Review

Genetic Insights into Ancient Kinship and Human History: Methods, Applications, and Implications

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ABSTRACT: Recent advances in ancient DNA analysis have transformed our understanding of kinship and underlying social structures in past populations. The application of next-generation sequencing technologies has enabled researchers to reconstruct the genetic makeup of ancient individuals with unprecedented precision, providing new insights into lineage, ancestry, and social organization. Ancient DNA evidence has revealed a wide range of kinship systems, including patrilineal and matrilineal descent, consanguineous marriages, female exogamy, and family-based burial practices. These findings underscore the complexity of human social relationships and the dynamic interactions between genetic inheritance, cultural traditions, and environmental factors in ancient societies. By examining case studies across different geographic and temporal contexts, this review highlights the transformative potential of ancient DNA in deciphering past human relationships. However, it also addresses key ethical concerns, including the importance of respecting cultural sensitivities and avoiding overly deterministic interpretations of genetic data. The integration of genetic evidence with archaeological and anthropological perspectives enables a more comprehensive reconstruction of ancient social systems, moving beyond simplistic genetic determinism to appreciate the intricate interconnections between biology, culture, and identity.

Keywords: Genetic kinship; Ancient DNA; Next-generation sequencing; Genetic data

1. The Nature of Ancient DNA

Ancient DNA (aDNA) refers to genetic material extracted from aged biological specimens, which is often highly degraded and present in only trace amounts. Over the past few decades, aDNA research has significantly advanced multiple disciplines, providing new insights into human migration, admixture, and kinship that traditional archaeological and anthropological methods alone may not fully capture [1]. The advent of advanced genomic techniques has enabled researchers to sequence increasingly older and more fragmented samples, providing an unprecedented direct view into the genetic composition of past populations.

One of the most significant contributions of aDNA studies in recent years has been the ability to reconstruct kinship and social structures in ancient communities. Previously, researchers primarily inferred these relationships from burial arrangements, artifact distributions, and osteological analyses. However, genetic analyses can now directly confirm or challenge these interpretations by identifying familial connections among individuals interred together. By analyzing autosomal single-nucleotide polymorphisms (SNPs), uniparental haplogroups (mitochondrial DNA and Y-chromosome), and runs of homozygosity, scientists can establish parent-offspring, siblings and cousin-level relationships, effectively mapping extended family networks in prehistoric societies. Such findings have profound implications for understanding social organization [2].

Genetic evidence can clarify whether burial clusters represent biological kin groups, whether cultural practices such as exogamy were enforced, and whether high-status individuals were closely related within a lineage. The application of next-generation sequencing (NGS) to ancient remains has thus become an essential tool for exploring social hierarchy, inheritance, and residence patterns, extending beyond the insights gained from material culture alone [2].

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Nonetheless, the power of genetic evidence necessitates careful contextualization, as ancient genomes do not exist in isolation; they are embedded within complex sociocultural systems that must be interpreted holistically and ethically [3].

1.1. The Significance of Kinship in Archaeology

Kinship is a fundamental structuring element of human societies, shaping inheritance, marriage patterns, social interactions, and identity. Traditional archaeology has inferred kinship relations from material culture, such as the spatial organization of graves, the distribution of grave goods, and the repeated use of certain mortuary sites. Despite this, these inferences often remain ambiguous, as multiple explanations can account for the same burial pattern. Ancient DNA provides a direct measure of genetic relatedness, helping resolve uncertainties and distinguishing whether collective burials represent biological families or individuals connected through social or ritual status [4,5].

Genetic studies have revealed diverse kinship practices across cultures. For example, patrilocal residence—where males remain in their natal community while females migrate—often results in limited Y-chromosomal diversity within a site but greater mitochondrial DNA diversity due to incoming brides. Conversely, matrilocal systems exhibit the opposite pattern. The detection of consanguineous marriages, such as a cousin or uncle-niece union, suggests that some societies practiced endogamy to preserve resources or social status within a lineage [2,6]. Moreover, ancient DNA can differentiate between biological kinship and socially recognized kinship, which refers to relationships that may not be reflected in genetic data but play crucial roles in community organization [7].

1.2. Moving Beyond Biological Determinism

Although aDNA enhances our ability to reconstruct familial ties, kinship extends beyond biological relationships to encompass social and cultural dimensions. Scholars caution against overly deterministic interpretations that equate genetic lineage with identity [3]. For example, a burial containing multiple women and children near a high-status male may reflect social organization rather than nuclear family structures. Additionally, patrilineal or matrilineal genealogical signals may intersect with broader cultural practices such as adoption, polygyny, or kin alliances. To avoid reductive interpretations, researchers must integrate genetic data with archaeological, environmental, and ethnographic evidence. Multidisciplinary approaches provide a more holistic perspective on ancient social structures, preventing the imposition of contemporary biases onto past societies that may have conceived of kinship in different ways.

2. Methodologies in aDNA Kinship Studies

2.1. Authentication of aDNA and Contamination Control

Ancient DNA is inherently low-quantity and highly susceptible to contamination from modern DNA, necessitating stringent authentication protocols. To mitigate contamination, researchers employ decontamination procedures, work in clean-room facilities, and identify characteristic patterns of DNA degradation, such as postmortem cytosine deamination and short fragment length. These measures help ensure the authenticity of aDNA sequences [8]. The gold standard for validation remains reproducibility through independent replication, which minimizes the risk of contamination and methodological artifacts.

2.2. Next-Generation Sequencing and Library Preparation

The advent of NGS platforms, such as Illumina, has revolutionized aDNA research by enabling the parallel sequencing of millions of short DNA fragments. DNA is extracted from powdered bone or tooth samples using specialized protocols, after which sequencing libraries are prepared by ligating platform-specific adapters to fragmented DNA. To mitigate damage-induced errors, samples are often treated with uracil-DNA glycosylase (UDG) to remove deaminated cytosines. The prepared libraries undergo amplification, cluster generation, and sequencing via the Sequencing by Synthesis (SBS) method. This approach is both rapid and cost-effective, generating large volumes of genetic data even from highly degraded samples. As a result, genome-wide analyses of ancient individuals, population-level comparisons, and direct kinship inferences have become increasingly feasible.

2.3. Statistical and Computational Methods

Ancient DNA datasets often contain high rates of missing data due to degradation, necessitating the use of computational approaches to maximize analytical accuracy. Genotype imputation algorithms leverage linkage disequilibrium patterns from high-quality reference populations to infer missing genotypes [9], while uniparental markers (Y-chromosome and mtDNA) are commonly used to trace paternal and maternal lineages, particularly in cases of low genomic coverage.

Autosomal kinship coefficients derived from shared alleles and runs of homozygosity (ROH) allow for the quantification of relatedness within and between archaeological samples [10–12]. The software READ, developed for aDNA kinship analysis, which applies "expected number of mismatches" to measure the amount of information available in kinship estimation, categorizes individual pairs into four classes: (1) identical individuals or monozygotic twins; (2) first-degree relatives (parent-offspring, full siblings); (3) second-degree relatives (grandparent-grandchild, avuncular, or half-siblings); and (4) unrelated individuals (kinship beyond the second-degree range), however, since third-degree classification in READ demands more data than second- or first-degree classifications, kinship classification for low-coverage data is likely to produce biased results [13–15]. Identical by Descent (IBD) analysis further refines kinship assessments by identifying shared genomic segments, differentiating between close familial relationships and more distant shared ancestry [16]. When it comes to this, the ancIBD method accurately detects IBD segments in human aDNA data, reliably identifying IBD segments longer than 8 cM in SNP capture data with at least 1× average coverage depth and whole-genome sequencing (WGS) data with coverage as low as 0.25×. Nevertheless, the model calculates genotype probabilities based on Hardy-Weinberg equilibrium and allele frequencies from modern reference populations, which may not be fully applicable to ancient populations with genetic structures involving recent admixture or isolation [17]. KIN can estimate genetic relatedness and IBD from low-coverage ancient DNA data, accurately classifying up to third-degree relatives and distinguishing between siblings and parent-child pairs using as little as 0.05× sequence coverage. KIN assumes the analyzed individuals originate from a single population; if a significant substructure exists in the actual population, the method may fail to infer relatedness accurately [18].

Population structure analyses, such as Principal Component Analysis (PCA), ADMIXTURE, and qpAdm, facilitate the clustering of individuals based on genetic similarity and the estimation of ancestry proportions from multiple source populations [19–22]. The outgroup *f3*-analysis, first proposed by Raghavan et al., measures genetic similarity between two populations relative to an outgroup using *f3(Outgroup; X, Y)*, where a higher f3 value indicates greater genetic affinity. To distinguish genetic similarity due to shared ancestry from admixture, f4-analysis employs the statistic *f4(P1, P2; P3, P4)*, where P4 typically serves as an outgroup [22]. For phylogenetic reconstruction and admixture modeling, Treemix infers maximum-likelihood population trees while incorporating gene flow between diverged lineages [23], and DATES estimates the timing of admixture events by analyzing linkage disequilibrium decay, providing an approximation of the number of generations since initial genetic mixing [24]. When combined with archaeological context, including burial arrangements or associated grave goods, these computational approaches provide powerful insights into ancient populations' kinship structures and demographic history.

2.4. Integrating Genetic Data with Archaeological Context

The integration of genetic data with archaeological evidence is crucial for accurately reconstructing ancient social structures. Burial practices, material culture, and isotopic analyses of diet and mobility provide key contextual information that complements genetic findings. For instance, if genetic analysis reveals close biological relatedness among individuals, yet isotopic data suggest different diets or geographic origins, this may indicate complex social dynamics such as fosterage, exogamous marriage practices, or the relocation of individuals during their lifetimes. Similarly, the presence of paternal haplotype clusters coinciding with shared mortuary traditions may suggest a patrilocal residence system, whereas greater variability in maternal lineages within a cemetery could indicate female exogamy. Interdisciplinary collaboration among geneticists, archaeologists, and anthropologists ensures that aDNA findings are interpreted within a broader cultural and historical framework rather than in isolation.

3. Applications and Case Studies

3.1. Revealing Complex Kinship Patterns

aDNA analyses have greatly enhanced our understanding of kinship structures across diverse societies and periods. In Neolithic Europe, certain groups exhibited strong patrilineal ties, as reflected by the clustering of Y-chromosomal haplotypes among adult males buried together [2]. A notable example is the adult male interred in the innermost chamber of the Newgrange passage tomb, whose genome revealed evidence of a first-degree incestuous union. Runs of Homozygosity (ROH) analysis confirmed that he was the offspring of either a sibling pair or a parent-offspring relationship. The elaborate burial treatment, including a central position within the tomb and rich grave goods, suggests that such mating strategies may have been employed to preserve lineage continuity, wealth, and social power.

This case contrasts sharply with broader patterns in Neolithic Ireland, where demographic modeling indicates that community sizes were sufficiently large and exogamous practices prevalent enough to maintain low inbreeding coefficients, avoiding consanguineous unions closer than fifth-degree relatives.

The extreme inbreeding observed at Newgrange represents a statistically rare phenomenon, aligning ethnographically with politico-religious elites who practiced sanctioned endogamy to consolidate hereditary power, as documented in divine kingship systems of ancient Egypt, Hawai'i, and the Inca civilization [25,26]. The deliberate placement of this individual at the ritual focal point of the monument, alongside isotopic evidence of privileged dietary access, suggests that consanguineous practices functioned as a strategic mechanism to reinforce lineage purity and centralized authority within Ireland's hierarchical passage-tomb societies. Notably, male individuals from the Poulnabrone portal tomb and Parknabinnia court tomb revealed significant divergence in the frequencies of two Y-chromosomal haplogroups, and kinship reconstruction demonstrated no evidence of close genetic ties among individuals interred within each tomb cohort. This absence of nuclear family groupings, coupled with patrilineally inherited haplogroup differentiation between neighboring megalithic sites, underscores the emergence of social stratification mediated through broad-scale patrilineal networks rather than localized kinship units[27]. Meanwhile, maternal DNA diversity often indicated exogamous wives moving between communities, suggesting the widespread exchange of females as a means to forge alliances [6].

Archaeological sites in Peru and Chile suggest that kin-based marriage selection may have been employed to preserve tribal or community identities, particularly in resource-scarce environments. Similarly, genomic analysis of individuals from the Pingliangtai site, associated with the Late Neolithic Longshan culture in China, indicates consanguineous mating practices. The three individuals analyzed in this study (M310, M311, and M312) shared maternal lineages, were identified as second-degree relatives, and were likely members of an extended family unit [28]. During the Longshan cultural period (YR_LN), genetic evidence from both the Haidai region (lower Yellow River basin) and the Central Plain region (middle Yellow River basin) reveals widespread consanguineous mating. ROH analysis identified extensive long ROH segments in individuals from the Dinggong site, such as M77 and M10, and the H6 individual from the Wadian site. These ROH levels significantly exceed background levels observed in earlier Neolithic populations, suggesting a broader sociocultural pattern rather than isolated cases. Consanguinity may have reinforced elite kinship networks or resulted from endogamous practices within small, geographically constrained communities [29]. The Sunghir site in Russia presents a more complex picture. Genomic data reveal a mix of closely related individuals and unrelated companions buried with elaborate grave goods [30]. This pattern suggests a social or ritual mechanism that extended beyond genetic ties, emphasizing communal bonds in early social organization.

The role of genetic affinity in shaping early social complexity is evident as kinship structures evolved alongside increasing stratification and resource specialization. The intensification of social complexity—marked by specialized labor divisions, refined resource allocation systems, and hierarchical power structures—likely facilitated the expansion of extended family networks beyond the nuclear family model, accommodating the demands of evolving socioeconomic dynamics [28]. A comparable phenomenon is observed in Corded Ware Culture burials at Eulau (Germany), where some co-burials included children who were not biologically related to the adult female interred with them. This pattern suggests the practice of adoption, fostering, or symbolic motherhood, reinforcing the role of non-biological kinship in early societies [3].

3.2. Gender Roles, Social Status, and Burial Practices

Ancient DNA has provided crucial insights into the intersection of gender, social status, and burial practices. In some Bronze Age European societies, the most opulent grave goods were associated with male individuals belonging to patrilineal lineages, suggesting a system in which wealth and social power were transmitted along paternal lines [16,31]. Conversely, in certain Central Eurasian pastoralist communities, aDNA evidence indicates that eldest males held high social status, as reflected in large, richly furnished graves. These findings also align with genomic evidence of polygamous or levirate marriage practices [32,33].

In Neolithic Ireland, genomic analyses of individuals from the Newgrange passage tomb reveal that first-degree relatives of an inbred elite individual were interred at other major passage tomb complexes, notably Carrowmore and Carrowkeel. These individuals exhibited fourth-degree kinship connections but lacked close nuclear family groupings within their respective tomb cohorts. This pattern suggests that elite power structures were maintained through networks of broad patrilineal descent rather than localized familial units. Genetic continuity was preserved through kinship alliances spanning multiple monumental centers, indicating that Ireland's passage-tomb-building societies possessed attributes of emerging social complexity. These attributes included institutionalized elite lineages and centralized resource mobilization, both of which were key precursors to early state formation [27].

Matrilocal residence patterns were prevalent in Iron Age Britain, with evidence suggesting a transition from earlier patrilineal social structures. Among the Late Iron Age Durotrigian tribe, female individuals were frequently buried with substantial grave goods, and genetic analyses revealed an extended kin group centered around a single maternal lineage. Notably, female members shared a rare mitochondrial haplogroup (U5b1 subclade), while Y-chromosomal diversity within the group was markedly heterogeneous. Intra-group relatedness among males was significantly lower, with 80% of non-maternal lineage members being male, consistent with male exogamy and marital migration into matrilocal communities. Osteological evidence and fortified settlement patterns suggest chronic male absence due to warfare, which may have driven the institutionalization of female socio-political authority and resource control [34].

In some contexts, women's burials feature high-status symbols traditionally associated with male roles, possibly reflecting more flexible gender roles or the ritual appropriation of masculine identity for socio-political purposes [35]. Additionally, collective and family-based burials provide further insights into kinship structures and their role in social organization. Neolithic and Chalcolithic cemeteries in Poland, Germany, and Normandy often contain nuclear families or extended kin clusters, underscoring their centrality in agricultural production and land inheritance [2,31]. These patterns reinforce the idea that early farming communities frequently organized production and resource management around immediate and extended family units.

3.3. Human Populations Migration and Admixture

Ancient DNA (aDNA) research has significantly advanced our understanding of population movements and admixture across Eurasia, often revealing patterns that extend beyond kinship structures within individual sites. This section synthesizes evidence from East and Northeast Asia to Europe and the Americas, highlighting key migratory and genetic transition events from the Late Pleistocene to the historical period.

3.3.1. From the Last Glacial Maximum to the Bronze Age: Trans-Eurasian and Native American Ancestry Formation

Ancient Northeast Asian genomes reveal a major population turnover after the Last Glacial Maximum (LGM). Pre-LGM individuals, such as Tianyuan individuals, suggest long-term isolation in the Amur Basin. Post-LGM populations, exemplified by AR19K and AR14K, exhibit marked genetic divergence from earlier groups and continuity with later Neolithic communities, forming the East Asian component of Ancient Paleo-Siberians (e.g., Kolyma, UKY). These Paleo-Siberians represent a genetic admixture of AR14K-related East Asians and Ancient North Eurasians (ANE), indicating the Amur Basin's central role in shaping the Late Pleistocene trans-Eurasian gene flow [36].

Genome-wide data link Upper Paleolithic Siberians to the founding populations of the Americas. The UKY individual (~14,000 BP) shows a dual ancestry from ANE and Northeast Asians (NEA), which also characterizes the 9800-year-old Kolyma genome. These individuals form sister lineages to ancestral Native Americans, suggesting repeated interactions between NEA and proto-Native American groups in Siberia before the trans-Beringian migration. Moreover, the genetic continuity of ANE ancestry is evident in the Baikal region from the Early Neolithic through the Bronze Age. Some LNBA individuals, such as KPT005, carry Yamnaya-related steppe ancestry, indicating eastward gene flow from the Pontic-Caspian region during the Early Bronze Age [37]. This steppe influence parallels linguistic hypotheses concerning Indo-European dispersals and alters local kinship structures [38,39].

Later, individuals from Siberian Inuit sites (Uelen, Ekven) reveal ~31% Native American-related ancestry, indicating a reverse gene flow from North America to Asia. This observation aligns with linguistic evidence for a back-migration of Eskimo-Aleut speakers. Additionally, genetic affinities between Na-Dene speakers and Paleo-Siberians (e.g., Kolyma1) suggest distinct population histories from Palaeo-Eskimo groups (e.g., Saqqaq) [40].

3.3.2. East Asian Prehistory Shaped by Farming, Language, and Genetic Exchange

Ancient DNA reveals dynamic genetic shifts across the Yellow River (YR), West Liao River (WLR), and Amur River (AR) basins. In the YR basin, continuity from the Yangshao period to the Late Neolithic supports a northern origin of Sino-Tibetan languages. In contrast, WLR populations correlating with the dispersal of Transeurasian languages show increasing YR affinity over time, likely due to intensified millet farming and admixture with southern groups during the Late Neolithic [41–45].

Upper_YR_LN individuals (e.g., Qijia culture, 2050–1850 BCE) exhibit admixture between YR farmers and AR foragers, a pattern retained into the Iron Age. Modern Tibetans inherit partial ancestry from these populations, supporting the role of YR expansions in Tibetan Plateau colonization post-1600 BCE. However, ancient AR groups—despite showing genetic continuity with modern Tungusic-speaking populations—did not directly contribute to Tibetan or Chinese ancestry, reflecting stratified population histories. Bronze Age gene flow from YR to WLR regions likely led to agricultural intensification and facilitated admixture with AR-related pastoralists. This coincided with a shift to nomadic lifeways and suggests environmental and economic drivers behind demographic transitions[41].

In the Haidai region, gene flow did not always accompany archaeological interaction with the Central Plain. Neolithic Haidai populations, such as Fujia_LDWK, exhibit mixed ancestry from YR_MN (Yangshao), local Shandong_HG (Boshan_EN), and a southern Amis-like component. During the Longshan period, Haidai groups remained genetically distinct from YR-related populations, despite cultural convergence. Only in the Bronze Age did substantial genetic homogenization occur, with Central Plain-derived YR_LN ancestry dominating both regions. The Erlitou group maintained continuity with earlier Longshan populations, forming a key node in northern China's genetic structure [29].

3.3.3. Genetic Networks Across East Asian Islands and Transcontinental Corridors

Prehistoric Guangxi and Fujian served as East and Southeast Asia crossroads, as reflected in late Pleistocene and early Holocene individuals like Longlin and Dushan. These individuals display divergent genetic lineages distinct from both Southeast Asian Hòabìnhian and northern East Asian populations, indicating multiple waves of migration and admixture before agriculture emerged. During 9000–6000 BP, Guangxi populations underwent complex admixture events, exemplified by the Baojianshan individual, who harbored ancestry from indigenous Guangxi, Fujian-related coastal, and Southeast Asian lineages. Over time, northern East Asian influence increased, especially after ~1500 BP, when Shandong-related ancestry became prominent [46].

In Japan, tripartite ancestry emerged through successive migratory episodes: Jomon hunter-gatherers, Yayoi farmers (linked to the WLR Bronze Age), and Kofun-period Han-related migrants. These lineages ultimately formed the genetic foundation of modern Japanese populations [47,48]. Similarly, Kofun individuals show significant gene flow from Shandong Longshan groups, highlighting coastal northern China as a major source of mainland East Asian ancestry in post-Yayoi Japan. Korean genetic continuity from the Three Kingdoms period onward suggests regional stability, contrasting with the layered demographic history of Japan [49].

3.4. Interdisciplinary Integration and Complexity Interpretation

While genetic data can reveal population shifts and kinship networks, these patterns are also shaped by ecological conditions, trade routes, linguistic influences, and sociopolitical institutions. For example, isotopic analyses can determine whether individuals with shared genetic ancestry had different diets, suggesting divergent social roles or economic niches. Similarly, linguistic reconstructions can align with aDNA-based models, providing insights into the timing and directionality of language spread [50]. Climate reconstructions further contribute to this interdisciplinary framework by identifying environmental disruptions that may have driven population movements or facilitated the introduction of new genetic lineages [51].

Crucially, aDNA findings sometimes challenge earlier archaeological interpretations. In Central Mexico, genomic data indicate that severe droughts around 1100 years ago did not lead to the replacement of local populations by nomadic outsiders. Instead, indigenous groups appear to have persisted, suggesting social resilience and the role of robust kin networks in ensuring survival under extreme conditions [51]. In regions such as the Tibetan Plateau and the Altai Mountains, ancient DNA reveals waves of admixture that correspond with evidence of high-altitude adaptation, demonstrating that kin-based groups incorporated new genetic lineages over time [52]. These cases illustrate the power of an integrative approach that combines genetics, archaeology, linguistics, and paleoenvironmental studies. By synthesizing multiple lines of evidence, researchers can develop a more nuanced understanding of human history, capturing the complexities of migration, adaptation, and social organization beyond what any single discipline can reveal alone.

4. Ethical Considerations and Challenges

The ability of aDNA research to uncover personal and ancestral information raises significant ethical concerns. While genetic data can confirm biological kinship, many societies define kinship through social and symbolic relationships—such as adoption, godparenthood, or communal affiliations—that remain undetectable through genetic testing alone [53]. Overreliance on genetic data risks marginalizing the lived experiences of past people by conflating biological ancestry with social identity [3]. The extraction of DNA from human remains also necessitates respect for descendant communities. Cases such as the Kennewick Man/Ancient One in North America and other contested remains highlight the importance of transparent communication and collaborative decision-making with Indigenous and local stakeholders. Researchers should obtain necessary permissions, respect reburial requests when appropriate, and recognize that some communities prioritize cultural interpretations of ancestry over genomic ones. Ethical best practices emphasize an approach that integrates community perspectives rather than privileging scientific analysis alone [54].

A further challenge concerns the public presentation of results. Simplistic framings of aDNA findings—such as defining entire populations by a particular haplogroup or suggesting that social behaviors are "genetically encoded"—risk reinforcing misconceptions about biology, race, and identity [54]. Scholars increasingly stress the importance of careful language and context-sensitive interpretations, ensuring that genetic data are presented as one component within the broader framework of human history.

Looking ahead, emerging techniques such as epigenetic and proteomic analyses of aDNA may provide new insights into ancient health and dietary patterns. However, these expanding research avenues also introduce additional ethical considerations regarding privacy and the respectful treatment of human remains. As the field advances, integrating ethical reflexivity into scientific practice will remain essential to balancing the pursuit of knowledge with respect for past and present communities.

5. Conclusions

Ancient DNA research, driven by next-generation sequencing, has fundamentally reshaped our understanding of past societies' kinship, social organization, and migratory patterns. By analyzing genomic material from individuals interred together, researchers can reconstruct intricate family trees, identify exogamous marriage practices, and examine social hierarchies that might otherwise remain obscured. When integrated with archaeological data on burial practices, artifact distributions, isotopic analyses, and environmental reconstructions, these genetic insights provide a powerful framework for interpreting how ancient populations lived, interacted, and adapted. However, the success of aDNA studies depends not only on scientific rigor but also on ethical responsibility. Researchers must remain attentive to the perspectives of descendant communities, avoid overly deterministic narratives, and acknowledge the social and cultural complexities that genetics alone cannot fully capture. A collaborative, interdisciplinary approach ensures that genomic data enhances, rather than overshadows, the historical, cultural, and environmental contexts that shape human societies. As analytical techniques continue to advance and genomic archives of the distant past expand ancient DNA research will remain a critical and rapidly evolving field in unraveling human history's genealogical and cultural tapestry.

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Author Contributions

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