LETTERS

Origin of the Jews and the Arabs: Date of their Most Recent Common Ancestor is Written in their Y-Chromosomes – However, There Were Two of Them

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A pattern of Y-chromosomal mutations in 37 and 67 marker haplotypes of the Jews and the Arabs indicates that their most recent common ancestor in haplogroup J1 (subclade J1e*) and that (a different one) in haplogroup J2 (subclade J2a*) lived 4300±500 years before present (ybp) and 4175±510 ybp, respectively, that is practically at the same time. Then a split between the Jewish and the Arabic lineages in both J1 and J2 haplogroups occurred, which is clearly visible on the respective haplotype trees. The data show that a common ancestor of Cohanim (Jewish High Priests) of haplogroup J1 lived 1070±170 ybp, while a common ancestor of Cohanim in haplogroup J2 lived 3300±400 ybp.

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DNA genealogy, the essential goal of which is to describe and to date the origins of human populations in terms of time spans to their most recent common ancestors, has evolved with an astonishing speed during the last decade. An application of principles of chemical kinetics to mutations accumulated in certain markers (loci) of Y-chromosome (a chosen combination of markers in Y-chromosome is called a haplotype) lays a well justified ground for the respective chronological calculations. Those, in turn, serve as a measuring stick with respect to the history of humanity.

Essentially, at the core of the methodology, is a translation of the average number of mutations per marker in Y-chromosomes in the chosen population into a respective timespan, that is a coalescence time focusing at the common ancestors' lifetime. To do this correctly, the right approach should take into account a contribution of reverse mutations as well as a degree of symmetry or asymmetry of mutations, which increase or decrease a number of tandem repeats in the haplotypes loci. Besides, a right choice should be made for mutation rate constants for the given (or chosen) haplotypes, which are different for different combinations of markers in haplotypes. It should also accomplish a separation of lineages descended from different common ancestors in the chosen population (in a case of mixed populations, which commonly happens in real situations). A rather comprehensive description of the approach resolving these complications, and including criteria for composing and analyzing haplotype trees (examples are shown below) is given in[1].

It is well known that many Jews and Arabs belong to haplogroups J1 and J2, as well as many other haplogroups[2-8]. For some, apparently, quite arbitrary reasons, haplogroup J1 has been considered as the most likely one to host the principal ancestor of Cohanim, or Cohens, the Jewish High Priests. Granted, the first studies of the origin of the Cohens did not resolve haplogroups J into J1 and J2[9,10], however, the subsequent papers on the subject have shifted that origin to haplogroup J1, specifically, subclade J1e[8]. It was repeatedly claimed that a certain "signature" of alleles in certain markers (DYS 19, 388, 390, 391, 392, and 393), namely 14-16-23-10-11-12, identified the so-called "Cohen Modal Haplotype" (CMH) in haplogroup J1[6,8].

Haplogroup J1

In this study we have collected 94 of 37 marker haplotypes of haplogroup J1, all having the CMH "signature" as above, Jewish and non-Jewish, including several Arabic haplotypes (ironically, they all had the "Cohen Modal Haplotype"), and composed the respective haplotype tree, shown in Fig. 1.

Each bar in Fig. 1 represents a haplotype[1]. The tree shows two rather distinct branches: one, on the left, which is compact, and contains Jewish haplotypes only and another, on the right, which is "fluffy", therefore indicating a significantly "older age" in terms of a timespan to a common ancestor of the branch. It contains mostly non-Jewish haplotypes, including all three Arabic haplotypes. All 44 haplotypes of the "older" branch contain 291 mutations in the first 25 markers (0.265 mutations per marker on average), and 543

mutations in the “faster” 37 markers from the base (deduced ancestral) haplotype as follows:

12 23 14 10 13 17 11 16 11 13 11 30 -- 17 8 9 11 11 25 14 20 26 12 14 16 17 -- 11 10 22 22 15 14 18 18 32 35 12 10

This translates into **4100±460** years to a common ancestor of the “older” Arabic-Jewish branch, as explained in the METHODS section at the end of this article (all other data on mutations and their calculations are given in that section).

The “younger”, Jewish only, branch has a common ancestor **1125±160** years before present (ybp) who had the following haplotype

12 23 14 10 13 **15** 11 16 **12** 13 11 30 -- 17 8 9 11 11 **26** 14 **21** **27** 12 14 16 17 -- 11 10 22 22 15 14 **20** 18 **31** 35 **13** 10

These two base haplotypes differ by 5.5 and 10.5 mutations in their 25 and 37 marker format, respectively, which places their common ancestor to **4300±500** ybp, and makes the common ancestor of the “older” branch the most recent common ancestor of both the Jews and the Arabs in both the mixed “older” and the Jewish “younger” branch.

In other words, we see the two lineages derived from a common ancestor who lived around 4300 ybp, one encompasses mainly Jews, and another – mainly non-Jewish people, among them the Arabs.

To verify this tentative conclusion and examine the time estimate for the split in finer detail, we analyzed 67 marker haplotypes, available from 34 individuals within the preceding population (see Fig. 1). The respective haplotype tree is shown in Fig. 2.

The 67 marker haplotype tree has provided even better separation of the "younger" (on the right) and the "older" (on the left) branches (Fig. 2). All 17 haplotypes of the "younger" branch belong to Jews, and 11 out of 17 haplotypes of the "older" branch were non-Jewish, including the only one Arabic haplotype reported in the 67 marker format. The base haplotypes in the 67 marker format were as follows:
"Older branch":

12 23 14 10 13 17 11 16 11 13 11 30 -- 17 8 9 11 11 25 14 20 26 12 14 16 17 -- 11 10 22 22 15 14 18 18 32 35 12 10 -- 11 8 15 16 8 11 10 8 11 9 12 21 22 18 10 12 12 15 8 12 25 21 13 12 11 14 12 12 12 11

and "Younger" branch:

12 23 14 10 13 15 11 16 12 13 11 30 17 -- 8 9 11 11 26 14 21 27 12 14 16 17 -- 11 10 22 22 15 14 20 18 31 35 13 10 -- 11 8 15 16 8 11 10 8 11 9 12 21 22 17 10 12 12 15 8 12 24 21 13 12 12 14 12 12 12 11

These haplotypes are identical with the above (for the respective branches) at the first 37 markers, and provide an extension with 30 more markers. A common ancestor for the "older", mixed branch lived **4225±545** years before present, which is within the margin of error with that for the 37 marker dataset (**4100±460** ybp).

The "younger", Jewish only branch on the right-hand side in Fig. 2 had a common ancestor who lived **1020±170** ybp. Again, this is within the margin of error with **1125±160** ybp obtained for the 37 marker dataset. The data is quite reliable, and calculations employing the 25, 37, and all 67 marker haplotypes in Fig. 2 gave 900±195, 1150±180, and 1000±140 ybp, respectively, to the lifetime of a common ancestor of the Jewish population (the "younger" branch on the right in Fig. 2), all of them having the "Cohen Modal Haplotype".

As in the preceding (37 marker) example, we see the two lineages derived from a common ancestor who lived around 4300 ybp, and he was the most recent common ancestor of both the Jews and the Arabs. He lived – taking into account both the 37 and 67 marker datasets **4300±500** years before present.

His Arabic descendants continued his direct lineage, while his Jewish descendants went through a population bottleneck at **1070±170** years ago (this is also called a genetic drift) and expanded, beginning at about the 10th century AD into what is now called the "Cohen Modal Haplotype" lineage.

In fact this should be called the "**Abraham Modal Haplotype**" when it is exhibited in Jews and Arabs.

Data, obtained by us in[11], provides additional support to this suggestion. In that study, haplotypes of actual Cohens (Cohanim) of haplogroup J1e*-P58*, collected by Hammer, Behar, Skorecki et al[8] were considered, and it was found that their common ancestor lived 1075±130 years before present[11]. Three ancestral haplotypes of J1e* Cohanim, identified in the study[11] were – in the 22 marker format available (the last shown allele is number 37th in the above extended haplotypes):

12 23 14 10 13 15 11 16 12 13 11 30 – 17 8 9 11 11 26 14 21 **26 --** 10

12 23 14 10 13 15 11 16 12 13 11 30 – 17 8 9 11 11 26 14 21 27 -- 10

12 23 14 10 13 15 11 16 **11** 13 11 30 – 17 8 9 11 11 26 14 21 **26 --** 10

One can see that the middle one exactly matches the first 21 markers, along with the 37th one, of the "younger" branch in Figs. 1 and 2. Two other base (ancestral) haplotypes differ from it by only one and two mutations (marked in bold), and a common ancestor of all the three base haplotypes lived in the range of **625-875** ybp[11].

To sum it up, the most recent common ancestor of Jews and Arabs of haplogroup J1 (subclade J1e) lived **4300±500** years ago, and he had the "J1 Abraham Modal Haplotype", former "Cohen Modal Haplotype" signature. From him a split occurred between the Jewish and the Arabic lineages in haplogroup J1 (J1e*). The split is clearly visible on the haplotype tree in the 37 and the 67 marker format (Figs. 1 and 2).

1070±170 years before present, in the 10th century (plus-minus a century), a line of Cohanim, haplogroup J1e*, split from that ancestral lineage.

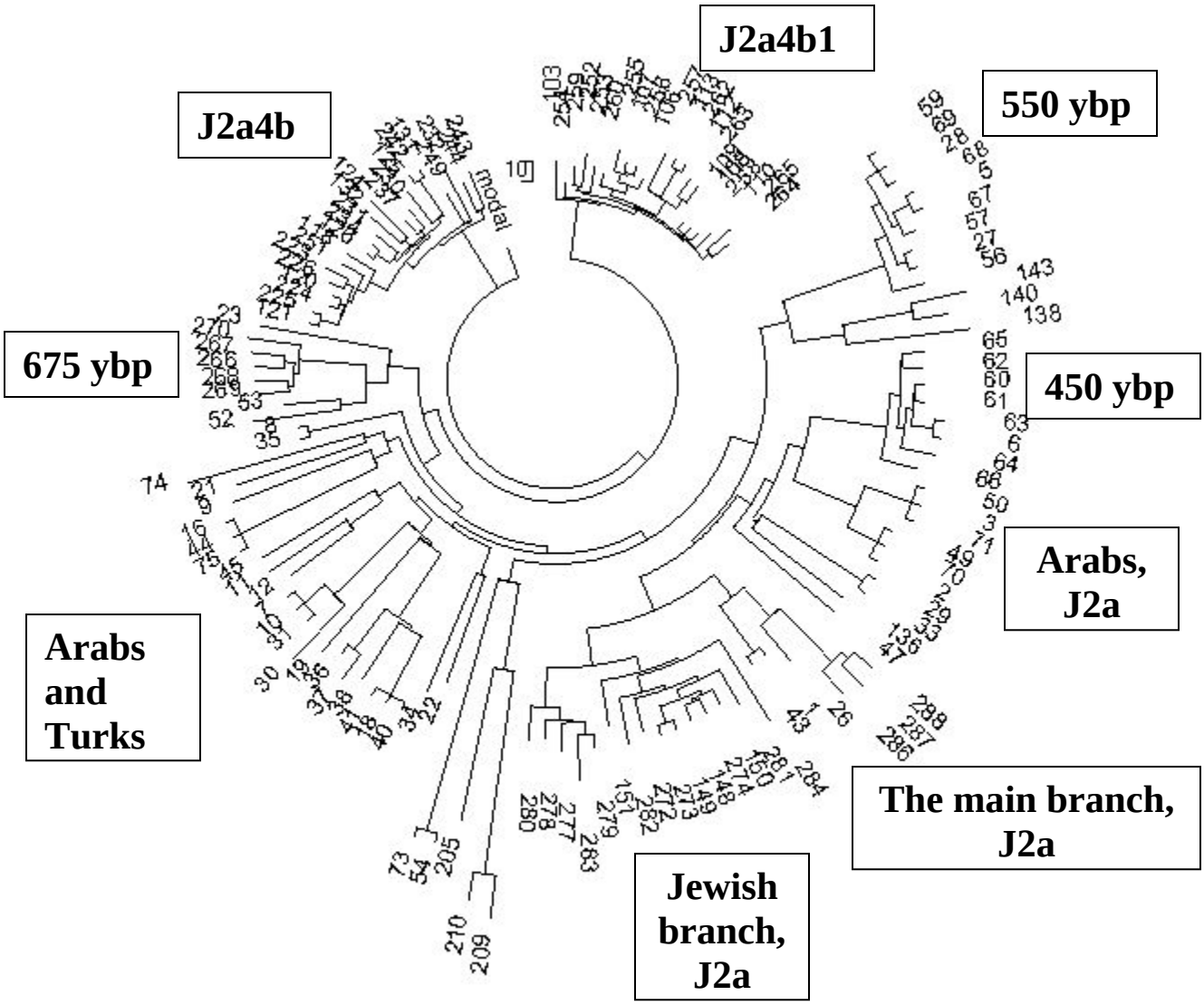
The most recent common ancestor of the Cohanim J1 (J1e*) lineage had a haplotype which still contained the "Abraham" six-marker signature 14-16-23-10-10-12 (see above), however, his haplotype already contained six mutations from the initial haplotype in that lineage.

Those six mutations were all inherited by Cohanim in haplogroup J1, and many of them continue to carry those mutations to the present time.

Haplogroup J2

We have collected 181 and 131 of 37 and 67 marker haplotypes, respectively, of haplogroup J2. All haplotypes were obtained from Jewish and Arabic Projects, such as Arabic World DNA, J2-Arab Project, Sharifs DNA Project, Jewish Heritage Project,

Cohen Project, Sephardic Heritage project, and from YSearch database. The respective haplotype trees are shown in Figs. 3 and 4.



Most of the branches in Fig. 3 contain either only Jewish haplotypes, or only Arabic ones, and cannot be employed for the main purpose of this work. Besides, some branches were not only mono-ethnic, but were too recent in terms of timespans to their common

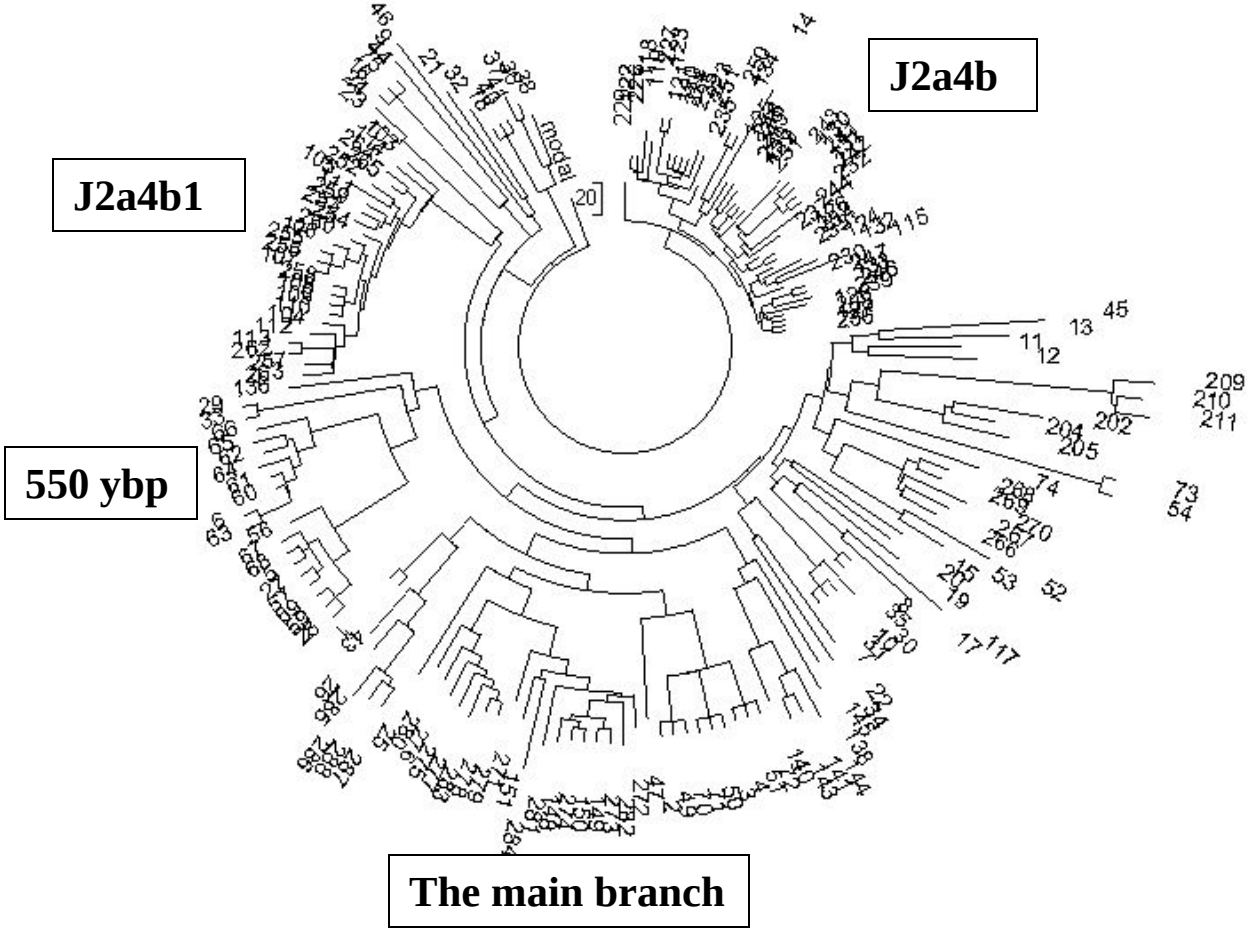
ancestors (see Fig. 3). Clearly, those branches represent rather recent lineages, and are not related to the genealogical split between the Arabs and the Jews. There is only one branch on the tree which appears appropriate for the analysis of the split. This is a double branch in the lower right-hand side of the tree, one half of which is represented with mainly Jewish haplotypes, and another with mainly Arabic ones. It is marked as "The main branch" on the tree. All haplotypes on the branch belong to J2a haplogroup. The branch has 39 haplotypes, however, eight of them form a sub-branch which is only 450 years "old" and its haplotypes noticeably differ from those of the rest of the branch. Clearly, it is a recent formation, and contains only Arabic haplotypes.

The rest of the branch containing 31 haplotypes (11 were Arabic and 20 were Jewish haplotypes) has a common – Jewish and Arabic – base (ancestral) haplotype of

12 23 15 10 14 17 11 15 12 13 11 29 -- 15 8 9 11 11 24 15 21 31 12 13 16 17 -- 10 10 19 23 16 14 18 18 36 37 12 9 – 11 7 14 15 8 11 10 8 11 9 12 17 17 14 10 12 12 15 9 12 22 21 14 12 11 14 11 12 12 12

A common ancestor of the joint Jewish-Arabic branch lived **4375±530** ybp, after which the joint population split.

The 37 marker haplotype tree (Fig. 4) contains more haplotypes compared to the 67 haplotype tree. The tree is essentially the same, with just a few branches switched their positions.



The base 37 marker haplotype of the main branch (containing 37 haplotypes) is identical to that in the first 37 markers of the base 67 marker haplotype (see above). A common ancestor of the joint Jewish-Arabic branch, according to the 37 marker haplotypes, lived **3975±480** ybp, after which the population split.

Hence, a common ancestor of both Jewish and Arabic lineages in haplogroup J2a-M410* lived – as an average of the timespans estimated from the 67 and 37 marker base haplotypes - **4175±510** years before present.

In other words, the time of the split between the Jewish and the Arabic lineages occurred at the same time in J1 (**4300±500** ybp) and J2 haplogroups.

It is remarkable that the base haplotype for descendants of Cohanim of the former Russian Empire (Russia, Ukraine, Belarus, Lithuania, and Poland) of haplogroup J2a-M410*, determined in paper[11]

12 23 15 10 14 17 11 15 12 13 11 29 -- 15 8 9 11 11 24 15 21 **32** -- 9

(the last allele belongs to the 37th marker in the extended haplotypes above) is practically identical with the respective 22 markets of the above extended haplotypes. The only mutation (in bold) is not a surprise, since a common ancestor of those Cohanim lived 325±190 years ago, and a common ancestor of the 37 and 67 marker haplotypes above lived 4175±510 years ago, almost four thousand years earlier. It is remarkable, though, that the joint Jewish-Arabic common ancestral haplotype has retained its pattern ca. 4,000 years after the lifetime of the founder of both the Jewish and the Arabic original lineages.

There is yet additional proof of the significance of the above ancestral haplotype in the J2 Cohanim lineage. This proof was presented in the Cohanim haplotypes themselves. President of the International Jewish Association of Cohanim, Latin America, Mr. Mashuah Pereira Cohen, has provided me with a list of twenty one verified traditional

Cohanim surnames from both Ashkenazi and Sephardic communities, which are – by their status – in good terms with the Association, along with their 12-marker haplotypes, obtained from FTDNA projects. Among them were Cohanim-Ashkenazim from Russia, Belarus, Poland, Lithuania, Hungary, Germany, Austria, Spain, Portugal, Ireland, as well as Cohanim-Sephardim from Spain, Portugal, Brazil, Morocco and the Netherlands. Their last names, according to the Association, include Cohen, Kahan, Mazer, Kaplan, Katz, Cowan, Coyne, HaKohen, Cohen Pereira, Cohen Rodrigues, Machado (Levy), Shapiro, Ben Ezra, Levy, Pereira Cunha, Garfinkel, Kagan, Kovacs, Kohn, Kohen, Cunha. Their haplotype tree is shown in Fig. 5.

Seven haplotypes of the Cohanim-Sephardim had 14 mutations from their base (ancestral) haplotype

12 23 15 10 13 18 11 15 12 13 11 29

which gives **2500±700** years from their common ancestor. 14 haplotypes of the Cohanim-Ashkenazim had 18 mutations from their base haplotype

12 23 15 10 **14 17** 11 15 12 13 11 29

which gives **1575±400** years from their common ancestor. One can see that there are only two mutations between the base Cohanim Ashkenazim and Sephardim haplotypes (shown in bold), which translates into 2500 years of mutational difference between their common

ancestors, and places their common ancestor to **3300±400** years before present. It fits into the pattern emerging here, that the 12-marker base J2 Cohanim (Ashkenazim) haplotype is identical with the first 12 alleles in the haplotype of the common ancestor of the Jews and the Arabs (shown above in the 67 marker format). .

To sum this section up, the most recent common ancestor of the Jews and the Arabs of haplogroup J2a-M410* lived **4175±510** years ago, and he had the "J2 Cohanim" signature in his haplotype. Again, it is rather "**J2 Abraham Modal Haplotype**". From him a split occurred between the Jewish and the Arabic lineages in haplogroup J2. The split is clearly visible on the haplotype tree in the 37 and the 67 marker format (Figs. 3 and 4). Around 3300 years before present, in the middle of the 2nd millennium BC, a line of Cohanim, haplogroup J2a*, split from that lineage and continued with the initial ancestral haplotype. Around 2500 years before present, in times of the Babylonian and the Assyrian exiles, the J2 Cohanim-Sephardim lineage split, and continued with the two mutations at DYS385a,b (13-18 compared to the initial 14-17) in the ancestral haplotype. The rest of J2 Cohanim continued with the same ancestral haplotype, and passed a population bottleneck (a genetic drift has occurred) in the middle of the 1st millennium AD.

This concurs with well-known historical data, according to which some 3300 years ago an institute of Cohanim was established, with its inheritance status. The Sephardim split from the main body of the Jewish population in the middle of the 1st millennium BC; and after the destruction of the Temple, in the middle of the 1st millennium AD, a new Jewish

community began to form in Europe, and gave rise to Ashkenazim, the “Jews of Germany”.

Why there were two “Abrahams”, whatever were their real names, one in haplogroup J1 and another in J2, with very similar, if not identical times of their lives? Furthermore, how is it that each of the “Abraham” lineages hosts the Cohanim, albeit the Cohanim of haplogroup J2 have their common ancestor at about 3300 years before present, while a common ancestor of the Cohanim of haplogroup J1 has appeared only around 1000 years before present?

A plausible explanation can be offered. Obviously, there were predecessors of the Jews and the Arabs in both haplogroup J1 and J2. They were practically the same people, and were called the Bedouins (or we call them Bedouins now). 4200±500 years before present they split, on the grounds of some apparently very serious reason, which likely had a religious, that is a cultural and spiritual connotation. The split was, judging from the sharpness of parting of their DNA genealogical lineages, quite a decisive one. Naturally, the split occurred not along the haplogroups J1 and J2, but across them. That was how the Jews and the Arabs had acquired both J1 and J2 haplogroups. The story of Abraham and his siblings, Ishmael, and Isaac and Jacob, the patriarchs of the Arabs and the Jews, respectively, was told and re-told by the Arabs and the Jews of all the haplogroups. Hence, it is reasonable to believe that each haplogroup which was involved in the separation process, would have had its own “Abraham”, who lived about 4,200 years ago.

(If some haplogroup does not show such a split involving both the Arabs and the Jews and going back to about 4,200 ybp and earlier, then either there were no Jews and Arabs with such a haplogroup in those times, or they were not involved in the split).

To verify this hypothesis, I have composed a 25 marker haplotype tree (not shown here) from 163 haplotypes of haplogroup R1b1b2, which included 108 haplotype of Jews and 155 haplotypes of non-Jews (mostly Europeans, including several Arabs, since only a very limited number of Arabic R1b1b2 haplotypes are available in databases). The Jewish haplotypes did not mix with the European haplotypes, and they form a number of different branches, while all the Arabic haplotypes were located only in the European branches. Hence, there was no a split of the Jewish and the Arabic haplotypes in haplogroup R1b1b2, though a common ancestor of the Jews in R1b1b2 lived 5650±710 years before present. However, those proto-Jews of R1b1b2 have not been involved in the alleged religious/cultural dispute with the emerging Arabs.

METHODS

Analysis of mutations and their rates. Principal methodology was described in[1]. Haplotype trees were constructed using PHYLIP, the Phylogeny Inference Package program[12], as was explained in detail in[1,13]. A "comb" around the wheel, a "trunk", in haplotype trees identifies "base" haplotypes, identical to each other and carrying no mutations compared to their ancestral haplotypes (e.g., in Fig. 5). The farther the

haplotypes lay from the wheel, the more mutations they carry compared to the base haplotype and the older the respective branch.

The "base" haplotypes are the ancestral haplotypes in an ideal case. However, since those haplotypes often are deduced ones, it would be inaccurate to call them "ancestral". Hence, "base" haplotypes.

The timespans to a common ancestor were calculated using both "logarithmic" and "linear" approaches. The logarithmic method is based on the assumption (which largely, or practically always holds true) that a transition of the base haplotypes into mutated ones is described by the first-order kinetics:

$$B = Ae^{kt,}$$

that is

$$\ln(B/A) = kt$$

where:

B = a total number of haplotypes in a set,

A = a number of unchanged (identical, not mutated) base haplotypes in the set,

k = an average mutation rate,

t = a number of generations to a common ancestor.

One can see that the logarithmic method does not consider mutations in haplotypes; only mutated and non-mutated (base) haplotypes are considered.

Mutation-counting methods are all based on accumulation of mutations in haplotypes over time. They include the "linear", "quadratic" (ASD) and "permutational" methods[1]. In this paper only the "linear" method is employed. In this method a total number of mutations in a set of haplotypes is counted, an average number of mutations per marker is calculated, a correction for back mutations is introduced, either numerically[1], or using a handy table[1], and a time span to a common ancestor is calculated, either using the Table[1] or applying the respective mutation rates. In other words, it is described by the following equation

$$n/N/\mu = t$$

where n is a number of mutations in all N haplotypes in the given series of haplotype, μ is an average mutation rate per haplotype per generation, and t is a number of generations to a common ancestor, corrected for back mutations.

Average mutation rates employed in this paper, are[1]:

For 12 marker haplotypes – 0.022 mutations per haplotype, 0.00183 mutations per marker,

for 25 marker haplotypes – 0.046 mutations per haplotype, 0.00183 mutations per marker,

for 37 marker haplotypes – 0.090 mutations per haplotype, 0.00243 mutations per marker,

for 67 marker haplotypes – 0.145 mutations per haplotype, 0.00216 mutations per marker.

These mutation rates were calibrated employing 25 years per generation. Time spans to a common ancestor were calculated typically employing the first 25 markers in haplotypes; these markers normally give the most reproducible data. In some cases calculations have been conducted using also 37 and 67 markers just to illustrate reproducibility of calculations.

Error margin for time spans to common ancestors are calculated as described in[1], and correspond to the 95% confidence interval.

Details of the calculations.

Haplogroup J1.

1) Fig. 1, 37 marker haplotype tree, the "older" branch of 44 haplotypes, 291 mutations in the first 25 marker haplotypes give 291/44/25 = 0.265 mutations per marker, 0.265/0.00183 = 145 generations to a common ancestor without correction for back mutations, or 169 generations with the correction, that is 169x25 = 4225 years to a common ancestor. 291 mutations determine[1] the margin of error equal to 5.86% for the

average number of mutations per marker, hence, 0.265±0.016 mutations per marker, and to 11.59% for the time span to a common ancestor, hence, 4225±490 years to a common ancestor .

2) Fig. 1, 37 marker haplotype tree, the "older" branch of 44 haplotypes, 543 mutations in all 37 marker haplotypes give 543/44/37 = 0.334 mutations per marker, 0.334/0.00243 = 137 generations to a common ancestor without correction for back mutations, or 159 generations with the correction, that is 3975 years to a common ancestor. 543 mutations determine the margin of error equal to 4.29% for the average number of mutations per marker, hence, 0.334±0.014 mutations per marker, and to 10.88% for the time span to a common ancestor, hence, 3975±430 years to a common ancestor.

An average of 4225±490 and 3975±430 ybp gives **4100±460** years to a common ancestor of the "older" branch in the 37 marker haplotype tree of the Jewish and the Arabic haplotypes.

3) Fig. 1, 37 marker haplotype tree, the "younger" branch of 50 haplotypes, 98 mutations in the first 25 marker haplotypes give 98/50/25 = 0.078±0.008 mutations per marker, 0.0784/0.00183 = 43 generations to a common ancestor without correction for back mutations, or 45 generations with the correction, that is **1125±160** years to a common ancestor.

4) Fig. 2, 67 marker haplotype tree, the "older" branch of 17 haplotypes, 118 mutations in the first 25 marker haplotypes give 118/17/25 = 0.278±0.026 mutations per marker, 0.278/0.00183 = 152 generations to a common ancestor without correction for back

mutations, or 179 generations with the correction, that is **4475±610** years to a common ancestor.

5) Fig. 2, 67 marker haplotype tree, the "older" branch of 17 haplotypes, 210 mutations in the first 37 marker haplotypes give 210/17/37 = 0.334±0.023 mutations per marker, 0.334/0.00243 = 137 generations to a common ancestor without correction for back mutations, or 159 generations with the correction, that is **3975±480** years to a common ancestor.

An average of 4475±610 and 3975±480 ybp gives **4225±545** years to a common ancestor of the "younger" branch in the 67 marker haplotype tree of the Jewish and the Arabic haplotypes.

6) Fig. 2, 67 marker haplotype tree, the "younger" branch of 17 haplotypes, 27 mutations in the first 25 marker haplotypes give 27/17/25 = 0.0635±0.012 mutations per marker, 0.0635/0.00183 = 35 generations to a common ancestor without correction for back mutations, or 36 generations with the correction, that is **900±195** years to a common ancestor.

7) Fig. 2, 67 marker haplotype tree, the "younger" branch of 17 haplotypes, 68 mutations in the first 37 marker haplotypes give 68/17/37 = 0.108±0.013 mutations per marker, 0.108/0.00243 = 44 generations to a common ancestor without correction for back mutations, or 46 generations with the correction, that is **1150±180** years to a common ancestor.

8) Fig. 2, 67 marker haplotype tree, the "younger" branch of 17 haplotypes, 93 mutations in all 67 marker haplotypes give 93/17/67 = 0.0817±0.008 mutations per marker, 0.0817/0.00216 = 38 generations to a common ancestor without correction for back mutations, or 40 generations with the correction, that is **1000±140** years to a common ancestor.

An average of 900±195, 1150±180, and 1000±140 ybp gives **1020±170** years to a common ancestor of the "younger" branch in the 67 marker haplotype tree of the Jewish and the Arabic haplotypes.

An average of 4100±460 and 4225±545 ybp gives **4160±500** years to a common ancestor of the "older" branch in the 37 and 67 marker haplotype tree of the Jewish and the Arabic haplotypes.

An average of 1125±160 and 1020±170 ybp gives **1070±170** years to a common ancestor of the "younger" branch in the 37 and 67 marker haplotype tree of the Jewish and the Arabic haplotypes.

Base haplotypes of the "older" and "younger" branches differ by 5.5 and 10.5 mutations on the first 25 and 37 marker haplotypes. This results in a difference between the two common ancestors of 3400 years, and places their common ancestor to **4300±500** years before present. This is the common ancestor of the "older" branch, within the margin of error.

Haplogroup J2.

1) Fig. 3, 67 marker haplotype tree, the main (subclade J2a) branch of 31 haplotypes, 211 mutations in the first 25 marker haplotypes give 211/31/25 = 0.272±0.019 mutations per marker, 0.272/0.00183 = 149 generations to a common ancestor without correction for back mutations, or 175 generations with the correction, that is **4375±530** years to a common ancestor.

2) Fig. 4, 37 marker haplotype tree, the main (subclade J2a) branch of 37 haplotypes, 231 mutations in the first 25-marker haplotypes give 231/37/25 = 0.250±0.016 mutations per marker, 0.250/0.00183 = 137 generations to a common ancestor without correction for back mutations, or 159 generations with the correction, that is **3975±480** years to a common ancestor.

An average of 4375±530 and 3975±480 give **4175±510** years to a common ancestor of the "younger" branch in the 67-marker haplotype tree of the Jewish and the Arabic haplotypes.

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Additional Resources:

Sharifs DNA Project, http://www.familytreedna.com/public/sharifs/default.aspx

The Jewish R1b Project, http://www.familytreedna.com/public/JewishR1b/default.aspx

J2-Arab Project, http://www.familytreedna.com/public/J2-Arab/default.aspx

Cohen DNA Project, http://www.familytreedna.com/public/Cohen/default.aspx

Jewish DNA Project,

http://www.familytreedna.com/public/JewishDNAProject/default.aspx

Jewish Ukraine West Project,

http://www.familytreedna.com/public/Jewish_Ukraine_West/default.aspx

JewishGen Scandinavia DNA Project,

http://www.familytreedna.com/public/ScandinaviaSIG/default.aspx

Sephardic Heritage DNA Project,

http://www.familytreedna.com/public/Sephardic_heritage/default.aspx

Ashkenazi-Levite DNA Project, http://www.familytreedna.com/public/Ashkenazi-Levite/index.aspx?fixed_columns

YSearch, a Free Public Service from Family Tree DNA, http://www.ysearch.org/

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FIGURE LEGENDS

Figure 1. 37 marker haplotype tree for the "Cohen Modal Haplotype", haplogroup J1. This 94 haplotype tree was composed of haplotypes obtained from YSearch database and private "Cohen Haplotype" projects. The tight, compact, hence "young" branch on the left encompasses the Jewish haplotypes only. The fluffy" and much more extended, therefore "old" branch on the right contains haplotypes, two-thirds of which belong to

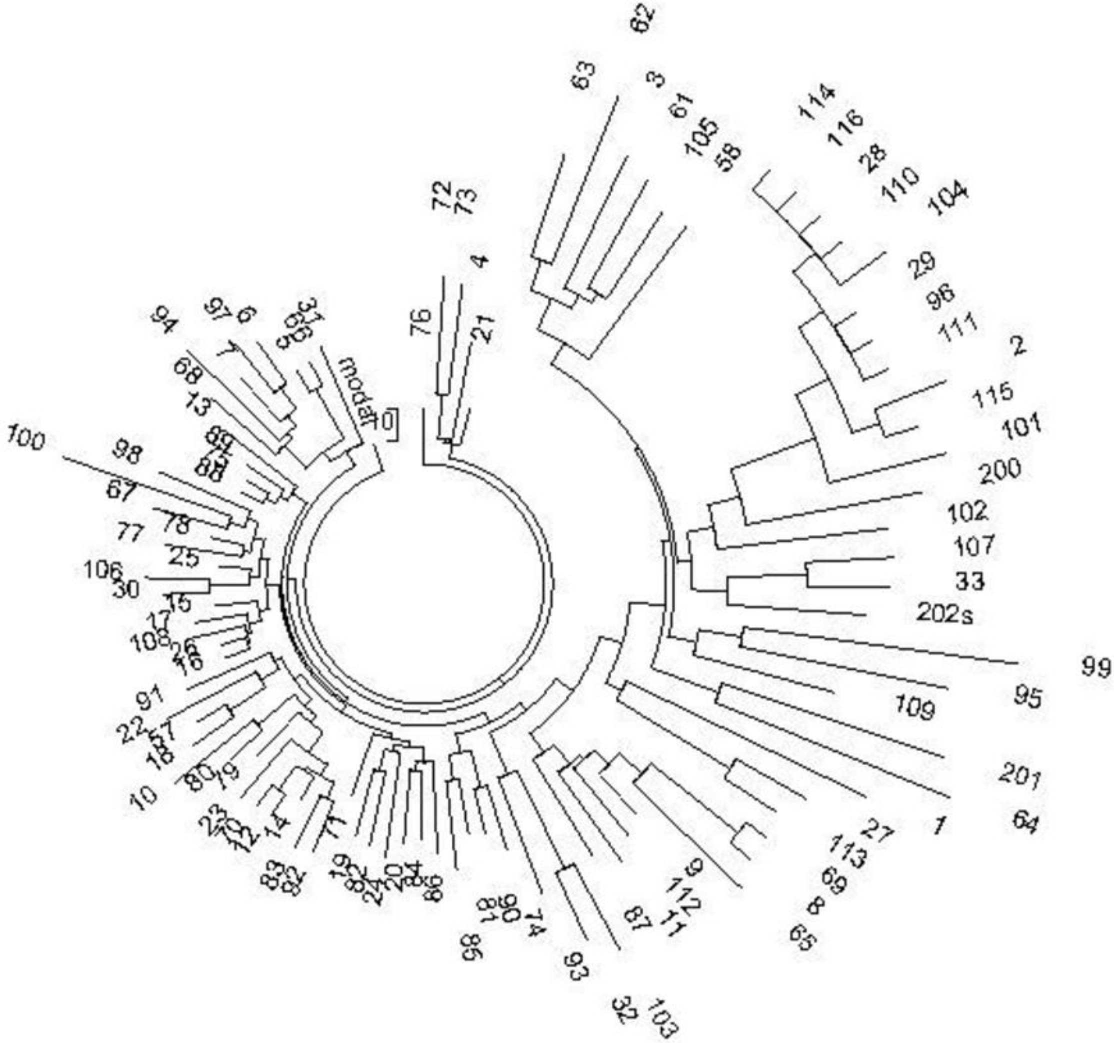
people claiming non-Jewish origin. Haplotypes 200, 201 and 202s belong to the Arabs and haplotype 202s belongs to Arab-Sayid/Sharif (Sharifs DNA Project).

Figure 2. 67 marker 34 haplotype tree for the "Cohen Modal Haplotype", haplogroup J1. For explanations see the legend to Figure 1.

Figure 3. 67 marker 131 haplotype tree composed of the Arabic (haplotype numbers below 100) and Jewish (haplotype numbers 100 and higher) haplotypes of J2 haplogroup. All haplotypes were collected from sources indicated in the text. Some subclades are indicated on the graph, as well as some timespans to common ancestors for "young" branches. Branches of subclades J2a4b and J2a4b1 contain only Jewish haplotypes, with the respective times to their common ancestors of 1200±210 and 700±150 years before present (NOTE for the publisher: the figure does not contain labels; they are added in the text format, see above)

Figure 4. The 37 marker 181 haplotype tree composed of the Arabic (haplotype numbers below 100) and Jewish (haplotype numbers 100 and higher) haplotypes of J2 haplogroup. The 450-ybp Arabic branch in Fig. 3 became more numerous 550-ybp branch in Fig. 4, that is essentially the same within the margin of error. For further explanations see legend to Figure 3 (NOTE for the publisher: the figure does not contain labels; they are added in the text format, see above) .

Figure 5. The 12-marker 21 haplotype tree composed of the Cohanim J2 haplotypes, provided by the International Cohanim Association (President, Mr. Mashuah Pereira Cohen).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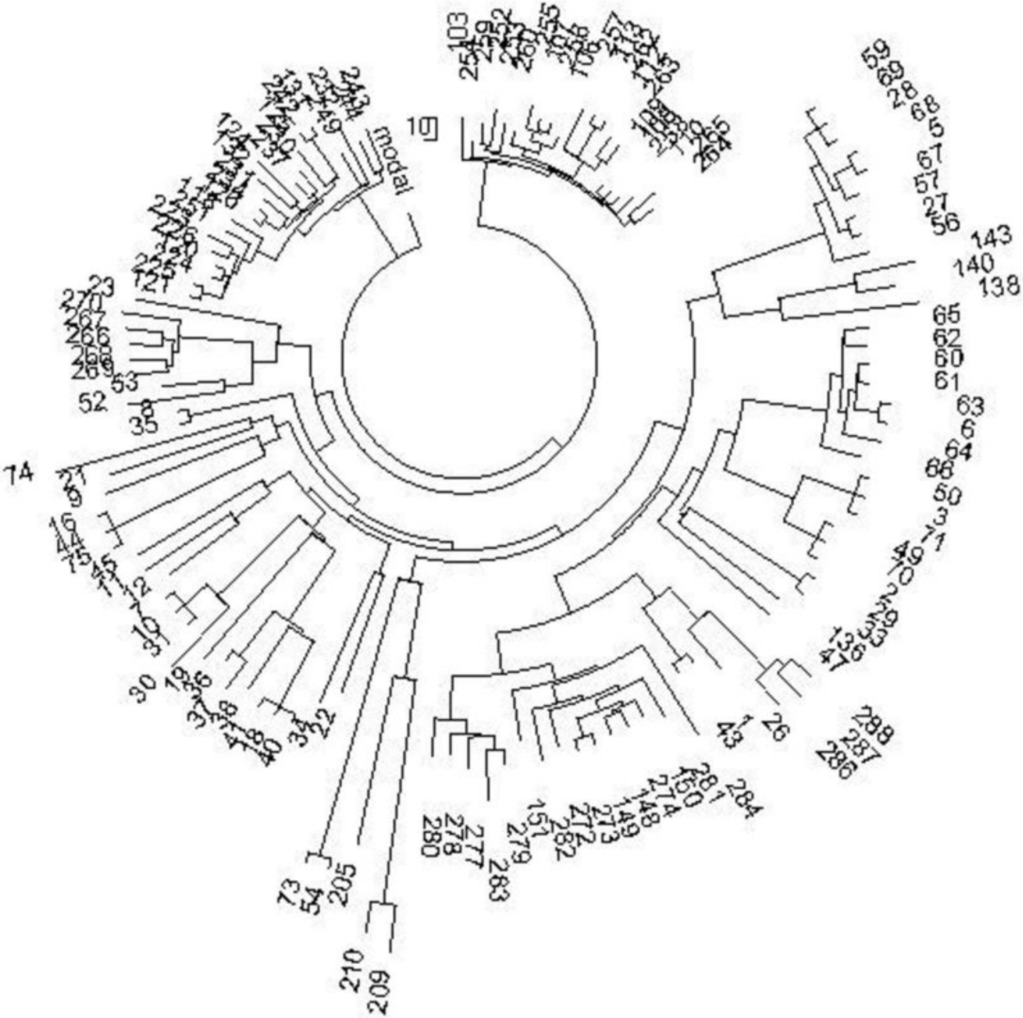

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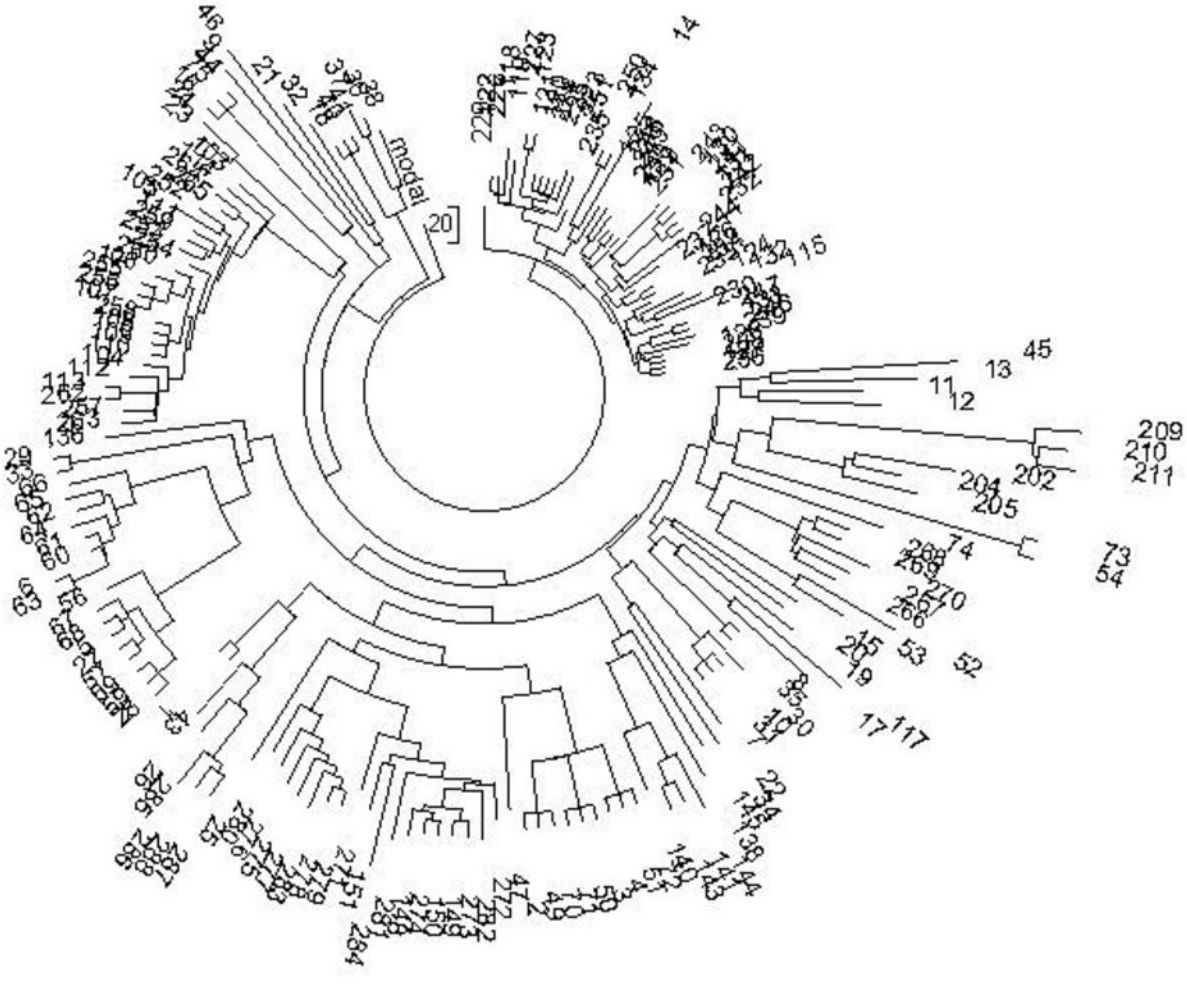
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