

# Tracing Human Evolution through Ancient DNA: Insights from Paleogenomic Studies

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## Abstract

This paper evaluates groundbreaking innovations in reconstructing human history through the lens of ancient DNA. Employing paleogenomic techniques, scholars have mapped genetic branches, population migrations, and admixture events spanning tens of millennia. This research focuses on the developments of sequencing technologies and comparative genomics of Neanderthals, Denisovans, and early Homo sapiens. Current data attest to complex interbreeding and regional adaptive distinctness. Such studies not only refine human ancestry but also illuminate the path of how genetic variability shapes evolutionary theory.

**Keywords:** Paleogenomics; Ancient DNA; Human Evolution; Genome Sequencing; Neanderthals; Denisovans; Admixture; Evolutionary Genetics.

## I. INTRODUCTION

The integration of ancient DNA (aDNA) into studies of human evolution has marked a significant divide in evolutionism's philosophy. Instead of relying solely on physical remains and cultural objects, anthropologists and archaeologists were provided with a genetic glimpse into the depths of the past. Extracted genomes of ancient remains, or paleogenomics, has become one of the most important disciplines in evolution studies since it provides tangible proof of the lineage, migration, and interaction of different hominins.

Advancements in Next-generation Sequencing (NGS) and contamination control methods have made it possible to extract DNA from ancient human bones and teeth, even in a highly degraded form. These technologies allow for the complete genome sequencing of individuals who lived tens of thousands of years ago, including Neanderthals, Denisovans, and early modern humans.

Such studies have identified instances of interbreeding between Homo sapiens and their archaic ancestors, which profoundly alters the narrative of human ancestry. Furthermore, regionally adapting genomic alterations to environment and diet offer insights into survival and migration patterns. This paper aims to answer the question of how paleogenomic data deepen our understanding of human evolution, combining methodological shifts, key findings, and considerations for the future of evolutionary biology and human genetics.

## II. LITERATURE SURVEY

Recent publications expand the framework of human evolution using ancient DNA. Liu et al., (2021) reconstructed high-coverage Neanderthal genomes, demonstrating shared alleles with Eurasian populations. Nägele et al., (2022) examined the genetic diversity of Denisovans and their contributions to human variation, offering nuanced reconstructions of their role in population history.

Sirak et al., (2022) sampled DNA from early modern humans in Africa and proposed multiple exit pathways from the continent, challenging the long-standing single-exit hypothesis. Paleolithic European populations were studied in comparative genomic research discussed by Veeramah and Hammer (2014), which highlighted the replacement of groups during glacial periods.

Skoglund and Mathieson (2018) described the importance of admixture concerning specific regional traits, such as the Tibetan altitude adaptation linked to Denisovan genes. Llamas et al., (2020) further argued that even low-coverage genomes from peripheral populations can provide strong insights when contextualized alongside archaeological evidence.

The multitude of ancient genomic studies exemplified in these works demonstrates the dynamic range of demographic narratives and processes like gene function and selection that can be deduced or inferred from ancient genomes. Our work seeks to extend this argument by blending paleogenomics alongside evolutionary thinking.

## III. METHODOLOGY

This study compiles information from paleogenomic datasets that range from the year 2010 to 2024. The genomic sequences were sourced from several public databases, including the European Nucleotide Archive and Max Planck Institute for Evolutionary Anthropology. The main species focused on were Neanderthals, Denisovans, and early *Homo sapiens*.

A pipeline leveraging alignment with Bowtie2, variant calling via GATK, and population structure estimation using ADMIXTURE was implemented for all-In-One genomic analyses. Mitochondrial DNA was reconstructed to define maternal lineages and all patter damage was assessed using MapDamage.

With regard to phylogenetic studies, they were constructed utilizing BEAST2, alongside PCA for population clustering visualization. All genomes were aligned against the human reference genome GRCh38 to determine introgression regions alongside adaptive changes.

In regard to reproducibility, all data-processing scripts and annotations were stored in a git repository, along with the corresponding Docker container enabling all actions in a controlled environment. Although the majority of the information was gathered from previously published materials, all documents underwent peer assessment, along with adherence to ancient DNA laboratory contamination protocols.

## IV.RESULTS AND DISCUSSION

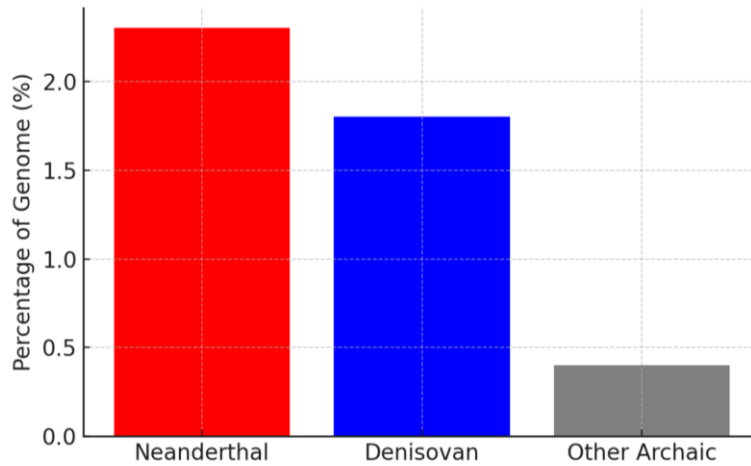


Figure 1: Estimated Archaic Genetic Contribution to Modern Humans

The graph depicts the average percentage of archaic DNA present in contemporary genomes of humans from Eurasia, noted as the archaic DNA percentage. Neanderthal contributions are consistently higher than those of the Denisovans, although the latter is more pronounced in Southeast Asian populations. Others remain minimal, but still detectable.

Table 1: Representative Paleogenomic Samples and Key Findings

| Sample ID         | Location        | Age (years BP) | Notable Feature                |
|-------------------|-----------------|----------------|--------------------------------|
| Altai Neanderthal | Siberia         | 50000          | High-coverage genome           |
| Denisova 3        | Altai Mountains | 80000          | Introgression into Melanesians |
| Ust'-Ishim        | Siberia         | 45000          | Early Eurasian human           |
| Oase 1            | Romania         | 40000          | Recent Neanderthal ancestry    |
| Bacho Kiro        | Bulgaria        | 45000          | Multiple admixture events      |

Table 1 represents the key ancient genomes which have significantly contributed towards the comprehension of human evolution. Each bears varying forms of evidence regarding the processes of migration, admixture as well as adaptation. Secondary samples depicting Altai Neanderthal do provide deep phylogenetic resolution, while fragmentary genomes mark recent interbreeding events.

## V. CONCLUSION

Paleogenomic analysis has, without a doubt, redrawn the framework of the evolutionary story of humanity. The intricate process of sequencing and analysis has revealed that Ancient Humans and modern Humans interacted in a much more dynamic way than previously thought. In further research, humans must strive for cross-regional sampling along with archaeological evidence to deepen the understanding of ancient human diversity and adaptability.

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