Archaeogenetics Without the Headlines

What ancient DNA measures, how inference works and where history exceeds genetics

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Direct answer. Ancient DNA can test biological relatedness, ancestry change, mixture and population continuity through time. It cannot directly identify a language, religion, archaeological culture, caste, nation or personal identity. Reliable archaeogenetics begins with secure provenience and dating, authenticates short damaged molecules, quantifies contamination, tests alternative population models and interprets results beside archaeology, history and linguistics.

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1 Scope and inferential chain

Ancient-DNA claims pass through excavation, sampling, extraction, sequencing, authentication, genotype processing, statistical modelling and historical interpretation. Error or bias at each stage propagates forward, so evidence must be audited along the whole chain.

2 Molecular preservation and authentication

Authentic ancient molecules are typically short and show characteristic post-mortem damage. Clean-room procedures, blanks and quantitative contamination estimates remain essential because modern human DNA is ubiquitous.

3 Data generation and representation

Shotgun and targeted capture designs answer partly different questions. Low-coverage pseudo-haploid calls permit population comparison but discard diploid information and require methods robust to missing data.

4 Population genetic models

PCA, clustering, f-statistics and admixture models describe relationships conditional on samples and assumptions. Proxy populations are not literal ancestral peoples, and model fit should be compared across plausible alternatives.

5 Sampling, chronology and scale

Preservation, excavation and permission generate geographic and social bias. Individuals must be dated and interpreted at the scale supported by the sample; extrapolation from a cemetery to a civilisation requires independent justification.

6 Identity and interdisciplinary interpretation

Biological ancestry is not equivalent to culture, language, ethnicity or nation. Genetics can reject or support demographic prerequisites for historical hypotheses, while archaeology and textual or linguistic evidence address different dimensions.

7 Ethics, damage and data stewardship

Research should comply with law, engage stakeholders, minimise destructive sampling and archive data with usable metadata. Scientific value does not remove obligations to human remains and communities.

8 Reporting checklist

A reproducible study reports provenience, permissions, dating, skeletal element, laboratory controls, damage, contamination, coverage, processing, reference datasets, code, model alternatives and uncertainty, and separates results from interpretation.

9 Evidence assessment

Strong	Authenticated ancient genomes can reveal biological relatedness, ancestry change, mixture and continuity across sampled times and places.
Probable	Well-sampled genetic shifts often reflect migration or changing mobility, when chronology and alternative models are adequately tested.
Contested	The scale, direction and social mechanism of many inferred movements, especially where sampling is sparse.
Unsupported	Directly equating genetic components with languages, archaeological cultures, castes, ethnicities or modern nations.

10 Conclusion

Archaeogenetics is most powerful as a time-resolved line of biological evidence. Authentication, representative sampling, explicit models and ethical stewardship determine its reliability. Its findings enrich history when they constrain demographic possibilities, while archaeology, linguistics and texts retain their own indispensable authority over culture and meaning.

References

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This paper is an evidence review for public scholarship.

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