
Alan Dickin

The Table of Nations and the Spread of Human Civilization: New Genetic Evidence

Alan Dickin

Adam is regarded as either the biological or the spiritual father of the human race. However, since all of Adam's descendants except Noah and his family were annihilated by the Flood, the biblical account of humanity's dispersal over the earth begins in the Table of Nations (Genesis 10). On the other hand, scientific evidence describes two episodes of mass human migration, when small groups of modern humans spread out geographically to cover much of the earth. The first of these was the "out of Africa" migration around 55,000 years BC, while the second was a lesser-known agriculturalist migration from the Middle East beginning around 8000 BC.

The objective of this article is to compare genetic evidence for the second of these two migrations with the biblical Table of Nations. Dating Noah's Flood to the Neolithic Period is a key step to bringing the Table of Nations and the agriculturalist dispersal event into harmony. Genomic evidence shows that the outward spread of agriculturalists from southeast Anatolia began slightly earlier than the most likely date of Noah's Flood in Mesopotamia. However, the outward migration of agriculturalists probably left behind deserted villages in southeast Anatolia and Northern Mesopotamia that resembled the ruined settlements of Southern Mesopotamia devastated by the Flood. Hence, it was natural that ancient peoples attributed the outward migration of Neolithic agriculturalists to the spread of Noah's descendants, conflating these movements out of Mesopotamia. It is concluded that Genesis contains a remarkably accurate picture of the Neolithic origins and spread of human civilization in the Middle East.

There have been many attempts to reconcile Genesis with a scientific account of origins. One approach envisages biblical Adam and Eve as the first modern humans, and hence as the biological ancestors of the human race. An African origin for the human race has long been implied by fossil evidence, and in the 1980s this was supported by mitochondrial DNA evidence, requiring a common origin of all human mitochondria from a single African woman who lived around 200,000 years ago.[1] Since that time there has been a flood of genetic and anatomical data that point to the origins of modern humans (*Homo sapiens*) in Africa around 300,000 years ago.[2] Nearly a quarter of a million years later, the principal exodus of humans from Africa occurred around 55,000 years ago,[3] but a smaller exodus that led to the populating of Australia may have occurred about 20,000 years earlier.[4]

In recent articles attempting to reconcile the genetic evidence with a view of Adam as the biological father of the human race, David Wilcox placed biblical Adam in Africa around 150,000 years ago.[5] He suggested that Adam might have emerged from a demographic bottleneck that allowed a small society of humans to undergo divine enculturation, when

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"divine revelatory activity programmed a new cultural operating system into the brain(s) of one (or a few) humans."[6] Wilcox speculated that this was also the point at which human sin entered the picture, as a conscious decision to disregard God's authority.

Theologically, it has been argued that common descent from Adam is necessary to preserve the "common dignity of all people."[7] However, this model raises problems of both a temporal and spatial nature. Temporally, it situates Adam in the remote prehistoric past, tens of thousands of years before the agricultural setting of his sons Cain and Abel. Spatially, it moves Eden from Mesopotamia to Africa, requiring Adam's descendants to be dispersed from there around the world. This is a problem because the Bible contains no hint of an epic migration out of Africa that led to human dispersal over the earth. On the other hand, Genesis does claim a major human dispersal event, beginning after Noah's Flood and commonly referred to as the Table of Nations (Genesis 10).

The Table of Nations comprises a family tree of Noah's three sons—Shem, Ham, and Japheth—who are claimed to be the ancestors of all Middle Eastern peoples. This account of human dispersal from Noah's sons could be connected with the migration out of Africa around 55,000 years ago. However, recent genetic evidence records a less well-known but equally dramatic migration event that occurred in the Neolithic Period after 9000 BC. This new evidence, published in the past five years, includes genome-wide DNA signatures obtained from hundreds of modern and ancient individuals. Hence, it seems logical to see whether this new evidence can help us understand the story of human dispersal told in the Table of Nations.

The Origins of Human Civilization

A Neolithic human dispersal event would be consistent with the more recent setting for Adam proposed by Denis Alexander, "God in his grace chose a couple of Neolithic farmers in the Near East, or maybe a community of farmers, to whom he chose to reveal himself in a special way."[8] If this view is correct, Adam cannot be the biological father of the human race. However, John Walton has argued that Adam's unique biblical status derives not from his biological parenthood, but from his election by God as a *priestly representative* of humankind.[9] In this way, all of humanity would have inherited the spiritual consequences of Adam's sin without being his biological descendants.

Placing Adam in a Neolithic setting suggests that Genesis is describing events associated with the origins and spread of human *civilization* rather than the human race as a whole. For example, several lines of evidence suggest that Adam's sons were not alone on the earth in Genesis 4: Cain fears retribution from unknown assailants; he mysteriously finds a wife; and he becomes a city builder, implying a significant number of people living together. The description of Cain as a city builder is critical because civilization literally means "life in cities." If Genesis is describing the origins of human civilization, this implies that the Table of Nations is describing the spread of civilization after the Agricultural Revolution. However, Genesis also claims that this spread of civilization was interrupted by Noah's Flood. Therefore, if the Flood was a real event, it is critical to understand its time and place in the story of human origins.

The Significance of Noah's Flood

The Great Flood is an important reference point in human history because it is reported in three different Mesopotamian accounts, allowing detailed comparison with the biblical Flood story. Since the nineteenth century, the common origins of the biblical and Mesopotamian accounts have been understood, based on minute similarities such as the sending out of birds to test the abatement of the floodwaters.[10] Based on this commonality, there has been strong reliance on Mesopotamian literary evidence to date Noah's Flood.

The most well-known version of the Sumerian King List (the Weld-Blundell prism) has been widely used to date Noah's Flood to around 2900 BC, at the beginning of the Early Dynastic Period of Sumerian history.[11] However, an earlier version of the Sumerian King List contains no mention of the Flood or the ante-diluvian dynasties that were supposed to have ruled Mesopotamia before the Flood.[12] Furthermore, these ante-diluvian dynasties are known to be mythical, since archaeological evidence shows that Uruk was the dominant city of ancient Mesopotamia prior to the Early Dynastic Period.[13] Therefore, it is evident that the King List does not provide any reliable evidence to date the Flood. However, both the biblical and Mesopotamian literary sources provide indirect evidence for its date.

All of the ancient sources agree that there were no known survivors of the Flood outside the Ark, and these claims of human annihilation are supported by the New Testament letters (Heb. 11:7; 1 Pet. 3:20; 2 Pet. 2:5) and the quoted sayings of Jesus (Matt. 24:38–39; Luke 17:26–27). Hence, these sources validate the ancient belief expressed in the Table of Nations that the earth was repopulated by Noah's sons after the Flood. This is important because this belief is credible only if the Flood is placed in the remote prehistoric past, not at the mature stage of civilization that is implied by the Weld-Blundell prism.

A Neolithic date for the Flood is supported by archaeological evidence, which reveals a complete continuum of mud-brick architecture in several cities of ancient Mesopotamia, going back to around 5500 BC.[14] It is highly unlikely that such architecture could have survived prolonged inundation without signs of water damage. When this evidence is coupled with the complete interruption of human civilization described in both biblical and Mesopotamian Flood stories, it points to a date for Noah's Flood before 5500 BC. This is supported by geological and paleoclimate evidence for a period of intense rainfall events in the first half of the sixth millennium BC, in the Late Neolithic period.[15] However, evidence that the Flood occurred in the Late Neolithic period has led some scholars to suggest that it was not the result of a catastrophic river flood, but was caused by sea-level rise after the last glacial period. One of the most widely known of these alternatives is the Black Sea deluge theory.

The Black Sea Deluge Theory

The Black Sea was isolated from the Mediterranean during the last Ice Age, when global sea-level dropped below the bottom of the Bosporus Strait (BS, fig. 1). During much of this time, the level of the Black Sea was maintained by river flow from the north. However, based on evidence for a period of aridity during the Younger Dryas event beginning around 11,000 BC, the level of the Black Sea could have dropped at that time. As a result, settlements might have been established on the ancient shoreline at depths up to 100 m below present-day sea-level (locations marked RP in fig. 1). Therefore, when rising sea-level overtopped the Bosporus Strait, any such settlements would have been submerged when the Black Sea was refilled. Since the level of the Black Sea could have risen by up to 10 cm per day, this might have led to ancient Flood myths.

Proposed by Ryan and Pitman,[16] the Black Sea deluge theory led to a vigorous debate that has continued over many years. Ryan has continued to defend the original model in several papers, including recent geophysical investigations.[17] However, the model has been weakened in several ways. Firstly, all authors now agree that the initial entry of Mediterranean water into the Black Sea had already begun by 7300 BC, and possibly as early as 7600 BC, approximately 2,000 years earlier than originally proposed.[18] This suggests that seawater incursion was much slower than originally thought.[19] In fact, seawater could have entered the Black Sea by seeping along the bottom of the Bosporus Strait, even if there was a net outflow of fresh water from the Black Sea at the same time.[20] This flow pattern exists at the present day, with brackish water flowing southwards along the Bosporus at the surface while salt water flows northwards at the sea bed.

These lines of evidence greatly weaken the idea that the flooding of the Black Sea caused catastrophic loss of human life. However, there is even more critical

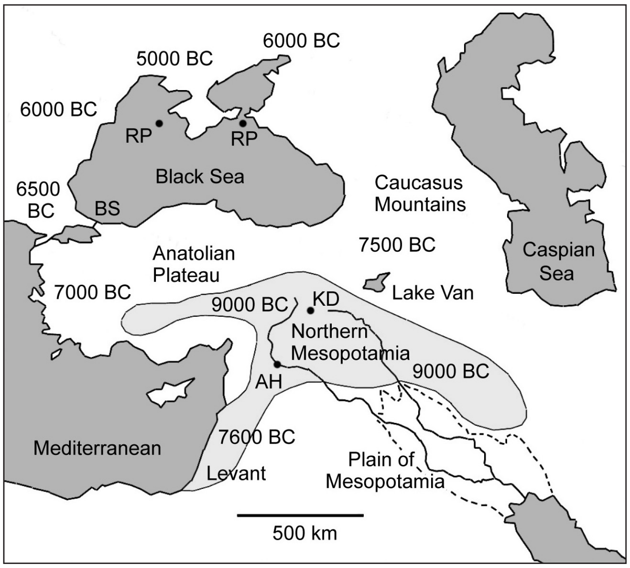

Figure 1. Map of the Middle East showing alternative sites of a Neolithic Flood (the Black Sea and Mesopotamia) relative to approximate dates for the appearance of Neolithic culture in different regions. Locations mentioned in the text: BS = Bosporus Strait; RP = sites examined by Ryan and Pitman; KD = Karaca Dag; AH = Abu Hureyra. Modified after Broushaki et al.[21]

literary evidence against the idea that the flooding of the Black Sea inspired the story of Noah's Flood. After the incursion of sea-water, the level of the Black Sea never subsequently went down, whereas the receding floodwaters and the drying of the earth are vitally important parts of the story of Noah's Flood. Therefore, given that the preceding and following chapters in Genesis are set in Mesopotamia, it is clear that Noah's Flood was a catastrophic river flood on the Mesopotamian plain. This location for the Flood is also closely adjacent to the earliest appearance of Neolithic culture arising from the Agricultural Revolution (grey shading in fig. 1).

The Agricultural Revolution

Although some claims have been made for early forms of agriculture in isolated populations during the last Ice Age, there is little doubt that the Agricultural Revolution as a world-changing event began around 9000 BC, initiating the Neolithic Period. Around this time, the first signs of animal husbandry are indicated by a change in the age and sex distribution of sheep and goat skeletons from ancient settlements.[22]

Based on skeletal remains, it was observed that earlier societies had focused their hunting efforts on the largest mature specimens of prey animals. During the Younger Dryas period, wild populations were probably stressed by the adverse cold, dry conditions.[23] In response, it appears that Neolithic humans reacted by beginning to manage wild sheep and goat populations, targeting young males and sparing females until they had reached menopause. This change in the skeletal assemblages suggests that domestication of sheep and goats began around 9000 BC, the former in northwestern Mesopotamia (SE Anatolia) and the latter to the east (Zagros Mountains), with an overlap in the Lake Van area of Eastern Turkey (fig. 1).

A short time later, around 8500 to 8000 BC, the domestication of pigs and cattle is also identified near the upper reaches of the Tigris and Euphrates rivers of Northern Mesopotamia (fig. 1). Subsequently, these domesticated groups spread out along the Fertile Crescent, which is the zone with sufficient rainfall to conduct subsistence farming without the need for irrigation. For example, domesticated goats reached the Levant around 7600 BC, followed shortly by sheep, pigs, and cattle.

Evidence for the domestication of cereal crops is recorded in a somewhat different form, by the selection of grain morphology that made cereals more suitable for harvesting and threshing.[24] In wild varieties of wheat and barley, the seed is weakly attached to the rachis (stem) of the ear, allowing individual grains to be easily detached, while the husk is strongly attached to the seed, promoting wind dispersal. In contrast, domesticated varieties have seeds that are more strongly attached to the ear (preserving it intact until harvesting), while the husk is more readily detached during threshing. In the earliest domesticated wheat variety, called Einkorn, the readily detached husk leads to what are called "naked" seeds. These seeds are also larger than wild wheat seeds, providing better nutrition. These changes in grain morphology (particularly the appearance of naked seeds) allow the appearance of domesticated cereals to be detected around 9000 BC at Abu Hureyra in Northern Mesopotamia (fig. 1).[25]

Because wild cereal populations persist to the present day as weeds, their genetic diversity is more readily compared with domesticated varieties than is possible for domestic animals (whose wild populations are depleted). This allows the geographical site of cereal domestication to be determined from genomic data on modern cereal varieties. The evidence suggests that cereal crops also originated from the region of Northern Mesopotamia. In the case of einkorn wheat, the genetic evidence suggests that all domesticated varieties arose from a single branch of the wild population (fig. 2). The wild einkorn population most closely related to domesticated wheat comes from the region of Karaca Dag, located in southeast Turkey between the headwaters of the

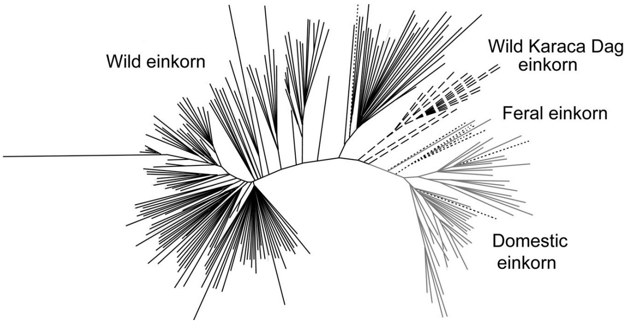

Figure 2. Genetic tree of einkorn wheat, showing the common origin of all domesticated varieties (grey lines) from wild Karaca Dag wheat (dashed lines). Feral wheat varieties (dotted lines) are a secondary mixture of wild and domesticated wheat. Modified after Salamini et al.[26]

Tigris and Euphrates (fig. 1). Therefore, it is inferred that the domestication of wheat occurred in this mountainous area of Northern Mesopotamia.

Human Genetic Studies

Archaeological evidence suggests that the practice of agriculture spread across the world in the millennia after the Agricultural Revolution. This spread was particularly dramatic in Europe, where it appeared to move from Eastern to Western Europe in an enormous wave of human migration.[27] Hence, this model was very attractive for testing using genetic analysis.

With the first developments of nuclear (autosomal) DNA analysis in the 1970s, it was realized that information from a large number of different gene loci on several chromosomes could be combined using the statistical method of principal component analysis (PCA). This technique identifies the greatest degrees of genetic variation (polymorphism) across a large number of chromosomal locations. The individual genetic variations are called single nucleotide polymorphisms (SNPs), commonly referred to as "snips," whereas the principal components of variation are termed "eigenvectors."

A genome-wide study of genetic variation in modern Europeans found large-scale trends along the axes of the principal eigenvectors, suggesting large-scale genetic mixing that was best explained by the spread of agriculture across Europe.[28] More recent principal component analysis of genome-wide SNP variations in modern human populations is shown in figure 3. This figure shows that the extremes of the distribution are present in relatively isolated people-groups, whereas less-isolated people groups are the products of genetic mixing. For example, the Turkish population field (dashed envelope) shows evidence of mixing with groups to the north and east, with additional mixing trends toward the Greek and Cypriot fields that are not shown in figure 3.

Although the genomic data from modern people are clearly indicative of population mixing, there is substantial ambiguity about the nature and date of mixing processes. For example, it is not clear whether the spread of agriculture across Europe and consequent genetic mixing was caused by mass human migration, or by "word of mouth" communication of the *idea* of agriculture, coupled with multiple local population mixing events. Genomic analysis of modern individuals cannot distinguish between these models, which can be resolved only by sampling ancient human DNA.

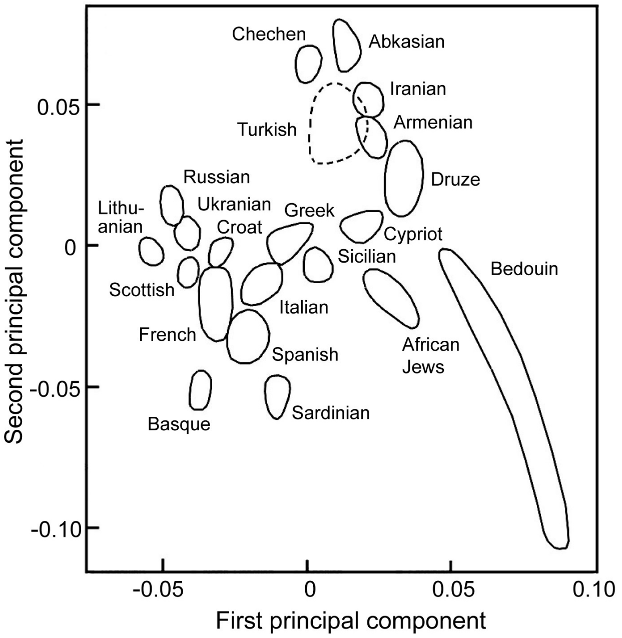

Figure 3. Genomic data for modern humans plotted to show two principal eigenvectors. Note that outliers have been omitted from the Turkish field. Modified after Lazaridis et al.[29]

Ancient DNA Analysis

Until recently, it was not possible to extract usable amounts of DNA from ancient burial sites and distinguish it from modern contamination. For this reason, the first genomic studies of ancient human DNA (*Homo sapiens*) were made on frozen bodies. For example, DNA analysis of hair from a 4,000-year-old Paleo-Eskimo from western Greenland yielded an autosomal DNA signature similar to eastern Siberians, and also showed that mitochondrial and Y-chromosomal DNA were derived entirely from the same northeast Asia haplogroup.[30] Because mitochondrial and Y-chromosomal DNA are defined by inheritance through only one parent, they are not as useful as autosomal DNA to characterize complex population mixing histories. However, they are very useful for testing modern contamination. For example, these data showed that no modern European contamination had been introduced during laboratory processing in Denmark.

Since DNA undergoes much more rapid deterioration as temperatures increase, it is much more difficult to recover usable amounts of DNA from (nonfrozen) skeletal remains. These samples typically contain only 1% of ancient human (endogenic)

DNA, the remaining 99% being largely bacterial and fungal DNA.[31] Therefore, the first successful genome-wide study of ancient human migration patterns was based on 5,000 year-old bones and teeth from Sweden[32] where DNA preservation was enhanced by the cold climate. As an additional precaution, samples were leached before DNA extraction with 0.5% bleach, which preferentially removes modern contamination.[33]

The techniques of DNA analysis in the Swedish study[34] were typical of modern "next-generation" sequencing.[35] These began with DNA extraction using a proteinase buffer and purification by centrifugation through columns containing silica-gel membranes.[36] Marker sequences were then added to the ends of DNA fragments, creating "adaptor-ligated sequence libraries." The method is based on the parallel method of sequencing modern DNA by deliberately fragmenting the genome into short pieces.[37] Since ancient DNA is already fragmented in short pieces (20–100 base pairs),[38] adaptor ligation was applied directly to the extracted DNA.[39] All DNA in the sample was then amplified and sequenced (shotgun sequencing) on the *Illumina* platform, after which the nonhuman data were discarded.

Due to the relatively cold conditions in the Swedish burial sites, useable fractions of endogenic human DNA were recovered (2.4–6.35%). However, samples from temperate latitudes are much more demanding, since they contain a lower fraction of preserved ancient DNA. The best recovery of ancient DNA is achieved from the interiors of teeth[40] and dense regions of bone such as the limbs and the base of the skull near the inner ear.[41] In addition, DNA extraction and purification methods have been adapted to enhance the recovery of very short fragments (< 40 base pairs).[42] However, the fraction of endogenous DNA may still be too low for cost-effective sequencing. Therefore, a method was developed to selectively target and extract short segments of ancient human DNA by attaching "capture probes." For genome-wide DNA studies, capture probes are obtained from short pieces of modern DNA corresponding to SNPs right across the human genome.[43] This DNA is used to make a "bait library" of RNA which is then amplified and reacted with ancient human DNA in the sample. The RNA probes are made to bind chemically to magnetized microbeads, allowing the attached endogenic DNA to be extracted magnetically, after which it is amplified and sequenced in the normal way.

The final stage of data collection is to merge overlapping sequence reads (e.g., > 15 bp length with 95% agreement)[44] into longer sequences, and then map these onto a human reference genome in order to identify SNPs.[45] The resulting data set can then be analyzed statistically.

Mesolithic and Neolithic Human DNA

The analysis of dated ancient samples is critical in order to move from speculative theories of ancient human migration to well-constrained models. This is now possible for the first time due to the publication of genome-wide DNA data from over 500 ancient humans.

To study human migration after the Agricultural Revolution, it is critical to define the genetic signature of local hunter-gatherer populations before the Agricultural Revolution. In this way, any migration of agriculturalists from one region to another can be clearly demonstrated by changes in the DNA signature through time. Therefore, some of the most important samples are from Mesolithic (pre-Neolithic) human populations (also called Epipaleolithic). These samples include hunter-gatherers from southern Anatolia, which represent the ancient DNA sample closest to the site of the Agricultural Revolution. These data are compared with other ancient and modern DNA signatures in figure 4.

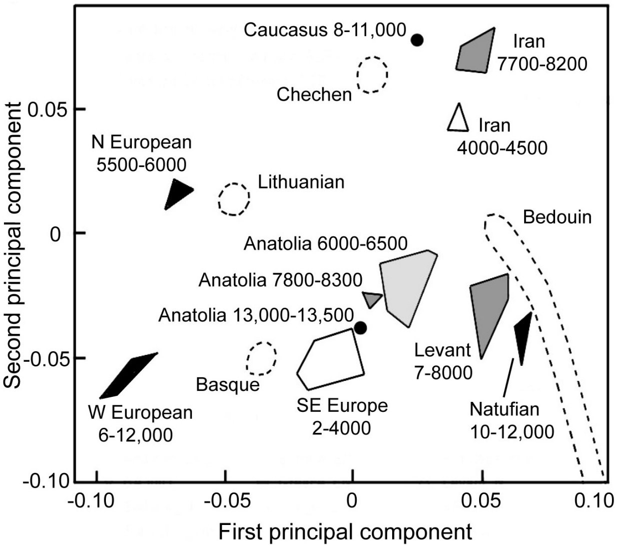

Figure 4. Principal component analysis of genomic data from the Middle East and Europe, with ages in years BC. Black = Mesolithic hunter-gatherers; dark grey = Pre-pottery Neolithic; pale grey = Pottery Neolithic; white = Chalcolithic; dashed = Modern. Data from Feldman et al.,[46] with age information and approximate SE Europe field from Lazaridis et al.[47]

The ancient genomic data in figure 4 are projected onto the two principal eigenvectors of SNP variation derived from modern human populations. Because these eigenvectors are defined by large modern populations (ca. 2,700 individuals), this allows small suites of ancient DNA data obtained by different research groups to be objectively compared. Also, for comparison with the ancient data distribution, four of the modern outlier population groups are shown as dashed envelopes in figure 4.

The DNA data in figure 4 show that Mesolithic hunter-gatherer populations (black points and fields) had very distinctive regional genomic signatures. Although these populations vary somewhat in age (labeled in years BC), they are shown by their archaeological context to be pre-agricultural.[48] Critically, the later Neolithic Anatolian populations have genetic signatures close to the Mesolithic Anatolian point (dated to 13,000 BC), showing that the genetic makeup of Anatolians remained relatively fixed for several thousand years during the Agricultural Revolution, with only minor inputs of genetic material from the Levant, the Caucasus, or Iran. Furthermore, archaeological evidence shows that the Anatolians adopted agriculture from the adjacent Northern Mesopotamian population soon after the Agricultural Revolution.[49]

Agriculture evidently gave these people a huge advantage in survivorship. As a result, they started to spread out in almost every geographical direction, intermixing with local hunter-gatherer populations in each area. Progressive migration over a period of several thousand years is demonstrated by the genetic make-up of human remains dating to the pre-pottery Neolithic, the pottery Neolithic and the Chalcolithic periods (dark grey, pale grey and white fields respectively in fig. 4). In most cases, the Neolithic and Chalcolithic fields are intermediate between the southeast Anatolian Mesolithic sample and local hunter-gatherer populations in the Levant (south), Europe (west), and the Caucasus and Iran (northeast).

Agricultural Migration and the Table of Nations

In the Genesis account, Noah represents a "new Adam," and the Table of Nations describes the outward spread of people groups after the Flood. This idea shows a strong correspondence with the genomic evidence for outward movement of people from SE Anatolia/Northern Mesopotamia beginning in the pre-pottery Neolithic (ca. 9–7000 BC) and gaining full force in the late (pottery) Neolithic (ca. 7–5000 BC).

If the Flood occurred in Southern Mesopotamia around 5700 BC, the genomic evidence suggests that the outward migration of people actually began up to two millennia before the Flood. However, such an outward migration would have had important consequences for the experience of those who survived the Flood on Noah's Ark. After the Flood, it is almost inevitable that the Ark would have become a holy site where human worship was strongly centred. The Genesis account supports this view, quoting the descendants of Noah in Mesopotamia as saying that they did not want to be scattered (Gen. 11:4). However, when these people did start to travel outwards from the new center of civilization in Southern Mesopotamia, they would have encountered a depopulated landscape. Their immediate surroundings on the plain had been depopulated by the Flood, which in the words of the Gilgamesh Epic "was flat as a roof" on which "all mankind had returned to clay."[50] But beyond the limits of the Flood, the descendants of Noah would probably have encountered a landscape depopulated by the outward Neolithic population migration. In fact, evidence from paleo-archaeology suggests that several villages in northern Mesopotamia were abandoned before the Flood and never resettled.[51]

The very factors that first led to the Agricultural Revolution in Northern Mesopotamia probably encouraged this abandonment. As suggested above, it was probably climatic pressure that first led people to adopt agriculture. Having done so, they would probably have discovered that the wetter, more consistent climate in the Levant, the Caucasus, and especially Europe, was more conducive to sustained agricultural production than Mesopotamia. Thus, the first waves of settlers would doubtless have reported back favorably to their home villages that conditions were better elsewhere.

The wave of agriculturalist migration is shown particularly clearly in the west.[52] Here, across Anatolia, the Balkans, and the Aegean, age-peaks of radiocarbon dates show that this was truly a westward wave of mass migration. Data from the Aegean (fig. 5) suggest that the peak of the westward-moving wave passed through just before 6000 BC, a few hundred years before the most likely date of Noah's Flood. This westward migration is described in some detail in the Table of Nations, which identifies the maritime peoples of the Mediterranean as being descended from Javan (a son of Japheth), who is identified in the book of Daniel with the Greeks. However, it is impossible that ancient peoples could have known the precise historical timing of this migration. Writing was not invented until thousands of years later, and did not comprise a system of recording dating information until at least 2750 BC.[53] Therefore, it is logical that the ancient biblical author assumed the westward migration to have occurred after Noah's Flood.

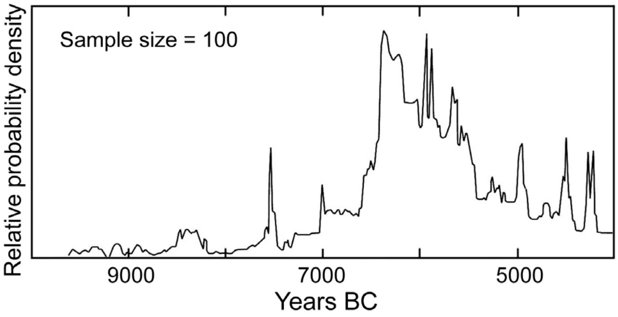

Figure 5. Probability density plot summarizing the relative number of radiocarbon ages as a function of time in the Aegean region. Modified after Silva and Vander Linden.[54]

The sons of Ham are even more important in the Table of Nations than the sons of Japheth, because they include the Egyptians and Canaanites, the principle enemies of Israel in later history. Linguistically, the Canaanites are part of the same Semitic language group as the Israelites themselves. However, this would not have concerned the ancient author, who was more interested in broad geographical and political identities.

Significantly, the southward migration of the sons of Ham into the Levant is supported by the principal component analysis in figure 4, which shows the pre-pottery Neolithic population of the Levant as having a DNA signature intermediate between Anatolia and the Mesolithic Natufians of the Levant. However, because the eigenvectors in figure 4 summarize genomic variation in the data set as a whole, they cannot provide a quantitative analysis of the relatedness of individual groups across a large number of SNPs. Therefore, some of these relationships were tested by Lazaridis et al. using *f*4 statistics (fig. 6).[55] This analysis will be used here to test the proposed southward migration from Anatolia to the Levant.

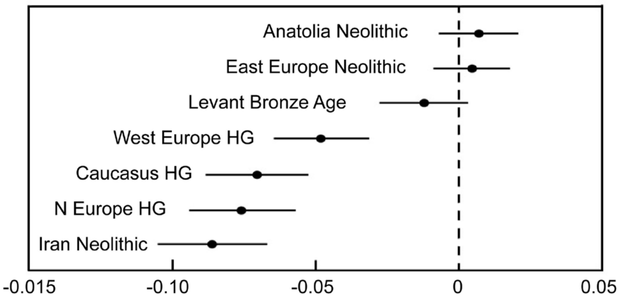

Figure 6. Results of the f_4 statistic (test-group, Natufian; Levant-Neolithic, chimp) to see if the Levant Neolithic population shares more alleles with a test population than the Levant Mesolithic. HG = hunter-gatherer. Error bars are +/- 3 standard errors. Modified after Lazaridis et al.[56]

Figure 6 shows results of the f_4 statistical test (test-group, Natufian; Levant-Neolithic, chimp). This test compares the relatedness of the Levantine Neolithic population to different test populations relative to the Mesolithic Natufians of the Levant, using the chimp genome as a yardstick for comparison. The positive result at the top of the chart shows that Levant Neolithic farmers shared a greater number of alleles with Anatolian farmers than with Natufian hunter-gatherers, whereas most other Mesolithic or Neolithic populations are more remotely related. This provides evidence for a migration of Anatolian farmers to the Levant. However, since the second closest population to the Levant Neolithic comprises Eastern European farmers, this suggests that the source of the migrants was not Anatolia specifically, but a general pool of Neolithic farmers from the whole region of the Agricultural Revolution.

Mitochondrial and Y-Chromosomal Evidence

Before the development of genome-wide (autosomal) DNA population studies, early work on the genetic relationships between human and primate lineages was based largely on the study of mitochondrial and Y-chromosomal (haploid) genetic inheritance.[57] Since these techniques reflect inheritance solely through the female and male lines respectively, this means that mitochondrial and Y-chromosomal DNA yield less-reliable evidence about the mixing of ancient people groups. However, because haploid DNA is more susceptible to local extinction events, it is very sensitive to population bottlenecks. It is also useful for dating these bottlenecks, because the simpler lines of descent make it easier to provide age calibrations based on haploid DNA mutation rates.

One of the most important of these bottlenecks is the "out-of-Africa" migration that occurred when small bands of modern humans left Africa.[58] Mitochondrial and Y-chromosomal evidence support the thesis that this bottleneck of human evolution occurred around 55,000 years ago, and was followed by an evolutionary diversification event (fig. 7) as the small bands of migrants spread out over the rest of the world.

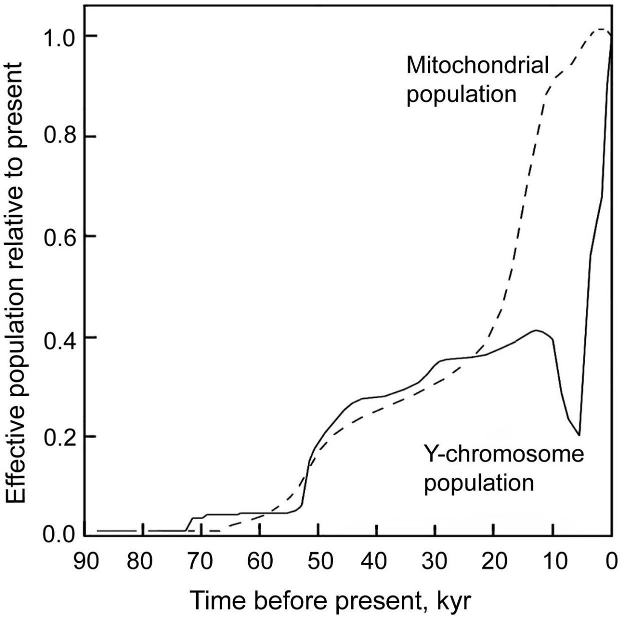

Figure 7. Variations in effective mitochondrial and Y-chromosomal population diversity, relative to the present day. Modified after Karmin et al.[59]

Y-chromosomal population diversification was more dramatic than the growth of mitochondrial population diversity after the 55,000 year dispersal event (fig. 7), and Y-chromosomal evidence also gives a signal for an earlier "out-of Africa" migration around 75,000 years ago (consistent with the date of human fossil remains in India[60]). On the other hand, mitochondrial population diversity increased more rapidly in the interval from 20 to 10 kyr before present. This mitochondrial diversification event began earlier in the Middle East than in Europe,[61] suggesting that it reflects migration into newly available landscapes as glaciers retreated at the end of the Ice Age. In contrast, there is only one case in the last 50 kyr in which haplogroup population diversity was markedly reduced, and this occurred less than 10,000 years ago, after the Agricultural Revolution.

The effective Y-chromosomal population diversity crashed at the beginning of the Neolithic Period and did not recover for several thousand years, whereas the mitochondrial population diversity shows no such decrease (fig. 7). Zeng et al. suggested that this difference reflects the different social structure of male and female kinship groups.[62] For example, if male kinship groups were in strong competition, there would be a high likelihood of small Y-chromosomal populations going extinct, so that during periods of intense competition, Y-chromosomal population diversity could crash. In contrast, females move more freely between kinship groups, keeping larger mitochondrial populations extant.

A dramatic demonstration of a kinship selection event of this type is given in the biblical Flood story. According to the biblical account, all of the survivors on the Ark were from one male kinship group (Noah and his three sons). On the other hand, we can infer that the four women on the Ark were probably less closely related. Therefore, if the account of human annihilation in the biblical and Mesopotamian Flood stories is based on a real event, we can see that this event would have caused an intense bottleneck in Middle Eastern Y-chromosomal populations, but less so for mitochondrial populations.

Modeling the history of effective male population diversity for different geographical regions provides evidence for this type of bottleneck. For example, the proposed Late Neolithic date of the Flood corresponds with a Y-chromosomal population minimum in the Middle East (fig. 8). However, we can see that the decline in Y-chromosomal population diversity actually began before the Flood, starting immediately after the Agricultural Revolution.

We can infer that the enhanced survivorship of male kinship groups practicing agriculture was so greatly enhanced that most hunter-gatherer kinship groups went extinct during the early spread of agriculture in the Middle East. These agriculturalists spread out over the known world, establishing the first complex civilizations. Within these civilizations, competition between male kinship groups was probably reduced, allowing a strong diversification of Y-chromosomal populations.[63] This model is dramatically confirmed by the behavior of European Y-chromosomal populations around 4000 BC (fig. 8). This is the approximate time when Steppe populations practicing agriculture swept across Western Europe, essentially annihilating native male kinship groups.[64] In contrast, the Steppe immigrants were highly successful, leading

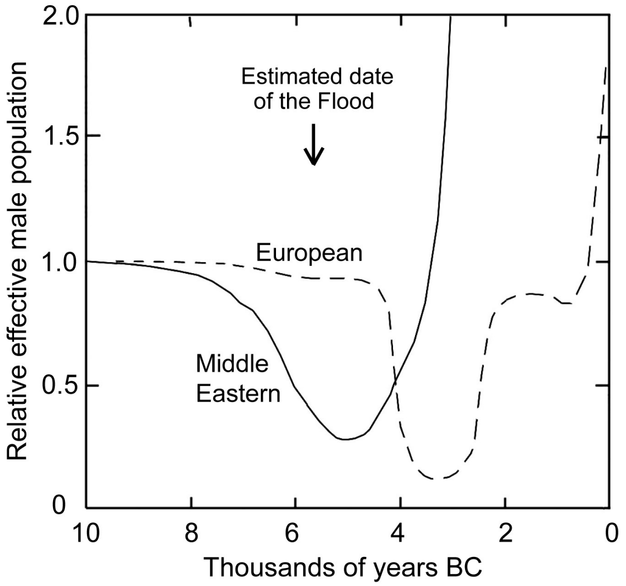

Figure 8. Effective Y-chromosome population diversity for the Middle East and Europe, normalized to their value before the Agricultural Revolution. Modified after Karmin et al.[65]

to massive Y-population diversification shortly afterwards.

It is significant that the autosomal and haploid DNA evidence gives a consistent picture of the timing of Neolithic migration events, despite their different sources of chronological information. Thus, the ages of the samples in figure 4 are "real time" ages of actual individuals derived from radiocarbon dating or archaeological contexts. In contrast, the ages of population bottlenecks in figure 7 are model ages based on the application of mutation rates to divergent modern haplogroup signatures. The fact that these two completely different sources of chronological information agree provides powerful evidence in support of the accuracy of the agriculturalist migration and diversification model.

Conclusions

In attempts to reconcile the Genesis account of human origins with scientific evidence, two different approaches have been taken. One approach has been to identify Adam as a Neolithic agriculturalist based on the occupations of his sons, one of whom is also described as the first city builder. This view locates Adam in Mesopotamia, reflecting his placement by God in the Garden of Eden, where the Tigris and Euphrates rivers met. In this view, Adam was the priestly father of humanity, and, through his descendant Noah, he played a formative role in the origin and development of Middle Eastern civilization. The other approach locates Adam in Africa 100–200 thousand years ago, where he is the biological father of the human race. This model requires tens of thousands of years of lost human experience, during which time Adam's descendants must have migrated out of Africa and spread over the rest of the earth. Genesis contains no hint of such a migration event, but it does claim that all Middle Eastern people groups were descended from the survivors of a catastrophic Flood in the Mesopotamian region.

If Noah's Flood occurred in the Neolithic Period, the spread of humanity across the Middle East ties in closely with genomic evidence for a massive outward migration from Northern Mesopotamia/southeast Anatolia after the Agricultural Revolution. Therefore, the overall portrait of Middle Eastern origins painted in Genesis is consistent with scientific evidence for the origins of human religion and civilization in the Neolithic Period in Mesopotamia. ♥

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