



Stephen L. Reinbold

# Pharaoh's Gift: Was Ancient Nubia the Land of Milk and Camels?

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*Did Abraham receive camels from Pharaoh? Many archaeologists contend that the presence of camels in the Genesis narrative is an anachronism that was added by later scribes. But what if camels were brought across the Red Sea from Arabia to Africa at an earlier date? I will propose a possible camel route from the coastal region to the Nile based on studies of the following: modern and ancient DNA, revealing camel movements after domestication; mutations for adult lactase persistence (LP) that were brought to Africa along with camels or that originated in Africa; and human Y chromosome mutations that can be associated with the LP alleles and the transport of camels. The cumulative evidence allows the possibility of camels to reach Nubia by about 2000 BC. Egyptians could have brought them to Pharaoh who gave them to Abraham.*

**D**id Abraham receive camels from Pharaoh, as recorded in Genesis 12? Did he send them to Aram to buy a bride for Isaac? Did Rebekah ride on one? An article posted on Time.com pronounced that Abraham's camels were "phantoms," an anachronism that was added by later scribes.<sup>1</sup> This announcement was not new to archaeology but was precipitated by an article in the journal *Tel Aviv* in which archaeologists stated that camel remains were found with human remains at a mining site in Israel dated about 1000 BC and not before.<sup>2</sup> When camels became essential to caravan trade is disputed. Most archaeologists already believed that no solid evidence from Egypt or the Levant was known prior to that time.

The existence of domesticated camels in Africa, particularly in Egypt, has been controversial among archaeologists. In the last century, William Albright declared that biblical Abraham could not have received camels from Pharaoh because there was no record of them or inclusion of them in accounts of Egyptian animals.<sup>3</sup> He believed that donkey caravans could have sufficed. Christina Köhler and colleagues explored ancient chert mines in an extremely dry area of Egypt that were dated to the Middle Kingdom. Yet, they believed that donkeys were used for transport despite the difficult logistics of supplying them with water

and food, because they did not believe that camels were domesticated then.<sup>4</sup> However, Michael Ripinsky summarized the opposition to this view, including finds in Egypt of a camel hair rope, pottery in the shape of camel heads, and rock art depicting camels.<sup>5</sup> These finds are disputed: for example, did the vague-looking pottery really depict camel heads? How old was the rock art? More convincingly, a camel skull was found in Egypt dating between 2000 and 1400 BC. In his classic book *The Camel and the Wheel*, Richard Bulliet reviewed the evidence, especially the similarities related to the early use of camels for milking in the southern Arabian Peninsula and in the Horn of Africa, and declared that the early second millennium BC arrival of camels on the continent, at least in small numbers, was a possibility.<sup>6</sup>

There are two possibilities for the introduction of camels to Egypt: (1) they may have entered by land caravans through the Arabian Peninsula and the Levant; or (2) they could have been brought across by boat to modern-day Somalia or Eritrea and then to the Nile Valley.<sup>7</sup> Archaeological work has concentrated on the Levant and Egypt. Excavations of early Bronze Age

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Arad in the Negev Desert revealed a small number of camel bones, interpreted by Ruth Amiran as coming from wild camels dated at about 2700 BC.<sup>8</sup> Camel bones in Jordan have been dated to the third millennium BC by the Camel Bone Dating Project as listed in Oxford AMS System.<sup>9</sup> There has been less archaeological work in the Horn of Africa near the Red Sea, partly because of political instability there for many years. Nevertheless, Bulliet thought that domesticated camels arrived by ship to Somalia between 2500 and 1500 BC.<sup>10</sup>

In this article, I will show that the East African camels were a separate introduction and that this introduction was earlier than that of camels arriving by the land route. I will examine the genetics of camels and the genetics of camel herders, who may have brought camels to Africa, by examining lactase persistence (LP) alleles and Y chromosome mutations.

### Genetics of Camels

Camel genetics reveals a history of movement of the animal post-domestication. Faisal Almathen and colleagues refer to pre-Iron Age camel remains as being "intrusive to the chronology" due to doubtful provenance or carbon-14 dating.<sup>11</sup> They do not believe that domesticated camels expanded out of Arabia before about 1500 BC. They believe that the biggest expansion in caravan trade developed after AD 1200 with the growth of the Ottoman Empire. They do, however, point out that East African camels are genetically unique, perhaps due to use (mainly for milk) and long isolation, and that they have a separate origin from the camels of North and West Africa, probably originating from South Arabia. South Arabian camels are more genetically similar to East African camels than to North Arabian camels. Using genome sequences and examining microsatellite diversity by performing coalescent simulations to work backward to discover when the sequences converged in the past, Almathen et al. found a severe bottleneck in East African dromedaries about 8,600 years ago, presumably long before domestication. They found that East African camels had the highest mitochondrial diversity which would be consistent with the shipping of primarily female camels (used for milk) to Africa, along with a small number of male camels. They lumped together North African camels, including Egyptian camels and western Saharan camels.

There may be, however, a discontinuity in Egypt compared to western Africa, such as in Algeria. Youcef Amine Cherifi and colleagues found a differentiation between Algerian and Egyptian camels, despite extensive back-and-forth movements.<sup>12</sup> Egyptian Sudani camels are from Sudan; Falahi camels used in the delta region of Egypt are bred in Upper Egypt and resemble

a description of camels from Somalia given by Hellmut Epstein.<sup>13</sup> Ahmed Ould and colleagues found that 91% of variation in Tunisian camels was *within* populations, not between populations, again showing that western camels were relatively homogeneous compared to those in Egypt.<sup>14</sup> According to Bulliet, even the type of saddle used with South Arabian camels is similar to that used in East Africa, in addition to the use of camel milk.<sup>15</sup> He did think that there was a break at the highlands north of the Afar Desert in Eritrea between the East African camels and camels of northern Sudan (Nubia) because he did not think that the Beja north and south of the narrow coastline strip raised camels (fig. 1). However, the Beja of Sudan still rely on camel milk for subsistence during famine.<sup>16</sup>

### Genetics of Camel Herders

#### *Methodology*

To understand how the populations who depended on camel milk were affected genetically, it was necessary to calculate changes in allele frequencies by generation in order to calculate the date of origin for alleles. The Hardy-Weinberg equilibrium is a general formula ( $p^2 + 2pq + q^2 = 1$ ) that calculates allele and genotype frequencies under certain conditions: no selection, no mutation, no migration, random mating, and large population size. Of course, these conditions are not always true. The homozygous recessive genotype is represented by  $q^2$  in the above equation and is the proportion of the population susceptible to negative selection. The formula for changes in allele frequencies when selection is present can be calculated using a selection coefficient  $s$  which represents the proportion of homozygotes that is eliminated each generation. If  $q$  is the original frequency of the recessive allele, then  $q$  can be recalculated for each generation ( $q - sq^2 / 1 - sq^2 = q'$ ) to give  $q'$  which is the frequency in the next generation.

The formula was entered into an Excel spreadsheet. The current allele frequency of a population is located by inspection, working down the spreadsheet generation by generation from the original  $q$  value. When particular values of  $q'$  are found in the Excel table, the number of generations to reach this point is given. However, what we are really interested in is the number of years to reach the current dominant  $p$  allele frequency. The frequency of the particular dominant allele of interest is found by  $p = 1 - q$ . Of course, certain assumptions have to be made. I consistently used a selection coefficient of 0.05, well within the range of estimates for lactase persistence in several sources. To estimate the frequency of a particular allele at its origin, a necessary starting point for the calculations, I used the frequency of 0.001. This would indicate a mutation rate of 1 in 1,000 for a large

population over an appropriate range of time, keeping in mind that mutation is always rare. However, when migration does occur, it can introduce a new allele to a population more quickly, and it is expected that a new allele will initially appear at a higher frequency than that of a new mutation.

The above represents the simple case of only two alleles for a gene in a population. A complication enters when there is more than one dominant allele represented in a population. The alleles of interest will be considered to have frequencies of  $p+r=1-q$ , where  $p$  and  $r$  represent two alleles, both of which are considered to be dominant to the recessive  $q$ . In terms of phenotypes, there will be no difference between the dominant alleles, and they will act as if there is only one dominant allele. It is only by gene sequencing that they can be distinguished. For simplicity, I usually estimated the time of origin for the alleles from the combined current frequencies of the dominant alleles, but the actual separate histories of the two alleles are not resolved. One of the dominant alleles might have entered the population later by migration, as would be expected from a much smaller current frequency. If I know the time when the two populations first came into contact, then I can resolve their separate

histories by locating, in the spreadsheet, the number of generations that transpired to reach the date of expected contact. The associated frequency  $1-q'$  will be that of the more common dominant allele  $p$  of the population when it received allele  $r$  from the other population. In this case, the initial frequency of allele  $r$  in the recipient population would be less than the frequency in the donor population.

### Arabian Lactase Persistence Allele

Most humans after childhood do not produce the enzyme lactase (coded by LCT gene on chromosome 2) responsible for breaking down lactose in milk. Mutations occur in the regulatory region for the lactase structural gene; these mutations allow lactase persistence (LP). An indirect method of examining the arrival of camels in Egypt is by looking for the unique variant of LP (G-13915, "the Arabic allele," showing substituted nucleotide and position) that originated in the Arabian Peninsula in association with the consumption of camel milk. This occurred presumably about 4,000 years ago as dated by Nabil Sabri Enattah and colleagues, using linkage disequilibrium of haplotypes and calculating the rho statistic, which is based on the average distance of a set of sequences from the most recent common ancestor.<sup>17</sup> This allele is found in northeastern Africa in Arabic and non-Arabic tribes (fig. 1).

I examined frequencies of the Arabic allele (G-13915) for LP in non-Arabic tribes in East Africa, including Afar from Eritrea, Beja from northeast Sudan, Tigray from central Ethiopia, Mahas (Nubians) from the upper Nile in Sudan, and Somali from Ethiopia (table 1). I also looked at two Arabic-speaking tribes in the upper Nile valley (table 1): the Gaali who may be Arabized Nubians, and the Shokrya (Juhayna) thought to have migrated from Arabia. These tribes, with already high frequencies of the allele, probably entered Sudan by AD 1000.

**Table 1.** African tribes with lactase persistence (LP) alleles G-13915 (Arabic allele) and G-13907 (Eritrean allele). The tribes are listed with their location, linguistic association, lifestyle, and total sample size included from research studies.

Tribe	Countries	Language	Lifestyle	Total N
Afar	Eritrea, Ethiopia	Cushitic	Nomadic pastoralist	37 <sup>18</sup>
Beja	Eritrea, Sudan	Cushitic	Pastoralist	71 <sup>19</sup>
Amhara, Tigray	Ethiopia	Semitic	Agro-pastoralist	40 <sup>20</sup>
Mahas	Sudan	Nilo-Saharan	Agriculturalist	69 <sup>21</sup>
Somali	Ethiopia	Cushitic	Pastoralist	109 <sup>22</sup>
Gaali	Sudan	Arabic	Agro-pastoralist	146 <sup>23</sup>
Shokrya	Sudan	Arabic	Pastoralist	40 <sup>24</sup>



**Figure 1.** Map of Red Sea Region. Tribe names are in script.



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However, Arabs, bringing camels with them, may have already entered Africa by the Red Sea route earlier, as discussed by Bulliet.<sup>25</sup> Somalia or Eritrea would be the likely part of Africa reached by sailors from southern Arabia. Coastal tribes include the Afar and the closely related Saho who may have interbred with the Arabs. Movement of the Arabic allele at that point could be up the coast through Eritrea among the Tigray. The highest frequency is found in northeastern Sudan, near the coast, among the Beja. This location is near a wadi that gives access to the Nile River Valley in the interior. The frequency found in the Somali from Ethiopia is 5%. The only Somali sample I have is from Ethiopia; therefore, I focused on Eritrea as the initial area of contact.

The difficulty is timing. Based on marker sequences near the LCT gene,<sup>26</sup> Enattah et al. estimated the date of origin at 4,000 years ago;<sup>27</sup> however, the dating method has very broad confidence levels, allowing at least two thousand years difference (rho statistic estimate of 4,091 +/- 2,045). Also note that milk can be used as food when fermented, even by nonlactose digesters, before the LP allele is present. Another LP allele, which may be older, will be helpful here.

### Endemic Lactase Persistence in Africa

The G-13907 allele was associated with Afar camel herders by Ingram et al.,<sup>28</sup> but I will henceforth refer to it more broadly as the "Eritrean allele." It has been shown to have LP activity. The allele is not found outside the Horn of Africa region. In addition to the Afar tribe of Eritrea and Ethiopia, it has been reported at high frequencies of about 20% in other Ethiopian tribes and in the Beja of Sudan. Table 2 shows possible dates of origin based on frequencies of the combined Arabic and Eritrean alleles. I used a twenty-five-year generation time and a thirty-year generation time.<sup>29</sup> The most uncertain number is the initial frequency, which affects the date of initial introduction into the population considerably. Enattah et al. used 0.001 as the initial frequency based on mutation in a population of 500, and they used a selection coefficient of 0.05.<sup>30</sup> Here the LP alleles are p and r which are dominant so that  $1-q=p+r$ . For Beja, the combined frequency for G-13915 and G-13907 is about 0.38, indicating that they originated about 3,375 years before present if the generation time was 25 years, or 4,050 years before present if the generation time was 30 years (table 2). The Beja appear to be a strong, independent tribe set off from the Arabs by language, and the Beja were known to the ancient Egyptians from 2000 BC. The Afar have only one data set, but the data are crucial in understanding when the G-13915 allele first arrived in Africa.<sup>31</sup> If G-13915 and G-13907 are combined, they may have originated prior to 2000 BC.

**Table 2.** Date of origin of combined Arabic (G-13915) and Eritrean (G-13907) lactase persistence (LP) alleles in African tribes based on selection coefficient  $s$  of 0.05, initial frequency  $q$  of 0.999 (recessive non-LP allele), and generation times of 25 and 30 years. Tribes are listed with the age of the LP allele in years before present (YBP), where frequency  $q$  in next generation  $q'$  is found by  $q' = q - sq^2 / 1 - sq^2$ .

Tribe	LP allele % <sup>a</sup>		Date of Origin YBP Generation time	
	Arabic allele G-13915	Eritrean allele G-13907	25 Years	30 Years
Afar	12.2	29.7	3550	4260
Beja	17.9	20.2	3375	4050
Amhara, Tigray	12.5	20.0	3200	3840
Mahas	12.5	1.0	2475	2970
Somali	5.0	5.5	2375	2850
Gaali	16.8	1.9	2750	3300
Shokrya <sup>b</sup>	27.5	2.5	3250	3900

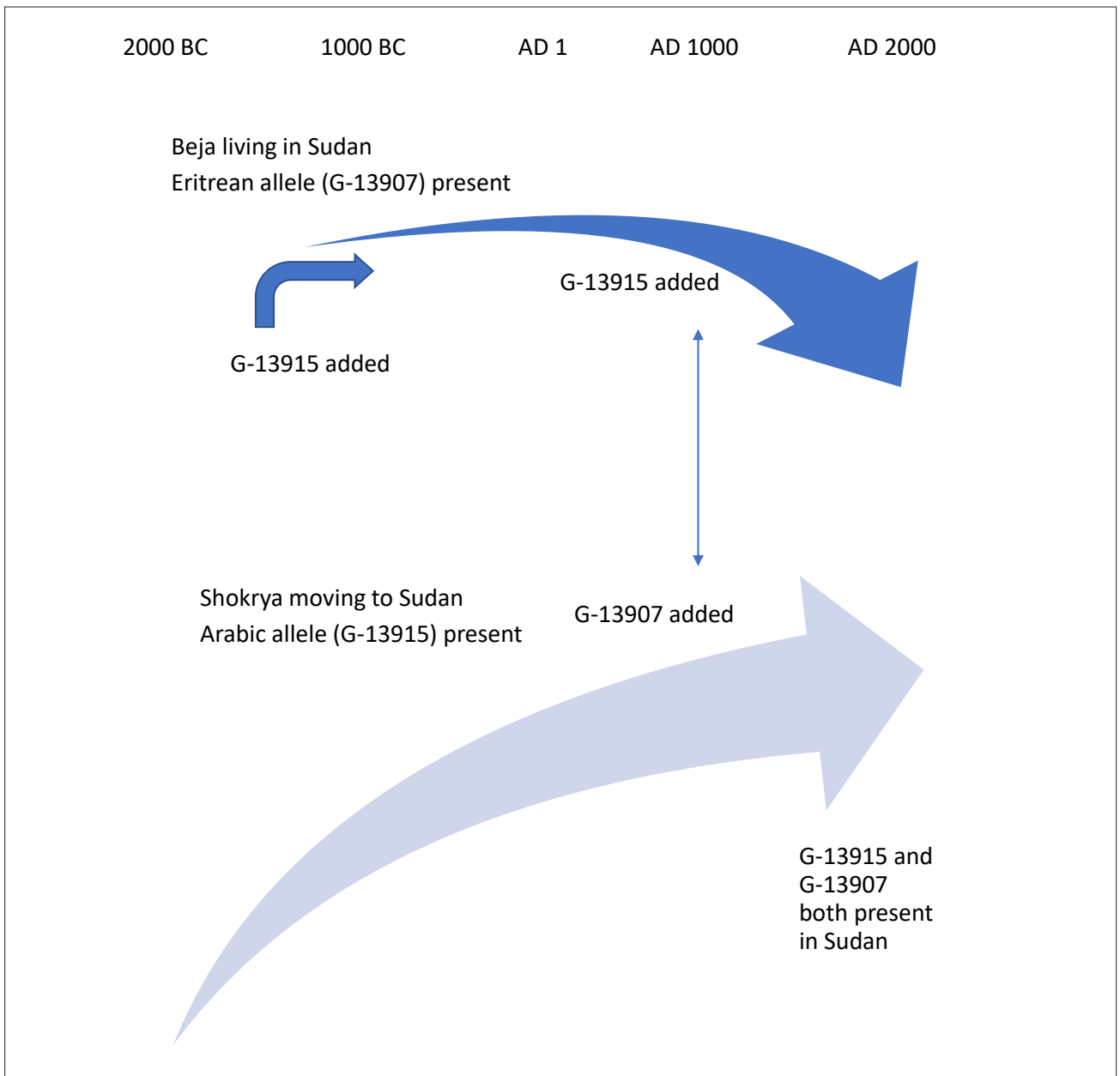
a = average of independent studies when more than one study  
 b = European allele G-13910 also present as 2.5%

Table 2 can be used to show possible dates when the Eritrean allele (G-13907) entered the Arabic tribes who migrated into the region. The Eritrean allele is not common in Arabic tribes of the region, which have frequencies of less than 5% (table 2). This suggests a different migration pattern for this allele compared to the Arabic allele (G-13915). In fact, this migration pattern difference suggests the relatively recent acquisition of the Eritrean allele by the Arabic tribes of the region. On the other hand, the roughly equivalent level of the Arabic allele in native Horn tribes, compared to that in Arabs, indicates that the Arabic allele was already present in the Horn tribes when Islam arrived. Muslim Arab conquest of the upper Nile was delayed by Christian kingdoms in Ethiopia and maintained by a peace treaty lasting from AD 700 to 1300.<sup>32</sup> Some of these tribes settled as agriculturalists, but they still retained the Arabic allele at about 17%. Others such as the Shokrya remained pastoralists, and the frequency of the Arabic allele continued to increase to about 27.5%. If the Arabic allele arrived with the Arab Muslims, who mixed freely with the natives despite language differences, then why did the level of the Eritrean allele not increase proportionately in the Arabs? The case is then made that minimal mixing occurred between the Beja and the Arabs, with the Arabic allele already present in African pastoralists independently, who gave a small input of the Eritrean allele to the Arabs (fig. 2).

Two scenarios are possible. First, according to Edita Priehodová and colleagues and other researchers, the Arabic allele arrived in the Horn of Africa, probably through the Levant into Egypt and up the Nile River,

only after the Muslim conquest, and it arrived later than in the north because progress up the Nile was blocked by Christian kingdoms from about AD 700 to 1300.<sup>33</sup> For this Islamic conquest proposal, only after about AD 1000, allowing for some interbreeding with Cushitic tribes during the time before AD 1300, would Arabs likely have introduced the G-13915 allele to these tribes, after which it was selected for along with the endemic G-13907 allele. According to this hypothesis (fig. 2), the high frequency of the Beja for the G-13915 allele was then realized along with the previous high frequency of G-13907.

According to the second proposal, the G-13915 allele had already arrived via the Red Sea by Arabic traders bringing camels and contributing an initially small amount to the gene pools of the Red Sea coastal tribes Afar and Saho. The Arabic allele then passed through other Eritrean and Ethiopian tribes to the Beja in Sudan and minimally to the agricultural Mahas. When the Arab tribes arrived after the Muslim conquest of Sudan, interbreeding had little effect on G-13915 frequency in the local tribes that already possessed it. In the meantime, the G-13907 allele passed minimally into the



**Figure 2.** Schematic of Arabic (G-13915) and Eritrean (G-13907) LP allele exchange between Shokrya and Beja tribes in Sudan about AD 1000. Arabic allele must have been added to Beja before AD 1000 as shown on left.

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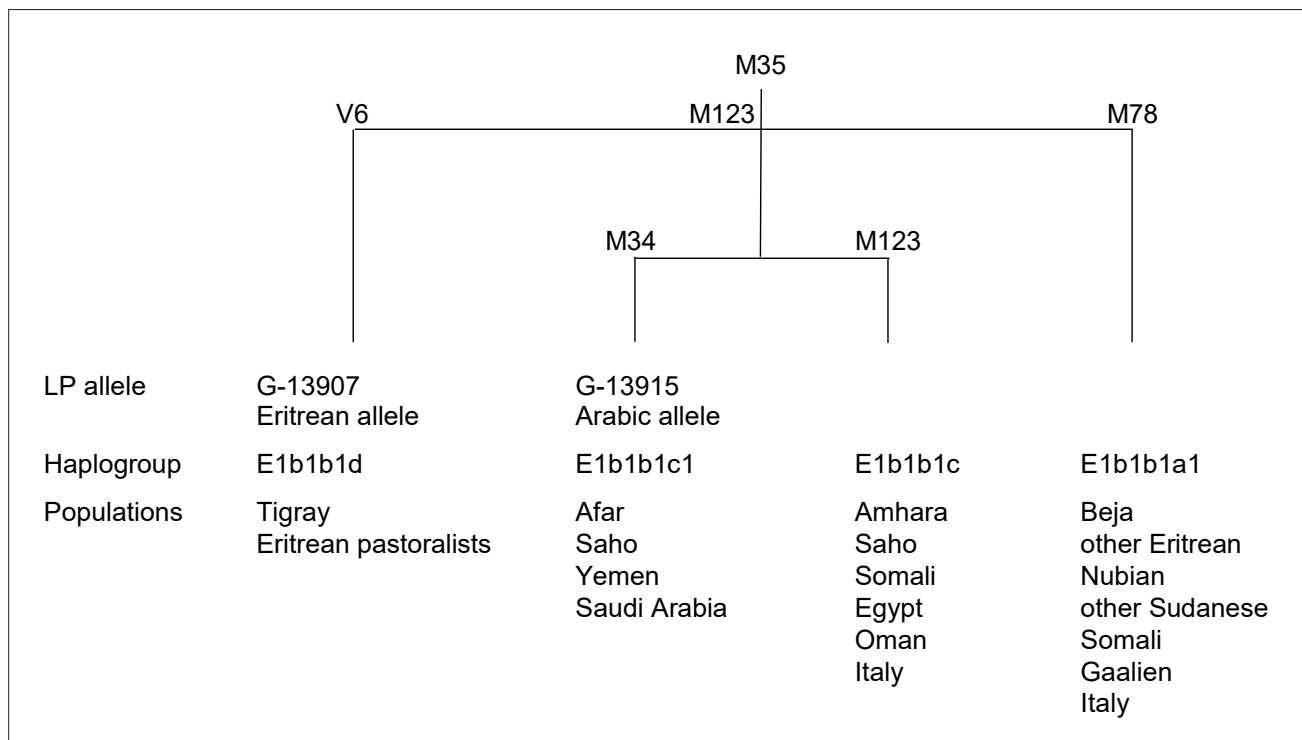
Arabic tribes, including the pastoralist Shokrya and partly pastoralist Gaali. Now we need to look at another line of evidence to choose between these two scenarios.

### Y Chromosome Evolution

There are advantages to examining the Y chromosome because it allows tracking of migrating males; mutations are considered random, not directly selected; and ages can be based on estimated mutation rates. Eyoab Gebremeskel and Muntaser Ibrahim examined Y chromosomes in Eritrea and, although they had small sample sizes for some groups, they also summarized data from other researchers.<sup>34</sup> Beniamino Trombetta and colleagues further updated Y chromosome evolution in the Middle East and Northeast Africa (fig. 3).<sup>35</sup> The M123 mutation is important, as one branch (M34, named by mutation), possibly associated with the Arabic allele for lactase persistence (LP), appears to have arisen in Saudi Arabia or Yemen and might have crossed the Red Sea to the Saho (n=11). No LP data are available for the Saho; however, the M34 Y chromosome is also found in the closely related Afar tribe (n=1), which has a high frequency of the Arabic allele. It is to be expected that sailors would be males, and, hence, there would be a one-way flow to the recipient tribe as evidenced by the M34 Y chromosome, at least in the first generations. The nearby Beja (n=22) could

have picked up the Arabic allele from the Afar or Saho, although the M34 Y chromosome has not been found in Beja, but any apparent linkage between M34 and G-13915 would be lost because they are not on the same chromosome. After the M123 split, the remaining M123 branch apparently does not associate with G-13915, as the M123 is also found in Italians not known to carry G-13915.

Using genomic sequence differences in Y chromosomes from many African samples to calculate the rho statistic and determine the age of the most recent common ancestor, Trombetta et al. found five African pastoralism-related alleles that originated in newly described clades of the E-V1515 Y group in Africa.<sup>36</sup> The E-V1515 clades split off from sister clades about 12,000 years ago (not shown). Trombetta et al. examined the number of mutations involved in detail. Dates of branch points were estimated from coalescence and rho statistic. These include the E-V1486 subclade associated with LP C-14010 ("Kenyan allele") and the E-V1700 subclade associated with G-13907 ("Eritrean allele"). They worked out details for the newly discovered E-V1515 branch, which they dated to have split into E-V1486 and E-V1700 branches 12,000 years ago. Nine mutations occurred in the E-V1486 branch until, during a span of 8,500 years, it split into three sub-branches about 3,500 years ago. The E-V1700 branch had six mutations



**Figure 3.** Partial tree of the E-M35 subgroup of haplotype E1b1b of the human Y chromosome. (Redrawn from Gebremeskel and Ibrahim; Trombetta et al.<sup>37</sup>) Haplotypes have standard nomenclature and new branches form at mutations. Two possible lactase persistence (LP) allele associations are shown.

during a span of 7,000 years, before giving rise to the V6 mutation (fig. 3) dated at 5,000 years before present. The V6 branch is also associated with the G-13907 mutation which might have originated at about 4,000 years ago in Eritrea.

Although the researchers did not find the V6 mutation in the Afar and Saho, the G-13907 allele could have originated in an adjacent Eritrean pastoralist tribe and been passed to them unlinked to the V6 mutation. These tribes are highly dependent on camels. Meanwhile, the G-13915 allele might have originated in the Arabian Peninsula at about that time (4,000 years ago). The M34 Y-branch from M123 might have been carried to northeastern Africa, perhaps modern-day Eritrea, by Arabs crossing the Red Sea with camels. The Saho may have interbred with them and then passed both the M34 Y chromosome and the G-13915 allele to the nearby Afar tribe, who are camel herders to this day. The G-13915 allele reached the Beja through interbreeding between adjacent populations, although the M34 Y chromosome did not. The Y mutation and the G-13915 allele would have drifted apart by then, as they are not linked.

Now let us return to the previous discussion of contact between the Arabic Shokrya and the Cushitic Beja in Sudan (fig. 2). Using the AD 1000 date as a good approximate date for when Arabic and Cushitic tribes came into sufficient contact for interbreeding, the Arabic pastoralist tribe Shokrya was set as having the G-13915 allele frequency of 0.10, by tracing back 1,000 years from its current level, and the Beja initial frequency was set lower at 0.012. The frequency of the G-13907 allele for the Beja predicted for AD 1000 was set at 0.05, and set lower for the same time for the Shokrya, with an initial frequency set at 0.006. Using a hypothetical reciprocal exchange, it was estimated that 100 out of 1,000 Beja, averaging six copies of the G-13907 allele, bred initially with Shokrya so that the latter received the G-13907 allele. The number of Shokrya was also set for 100 out of 1,000 initially breeding with Beja, averaging twelve copies of the G-13915 allele received by the Beja.

From this hypothetical initial frequency in AD 1000, the frequency of the Beja for the G-13915 allele in AD 2000 was calculated and found to be much below the actual current frequency. Using the approximate frequency based on the AD 1000 contact date and starting with the G-13915 allele at 0.012, the Beja would require hundreds of years *after* AD 2000 to reach the current level for the allele (0.18). Therefore, the Beja must already have had a high level of G-13915 when the tribes came into contact. In this example, it was assumed that the Beja had limited contact with Shokrya at AD 1000; otherwise, the Shokrya would be expected to have a much higher level

of G-13907 than it now has, if interbreeding with Beja had been more frequent.

There are many uncertainties in this dating method and, to be sure, other reciprocal exchanges are possible, but they will be limited by this constraint in G-13907 frequency. However, nonreciprocal gene flow is possible and must be considered. If the mating had been directional with Arab males carrying G-13915 to Beja, while Beja females did not carry G-13907 to Arabs, then Beja males resulting from Arab fathers would be expected to carry a specific Arabic Y chromosome in substantial numbers. Instead of an Arab-specific Y chromosome, most Beja (fig. 3) share a very widespread Y chromosome (M78) with populations in Africa, west Asia, and Europe who are not associated with G-13915.

## Conclusions

Both the genetics of camels and the genetics of camel herders show that East Africa is distinct from North Africa. The camels of East Africa are of the milking variety which is presumed to indicate the original use of the camel that developed on the Arabian Peninsula. Even camels in northern Egypt show some similarity to the East African camels; it was only later that the caravans from the peninsula arrived through the Levant and traveled west across the Sahara.

The camel herders show a similar distribution. The Arabic lactase-persistence (LP) allele (G-13915) arrived on the Red Sea coast from Arabic tribes bringing camels, continued on to pastoralist tribes in what is now Eritrea, perhaps arriving among the Afar or Saho first, coming next to tribes that live along the coast, eventually reaching inland to the Beja and north into Sudan, and then into the Nile Valley, probably traveling through a wadi in northeastern Sudan to the Nubian Mahas. These non-Arabic tribes have the Arabic allele in higher frequency than many of their Arabic neighbors who did not enter Sudan until after AD 1000, thus discounting the need for the Arabic allele traveling by caravans, crossing through the Sinai into Egypt, and then up the Nile Valley. In this same time range, the G-13907 allele appeared in Eritrean pastoralists and was passed into the Tigray and the Afar and Saho, who in turn passed it to the Beja and eventually to the Nubian Mahas and the Arabic Gaali and Shokrya. Cultural evidence for camels in this time period includes rock drawings near Laga Oda in Ethiopia, showing camels on a wall with drawings similar to C-group Nubian drawings.<sup>38</sup> The C-group culture is dated from 2400 to 1550 BC.

Although none of these possible dates for arrival of camels in Africa may be sufficient by themselves,



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cumulatively, they point consistently to a date between 3,500 and 4,000 years ago. If pastoralism swept from northeast to southwest as seems likely, it originated in Asia Minor perhaps 8,000 years ago, about the time that dairy culture began with cattle. The arid Red Sea region was not suitable for cattle, but the Arabs may have utilized camels starting at least 4,000 years ago and introduced them to the Afar and Beja. They could have introduced camels to the arid south Red Sea coast of Africa between 3,500 and 4,000 years ago. They may also have contributed to the local gene pool, including both the G-13915 allele and the Y chromosome with the M34 mutation currently found in Yemen, Saudi Arabia, and Eritrean Afar and Saho. Coincidentally, the G-13907 allele, being useful when camels arrived and associated with branch V6 of the E-V1700 Y chromosome in the Afar or other Eritreans, may have originated at the same time. Furthermore, based on current combined frequencies of LP alleles G-13915 and G-13907 in African populations, the alleles originated between 3,500 and 4,300 years ago.

About 2000 BC, Egypt had just emerged from the First Intermediate Period of internal strife and weakness toward Nubia and built the Middle Kingdom, which was a period of strength, both internally and externally. Abraham would have encountered a Pharaoh fully in charge and fresh from victories over Nubia and sitting astride the ancient pathway out of Africa into Asia. Abraham trod the path that was used back and forth between great civilizations.

Since the Egyptians received their meat, milk, and transportation needs from cattle, goats, sheep, and donkeys, camels would have been a mere curiosity to Pharaoh—perhaps received as tribute from the conquered Nubians or from a trade for exotic animals. Even if there was no extensive caravan trade between the southern Red Sea and Egypt, Nubians might have occasionally received camels from the Beja, their neighbors along the desert coast on the Red Sea. The Beja might have immediately utilized camels as a source of milk, just as the Arabs who brought them to their coast did. The Egyptians could have received camels directly from the Beja, who were known to them as early as the twelfth dynasty about 2000 BC. Egypt was in a period of Imperial equilibrium toward Nubia at the time, wherein Egypt interacted through trade with the native C group, including trading for exotic animals, but Egypt did not settle or form an integrated system of state control.<sup>39</sup> Abraham from Mesopotamia may have already been familiar with two-humped camels used as pack animals, in that camel rations are recorded by carvings on a Mesopotamian cylinder dated from 3800 YBP, and he

may have gladly received similar one-humped camels as a gift from Pharaoh.<sup>40</sup>

The biblical uses of camels during the Patriarchal period included transporting light loads (gifts for Rebekah's family, and later for Rebekah and Rachel to ride on). Camels may not have been common in Nubia, and certainly not in Egypt, but warfare in Nubia previous to Abraham's arrival in Egypt could have netted Pharaoh tribute—including camels. It would have been natural for him to re-gift these to Abraham as tribute in order to find favor in pursuit of Sarah for a wife. ●

### Notes

- <sup>1</sup>Elizabeth Dias, "The Mystery of the Bible's Phantom Camels," February 11, 2014, <https://time.com/6662/the-mystery-of-the-bibles-phantom-camels/>.
- <sup>2</sup>Lidar Sapir-Hen and Erez Ben-Yosef, "The Introduction of Domestic Camels to the Southern Levant: Evidence from the Aravah Valley," *Tel Aviv* 40 (2013): 277–85, <https://doi.org/10.1179/033443513X13753505864089>.
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