RA04

THE THIRTEENTH TRIBE & THE ANCESTRY DEBATE

A book, a hypothesis and the evidence

COMPLETE SOURCE-BASED STUDY

A critical examination of the Khazar ancestry hypothesis and its use in Peter David Beter's account.

Koestler · Khazars · Yiddish · genetics · Beter

Tempus omnia revelat.

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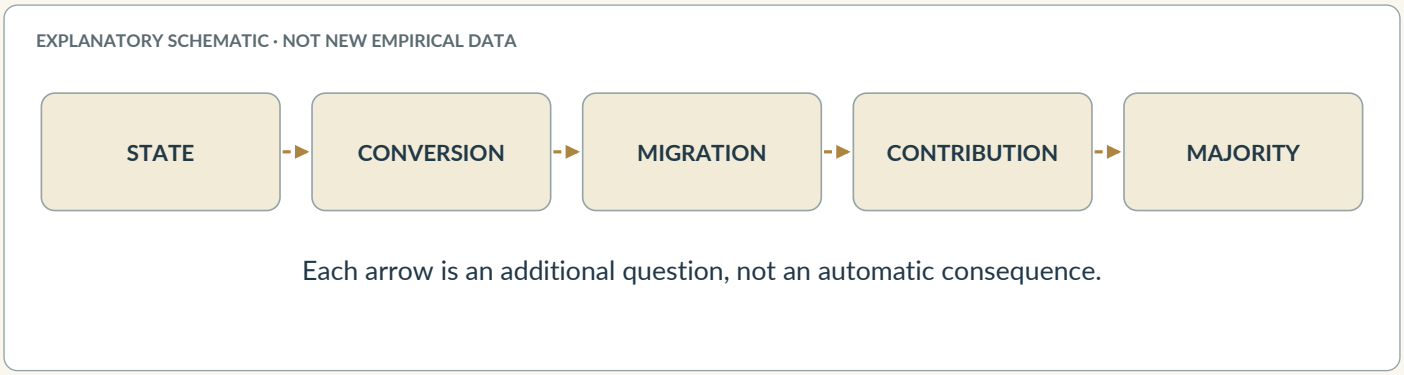
What this volume examines

RA04 asks how a claim about a medieval conversion becomes a claim about the ancestry of a later population. At its centre is Koestler's 1976 book, explicitly recommended in Topic 3 of Beter's AL50. The object of inquiry is not human worth or a licence to assign identities to other people. [S01–S03]

The core question has several levels: did a Khazar state exist; did some inhabitants adopt Judaism; did their descendants join other communities; did they supply the predominant ancestry of Ashkenazi Jews? Each step requires additional evidence. Political organisation, religious affiliation and population ancestry are not interchangeable quantities.

The selected genetic studies support combined European and Middle Eastern ancestry in the Ashkenazi population. Elhaik offered a different interpretation supporting the Khazarian hypothesis, so his assumptions are compared with criticism and additional evidence. This is not a contest between two equally simple family trees. [S06, S07, S10–S12]

The result is a distinction between well-supported broad relationships, uncertainty about the contribution of a specifically named medieval population, and claims that genetics cannot establish at all. "Not demonstrated" does not mean an exact zero; the possibility of an individual ancestor does not establish predominant ancestry.



The possibility of ancestry, the size of a contribution and political continuity are three different questions.

Sources / notes: S01, S02, S03, S06, S07, S10, S11, S12

Method, scope and source access

This is a selective source and methods analysis, not a systematic review of every publication or a new analysis of raw genomes. Calculations in the examples are educational. They are not measurements of Ashkenazi or Khazar populations. The source cut-off is 11 October 2026; that date does not imply that every question in the field has been settled.

Koestler was read in an available electronic transcription, particularly the argumentative passages and appendices. The entire transcription was not collated against the first printed edition. The hosting website's introduction and evaluative claims are not treated as Koestler's words or as scholarly evidence. We therefore identify sections rather than invent precise original page references. [S01, S02]

For Behar's 2013 study we use the authors' abstract in a university repository. For the Das team's 2016 reply we use a preprint abstract. The other scholarly texts and the portions accessible are identified in the source register. A title in the bibliography does not itself mean that every supplement has been inspected. [S07, S13, S17]

Source wording, authorial interpretation and our assessment are kept separate. Brief quoted labels remain the author's labels; the remaining text is our paraphrase or analysis. The illustrated edition condenses the discussion but must not increase the certainty of its conclusions. Historical hypotheses are not tested by voting according to sympathy for their authors.

Reused AI illustration / imagined historical scene — not an archival image

> **First AI-assisted editorial edition; not a peer-reviewed monograph or a laboratory replication.**

Sources / notes: S01, S02, S07, S13, S17

01 / The 1976 book and the question it raised

Arthur Koestler published The Thirteenth Tribe: The Khazar Empire and Its Heritage in 1976. The catalogue lists the American Random House edition at 255 pages. It is not a genomic study; present-day findings cannot be attributed to its original evidentiary procedure. [S02]

His central hypothesis assigned Khazar descendants a major, potentially predominant role in the ancestry of Eastern European Jews. His opening rationale hoped that this account would undermine racial foundations of antisemitism. [S01]

We separate two questions here. One is empirical: what historical process and what data would support the proposed contribution? The other is ethical: must hatred of people be rebutted by changing their pedigree? The answer to the second question should not depend on success with the first. Persecution remains unacceptable even if a historical account of ancestry proves correct.

The book is useful to read as an influential argument, not as an original register of births. Readers should mark separately a described event, a transmitted report, a plausible reconstruction and a bold estimate. Movement between those levels, rather than the unusual nature of the subject, determines the strength of the evidence.

The same rule applies to critics: lack of present agreement does not remove the book from the history of debate. Its historical significance, however, does not substitute for testing its demographic conclusion.

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> **An author's intention does not settle an empirical question. An empirical result does not determine human dignity.**

Sources / notes: S01, S02

02 / The argument contains more than one link

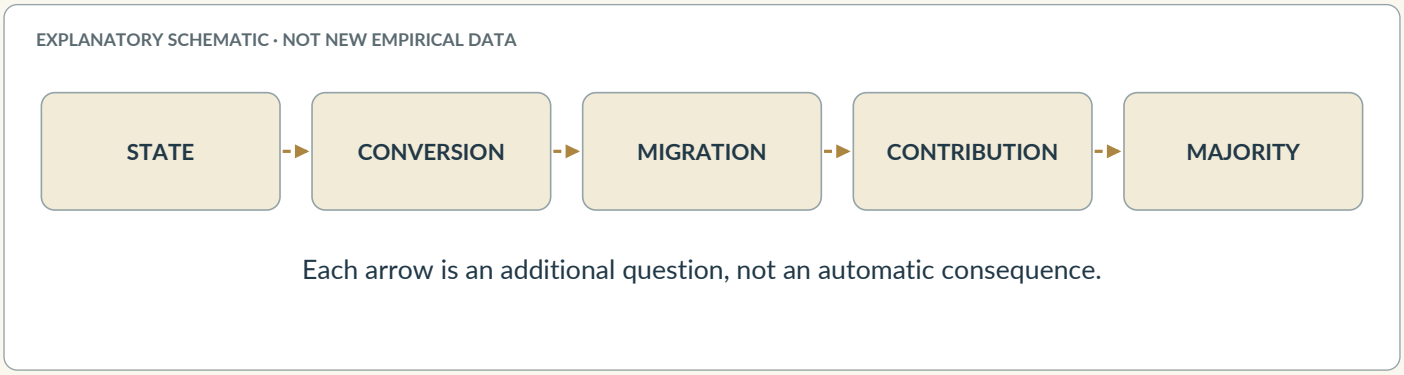
The appendix on modern literature shows that Koestler drew, among others, on D. M. Dunlop and A. N. Poliak. We describe that use through Koestler; this is not a claim to have independently checked all their original books. [S01]

Construct the analytical chain without skipping steps: political state → religious conversion → migration → reproductive contribution → predominant ancestry. An arrow denotes a question here, not an established consequence. Evidence that a particular ruler was Jewish, for example, does not count converts; the number of migrants does not determine their later proportion without information about other communities.

A large number of bibliographic references does not automatically equal a large number of independent testimonies. If a modern author borrows from an earlier monograph which repeats a single medieval text, there is still only one branch of transmission. Repetition may make a claim familiar without increasing the number of directly recorded events.

At each transition we therefore ask what information is missing. We need a time, place, identification of the group, numbers or defensible ranges, and comparison with other sources of migration. A reasonable procedure allows the first two links to have a different evidential status from the last two.

Political continuity would require a further, separate chain: institutions, identified actors, communications and decisions. Family ancestry cannot supply that chain.



> **One true link does not automatically validate the entire story.**

Sources / notes: S01, S18

03 / Khazaria: territory, state and a diverse population

In Encyclopaedia Iranica, Dan Shapira describes the Khazars as a multiethnic confederation led by a Turkic group. His discussion of Judaization distinguishes the ruling circle from the wider population and identifies the extent of conversion as unknown. This already cautions against imagining one homogeneous “Khazar genome.” [S18]

A genetic hypothesis must specify whose ancestry is being discussed. An urban resident? A member of the political elite? A Turkic-speaking nomad? A Jewish immigrant to the realm? These categories can overlap, but are not identical. Finding a skeleton within the former khaganate does not, by itself, establish that person’s religion or ancestry.

Migration into Khazaria is not evidence against Middle Eastern ancestry either: a person could have entered the realm from elsewhere, with a descendant subsequently leaving it. A model of “Khazars or the Levant” may wrongly exclude two stages of the same family history. The time horizon has to be defined before the test begins.

Rejecting a universal conversion would not establish that no convert ever had descendants elsewhere. Confirming a Jewish ruler would not establish a mass population transfer. RA01 examines the medieval foundation; this volume asks what additional assumptions are needed to infer a later majority.

The question is not whether people could move, but which specific movement explains the available evidence better than the alternatives.

Reused AI illustration / imagined historical scene — not an archival image

> **A territorial label must not become a biological population without a test.**

Sources / notes: S18, S04

04 / Yiddish: contact is not a complete pedigree

Language evidence matters, but it must remain language evidence. Marion Aptroot emphasises the Germanic grammatical structure of Yiddish and documented medieval use of Ashkenaz for German lands. Slavic contact features do not themselves overturn that foundation. Her discussion also addresses Wexler's hypothesis of a relexified Slavic language. [S05]

The decisive procedure is not to count all borrowed words and declare a winner. Historical linguistics compares regular relationships between forms, grammar, earlier texts and datable contacts. Script is another separate dimension: using Hebrew letters does not place Yiddish in the same linguistic branch as Hebrew.

Yet a Germanic language does not entail exclusively Germanic ancestry among its speakers. A group may adopt its neighbours' language while some earlier ancestors came from elsewhere. Equally, a demonstrated genetic contribution from another region does not automatically reclassify a language. The disciplines can cooperate only without circular proof.

Similar place names require earlier spellings and dates. A name resembling Ashkenaz is not a migration record by itself. If a genetic location is interpreted through a proposed etymology, and that etymology is then defended through the genetic location, two independent proofs have not been obtained.

In our analysis, Yiddish therefore supplies evidence about the history of language contact, not a universal detector of Khazar ancestors.

Reused AI illustration / imagined historical scene — not an archival image

> **Script ≠ language family ≠ the complete ancestry of speakers.**

Sources / notes: S05, S14, S15

05 / A demographic puzzle needs denominators

An argument about “excessively rapid growth” is meaningful only with verifiable starting figures. Aptroot notes incomplete and unreliable earlier population information. A record of taxpayers, households or settlements is not a census of the entire population without appropriate conversion. [S05]

An educational example: suppose a population begins at 50,000 and reaches 5,000,000 after 400 years. In a purely exponential model, this hundredfold increase requires an average net growth rate of approximately 1.158% per year: r = 100^(1/400) − 1. These numbers were chosen to illustrate the calculation. They are not estimates of a particular Jewish population or a claim about its actual history.

The calculation says nothing about real mortality, epidemics, forced movements or migration. It shows only that “impossible” must become a test of assumptions. Mathematical possibility does not establish an event; an incomplete starting count does not establish the necessity of one particular migration source.

A sound historical model would need the same territory and population definition at both ends, evidence on migration, families and losses, and uncertainty intervals. Changing the boundaries of enumeration can create apparent growth without a single extra birth.

Even a successful demographic reconstruction does not by itself establish the religion or ethnic designation of ancestors; those require other kinds of evidence.

EXPLANATORY SCHEMATIC · NOT NEW EMPIRICAL DATA

50,000 → 5,000,000

400 years · 100-fold increase · r ≈ 1.158% per year

A purely hypothetical model; not a historical population estimate.

> **Educational model, not a historical measurement: 50,000 × (1 + r)^400 = 5,000,000.**

Sources / notes: S05

06 / Three meanings of ancestry

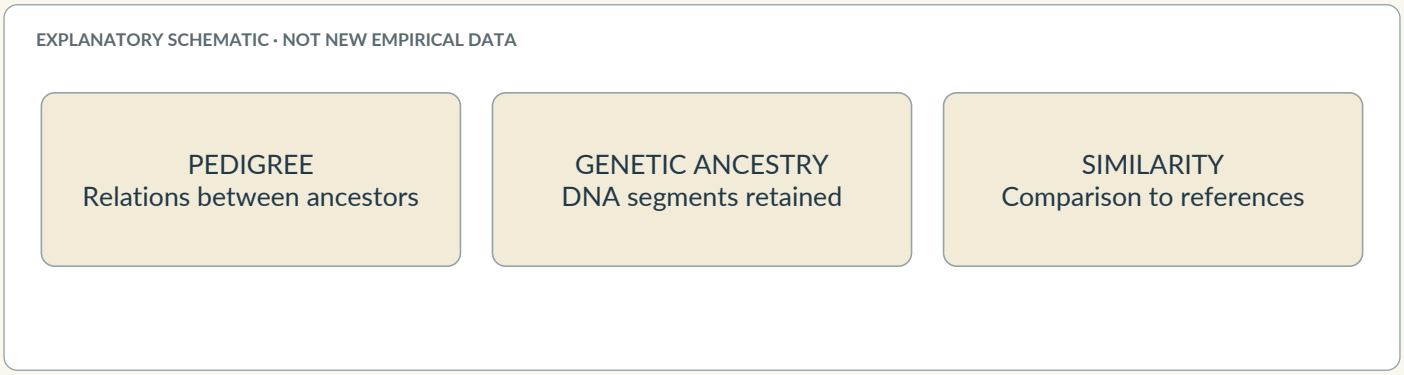
Mathieson and Scally distinguish genealogical ancestry, genetic ancestry and genetic similarity. Genealogy concerns ancestors in a pedigree; genetic ancestry concerns the paths through which DNA segments were transmitted; similarity concerns comparisons between sampled genomes. A comparison result is not a complete list of identifiable ancestors. [S04]

A remote genealogical ancestor need not have left an identifiable DNA segment in the particular person being studied. “The method detected no contribution” therefore does not automatically mean “no such person occurred in the pedigree.” The reverse mistake is equally serious: a possible remote ancestor does not justify claiming that most of a genome came from that group.

Geographical labels require a time reference. An ancestor living in a medieval Italian town could have had earlier ancestors in the eastern Mediterranean. “Italian” and “Middle Eastern” need not be mutually exclusive across different time horizons. A present-day reference dataset is not a frozen ancient population.

In practice, every percentage needs the question: a percentage of what? A maternal lineage, classified segments, pedigree branches or a sample average? Without that information, even a precise-looking number is an incomplete claim.

Religious status and citizenship do not belong in this threefold distinction as an additional genetic metric. They are different social and institutional questions which a similarity plot cannot decide.



An undetected genetic signal and an impossible genealogical ancestor are not synonyms.

Sources / notes: S04

07 / Three genetic windows, not three complete histories

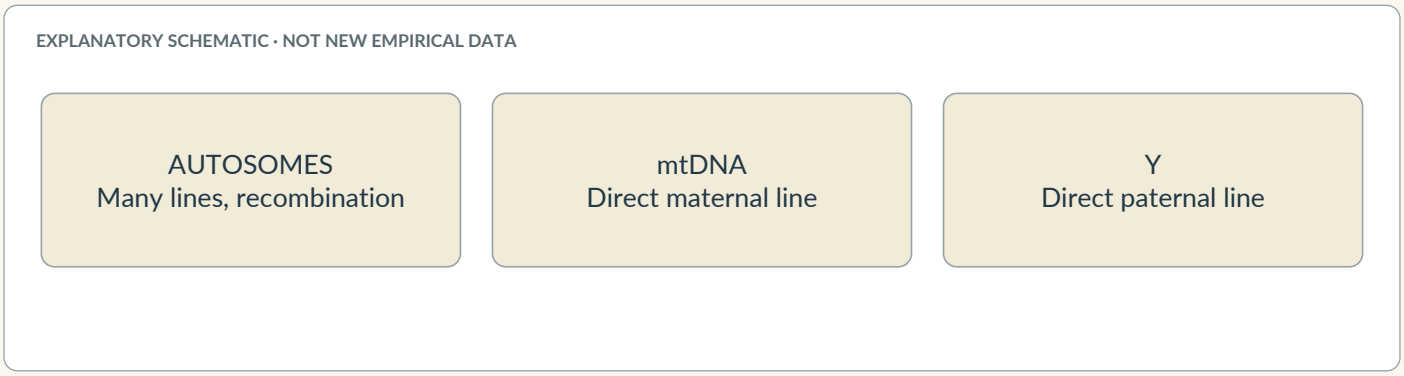
Autosomal data examine much of the genome inherited through many family lines. Mitochondrial DNA is used to trace the direct maternal line; the non-recombining part of the Y chromosome traces the direct paternal line. The studies by Costa, Rootsi and Xue therefore do not ask exactly the same question. [S08, S09, S11]

Imagine a person whose direct maternal line leads back through eight generations to one woman. That woman occupies only one position in a pedigree whose branches repeatedly intersect. A finding about her mitochondrial lineage does not fill every other position. Nor does a man's Y chromosome represent his mother's family history.

A haplogroup is a branch of genetic relatedness marked by shared variants. Its broad designation may encompass very old divisions and a large geographical area. Finer resolution matters: a result for R1a in general need not equal a result for one particular sub-branch of R1a. [S09]

When comparing studies, read the unit of measurement before the headline. An apparent contrast between predominantly European maternal lineages and mixed autosomal ancestry can reflect different histories of male and female lines, rather than automatically demonstrating fraud.

That is not a licence to assemble results arbitrarily. A suitable combined model must respect the sampling, temporal estimates and uncertainty of each study. It cannot be obtained by averaging three incomparable percentages.



Mitochondrial DNA, the Y chromosome and autosomes have different scopes.

Sources / notes: S04, S08, S09, S11

08 / Elhaik 2013: a hypothesis and its proxies

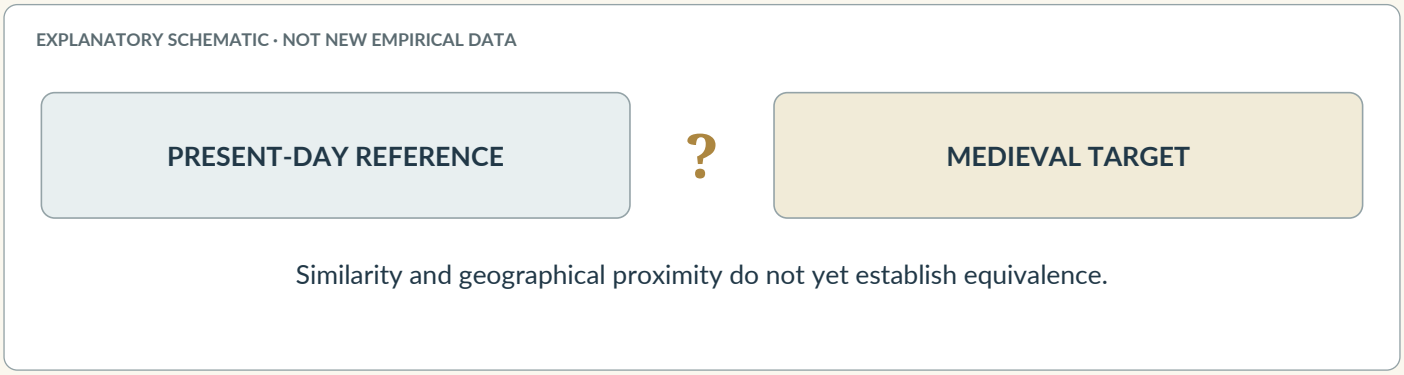
Eran Elhaik analysed 1,287 unrelated individuals from eight Jewish and 74 non-Jewish populations. The autosomal dataset initially contained 531,315 markers; after pruning correlated markers, 221,558 were used for most analyses. His conclusion supported the Khazarian hypothesis and described composite ancestry, not an exclusively single biological branch. [S06]

The key interpretative step used present-day Armenian and Georgian samples as proxies for Khazars, and Palestinian samples as proxies for earlier Judean ancestors. These are modelling assumptions. They are not direct genetic measurements of medieval khaganate inhabitants or automatic demonstrations of unchanging populations. [S06]

Readers should see why such a test is attractive: contemporary data allow similarities to be examined that an earlier book could not measure. They should also be told whether the chosen similarity distinguishes a specifically Khazar contribution from older shared West Asian ancestry.

Our assessment therefore says neither “the publication does not exist” nor “genetics has confirmed Koestler exactly.” It is a published analysis whose interpretation depends on proxy samples. A persuasive test would need to show that the result remains specific under other reasonable panels and competing historical models.

Criticism should address that discriminatory power. A researcher’s personal ancestry or a reader’s sympathy with the conclusion is not a measure of correctness.



A proxy sample is a testing tool, not an already established identity of historical ancestors.

Sources / notes: S06, S07

09 / Behar 2013: a broader panel and a bounded conclusion

Behar and colleagues report 1,774 samples from 106 populations, including 261 newly analysed samples from 15 populations in the Caucasus and its northern vicinity. Their abstract describes the strongest Ashkenazi relationships with other Jewish populations and, among non-Jewish groups, with Europe and the Middle East. They detected no distinctive substantial contribution from the proposed Khazar region. [S07]

The authors also identify a problem frequently lost in popular accounts: there is no unambiguously identified present-day Khazar reference population. Similarity to a Caucasian sample can reflect older shared Middle Eastern relationships rather than a particular medieval conversion and migration. [S07]

For this edition we have the authors' abstract and bibliographic record, not a complete detailed reanalysis of every supplement. We therefore add no invented confidence interval for a "Khazar percentage," and do not claim to have reproduced their computation.

Both the force and the boundary of a negative finding matter. A broader regional panel weakens a particular argument based on selected modern proxies. It does not erase every possible individual Khazar ancestor from every pedigree. Absence of a substantial signal is not a universal statement that the number of such ancestors was zero.

The study is thus not simply a mirror image of Elhaik's article. It seeks to reduce ambiguity in the reference panel, although the fundamental problem of historical identification does not disappear entirely.

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> **No detected substantial contribution is not proof of an absolute genealogical zero.**

Sources / notes: S07, S04

10 / Comparison without false equivalence

When two studies reach different conclusions, their results should not simply be averaged, nor should an author be selected by name. First determine whether the same claim is being tested. Elhaik uses particular modern populations as proxies; Behar's broader panel challenges the specificity of that interpretation. [S06, S07]

Sample count is not the only criterion. A larger panel of inappropriate proxies could still answer the wrong question. Conversely, broader and more relevant regional coverage can reveal that an apparently exclusive similarity was not exclusive at all. Sensitivity to population selection and analytical procedure matters.

Our assessment asks whether the model distinguishes a Khazar contribution from alternatives producing similar observations. For mixed West Eurasian ancestry, finding a point between Europe and the Caucasus is insufficient. Predictions are needed on which the competing historical models actually differ.

Later autosomal and medieval data add further constraints. They do not reproduce every sentence in an earlier controversy, but they allow a proposed history to be tested against independently dated individuals and patterns of admixture. [S10–S12]

Weighing evidence does not mean assigning every hypothesis the same probability. It means explaining why one result discriminates between alternatives more effectively, and specifying exactly what it still leaves unresolved.

Reused AI illustration / imagined historical scene — not an archival image

> **Objectivity means applying the same tests, not dividing the truth equally between positions.**

Sources / notes: S06, S07, S10, S11, S12

11 / GPS: a coordinate is not an ancestral birthplace

Das, Wexler, Pirooznia and Elhaik linked genetic geolocation to a hypothesis about Yiddish origins in 2016; their reply describes 367 Ashkenazi participants and locations concentrated in northeastern Turkey. Their 2017 perspective defends an Irano-Turko-Slavic account and answers critics. We do not portray this position as one that could not be published. [S13, S15, S17]

Flegontov and colleagues object that GPS operating on modern references is not a machine for reconstructing a millennium of migration. They also challenge the linguistic argument; Aptroot separately discusses Yiddish and historical use of the name Ashkenaz. [S14, S05]

A simple analytical objection is that averaging the locations of two related reference groups can produce a point where their ancestors never met. A different reference panel can move the point without changing the sampled person's history. This does not make geolocation universally useless; it means that its temporal interpretation requires evidence.

The defence and the objections must be read together. We do not run a new GPS analysis or decide the matter by citation count. We ask whether the data contain the information required to identify a particular medieval village, and whether the linguistic evidence remains independent of the selected location.

A coordinate without a validated temporal reconstruction is not an ancient ancestor's address.

EXPLANATORY SCHEMATIC · NOT NEW EMPIRICAL DATA

A model point between references ≠ an established place of origin.

> **A weighted average of present locations can arise without migration through the resulting point.**

Sources / notes: S13, S14, S15, S17, S05

12 / Maternal lineages: what a European result means

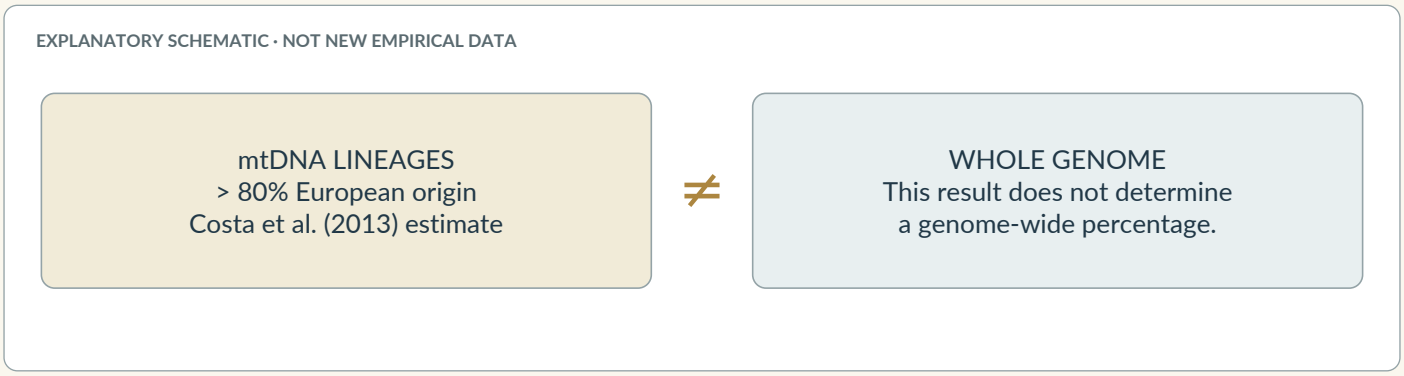
In 2013, Costa and colleagues examined Ashkenazi mitochondrial lineages. They traced four major founder lineages, associated with approximately 40% of mitochondrial variation, to prehistoric European branches. Their broader estimate proposed European origins for more than 80% of Ashkenazi mitochondrial lineages. [S08]

That conclusion must not be rewritten as “80% of all ancestors” or “80% of the entire genome.” The unit is a mitochondrial lineage. Nor does a result emphasising ancestry outside the Middle East confirm the Khazar hypothesis merely for that reason. Europe is not synonymous with Khazaria.

The authors discuss their findings against an earlier proposal of Middle Eastern maternal founders. This edition does not claim an independent reanalysis of those phylogenies. The essential distinction is between the origin of a branch, its age, and when it entered a particular community. An old common ancestor of a lineage does not date a religious conversion. [S08]

A responsible popular account would name the marker, samples and temporal uncertainty. It would then explain why the finding can coexist with different paternal and autosomal histories. It would not use the result to erase every Middle Eastern relationship or declare a religious identity false.

Equally, European contributions should not be hidden because somebody dislikes them. The appropriate response is to specify the denominator, not to select congenial numbers.



> **>80% of mitochondrial lineages ≠ >80% of the whole genome.**

Sources / notes: S08, S04

13 / A paternal R1a lineage: resolution changes the inference

Rootsi and colleagues examined finer Y-chromosome branching among Ashkenazi Levites in 2013. The broad designation R1a had previously suggested a possible Eastern European source. Their sequencing and investigation of marker M582 instead supported a Near Eastern source for the particular founder lineage. [S09]

The example is methodologically useful: one broad haplogroup can contain different sub-branches with different histories. It does not imply that every R1a lineage is Near Eastern or that every Ashkenazi man carries this branch. The object of the study is a particular paternal lineage group, not the entire population.

Nor does an association between a biological lineage and an inherited religious designation automatically identify a named biblical ancestor. A laboratory finding can support shared paternal ancestry in a group, but a historical name needs its own evidential chain. Deep shared ancestry and an identified pedigree are not the same output.

For the Khazar hypothesis, rejecting one supporting argument differs from excluding every possibility. If finer resolution weakens a particular Eastern European explanation for this lineage, it has not thereby recalculated the population's entire autosomal ancestry.

The appropriate conclusion remains bounded: a large haplogroup's name is insufficient to choose a medieval ethnic group. Higher resolution can change a geographical interpretation, but cannot by itself supply an ancient carrier's religion, language or political beliefs.

Reused AI illustration / imagined historical scene — not an archival image

> **A sub-branch is more precise than a broad haplogroup, but is still not an ethnic identity card.**

Sources / notes: S09, S04

14 / A founder event is not a population census

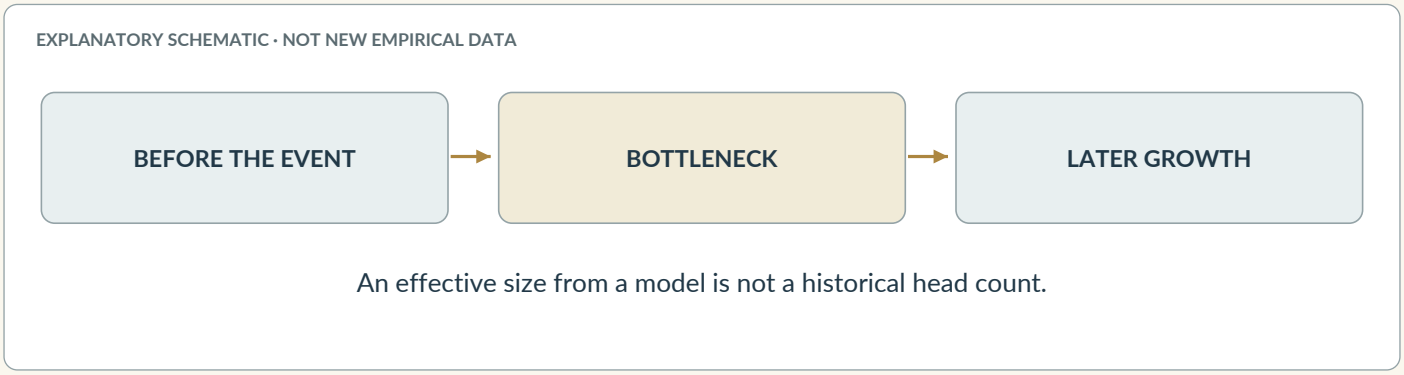
Carmi and colleagues analysed 128 Ashkenazi genomes and modelled a strong recent bottleneck involving approximately 350 individuals. The older branches of their model supported approximately balanced European and likely Middle Eastern components. [S10]

The figure of approximately 350 is not a list of named people, nor evidence that exactly 350 Jews lived throughout Europe in a particular year. It is a parameter of a reproductive-history model. A genetically inferred founder population size need not equal the total number of inhabitants of a historical territory.

A founder effect means that many later descendants can carry substantial variation from a relatively narrow circle of earlier lineages. It can accentuate similarities without requiring a separate recent arrival for every currently numerous branch. It still does not, by itself, locate those founders or identify their religious affiliation.

The important distinction is between “few founder lineages” and “a biologically uniform people.” The founders may themselves have been genetically diverse. Migration and further mixture may have followed the bottleneck, and a simple model need not capture every step.

This study therefore helps explain demographic structure. It is neither a direct signature of Khazaria nor a substitute for historical documents on the formation of communal institutions.



A genetically inferred founder size ≠ an exact census of all living inhabitants.

Sources / notes: S10, S16, S12

15 / Admixture through time: two problems with one percentage

In 2017, Xue and colleagues investigated the timing and location of European contributions to Ashkenazi history. Their findings supported a substantial Southern European component within the European contribution and more than one episode of admixture. The range of 60–80% concerns the Southern European share of European ancestry, not every Ashkenazi individual's entire genome. [S11]

The first problem is the denominator. As a purely educational example, if a model contained 50% European ancestry and 60–80% of that component were Southern European, the result would be 30–40% of the whole. This explains multiplication of proportions; it is neither a personal DNA test nor a new universal population percentage.

The second problem is time. A single generational estimate can summarise multiple events, rather than date one marriage, conversion or migration. The authors combine methods and discuss earlier and later components. Their interpretation is more complex than a single arrow on a map. [S11]

In comparison with Koestler, the important point is that European ancestry need not derive from one northeastern source. Different parts of Europe and different centuries constitute distinct testable scenarios. Without these distinctions, "European" is too coarse a label.

Modern reference groups must not be turned into eternally unchanged nations here either. The result reconstructs population relationships under specified assumptions; it is not a list of every ancestor's citizenship.

EXPLANATORY SCHEMATIC · NOT NEW EMPIRICAL DATA

Hypothetical example: 50% × 60–80% = 30–40% of the whole.

Identify the denominator before comparing percentages.

Sources / notes: S11, S04

16 / Erfurt: medieval DNA beyond modern proxies

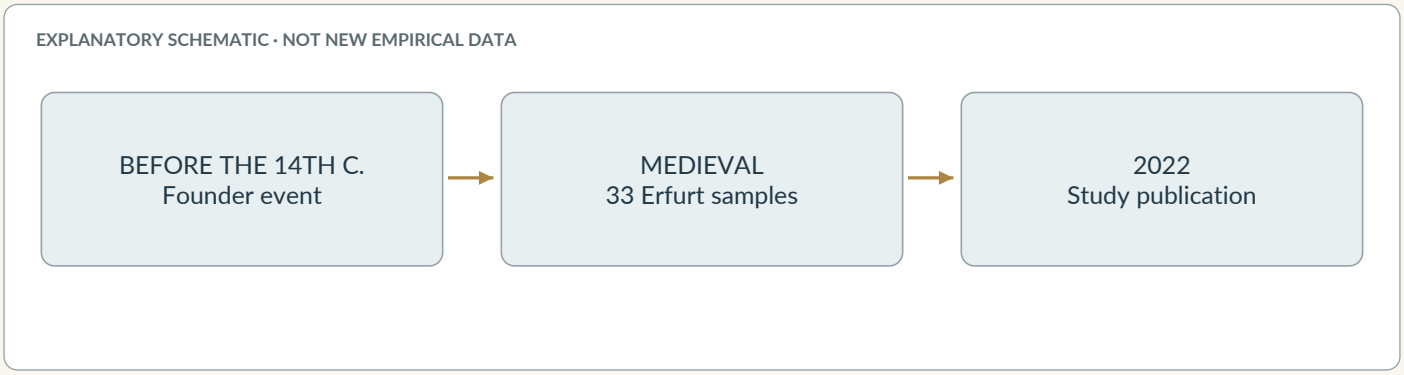
Waldman and colleagues published genome-wide data from 33 individuals from the medieval Jewish cemetery in Erfurt in 2022. The sampled community showed genetic continuity with present-day Ashkenazi Jews, but also greater internal variation. The inferred founder event preceded the fourteenth century. [S12]

Dated remains constrain hypotheses differently from present-day coordinates alone. We can ask not only whom somebody resembles today, but whether a particular profile existed in a specified place and period. That matters when testing accounts that place the formation of the entire population only in later centuries.

The authors explicitly caution that the study concerns one site and time window. Their qpAdm models should not be read as exact direct percentages contributed by named modern populations. They acknowledge a wide range of models and limits to complete demographic reconstruction. [S12]

Erfurt is consequently not a universal pedigree for every Ashkenazi person. By itself it neither identifies nor excludes every remote Khazar ancestor. It does provide an independently dated point with which a broader historical account must be compatible.

The finding cannot simply be dismissed as “a theory,” but neither can it be inflated into an exhaustive explanation of all preceding migrations. Its specific temporal anchor is its strength; overgeneralising from one locality is the principal popularisation risk.



33 medieval individuals provide valuable evidence, not the whole past population.

Sources / notes: S12

17 / Coloured plots are not primordial peoples

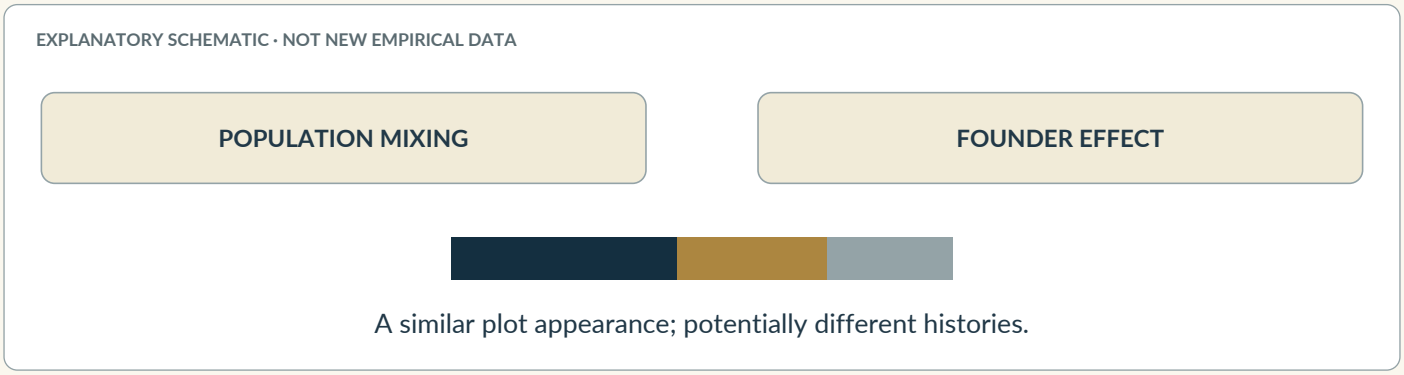
PCA summarises differences between samples; ADMIXTURE partitions genetic variation under a particular model and a chosen number of components. Neither abbreviation means automatic historical reconstruction. Lawson, van Dorp and Falush use simulations and examples to show that similar coloured results can arise under different demographic scenarios. [S16]

Consider two explanations: recent mixture of two sources, and older shared ancestry followed by strong genetic drift. If the chosen plot represents both scenarios similarly, it has not distinguished between them. Calling one colour “Khazars” and then presenting that label as a measured historical event is insufficient.

Responsible reading asks about the effects of reference panels, relatives in a sample, missing populations, temporal resolution and model fit. Different methods can help precisely because their assumptions differ; agreement matters only if it is not merely a repetition of the same initial assumption. [S04, S16]

This caution is not intended to invalidate genetics. It prevents a useful statistical shorthand from becoming a narrative which the data do not distinguish. Likewise, failure of one model does not automatically establish its best-known competitor.

Our diagrams therefore contain no real population data unless explicitly identified. A schematic explains the logic of a question; it is not a new scientific figure demonstrating particular ancestry.



A colour identifies a model component. A historical name requires additional evidence.

Sources / notes: S16, S04

18 / What would make a stronger test of a Khazar contribution

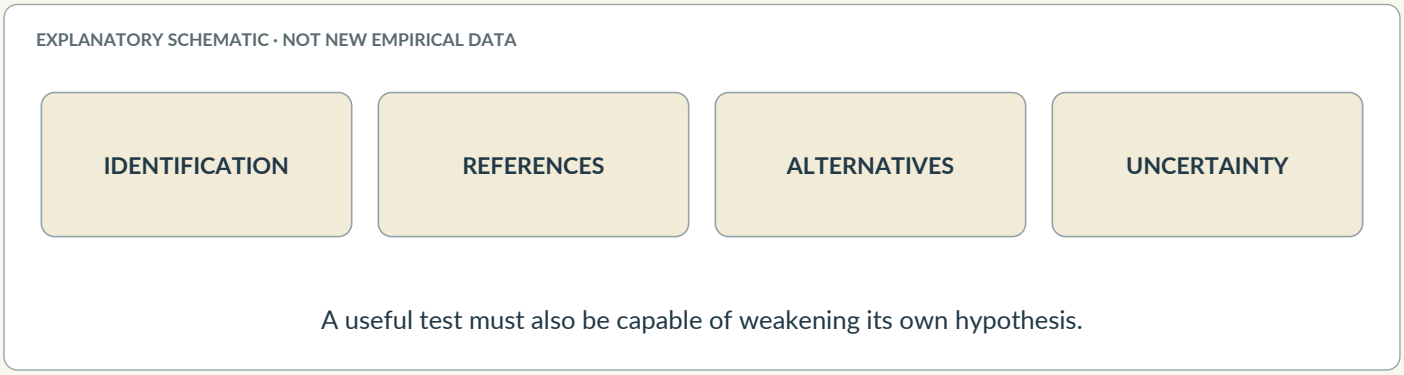
The population studies compared here do not directly examine a representative, historically well-attributed panel of Jewish inhabitants of the Khazar state. This is not a claim about every archaeogenetic project worldwide; it states a boundary of this body of evidence. [S06, S07, S12]

A stronger test would require secure dating, archaeological context, checks for contamination and biological relatives, and multiple sites. It would need to distinguish inhabitants of the realm from a particular converted circle. A grave inside the khaganate does not automatically belong to a Jewish person, and genetic similarity cannot supply a religion.

Competing models should then be specified in advance. What contribution, in which century, to which later community is proposed? What would the model predict differently from older Middle Eastern and European relationships? How large a contribution can the available data distinguish, and what remains below the detection threshold?

Such research must not turn unavailable samples into positive evidence for a preferred hypothesis. It should equally avoid claiming a definitive zero when the test lacks the necessary sensitivity.

Human remains also raise ethical questions. The Erfurt study explicitly records approval by the local Jewish community. People are not merely material for a polemic; the necessity of sampling, respect for remains and responsible communication belong within research design. [S12]



Before testing, specify the population, period, alternatives and discriminatory limits.

Sources / notes: S06, S07, S12

19 / Beter: citing a book and adding a political thesis

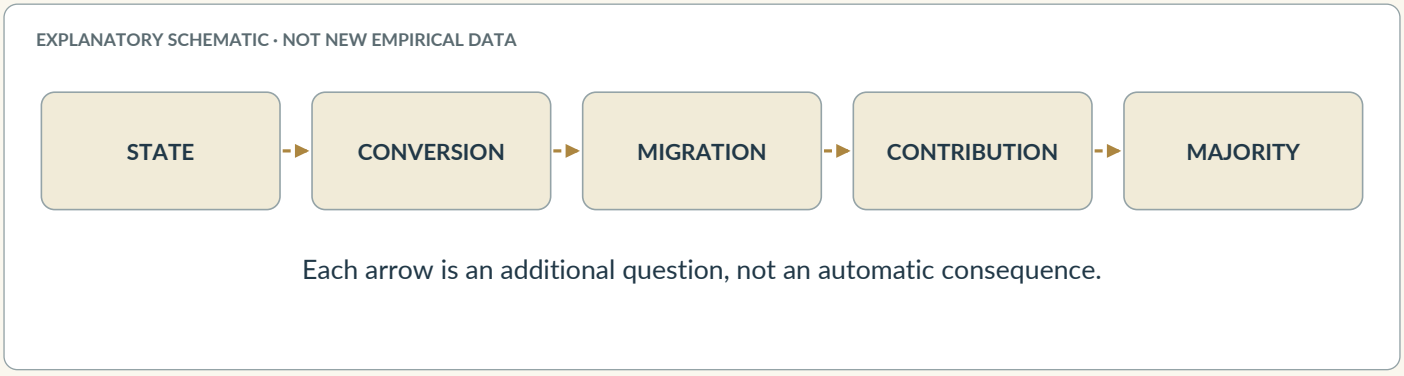
In AL50, Beter explicitly recommends Koestler's book and connects the Khazars to a long conflict with Russia. His subsequent account attributes intergenerational hostility to "Khazar Jews" and connects it with Bolshevism and Zionism. These are his claims under examination, not our designation of a present-day population. [S03]

The book's relationship to that conclusion must be disentangled. Even a confirmed biological contribution would not establish an enduring political organisation, secret coordination or an inherited intention of revenge. Those claims require historically identified people, institutions and actions.

In Appendix IV, Koestler also explicitly rejects using the ancestry hypothesis to deny Israel's existence. This does not automatically validate his political argument; it does show that his book cannot be equated indiscriminately with every later use of it. [S01]

Beter's recordings predate the genomic studies compared here. It would be unfair to say that he ignored evidence not yet published. It is nevertheless appropriate to reject the idea that later scientific terminology retrospectively validates his entire theory. Chronological succession does not confirm every earlier statement.

A label for a historical group must not quietly become a general indictment of people today. Each alleged political connection needs its own evidence; it cannot be inferred from a pedigree.



> **DNA does not test a thousand-year revenge. Citing a book does not demonstrate political continuity.**

Sources / notes: S01, S03

20 / Conclusion: precision without pretending completeness

Koestler's hypothesis belongs to the history of the ancestry debate. Its strong demographic version is not sufficiently established by the existence of a Khazar state, accounts of a Jewish ruling circle, or European ancestry among Ashkenazi Jews. Each statement has a different scope. [S01, S18, S07]

Our assessment of the selected studies favours multilayered European and Middle Eastern ancestry over a demonstrated Khazar majority. The reason is not the comfort of a traditional narrative, but the combination of regional comparisons, different genetic lineages, admixture timing and a medieval data point. Specific proportions and routes remain matters of modelling. [S07–S12]

The weaker possibility of an individual or minor Khazar contribution must not be substituted for the stronger majority claim. Leaving it open is not positive evidence for it. These studies do not provide the direct, adequate reference panel needed to quantify such a contribution precisely.

Language, religion, genetic similarity and citizenship do not answer the same question. None of the findings discussed here supports biologically inherited political hostility or collective guilt assigned by ancestry.

Later volumes examine political movements and historical events separately. RA04 supplies no genetic shortcut for them. It supplies a procedure: an exact claim, matching evidence, a competing explanation and an acknowledged degree of uncertainty.

Reused AI illustration / imagined historical scene — not an archival image

> **What is possible, what is probable and what is demonstrated must not be conflated.**

Sources / notes: S01, S07, S08, S09, S10, S11, S12, S18

Comparing studies / I

The dataset, the authors' conclusion and the interpretative limit are different things.

Elhaik · 2013 · Modern samples; 1,287 people

FINDING	Support for a Khazarian interpretation under the chosen proxies.
LIMIT	No direct panel of medieval Khazars.

S06

Behar et al. · 2013 · Modern samples; 1,774 people

FINDING	European and Middle Eastern relationships; no substantial specific Caucasian signal.
LIMIT	Abstract access in RA04; not a genealogical zero.

S07

Costa et al. · 2013 · Mitochondrial lineages

FINDING	Substantial European maternal contribution.
LIMIT	Not a percentage of the entire genome.

S08

Rootsi et al. · 2013 · Y, R1a/M582

FINDING	Near Eastern source for a particular Levite lineage.
LIMIT	Not all Ashkenazi Jews or all R1a lineages.

S09

Comparing studies / II

The dataset, the authors' conclusion and the interpretative limit are different things.

Carmi et al. · 2014 · 128 sequenced genomes

FINDING Founder bottleneck and a mixed-ancestry model.

LIMIT Modelled size is not a population census.

S10

Das et al. · 2016/2017 · GPS; modern references

FINDING Alternative geographical and linguistic interpretation.

LIMIT The temporal meaning of coordinates is disputed.

S13–S15, S17

Xue et al. · 2017 · Autosomal segments and timing

FINDING Substantial Southern European share of European contributions; multiple episodes.

LIMIT A share of a component is not a share of the whole.

S11

Waldman et al. · 2022 · 33 medieval individuals; Erfurt

FINDING Continuity, variation and an earlier founder event.

LIMIT One locality; not a complete migration chronicle.

S12

Claim register / C01–C05

C01 · DOES NOT FOLLOW

A historical Khazar state establishes predominant Khazar ancestry among Ashkenazi Jews.

State existence and reproductive contribution to a later population are different claims. Migration and descendant evidence are also needed. [S18, S07]

C02 · UNWARRANTED GENERALISATION

Conversion of an elite means every inhabitant converted.

The historical entry identifies the extent as unknown. A religious elite is not automatically the entire population. [S18]

C03 · CATEGORY ERROR

European features in Yiddish prove exclusively European biological ancestry.

Language contact and genetic transmission are not the same event. Yiddish's Germanic classification does not fill a speaker's pedigree. [S05, S04]

C04 · INCORRECT METHOD DESCRIPTION

Elhaik directly tested medieval Khazar genomes.

The central comparisons use modern proxies. Their historical representativeness is part of the dispute, not an established result. [S06, S07]

C05 · STRONGER THAN THE RESULT

Behar proved no Ashkenazi person could have any Khazar ancestor.

The abstract reports no substantial regional signal under its panel. It does not inspect every individual pedigree. [S07, S04]

Claim register / C06–C10

C06 · WRONG DENOMINATOR

European origins for over 80% of mtDNA lineages mean over 80% of the entire genome.

Maternal lineages are not autosomal proportions. A European result alone also does not identify a Khazar source. [S08, S11]

C07 · MISREAD MODEL PARAMETER

A model of approximately 350 founders is an exact historical census.

This models reproductive history, not all living people within a specified territory. [S10, S12]

C08 · UNDEMONSTRATED LOCALISATION

A GPS point identifies the village of all medieval ancestors.

Modern coordinates do not establish this without a validated temporal reconstruction. Both critique and authorial defence are identified. [S14, S15, S17]

C09 · OVERGENERALISATION

Erfurt exhaustively explained all Ashkenazi migrations.

The dated sample of 33 supports continuity and an earlier founder event. The authors explicitly limit it to one place and time. [S12]

C10 · DOES NOT LOGICALLY FOLLOW

A confirmed Khazar ancestor would prove a thousand-year political revenge.

Ancestry identifies no institution, order, political intention or action. This is an additional Beter thesis requiring separate evidence. [S03, S04]

Chronology

7.–10. storočie / 7th–10th c.	Historical period of the Khazar state; not a single biological pedigree. [S18]
1976	Koestler's book; a historical-demographic hypothesis before the genomic era. [S01, S02]
1979	Beter recommends the book in AL50 and develops a broader political interpretation. [S03]
2013	Elhaik and Behar: different regional interpretations. Costa and Rootsi: distinct uniparental lineages. [S06–S09]
2014	Carmi: sequenced genomes and a founder-bottleneck model. [S10]
2016–2017	GPS and language debate; authorial reply and perspective. Xue: timing and location of European contributions. [S05, S11, S13–S15, S17]
2018–2020	Methodological clarification of model plots and meanings of ancestry. [S04, S16]
2022	Waldman: dated medieval genomes from Erfurt. [S12]

Glossary

Ashkenazi Jews

Historical-cultural Jewish communities associated with German lands and later other regions; not one unchanging genome.

Autosomes

Chromosomes other than sex chromosomes; provide a broader picture of transmission through many lines.

Genetic drift

Random changes in variant frequencies, especially pronounced in small populations.

Haplogroup

A branch of genetic relatedness marked by variants; not a religious or citizenship category.

IBD

A segment inherited from a common ancestor; its length can contain information about time.

Mitochondrial DNA

A marker of the direct maternal line; not the whole genome.

PCA

A statistical summary of variation among samples into fewer axes; not an automatic migration map.

Proxy

An available sample standing in for an indirectly investigated historical population.

qpAdm

A method for testing models of genetic relationships and contributions relative to reference groups.

Reference panel

A set of comparative samples; its selection affects interpretation.

ROH

Runs of homozygosity; useful in investigating relatedness and demographic history.

Founder effect

A later population carries substantial variation from a comparatively restricted earlier circle.

Sources / S01–S05

Access checked for this edition; source cut-off 11 October 2026.

S01 · Arthur Koestler

The Thirteenth Tribe: The Khazar Empire and Its Heritage

1976; electronic transcription

https://www.heritage-history.com/index.php?author=koestler&book=tribe&c=read&readAll=true

ACCESS: Available transcription of the main text; argumentative passages and Appendices II–IV examined. Not fully collated with the first edition. The host introduction is excluded. The book is not reproduced in this package.

S02 · Google Books / Random House catalogue record

The Thirteenth Tribe: The Khazar Empire and Its Heritage

Random House, 1976; 255 pp.; ISBN 0394402847

https://books.google.com/books/about/The_Thirteenth_Tribe.html?id=UOFoAAAAMAAJ

ACCESS: Bibliographic record for date, publisher and extent. Not evidence that the book's thesis is correct.

S03 · Peter David Beter

Audio Letter No. 50

30 September 1979; Topic 3

https://www.peterdavidbeter.com/docs/all/dbal50.html

ACCESS: Topic 3 transcript, including the book recommendation and wider theory. The recording was not newly audio-collated for this edition.

S04 · Iain Mathieson; Aylwyn Scally

What is ancestry?

PLOS Genetics 16(3), e1008624 (2020). DOI: 10.1371/journal.pgen.1008624

https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1008624

ACCESS: Full available text of a methodological opinion piece. Not a separate dataset testing the Khazar hypothesis.

S05 · Marion Aptroot

Yiddish Language and Ashkenazic Jews: A Perspective from Culture, Language, and Literature

Genome Biology and Evolution 8(6), 1948–1949 (2016). DOI: 10.1093/gbe/evw131

https://academic.oup.com/gbe/article/8/6/1948/2574117

ACCESS: Full available scholarly comment. Earlier printed sources are used through the author's account; we did not independently analyse their palaeography.

Sources / S06–S10

Access checked for this edition; source cut-off 11 October 2026.

S06 · Eran Elhaik

The Missing Link of Jewish European Ancestry: Contrasting the Rhineland and the Khazarian Hypotheses

Genome Biology and Evolution 5(1), 61–74 (2013; online 2012). DOI: 10.1093/gbe/evs119

https://pmc.ncbi.nlm.nih.gov/articles/PMC3595026/

ACCESS: Full available article; proxy selection, dataset size and interpretation examined. No new computation on raw data.

S07 · Doron M. Behar et al.

No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews

Human Biology 85(6), 859–900 (2013). DOI: 10.3378/027.085.0604

https://digitalcommons.wayne.edu/humbiol/vol85/iss6/9/

ACCESS: Authors' abstract and publisher/university record. The full article and table supplements were not fully available in this working access.

S08 · Marta D. Costa et al.

A substantial prehistoric European ancestry amongst Ashkenazi maternal lineages

Nature Communications 4, 2543 (2013). DOI: 10.1038/ncomms3543

https://www.nature.com/articles/ncomms3543

ACCESS: Full available mitochondrial-lineage article. Its estimates are not presented as autosomal proportions. The earlier competing account is described through the authors' discussion.

S09 · Siiri Rootsi et al.

Phylogenetic applications of whole Y-chromosome sequences and the Near Eastern origin of Ashkenazi Levites

Nature Communications 4, 2928 (2013). DOI: 10.1038/ncomms3928

https://www.nature.com/articles/ncomms3928

ACCESS: Full available article, especially abstract, introduction and M582 results. The conclusion concerns a particular paternal lineage, not the whole population.

S10 · Shai Carmi et al.

Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins

Nature Communications 5, 4835 (2014). DOI: 10.1038/ncomms5835

https://www.nature.com/articles/ncomms5835

ACCESS: Full available article; historical modelling using 128 genomes. No health recommendation or individual genetic counselling is provided here.

Sources / S11–S14

Access checked for this edition; source cut-off 11 October 2026.

S11 · Xue et al.

The time and place of European admixture in Ashkenazi Jewish history

PLOS Genetics 13(4), e1006644 (2017). DOI: 10.1371/journal.pgen.1006644

https://pmc.ncbi.nlm.nih.gov/articles/PMC5380316/

ACCESS: Full available article; timing and regional shares within European contributions. The multiplication example in RA04 is explicitly our own educational illustration.

S12 · Waldman et al.

Genome-wide data from medieval German Jews show that the Ashkenazi founder event pre-dated the 14th century

Cell 185(25), 4703–4716.e16 (2022). DOI: 10.1016/j.cell.2022.11.002

https://reich.hms.harvard.edu/sites/reich.hms.harvard.edu/files/inline-files/2022_Waldman_ErfurtMedievalJews_Cell%5B15%5D_0.pdf

ACCESS: Available author PDF, including Limitations of this study and methods. Its in-press pagination differs from the published bibliographic pages. External supplementary datasets were not reanalysed.

S13 · Ranajit Das; Paul Wexler; Mehdi Pirooznia; Eran Elhaik

Localizing Ashkenazic Jews to Primeval Villages in the Ancient Iranian Lands of Ashkenaz

Genome Biology and Evolution 8(4), 1132–1149 (2016). DOI: 10.1093/gbe/evw046

https://pubmed.ncbi.nlm.nih.gov/26941229/

ACCESS: Identifying bibliographic record. Our description and defence of the procedure rely mainly on the authors' S15 and the reply abstract S17; we do not claim full inspection of the original article.

S14 · Pavel Flegontov et al.

Pitfalls of the Geographic Population Structure (GPS) Approach Applied to Human Genetic History: A Case Study of Ashkenazi Jews

Genome Biology and Evolution 8(7), 2259–2265 (2016). DOI: 10.1093/gbe/evw162

https://academic.oup.com/gbe/article-pdf/8/7/2259/20711100/evw162.pdf

ACCESS: Full available PDF text of the methodological and linguistic critique. RA04 diagrams are new explanatory schematics, not copied scientific figures.

Sources / S15–S18

Access checked for this edition; source cut-off 11 October 2026.

S15 · Ranajit Das; Paul Wexler; Mehdi Pirooznia; Eran Elhaik

The Origins of Ashkenaz, Ashkenazic Jews, and Yiddish

Frontiers in Genetics 8, 87 (2017). DOI: 10.3389/fgene.2017.00087

https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2017.00087/full

ACCESS: Full available perspective by the alternative account's authors, including their defence against linguistic and genetic criticism. It is not a new independent sample of medieval Khazars.

S16 · Daniel J. Lawson; Lucy van Dorp; Daniel Falush

A tutorial on how not to over-interpret STRUCTURE and ADMIXTURE bar plots

Nature Communications 9, 3258 (2018). DOI: 10.1038/s41467-018-05257-7

https://www.nature.com/articles/s41467-018-05257-7

ACCESS: Full available methods article, especially model scenarios, discussion and interpretative limits. Not a separate direct test of Ashkenazi origins.

S17 · Ranajit Das; Paul Wexler; Mehdi Pirooznia; Eran Elhaik

Responding to an enquiry concerning the geographic population structure (GPS) approach and the origin of Ashkenazic Jews – a reply to Flegontov et al.

arXiv:1608.02038v2 (17 August 2016). DOI: 10.48550/arXiv.1608.02038

https://arxiv.org/abs/1608.02038

ACCESS: Abstract and metadata of the preprint. Its preprint status is distinguished from peer-reviewed publication; the full 32-page reply is not analysed here.

S18 · Dan (D. Y.) Shapira

Khazars

Encyclopaedia Iranica XVI/5, 511–528; online 14 December 2020

https://www.iranicaonline.org/articles/khazars/

ACCESS: Available scholarly encyclopaedia entry; historical definition, diversity and the uncertain extent of conversion used. Not a genetic study.

Reader checklist and edition notes

Reading procedure: specify the exact claim and its time; locate the original publication; distinguish full text from abstract; check population and marker; identify proxies; look for an alternative model; read the limitations; do not mix percentages with different denominators; separate a finding from a political or ethical conclusion.

This is an independent AI-assisted editorial study. It is not written by Peter David Beter or Arthur Koestler, a peer-reviewed monograph, a new genetic experiment, or individual medical or legal advice. Its selection of sources is explicitly bounded.

Atmospheric illustrations are reused from earlier RA01/RA02 editions. They are historicising images, not photographs of evidence, authentic portraits of sampled ancestors or precise archaeological reconstructions. RA04 schematics are our own explanations; hypothetical numbers are labelled.

Numbered citations lead to this volume’s source register. Technical filenames are shared across EN/SK, while their contents remain linguistically separate. This edition does not alter RA01, RA02 or RA03. The issue date and version identify later corrections without rewriting publication history.

The closing principle is simple: a finding about ancestors is not a verdict on descendants. Protecting innocent people and recognising equal dignity do not require a successful test of any ancient-ancestry hypothesis.

> **Tempus omnia revelat. · Time reveals all.**