



Utilization of wild animal resources on the silk road: Ancient DNA study on *Saiga tatarica* unearthed from Tangchaodun Ruins

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ABSTRACT

The utilization of animal resources caters to human material needs for survival and development, reflecting the evolutions of culture and social structure, technological advancement, and the dynamics of human-environment relationship. The present ancient DNA study analyzes four samples excavated at Tangchaodun Ancient City Site which were morphologically identified as sheep. Alignment analyses, phylogenetic analyses, and genetic distance calculations reveal that these samples belong to the nominate subspecies of the Saiga antelope. In a broader sense, the results and findings of this study further confirmed the promising future of ancient DNA technology as a state-of-the-art method in subspecies identification and classification. Mitochondrial D-loop region analysis indicated that the ancient Saiga antelope population had remarkably high genetic diversity and thus a more complex population structure than its contemporary one. This finding offers valuable insights into historical distribution and conservation of Saiga antelope. From the perspective of historical geography, since ancient Saiga antelope population was discovered in Tangchaodun ruins, it's deduced that the ancient residents there might have hunted and used the Saiga antelope to obtain materials for living and production. Specifically, as suggested by archaeological findings and recorded documents, the excavated Saiga antelope horns might be for medical and aesthetic uses. The findings and deductions made thereby provides clues about the hunting, tribute, and trade activities in that period, which helps draw a full picture of the economic and cultural exchanges along the Silk Road at that time.

1. Introduction

Located at the northern foot of the Eastern Tianshan Mountains, Tangchaodun Site was an important political-military establishment and transport hub during the Tang Dynasty (618–907 CE). It was built during Emperor Taizong's "Zhenguan" reign (627–649 CE) and remained in use through the Gaochang Uyghur Kingdom (843–1275 CE), the Western Liao Dynasty (1124–1218 CE), and the Yuan Dynasty (1271–1368 CE) (Wei and Zheng, 2022), but was gradually abandoned during the Chagatai Khanate (1227–1346 CE) in the 14th century due to numerous wars (Wei et al., 2023). The city's eastern wall aligned with the natural river course, while the other three walls were straight, making it roughly rectangular. The name "Tangchaodun" derives from the elevated platform at the center of the northern wall (Ren and Wei, 2021). Since 2018, archaeological excavations have revealed the site, with various artifacts and remnants unearthed. The site's sedimentary layers show multiple

historical periods, and the sorted pottery evolution sequence from the Tang to Yuan Dynasties has enhanced the understanding of the cultural features of the remains (Wei and Zheng, 2022). Multiple architectural relics witnessed the cultural interactions and integrations along the New Northern Route of the Silk Road, as well as religious and ethnic amalgamation in Xinjiang. A prominent one is a Tang Dynasty Buddhist temple complex in the city center, facing east and sitting west, used until the Gaochang Uyghur Kingdom and the Yuan Dynasty. In central north Tangchaodun, a Nestorian church site with two architectural clusters and abundant wall paintings was discovered, which is academically significant due to its historical, religious, and cultural implications (Ren and Wei, 2022). Also, a Roman-style semi-subterranean bathhouse with two tiers of chambers was found in the city's northeast. It incorporated Central Plains attributes in its original design, was established in the Gaochang Uyghur era, underwent renovation, and remained in use until the Yuan Dynasty. Additionally, a Tang courtyard that might have

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served as an official storage facility was excavated.

After the unification of the Western Regions in Tang dynasty, the “Steppe Route of the Silk Road” (Zhang and Dang, 2023), which ran along the northern foothills of the Tianshan Mountains with Tingzhou as its center, extended eastward to Yizhou and westward to Suiye. The Northern Route along the northern foot of the Tianshan Mountains functioned as an important passage for trade and military defense, which brought about convergence, clash and blending of nomadic and agricultural civilizations there (Yang, 2017). From the perspective of zooarchaeology, the studies on the subsistence economy of ancient cities along the Silk Road on the northern slope of the Tianshan Mountains have laid particular emphasis on domestic animals, yet relatively little research has been conducted regarding the utilization of wild animal resources. (Ling et al., 2016; Wang et al., 2021; Dong et al., 2022; Li et al., 2022). In fact, wild animals served as important sources of meat and fur, and their bones, teeth, and horns could be used as rare medicinal materials and for high-quality handicrafts (Song et al., 2025). Especially along the Silk Road, wild animals and their by-products were indispensable in promoting commodity trade and exchanges (Yang, 2009). Given the importance of wild animal resources to economic and social development in ancient dynasties, this study conducted an ancient DNA analysis of morphologically identified “sheep” samples to further identify the species and, more broadly, uncover new findings regarding the economic and social development in ancient regions along the Silk Road. In the early archaeological work, the four unearthed samples were initially identified as sheep through the method of morphometrics. However, morphometric identification is limited by factors such as the preservation state of samples and the overlap of species' morphological characteristics, and its results may be subject to deviations—especially when the morphological similarity between the bones (such as horns) of wild animals and domesticated animals is relatively high, it is difficult to achieve accurate distinction relying solely on morphological features (Wang and Joris, 2023). To verify this preliminary identification conclusion and clarify the species classification, this study further analyzed the samples using ancient DNA technology. The results showed that they were actually the remains of Saiga antelopes.

The saiga antelope (*Saiga tatarica*), a critically endangered antelope that once inhabited a vast area of the Eurasian steppe in antiquity, belongs to the class Mammalia, order Artiodactyla, family Bovidae (Wu, 1997). The saiga antelope possesses therapeutic properties. (Meng and Wang, 1999). Adults feature an elongated nose and an anterior part curling slightly downward, and are often called the “high-nosed antelope” due to its distinctive morphological traits. China is one of the native habitats of the saiga antelope. During antiquity, northwestern Xinjiang, western Inner Mongolia, and northwestern Gansu were the peripheral distribution zones of the saiga antelope in China. Due to habitat degradation, rampant poaching, and other reasons, the species has experienced dramatic population declines in China (Meng and Wang, 1999). Currently, saiga antelope are reintroduced and raised in a semi-wild state in Gansu and Xinjiang for experimental and research purposes (Olga et al., 1998). Globally, the saiga antelope is distributed mainly in the arid steppes and semi-desert areas of Central Asia, specifically in Kazakhstan, Mongolia, Russia, Turkmenistan, and Uzbekistan (Wang and Jin, 2019).

The horns of the saiga antelope are a valuable traditional Chinese medicine. They can regulate liver metabolism to maintain normal liver function, alleviate ophthalmic discomfort caused by hepatic disorders for better eye health, improve blood circulation to ensure proper nutrient and oxygen delivery, facilitate body detoxification to remove accumulated toxins, and regulate blood pressure and relieve physical pains (Zhao, 1992). Due to the significant role saiga antelope played in ancient Chinese medicine as well as its historical, ecological, and cultural implications, the distinctive species has captivated the interest of conservationists, biologists, and wildlife enthusiasts worldwide. This study conducts ancient DNA study on previously identified “sheep” remains unearthed at the Tangchaodun Site (Ren and Yu, 2020). To verify

or refute the previous identification conclusion and determine its subspecies, alignment analyses, phylogenetic analyses, and genetic distance calculations, followed by molecular genetic investigations were performed on the samples. Based on the results, relevant documents and archeological reports, the distribution, utilization and evolution of saiga antelope were discussed.

2. Materials and methods

2.1. Tangchaodun site and sample collection procedure

The Tangchaodun Site is located at the northeast corner of Qitai County, Changji Hui Autonomous Prefecture, Xinjiang, also on the Northern Route of the Silk Road which runs along the northern foot of the Tianshan Mountain range. The four samples investigated in this study (Fig. 1B) were unearthed from three excavation areas (namely Area A, Area B, and Area D) at Tangchaodun. They were morphologically identified as “sheep”, yet further investigations are called for to prove/disprove the assumption and specify its subspecies (Wang and Joris, 2023). The samples in this study were deposited at Bioarchaeology Laboratory of Jilin University. The site and the samples are shown in Fig. 1A and Table 1.

2.2. DNA extraction, library construction and high-throughput

Firstly, we use an electric sanding tool and sterilized disposable drill bits to remove 1–2 mm of the sample surface so as to minimize external contamination. After that, we soak the horns in a 10 % sodium hypochlorite solution for 15 min, rinse them with diethylpyrocarbonate (DEPC) water, and then soak them in anhydrous ethanol for 5 min. Next, we expose the samples to a UV lamp until they are completely dried. On the next day, we further sand the horns with the electric sanding tool and sterilized disposable drill bits to obtain a powder sample weighing 50–100 mg. The method for ancient DNA extraction in this study is based on the one described by Dabney (Dabney et al., 2013). We obtain the extraction solution by using the MinElute® PCR Purification Kit.

For library construction, we adapt and optimize the experimental method for Double-stranded DNA sequencing developed by the Max Planck Institute in Germany (<https://www.protocols.io/view/a-z-of-an-ancient-dna-protocols-for-shotgun-illumina-36wgq529xgk5/v2/guidelines>) (Meyer et al., 2012). Mitochondrial capture is carried out by iGeneTech Bioscience. Finally, we perform double-end sequencing using the Illumina Hiseq X Ten platform, which is a high-throughput sequencing technology.

2.3. Authenticity of the sequencing results

In accordance with the ancient DNA contamination prevention techniques (Gilbert et al., 2005; Willerslev and Cooper, 2005; Fulton, 2012), all pre-PCR procedures were conducted in a dedicated ancient DNA laboratory at Jilin University, while the post-PCR steps were carried out in a separate and geographically distant laboratory. Prior to each experiment, the workspace was exposed to ultraviolet light for 30 min. Throughout the experiment, pipettes and the super-clean table were regularly wiped with bleach. All personnel in the laboratory wore protective clothing, including sterile disposable caps, masks, and gloves. Additionally, all disposable consumables used during the experiments were DNA-free grade. To detect any potential contamination, blank controls were included at each stage of DNA extraction and amplification, all of which yielded negative results. We used MapDamage v2.2.1 (Jonsson et al., 2013) to assess damage profiles of sequenced DNA to ensure authenticity (Supplementary Fig. 1). To reduce the impact of ancient DNA damage on subsequent analyses, we performed rescale and trim processing on the sample data.

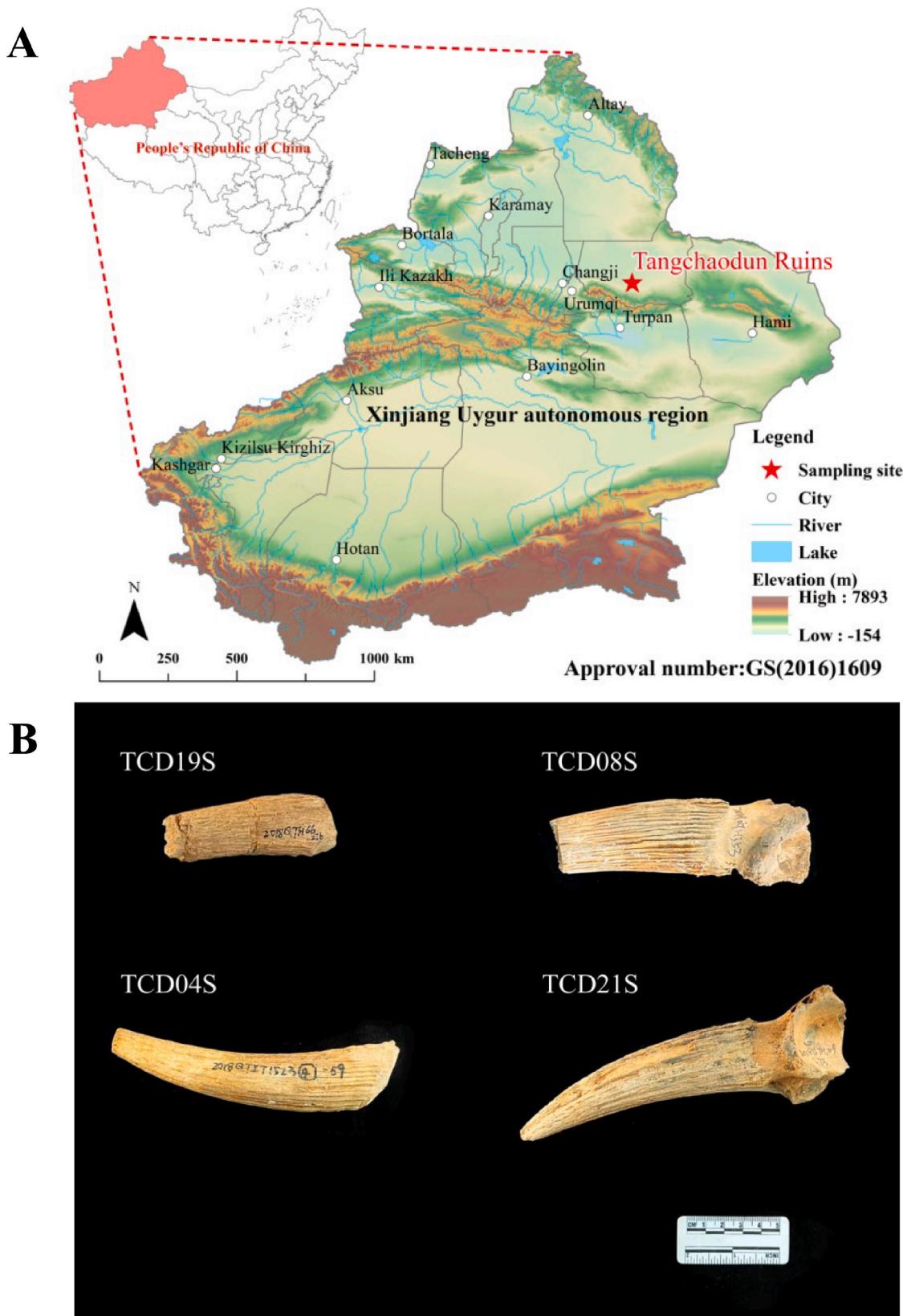


Fig. 1. (A) Location of the Tangchaodun Ruins; (B) Sample of remains analyzed in this study.

2.4. Data processing

Raw data were processed using the PALEOMIX v1.3.7 pipeline (Schubert et al., 2014). Firstly, adapter sequences were identified and

removed using AdapterRemoval v2.2.0 (Schubert et al., 2016). During the processing, reads below 35 base pairs (bp) in length were filtered out, and bases with a quality below 20 were discarded. The double-end data was then merged. A total of 149 mitochondrial genomes including

Table 1

The information concerning the ancient samples analyzed in this study.

Lab Code	Archaeological code	Element	Dynasty	Morphology	Experimental result
TCD04S	2018QTIT1523④-59	Horn	Tang ~ Yuan (618–1368 CE)	Sheep	success
TCD08S	2019QTH353-5	Horn	Tang (618–907 CE)	Sheep	success
TCD19S	2018QTH166-276	Horn	Tang (618–907 CE)	Sheep	success
TCD21S	2018QTH109-73	Horn	Yuan (1271–1368 CE)	Sheep	success

two different families of animals—Bovidae and Cervidae ([Supplementary Table 1](#))—were selected as reference sequences and aligned with them simultaneously using the BWA v0.717 aln algorithm ([Li, 2013a](#), [Li, 2013b](#)) to identify the specific species (We denote this method as separate mapping). Considering that the mitochondrial genomes of related species are similar, which may lead to very close results between the number of reads and coverage aligned to reference of the separate mapping, thus affecting the identification, we adopted competitive mapping strategy. We combined 149 mitochondrial genome reference sequences of Bovidae and Cervidae species into one reference sequence. This combined reference sequence, containing 149 mitochondrial genomes which are equivalent to 149 chromosomes of this reference sequence, was then used to analyze the four samples against the aligned reference sequence ([Song et al., 2024](#)). Based on the total number of base pairs and coverage of each chromosome, the species of the samples were determined.

After that, the mitochondrial genomes of the identified species were used as the reference sequences for alignment, and then MinQuality was set to 25 PCR duplicates were discarded using the MarkDuplicates command in Picard v2.20.0 ([Sacco et al., 2017](#)). All local realignments around indels were performed using GATK v3.7.0 for base quality rescaling and end trimming ([McKenna et al., 2010](#)). Sequencing quality and mitochondrial coverage were assessed using Qualimap v2.2.1 ([Okonechnikov et al., 2016](#)). Mitochondrial consensus sequences were extracted using ANGSD v0.931 (–doFasta2 –setMinDepth 3 –minQ 20 –minMapQ 30 –trim 4; [Korneliussen et al., 2014](#)). Finally, the resulting mitochondrial consensus sequences were searched online using BLAST (<https://blast.ncbi.nlm.nih.gov>) to obtain the species information of sequences and to further identify the species type.

2.5. Data analysis

To further explore the species relationships of the excavated samples, we downloaded 30 mitochondrial genome data of Antilopinae from NCBI GenBank (<https://www.ncbi.nlm.nih.gov>) to construct a dataset called database1 ([Supplementary Table 2](#)). Multiple sequence alignment of data in database1 and four samples in this study was performed using MUSCLE v3.8.1 ([Edgar, 2004](#)). We used the species *Ovis moschatus*, which belongs to the genus *Ovis* within the family Bovidae mitochondrial complete genome sequence NC_020631.1 as the outgroup. The best alternative models were determined using ModelTest-NG v0.1.6 ([Darriba et al., 2020](#)). The model was selected GTR + I + G4. The phylogenetic tree was constructed using RAxML-NG v0.9.0 ([Kozlov et al., 2019](#)), and the final tree visualization was done using iTOL ([Letunic and Bork, 2021](#)). In addition, we calculated the genetic distances between individuals by utilizing the “Compute Pairwise Distances” function in MEGA 11 ([Tamura et al., 2021](#)), with the “Bootstrap Replications” set to 1000 and the “p-distance” model selected. Based on the calculated results, we then used the R package “pheatmap” ([Kolde, 2019](#)) in conjunction with R v4.1.2 ([R Core Team, 2022](#)) to draw heatmaps.

To determine the specific subspecies of the samples in this study, we downloaded the published mitochondrial D-loop region sequence (454 bp) data of the nominate subspecies (*Saiga tatarica tatarica*) and the Mongolian subspecies (*Saiga tatarica mongolica*) of the saiga antelope from the NCBI GenBank to construct database2 ([Supplementary Table 3](#)). Meanwhile, we also extracted the 454 bp D-loop region

sequences of the four samples in this study. Multiple sequence alignment was performed using MUSCLE v3.8.1. We used the species *Antidorcas marsupialis*, which belongs to the genus *Antidorcas* within the family Bovidae mitochondrial complete genome sequence NC_020678.1 as the outgroup. The best alternative models were determined using ModelTest-NG v0.1.6. The model was selected TPM2uf + G4. The phylogenetic tree was constructed using RAxML-NG v0.9.0, and the final tree visualization was done using iTOL. In order to analyze the samples unearthed from the site within a broader spatio-temporal scope, we constructed database3 ([Supplementary Table 4](#)) by using the D-loop region (940 bp) of the samples in this study and that of the nominate subspecies of the saiga antelope (*Saiga tatarica tatarica*). Then, we calculated the Nucleotide Diversity (π) through DnaSP v6.0 ([Rozas et al., 2017](#)).

3. Results

3.1. Sequencing and identification results

After being aligned with 149 mitochondrial genome reference sequences, five species with the highest coverage of the alignment reference sequences were initially selected ([Supplementary Table 5](#)). Then the mitochondrial consensus sequences of the five corresponding species were extracted and online BLAST search was performed to obtain the species information of the sample sequences. It turned out that the four samples in our study showed the highest number of base pairs and coverage in mitochondrial reference genome alignment, and the four samples all fell into the Bovidae family, Antilopinae subfamily *Saiga tatarica*. Furthermore, 149 mitochondrial genomes were merged into a single reference sequence for alignment analysis. All four samples were aligned to *Saiga tatarica*, which showed the highest number of base pairs and coverage ([Supplementary Table 6](#)). The outcomes of the two alignment techniques were consistent with each other, confirming the reliability of the identification results. Then with the whole mitochondrial genome of *Saiga tatarica* (NC_020746.1) used as the reference sequence, separate alignment analysis were performed on the four samples. As it turned out, all of the mitochondrial genome coverage multipliers were greater than 1X, and the number of sites covered by the mitochondrial genome was greater than 10,000 ([Table 2](#)).

3.2. Results of mitochondrial genome analysis

3.2.1. Phylogenetic analysis

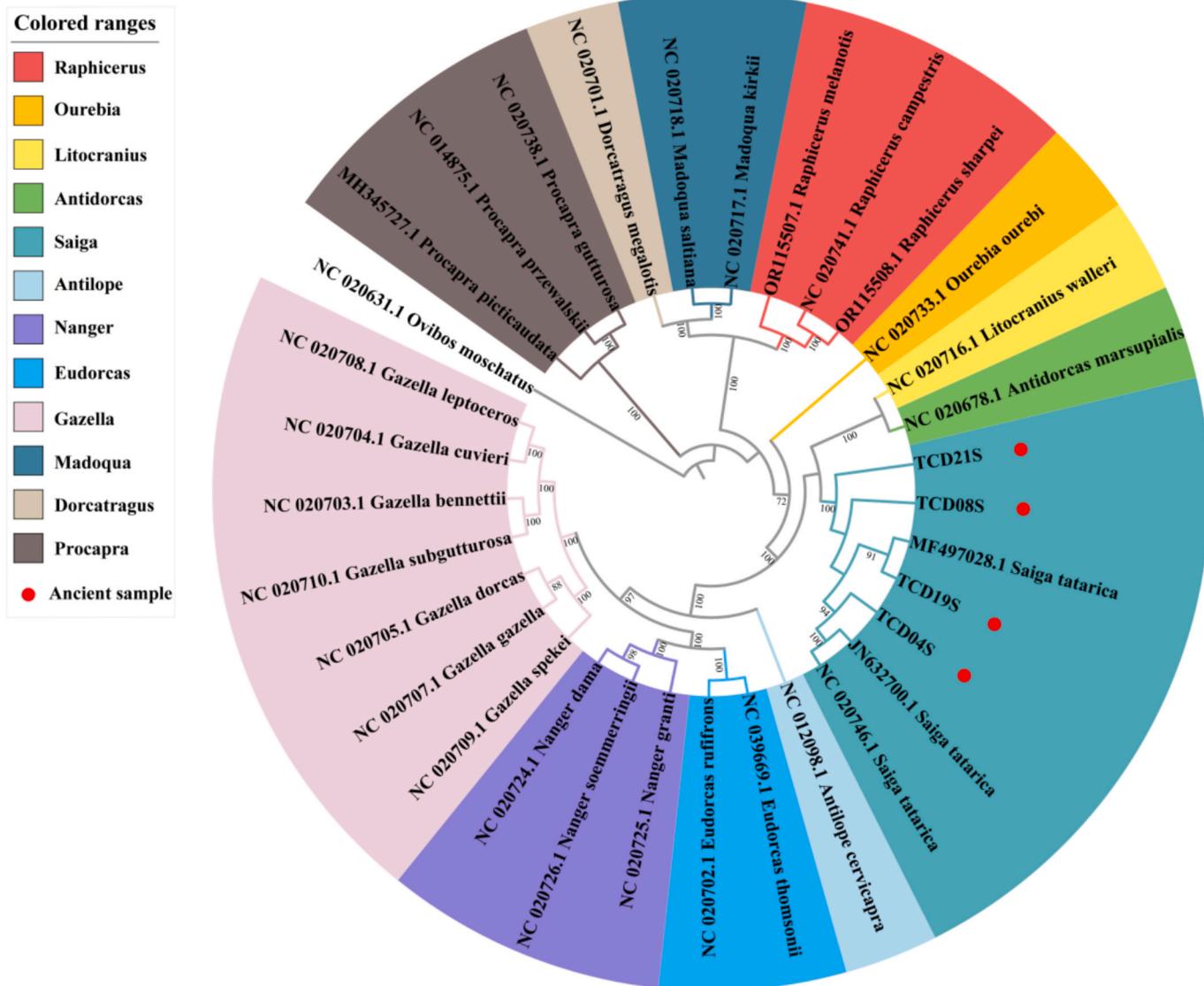
To determine the phylogenetic position of the ancient samples, a phylogenetic analysis was carried out by combining the four ancient samples with the sequences in database1. Using the muskox (*Ovis moschatus*) as an outgroup, a maximum-likelihood tree ([Fig. 2](#)) was constructed.

As depicted in the maximum-likelihood tree, a distinct separation of the 11 genera of Antilopinae can be observed. Each species was associated with a branch that corresponded to its relevant genus. TCD04S clustered with the contemporary *Saiga tatarica* samples, JN632700.1 and NC_020746.1. Additionally, TCD04S together with the clade consisting of TCD19S and MF497028.1 gave rise to a higher-level clade. Likewise, TCD08S and TCD21S clustered within the branch of the genus *Saiga*.

Table 2

Sequencing information of ancient samples analyzed in this study.

Experimental Code	Total Number of Base Pairs	Species with the Highest Coverage of Aligned to Reference	Coverage of Aligned to Reference (X)	Number of Reads Aligned to Reference	Number of Sites Aligned to Reference	Number of Sites in the Reference	Average Fragment Length (bp)
TCD04S	24,886,576	<i>Saiga tatarica</i>	4.9908	1545	15,952	16,375	57.35
TCD08S	39,493,932	<i>Saiga tatarica</i>	8.2129	2950	16,113	16,375	56.55
TCD19S	25,378,866	<i>Saiga tatarica</i>	24.0322	14,605	16,193	16,375	56.44
TCD21S	32,956,928	<i>Saiga tatarica</i>	1.8001	724	13,015	16,375	49.54

**Fig. 2.** ML phylogenetic tree based on mitochondrial genome of Antilopinae subfamily.

3.2.2. Genetic distance calculation

To validate the above species identification results, genetic distances among individuals were calculated based on the data in Section 3.2.1. The calculated results were visualized (Fig. 3). It was shown that, in contrast to other genera within the Antilopinae subfamily, the four ancient samples in this study demonstrated relatively closer genetic distances to the modern *Saiga tatarica* samples. These outcomes further proved the accuracy of ancient DNA technology in species identification when considering genetic distances among species.

3.3. Results of mitochondrial D-loop region analysis

3.3.1. Phylogenetic analysis

A phylogenetic analysis of the sequences from database2 and the mitochondrial D-loop region sequences (454 bp) extracted from the four ancient samples were performed. The results, as demonstrated in Fig. 4, showed that all four ancient samples belonged to *Saiga tatarica tatarica*.

3.3.2. Nucleotide diversity calculations

The mitochondrial D-loop region sequences (940 bp) of the four ancient samples and those from database3 were classified into two

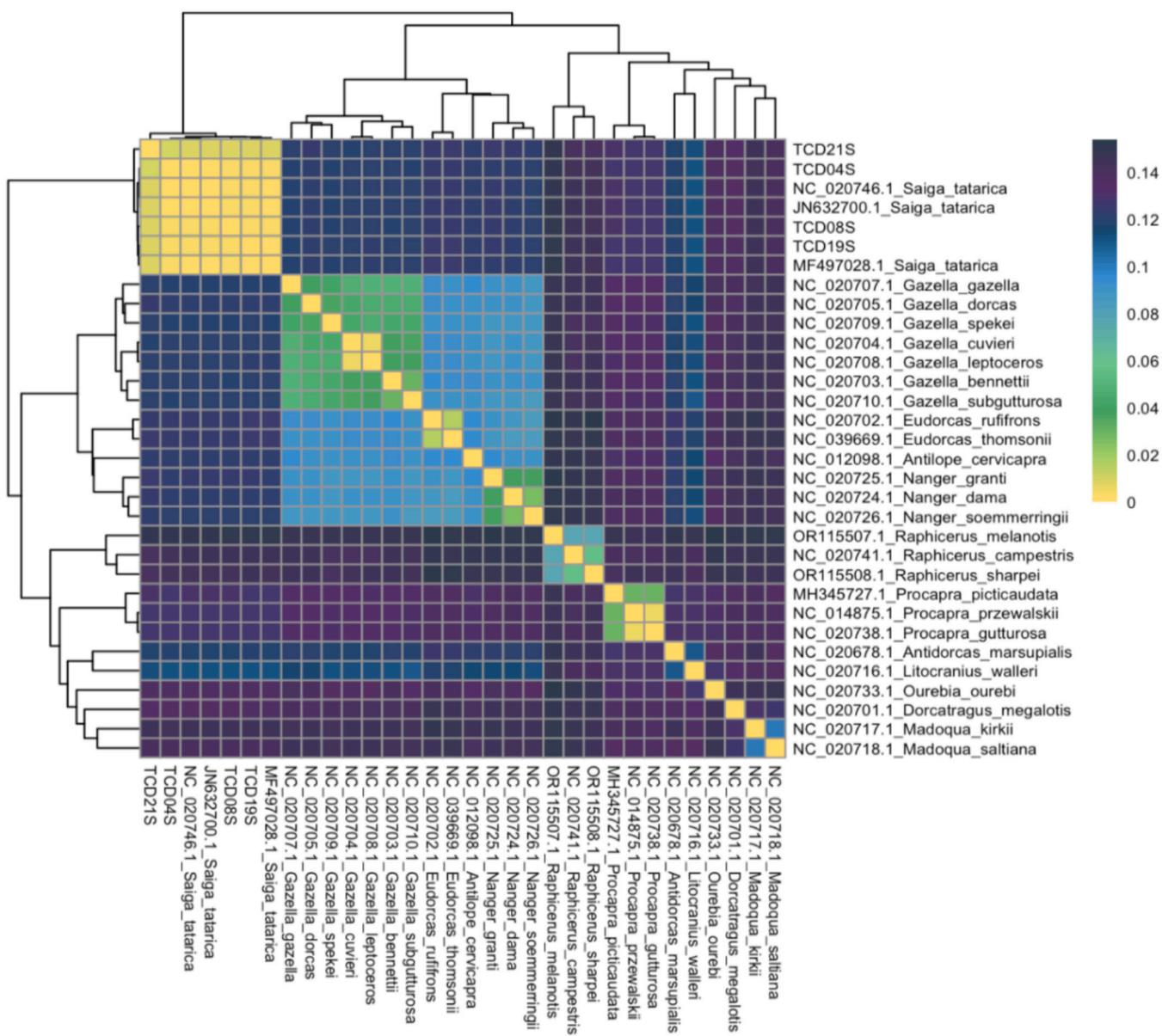


Fig. 3. Pairwise Distances heatmap based on mitochondrial genome of Antilopinae subfamily.

distinct groups: the Tangchaodun ancient samples (TCD) and the modern samples. Upon calculating the nucleotide diversity ($\pi = 0.02885$) compared to the modern group ($\pi = 0.02723$).

4. Discussion

4.1. Molecular Genetics of *Saiga tatarica*

The Tangchaodun Ruins lie within the historical distribution range of *Saiga tatarica* (Wang et al., 1998). Through ancient DNA analysis, this study successfully identified four archaeological samples as *Saiga tatarica*. The earliest unearthed stratum dates back to the Tang Dynasty (618–907 CE), and the latest to the Mongol Yuan Dynasty (1271–1368 CE). Although abundant zooarchaeological materials from Xinjiang have been published (Ling et al., 2016; Wang et al., 2021; Dong et al., 2022; Li et al., 2022; Qiu, 2024), ancient remains of *Saiga tatarica* are seldom reported. These findings not only enrich the archaeological documentation of this species but also provide a new perspective for re-evaluating how ancient humans utilized wild animal resources along the Silk Road.

Mitochondrial D-loop region analysis shows that all four ancient samples belong to the subspecies *Saiga tatarica tatarica*. Historically, there were five subspecies of saiga antelope, three of which are extinct, leaving only *S. t. mongolica* and *S. t. tatarica* (Wang & Zhao, 2015). *S. t. tatarica* was widely distributed across Central Asia and parts of China, while *S. t. mongolica* was confined to the Great Lakes Basin in north-western Mongolia (Rey-Iglesia et al., 2022). Male *S. t. tatarica* can weigh up to 45 kg, with females around 36 kg, and male *S. t. mongolica* typically do not exceed 32 kg, having a smaller body size and thinner horns (He, 2021). Previous studies suggested that the Altai Mountains divided saiga distributions into Chinese and Mongolian populations (Cui et al., 2017), implying that ancient Chinese populations belonged to the larger *S. t. tatarica*. Our results genetically confirm this hypothesis, offering molecular evidence for ancient zoogeographic patterns.

In archaeology, this molecular identification compensates for the limitations of traditional morphological zooarchaeology. Ancient DNA techniques thus help reveal the patterns of wildlife utilization that were previously overlooked, prompting a reconsideration of human-animal interactions along the Silk Road. For instance, the horns, meat, and fur of the saiga antelope might have entered human society through

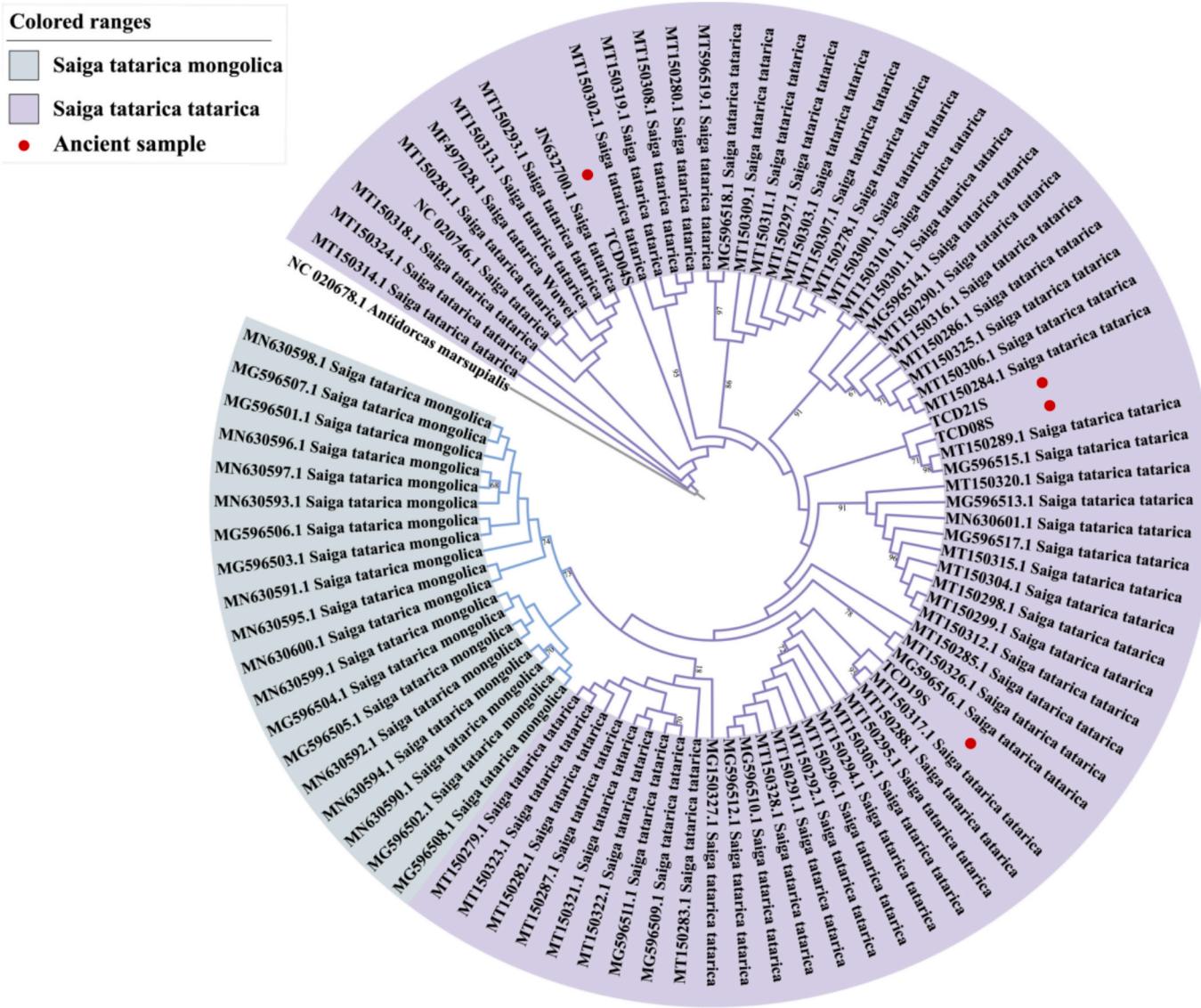


Fig. 4. ML phylogenetic tree based on the mitochondrial D-loop region (454 bp) of *Saiga tatarica*.

hunting or trade, yet their specific uses (such as for food, in rituals, or for medicinal purposes) still need the support of more archaeological background information. Besides identifying the subspecies and understanding their historical distributions, genetic diversity analysis also sheds light on the evolutionary history of *Saiga tatarica*. Nucleotide diversity analysis indicates higher genetic diversity in ancient saiga populations than in modern ones (Fang, 2021; Song et al., 2024). This discrepancy may reflect either historical broader distributions supporting richer genetic structures or severe genetic bottlenecks in modern populations due to habitat loss (Li, 2013a, Li, 2013b) and overhunting (Wang, 2019).

4.2. Antelopes' horns and *Saiga tatarica*

In traditional Chinese medicine, antelope's horn, known for its liver-pacifying, heat-clearing, and toxin-releasing effects, has long been recognized and employed in medical practices (Meng and Wang, 1999). The earliest record of antelope's horn used as a medicine dates back to *The Divine Farmer's Materia Medica* 神農本草經 (Yang, 1998) over two thousand years ago in the Qin and Han Dynasties. Antelope horn as burial item for its medicinal values was discovered in the Western Han Dynasty Mausoleum of the Nanyue King as well (Cultural Relics

Management Commission of Guangzhou Municipality et al., 1991). Descriptions of antelope's horn in some Chinese medical texts probably refer to Saiga antelope horns. For instance, *The Newly Revised Materia Medica* 新修本草 (Su, 1994a, Su, 1994b) from the Tang Dynasty described antelope horns as “having numerous nodes and coiling in a crinkled circular fashion” 角甚多節，蹙蹙圓繞, while *Illustrated Classic of Materia Medica* 本草圖經 (Su, 1994a, Su, 1994b) from the Song Dynasty noted that “the antelope horns measure one to two feet in length, possess nodes resembling human finger grip marks, and are exceptionally firm and tough.” 其角長一、二尺，有節如人手指握痕，又至堅勁。These morphological traits closely match those of contemporary Saiga antelope horns. Saiga antelope horn has 10 to 20 elevated annular ridges extending from the base, with inter-ridge distances of about 2 to 3 cm, allowing for finger insertion, known as the “hand-fitting grasp”. Such features remain key indicators in morphological antelope species identification. During the Ming and Qing Dynasties, the medicinal properties of antelope's horn were specified (Liu, 2019), and antelope horn descriptions further matched with Saiga antelope horn. *Collected Sayings on Materia Medica* 本草匯言 (Ni, 2005) in Ming dynasty stated that “Antelope horns as white and shiny as jade are seven to eight inches long.” 犀羊角白亮如玉，長七八寸。*New Compilation of Materia Medica* 本草從新 (Wu, 2013) in the Qing Dynasty noted: “Antelope's horns bright and

have sharp tips without being black are of good quality.”明亮而尖不黑者良。Although the antelope horns used medicinally before the Ming Dynasty might have come from various antelope species, the therapeutic potential of Saiga antelope horn has been more widely recognized since the Ming and Qing Dynasties (Jin, 2007), and it was actually used in medical practices as early as the Tang and Song Dynasties.

4.3. The sources and utilization of Saiga antelope

According to relevant archaeological material (Ren and Yu, 2020), the four samples (TCD04S, TCD08S, TCD19S, and TCD21S) in this study (Fig. 1B) were excavated from test pit IT1523 and ash pits H353, H66, and H109 respectively. Plentiful accompanied artifacts of TCD08S and TCD19S were unearthed as well, and all their excavation units (H353, H66) can be identified as cultural remains of the Tang Dynasty. H353, located in the courtyard section of the site, was a regular bag-shaped ash pit, with visible mud plastering traces on the walls, indicating it underwent artificial modifications during its construction. The excavated items included pottery (such as jars, bowls, basins, and lids), ironware, copper belt ornaments, stone bowls, coal lumps, and charcoal, demonstrating the prosperous domestic and production activities during ancient period here (Supplementary Fig. 2). In ash pit H66, pottery (basins, jars, urns, and ink stones), copper hairpins, bone awls, along with *Kaiyuan Tongbao* copper coins and other items were unearthed (Supplementary Fig. 2). Considering the pit location, human-induced traces, and excavated items (Tuo and Wen, 1995), it is hypothesized that H353 and H66 may have served as storage facilities, akin to cellars, and that special items not limited to food and everyday requirements may have been stored there. Because of its medicinal importance and aesthetic appeal, Saiga antelope horn may have been stored alongside valuable items like *Kaiyuan Tongbao* copper coins in the pits.

Saiga antelope provided important supplements to meat resources and other materials, including its horns and furs (Meng and Wang, 1999). It's assumed that the Saiga antelope horns unearthed from Tangchaodun reflect the prevalent hunting practices across all social classes in the Tang dynasty (Tian, 2018). Hunting activity among the royal and noble class is well documented in Tang poetry and evidenced by the numerous pottery hunting figurines and hunting murals found in prestigious Tang tombs (Tomb of Crown Prince Zhanghuai, Tomb of Princess Yongshou, and Tomb of Zheng Rentai) (Jia, 1991). For ordinary people, hunting closely related to economic production, and quite a lot of people depended on hunting to make a living at that time (Zhang, 2022). Tangchaodun was initially the seat of Pulei County government and a military, administrative, and transit hub along the New Northern Route of the Silk Road (Ren and Du, 2024). Antelope's horn, a valuable resource for medicine and handicrafts production, might have been exchanged as an important commodity there. As recorded in *The Six Codes of the Tang Dynasty* 唐六典 (Li, 1992) and *The New Book of Tang (Geography)* 新唐書·地理志 (Ouyang and Song, 1975), Tingzhou (specifically Beiting, which administrated Pulei County then) presented *Su Huo Horns* 速霍角 (antelope horns in Turkic languages (Xia, 2004)) as tribute to the imperial court.

Even after the Tang and Five Dynasties, the nations in China's Western Regions presented antelope horns to the central government, as pointed out in historical documents. *Cefu Yuangui* 冊府元龜 (Wang, 1989) Volume 972 reads that “in the first year of Yingshun, the Khagan of the Uyghur, Renmei, dispatched envoys to offer tribute items including saddled horses and weaponry left by the previous Khagan, Renyu, as well as horses, two lumps of jade, horse harnesses, sal ammoniac, antelope horns, Persian silk textiles, and jade belts given by himself.”應順元年，回鶻可汗仁美遣使獻故可汗仁裕遺留貢物鞍馬、器械，仁美獻馬、二團玉、鞚轡、硇砂、羚羊角、波斯寶織、玉帶。“In the third year of Tianfu, The Khagan of the Uyghur, Renmei, presented wild horses, one-humped camels, jade bridles, borax, sal ammoniac, sea otter testicles, diamonds, antelope horns, and other items.”天福三年，可汗回鶻王仁美進野馬、獨峰駝、玉轡頭、大鵬砂、硇砂、膾肭臍、金剛鑽、羚羊角等

物。“In May of the first year of Qianyou under the reign of Emperor Yin of the Later Han Dynasty, the Khagan of the Uyghur dispatched envoys to present tribute... antelope horns, sal ammoniac, and other medicinal substances were offered by Khotan.”漢隱帝乾祐元年五月，回鶻可汗遣使入貢……又羚羊角、硇砂諸藥于闐國遣使朝貢。Saiga antelope horn, as a valuable natural resource, exerted a significant influence on human society throughout historical time periods. They were not only the byproducts of hunting in border regions but also a vital commodity within the Silk Road trade network, showcasing the multifaceted economic activities and intricate cultural interactions in ancient human society (Tang, 2010).

5. Conclusion

In this study, an ancient DNA study was conducted on four animal remains from Tangchaodun Ruins to identify the species of the samples. Results of comparative analyses, phylogenetic analyses, and genetic distance calculation indicate that all the samples were Saiga antelopes, precisely *Saiga tatarica tatarica*, demonstrating the efficacy of ancient DNA techniques in accurate subspecies-level identification. The analysis of the mitochondrial D-loop regions showed that the genetic diversity of ancient Saiga antelopes exceeded that of contemporary populations, which provided clues for the historical distribution of Saiga antelopes and insights for the conservation of current populations. It can also be assumed that the inhabitants of Tangchaodun Ruins hunted and exploited the resources of Saiga antelopes, enriching the research findings on human activities in Xinjiang. The Saiga antelope horns unearthed in Tangchaodun Ruins might have been preserved due to their medicinal and aesthetic values, which can be evidenced by historical records of Saiga antelopes used as traditional Chinese medicine. Meanwhile, as revealed by historical documents, they played a vital role in tribute and in establishing the east–west trade network, indicating the vibrant economic and cultural interactions in the Tang Dynasty.

This work deepens our understanding of historical animal resource utilization and, more broadly, the role of the Silk Road as a long-established and permanent hub for exchange, influence, and cooperation among communities.

CRediT authorship contribution statement

Xinyan Zhang: Writing – review & editing, Writing – original draft, Project administration, Investigation, Formal analysis, Data curation, Conceptualization. **Guangjie Song:** Writing – review & editing, Validation, Supervision, Formal analysis, Conceptualization. **Zhuowei Tang:** Writing – review & editing, Supervision, Conceptualization. **Jian Wei:** Writing – review & editing, Supervision, Investigation. **Guan Ren:** Supervision, Resources, Funding acquisition. **Dawei Cai:** Writing – review & editing, Supervision, Resources, Funding acquisition, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jasrep.2025.105384>.

Data availability

Data will be made available on request.

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