Review

Genetic History of Ancient Xinjiang Revealed by Ancient DNA Study: A Hub of Eurasian Population Migration and Cultural Exchange

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ABSTRACT: Xinjiang, a “genetic crossroads” of Eurasia, offers critical insights into transcontinental population migrations, cultural exchanges, and genetic fusion. This review synthesizes ancient genomic data from about 200 individuals (from the Bronze Age to the Historical Era), alongside archaeological, paleo microbial, and environmental evidence. Key findings include: (1) Bronze Age genetic heterogeneity: Tarim Basin populations (e.g., Xiaohe culture) retained high Ancient North Eurasian (ANE) ancestry, while northern Xinjiang groups exhibited tripartite admixture among ANE, Afanasievo pastoralists, and Baikal hunter-gatherers; (2) Stratified admixture patterns emerged during the Iron Age to Historical Era, shaped by Xinjiang’s “barrier-and-connection” geography traits; (3) Trans-Eurasian interactions were propelled by technological diffusion (e.g., metallurgy), socio-political transformations (e.g., Silk Road governance), and adaptive strategies (e.g., lactose fermentation), positioning Xinjiang as a nexus of Eurasian mutil-connectivity. Our synthesis bridges genetics, archaeology, and environmental clues, highlighting Xinjiang’s critical role in Eurasian population dynamics. Future research should employ high-resolution spatiotemporal sampling and interdisciplinary approaches to unravel genetic-societal coupling during vital historical phases (e.g., Xiongnu expansion) and molecular mechanisms of environmental adaptation.

Keywords: Ancient DNA; Xinjiang; Population dynamics; Silk Road

1. Introduction

Xinjiang, located at the heart of the Eurasian continent, serves as a crucial corridor connecting surrounding civilizations. The region’s unique geography is shaped by the Tianshan Mountains, which run from east to west. These mountains divide Xinjiang into two distinct areas: the Dzungarian Basin in the north and the Tarim Basin in the south. This natural division creates a wide range of environments across the region. The grasslands in the north are well-suited for pastoralism, while the oases in the south support irrigation farming. To the west, the Tianshan Mountains connect Xinjiang to the Eurasian Steppe. To the east, the mountains link to the heart of East Asia through the Hexi Corridor. This geographical diversity attracted people with different subsistence to migrate and settle [1]. Over time, Xinjiang also became a ‘genetic bridge’ that helped exchange culture and ideas between the East and the West [2]. In Xinjiang, barley and wheat from West Asia came into contact with millet and rice from East Asia [3]. Livestock such as cattle and horses also spread across Eurasia through this region [4]. Thanks to its rich mineral resources, Xinjiang became a key center for the spread of metalworking technologies as well [5]. Geographic barriers like deserts and mountains naturally isolate local populations. Meanwhile, the oasis-pasture corridors allowed the interaction of technologies, languages, and genes across Xinjiang. This delicate balance of barrier and connection’ makes Xinjiang a key location for studying Eurasian population migrations and cultural exchanges over time.

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Genetic studies of modern populations in Xinjiang have begun to uncover complex patterns of exchange and adaptation over time. In 2017, Xu et al. discovered that the Uyghur population in Xinjiang resulted from several admixture events between Eastern and Western Eurasian populations, leading to a northeast-southwest genetic differentiation within the Uyghur population [6]. In 2023, Xu et al. conducted a study on the genetic structure of a broader range of populations in Xinjiang, including Kazakh, Uyghur, and Hui. They also explored genomic and transcriptomic features in greater detail. The study showed that the higher proportion of East Asian-related ancestry influenced the frequency of genes associated with phenotypic traits, such as EDAR. At the transcriptomic level, the more balanced genetic contributions from different populations resulted in higher levels of gene expression regulation. Additionally, population-specific environmental adaptations played a key role in shaping immune and metabolic function adaptations. The geographical features of Xinjiang's mountain basins create natural barriers that isolate populations, and the unique genetic histories of these isolated groups make Xinjiang a key research hotspot [7]. In 2025, Xu et al. studied the genetic evolution of the Lop Nur people, an isolated group in southern Xinjiang, and examined the evolutionary genetic mechanisms behind hypertension. They found a predominant admixture pattern of Western males and Eastern females. The population had been completely isolated until about 300 years ago, after which it began genetic exchanges with surrounding groups. The long-term desert environment drove the diversity of the UGT2B17 gene family, which is linked to toxin metabolism and energy balance. Meanwhile, the high-salt, high-fat diet created strong selection pressure on lipid metabolism pathways [8].

While genetic research has shed light on the admixture and adaptation of modern Xinjiang populations, its conclusions are limited when attempting to trace deeper historical events. For populations in Xinjiang, which have been intermingling for thousands of years, early admixture events are often obscured by later hybridization. Modern genomics cannot fully reconstruct extinct ancient genetic branches or precisely identify the evolutionary nodes of key genes. Ancient DNA, with its unique 'time scale' attribute, allows for direct analysis of the ancestral components' sedimentation process at different historical stages. It can trace the evolutionary trajectory of functional genes and connect phenotypic adaptations to specific environmental pressures of particular periods. This spatiotemporal depth makes ancient DNA an essential tool for reconstructing the genetic history of Xinjiang's populations, particularly in unraveling the complex relationships between language spread, technological diffusion, and population migration. The study of ancient populations in Xinjiang has developed alongside advancements in ancient DNA (aDNA) research. In 1984, Higuchi et al. first extracted ancient mitochondrial DNA from preserved Quagga specimens [9]. The following year, Svante Pääbo obtained mitochondrial DNA from an Egyptian mummy [10]. Mitochondrial DNA, with its high copy number and maternal inheritance, provides high-quality data for tracing maternal genetic history [11]. During this period, studies of ancient populations in Xinjiang also focused on mitochondrial DNA. Cui et al. sequenced the highly variable regions of mitochondrial DNA. They performed SNP genotyping of the coding regions from individuals at the Shampula, Yuansha, and Niya sites in the Tarim Basin, dating back to around 2200–2000 BCE [12]. The data indicated that ancient populations in the Tarim Basin were formed through the fusion of East and West Eurasian lineages, which had already differentiated. This marked the first significant attempt to understand the genetic history of Xinjiang's populations using genetic data, laying the foundation for aDNA research in the region. However, mitochondrial DNA can be affected by back mutations and parallel mutations, which can significantly complicate the construction of phylogenetic trees.

With the advancement of Polymerase Chain Reaction (PCR) and next-generation sequencing, aDNA research progressed rapidly. Since then, integrating aDNA data with multidisciplinary approaches to analyze the genetic interactions of ancient populations has become a central focus of research. To accurately reconstruct the genetic history of Xinjiang's populations, it is essential to place them within the broader context of Eurasian population history.

2. Advances in Eurasian Population History: The Foundation of Ancient Population History in Xinjiang

Eurasian populations have followed distinct genetic differentiation trajectories since the Late Pleistocene. Early European hunter-gatherers exhibited different genetic structures, with southwestern populations maintaining genetic continuity for over 20,000 years, while populations in central and southern Europe were replaced by another group of hunter-gatherers from the Balkan region after the Last Glacial Maximum. This regional differentiation persisted until the Neolithic Revolution, when Anatolian farmers spread agricultural practices through genetic admixture with local hunter-gatherers [13,14]. The Bronze Age witnessed transformative population movements driven by the Yamnaya pastoralists, who originated from the Pontic-Caspian steppe [15–19].

The expansion of the Yamnaya population not only reshaped the genetic landscape of Europe but also extended across Eurasia to Mongolia, spreading advanced pastoral technologies and Indo-European languages. Before the arrival of Steppe-related populations, eastern Eurasia was already home to diverse hunter-gatherer and agricultural communities. These included the Ancient North Eurasian (ANE) populations. ANE ancestry refers to a genetic component linked to Upper Paleolithic hunter-gatherers from northern Eurasia, which contributed to populations across Eurasia and the Americas [20], the Ancient Northeast Asian (ANA) populations in the Russian Far East, the Ancient Palaeo-Siberian (APS) groups formed through their admixture [21], and the YR_MN populations from the Yellow River Basin in East Asia during the Neolithic [22]. In southern Central Asia, the Neolithic Geoksyur_EN populations emerged through admixture between Anatolian farmers, Iranian farmers, and Western Siberian hunter-gatherers (WSHG), and later incorporated ancestry from Andamanese hunter-gatherers (AHG), eventually contributing to the formation of the Bactria-Margiana Archaeological Complex (BMAC). BMAC denotes a Bronze Age civilization in Southern Central Asia, characterized by urban communities, and mainly genetic links to Iranian farmers [15]. The arrival of steppe pastoralists around 2000 BCE triggered a significant genetic turnover across the region. Late Bronze Age (LBA) technological innovations, particularly chariot warfare, facilitated the rapid expansion of Sintashta-related populations from the Ural Mountains. These populations carried enhanced European farmer ancestry and expanded eastward to establish the Andronovo cultural complex, significantly increasing the presence of western steppe genetic components throughout Eurasia [15,18]. The Iron Age and the Historical Era were pivotal periods of increased circulation across Eurasia, significantly shaping the genetic structure of modern populations. The Scythian-saka populations that dominated the Eurasian steppe during the Iron Age had a significantly different genetic structure, which was related to the geographic location. The Hungarian Scythians in Europe mixed European farmer ancestry with that of Late Bronze Age steppe populations, while the Inner Asian Sakas exhibited significantly different genetic structures depending on their geographic location. The Targar culture population in southern Siberia formed from admixture between LBA Steppe populations, Baikal hunter-gatherer populations (admixture of ANE and ANA related populations), and Paleolithic MA1 (ANE-related population), whereas the Central Asian Tasmola culture population lacks MA1-related genetic component; closer to southern Central Asia, the TianshanSaka populations require additional Neolithic Iranian-related ancestry instead of ANE-related ancestry [23]. This suggests that population mobility increased during this period, but with clear regional specificity.

The emergence of the Xiongnu confederation in the eastern Eurasian steppe exhibited genetic heterogeneity. In the late Xiongnu and historical periods, the continuous westward migration of the Xiongnu people led to further genetic mixing between various nomadic empires across the Eurasian steppe [23,24]. This mixing, however, saw a gradual increase in eastern Eurasian-related ancestry. The genetic pattern of east-west differentiation and north-south intertwining across Eurasia provides an indispensable reference for studying populations in Xinjiang as a contact zone.

3. Paleogenetic Insights into the Genetic History of Xinjiang Populations

Recent advances in aDNA have greatly enhanced our understanding of the complex population dynamics in Xinjiang, providing unprecedented insights into Eurasian demographic history. This review systematically examines the dynamic evolutionary history of populations in Xinjiang from the Bronze Age (BA) to the Historical Era (HE), drawing on published ancient genomic data from hundreds of individuals (Figure 1). We also elucidate the potential driving factors behind the formation of regional differences, evaluate Xinjiang's critical role as a key hub in ancient Eurasian population interaction, and provide a theoretical framework and foundation for future interdisciplinary studies in ancient genomics.

The earliest evidence of human presence in Xinjiang dates back to about 45,000 years ago at the Tongtian Cave site in Altai [3], although human remains are only found dating back to approximately 5000 BP. The genetic structure of the earliest inhabitants of Xinjiang has been a topic of intense debate among researchers, with both the steppe hypothesis and the oasis hypothesis being proposed [25]. However, the discovery of aDNA studies has provided a completely new answer to this crucial question. In 2021, Zhang et al. reported genetic data on the earliest populations in Xinjiang, revealing that the ancient populations in southern and northern Xinjiang exhibited distinctly different patterns of genetic evolution. Populations from three contemporaneous sites in the Tarim Basin in southern Xinjiang exhibit a high degree of genetic homogeneity. The Xiaohe culture populations display a significant proportion of Paleolithic ANE-related genetic components, with little evidence of recent admixture from steppe nomadic or agricultural populations from southern Central Asia. This stands in stark contrast to the agricultural and dairy livestock economy uncovered at the site [26]. This suggests that the Bronze Age populations in southern Xinjiang maintained a strict genetic barrier and were connected to neighboring groups primarily through cultural exchange. The discovery of the ANE ancestry in Xinjiang not only clarifies the genetic structure of initial populations but also extends the known distribution of ANE-related groups across Eurasia. In contrast, Bronze Age populations in northern Xinjiang exhibited a three-way admixture involving ANE-related ancestry, Early Bronze Age steppe populations (Afanasievo/Yamnaya), and hunter-gatherers from the Baikal region [26]. The later Chemurchek population near the Altai Mountains also showed genetic admixture from BMAC-related groups, highlighting the Inner Asian Mountain Corridor (IAMC) as a key conduit for rapid population and cultural transmission [18,27]. Despite the discovery of Chemurchek cultural sites in other parts of northern Xinjiang, the lack of genomic data hampers a comprehensive understanding of the dispersal routes of the BMAC-related population along the IAMC, as well as the patterns of their distribution within Xinjiang.

During the Middle to Late Bronze Age (MLBA), steppe populations near the Ural Mountains emerged with advanced technologies in chariotry and metallurgy. These groups, characterized by increased European farmer ancestry, subsequently expanded eastward, giving rise to the genetically related Andronovo populations. Archaeological evidence suggests that, compared to the Early Bronze Age (EBA), Late Bronze Age (LBA) Xinjiang experienced more widespread influence from western Eurasian steppe pastoralists, particularly the Andronovo culture population, which was concentrated in the western Tianshan region and expanded eastward [28]. Ancient DNA analysis of seven individuals from the Ili River Valley reveals considerable genetic heterogeneity, indicating early stages of population admixture. These LBA populations retained genetic components from EBA ancestries—including Xiaohe, BMAC, Northeast Asian hunter-gatherers, and Afanasievo ancestry—while incorporating substantial ancestry from LBA Steppe nomads, confirming the simultaneous cultural and genetic influence of these groups on Xinjiang [29]. As a key region within the Andronovo Culture Complex, Xinjiang plays a crucial role in understanding the development of Late Bronze Age pastoralism across Eurasia. However, the limited availability of genomic data hampers a comprehensive understanding of the distribution, genetic differentiation, and interactions of Andronovo-related populations within Xinjiang, as well as their broader connections to the Eurasian steppe. In particular, it remains unclear whether the populations of southern Xinjiang, who maintained a genetic barrier during the EBA, were later influenced by the rapidly expanding LBA Steppe populations., Additionally, considering the advanced metallurgical technologies mastered by the LBA Steppe populations and the rich metal resources in Xinjiang, their distribution, expansion, and social organization in the region were likely closely tied to mining and metallurgy. Addressing these questions is crucial not only for understanding the differential impacts of Early and Late Bronze Age populations on Xinjiang but also for gaining insight into the formation and development of diverse nomadic groups in the region during the Iron Age.

In contrast to the significant influence of Western Eurasian populations during the Bronze Age, the Iron Age across much of Eurasia is marked by a widespread increase in East Eurasian ancestry [23]. Distinct from contemporaneous populations elsewhere on the continent, Iron Age populations in Xinjiang show a marked increase in ancestry related to Neolithic farmers from the Yellow River Basin. Genetic analyses have revealed up to 80% Yellow River-related ancestry in Iron Age individuals from central and southern Xinjiang [30,31], underscoring the significance of the eastern Tianshan region and the Hexi Corridor as key hubs facilitating interactions between East Asian farmers and steppe pastoralists. In addition to the prominent East Asian component, steppe-related ancestry in Iron Age Xinjiang populations displays considerable regional heterogeneity. At the Shirenzigou site in eastern Xinjiang, genetic data reveal the continued presence of EBA steppe ancestry linked to the Afanasievo population [32]. This discovery offers fresh insights into the genetic history of Xinjiang and calls for a reassessment of the expansion of early steppe populations and the continuity or replacement of steppe ancestries in particular regions. Ancient genomic studies have also confirmed the genetic similarity between Iron Age populations in Xinjiang and various Eurasian steppe nomadic groups, indicating extensive interactions with Scythian populations during this period. The genetic impact of various Scythian populations on different regions of Xinjiang may have varied. Moreover, the genetic affinity between Xinjiang populations and the BMAC-related agricultural populations became more pronounced [29]. Driven by both steppe nomadic and agricultural populations, cultural exchanges accelerated across the continent, with Xinjiang serving as a central mediator. This exchange facilitated the spread of production techniques, burial customs, and other cultural practices, establishing a comprehensive and interconnected network of interactions. This network likely laid the foundation for the precursor to the Silk Road, which later enabled the establishment of the Silk Road during the Han Dynasty. As a result of these frequent exchanges, population genetic structures became increasingly homogeneous, complicating efforts to obtain detailed genetic histories. Therefore, innovative methodologies are essential to reconstruct population connection networks using high-quality genomic data.

Due to Xinjiang's strategic geographical location and its active population interactions, the Han Dynasty established the Silk Road, a trade route stretching from Luoyang to the Mediterranean. The Silk Road, centered in

Xinjiang, saw multiple routes converging in the region. The opening of these routes significantly facilitated the exchange of culture and the flow of genetic material between East and West Eurasian populations through Xinjiang. During this period, the genetic makeup of populations in Xinjiang continued to reflect the mixed model established during the Iron Age. The majority of individuals can be modeled as a mixture of Steppe, BMAC, and East Asian-related ancestry. Notably, Xiaohe-related ancestry persists in the populations of Xinjiang during the Historical Era. This suggests that, despite the extensive movement fostered by the opening of the Silk Road, the genetic structure of populations in Xinjiang maintained a degree of continuity [29]. Meanwhile, to ensure the stability of the Silk Road, the Han Dynasty and subsequent rulers implemented policies such as the establishment of military garrisons and the promotion of agricultural settlements in the region. These measures had a profound impact on the population structure and lifestyle. Dietary patterns also show distinctions between agricultural and pastoral groups. However, both groups shared the same burial site, indicating a deep integration between these distinct populations [33]. The genetic structure of populations in Xinjiang underwent significant changes, with a notable increase in East Asian components during the Historical Era. This dynamic and stable mixed pattern reflects the ongoing, rather than explosive, nature of population mobility driven by Silk Road trade. With a clearer understanding of the primary genetic characteristics of historical Xinjiang populations, future research should focus on refining the details. This can be achieved by fully leveraging ancient DNA technology and integrating findings from other disciplines to deepen our understanding of population genetic history and societal structures during the Historical Era. This is particularly important in relation to the Silk Road, which had a profound influence on the entire Eurasian continent (Figure 2).

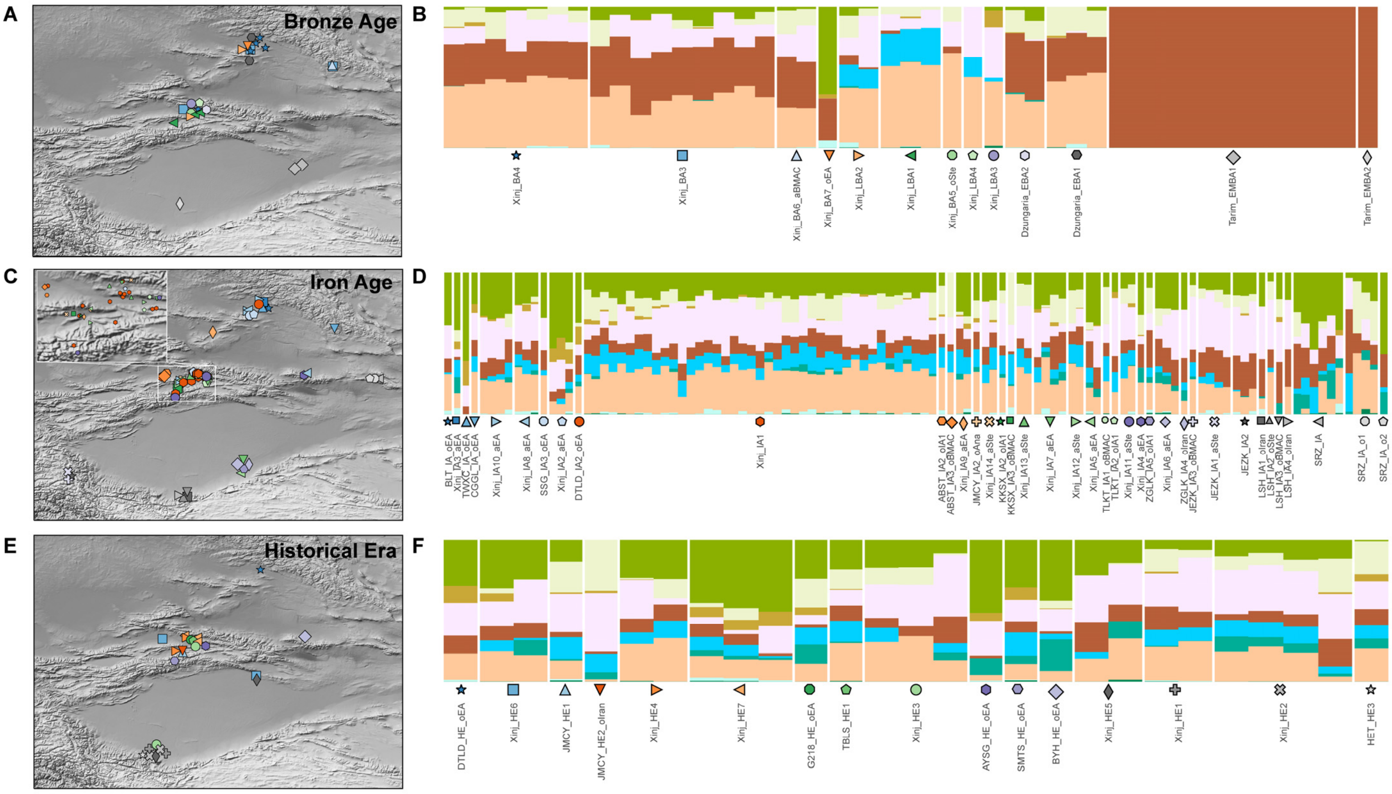

Figure 1. The geographic distribution and genetic structure of published ancient Xinjiang populations from Bronze Age to Historical Era. (**A**). Geographic location of ancient individuals during the Bronze Age. (**B**): ADMIXTURE analysis of ancient individuals during the Bronze Age. (**C**). Geographic location of ancient individuals during the Iron Age. (**D**): ADMIXTURE analysis of ancient individuals during the Iron Age. (**E**): Geographic location of ancient individuals during the Historical Era. (**F**): ADMIXTURE analysis of ancient individuals during the Historical Era. In (**B**), (**D**) and (**F**), the six major color are maximized in the following populations: brown (ANE), green (ANA), blue (Sardinian), cyan (Ami), yellowish (Steppe_EMBA), light green (Namazga_CA).

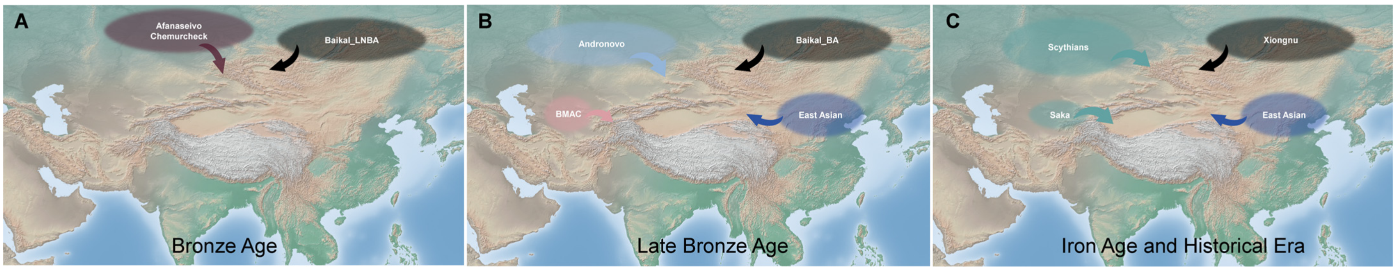

Figure 2. The genetic history of Xinjiang populations in the context of population dynamics in Eurasia. (**A**). Population dynamic during the Bronze Age. (**B**). Population dynamic during the Late Bronze Age. (**C**). Population dynamic during Iron Age and Historical Era.

4. Driving Force behind Population Migrations and Cultural Diffusion in Xinjiang under the Trans-Eurasian Context

Xinjiang has distinctive geography, characterized by a mosaic of basins and mountain ranges, forming natural networks of oasis corridors and steppe routes that facilitated sustained exchanges among diverse subsistence communities. Existing research underscores that a comprehensive understanding of Xinjiang's population history is crucial for reconstructing broader patterns of human genetic legacy across Eurasia. It also sheds light on the intricate interplay between human populations, environmental conditions, subsistence strategies, and social organization throughout history. Throughout human history, changes in subsistence strategies and major technological innovations have frequently coincided with shifts in genetic structure, catalyzing migration and cultural transmission. Population movements across different periods were shaped by diverse and evolving drivers, resulting in varied migration dynamics. This review synthesizes insights from ancient genomic studies to explore these potential driving forces and identifies key unresolved questions, outlining future directions for aDNA research in the region.

4.1. Bidirectional Drivers of Technological Diffusion and Economic Demand

The bidirectional forces of technological transmission and economic demand have been pivotal in shaping human migration and cultural exchange across Eurasia. From the early use of stone tools in the Paleolithic to the agricultural transformations of the Neolithic and the advent of metalworking in the Bronze and Iron Ages, each major technological milestone not only improved practical capabilities but also triggered far-reaching changes in social structures and interregional connectivity. These shifts supported increased human mobility, emerging occupational specializations, and the expansion of trade networks. Given its geographically diverse landscape, ranging from fertile oases to steppes, Xinjiang provided a conducive setting for a variety of subsistence strategies, thus becoming a central nexus for technological diffusion and cultural convergence.

During the transition from the Bronze Age to the Iron Age, Xinjiang's role in the Eurasian metallurgical network became increasingly prominent, as evidenced by numerous metallurgical remains [34]. The earliest evidence of pure copper and copper smelting slag at the Narensu site suggests that northern Xinjiang communities had developed localized metallurgical practices as early as the Early Bronze Age [35,36]. The Ural Mountains, a key early metallurgical hub in Eurasia, served as a technological foundation for the LBA steppe nomads. Driven by a mix of climate change, resource pressures, and the expansion of pastoralism, these nomads migrated eastward from the Urals and Central Asia into Xinjiang, carrying with them metallurgical knowledge that facilitated the integration and adaptation of bronze technology in the region [37]. Xinjiang's steppe-based metallurgical communities took advantage of local metal deposits and natural resources to produce weapons, tools, and other metal goods. By blending metallurgical practices with pastoralism and agriculture, these communities developed a complementary subsistence and technological system. As the Iron Age progressed, Xinjiang emerged as a convergence zone for multiple metallurgical traditions, resulting in a regionally distinctive metallurgical system. Through processes of localization and innovation, Xinjiang cultivated specialized crafts and material exchange networks, establishing itself as a key hub connecting Eastern and Western Eurasia. Metal objects became central to cross-regional exchanges, paving the way for the early trans-Eurasian trade routes—precursors to the Silk Road—that emerged within the context of metallurgy and migration.

4.2. Social Structure and Cultural Exchange as Drivers of Change

The development of metalworking technology played a key role in changing the social structure of the Eurasian steppe. In the Bronze Age, the Afanasievo culture already showed signs of social differences. However, these were more likely based on spiritual authority, such as rituals and ancestor worship, rather than economic wealth. As time passed, particularly with the Sintashta culture and nearby groups, the growth of metalworking techniques led to clearer divisions of labor [37]. These divisions likely formed around household production, metalworking specialists, or specific technical groups. This process marked the early stages of a social hierarchy based on labor. During the Iron Age, different nomadic states began to form across the Eurasian steppe, leading to more distinct social hierarchies. Political power during this time was reflected not only through military conquests and control of land but also through the management and competition for resources and trade routes. Xinjiang became an important region for interactions between various political groups. The Han Dynasty, for example, used both military force and political alliances, like the “heqin” (marriage alliance) policy, to strengthen their position. They built on the proto–Silk Road’s trade networks and officially established the Silk Road as a major trade route. To ensure the security of these routes and stabilize the border, the Han set up military-administrative systems, such as garrison settlements and the Western Regions Protectorate [38]. The development of political and economic systems had a significant influence on the genetic makeup of Xinjiang. During the Iron Age and later periods, southern Xinjiang and the eastern Tianshan region began to show genetic signs of mixing with Yellow River farming populations [30]. This reflects the integration of agricultural settlers with local communities after the Han dynasty took control. However, there is still a lack of detailed studies on the social organization of populations from the Bronze to early Iron Age, particularly regarding how social stratification and kinship structures were reflected in genetic data. While much has been written about the Silk Road, research on ancient DNA from its institutionalized phase is still in the early stages. Current studies have limited coverage in both time and geography, with too few samples to allow for in-depth analysis of social evolution. Future research should focus on collecting time-series data, examining a variety of site types, and ensuring a broader range of samples. This would help create a more complete model that integrates social structures, political networks, and genetic interactions.

5. Insights and Future Directions of Ancient Genomic Studies in Xinjiang

Genetic studies of ancient populations in Xinjiang have confirmed its significant role in exploring cultural exchanges between East and West Eurasia. Xinjiang is connected to several corridors for the rapid migration of populations, such as the Inner Asian Mountain Corridor in the west and the Hexi Corridor in the east. Collectively, these corridors have facilitated the exchange of populations; however, Xinjiang performs different functions from these corridors. In contrast to the high altitude of the Inner Asian Mountain Corridor and the Gobi Desert of the Hexi Corridor, the expansive geographic area of Xinjiang, interspersed with numerous oases and grasslands [1], offered conducive long-term development sites for pastoralism and agriculture, thereby facilitating genetic fusion and cultural exchange. Xinjiang and the Hexi Corridor, which also served as important parts connecting East and Central Asia and subsequently the Silk Road, are genetically distinctly different. From the Bronze Age to the historic period in Xinjiang has shown genetic admixture of East and West Eurasian populations [29], whereas the ancient populations of the Hexi Corridor region have maintained genetic continuity with East Asian populations, only a few individuals show genetic affinity with Western Eurasian populations [39]. The 5000-year genetic continuity in Xinjiang has transformed our understanding of population integration across Eurasia, emphasizing that admixture, rather than replacement, has been the primary process in human evolution on the continent. This ongoing interaction is deeply influenced by Xinjiang’s unique geography, ecological variety, and intricate social structures, making it a key region for studying migration and cultural exchange.

However, there are still significant gaps in our understanding, particularly regarding Xinjiang’s interactions with the broader Eurasian context, which have not been systematically or precisely analyzed. Ancient genomic studies show that by the Late Bronze Age to the Iron Age, populations in northern and western Xinjiang had developed a variety of physical traits linked to Eurasian ancestry. For instance, lighter hair and skin pigmentation were present in the Late Bronze Age, and traits like blue eyes appeared during the Iron Age, characteristics typically associated with Western Eurasian ancestry. As time passed, especially in later historical periods, genetic influences from East Asia, South Asia, and Central Asia became more prominent, leading to a shift toward darker hair and eye colors [29]. This change in physical traits reflects not just shifts in genetic composition but also environmental selection pressures. Such genetic diversity likely played a crucial role in helping ancient populations adapt to a variety of ecological environments, contributing to their long-term survival. Genetic studies of plants and animals in Xinjiang provide valuable insights into the complex relationship between human technological practices and biological evolution. While Bronze Age populations were mostly lactose intolerant, they used lactic acid fermentation to reduce the lactose in dairy products, an example of gene-culture co-evolution. Over time, lactic acid bacteria adapted, developing resistance mechanisms that reflect long-term human–environment interactions [40]. Domesticated plants and animals from both Eastern and Western regions met and spread through Xinjiang, with ancient DNA studies of wheat and horses offering new evidence of these exchange processes [41,42].

Additionally, research on ancient pathogens has shed light on the links between population health and migration routes. For example, at the Quanergou site, a Bronze Age population carried a strain of Salmonella enterica that had acquired the virulence factor Paratyphi C. Studies on hepatitis B virus (HBV) further reveal that Xinjiang acted as a crossroads for multiple genotypes (A, B, D, and WENBA), with genotype D likely emerging from recombination between genotypes A and WENBA [43].

Overall, Xinjiang serves as a vital link in trans-Eurasian migration and cultural exchange, playing a central role in the co-evolution of genes, microbes, and environmental adaptation. From the evolution of physical traits and dietary practices to the development of microbes and the spread of pathogens, Xinjiang's history offers a unique perspective on human evolution and the integration of civilizations across Eurasia. Future research should focus on clarifying connections with different parts of Eurasia and mapping the specific routes and mechanisms of population movement, admixture, and diffusion over multiple spatial and temporal scales. Key areas for further exploration include: (1) investigating how the integration of populations with varying subsistence strategies influenced social organization; (2) reconstructing detailed genetic changes around key historical moments, such as the rise of the Silk Road; and (3) integrating genomic and phenotypic data to explore the molecular underpinnings of disease susceptibility and environmental adaptation, shedding light on the co-evolution of genes, culture, and ecology. Through interdisciplinary collaboration, future research in Xinjiang will provide essential insights for reconstructing the human evolutionary network across Eurasia.

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Author Contributions

Conceptualization, Y.C., X.Z. and R.S.; Validation, Y.C., X.Z., R.S. and C.L.; Writing—Original Draft Preparation, Y.C., X.Z. and R.S.; Writing—Review & Editing, Y.C., X.Z. and R.S.; Visualization, X.Z. and R.S.; Supervision, Y.C. and C.L.; Funding Acquisition, C.L.

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Not applicable.

Informed Consent Statement

Not applicable.

Data Availability Statement

We did not generate new data.

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Author Statement

During the preparation of this work, the authors used DeepL in order to improve readability and language. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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