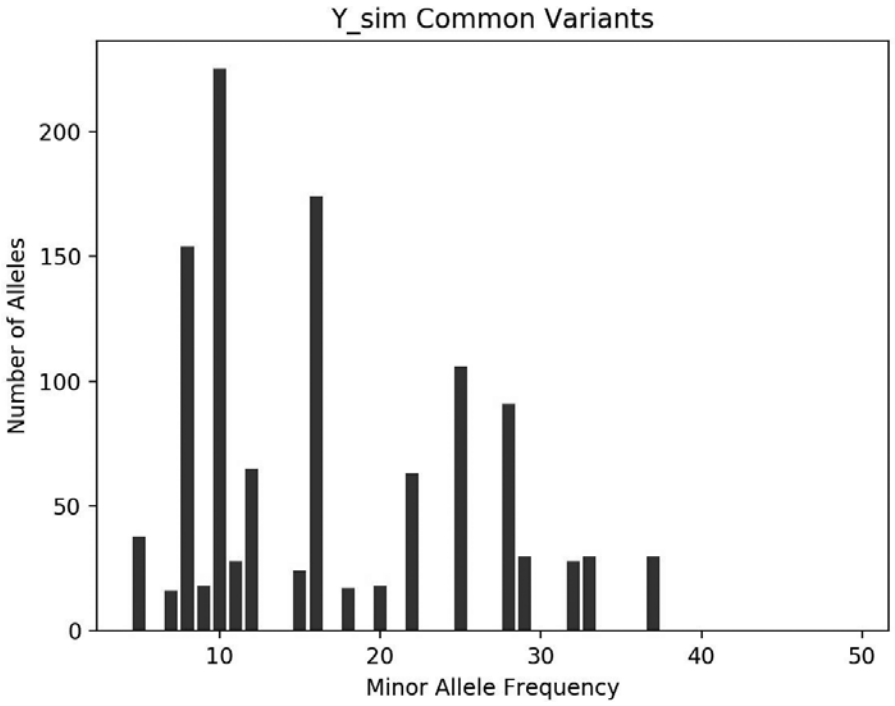

Figure 4. The allele frequency distribution for a run of the model Y_sim_Pdrive.py for 25 generations with Bottleneck Mortality 80%, GK sons 100, and Patriarchal Drive Coefficient 30.

files) would remain common variants in Gen_1, with slight shifting of their AFs due to the changes in lineage numbers. Shem's signature would be in his 5 sons at AF of 5/16 (31%). Ham's signature would be in his 4 sons at 4/16 (25%). Japheth's signature would be in his 7 sons at 7/16 (44%). But the unique, new mutations in Gen_1, received in these 16 grandsons of Noah, would each be at 1/16 (6%), a frequency just enough for them to be called common variants. For all subsequent generations, the patriarch signature mutations would remain common (unless a patriarch lineage fell below 5%), but no more new mutations would become common variants because those who carried these new mutations would be less than 5% of the population. From the third generation on, no new mutations could become common variants without major demographic changes. Such changes which occur when the population is very small are expected to increase common variant numbers since the future impact of new mutations is inversely related to population size (Carter, 2019). For this reason, the many common variants seen in the 1000G Y chromosome data is remarkable in that they indicate major demographic stirring in the first few generations that followed the Flood (Sanford et al, 2018, pp. 200–216).

What kind of demographic changes would produce more common variants in Gen_2 and after? Many men would have to die without producing any sons, and a surviving man would then need to produce more than 5% of the sons in the next generation in order for his unique variants to become common variants in that generation. Turning on additional functions in the model caused this to happen, producing output closer to the real data. A "Mortality" function causes each generation to lose 20–30% of the men at random before they produced any sons. A "Bottleneck" function causes the population to collapse by as much as 80% every few generations by randomly culling away men. Lastly, a function causes one randomly selected man in each generation to produce 50 to 150 sons, the exact number randomly selected. For lack of a better name, this function is called the "Genghis Khan" (GK) function.

Figure 4 shows a typical common allele frequency distribution from the model's output after the Mortality, Bottleneck, and GK functions are activated to produce demographic stirring. Each run of the model produces a unique picture due to the randomness programmed into the functions, so Figure 4 represents only one example, with close approximation to the real data. Notice that 10 variant peaks now have AF between 16% and 35% so this plot more closely resembles Figure 2.

Modeling with Biblical Parameters

The model was set to reflect the historical record of Genesis 9–11 by setting the first two generations to Noah's three sons and 16 grandsons. Assuming that each of Noah's sons received many mutations on the Y chromosome inherited from their father, the patriarchal drive coefficient was set to 30. Bottleneck events were set to occur for the generations listed on Table 1, according to major historic events recorded in Genesis and Exodus (Austin, 2019; Whitcomb, 1993) and an assumed Ice Age (Snelling and Matthews, 2013). The Babel event was set to Gen_4. The Ice Age was assumed to suppress population size in generations 5 and 6 so that the initial population bottleneck lasted 3 generations. With these settings, the population at Gen_3, one generation before the Babel event,

Table I. Potential bottleneck (population collapse) events recorded in Genesis and Exodus. (Austin, 2019; Whitcomb, 1993; Snelling and Matthews, 2013)

Event	Reference	Date	Generation
The Flood	Gen. 6-9	2391 BC	0
Babel	Gen. 11	2250 BC	4
Ice Age	? Job 38:22	? 2100 BC	5–6
Abram Famine	Gen. 12:10	2000 BC	9
Isaac Famine	Gen. 26:1	1950 BC	10
Joseph Famine	Gen. 41:29-30	1875 BC	12
Moses's birth	Exodus 1	1525 BC	22

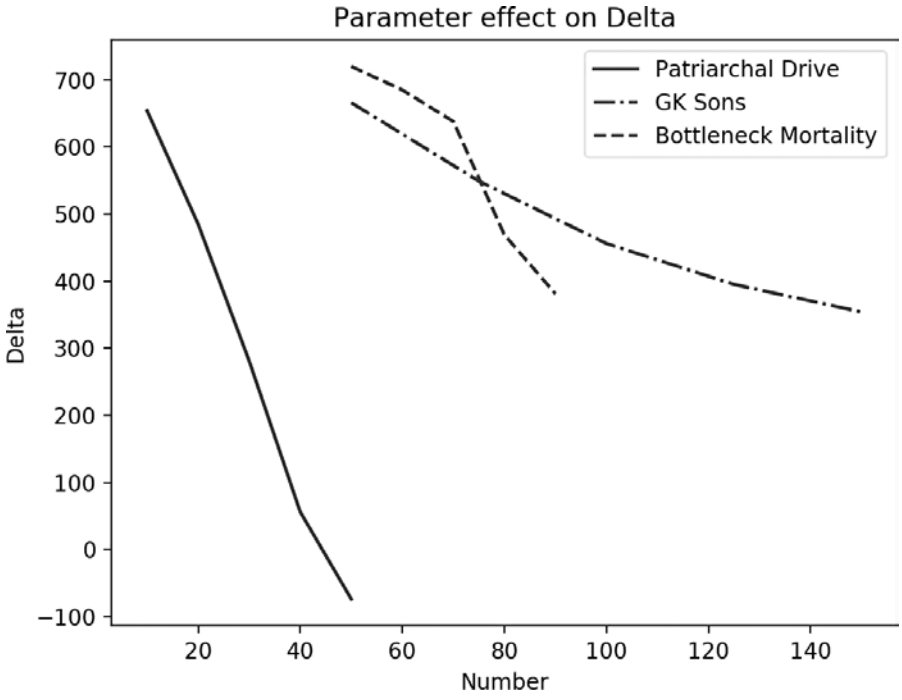

Figure 5. Parameter effect on Delta using program "Y_sim_Pdrive.py." Patriarchal Drive Coefficient C (see Equation 1) varied from 10 to 50 mutations. GK sons varied 50 to 150 sons, Bottleneck Mortality varied 50% to 90%. Delta is the average of 861 minus the number of variants between AF 16–32% after 25 simulated generations.

averaged 560 men. These represent the fathers, with their wives and the children, who were scattered from Babel, altogether several thousand people. Since the model does not cull the population (causing men to die) until the set maximums are exceeded, and these had not been exceeded by the time of the Babel event, the model includes Noah and his sons among those who dispersed from Babel (Carter and Lightner, 2016).

Model Optimization

A target, Delta, was devised to compare the model's output to that of the 1000G data. Delta was the number of variants of AF between 16% and 32% in the 1000G data (861 variants fell in this range) minus the number in this range in the model's output at the end of each run of 25 generations. The more closely Delta came to zero, the more closely the model matched the 1000G data. The parameters were optimized one at a time with the model's other settings not changed. Using this method, it was found that the number of sons (GK function), the bottleneck mortality, and the Patriarchal Drive Coefficient had a major effect on Delta and could be adjusted to make the model's output resemble the 1000G data. Figure 5 shows the effect of these three parameters on Delta. Delta was most sensitive to the Patriarchal Drive Coefficient, which gave a slope of -18.2 as the maximum number of mutations, C in Equation 1, increased from 10 to 50. Figure 6 shows the average number of new mutations added per male per generation for various settings of the Patriarchal Drive Coefficient, C. Table II gives the model's parameters and their standard settings during the optimization procedure. Tables III–V show the data displayed in Figure 5. As the number of GK sons, bottleneck mortality, and Patriarchal Drive Coefficient increased, Delta decreased.

Model Analysis

The program was analyzed in a Monte Carlo fashion by running it three hundred times with these optimized parameters: GK sons 100, Bottleneck mortality 75–85%, Patriarchal Drive

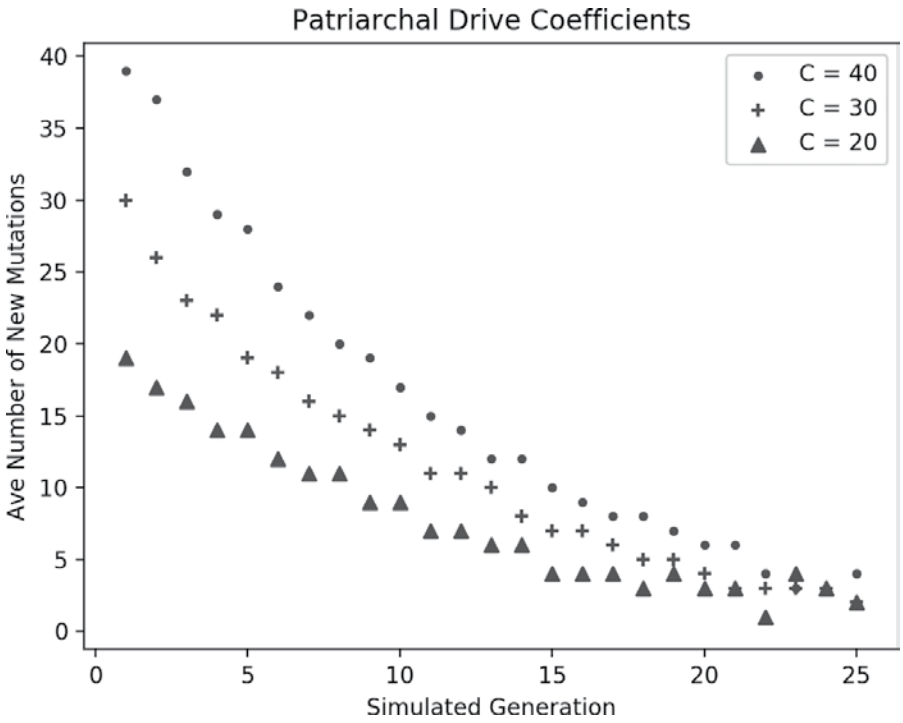

Figure 6. Model "Y_sim_Pdrive.py" output for various Patriarchal Drive Coefficients, C, showing average number of new mutations per male at each simulated generation. Based on Equation 1, $u(g) = C\ e^{-0.09g}$, with added random variation of 2 standard deviations around a Gaussian of mean u(g).

Table II. Parameters of the model (Y_sim_Pdrive.py) and their standard settings during the optimization procedure.

Parameter	Setting
growth rate	random 4–7 per male per generation
mutation rate	$u(g) = C\ e^{-0.09g}$, C = 30, g = generation
annual mortality	20–30% per subpopulation
subpopulation maximum	S = 400, H = 500, J = 600
GK sons	random selection of 50–150 sons
Bottleneck events	Gen. 4, 5, 6, 9, 10, 12, 22
Bottleneck mortality	random between 65% and 85%

Coefficient 42. Figure 7 shows the distribution of Deltas produced. Figure 8 shows a Q-Q plot of the Deltas versus a normal distribution. The mean Delta was 7.46, the SD was 188, and the 95% confidence interval was -18.9 to 33.9 (n = 200). Since a Delta of zero falls within the 95% confidence interval, the model run on these settings yields results closely matching the 1000G data.

The effect of population bottlenecks on mutation accumulation was analyzed by running the model for 25 generations with and without bottlenecks, other parameters being held constant. At 10 generations, the total number of mutations, number of extant mutations, and number lost to drift were 773162, 95023, 678139 for the run with no bottlenecks and 520002, 11683, 508319 for the run with bottlenecks. Total mutations were lower in the run with bottlenecks due to lineage losses caused by population collapses. Figure 9 shows the percent of mutations lost due to drift for the two scenarios. By generation 10 without bottlenecks, 88% of the total mutations had been lost due to drift. With bottlenecks included, 98% of total mutations had been lost due to drift by generation 10. Thus, the model demonstrates the effects of population bottlenecks, which increase the loss of mutations by drift (Carter, 2009), thus altering the allele frequency distribution. Since the most likely lost mutations are rare, the percentage of common variants is increased, consistent with the common variant pattern seen in the 1000G data.

Patriarch Profiles

One interesting result supported by the model is the persistence and prominent location of AF bins containing the original mutations of the three sons of Noah. These "Patriarch Profiles" should exist on the Y chromosomes of all men, according to which of the three lineages they belong, due to the clonal inheritance of mutations on the Y chromosome. The model's output, in the graphic form of the allele frequency distributions, always displays the three patriarch AF bins as the highest frequency variants for each lineage. When the number of men carrying each patriarch

Table III. Optimization of Number of Sons fathered by opportunistic reproducers (GK function). One man in each generation in each subpopulation fathered many sons. Delta = 861 minus average number of variants of AF 16–32% (100 iterations). S. D. = 1 standard deviation.

Sons	Delta	S. D.
50	666	92.5
75	549	117
100	456	127
125	395	137
150	354	143

Table IV. Optimization of Bottleneck Mortality. Average Delta over 100 runs of 25 generations with Mortality 50 to 90%. Delta = 861 minus average mutation count between AF 16–32% (100 iterations). S. D. = 1 standard deviation.

Mortality %	Delta	S. D.
50	720	57.5
60	685	76.7
70	638	99.2
80	469	124.0
90	381	119.0

Table V. Optimization of Patriarchal Drive Constant, C, in the mutation function where the number of new mutations per man per generations is $u(g) = C\, e^{-0.09g}$ (equation 1). Delta = 861 minus average number of mutations between AF 16–32% (100 iterations). S. D. = 1 standard deviation.

C	Delta	S. D.
10	654	127.0
20	485	96.4
30	281	106.7
40	56	167.9
50	-74	213.9

signature are added, the sum is the total population at the end of the model run. The mutations that accumulate in the lineages that branch off and descend from the three patriarchs are always in AF bins of lower frequency than the patriarch bin. Some of these "descendant" bins become common AF bins due to demographic events, but most of them remain uncommon or rare.

Discussion

A biblical model of human history requires an explanation of how the Y chromosome genetic diversity found in the world today has developed within the 4,500 years since the Flood. The large number of rare variants found on Y chromosomes today are due to rapid population expansion, which is amply detailed in historic records. These rare variants have accumulated as mutations were passed down in a clonal fashion to the rapidly increasing number of new male lineages. But simple clonal inheritance of mutations cannot explain the common variant pattern of the Y chromosomes found in large databases because new mutations in a rapidly expanding population produce rare variants. Major demographic events, such as population bottlenecks and the fathering of many sons by a few men, must have occurred while the population was small in order to produce these common variants. The historic events recorded in Genesis provide the basis of an explanation for the Y chromosome common variants. With this in mind, the computer model presented in this paper was calibrated to show how population collapses and opportunistic male reproduction, together with increased mutation rates in the early post-Flood world, could produce the common variant pattern.

At 25 generations, the model matches the real data when the optimized parameters are set according to the events recorded in Genesis and Exodus. But how realistic are these parameters?

Population Collapses (Bottlenecks) Due to Historic Events

After the Flood, the next bottleneck in human population was the Babel event, where people scattered from a civilization into an uncharted wilderness. Some may argue that these people were primitive, bronze-age nomads used to survival in adverse circumstances. The biblical record says otherwise. The city of Babel was a civilized place, for they had a common language and culture (Genesis 11:1), a ceramic industry (Genesis 11:3), engineering and architecture (Genesis 11:4), a long term strategic plan (11:4), and they were organized with an administration or government (Genesis 11:3–4). The industries of the pre-Flood world were known to Noah and his sons, who lived until after the Babel event. For example, they knew how to build cities (Genesis 4:17), they knew about metallurgy in copper and iron (Genesis 4:22), and animal husbandry (Genesis 4:20). Furthermore, Noah and his sons had built the largest, ocean-going boat the world has ever seen until the advent of twentieth century supertankers and container ships. Such activities require mathematical and engineering knowledge as well as organization. These are the trappings of civilization.

However, the world into which the refugees of the Babel civilization were scattered was completely unknown and unpeopled. Recent historical examples of people leaving civilizations to live in unknown and under-populated areas give some measure of how much of a population collapse might accompany such a migration. The Pilgrims, who established the Plymouth Colony in AD 1620, lost 47 of the 102 passengers of the Mayflower by the end of their first winter in the New World, due to starvation and disease (Bradford, 1920, p. 85). The 121 of Roanoke Colony in AD 1518 completely vanished (Lawler, 2017). The Jamestown Colony of AD 1607 was nearly wiped out, and so was abandoned after 3 years, when 80 to 90% of the original 100 settlers were dead (Stebbins, 2011). Starvation and disease played a big role in the failure of these colonies, but strife with the local American Indians was also a contributing factor. While those who left Babel had no natives to contend with, neither did they have help from friendly natives, as Squanto helped the Pilgrims (Bradford, 1920, p. 85). Also, the Ice Age was building up soon after the Babel event (Snelling and Matthews, 2013), which would cause crop failures and starvation to those who had settled in Europe and northern Asia. Given these historic events and considerations, it does not seem inappropriate to set the bottleneck collapses in the range of 80%.

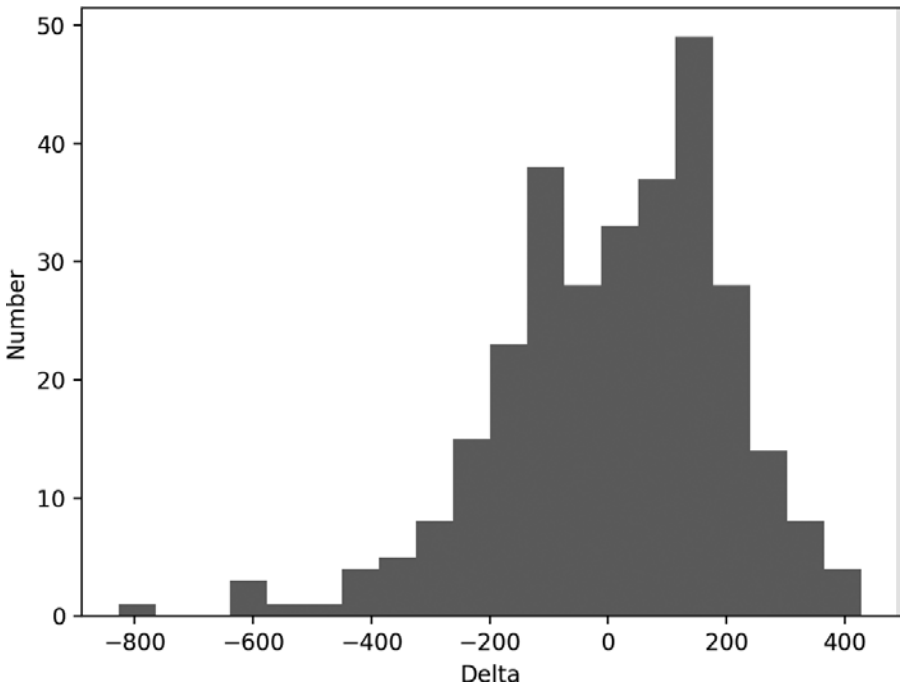

Figure 7. Distribution of Deltas from 300 runs of " Y_sim_Pdrive.py" with optimized parameters: GK sons 100, Bottleneck Mortality 75–85%, Patriarchal Drive Coefficient 42. Delta is the number of variants of AF 16–32% in the 1000G data (861 variants) minus the number in this range in the model's output at the end of each run of 25 generations.

For most of the recorded events, the Bible gives no hint regarding how much of a population collapse occurred (Carter and Lightner, 2016). The record is silent on the degree of population decline at Babel, the Ice Age, and the famines in Canaan during the days of Abraham and Isaac. However, the famine of Joseph's day was said to be worldwide (Genesis 41:57), in which case a 50% or greater collapse does not seem unreasonable. "Worldwide" need not include the Americas or Oceana and Australia in 2000 BC, because the population then is estimated to have been only a few million (Jeanson, 2019). Likely, migration farther than Asia had not yet occurred, or only to a limited extent. Such a worldwide famine probably caused a population collapse similar to

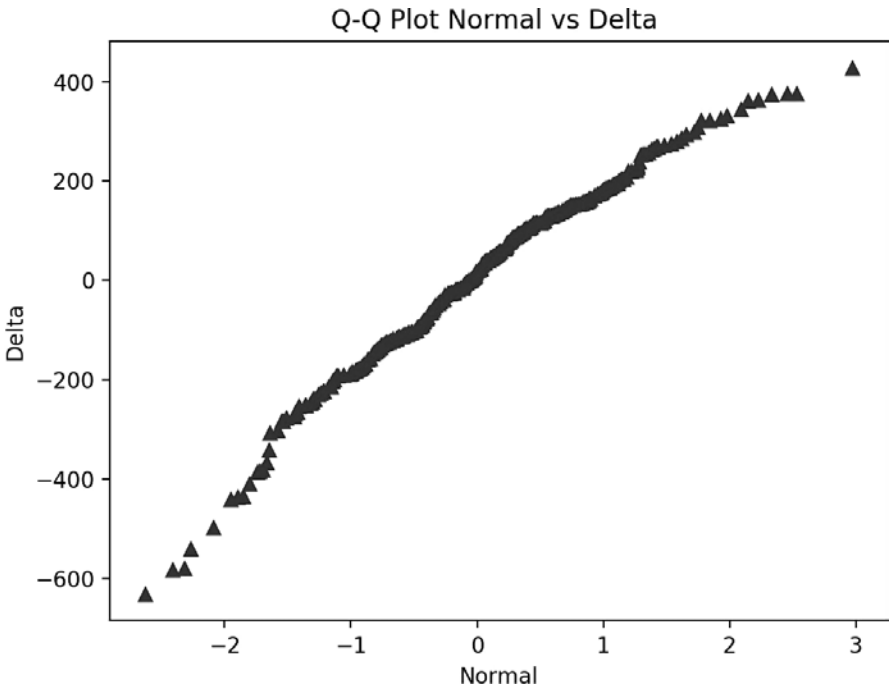

Figure 8. Normal Q-Q Plot of Deltas vs Normal distribution from 300 runs of "Y_sim_Pdrive.py" with optimized parameters: 100 GK sons, Bottleneck Mortality 75–85%, Patriarchal Drive Coefficient 42. Delta is the number of variants of AF 16–32% in the 1000G data (861 variants) minus the number in this range in the model's output at the end of each run of 25 generations.

that of the Babel event. Regarding the population collapse of generation 22, since the children of Israel in Egypt were a large part of the population (Exodus 1:7), the genocide practiced by Pharaoh at the time of Moses' birth, directed as it was against the male children, may have caused a loss of male lineages similar to that of major wars throughout history.

The high values of parameters required to match the 1000G data within 25 generations raises the question whether demographic events later in history, up to the present, have contributed to the common variant pattern. The program might generate the same common variant pattern with smaller parameter values if the simulation were extended to 100 or more generations with frequent bottlenecks. The question then becomes whether population bottlenecks of 80% have occurred in recent times of larger world population.

The bottleneck events recorded in Genesis occurred when the world's population was small, likely no more than a few thousand during the Ice Age. By the time of Moses, 22 generations post-Flood, the population had increased to several million, a 6-fold increase from Noah's family (Jeanson, 2019). The demographic effects of bottlenecks on genetic data will be greater for small populations than for large and rapidly growing populations. Given the large population today, even the catastrophic losses of male lineages in the 20th century (White, 2016; Satter, 2017) would not be expected to alter the common variant pattern of Y chromosome data drawn from the entire world of over 3 billion men. Simply put, population collapses of 80% have not occurred upon a worldwide basis in recent times. The loss of male lineages from the very large population of modern times would not affect genetic variant frequencies to the same degree as population collapses much earlier in history when the total population was only a few million or less (Carter, 2019).

Massive population bottlenecks are more likely to have occurred in the Middle Ages, when the total population was less than 200 million (Jeanson, 2019). In the 13th century bubonic plague may have wiped out a half of Europe (Benedictow, 2005). History does not record the mortality suffered in China, where the plague originated, but it may have been even greater. A case can be made for 50–80% population collapses during the Middle Ages. The effect of bubonic plague on the genetics of the Y chromosome have yet to be investigated.

Other than population collapses, demographic factors such as differential reproduction within subpopulations, have likely contributed to the production of some common variants by favoring some male lineages over others. This may explain the haplogroup of R1b3 found in Ireland in 20% of the men living there today. This variant originated from a man in Asia around AD 1000 (Moore et al., 2006). The R1b3 is denoted by SNP M269, which falls in minor AF bin 17% in the 1000G data. This mutation is an example of a recent demographic trend producing a common variant on the Y chromosome in the 1000G data. But on a worldwide scale, such more recent demographic events have less effect than similar events in ancient times. So, based on these theoretical considerations, the bottleneck events recorded in Genesis and Exodus are likely the major cause of the common variant pattern seen in the Y chromosome data.

Opportunistic Male Reproduction

Adjusting the model to produce variant patterns similar to the 1000G data also required the advent of men who fathered 50 to 100 sons or more. These opportunistic breeders are well documented in the Bible and throughout history up to the present. A recent, notorious example is an NBA basketball star of the 1970's, who claimed to have had sexual relations with 20,000 different women during his life. If 1% of these women had given birth, he could have fathered 100 sons. Similar feats of male reproductive prowess stretch back to ancient times. Solomon had 700 wives and 300 concubines (I Kings 11:3). If half of these became pregnant, 250 sons may have been born. Like Solomon, Genghis Khan is thought to have had many wives and many sons (Zerjal et al., 2003; Carter, 2009). Unlike Solomon, Genghis Khan slaughtered many young men as his armies ranged over half the world (Zerjal et al., 2003). It is a sordid fact of human history that those who achieve great military victories and slaughter entire male populations tend to celebrate their victories by impregnating all the wives and daughters of the defeated. Thus, wars often have resulted in the extinction of large numbers of male lineages and repopulation by the sons of the conqueror. When this aspect of history was incorporated into the model, combining opportunistic male reproduction with population bottlenecks, the common variant pattern more closely resembled the 1000G data.

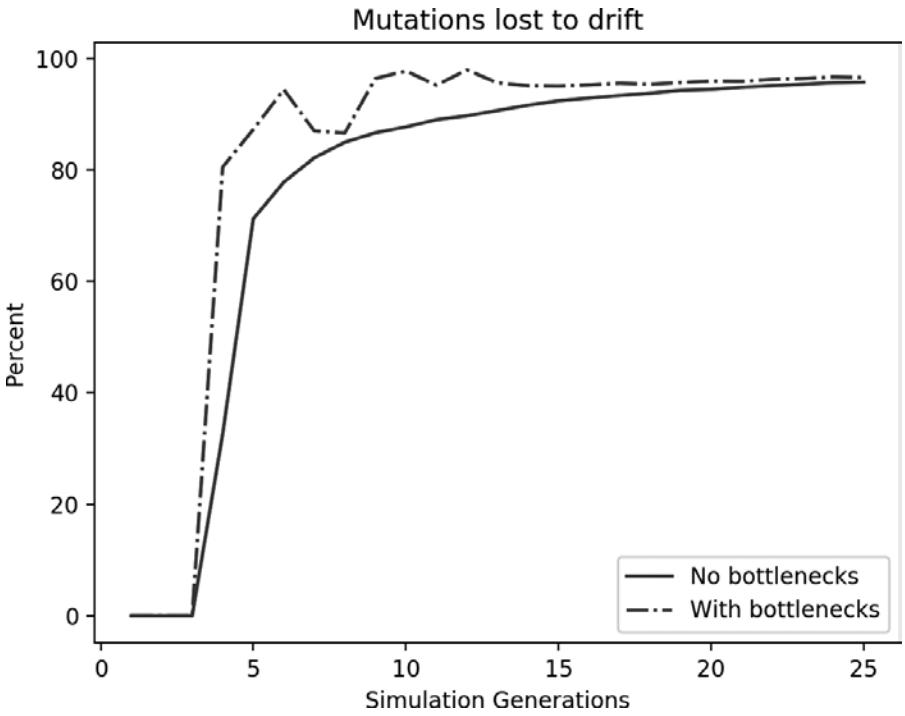

Figure 9. Mutations lost to drift over 25 simulated generations for the model "Y_sim_Pdrive.py" run with and without population bottlenecks at generations 4, 5, 6, 9, 10, 12, 22. All bottlenecks were 80% mortality. Percent = 100 X (number of mutations lost / total mutations).

Patriarchal Drive

Patriarchal drive may also have contributed to the formation of the common variant pattern. Patriarchal drive refers to the genetic effects of very old men fathering children in small populations. A mutational load builds up in the sperm of aging fathers as the germ cells continue to divide throughout the man's life (Carter, 2019) so that older fathers pass on more mutations. Since Noah was 500 years old when his sons were born (Genesis 5:32), assigning 30 or more unique mutations to each of his sons is justified. The increased mutation rate of patriarchs is implicated as a cause of the deep-node structure of the Y chromosome phylogenetic tree, where the ancient branch lengths are much longer than recent branches. This explanation for the branch-length disparity is confirmed by Carter's computer model of patriarchal drive (Carter, 2019). Another explanation could be that the long branch lengths are due to population collapse, as implicated for the structure of the Native American phylogenetic tree analyzed by Jeanson (2020). The loss of many male lineages due to population collapse also lengthens branches of the phylogenetic tree.

The Patriarchal Drive Coefficient had to be set to 42 to cause the model's output to approach a Delta of zero. Lower values of C would not allow the Delta to approach zero in 25 generations even with bottleneck mortality set to 90%. Extending the simulation to 180 generations and adding 80% bottlenecks every 5 generations caused the model to produce a Delta approaching zero with no patriarchal drive mutations added. Because these different sets of parameters were both able to force Delta to zero, the model alone does not allow conclusions regarding historically accurate parameter settings.

Other Implications of the Model

The model's output suggests several conclusions about human population growth. The population at Babel was several thousand when the reproductive rates of Shem, Ham and Japheth are extended to Generation-4. The world's population would have reached billions before 1000 BC had not bottleneck events intervened to severely limit population growth. In the model, the population recovers rapidly following bottlenecks. This is consistent with historical records which indicate that, by 1000 BC, a 7-fold population increase had occurred from after the Flood (Jeanson, 2019).

Since the model does not account for the effects of mutations on individual fitness and reproductive success, and since the common variant pattern of the 1000G data can be modeled by demographic changes alone, natural selection of beneficial over deleterious mutations appears to be irrelevant. This is consistent with the observation that today a man's reproductive success has to do with survival from war and famine, and decisions regarding marriage and family, rather than any apparent fitness conferred by superior genes.

With each run of the model, the patriarch signatures of Noah's sons remain as prominent common AF peaks on the plot. If the model is an accurate representation of Y chromosome inheritance, the patriarch signatures of Noah's sons should be evident in the 1000G data, as the highest AF bins for each lineage. This idea is currently under investigation. However, if the model's assumptions are not true, then patriarchal variant signatures may not be discernible today. For example, the model assumes no crossing over, no gene conversion and no homoplasy (Carter, 2009). If these processes frequently occur for the Y chromosome, then the Y chromosome common variants may not contain patriarchal signatures.

Summary

Based on the historical events recorded in Genesis, the common variant pattern found on the Y chromosomes in the 1000 Genome database was reproduced by a computer model in 25 simulated generations post-Flood when population bottlenecks, opportunistic male reproduction, and high patriarchal mutation rates were added to the Growth, Mutation, and Famine functions. This indicates that major demographic disruptions, in the form of massive extinctions of male lineages, may have accompanied the Babel event, the Ice Age, and the famines and genocide recorded in Genesis and Exodus. The establishment of new male lineages by feats of reproductive prowess, is also implicated as a cause of the many common variants on the Y chromosomes of the world. Truly, this gives a dark picture of the character of the human male and his blood-stained history, yet this fallen character is well documented in the pages of the Bible. The reign of death due to sin described in Genesis has left a genetic record on the Y chromosome. Because mutations in the model were neutral with respect to survival and reproduction, it can be inferred from this study that natural selection, favoring beneficial mutations and eliminating unfavorable ones, has played a minor role, if any, in producing the current pattern of variants on the Y chromosomes of the 1000G database. Rather, high patriarchal mutation rates, the demographic events recorded in Genesis causing massive extinction of male lineages, and the advent of occasional men fathering hundreds of children, is the major cause of these patterns. The model indicates that the patriarchal patterns of mutations should still be discernible in the Y chromosome databases, an area of ongoing study.

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