

Ancient DNA helps compare the proposed paternal families. It does not yet identify a patriarch.

The ancestry containing CB-01, the principal Cohen branch called J-ZS222, currently provides the strongest starting point for the connected family history. Its advantage comes from an independently recorded priestly tradition across several Jewish communities. The preference is provisional. CB-02 and CB-03 remain serious alternatives. Z642 has useful Samaritan and regional evidence, but its country pattern does not currently outweigh the priestly evidence. None of these results establishes an identification of Aaron, Jacob, Abraham, Noah or Adam.

Existing ancient DNA does contain a strongly supported member of CB-01. The man is I37241. His published central date is about AD 100. I independently checked his DNA reads and found eleven defining CB-01 mutations that survive strict quality and end-trimming checks. Two additional mutations support a probable position inside its Z18271 branch. His archaeological location and community are withheld. He establishes ancient membership of the genetic branch; he does not establish priestly or Israelite identity.

[Akbari and colleagues, 2026, original tables](#)

The published Erfurt individual I14846 offers a different kind of evidence. His medieval Jewish cemetery gives a meaningful community context. His precise CB-01 placement rests on one surviving informative DNA read, however. The older Megiddo individual I4517 does not supply the missing ancient identification: two reads retain the earlier base at a mutation defining CB-01. The distinction between a strong genetic placement and a strong archaeological context matters throughout this report.

[Waldman and colleagues, 2022](#) · [Agranat-Tamir and colleagues, 2020](#)

Alcuin directed the investigation, checked the decisive sources and calculations, and made this assessment. Sonnet 5.5 completed the detailed tree, archaeological and population-model research. Focused review assignments corrected errors and challenged the conclusions. The [technical record](#) describes the checks, unresolved evidence and model execution. The [research files](#) preserve the calculations and working evidence.

The investigation accepts Scripture as authoritative and uses the project's particular historical interpretation.

That interpretation places Noah's arrival in an already inhabited world in 2903 BC. It does not require a worldwide human genetic bottleneck. It allows Adam's chromosome to have been copied from an earthly source. These are the premises of this comparison, rather than discoveries made by DNA.

The chronology places Adam at about 5159 BC, Abraham's birth in 1771 BC, Ishmael's in 1685 BC, Isaac's in 1671 BC, and Jacob and Esau's in 1611 BC. It places the entry into Egypt in 1481 BC and the Exodus in 1266 BC. I have not altered genetic mutation rates to fit those dates. Estimates of genetic age retain their published uncertainty. The effects of the unusually late fatherhood in the interpretation remain uncertain.

The genealogy requires one father-to-son history from Noah through Shem, Abraham, Isaac and Jacob to Levi and Aaron. A proposed Aaronic branch therefore also proposes an ancestry for those earlier men. It does not give the same amount of evidence for each name. The arrival date, the date when a mutation appeared, and the date of the shared ancestor of tested descendants are different events.

A growing family need not become a larger share of its neighbours.

Its sons must survive and have sons. Their families must reach the place later excavated. Other families may grow just as quickly. Marriages can spread genealogical descent widely while leaving a paternal line rare. Burial practice, preservation, excavation and readable mutations then determine which descendants can be recognised.

The models follow different kinds of ancestry.

Quantity	What the number means	What the existing model supplies
G: genealogical descent	Residents with any ancestor from the ark, divided by all residents.	The map follows descendants of one seed man. It does not calculate this full ark-wide quantity.
A: expected overall ancestry	The expected share of the rest of the genome assigned to ark founders.	The pedigree assigns this share to followed people. It is not measured ancient DNA.
H(t): ancestry above a threshold	Residents whose assigned overall share is at least t , divided by all residents.	The pedigree reports thresholds such as one-half and one-quarter. It drops people below one-eighth.
Y: paternal descent	Men whose chain of fathers reaches Noah, Abraham or Jacob, divided by the relevant male population.	The later community model follows Jacob's paternal line. The early pedigree needs a separate father-chain calculation.
O: recognised paternal descent	The fraction of the actual tested men whose DNA permits recognition of the specified branch.	No existing model estimates this reliably for the archaeological collections. A broad J1 or J2 call is insufficient.

A son of an unrelated mother still inherits his father's Y chromosome. His expected overall ancestry is diluted, but his paternal line is not. The pedigree model's one-eighth threshold therefore removes some men who still belong to the paternal family. It also stops forming new marriages above 1,500 followed people in a region and stops generating births after 1736 BC. Its later decline cannot be interpreted as the disappearance of Noah's male-line descendants.

Sonnet extended the calculation to compare declining, equal, slowly increasing and faster increasing paternal shares. The scenarios use the model's staggered Levant arrivals and explicitly vary how many incoming men belong to Noah's father line. They include population growth and, in the stochastic version, extinction of male lines. The calculations use a broad Levant-and-Cyprus region. They do not establish the frequency at Megiddo, Jerusalem or any particular cemetery.

Alternative assumptions produce very different shares of resident Levant-region males.

Assumed reproduction relative to other men	2000 BC	1611 BC	1266 BC	586 BC	AD 100
The line has 5% fewer surviving sons per generation than other men.	0.0011%–0.011%	0.000565%–0.00565%	0.000313%–0.00313%	9.79e-05%–0.000979%	3.04e-05%–0.000304%
The line has the same number of surviving sons per generation.	0.00201%–0.0201%	0.00201%–0.0201%	0.00201%–0.0201%	0.00201%–0.0201%	0.00201%–0.0201%
The line has 5% more surviving sons per generation.	0.0036%–0.036%	0.00678%–0.0678%	0.0119%–0.119%	0.0359%–0.358%	0.109%–1.08%
The line has 15% more surviving sons per generation.	0.0107%–0.107%	0.0658%–0.654%	0.327%–3.18%	7.24%–43.8%	65.5%–95%

Every range in this table compares an assumed 10% with an assumed 100% of arriving household males belonging to Noah's father line. It is not a confidence interval. The calculation assumes half of household members are male, about 501,000 resident males near the first arrivals, and 30-year generations. The model's principal arrivals occur near 2369 BC; other households arrive later. Its population growth is extrapolated beyond the period of its saved population estimates. These deterministic calculations omit chance extinction. The separate stochastic calculations in the technical record include it. A persistent reproductive advantage over many centuries is a strong assumption, not a finding.

For illustration only, Sonnet also simulated 100 unrelated men chosen without burial or recovery bias, with a 20% chance of reading enough DNA in each carrier to recognise the branch. Under the full-founder, equal-reproduction scenario, the probability of recognising at least one carrier near AD 100 is about 0.4%. Under the full-founder, 5%-greater-reproduction scenario it is about 19%. Those are probabilities for an invented unbiased collection under stated histories. They are not probabilities for the actual ancient collections, or for identifying Noah.

These alternative histories show why a fixed waiting period would be misleading. Under equal reproduction, more descendants can exist while their proportion stays small. Under declining reproduction, a later collection can be less likely to contain a descendant. Under sustained greater reproduction, later specimens become more informative. A positive early specimen can establish presence under any scenario. An early negative result requires a credible chance of detection before it can count against a history.

The following table places model outputs beside the evidence available for the same broad periods.

“Not calculated” means that the model supplies no valid number. It does not mean zero descendants. The regional archaeological counts use the current AADR index and original papers. Intervals crossing a period boundary remain separate. The model’s Levant-and-Cyprus region and the four modern-country search area are approximations to different geographical populations.

AADR, v66.p1, Dataverse release 14.0

The periods join observations to the quantities the models actually calculate.

Place and period	G	A and H(t)	Paternal Y quantity	Observed evidence and denominator	What O permits
Before 2903 BC; receiving populations	No arrival-derived G applies.	The background populations are not assigned ark ancestry by this interpretation.	Related earthly paternal branches may already exist.	Earlier Near Eastern J and E branches supply regional background.	A broad ancestral branch cannot distinguish an introduced family from relatives already present.
2903–2000 BC; Shinar and dispersal	Not calculated for all ark ancestors.	The central pedigree follows a median 882 Shinar people at 2372 BC, with mean assigned A ≈70.5%. These are followed people, not all residents.	A father-chain can be traced only for the retained example pedigree; the whole regional share is not supplied.	The examined southern Mesopotamian coverage does not provide a matched arrival test. Later Bakr Awa lies in northeast Mesopotamia.	No calibrated probability of recognising initial descendants exists.
2903–2000 BC; broad Levant region	The separate map tracks one seed man, not full G.	At 2200 BC, the pedigree’s median H(½) is 429/1,065,295 residents (0.040%); H(¼) is 741/1,065,295 (0.070%).	At 2000 BC, the scenarios above range from 0.0011% to 0.107% of resident males across their assumptions.	AADR indexes sparse Early Bronze evidence. The strict 2903–2000 BC four-country search has four Y-called men wholly within it and three whose dates cross 2000 BC. None crosses 2903 BC. The earliest inside interval starts at 2700 BC.	Broad J1/J2 evidence tests regional background. It does not identify Noah’s descendants.
2000–1481 BC; Levant and patriarchal interval	Not calculated consistently across models.	The pedigree’s later regional totals are limited by its marriage ceiling and ancestry cutoff.	At 1611 BC, the alternative regional shares above span about 0.000565%–0.654%.	The four-country AADR search has 24 Y-called men wholly within this interval and 17 straddling its edges. A known father–son pair reduces the 24 to at most 23 close-kin-independent men.	I10268 has older-related J1 evidence. His dated interval precedes Abraham’s birth. He cannot be Abraham’s descendant.

Place and period	G	A and H(t)	Paternal Y quantity	Observed evidence and denominator	What O permits
1481–1266 BC; modelled Israelite household in Egypt	Not supplied.	The forward calculation begins with A $\approx$ 10.1% for Jacob's sons; its middle Exodus result is A $\approx$ 3.43%.	Y_J starts at 100% by construction and reaches 92.2% under the middle delayed-incorporation calculation.	No matched Egypt collection from this interval was identified in the examined sources.	The household proportion cannot be applied to all Egyptian men.
1481–1200 BC; regional Late Bronze Levant	Not supplied.	No valid continuation of the early pedigree provides a regional A or H.	The separate regional scenarios at 1266 BC span about 0.000313%–3.18%.	Baq'ah has eleven published Y-called men across wider Late Bronze intervals; seven share a broad J-Y2919 assignment. Known relatives and repeated families reduce independence.	These regional men test presence and spread of branches. They are not a direct sample of the model's Egyptian household.
1200–586 BC; Iron Age Levant and modelled Israel/Judah	Not supplied.	At the design stage ending 586 BC, middle A is 2.06% among the modelled community.	Middle Y_J is about 71% among community men, not all regional men.	The strict four-country interval contains three Y-called men plus seventeen straddlers. I4517 is from Megiddo; I2201 is T-L208 at Abel Beth Maacah; ASH087 is L at Philistine Ashkelon.	The collection does not represent Judah or permit a candidate-specific absence probability. I4517's reads oppose his deepest automatic CB-01 label.
586 BC–AD 70; later Levant and Mediterranean	Not supplied.	The community model continues; it does not distinguish individual archaeological sites.	Middle Y_J is about 64% at the design stage ending AD 70.	Beirut has regional J1 and other branches. R835's Roman interval extends from 27 BC to AD 300 and straddles this boundary.	R835 supplies an older-diverging relative, not a verified CB-01 man.
AD 70–1000; dispersed and partly anonymised men	Not supplied.	The model calculates different community trajectories. It cannot assign an anonymised individual to one.	At about AD 1000, its middle Ashkenazi Y_J is 57%; A is 1.11%.	I37241 (mean AD 100) is CB-01; I45358 (mean AD 750) is an earlier-diverging relative. Both lack public site and community context.	These men establish dated genetic relationships. They do not measure a Jewish or Levantine population share.
AD 1000–1700; medieval Jewish contexts and later persistence	Not supplied.	At about AD 1700, the middle Ashkenazi model gives A $\approx$ 0.84%.	The same conditional path gives Y_J $\approx$ 52%.	Erfurt, Norwich and Tàrrega supply 17 men with published Y calls. I14846 has thin CB-01 evidence; ROQ2 belongs to a related E branch. Anonymised I43272, mean AD 1700, is inside Z642.	Cemetery exposure and branch readability are not calibrated. I43272 cannot be added to the Jewish denominator.

Place and period	G	A and H(t)	Paternal Y quantity	Observed evidence and denominator	What O permits
Present Jewish communities	Not supplied.	Middle A is $\approx 0.745\%$ for Ashkenazi and $\approx 1.269\%$ for Iraqi/Iranian model communities.	Middle Y_J is $\approx 49.9\%$ and $\approx 58.2\%$, respectively. The low/high Ashkenazi cases are 91.4%/12.6%.	Lipson recruited 104 Cohanim; 47 belong to CB-01, four to CB-02 and six to CB-03. Other studies recruited broader Jewish groups.	A fraction among priests or project participants cannot measure Y_J among all community men.
Present Samaritans and Arabian regional comparisons	Not supplied for the communities.	The forward model gives two different Samaritan histories. Its fixed outsider-ancestry values are rough approximations.	Middle Samaritan Y_J is $\approx 69.7\%$ without, or $\approx 41.8\%$ with, the model's specified 722 BC incorporation event. No matched Arabian Y prediction was generated.	Shen tested twelve Samaritan men from four families. Regional sequencing and commercial projects document diverse Arabian branches with different recruitment.	Deeply separated Samaritan families cannot all be one recent paternal line. Arabian countries cannot identify Ishmael or Keturah.

These entries preserve source-model meanings rather than combine incompatible models. The later design-stage dates omit a separate 40-year wilderness interval and round generations; they are approximate stage labels. The detailed evidence file contains the longer output series.

[AADR, v66.p1, Dataverse release 14.0](#) · [Agranat-Tamir and colleagues, 2020](#) · [Feldman and colleagues, 2019](#) · [Haber and colleagues, 2020](#) · [Akbari and colleagues, 2026, original tables](#) · [Waldman and colleagues, 2022](#) · [Pallarés-Viña and colleagues, 2026](#)

The later community calculation gives Jacob-paternal shares of 91.4%, 49.9% and 12.6% among its present Ashkenazi male population under its low-, middle- and high-incorporation assumptions. I independently reproduced those three numbers. They are conditional model outputs. They cannot be compared directly with 47 CB-01 men among 104 recruited Cohanim. One denominator contains all modelled community men; the other contains recruited priests. A valid comparison also needs the community frequency of the larger branch that would include Jacob's other descendants.

Increasing the model's incorporation of outside fathers lowers its expected Jacob-paternal share. Choosing the top of its assumed male-incorporation ranges lowers the middle result from 49.9% to 33.8%. Choosing the high values for all incorporation inputs lowers it to 12.6%. These are explicit revisions after inspecting the results. They are not independent predictions or evidence that any particular branch belongs to Jacob.

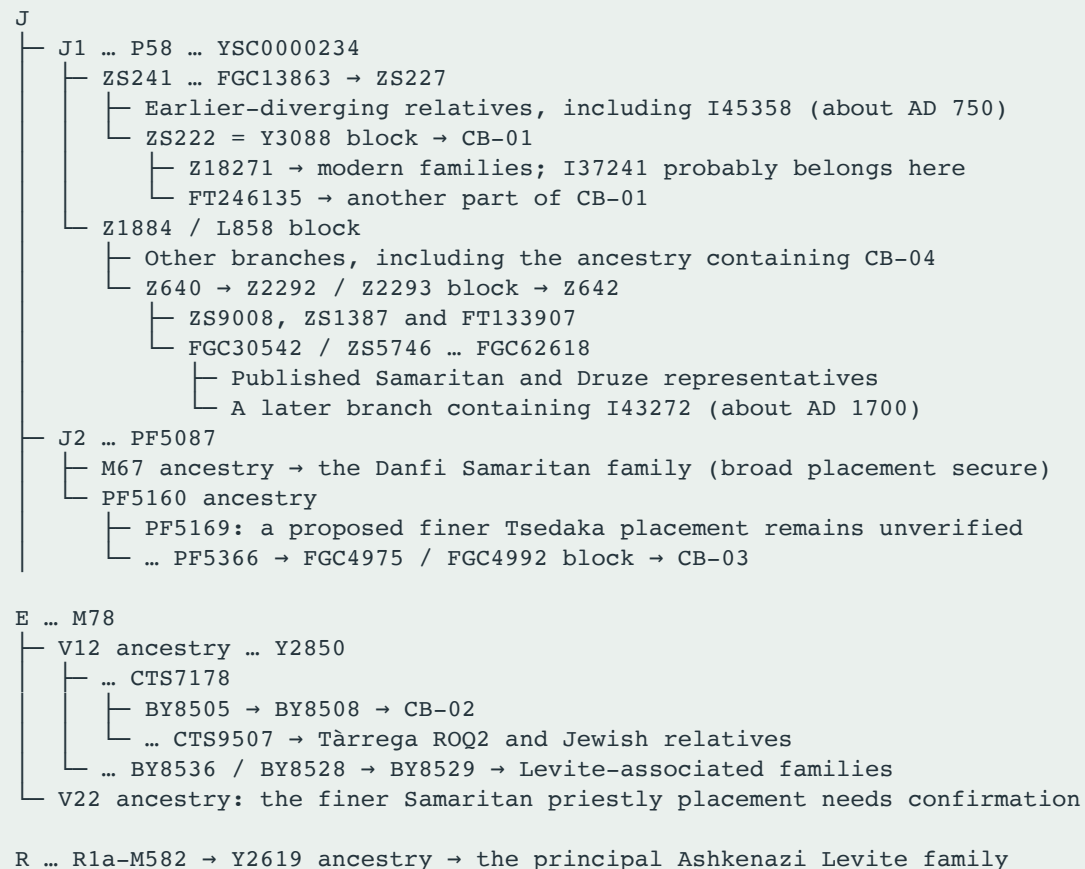
The demographic calculation does not by itself choose a haplogroup. Assigning Jacob's paternal family to the ancestry containing CB-01, CB-02 or CB-03 produces the same conditional paternal shares until evidence supplies different histories of survival, growth or incorporation. Each present priestly branch would represent only a subset of Jacob's sons' descendants. Predicting its frequency therefore also requires the proportion descending through Levi and Aaron. That proportion is not supplied by the model. Z642 presents the converse problem: a proposed Abraham-level branch could include descendants outside Jacob's family. Its whole frequency cannot be substituted for Jacob's share.

The proposed branches form alternatives within a connected tree.

A haplogroup is a branch defined by shared mutations on the Y chromosome. The outline below omits many intermediate branches. An equals sign means alternative names for the same marker or mutation-defined block at the resolution used here.

[Sahakyan and colleagues, 2021](#) · [Lipson and colleagues, 2025 preprint](#) · [YFull public tree data](#)

The human paternal tree separates E, J and R long before the proposed patriarchs.



CB-01 and Z642 meet at YSC0000234. FamilyTreeDNA estimates that shared ancestor at 3352 BC, with a reported 95% interval of 4117–2682 BC. The central estimate is earlier than the proposed Noah arrival, and much earlier than Abraham. Their separate histories cannot both identify Abraham's and Aaron's paternal branch under the ordinary tree and clock. Their shared older ancestry does not identify Noah. The previously withdrawn identification of Noah with L858 is not restored.

[FamilyTreeDNA Discover](#)

CB-01 and CB-03 meet much earlier, at the division between J1 and J2. The J1 and two J2 Samaritan families also have ancient separations. Loss of other sons’ lines cannot make these surviving, deeply different chromosomes descend from one recent paternal founder. At least some present tribal or priestly traditions require a different history of family membership. The same scrutiny must apply to Jewish and Samaritan traditions.

[Shen and colleagues, 2004](#) · [Oefner and colleagues, 2013](#)

A branch’s “formation” estimate generally refers to its separation from the parent branch. Its common-ancestor estimate refers to the tested descendants within it. Neither date names a historical person. CB-01’s published shared ancestor is around 833 BC, with a reported 95% interval of 1289–440 BC; Table 3 gives the slightly different 834 BC and 1291–440 BC. Descendants of an earlier Aaron could still share a later surviving ancestor. No clock adjustment is needed for that possibility.

[Lipson and colleagues, 2025 preprint](#)

The comparison favours continuity of CB-01’s priestly family, but does not establish it.

A coherent history must explain both the surviving branch and the other families whose traditions would need incorporation, mistaken attribution or loss of earlier lines. An unidentified paternal family must also explain why the recognised priestly lines survived and acquired their traditions. It is not an assumption-free alternative.

The alternatives explain different observations and require different historical links.

Proposed history	What it explains	What it requires	What is missing or difficult
CB-01 ancestry (J-ZS222)	It is the strongest present starting point. It joins a large, geographically diverse priestly association with a now verified ancient member.	The proposed Aaronic line must retain or regain priestly identity. Other priestly Y families require different paternal origins. Jacob’s other sons may be lost, untested or on earlier-diverging branches.	The ancient member lacks a public community identity. A German Jewish non-priest joins earlier, around 2150 BC in the preprint; this is not demonstrated descent from another son of Jacob. No secure Israelite family links the branch to Aaron.
CB-02 ancestry (E-BY8508)	Four of the 104 recruited Cohanim belong here. A real Levite-associated E family and the Jewish Tàrrega ROQ2 lineage give additional relatives to test.	The proposed Aaronic history requires continuity in this smaller priestly family. A claimed Levi-level relationship to the other E family needs correct timing and a tradition that extends beyond surname evidence.	The Levite labels concentrate in a much younger part of the related family. The shared E-Y2850 ancestor’s usual point estimates precede Jacob and Levi. The combined arrangement does not name them.

Proposed history	What it explains	What it requires	What is missing or difficult
CB-03 ancestry (J2-FGC4992/FGC4975)	Six of the 104 recruits belong here, all Ashkenazi. Database relatives give a western and an eastern branch. This is a serious alternative priestly history.	Its proposed Aaronic family must survive through the later common ancestor. The eastern branch's priestly records need clarification. The other Cohen branches require different origins.	The four reported eastern relatives include men whose priestly status is unknown. Unknown status is not evidence of non-priestly status. The older regional part of its long branch does not need to have been priestly.
Z642 ancestry as Abraham's family	It contains a published Samaritan-labelled representative, Sephardic Jewish relatives and Arabian-heavy branches. Its branching estimates can be compared with the stated chronology.	The proposed Isaac/Jacob/Aaron family must lie within Z642. The large CB-01 priestly family then needs a separate origin. Country patterns must be replaced with documented community histories.	Its statistical comparison was developed after noticing the pattern, includes overlapping branches, and uses Germany as a proxy for Ashkenazi identity. No verified Aaronic branch has been identified inside it.
Danfi or Tsedaka Samaritan ancestry	Each has a family tradition and a secure broad J2 placement in the original Samaritan study. Each deserves a separate comparison.	One such family could preserve an earlier Israelite paternal line. The other incompatible tribal traditions would require incorporation or attribution changes.	Their deeper public labels are incompletely sourced. They are deeply separate from CB-03 and from the J1 Samaritan family. None presently has a dated ancient family link.
R1a-M582/Y2619 Levite ancestry	Rootsi's recruited dataset found M582 in 63 of 97 Ashkenazi Levites and eight of 51 other Levites. It supplies a strong alternative Levite association.	If it were Levi's line, an Aaronic descendant branch must also lie in that ancestry. All proposed E and J Aaronic identifications would then be alternatives.	A later surviving common ancestor does not exclude an earlier Levi. The required connected Aaronic branch has not been demonstrated. The recruitment design limits population estimates.
Other recorded Cohen families, including Samaritan priests	Lipson's CB-04–CB-09 and the Samaritan priestly E-M78 family represent additional paternal origins. Their later surviving common ancestors do not exclude an earlier Aaron.	Each history must connect its family to Aaron and explain the other incompatible priestly traditions. Relatives who split later than Aaron would also have to descend from him, even if they lost priestly status.	These histories have less present support from breadth of documented tradition or from independently connected relatives. The finer Samaritan V22 assignment needs confirmation. They are not excluded by a young common-ancestor date alone.
A presently unrecognised family	It accommodates extinction, missed testing, loss of status and other paternal branches. It remains possible across the tree.	The history must explain why its descendants were not recognised and how the recognised priestly families obtained their traditions. It may survive in a community absent from existing recruitment.	It offers less specific predictive structure. No unique present observation selects it. Its flexibility must not count as positive evidence.

[Lipson and colleagues, 2025 preprint](#) · [Shen and colleagues, 2004](#) · [Oefner and colleagues, 2013](#) · [Waas and colleagues, 2019, Figure 1 and Table 1](#) · [Rootsi and colleagues, 2013](#) · [Levy-Toledano and colleagues, 2026](#)

The strongest modern observation is CB-01's priestly association. Lipson's researchers recruited 104 men with reported priestly practice in their own, their fathers' and their grandfathers' lives. They deliberately sought diverse origins. CB-01 contains 47 of those 104 men, including 27 of the 43 Ashkenazi recruits and 20 of the 61 others. These are recruitment-sample fractions, not estimates for all Cohanim or all Jewish men. The preprint remains version 1, posted in December 2025, with no journal version recorded in the checked bioRxiv metadata.

[Lipson and colleagues, 2025 preprint](#)

Z642's geographical pattern survives as an observation in the saved commercial data. Its purported statistical strength does not. I reproduced one qualifying result among 66 resolved rows, but the rows represent 65 distinct branches. At least 33 of those branches lie within other selected branches. The Arabian condition was at least 80% of known origins in six specified countries, rather than exclusively Arabian origins. The eight men assigned to the "Ashkenazi countries" category within the relevant Z642 child all reported Germany. They lie in one younger paternal family. The country does not establish Jewish membership.

The criteria file was written after the saved Z642 country pattern had already been printed. That makes the comparison an exploration of a noticed pattern. It cannot be presented as an independent prediction. Changing several count thresholds leaves Z642 distinctive in this dataset, but that does not repair the missing community labels or the overlapping branches. One result among 66 rows is not a probability that Z642 is Abraham's family.

The Samaritan evidence strengthens the case for taking Z642 seriously. Waas's published Figure 1 places a Samaritan-labelled man with a Druze-labelled man within FGC62618, below Z642. I inspected that figure and its original age table. Identifying that particular Samaritan sample as the Marhiv family remains an inference. Shen's original study securely distinguishes the Marhiv J1 family, the Danfi J2-M67 family, and the Tsedaka J2 family outside M67. The public evidence does not justify treating all three traditions as equally precise genetic pedigrees.

[Waas and colleagues, 2019, Figure 1 and Table 1](#) · [Shen and colleagues, 2004](#) · [Oefner and colleagues, 2013](#)

The E alternative has become more concrete. Levy-Toledano's 2026 paper shows Levite-labelled Moroccan and Ashkenazi descendants within E-BY8529, below E-BY8528 (called BY8536 in the saved YFull tree). That family joins the CB-02 ancestry at E-Y2850. The medieval Jewish ROQ2 lineage joins CB-02 more recently, at E-CTS7178. I checked both relationships in the tree and inspected the paper's figure. The paper combines surname and tradition evidence and gives inconsistent Moroccan subgroup counts, so I have not converted its labels into a population frequency or a Levi identification.

[Levy-Toledano and colleagues, 2026](#) · [Pallarés-Viña and colleagues, 2026](#)

Older studies independently support priestly and Levite associations, but they measured different markers. Hammer’s extended Cohen pattern used twelve repeating Y markers; it was not an exact J-ZS222 test. Rootsi’s Levite study found marked R1a-M582 enrichment, but some contributing collections deliberately recruited priests and Levites. Its 63/97 and 8/51 results describe those Levite recruits. Broad regional Middle Eastern sequencing helps explain shared ancestry and uneven growth of paternal families. It does not identify a particular modern Arabian branch with a named son of Abraham.

[Hammer and colleagues, 2009](#) · [Rootsi and colleagues, 2013](#) · [Almarri and colleagues, 2021](#)

The earlier claim of an 85–100% chance of detecting another Jacob line does not yet supply a valid test of these candidates. The simulation gives every man a perfectly known tribal label. Real DNA does not supply those labels. Its result also depends on imposed modern family shares and on how it conditions on Aaron’s survival. Separately, its Erfurt calculation mistakenly drew 33 men: the paper studied 33 people, including 14 males, of whom ten received Y assignments. Correcting that denominator changes its Erfurt carrier probability; it does not by itself invalidate or repair the separate modern-tester calculation.

[Waldman and colleagues, 2022](#)

The ancient individuals provide dated genetic relationships with different levels of contextual support.

“Earlier base” below means that a readable position retains the state before the mutation defining the proposed branch. A position with no usable reads supplies no evidence either way. Dates from the anonymised 2026 dataset are published means; an individual interval or dating method was not supplied in the examined table.

The individual’s context and the quality of his Y placement are assessed separately.

Individual	Archaeology and date	Verified genetic evidence	Question the man can answer	Sequence accession and primary source
I10268	Megiddo infant burial; original direct date 2010–1779 cal BC. The authors flag a mismatch with stratigraphy.	J1-P58 ancestry. Sonnet found an upstream derived mutation and earlier bases at CB-01 positions.	Regional ancestry before Abraham’s birth; no Israelite or priestly identification.	ERR4193019; Agranat-Tamir and colleagues, 2020

Individual	Archaeology and date	Verified genetic evidence	Question the man can answer	Sequence accession and primary source
I4517	Megiddo boy, about 10–11, killed in a late Iron I house fire. Original direct date 1107–923 cal BC (95.4%); AADR recalibrates the older end to 1109 BC.	Two distinct reads retain G at hg19 Y:7,833,897 (ZS231). They survive mapping/base quality ≥ 30 and seven-base end trimming. They contradict the automated deep CB-01 call. A single derived ZS2434 read conflicts with that result; it is a damage-prone G→A change, unlike ZS231's G→T change.	A related J1 man, probably outside the modern CB-01 mutation block. The city and date do not identify his tribe.	ERR4174101; Agranat-Tamir and colleagues, 2020
ERS1790733	Sidon Middle Bronze jar burial, boy aged about 8–12; 1950–1730 cal BC.	Original J1-P58 call is based on very limited reads. The proposed finer FGC13863 placement was not verified here.	An early regional comparison. It does not yet establish the claimed precise relationship to CB-01.	PRJEB21330; Haber and colleagues, 2017
I2201	Abel Beth Maacah; grave cut into an older building; direct date 1011–846 cal BC.	Published T ancestry; AADR T-L208. No new read audit here.	A northern frontier-town comparator. Biblical place names do not establish individual Israelite identity.	PRJEB37057; Agranat-Tamir and colleagues, 2020
ALAO26, ALAO18 and SFI-42	Alalakh: ALAO26, 1746–1616 cal BC; ALAO18, 1499–1323 cal BC. Beirut: SFI-42, 542–395 cal BC.	ALAO26 and SFI-42 have L858/Z1884-related placements. Sonnet traced ALAO18's automatic FGC97306 label to Z640, outside Z642. These precise records were not rechecked from raw reads.	Earlier presence and later regional persistence on the Z642 side of the older tree. They are not demonstrated Z642 descendants.	ERR4027249; ERP121575; AADR, v66.p1, Dataverse release 14.0 · Haber and colleagues, 2020
R835	Civitanova Marche, Italy; published contextual interval 27 BC–AD 300.	The older B877 label combines markers now divided among several branches. I found earlier bases at four CB-01 sites and at ZS227. AADR flags estimated X-chromosome contamination of 1.8–2.9%; sparse positive calls require caution.	An earlier-diverging relative. He does not confirm ancient CB-01 membership or Jewish identity.	ERR3559877; Antonio and colleagues, 2019 · Sahakyan and colleagues, 2021
I37241	Site, country and cultural context withheld. Published mean 1850 years before AD 1950 = about AD 100; no individual interval in the examined table.	Eleven CB-01-defining positions retain derived reads at mapping/base quality ≥ 30 with seven-base end trimming. ZS222 has six such reads. Two further mutations support probable Z18271 membership; one is a damage-prone change.	Strong ancient CB-01 membership. His community and priestly status remain unknown.	ERR16131894; Akbari and colleagues, 2026, original tables

Individual	Archaeology and date	Verified genetic evidence	Question the man can answer	Sequence accession and primary source
I45358	Site and context withheld; published central date about AD 750.	Derived ZS227; multiple earlier bases across the CB-01 block, including five reads at ZS222. I reproduced the distinction independently.	A related paternal family survived into the first millennium AD. He does not divide the defining CB-01 block or establish another Jacob tribe.	ERR16131295; Akbari and colleagues, 2026, original tables
I14846	Erfurt Jewish cemetery; grave 16, boy aged about 11–13. Cemetery period about AD 1250–1400; no individual radiocarbon date.	Published J-Y3088. One derived transversion read at ZS231 survives strict checks; the other 24 block positions lack readable evidence. Sonnet withdrew earlier conflicting calls because they came from unreliable alignments.	Strong Jewish burial context with a supported, but single-site, CB-01 placement. The published manual assignment agrees. Existing reads do not provide multiple defining sites.	ERR9847014; Waldman and colleagues, 2022
SB604, SB676, SB696	Norwich well burial; combined radiocarbon interval AD 1161–1216, consistent with the 1190 attack.	Three different published paternal lines: J1, E and T. SB604 has high overall genome coverage, but I did not audit his defining Y reads.	Later Jewish community diversity and a useful high-coverage J1 comparison. Overall genome coverage is not a guarantee at every Y position.	PRJEB55223; Brace and colleagues, 2022
ROQ1, ROQ2, ROQ4, ROQ7	Tàrrrega Roquetes mass graves, mid-fourteenth century, linked archaeologically and historically to the 1348 pogrom.	Published calls: J-Y31564, E-CTS9507, G-PH1944, E-Y231455. ROQ2's E branch is related to CB-02 through E-CTS7178.	Four later Jewish paternal families. ROQ2 is neither a demonstrated CB-02 member nor a known Levite or Cohen.	PRJEB107193; Pallarés-Viña and colleagues, 2026 · Levy-Toledano and colleagues, 2026
I43272	Site and community withheld; mean 250 years before AD 1950 = about AD 1700.	Sonnet verified FT416287 and upstream markers below Z642 and FGC62618. My independent checks support Z642 at two positions.	Later persistence in a branch containing Samaritan and Druze relatives. No individual Samaritan, Jewish or Levantine identity follows.	ERR16135824; Akbari and colleagues, 2026, original tables

The three medieval Jewish collections supply seventeen men with published Y assignments and no identified close male-to-male relationships that require their removal: ten at Erfurt, three at Norwich and four at Tàrrrega. They show several paternal families in later Jewish communities. They do not represent seventeen independent chances to recognise a specific deep branch: coverage, mutations tested, cemetery selection and more distant kinship differ. Their existence is a reason to investigate persistence and spread, rather than stop at sparse Bronze Age evidence.

[Waldman and colleagues, 2022](#) · [Brace and colleagues, 2022](#) · [Pallarés-Viña and colleagues, 2026](#)

The direct read checks are targeted reanalyses of existing aligned DNA, not new laboratory results. I checked mapping and base quality, removed problematic alignments, varied trimming of read ends, and distinguished independent molecules where possible. Published damage and mitochondrial-consensus measurements support ancient origin for I37241’s libraries. I did not estimate contamination anew. The technical record retains the precise mutations, qualities, missing positions and conflicting calls.

The amount that can be inferred falls as the proposed history moves back from the observed families.

The same chromosome does not give equal evidence for every ancestor.

Proposed ancestor	What the present evidence supports	What the evidence does not yet establish
Jacob	If CB-01 is Aaronic, its earlier paternal ancestry must contain Jacob. CB-02 and CB-03 provide alternative priestly routes.	No securely identified ancient Israelite or Judahite in the examined evidence joins a named Jacob family to one of these precise branches.
Isaac	If the proposed Jacob family is correct, its immediately earlier paternal ancestry must include Isaac.	No independently identified Esau or other Isaac-descended family currently fixes his position on this tree.
Abraham	The tree can test whether proposed Isaac, Ishmael or other paternal families could share an ancestor in the relevant interval. Z642 is worth comparing on that basis.	Modern countries do not identify Abraham’s sons. CB-01 and Z642 cannot both provide the proposed Abraham-to-Aaron line.
Shem	If the proposed Abraham family is correct, its earlier paternal ancestry must include Shem.	The examined genetic evidence supplies no separate Shem-specific identification. His relationship follows from the accepted genealogy.
Noah	Any accepted Abrahamic paternal history also proposes Noah as an earlier ancestor. Arrival, survival and dispersal scenarios describe where descendants could later appear.	A regional J1 expansion, or a date near 2903 BC, cannot identify Noah. Pre-existing related earthly chromosomes must be separated from his particular descendants.
Adam	The copied-chromosome interpretation allows a genetic relationship to an earthly source family. It does not require Adam to be the common paternal ancestor of all humans.	The copy premise provides no unique mutation or branch date that identifies Adam. Current DNA does not locate him independently.

The provisional preference for CB-01 is most stable when recorded priestly continuity receives substantial weight and when surviving branches can pass through later bottlenecks. CB-02 could gain substantially from a securely documented related Levite family with the correct branching time. CB-03 could gain from verified priestly continuity in its eastern branch. Z642 could gain from documented Jewish community identities and securely contextualised ancient descendants on different relevant branches. A low survival rate for original priestly lines would weaken all three Cohen candidates and make an unrecognised line more plausible. None of those assumptions has a measured probability here.

Existing material can improve this comparison before new laboratory work is proposed.

The best next work has two parts. First, use the available higher-coverage or indexed DNA files for known-context Bronze, Iron, Roman and medieval men. Test the specific mutations that separate CB-01, its earlier relatives, Z642, CB-03 and the E alternatives. Second, verify the family and community records attached to modern men who may divide those branches. Neither broad haplogroup labels nor commercial page headings can substitute for those checks.

The most useful next medieval read checks are Norwich's high-coverage J1 man SB604 and Tàrrega ROQ2's E branch. The present Erfurt file supplies only one decisive CB-01 read; repeating the same check cannot create missing sequence. Recovering the original analysts' exact mutation evidence could clarify their published manual assignment. The best earlier regional comparisons include Alalakh ALA026 and ALA018, enhanced Baq'ah data, Sidon and Beirut. Each can test a different part of the tree. A confirmed older relative can constrain ancestry without being a descendant of the patriarch proposed for a later branch.

The new anonymised men already improve genetic timing. Their withheld archaeological information prevents a corresponding improvement in historical identification. A search snippet does not establish the proposed Judahite burial identity of anonymised I14918. His public region label and point date do not supply that missing context. Mödling's proposed CB-01 men remain useful leads, but their public raw reads need alignment and their cemetery context needs its own assessment. Those tasks require analysis, not fresh sampling.

The Ancient Genome Diversity Project was inspected rather than dismissed from its title or age. Its higher-coverage material includes an Early Bronze Age J2b man from 'Ain Ghazal. It does not presently supply a known specimen that decides among the principal proposed families. Some enhanced older samples are now public through the 2026 study. Restricted files and archaeological metadata were not requested from researchers.

[Ancient Genome Diversity Project](#) · [Akbari and colleagues, 2026, original tables](#)