Holstonia Bigfoot Investigations
Genesis Series No. 8

Genomic, Forensic, and eDNA Approaches to Detecting a Putative Relict Homo Species

Holstonia Bigfoot Investigations
From Anomaly to Analysis

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Dedicated to the memory of Dr. Jeff Meldrum and Dr. Jane Goodall

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Abstract

Recent advances in ancient DNA analysis, forensic genetics, and environmental DNA (eDNA) sampling have enabled detection of rare or cryptic taxa from minimal biological material. This paper evaluates the feasibility of identifying a hypothetical relict *Homo* lineage using non-invasive molecular approaches, including soil, sediment, water, keratinous material, shed epithelial cells, and trace forensic residues. We review genomic divergence patterns among known *Homo* lineages, outline contamination and authentication challenges specific to hominin-adjacent DNA, and discuss ethical considerations associated with sampling organisms closely related to *Homo sapiens*. A conservative predictive framework is proposed for detecting divergent hominin DNA and distinguishing it from modern human contamination. This synthesis establishes a methodological roadmap for molecular investigation while emphasizing inference, validation, and ethical restraint.

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1. Introduction

Molecular anthropology has substantially revised understanding of the genus *Homo*, revealing multiple late-surviving lineages and complex histories of divergence and admixture (Pääbo, 2014; Meyer et al., 2012). The identification of Denisovans from minimal skeletal material demonstrated that genetically distinct hominin populations can be recognized despite an extremely sparse fossil record (Meyer et al., 2012). These findings illustrate that biological presence and fossil visibility are not tightly coupled and that molecular evidence can reveal lineages otherwise invisible to archaeology or paleontology.

For a hypothetical low-density, cryptic hominin population, molecular approaches represent the most plausible avenue for detection. This paper evaluates genomic signatures, DNA recovery strategies, contamination controls, and ethical considerations relevant to assessing the feasibility of identifying a relict *Homo* lineage using non-invasive methods.

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2. Distinguishing Genomic Signatures Among *Homo* Lineages

Detection of a divergent lineage requires understanding genomic variation within and between known *Homo* groups.

2.1 Nuclear DNA Divergence Patterns

Comparative genomic studies indicate approximate nuclear divergence levels of ~0.12–0.15% between modern humans and Neanderthals and ~0.15–0.18% between modern humans and Denisovans, with substantially lower variation among modern human populations (Fu et al., 2014; Meyer et al., 2012). A hypothetical relict lineage related to late archaic *Homo* would be expected to fall within or above this range, depending on divergence time and subsequent gene flow. These values are best treated as heuristic benchmarks rather than strict thresholds.

2.2 Mitochondrial DNA Utility

Mitochondrial DNA (mtDNA) is abundant and often recoverable from degraded samples, making it useful for initial screening. However, mtDNA alone cannot establish taxonomic distinctiveness due to lineage replacement, introgression, and stochastic inheritance (Knapp et al., 2012; Willerslev & Cooper, 2005).

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2.3 Conserved Regions and Candidate Loci

Candidate loci frequently examined in hominin genomics include genes associated with speech and cognition (e.g., *FOXP2*), craniofacial development (*RUNX2*), brain growth (*ASPM*, *MCPH1*), pigmentation (*HERC2/OCA2*), and immune response (HLA/MHC regions). Divergent or archaic alleles at such loci could be informative but must be interpreted cautiously and in a multi-locus framework (Der Sarkissian et al., 2015).

3. Methods for Recovering DNA from a Cryptic Hominin

Advances in molecular recovery techniques permit DNA extraction from trace biological material under favorable conditions.

3.1 Environmental DNA (eDNA)

Environmental DNA has been successfully recovered from sediments, soils, and water sources, including contexts associated with large terrestrial vertebrates (Pedersen et al., 2015; Slon et al., 2017). Potential substrates include sediments from resting areas, track impressions, or frequently contacted surfaces. Analytical approaches include metabarcoding, shotgun sequencing, and targeted capture.

3.2 Trace and Contact DNA

Forensic studies demonstrate that small quantities of shed epithelial cells or biological residues can yield amplifiable DNA under controlled conditions (Zavala et al., 2023). Recovery is highly variable and sensitive to environmental exposure.

3.3 Keratinous Materials

Hair shafts and other keratinous tissues may preserve mtDNA and, less frequently, fragmented nuclear DNA. Keratin's resistance to degradation makes such substrates valuable but not reliably informative for full genomic reconstruction (Gilbert et al., 2005).

3.4 Contamination Controls

Stringent contamination controls are essential for hominin-adjacent DNA work. These include reagent blanks, negative controls, dedicated clean facilities, and independent replication using established ancient DNA authentication criteria (Cooper & Poinar, 2000; Gilbert et al., 2005).

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3.5 Challenges Unique to Hominins

Because humans are genetically close to other *Homo* lineages, distinguishing endogenous sequences from modern contamination requires multi-locus validation and statistical evaluation of divergence and damage patterns (Der Sarkissian et al., 2015).

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4. Forensic Approaches to Trace DNA Detection

Forensic methodologies developed for human DNA analysis can inform non-invasive sampling strategies but must be applied conservatively.

4.1 Trace and Touch DNA

Trace DNA may be recoverable from manipulated objects or contacted surfaces using sterile swabs or tape-lift techniques, though success rates are variable and context-dependent (Zavala et al., 2023).

4.2 Hair and Keratinous Residues

Hair shafts without follicles can yield mitochondrial genomes and limited nuclear fragments. Morphological assessment may guide prioritization but cannot substitute for genetic analysis (Gilbert et al., 2005).

4.3 Environmental Structures

Surface residues on environmental features may contain biological microdebris. Tape-lift sampling minimizes disturbance but carries elevated contamination risk.

4.4 Trackway Sampling

Track sediments may preserve trace biological material under rare conditions. Sampling should prioritize compressed or protected layers, recognizing low expected recovery rates (Pedersen et al., 2015).

4.5 Authentication

Authentication requires independent replication, consistency across loci, and degradation profiles consistent with environmental exposure rather than laboratory contamination (Cooper & Poinar, 2000).

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5. Expected Genomic Profiles Under a Relict *Homo* Model

Any detected genome would reflect divergence history, demographic size, and potential admixture.

5.1 Nuclear Divergence

Nuclear divergence provides the strongest evidence for lineage differentiation, with deeper splits producing larger divergence values. These expectations are probabilistic rather than diagnostic.

5.2 Mitochondrial Outcomes

Possible outcomes include archaic haplogroups, novel lineages, or modern human mtDNA due to introgression. mtDNA must be interpreted in conjunction with nuclear evidence.

5.3 Population Genetic Signatures

Low effective population sizes predict reduced heterozygosity, elevated linkage disequilibrium, and bottleneck signatures, though such patterns are not unique to relict populations (Fu et al., 2014).

5.4 Adaptive Regions

Alleles associated with environmental adaptation may be informative but are subject to convergent evolution and should not be overinterpreted (Der Sarkissian et al., 2015).

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6. Ethical, Legal, and Cultural Considerations

Investigation of a potential relict *Homo* lineage raises ethical issues due to cognitive and cultural proximity to *Homo sapiens*.

6.1 Non-Invasive Ethics

Sampling should remain strictly non-invasive, avoiding pursuit, capture, or disturbance. Environmental and trace sampling represents the ethical minimum.

6.2 Consent and Moral Standing

If a lineage exhibits advanced cognition or social structure, ethical considerations may parallel those applied to great apes or uncontacted human populations, though such issues remain hypothetical.

6.3 Legal Implications

Confirmation of a relict hominin would raise unresolved legal questions regarding species protection, human rights frameworks, and conservation law.

6.4 Indigenous Knowledge

Indigenous narratives should be approached respectfully and collaboratively, recognizing cultural sovereignty and avoiding extractive research practices.

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7. Conclusions

Molecular approaches offer the most plausible means of evaluating the hypothesis of a relict *Homo* lineage in the absence of skeletal remains. Environmental DNA, forensic trace analysis, and targeted genomic sequencing can, under favorable conditions, detect divergent hominin signatures. However, all findings must be interpreted conservatively, validated rigorously, and framed as probabilistic inference rather than confirmation.

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Key conclusions include:

- DNA may persist where skeletal material does not.
- Nuclear genomic evidence is essential for lineage differentiation.
- mtDNA is a useful screening tool but insufficient alone.
- Authentication must meet ancient DNA standards.
- Ethical constraints are central to study design.

A carefully designed molecular program could test the relict *Homo* hypothesis while remaining scientifically and ethically defensible.

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