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Influence of the Silk Road Trade on the Craniofacial Morphology of Populations in Central Asia

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INFLUENCE OF THE SILK ROAD TRADE ON THE CRANIOFACIAL MORPHOLOGY OF POPULATIONS IN CENTRAL ASIA

by

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ABSTRACT

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Advisor: Ekaterina Pechenkina, Vincent Stefan.

Large-scale human migrations over long periods of time are known to affect population composition. In the second century B.C the demand for silk threads in the West opened trade opportunities between China and the Europe. This allowed for new pathways to be established and old ones reinforced across the vast region of Central Asia; a network of overland and sea routes linking East with West for sixteen hundred years that became collectively known as the Silk Road. Populations living along these routes were affected by a constant influx of traders, merchants, and invading armies attempting to control the region. Although Central Asian populations have always exhibited some degree of admixture, genetic, archaeological, socio-cultural and linguistic evidence indicate an increase in admixture within these populations during the period when the Silk Road was active. Very little work has been done to confirm these findings from a morphological perspective.

This study investigates the craniofacial variation seen in populations living during the time of the Silk Road and analyses the patterns of admixture as a result of population migrations during this time. This was accomplished using 3D geometric morphometric analysis to assess the differences in craniofacial morphology of Central Asian populations living along the Silk Road before the opening of the trade routes with those living in the same region at the height or the close of the trade routes. Cranial series were selected from three locations: China/Mongolia, Central Asia, and Western Europe. Specimens were chosen to correspond with the time period and geographic span of the Silk Road. The data collected was analyzed using multivariate statistical methods and the results offer a morphological explanation for the population diversity seen in the region during that period.

The craniofacial morphology of this Central Asian sample fell between those examined from European and East Asian contexts, with a mosaic of traits that marked them as part of a statistically significant group distinguishable from those to the east or west, within the broader Eurasian human population. In this framework, they were considered an admixed group. Large cranial breadth, broad zygomatic area, a prominent glabella, and a specific nasal configuration (i.e., wider, long, and projecting) are characteristic of this population sample. Admixture in this population was found to have increased over the time span of the Silk Road, with the most pronounced jump observed in the early to middle period of the Silk Road from around the 5th to the 15th Century AD. This rapidly evolving craniofacial morphology cannot be characterized as secular change, but rather was strongly influenced by large migrations of people through the region mixing with the local population.

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INTRODUCTION

Around 200 BC, the establishment of the Silk Road trade routes spanning from Eastern China to the shores of Europe forever changed the landscape and makeup of Central Asia by creating corridors through which populations and goods passed across continents for 1,600 years (Figure 1.1). While the term "Silk Road" was not coined until the 19th century, roads tracing through the vast region of Central Asia crossing east to west have long been recognized as historically important trade routes along which goods were transported and sales were negotiated (Chin,2013; Wood, 2002: 9). The initial focus of the Silk Road trade was to bring silk from China to the people of the Greek Empire and later to Rome (Feltham, 2009; Wood, 2002:11).

Figure 1.1: Map of region

Adapted from http://worldmap.harvard.edu 2016 Silk Roads metadata and Eurasia lesser routes by Tim Williams, Institute of Archaeology, University College London.

As the routes became trodden through, goods were routinely exchanged and sold not only between the two poles of the road itself but along the way. Families, tribes, clans, and merchants settled into foreign lands and established themselves there interacting and integrating with local populations over generations (Hitch, 2009). Most historians agree that the main Silk Road trading routes were not established until 200BC-139BC (Whitfield, 1999:9; Whitfield, 2004:13; and Wood, 2002:11). However, some archaeological evidence shows that migrations through Central Asia to the Near East and Europe occurred well before then, just not with the same intensity, regularity, and purpose of the Silk Road (Han, 1994; Wood, 2002:27). Alexander the Great, a hundred years prior, had made incursions into Bactria and the high plains of Central Asia, reaching as far as the Pamirs (Holt, 1988:9). While it is certain that Alexander himself and many of his men contributed to a small percentage of admixture in the region through intermarriage and coupling, they occupied a narrow swathe of Central Asia for fifty years which is a relatively short time to have made an imprint on the population at large. However, there are potential traces of admixture left in an enclave of northwestern Pakistan, where a small population known as the Kalash living in an inaccessible mountainous area claim descent from Alexander the Great and his armies. Conflicting genetic studies undertaken have shown either none or some small amounts of Western European contribution to their genetic lineage; an event that corresponds loosely with Alexander's invasion of the mountains around 356-323BC (Hellenthal *et al*., 2014). In this population, facial features and light coloring distinguish them from other groups in the region as particularly European-looking, and as such, they trace their history to Alexander the Great and his invasion of their homeland. Because this unique population was geographically isolated from others in the region, they interbred and thus conserved the physical traits of the admixture throughout the generations.

Within the span of a generation or two, and given the right conditions Alexander and his companions left a trace of their heritage in the region. By comparison, the Silk routes brought sixteen centuries or roughly eighty generations worth of potential admixture to the peoples throughout the vast territory they crossed. This time period saw the creation of urban centers in Central Asia to which Western and Eastern populations migrated and where they established themselves and their families for trade purposes.

Intensive demographic changes occurred in these burgeoning trade centers at key points along the northern and southern routes (Hitch, 2009). New cities emerged and welcomed migrants from distant lands as well as successions of invading armies, creating a level of diversity on a larger scale than had been observed before.

It seems likely, given the geographic scale of these migrations and the time depth at hand that there would be substantial changes due to admixture in the genes of Central Asian populations, particularly changes that would be observable in craniofacial traits. However, it is equally possible that because these changes may have arisen more gradually and populations were not geographically isolated, that the various groups may not have mingled in any significant way other than through trade.

While there has always been some degree of admixture in Central Asia between East Asian and European traits (Xu *et al*, 2008), there has been little research showing the impact that the trade routes might have had on the local populations. Diverse populations from around Central Asia, the Middle East, Europe, and East Asia established themselves in these large cities and contributed even more genetic complexity to an already admixed population. While this could make it difficult to tease out what direct impact the trade routes might have had on these people, the purpose of this project, as an approach that complements the genetic studies of the area, is to investigate how potential admixture between East Asian and European populations is manifested on the cranial and facial skeleton, and whether this admixture increased over time due to migrations along the Silk Road.

PRESENT RESEARCH

Few studies have addressed the issue of admixed human populations, and even fewer have looked at how hybridization is represented in the skeleton. Most of the work on modern human admixture has come from the field of population genetics which, while incredibly informative on a historical level and for understanding large scale events, has its limitations. The identification of ancestral geographic origin from ancient DNA analysis is often difficult due to significant degradation and contamination issues, and more importantly it damages rare or difficult to access skeletal remains. Furthermore, at this stage, genetic studies cannot identify which genes affect which specific set of craniofacial traits. Genetic studies have primarily contributed to the current understanding of Central Asian population history, with most of the analyses conducted on living populations. This study will contribute to an increased understanding of how biological variability manifests in diverse groups and populations through the analysis of cranial remains. By quantifying and describing the range of variability in craniofacial features exhibited by admixed individuals, this study will contribute to the body of knowledge currently available on Central Asian populations. Methodologies applied to identify admixture in historical populations may also be applied to modern forensic cases. Some craniometric studies, using both modern and ancient crania for analysis, have found that populations from the same geographic region, regardless of time period, clustered much more closely together than with other contemporaneous groups from disparate geographic regions (Schmidt *et al.,* 2011; Seguchi *et al.,* 2010).

The study of human variation is incredibly important within the field of forensic anthropology, as the principal function is to construct a biological profile from skeletal remains, including estimating ancestry. Ancestry estimation methods are only as accurate as the data from which they are derived. Forensic anthropologists routinely use FORDISC, a software program which utilizes discriminant function analyses to assign likely ancestry and sex to a set of unknown remains, based on an in-built database of thousands of craniometric measurements (Ousley and Jantz, 2005). While this databank includes a large number of ancient and modern crania from Europe and some from East Asia, there is not a single specimen from Central Asia (Ousley and Jantz, 2005). 3D-ID, a newer software package which fulfills the same function but uses 3D GM landmark data, has an even smaller sample of crania from East Asia and none from Central Asia (Slice and Ross, 2009). Forensic anthropology has gained in prominence in recent years, with more interest from abroad than ever before, specifically in using applied techniques from the field to identify the missing. Standards based on populations from the US should not be used for populations from other regions, thus the dire need to contribute cranial morphological data on regions for which there is no information.

In addition, highlighting not only the occurrence but also the phenotypic effects of large admixture events on craniofacial features over the last few millennia will help us understand more about our distant human origins and retrace the path of our deep-past ancestors. Exploring the mixed inheritance of groups throughout history, and how these changes might be represented phenotypically, will also aid in clarifying the origins of current populations. More generally, this study helps us think about how to characterize craniofacial morphological variation in human populations that are rapidly becoming more and more intermixed. This project will contribute to the current and very relevant debate of how to define and identify admixture, an issue that affects the entire spectrum of anthropology and which touches all facets of daily life in America and around the world as globalization increases.

STRUCTURE OF DISSERTATION

This dissertation opens with an introduction to the Silk Road and presents the research at hand (Chapter 1). It is followed in Chapter 2 by an overview of the geographic boundaries and topography which make Central Asia a challenging and diverse region to study. A brief historical context for the region is provided along with a concise account of cultural practices and lifestyles of Central Asians from the late Bronze Age until the closing of the Silk Road. Special attention is paid in this chapter to the interactions and meetings of Eastern and Western peoples throughout the early history of the region. In Chapter 3, Central Asian population migration patterns and history are explained by reviewing the literature on genetic, archaeological, and linguistic research and forming a cohesive narrative of these peoples' history where possible. Chapter 4 reviews osteological research as it relates to admixture in modern humans and specifically examines craniofacial evidence of admixture in Central Asia. Also laid out in this chapter are the aims, research questions, and expected outcomes for this project. Chapter 5 addresses ancestry and population assessment methods as well as race concepts in anthropology. Terminology used in this paper is also discussed here.

Chapter 6 extensively details the museum collections analyzed in this study and lists the cranial specimens and series by provenance, time period, and sex. In Chapter 7, the methods used to collect and statistically analyze craniofacial landmark data are described. The next two chapters deal with data analysis for all the samples. In Chapter 8, the analysis focuses on inter-group comparisons of European, Central Asian, and East Asian craniofacial morphology. Chapter 9 examines craniofacial changes in three time-differentiated Central Asian groups looking for evidence of fluctuating admixture and secular growth. In the penultimate chapter (10), the outcomes of the three research questions are reviewed and the results are discussed within the framework of historical, genetic, archaeological, and linguistic evidence provided by previous research. The final chapter (11) presents potential future lines of analysis and offers a summary of the results obtained with the general implications of this research.

Chapter 2: Cultural, Historical, and Geographical Context

GEOGRAPHICAL CONTEXT

Central Asia, as a geographic entity, represents a vast area with borders variably defined in the literature. Often treated as a uniform region, Central Asia is anything but. Much of its landscape is inaccessible, with steppes, mountainous regions, large deserts, and little coastline. The steppe, itself the defining feature of the region, changes in character across the continent abutting deserts and oases in the East and South, the taiga and forests in the North, the rocky river-dense regions of the center and the desolate barren plateaus surrounding it (Kuzmina, 2008:11). Despite the difficult and varied environment, Central Asia has always been an area through which intense migration and resettling has occurred (Beckwith, 2009: xx). Generally, Central Asia may be thought of as extending from Western China to Anatolia. The Northern border includes Mongolia and in some of the literature even as far as Southern Siberia (Derenko *et al.*, 2007; Krause *et a*l., 2007; Zerjal *et al.*, 2002), while the Southern border extends down into the Indo-Gangetic plains of Northern India. Parts of South Asia are sometimes included because of the impact and reach of the Silk Road trade routes (Andrea, 2003; Beckwith, 2009: xx). As a consequence of its far-reaching borders, such a wide description of the region poses many problems because the level of diversity of the people, the languages, and cultures is extraordinary. Hundreds of ethnic groups reside in this land: some flourished in high-altitude settings while others adopted a nomadic lifestyle in the desert or pastoral economies in the steppes, some joined urban centers along the sea trade routes, and yet others settled inland to create large urban trade centers along the Silk Road.

Because of its diversity and size, Central Asia is often broken up into areas that are defined by social, cultural, and ethno-linguistic similarity. For this project, Central Asian populations have been chosen from an area covering western Turkmenistan to eastern Kirghizstan and from southern Kazakhstan to northern Iran. Most of the collection originates from the former soviet republics of Central Asia. The Central Asian republics of Kazakhstan, Kirghizstan, Uzbekistan, Tajikistan, and Turkmenistan are joined together based on the common heritage of the people, from their religion to their ethnicity, language, and long periods of shared history (Olcott, 1994). Although much commonality exists between groups, movements of populations through the region have created a constantly changing diverse population within the borders of each of these states. Substantial migrations in and out of these lands in ancient and recent history have created demographic changes in the region that are heavily dependent on political and economic fluxes of the governments and empires that surround them (Olcott, 1996).

Currently, much of the research on population origins and ethnography is focused on two very distinct periods in the history of the region: the deep past of Central Asia with genetic studies homing in on early human origins and migrations routes out of Africa, and archaeological studies centered around the influence of the Silk Road. Unfortunately, because of the marked separation between these two glimpses in time, a continuous picture of human migration and settlement in the region has yet to be formed.

HISTORICAL CONTEXT

Figure 2.1: Central Asian history timeline

	3000-1000 BC	1000-200 BC	200 -50BC	50BC- 300 AD	300-700 AD	700- 1100 AD	1100-1300 AD	1300-1400 AD	1400-1600 AD
ERA	**BRONZE**	**IRON**	**SILK ROAD**	**EMPIRES**	**TURKS/ARAB / TIBETANS**	**RELIGION**	**MONGOLS**	**TAMERLANE**	**CLOSING**
East C.A	2000 BC First East-West interactions: western mummies and fabrics found in West China	300-200BC Xiongnu of East Asian descent control eastern region and trade with Scythians	Emperor Wu of Han Dynasty explores trade with central & west Asia marking opening of Silk Roads 200BC	Chinese Empire under the Han expands West, by 50 AD conquers the Xiongnu in Tarim Basin	Tang Empire conquers Xi'an, largest urban ctr in East. Tibetans win Khotan and trade with Turks.	Tang lose territory north and west. Tibetan kingdom collapses in 9th C, China turns inward to protect itself	1215 Beijing falls to Mongols. Uighurs join army voluntarily but most eastern peoples are conquered by force	1300s Bubonic plague in China is catalyst for Mongol Khanate's fall. They are expelled back to Mongolia	China rarely uses SR, while coastal trading partnerships are made across world until overland routes become defunct
West C.A	17th C BC Large migration of IndoEuropean male warrior bands from Ural to west Central Asia	700 BC Scythians emerge and become primary force in region, trading with Greeks and Persians	Alexander the Great conquers western Central Asia setting the stage for SR trade opportunities 330 BC	Roman Empire dominates West and battles Alans/Sarmatians of Iranian origin on frontiers 100 AD	Arab expansion to Merv largest urban center of time, controlling trade opportunities with Rome	8th C spread of Islam pushes heart of SR west. Harsh climate in 9th C cause collapse of Arab empire	Shah of Khwarizm succumbs to Mongols in 1200s, cedes Iran and western & southern C.A	1390s Tamerlane conquers west and north all the way into Persia and Caucasus moving towards Moscow	Death of Tamerlane 1405 & last of unifying leaders of C.A. Ottomans take west and Safavids recapture Persia
Central	Indo Europeans mix with indigenous peoples. Interactions with East are limited	Nomadic Scythians move from western C.A. across central area and dominate region for centuries	After 200 BC alliances forged between nomadic& pastoralist communities to control flow of goods on SR	Unrelenting attacks /expansion of territory by Empires at poles of SR create instability &drop in commerce for C.A	Return to nomadic life bc of instability. Turks conquer C.A in 6th C establishing common language &culture in region	Literacy spreads: goods and ideas are traded. 9th C Seljuks (Turks) rise & fall, 200 yrs of changing rulers ensues	Mongols expand territory over 100yrs, create stable unified commercially thriving area with trade opportunities	Tamerlane defeats Mongols& expands realm. Builds Samarkand as cultural heart of Eurasia and model city for world	Maritime exploration begins in Europe causing slow decline and decay of the overland SR routes. Reversion to nomadic lifestyle

Neolithic to Iron Age

The early historical sources on the first millennium BC depict this region as a vast land occupied by nomadic tribes and farmers whose interactions with populations from afar are limited (Masson and Sarianidi, 1972: 155). While it is difficult to pinpoint when the first interactions between more distant Eurasian populations occurred, it is certain that these pre-dated the opening of the Silk Road by over 1,000 years, as early as the second millennium BC. This information has been gleaned from the discovery of human remains and fabrics originating from the Near East and excavated in Eastern Central Asia (Li, 1999; Thornton and Schurr, 2004). The archaeological record of that early period, east of the Fertile crescent (Near East), is discontinuous making it hard to form a fluid picture about the cultures and people of the time (Bellwood, 2013:151), but it is the climatic changes from the Neolithic to the Bronze Age which seem to have influenced population migrations into and through the region. From 2,000 BC onward periods of cooling and warming caused the deserts to shrink and encouraged the spread of the steppe grasslands across Central Asia creating favorable conditions for human occupation further inland than before (Kuzmina, 2008:16). Technological innovations such as the spoke-wheeled chariot found in burials in the Steppe region as early as 2000 BC and the presence of smelt furnaces in dwellings are characteristic of the period and likely indicative of early population movements across the region and the beginnings of metallurgy trade (Hanks, 2010). Little is known about the Indo-European speaking people who migrated roughly four thousand years ago from the steppe-forest region south of the Ural Mountains near the Black Sea and penetrating Central Asia mixing with the indigenous peoples of the region. Three large migration waves have been identified ranging from the third millennium BC to early in the first millennium BC. Around the 17th Century BC, the largest outflow of people saw these Indo-European speakers, mostly male warrior bands, moving as far as China, India, Western Europe, and the Near East eventually settling there and taking up local wives (Beckwith, 2009:30). Southern Central Asia (Turkmenistan and Northeastern Iran) in the Bronze Age is known to have hosted the Anau Culture a society based around irrigation farming while the Eastern and North-central areas (Kirghizstan and Kazakhstan) were home to pastoral nomads, primarily livestock-herding peoples (Kuzmina, 2008:86).

The Xiongnu of East Asian descent directed and organized the nomadic groups of Eastern Central Asia during the 2nd and 3rd century BC, while the Scythians controlled western and southern regions of Central Asia (Phillips, 1965: 111, 54). Much is known about the Scythians, a group of Iranian origin speaking an Indo-European language, about whom the first historical records of the region are written (Hambly, 1966: 19; Phillips, 1965:54-55). Anthropological research on the period preceding the Silk Road has primarily been conducted on the Saka, the largest and most long-standing Scythian tribe. Cranial series from this population exhibit facial features in the early specimens that are characteristically Near Eastern. As time progressed the Saka migrated eastward and mingled with Mongolian populations which led to more East Asian features being integrated into the later series (Khodzhayov, 2008).

Early trade and Alexander the Great

While archaeological evidence shows limited interactions between Europe and Central or East Asia in the second millennium BC, the conquest of the region by northern pastoral nomads on horseback is well documented from the first millennium BC onwards (Hanks, 2010). Around 800 BC, the Scythians a northeastern Iranian population known for their prowess on the battlefield through the use of cavalry (Barfield, 1989:1) emerged and over time established one of the most expansive early trading networks connecting them through wheat and corn trade to Greece in the west, Persia in the south, and with the Xiongnu further east (Rolle, 1989:110). Goods but also ideas might have been exchanged among these groups, the time frame of which corresponds roughly with the emergence of classical philosophical thought in China, India, and Greece (Beckwith, 2009:59). The prosperous Scythians as described by Herodotus around 440BC waged wars across the Near East and formed alliances with the Assyrians, also established one of the first cities, Gelonus, heavily influenced by Greek design, from which they conducted their transnational commerce in both Greek and Scythian languages (Rawlinson, 1992:342). But at heart, the Scythians were nomads, which made it difficult for the Persians and Greeks to wage wars against them. Persian and Greek wars raged on for the next few hundred years and it is in this context that Alexander the Great and his invading armies set the stage for the Silk Road around 330BC. This period provides one of the first historical accounts of meetings between societies from the East and West (Holt, 1988). Alexander, a Macedonian prince turned his attentions to conquering Persia after colonizing Bactria and bringing with him Greek culture, thought, and a large army. After the defeat of the Persians in 334BC, Alexander crowned himself Emperor of Persia and married the daughter of a baron from Balkh (northern Afghanistan) to prove his intent on integrating with the local populations. He also encouraged his men to take up wives from Bactria and Persia.

On the Eastern front, it is believed that a small contingent of the early nomadic pastoralists of the same stock as the Scythians emigrated in the first millennium BC eastward. West of the Altai mountainous region was therefore inhabited by North Iranian peoples while the eastern region south of the mountains was inhabited by people speaking different languages and with characteristically East Asian features (Di Cosmo, 2002: 163-166). The Scythians traded peacefully for centuries with the Xiongnu, the dominant people occupying agriculturally valuable lands from the Eastern Steppe to the Ordos plateau by the Yellow River. Presumably because of their lands, the Qin Dynasty around 215BC invaded them and they were forced to flee northward reverting to a nomadic steppe lifestyle for many years, but eventually returning and settling in the Tarim Basin (Beckwith, 2009: 71-73). It is under Emperor Wu of the Han Dynasty that the influence and reach of the Chinese Empire extended to Central Asia's nomadic communities and beyond. Central Asia from 200BC onwards is a changing region and its people are strongly affected by the geographic, commercial, economic, cultural, and religious novelties that the routes bring with them (Soucek, 2000). Alliances are made between nomads and pastoralist communities to control and monitor the flow of people and goods along portions of the Silk Road (Barfield, 1989:7; Sinor, 1977) and urban centers slowly develop along traffic chokepoints of the major routes. Emperor Wu is known to have sent envoys and armies westward to the Tarim Basin and Iran to survey the lands and report on their observations and any information they gathered from traders there about Greece and the Roman Empire (Di Cosmo, 2002: 206).

The Empires

From the opening of the Silk Road to around 200 AD, the various people of Central Asia are heavily involved in settling trading outposts and engaging in the numerous international trade opportunities proffered by the growth of the Chinese and Roman Empires at first at the poles of the region and later encroaching deeper into the heart of Central Asia (Beckwith, 2009:78). In Western Central Asia, around 100 AD, the dominant groups (Alans and Sarmatians) who were of Iranian origin occupied the territories from the Pontic-Caspian steppe to the eastern edge of the Roman lands until their most western provinces were forcibly incorporated into the Roman Empire. Similarly, on the eastern end of Central Asia, the Chinese dynasties expanded further west into the Tarim Basin area, unsuccessfully attempting to conquer and subjugate the Xiongnu at first. But around 50 AD, the Xiongnu in the South finally yielded to the Han and were assimilated into the Empire (Grousset, 1970:39). The Northern Xiongnu however managed to fight back mainly by raiding the northern Chinese frontier (Barfield, 1989:79) and they retained their kingdom extending as far as Sogdiana or modern day Bukhara (Beckwith, 2009: 89), essentially becoming the de-facto rulers of Central Asia for a few decades. In the same decade, the creation of the powerful Kushan Empire extending all the way south to the Indus river allowed for direct trade with the Romans via maritime connections further enriching this Empire. Not much is known about the Kushans except that they are of Tokharian stock and were the main catalysts for the spread of Buddhism throughout the region (Harmatta, 1999:491). Unrelenting attacks and attempts at expansion by the Empires at both extremes of the region created instability in the center and a marked drop in commerce. The urban centers along the Silk Road withered and in some cases disappeared not only affecting the economies of Central Asia but also of Rome and China (Beckwith, 2009:92).

Early Medieval to Middle Ages

Major population movements characterize the period after 200 AD. While the erosion of the great empires at the poles created porous borders for people living on the frontiers to move further inward, populations of northern and largely Germanic stock migrated south in vast numbers to the western regions formerly occupied by the Romans (Beckwith, 2009:93). The Hephthalites, probably of Iranian origin, formed a large kingdom by invading the lands north of Persia into the heart of Central Asia (Sinor, 1990:173, 229, 300) while populations of Mongolian stock moved further north and east into areas that had been occupied by the Chinese (Beckwith, 2009:93).

At this time, and for a few hundred years, the eastern end of the Silk Road consisted of fragmented realms with kings of non-Chinese origin reigning over a majority of ethnic Chinese in the North, while Chinese dynasties governed a mix of ethnic groups in the Southern area.

During this period of instability with mass migrations and reorganization of borders, Central Asians returned to a mostly nomadic or semi-nomadic lifestyle and their allegiance did not lie with a nation or an Empire but with their ruler and his companions. As such the history of the region is very complex and consists of a catalogue of quickly rising and falling clans and ever-shifting regional borders. Throughout their history and despite the constant ebb and flow of the powerful Empires and kingdoms surrounding them, the people of Central Asia managed to preserve their culture and language by creating their own organizational state whose underpinnings were nomadic pastoralism, or mobile livestock herding, and whose economy was supplemented by control of portions of overland trade routes by loosely organized kinsmen, clans, and tribes (Barfield, 1989:3-7; Beckwith, 2009:107; Foltz, 2010:2).

Perhaps the second-most important ethnic group to conquer the region and set up an Empire was the Turks towards the middle of the 6th Century AD (Millward, 2007:42). Originating from the Eastern Steppe, the Turks fought and defeated the Avars who were governing them at the time and pursued them to the edge of the Aral Sea (Sinor, 1997:146). The Turks traded freely with Rome but were unable to form a lasting alliance with Persia and thus remained at war with them. Nonetheless, the Turks ruled over an enormous territory encompassing most of modern Central and large parts of East and northeast Asia (Millward, 2007:31). Meanwhile the Arab expansion and conquest of parts of Tokharistan (roughly modern day Afghanistan) and southwest into Merv (Turkmenistan) allowed them control of one of the largest urban centers of Central Asia and facilitated trading opportunities (Beckwith, 2009: 123). Written historical accounts of Justinian's interactions and exchanges of Silk Road goods with China, Central Asia, and the Near East in the mid-6th century AD highlight the diversity of human populations participating in these commercial endeavors (Feltham, 2009). The Chinese Empire during that time was governed by the Tang dynasty who sought, like all the empires before them, to expand their borders westward. The acquisition of Xi'an (Chang'an) as the western capital of China was particularly important as it was the largest and most populated city in the world with the largest contingent of foreign residents anywhere (Grousset,1970:126). The Tibetans and Chinese battled each other for territory, both expanding westward but the Tibetans ultimately conquered Khotan and forged an alliance with the Turks (Stein, 1907: 148). Once again, a politically unsettling time for Central Asians ensued as the Arabs, the Chinese, and the Tibetans alternatively governed various areas of the central region, forcing the local populations to assimilate with whoever was governing them at the moment. The Arabs invaded Khorasan (covering parts of modern-day Turkmenistan, Iran, and Afghanistan) and settled into the region by assimilating with the local populations and buying land (Beckwith, 2009:132). While alliances between the great powers were in constant flux, the economy and prosperity of the Silk Road was ever increasing, and the local populations benefited financially, culturally, and politically during this period.

Towards the middle of the 8th Century AD, religious fervor took hold of the region, each empire building grand monuments in the name of Christianity, Islam, and Buddhism. Missionaries of all faiths (except for Judaism and Zoroastrianism) traveled the Silk Roads spreading the word and recruiting converts along the way (Foltz, 2010:12-17). With the embrace of religion as the catalyst, literacy swept across Central Asia particularly the western front as the new heart of the Silk Road was pushed further west. This resulted in the trade routes being pushed further north and west towards the Volga (Beckwith, 2009:141). On the Eastern front, the trade routes also started to move further north through Uighur lands. Major rebellions in the Chinese (Tang) and in the Arab (Umayyad) empires both shared the Sogdians (aided by Uighurs in the case of the Xi'an rebellion) as the primary instigators of these uprisings lending credence to the idea that they had orchestrated these revolts in tandem and using communication lines through the Silk Road (Beckwith, 2009:146; Barfield, 1989:153). Through their skill at translation, the Sogdians facilitated the transmission of religious and literary texts, music, paper-making techniques, and continued trading goods despite the slow erosion of some of the great powers (Andrea, 2003b). The Tang dynasty in particular suffered throughout this period losing western and northern lands to the Uighur and the Tibetans (Drompp, 2005:197), and being forced to turn their attention far south to maritime trading routes with Canton.

In the ninth Century, economic hardship in the region caused by climate change led to the breakdown of the Arab empire, the contraction of the Tibetan empire, and forced the Chinese to turn inward (Barisitz, 2017; Beckwith, 2009; Brown, 2001). This left the central regions to revert to a nomadic lifestyle with the great steppes as borders east and west between nomadic peoples and semi-nomadic pastoralist or agrarian communities. The new traders in the western area were the Vikings who reached Islamic territories arriving to the shores of the Caspian Sea by way of the Volga (Noonan, 1998:53). With the collapse of the Arab caliphate, the new rulers were mostly of Iranian or Central Asian origin. The Seljuks were the exception being of Turkish origin, but they conquered lands through Persia and into Anatolia spearheading the Turkicization of the region (Bosworth, 1968: 15-16). The Khitan, of Mongolian origin, governed the northeastern border of China to the Eastern Steppe ruling over a mix of Chinese and Central Asian peoples (Drompp, 2005: 200-205). Over the next three centuries changes in leadership were frequent but not so much to cause havoc in the region, however large groups of diverse people across Central Asia were consistently governed by leaders of changing ethnic background creating instability in these communities where one or another group were constantly vying for majority and recognition. In 1147, the Mongols led by Kabul Khan rose to power and took over the whole of the Eastern steppe, setting the stage for one of the most important periods in Central Asian history (Beckwith, 2009:176).

Mongol Invasions to the Closing of the Silk Roads

At its apogee, the Mongol Empire had spread from the Eastern Chinese shores to Poland, extending from the Arabian Sea to central Siberia unifying all Central Eurasia through conquest.

In 1206, the grandson of Kabul Khan, Temujin, was crowned Universal Ruler (Genghis Khan) by a confederacy of Mongol tribes (Chaliand, 2014:142). His power was considered God-given and his decree was to expand the empire in all directions; he expected allegiance to be paid to him directly and solely, not to the tribe at large, differing from previous nomadic political structures (Barfield, 1989:191). Many including the Uighurs and the Karluks voluntarily joined the Mongol Empire, but many more were conquered through force as large waves of Mongol armies rushed across Central Asia by way of the Silk Road, contributing yet again to the evolving ethnic makeup of the Central Asian people (Wood, 2002). In 1212-15, Beijing fell to the Mongols, extending their realm all the way East (Chaliand, 2014:142). A few years later, the shah of Khwarizm also succumbed to the unrelenting Mongol attacks ceding Iran and all Western and Southern Central Asia (Beckwith, 2009:188). The sons and grandsons of Genghis continued his campaign of war and subjugation across Eurasia for roughly a hundred years. A decade after Genghis' death, the Mongols invaded the Turkic, Finnish, and Ugric people living north of the Volga as well as the Russians all the way to Vladimir (near Moscow), down into Ukraine and finally reaching Poland and Hungary (Chaliand, 2014:147-148). Tibet fell easily without much bloodshed. The Mongols invaded Baghdad in 1258 and moved westward until they were rebuffed and badly beaten by the Syrian Mamlukes, one of their first defeats (Chaliand, 2014:149).

One of the major achievements of the Mongol campaign was creating a thriving, stable expanse across all of Central and most of East Asia governed by a highly capable and unifying force with one script that all could learn despite the multitude of languages spoken and diversity of the peoples (Beckwith, 2009:194). Merchants all the way from Europe, notably the Polo family from Italy, profited from the opportunity to visit and trade directly with this extensive and greatly powerful kingdom, bringing goods and people from the extremes of the road in direct contact with each other (Wood, 1998:5-6). The downfall of the Mongol Empire coincided closely with the outbreak of the bubonic plague across China and then Europe, decimating populations and ravaging economies (Beckwith, 2009:195). Portions of the Khanate fell in the 1300s starting with most of Iran and parts of China expelling the Mongols back to Mongolia.

This turbulent time saw the rise of one last leader who would retake lost territories and control the region for a brief time, Tamerlane, of Turkic-Mongol origin and from modern day Uzbekistan (Chaliand, 2014:150). Tamerlane defeated the Mongols in northern Central Asia then Iran and the Caucasus, and moved North to Moscow (Chaliand, 2014: 151). Around 1400, he set his sights on Northern India capturing Delhi, then doubling back to invade parts of Mameluke Syria and over the ensuing years battled his way through Ottoman lands (Manz,1989:70-73). During his reign, he poured his finances into building up the Central Asian city of Samarkand, so it would become the cultural heart of Eurasia and a model city for the world (Beckwith, 2009:202-203).

In the early 15th Century, Tamerlane died and with him the last of the large Central Asian empires. The Ottomans seized control of the western portions of Tamerlane’s empire and the Safavids took over the old Persian realm (Chaliand, 2014: 5, 140, 170). Meanwhile, in Western Europe, a new form of trade was taking root with the Portuguese leading the charge. Maritime exploration began and with it the slow decline and decay of the overland routes (Beckwith, 2009:209-211). As new Empires rose to prominence in the West the focus on trade with other regions became more important and new alliances with coastal countries were formed.

While the routes continued to be used, on the Eastern front and only sporadically, the story of the Silk Road trade routes stops here when most of the roads became unused and eventually defunct from the 15th Century onwards.

CULTURAL CONTEXT

Much like the history of Central Asia itself, the cultural context from which the Silk Road emerged is equally complex and diverse. Over the long span of 1600 years, the influence of the major world religions, warring invaders from faraway lands, and the constant migrations of peoples in the region have provided a very nuanced and diverse culture across Central Eurasia. Despite the disparity of ethnicities, languages, and socio-cultural mores, there is at the core a similar pattern that has in many instances endured until present.

Christopher Beckwith, noted scholar and historian of Central Asia and the Silk Road, has presented a paradigm that forms the basis from which has evolved all Central Asian socio-cultural relations: the Central Eurasian Culture Complex. The essential component of this Culture Complex is that each clan, tribe, or population have a ruler that looks over them governing and protecting the people and this ruler is surrounded by what Beckwith calls the *comiatus* (2009: 12-13), a close-knit troupe of friends or blood-brothers who protect the ruler and enforce his policies. The comiatus comes in many forms: they can be family members, friends, or elected officials, and this court of sorts can be comprised of a few or an entire assemblage with tiers and classes within in it. Through an oath, they pledge their undying loyalty to their leader and, upon the ruler's death, they commit ritual suicide and are buried alongside him (Rolle, 1989: 61, 64). The presence of a comiatus is confirmed through historical sources and archaeological evidence in the Scythians, the Xiongnu, the Persians, the Hephthalites, the Turks, Uighurs, Sogdians, Tibetans, the Mongols, the Byzantines, the Chinese and the Arabs post-Islamization (Beckwith, 2009:15-16). With the increasing influence of world religions on the people of Central Asia, the idea of ritual suicide became anathema and its importance in the comiatus faded but the structure of the relationship between ruler and consort endured and was adopted and adapted by new groups conquering the region.

The espousal of a nomadic lifestyle in diverse populations of Central Asia in the first millennium BC triggered the development of shared cultural traits among these otherwise linguistically and culturally different groups (Dani and Masson, 1999: 459). Much of the early literature on Central Asian populations describes the opposing values of the urban and agrarian peoples versus the nomads, with a romanticized notion of the great Nomadic cultures of the steppes as being unique in their mores and traditions, and particularly hungry for war (Herodotus for example barely mentions agriculturalists in Scythian times, preferring to focus on nomads and their warring ways). But modern scholars have postulated that the desires and ambitions of both the nomadic and the urban or pastoral peoples were probably quite similar. Both needed to keep crops or livestock thriving and thus both participated equally in commercial trade along the Silk Road to provide for their rulers who in turn would ensure the welfare and protection of their communities and lands. The Nomads were no more bent on war than any other peoples of the region, but would fight for their right to trade along the routes.

The influence of the nomadic culture on Central Asian population composition however was probably significant. Nomads and semi-nomadic people contributed to the ever changing character of Central Asia as borders became for the most part futile. Statehood was defined by the people and their relationship to each other, not by their geographic relationship to frontiers. When rulers died or were killed the people quickly pledged allegiance and united with their conquerors or neighboring states while still preserving their traditions and language for hundreds of years (Beckwith, 2009). This led to a cycle seen throughout the history of the region: one group rising quickly to ascension and acquiring enormous swathes of land and diverse populations under its wing, until the next big power would blast through, taking over and repeating the same pattern. The three most successful, those whose impact lingered for generations, were the Scythians, the Turks, and the Mongol invaders.

The Silk Roads were a lifeline to the people of Central Asia and the lifeblood of Central Asian economics. However, it is not only the trade of goods and products that marked the region but the exchange of ideas, philosophies, religions, and people along the way. And these exchanges were not exclusive to the extremes of the road in fact most of the trading whether cultural or material occurred in the center of the region and over short distances.

The collapse of the large Roman and Chinese Empires on the edges of Central Asia created an opportunity for border-dwellers to move further into the central zones of the empires and become integrated into the fold. Large numbers of individuals migrated over relatively short distances creating significant movements that affected the makeup of societies on the fringes of Central Asia. It was not until the early Middle Ages however that great kingdoms or empires on either side finally met and acknowledged each other's existence. Previously, trade and communication had always gone through intermediaries, such as the Sogdians, who for a few hundred years controlled much of the routes more or less exclusively.

With the spread of Buddhism by way of the Kushans and the rapid sweep of Islam across the region via the Arabs the model of ruler and comiatus persisted but adapted. In Buddhism, the comiatus became synonymous with the monastic tradition: groups of men dedicated to a spiritual teacher until they achieve nirvana, while in Islam the Comiatus morphed into the Ghulam system (guards or soldiers of the religion) much later adopted by the Ottomans (Beckwith, 2009). Medieval culture became religious in nature: monastic institutions were built and literacy across the region increased. The people of Central Asia, particularly in urban centers such as Merv and Samarkand, renowned international centers for education and high culture, influenced medieval Western European culture particularly through exchanges with Spain and the Near East. The golden age of the Islamic period saw a shift in the heart of scientific research and philosophy to Central Asia, and no longer in the Arab world. As a result, during this period an increase in agrarian and urban culture was seen across the region and in the Eastern Steppe.

It is not surprising that because of the deterioration of the Silk Roads the power of these former urban centers of learning slowly faded and the cities eventually disappeared leaving the residents to emigrate towards Europe or East Asia in search of new places to settle or to revert to nomadic and semi-nomadic lifestyles.

CONCLUSIONS

Through a long fluctuating history, and because of a challenging topography, the survival of the Silk Road for 1600 years and its continued existence through periods of incredible upheaval and instability was in no small part due to the Central Asian peoples nomadic, urbanized, or land owners' efforts to keep it alive. It is in this context that we must consider not only what the Silk Road brought to Central Asians but also how widely certain aspects of Central Asian culture from goods to ideologies were exported across the world from the first millennium BC to the 15th Century.

Chapter 3: Genetic, Linguistic, and Archaeological Evidence

INTRODUCTION

Information about unrecorded aspects of human history can be garnered by gathering evidence from the fields of human genetics, linguistics, archaeology, and anthropology to reconstruct social, cultural, and environmental settings as well as population movements and admixture. These bits of data and materials have helped historians reconstruct as accurate a timeline and telling of events as possible. Although this dissertation is focused on changes in craniofacial morphology, the information that artifacts, historical narratives, and language can provide is extremely valuable in forming a more complete picture of the people of that time period. Archaeological data on excavations and finds from 1900 onwards (Belenitsky, 1968;Romgard, 2008), country-specific chronologies (Frumkin, 1970), information on funerary practices and rites (Minyaev, 2009; Van Noten and Polosmak, 1995), full skeletal osteological analyses for evidence of trauma and lifestyle indicators (Jordana *et al*, 2009) and studies linking osteological data with linguistic, cultural, and genetic evidence (Thornton and Schurr, 2004) all help give a context to the cranial analysis in this current research. Because little osteological research has been conducted on this region and time-frame, it is important to consider the contribution and information that recent genetics studies on the admixture of people in the region have provided.

GENETICS OF REGION AND CURRENT RESEARCH

Large-scale events create conditions ripe for populations to mix: the rise and fall of empires, wars and invasions, the slave trade and colonialism, and trading routes such as the Silk Road which facilitated population movements and interactions for centuries. An admixed individual will possess DNA segments from both parents and thus from any of their ancestral populations. These segments of DNA shrink with each passing generation so it is possible to date the advent of admixture by determining the size of the ancestral segment (Hellenthal *et al.,* 2014). A loose timeline correlating historical migrations and events with admixture can be derived from the genetics studies conducted on Central Asian populations in the last two decades.

Early Bronze and Iron Ages

The initial population of Central Asia by anatomically modern humans dates back to around 40,000 BP with subsequent waves of migration radiating from the region outwards (Wells *et al*., 2001). An ancient DNA study on Bronze Age and Iron Age human remains from the Tarim basin showed that these individuals had the highest frequency of mtDNA haplogroup C, seen primarily in Siberian and Central Asian modern people and in lesser amounts in some East Asian peoples, and haplogroup H found most frequently in Northwestern Europe and the Iberian Peninsula. This study puts a significantly earlier date of contact between East and West than the opening of the Silk Road, and considers a Siberian Afanasevo or Andronovo origin for Tarim Basin populations of the Bronze Age (Li *et al*., 2010). An earlier genetic analysis of 49 Eurasian populations looking at frequencies of 23 biallelic Y-chromosome polymorphism haplotypes also confirms this based on the paternal lineage: around 3000 BC, the Kurgan, thought to have spoken a proto-Indo-European language (Haak *et al.,* 2015), migrated from Siberia across Central Asia and also south to India (Wells *et al.,* 2001). In a 2004 study by Lalueza-Fox *et al.,* mtDNA from ancient human teeth from Kazakhstan dating from the 14th Century BC to the 5th Century AD is analyzed. The results show that prior to the 13th-7th Centuries BC (Bronze Age) all the individuals belonged to European or Western Eurasian lineages. This corresponds well with historical accounts of Indo-Europeans populating the area early on and the linguistics evidence of the early Indo-European language Tokharian being spoken in the region. From the 6^{th}-5^{th} Centuries BC (Iron Age,) East Eurasian sequences begin to appear in the samples alongside the Western Eurasian haplotypes. This date of Eastern addition to the Kazakh genome corresponds closely with the emergence of the Xiongnu, East Asian nomads, sweeping through the region. European groups in another analysis showed an uptick in Northeast Asian and East Asian contribution from 1080 to 440BC directly linked to the conquests of Xiongnu from the Asian Steppes to the eastern borders of Western Europe (Hellenthal *et al.,* 2014).

Early Silk Road to Mongol Period

A potential admixture event, with contributions from a western European population, was identified in the Kalash, an isolated population in the mountains of Pakistan claiming descent from Alexander the Great, sometime shortly before 200 BC (Hellenthal *et al.,* 2014). This corresponds with the historical timeline and records of Alexander's invasion of the Hindu Kush.

In a landmark study that considered mitochondrial DNA, linguistic, and historical data as a cohesive entity, 200 individuals from four diverse Central Asian populations were selected to determine their genetic ancestry (Comas *et al.,* 1998). Mitochondrial DNA analysis (mtDNA) can reveal relationships along the maternal lineage, and four key Central Asian populations (Kazakh, Uighurs, Highland and Lowland Kirghiz) had mtDNA sequences that combined many European and East Asian characteristics. Researchers concluded that this was most likely due to admixture over long periods of time and in great amounts of European and East Asian populations, correlating temporally with the creation and maintenance of the Silk Road which facilitated gene flow through the region for 1600 or more years (Comas *et al.,* 1998). However, it is the Turkic invasions from 300 AD that explain the common origin of the Kazakh, Kirghiz, and Uighur people and languages (Comas *et al*., 1998).

Other studies, such as Ulivi *et al*. (2013), show a gradient from west to east with a higher proportion of Western European/Eurasian genetic contribution decreasing steadily across the continent and an admixture dated to the middle period of the Silk Road. Through the analysis of iris color heritability, the researchers found that the frequency of blue or green iris color decreases steadily and substantially compared to brown iris color as one moves eastward along the Silk Road trade routes.

The modern diversity of the people in the region though is primarily due to later migrations along the Silk Road and much of their genetic heritage can be traced to the Mongol period (Wells *et al*, 2001).

Mongol Period

Hellenthal *et al*. (2014) compiled a global genetic atlas of modern human admixture over the past 4000 years. Their analysis shows the strong influence of the Mongol expansion into Central Asia in the 13th and 14th Century AD affecting the Uighur, the Hazara (of Afghanistan), and the Turkish with a gradient of East Asian genetic contribution progressively decreasing from east to west.

While most of these studies have focused on the common origin and similar genetic contributions from East and West to Central Asian groups it is worth pointing out that not all populations end up mixing with occupying forces or with other groups. Interestingly, an Eastern Kazakh group was not genetically influenced by the Mongol invasion and occupation of their region over 200 or more years: there were no traces of any admixture event correlating with Genghis Khan and his armies (Tarlykov *et al*., 2013). This makes them unique among other Kazakh tribes and clans who all showed that their Y-chromosome diversity was strongly influenced by the Mongol expansion from the 13th to the 15th Century (Dulick *et al*., 2011). This is even more surprising given that Zerjal *et al*., 2003 identified a Y-chromosomal lineage present in 16 populations across Asia in high frequency (8%) attributable to Genghis Khan and the rapid Mongol expansion through the region.

Populations on the Eastern end of the Silk Road seem to have been much more affected by the Mongol expansion than the more westerly groups. A recent study (Mezzavilla *et al*., 2014) of the genetic landscape along the Silk Road collected and analyzed genetic information from populations in Georgia, Armenia, Azerbaijan, Uzbekistan, Kazakhstan, and Tajikistan. The Uzbeks and Kazakhs presented the greatest genetic diversity among all the groups, in line with the great span and size of their territories. More importantly, this study shows a clear West/East divide along the Silk Road with populations from Armenia, Georgia, and Azerbaijan showing more contribution from Europe and the Near East while populations from Uzbekistan, Tajikistan, and Kazakhstan have more genetic contribution from East Asia. As a whole, populations along the Silk Road have about the same amount of European ancestry but the populations from the Eastern Silk Road were more admixed than the western ones. The study also found that inbreeding was not high in any of the groups except for Tajikistan where genetic variation was quite low. The migration patterns in the region are complex: there is very little gene flow in the western region (except for Azerbaijan which had some East Asian contribution) and gene flow in the East runs in one direction only from East Asia to the more central region of East Asia but does not progress further (Mezzavilla *et al*., 2014). The Tajiks show a small contribution from the southern region of Central Asia while the Kazakhs mainly received contributions from East Asia. This indicates long periods of isolation and therefore relatively low gene flow in the furthest Eastern Silk Road territories except for a brief time corresponding yet again to the Mongol expansion in the 13th Century which reached all the way to Azerbaijan.

Ottoman Influence

Looking into the specifics of extant Turkish populations and whether their levels of admixture correlate with known historical population movements, Hodoglugil and Mahley (2012) found that Turkish populations were quite diverse in their genetic makeup but that the relative contributions from East, West, North, and South varied depending on which regional population was being studied. Regardless, the two major contributors to the Turkish genome are European (38-40%) and Middle Eastern (35-45%) with some contribution from Central Asia (9-15%) and South Asia (0-18%). Although the Central Asian contribution is lower than anticipated, recent historical events like the shrinking of the Ottoman Empire and the more recent emphasis on Turkish national identity may have insulated this society and heightened xenophobia which would have led to a slow decline in Central Asian genetic contribution.

Xinjiang

Numerous genetic studies have examined the extant population from Xinjiang in Western China to offer more information on the unique origins of the modern people in that area. The Uighur population has craniofacial traits that indicate admixture between East and West, Asian and European, which corresponds with the region's reputation as a major historical contact point between Europe, the Near East, Central Asia and East Asia (Xu *et al.*, 2008). In Li *et al.* (2010), a team of geneticists analyzed paternal and maternal DNA in human remains in the Tarim Basin from the Bronze and Iron Ages, dating the earliest occupation of the region around 3980 BP. A population from Xiaohe in the Northwestern Chinese province of Xinjiang showed different provenances for their maternal and paternal lineages: the maternal genetic contribution was from eastern and western regions while the paternal contributions were solely western. As indicated at the beginning of this section, Li *et al*. (2010) considers a Siberian Afanasevo or Andronovo origin for Xinjiang populations from the Bronze Age.

Genetically, modern Uighurs have Western Eurasian (<60%) and Eastern Eurasian ancestry (40%), proportions that are attributed to an admixture event that occurred 2,100-3,000 years ago (Xu *et al*., 2008). These dates correspond with the historical record of major trading routes passing directly through Xinjiang linking East and West, consistent with the establishment of the Silk trade routes (200 BC).

In another study (Yang *et al.*, 2008) investigating the genetic makeup of three populations from the Gansu corridor (northeastern part of the trade routes near Xinjiang) and two Uighur populations from Xinjiang proper, the admixture proportion of the Uighur populations coincided exactly with the Xu *et al.*, 2008 study. The Gansu corridor populations were genetically intermediate between East Asian and Central Asian, but also had a significant maternal contribution of European-specific haplogroups linked to the time frame of the Silk Road; these results indicate gene flow and therefore admixture through the corridor from west to east (Yang *et al*., 2008). Another genetic study (Patterson *et al*., 2012) which looked at Uighur populations presented a slightly more detailed picture of the history of admixture in this population. The researchers found that an admixture event involving Western Eurasians occurred much earlier lending a European admixture proportion of about 50% (similar to Xu *et al.,* 2008 and Yang *et al*., 2008). However, they noted a more recent admixture event dated to around 1200 AD which corresponded with East Asian genetic contribution and was attributed to the Mongol invasions (Patterson *et al*., 2012).

In a 2004 study by Yao *et al*. looking at the mtDNA of six different groups from Xinjiang, the proportion of western Eurasian contribution was found to decrease moving eastward from the Uzbeks (41%) to the Kazakhs (30%) followed by the Mongolians and the Hui at 6.7%, and finally the Han Chinese who had no western Eurasian contribution at all. The only group that did not fit neatly along the gradient was the Uighurs who had the highest proportion of western Eurasian contribution despite their more easterly location of origin compared to the Uzbeks and Kazakhs. However, this makes sense given their history of ancient admixture with Western Eurasia since the Bronze Age and their longtime residence in Xinjiang, the Han Chinese in comparison only moved to Xinjiang 60 years ago.

Sex Differences

Generally, genetic studies have shown strong parallels between Y-chromosome variation and language differences in populations, while mtDNA variation has explained female driven sex-specific migrations seen in Central Asia and around the world (Owens and King, 1999).

Studies comparing mtDNA and Y-chromosome sequences within Central Asian groups show more pronounced female migration probably because of women marrying outside of their own tribe. The patterns of admixture, therefore, differ not only between populations but within the same population they can also differ between the sexes (Chikisheva, 2008). These differences are magnified during the timing of the Silk Road (Owens and King, 1999; Perez-Lezaun *et al*., 1999). mtDNA diversity in lowland and highland Kirghiz communities is equivalent because of the exogamous social structure where females leave their tribe for marriage (Perez-Lezaun *et al*., 1999). However, haplotype diversity is lower in high altitude populations due to a male-driven founder effect in the settlement of high altitude lands (Perez-Lezaun *et al*., 1999). A study by Tarlykov *et al* in 2013 analyzed paternal and maternal DNA in Eastern and Southern Kazakh tribes. The results showed substantially different migration patterns between men and women, with women migrating to other regions and from other tribes as evidenced by data that are consistent with other ethnic groups in Central Asia. The paternal lineage, however, presented a completely different picture. The Eastern Kazakhs had very low paternal genetic diversity and all shared a common paternal ancestor, consistent with their orally related story of origin. The geneticists then analyzed the Y-chromosome haplotype diversity in Southern Kazakh tribes and found the two tribes although not geographically distant had completely different paternal origins. This was due to the extensive genetic isolation of the males in the eastern region and the exogamous structure of the tribe.

mtDNA analysis and therefore the maternal lineage carries the best evidence of a population's migration history. The Hui are descendants of Persian traders (almost exclusively men) who arrived to the southern coast of China in the 7th Century AD. They moved northward and married Han Chinese women along the way for generations, eventually settling in Xinjiang (Yao *et al*., 2004) thus the low percentage of Western Eurasian contribution in their maternal lineage at 6.7% (Yao *et al*., 2004).

These studies further emphasize that genetic diversity is heavily affected by the social structures and cultural norms of populations.

LINGUISTIC PATTERNS AND HISTORY

Additional evidence of population admixture can be gathered from linguistic sources, helping to guide genetic and morphological studies. Language, much like genes, is influenced by drift, migrations, and divergence, with modifications occurring as it is passed along to new generations (Creanza *et al*.,2015). For this reason, it is possible to correlate or at least compare the changes in language to the changes in genes and in some cases their evolution is synchronized. The two major languages of origin for the region are Proto-Indo-European covering most of the western and central Silk Road including western China and Proto-Sino-Tibetan in the eastern region (LaPolla, 2013). The case has been made for a third linguistic family the Altaic line which comprises Turkic, Mongolian, and Tungus, with the potential addition of Korean and Japanese (Vovin, 2015: 197; Heyer and Mennecier, 2009:163).

A 2015 study by Creanza *et al*. tested whether human demographic history leaves the same imprints on language, in particular, on phonemes (smallest unit of sound in a language that differentiates one word from another) as it does in genes. The team found that both genomes and language carry the imprints of their geographic location and therefore are good indicators of human migrations within a region. But while genes can only be transmitted vertically from one generation to the next, units of language (or phonemes) can be exchanged by speakers of different languages so they are often transmitted horizontally. Populations in long-term proximity to one another would therefore show an increase in phoneme similarity and share large parts of language. This is especially true for cities where many people from different populations had to communicate for commerce and as they traded goods and lived side by side their languages grew more similar to one another (i.e., a decrease in phoneme diversity). Isolated populations, on the other hand, show more phonemic diversity. Genetically, however, it is the exact opposite, these small, geographically isolated populations show a decrease in genetic diversity. While human migration patterns leave signatures on the genome and in language, the same processes do not always yield the same results. Creanza *et al.* (2015) find that geography affects both genes and language, but the evolution of language occurs much faster than evolving genes.

The original Indo-Europeans are thought to have left their homeland around 8000-9000 years ago and spread across Central Eurasia in two or three waves, though the expansion dates and directions are still being debated (Anthony, 2010; Mallory, 1989). They arrived in these new areas and settled in with pre-existing groups with their own culture, mixing in with them, imprinting on the local populations parts of their language and culture. Anthony (2010:59) posits that early Proto-Indo-European may not have been spoken until after 4000-3500 BC. All Indo-European languages can be classified into three groups: first wave languages (Anatolian and Tokharian around 2000 BC), second wave languages (Italic, Greek, Indic, Armenian and Germanic) and third wave languages (Iranian, Slavic, Baltic, Celtic, and Albanian) (Beckwith, 2009: 365). Daughter languages of Proto-Indo-European are very similar to the original language but they have acquired "loan words" (Beckwith, 2009:369) from local peoples and a new characteristic phonology. Beckwith describes the changes that have occurred in the daughter-languages as a creolization of the original language, acquiring and undergoing important changes as they converged with local languages (2009:370). Overall, Indo-European languages conserved much of their original specificities compared to other prototypic languages (Anthony, 2010). Two stages of migration are characteristic of Indo-European language evolution: one from the ancestral homeland, probably east or central Anatolia (Bellwood, 2013:159), to a transitional location and then another migration from there to the final place where the modern language family is known from (Beckwith, 2009:373).

The Tokharian language, classified as an Indo-European language but spoken in Eastern Asia, particularly greater China, tells of the origin of the populations speaking it: residents from Kucha in the first century BC with European features who probably migrated from the Iranian plateau along the northern Silk Road to reach the north edge of the Taklamakan desert where they settled

(Walter, 1998). Analyses of the origins and evolution of languages and dialects along the Tarim basin and in ancient cities like Turfan have explained in part population movements in the region (Hitch, 2009).

Renfrew (2004) suggests that the spread of Proto-Indo-European language correlates closely with the dispersal of the first farmers from Southwestern Eurasia or Anatolia towards the Northwest from 8500-9500years BP (also confirmed by phylogenetic linguistic studies by Gray *et al*., 2011). This seems to correspond with evidence from genetic and craniometric studies pointing to a demic diffusion migration across the region (Pinhasi and von Cramon-Taubadel, 2009). While Renfrew stresses that the advent and dispersal of farming is probably only one of many reasons that Proto-Indo-European expanded as far as it did, he does suggest that it could be the key to understanding how languages spread across the world (Gray *et al*., 2011). Nettle and Harriss (2003) expanded on this theory and investigated how genetic distance relates to linguistic affiliation in populations from across the world. They found that these two are linked only under very specific circumstances: where large-scale demic diffusions have occurred in the last few thousand years and are followed closely by long-periods of sedentism. They find this to be true for Indo-European, Sino –Tibetan, and Altaic language families (Nettle and Harriss, 2003).

The ancestral homeland of Proto-Sino-Tibetan was probably located somewhere in the sub-Himalayan region and its disintegration into various initial daughter-languages started around the fourth millennium BC when original populations migrated to Southern China and much later to Northern China (Pejros and Shnirelman, 1998:381). From the second millennium BC onwards, these waves of migrations were often supported and sponsored by the various Chinese dynasties and governments (LaPolla, 2013). Much like Indo-European, Sino-Tibetan's spread across vast swathes of Eastern Asia is thought to be linked to the spread of rice cultivation or in some cases millet (Pejros and Shnirelman, 1998:382).

In a comprehensive genetic and linguistic study of peoples along the Silk Road Heyer and Mennecier (2009:166) first analyzed the genes of 26 different populations from Western Uzbekistan to Eastern Kirghizstan. They then analyzed the languages of these peoples: about half speaking Indo-Iranian dialects (from the Indo-European language family) and the other half speaking various Turkic dialects (from the Altaic family). Their results showed no correlation between geographic distance and genetic distance among these populations (2009:171), however, they did find that linguistic distance correlated with genetic distance. These populations could roughly be divided into two genetic groups which cleaved according to language family: populations speaking Indo-European languages and populations speaking Altaic languages.

From all the linguistics research on the region, it seems that Central Asia is a unique place where linguistic origin and not geographic location affects genetic diversity. This is yet another example of how a cultural trait- language in this case- can shape genetic diversity (Heyer and Mennecier, 2009: 163-180).

ARCHAEOLOGICAL DIGS AND CURRENT RESEARCH

Archaeological data from 1900 onwards have provided pieces of information on the life of Central Asian populations. These include the discovery of the mummies with European features in Xinjiang dating from 2000 BC, and the influence of Alexander the Great's armies on populations from Iran to Tajikistan (Belenitsky, 1968:58). Through the analysis of funerary practices, artifacts, and rites information can be gleaned on the cultural, linguistic, and ethnic heritage of the deceased and the world they lived in. It bears mentioning that the pre-history of Central Eurasia and migration as an explanation for the important social change seen during this time is somewhat contentious in the field of archaeology. As such, there is a division in the literature concerning reasons, direction and dates of these movements, and the technological or climatic changes that may have catalyzed them. Frachetti (2011: 196) points out that in the case of Central Asia, unlike the vast research available on migration from the Paleolithic onward in western Europe, "migration appears as an inferred explanation without positive archaeological signatures" due to the lack of extensive data from archaeology, genetics, linguistics, and osteology for the region. Despite this, Frachetti's (2011) review current and past literature concludes that migration, due to a confluence of climatic changes, technological advancements (e.g., metallurgy, invention of the spoked-wheel), domestication of the horse, and social changes still remains a "strong explanatory voice in Eurasian scholarship" (pg: 206).

The Neolithic transition (10,000BC to Bronze Age) is defined by population growth and expansion due in part to more abundant and consistent food production (Bellwood, 2013; Xue *et al.,* 2006), and major human population developments. In Central Asia, presumably because of the climate and harsh environment, pastoral nomadism took over primarily in the steppes (Bellwood, 2013) leading to a low density population easily affected by demographic changes (Zerjal *et al*., 2002, Lockard, 2008:24). By 4,000 BC, the middle of Central Asia was occupied by a mix of pastoralists and farmers who lived side by side (Chaix *et al*., 2007).

Information about the lifestyle and people of north Central Asia during the Bronze Age is still being uncovered, but the discovery of archaeological sites in the Baraba forest-steppe of western Siberia has yielded some interesting insights. From around 3,000-700BC, large migrations from Kazakhstan and southwestern Central Asia towards Siberia led to the establishment of a culturally mixed population in the north. Most of the evidence for this comes from beads and beading techniques originating further south that were found during excavations in the northern forest-steppes, as well as ancient DNA analysis of infant remains (Pilipenko *et al.*, 2008). The late Bronze Age and the Iron Age saw intermittent movement through the area. Although much of the archaeological data available deals with China, Siberia, and the far borders of Central Asia, this has more to do with a lack of information on the inner regions (not as many sites and digs) than a lack of human activity there.

In Western China, mummies dated between 2,000 BC and 200 BC, were found in the Tarim basin causing a stir in the archaeological and anthropological community because of their more western features and fair hair (Romgard, 2008). Two different conclusions were drawn based on the analysis of these mummies: that these individuals came into the region from the north where they migrated from Siberia via the Irtysh Valley (Kozintsev, 2009), or that these individuals are of Near East origin and would have migrated from the south (from the Near East or South Asia) before the Silk Road trade started (Thornton and Schurr, 2004). As some studies indicate, the appearance of individuals of different ethnic makeup in areas where they are not indigenous was a more frequent occurrence during the Iron Age (1300-200 BC).

Burial practices of the Xiongnu and the Scythians offer glimpses of pre or early Silk Road populations and their probable ethnic affiliations (Minyaev, 2009). Full skeletal analyses of remains found in burials can determine if trauma or violence occurred in these populations and provides lifestyle indicators (Jordana *et al*, 2009). The discovery of frozen tombs in Mongolia with remains of individuals of western Eurasian and admixed descent as well as funerary artifacts indicating an Indo-European origin helped extend the range of the Scythian population further east than previously thought (Van Noten and Polosmak, 1995). Thornton and Schurr, in their 2004 paper linking osteological data with linguistic, archaeological, and genetic evidence, describe a high level of cultural and biological continuity over time in the Tarim Basin (Xinjiang, Western China) considering all the migrations traversing the region from both sides.

At a cemetery in Xiaohe, Xinjiang 167 graves were analyzed (Abuduresule *et al.,* 2007). Grave goods such as woolen fabrics, wheat grains, and animal bones (e.g., sheep) revealed that these Bronze Age to Iron Age remains belonged to those of agricultural and stockbreeding peoples who had come from the West (Romgard, 2008). The osteological analysis confirmed the older western lineage but also indicated that over time and in stages from the Han Dynasty onwards (from 200 BC) an influx of people came from the east to this area of the Tarim Basin (Li *et al*., 2010). In Hami, on the northern Silk Road, Bronze Age graves were found with walls made of mud bricks and stamped earth, a technique found in Bactrian graves indicating an exchange of funerary traditions between western central Asia and the Northeastern Tarim Basin (Romgard, 2008). Excavations from the Ili River Valley (part of China but within the Kazakh Autonomous Prefecture) have revealed pottery, wooden objects, and gold rings with ruby intaglio dated to around the 4th Century BC and with classical Greek mythology motifs printed on them. This provides evidence of the spread of Western Greek culture towards the East, probably in conjunction with Alexander the Great's conquests (Romgard, 2008).

Archaeological digs of burial and memorial mounds at Tuva (NW Mongolia, currently part of Russia) and in Central Asia proper revealed an ethnic shift that occurred early on: before the 6th Century BC the peoples of Tuva were culturally and ethnically more East Asian (but still admixed) but around the 2nd Century BC, with the expansion of the Scythians, the communities were influenced by Indo-European cultures and peoples and became more admixed with gene flow coming from the West (Chikisheva, 2008). The cranial analysis of the peoples buried at

Tuva matches the conclusions gleaned from analyses of the funerary constructions and associated artifacts (Chikisheva, 2008).

Chikisheva *et al*. (2009) conducted a dental analysis on a human skeleton buried in a Xiongnu grave in Northern Mongolia which identified the remains as being from a female of Northwest Indian origin. Also found in the grave was a woolen cloth of Parthian origin and embroidered curtains. Parthians, of northeastern Iranian origin speaking the Indo-European language of Parthian, were used as trading intermediaries between China and Rome. The Xiongnu during that period (300-200 BC) occupied the territories in the north between China and Parthia. This matches the historical data as large population of Indians had migrated to Eastern Turkestan by around 100 AD. These Indian women were known to have worked for the Xiongnu embroidering curtains and fabrics. Integrated within the Xiongnu were not only Chinese populations, but also western and southwestern Asians.

Typical "wooden-frame" burials in Northeastern central Asia are widely attributed to the Xiongnu, as are the presence of a comiatus dead by ritual suicide in the chamber of high-ranking war chiefs (Minyaev, 2009). Also, frequently found in Xiongnu graves are dismantled chariots still heavily ornamented in bronze and iron (Minyaev, 2009), but these are emblematic of the wider early cultural influence of Indo-European groups bringing the Central Eurasian Cultural Complex to the region and the chariot culture eastward (Rolle, 1989:114-116).

Archaeological finds not only verify or refute historical accounts but also provide concrete evidence of the lifestyles and cultural traditions of a population. For a long time, all that was known about Iron Age nomadic groups included excerpts from the historical anecdotes and observations of Herodotus who characterized them as violent and cruel people practicing human ritual sacrifice and cannibalism. Archaeological discoveries have helped fill in the gaps and build the narrative about this incredibly long lasting and far-reaching group. Excavations from the Altai mountain region of Mongolia tell us about the Pazyryk, also called the Eastern Scythians (5th-3rd Century BC), where their remains and the burial chambers were analyzed (Jordana *et al.*, 2009). The warrior-culture and comiatus burials are present in this population: the men are buried with their horses and weapons armed for the afterlife. In addition, osteological analysis showed great violence inflicted on men and women of this group with multitudes of injuries many times fatal, and thus concord to some extent with the accounts of Herodotus (Jordana *et al.*, 2009). While not directly considered Scythians, the parallels and similarities of the Pazyryk tombs with traditional Scythian tombs, primarily in the funerary artifacts and art indicate a historical relationship between the two and a cultural transference from the Scythians to the Xiongnu (Van Noten and Polosmak, 1995). Osteological analysis of Xiongnu burials in Mongolia show great craniofacial diversity, but overall, this population's cranial morphology aligns most closely with Chinese populations (Schmidt, 2012: 170,245). As Scythians inhabited areas closer to Greece, it is no surprise to find artifacts influenced by Greek aesthetic buried with them; similarly because of the proximity of the Xiongnu to China, the presence of Chinese goods, such lacquered boxes and silk in their graves is not unusual (Van Noten and Polosmak, 1995).

More recent exchanges between cultures are widely reported in historical documents even if archaeological material is rare. In a 9th Century Viking burial in Sweden, grave goods included a silver and violet glass ring engraved with the words "for Allah" in ancient Arabic script. These decorated glass objects are infrequently found but indicate a trade between the seafaring Scandinavians and the Islamic world roughly one thousand years ago (Bower, 2015).

CONCLUSION

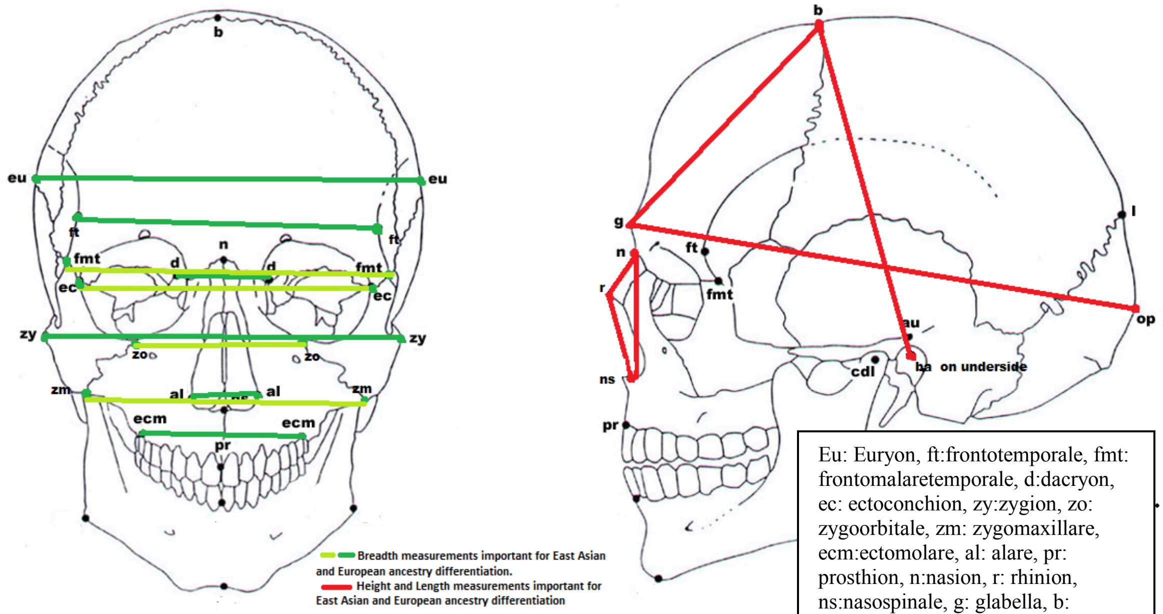
Archaeological evidence from Bronze and Iron Age burial grounds and excavations have revealed an early spread of technology, art, and culture from west to east related to the Andronovo culture, Bactrians, and early Scythians. This movement from west to east is further reinforced by the time-frame of the spread of Indo-European languages across the region from West to East. The genetic evidence is consistent with the west to east movement in the Bronze Age but then highlights a later strong influence and gene flow in the opposite direction due to the Mongol expansion. Many smaller waves of migration occurred across shorter-distances, in particular within Xinjiang Province where populations have been admixing in varying degrees over the last few millennia as confirmed by genetic, linguistic, archeological and osteological evidence (Li, 1999). Morphological studies of cranial features from large population samples have, in addition to the historical record, archaeological finds, and genetic analysis, been critical in shedding light on population movements and providing additional support for undocumented migrations.

Chapter 4: Craniometrics in Central Asia, Aims, and Research Questions

OSTEOLOGICAL STUDIES ON ADMIXTURE

Of relevance to this project are craniometric studies on East Asian and European remains that identify the principal traits that define the range of craniofacial morphology for these groups. A series of analyses have compared European and East Asian samples through linear and 3-D measurements and found that the main differences between these groups were in the upper and mid -face. In East Asian groups, the breadth of the face in particular was larger, the mandible and chin less pronounced or protruding, and the calvarium was rounder with a more flattened occipital region when compared with European groups (Alcade *et al.*, 1998; Ball *et al.*, 2010; Fraser *et al.*, 2003). Horizontal measures of the face such as wide bialare breadth, large bizygomatic breadth, wide intercanthal distance, as well as elongated upper face height, a more anteriorly positioned glabella, and lower nasal projection are all characteristic of East Asian ancestry (Abdushelishvili *et al.*, 1968; Le *et al.*, 2002; Scavone *et al.*, 2006). Figure 4.1 outlines the most important landmarks and measurements for distinguishing between European and East Asian groups.

Figure 4.1: Most important craniofacial landmarks and measurements for distinguishing between East Asian and European groups.



Adapted from Standards by Buikstra and Ubelaker (1994) http://www.cleber.com.br/standard.html

Eu: Euryon, ft:frontotemporale, fmt: frontomalaretemporale, d:dacryon, ec: ectoconchion, zy:zygion, zo: zygoorbitale, zm: zygomaxillare, ecm:ectomolare, al: alare, pr: prosthion, n:nasion, r: rhinion, ns:nasospinale, g: glabella, b: bregma, au: auriculare, l:lambda, op:opisthocranion, ba:basion

A small study testing the efficacy of a craniofacial identification using a 3D facial shape range-finder and a superimposition software program showed that it was able to differentiate between Japanese and Irish/Australian individuals with a 95% success rate based on three measurements alone: nasal width, nasal height, and lower facial height (Fraser *et al*., 2003). It is important to note, however, that there is much variation in craniofacial morphology among individuals of a given population (Roseman and Weaver, 2004), as well as between different populations. A study by Lee and Park (2008) comparing Korean and Japanese individuals by assessing shape differences with a three-dimensional analysis of laser scans showed that the two groups differed significantly in head and mid-facial length and breadth, and in length and breadth of the nasal aperture. The Japanese group was longer and broader in all these traits (Lee and Park, 2008). In a 3D geometric morphometric study looking at craniofacial variability among European, African, Native American, Oceanian, and Asian populations, it was found that using facial length, width, and upper facial flatness landmark information led to a high accuracy of classification for the European population as a whole (Spain, France, Italy, Portugal, Croatia, and Finland) compared to groups from the Americas, Asia (Turkestan, Syria, Dungan, Suse), Africa, and Oceania (Badawi-Fayad and Cabanis, 2007).

Craniometric studies frequently use cranial specimens from different time periods to assess the position of a particular population in comparison with other groups of known geographic origin. This is because it is often difficult to find and access cranial collections from a wide geographical range that are contemporaneous. One such study, sought to assess the ancestral origin of a small group of modern individuals listed as originally from China, and buried in North America (Schmidt *et al.,* 2011). This group was compared to cranial specimens from across the world and from different time periods (modern Africa, ancient Egypt, modern South America, Easter Island, Neolithic to modern China, ancient and modern Japan). This group was found to cluster most closely with Chinese specimens from all periods, and within a larger East Asia cluster which included all crania from China and Japan. Within-group diversity was found to be low across all time-periods in this population (Schmidt *et al.,* 2011). Similarly, another craniometric study investigating craniofacial diversity of Turkish populations (from Bronze Age to modern) within a worldwide sample of ancient and modern crania (Neolithic Greece, ancient and modern Britain, Medieval France, Iraq, ancient and modern East Asia, among others), found that European and Middle-Eastern populations clustered closely together while East Asian groups formed their own separate cluster regardless of the time period the crania were from (Seguchi *et al*., 2010). These results point to the viability of using cranial specimens from disparate time periods to assess craniofacial variation among geographically-differentiated groups.

Admixture occurs when individuals from two geographically distinct populations previously isolated from one another mate (Rosenboom *et al*., 2016); admixture is therefore the consequence of gene flow. Because the Silk Road opened trade routes through Central Asia spanning from Greece and Rome to China and Mongolia, the potential for admixture between populations that are morphologically quite distinct from one another might have increased during that time period (Eroglu and Erdal, 2008). Assessing admixture in the skeleton is difficult because admixed individuals can have highly variable morphologies either resembling one parent or with a completely new series of traits (Ackerman *et al.*, 2006). While most anthropologists use metric analysis to ascertain admixture, nonmetric analysis has also proved useful in identifying mixed origins for populations. In a study attempting to reveal the origins of Japanese populations, Kozintsev (1992), identified seven cranial nonmetric traits (e.g., occipital index, sphenomaxillary suture, transverse zygomatic suture, infraorbital pattern complexity, transverse palatine suture index, supraorbital foramen, and hypoglossal canal bridging) in ten skeletal series from Ancient and modern Japan and China and found that the modern Japanese population showed hybridization between East Asian and Jomon traits. Moiseyev (2009) also came to a similar conclusion of admixture in his analysis of cranial metric and nonmetric traits of Ryukyu islanders (archipelago belonging to Japan).

Studies that have looked at identifying admixed populations utilizing standard craniometric and 3-D geometric morphometric measurements have focused on highlighting not only the differences between the groups that have mixed together, but also identifying the new features that are characteristic of admixed individuals in those populations. In a US-army sponsored study looking at admixed soldiers, results indicated that the admixed population’s craniofacial traits fell within the range of variation of one or the other contributing groups (Yokota, 2004). In two studies examining modern human crania of Hispanic individuals compared to historical samples of Spanish crania, African-Americans, and pre-contact populations from South America, strong differences between these groups in craniofacial morphology were identified and may have contributed to a highly variable admixed Hispanic population (Ross *et al*., 2002; 2004); these results emphasize a need for specific standards for admixed populations (Spradley *et al*., 2008).

Craniofacial morphology can be altered over time due to changes that have nothing to do with admixture but are due to genetic drift, mutations, selection, adaptive pressures, or secular changes. Secular changes are non-genetic changes, or "how time brings about changes in biology […] due to changing variables in the environment" (DiGangi and Moore, 2013: 527). Changes in living conditions, improved nutrition, access to medical care, and better health, are known to cause increased growth in parts of the skeleton, including the craniofacial skeleton, often over one or two generations (DiGangi and Moore, 2013; Westcott and Jantz, 2005; Kouchi and Koizumi, 1992). Cranial changes due to secular growth are typically seen along vertical planes such as cranial vault elongation instead of horizontal measures (Jantz and Meadows Jantz, 2000), and care must be taken to not confuse these secular changes with changes due to gene flow, nor those due to adaptive pressures. For example, when analyzing ancient populations of hunter-gatherers in contrast with agriculturalists one must consider changes in subsistence strategy, which can morphologically alter the masticatory apparatus in particular. However, studies have shown that while the mandible can be significantly affected by changes in diet, these do not seem to affect the cranium which retains a more neutral genetic pattern (von Cramon-Taubadel, 2011a).

Depending on the population being analyzed there may be significant differences in cranial shape between males and females not due to allometric factors (Kranioti *et al*., 2008; Green and

Curnoe, 2009). A 3D morphometric analysis of a Southeast Asian sample showed that the most pronounced difference between male and female crania were in zygomatic and postorbital breadth closely followed by cranial vault breadth (Green and Curnoe, 2009). Of course, these feature differences may be characteristic to this specific population and different traits may be more significantly affected in other populations.

CRANIOMETRIC STUDIES IN CENTRAL ASIA

Historically, Central Asia has shown a clinal distribution of craniofacial traits that are more Near-Eastern or European as one moves west, and more typically East Asian eastward (Abdushelishvili *et al*., 1968:1-7; Keith, 1929). Cities like Turfan, Kashgar, Samarkand, Merv, Bukhara, and Khotan absorbed the majority of migrants and were important urban centers during the height of the Silk Road (Wood, 2002:13). Populations residing in these centers were more likely to intermingle. Therefore, there is an expectation that they would show more admixture than smaller and more isolated populations residing around the eastern and western extremities of the routes. We expect more craniofacial trait diversity in human remains from these large urban centers than in other areas. Yet, there is no evidence that diversity of traits is directly linked with the degree of exposure to other groups, thus these populations could have been living in proximity to each other but not mixing due to socio-cultural reasons (Ross, 2004). Additionally, evidence of material culture spread to a community where it had not been present before does not in itself prove migration, admixture, or even direct contact between groups. Coupled with skeletal and genetic evidence, however, it makes the case much more convincing, thus the need to consider threads of evidence from across the field of anthropology.

Pastoral communities that dominated western Central Asia for hundreds of years were constantly on the move and less likely to settle down near urban centers where Eastern and Western populations were meeting. The nomadic populations did, however, regularly interact with the salesmen and caravans along the way and they traveled to the cities to sell women of their tribes to urban slave owners (Feltham, 2009). Genetic studies have shown differential rates of migration between the sexes, with females migrating outwards more rapidly and in larger numbers due to the exogamous social structure of the highland and lowland pastoral and nomadic communities (Perez-Lezaun *et al.*, 1999). Thus, it is probable that the patterns of admixture might differ between the sexes in osteological analyses of populations from the region (Chikisheva, 2008).

Several studies have been conducted on cranial series across Central Asia revealing some populations that are highly admixed and others that are not, depending on the location and time-period in question (Chikisheva, 2008; Eroglu and Erdal, 2008; Han, 1994; Hemphill and Mallory, 2004; Khodzhayov, 2008; Kozintsev, 2008; Lee and Zhang, 2013; Tan *et al.,* 2013). In terms of skeletal analysis for Central Asia, the current literature available provides us with detailed information only for narrow geographic areas, thus the critical need to contribute more data to the field. The osteological data that have been published are heavily weighted towards the study of admixture in Bronze/Iron Age or late Medieval populations with less known for the time period in between and mostly covers populations on the fringes of Central Asia, not Central Asia proper.

Xinjiang Cranial Series

Han (1994) studied the physical characteristics, by means of observational qualitative analysis, of 274 crania from nine burials across Xinjiang Province dating from 1800 BC-300 AD (most were from the Bronze Age). The crania were classified according to ancestry group based on general morphological characteristics of the vault and face. His results indicated that only a small percentage (10%) of all the skulls analyzed were attributable to East Asian ancestry, as the majority had long vaults and narrow faces indicative of European ancestry. He infers that during the early to mid-Bronze Age populations of western Eurasian or European ancestry were moving eastward at a much faster rate and in much greater numbers than East Asians were migrating westward.

Romgard (2008) describes the skeletal remains found in three regions of Xinjiang dating from the Bronze Age and summarizes the findings according to location. In Hami, located in Northeastern Xinjiang at the Southern border of Mongolia, early Bronze Age crania were examined and a little over 25% of these were classified as European or Western Eurasian while the rest were found to be East Asian. In the Tian Shan mountainous area, bordering modern day Kirghizstan, early Bronze Age crania studied there revealed a community of East Asian and Europeans living side by side but not mixing. Finally, a Bronze Age cranial series from the South near modern day Jammu and Kashmir, was found to be of European ancestry. All of these finds indicate early Bronze Age populations that were in many cases diverse, but not necessarily admixed.

Hemphill and Mallory (2004) analyzed eight craniometric variables in over 1300 Bronze Age skulls from Xinjiang, Kazakhstan, Central Asia, Iran, and China. Before 1200BC, or in the Early Bronze Age, the population of the Tarim Basin was of unknown origin, but the mid and later Bronze Age populations can be classified as Indo-Iranian. It is highly likely therefore that gene flow came from highland Pamir (Tajikistan) and Ferghana Valley (Eastern Uzbekistan) populations moving east. These populations are inferred to be the Saka, an Indo-Iranian group who brokered the east-west trade along the Silk Road.

Lee and Zhang (2013) looked at 26 morphological nonmetric dental traits in 57 Bronze Age to Medieval (700BC –AD420) samples from across China including Xinjiang and Mongolia. They found that the Western Chinese populations were the most different from all the others both in geographic distance and biologically. This is probably because the people of Xinjiang are derived from western Eurasians, as confirmed by skeletal analysis (cranial: Han, 1994; Romgard, 2008; Hemphill and Mallory, 2004; and dental: Lee and Zhang, 2013), genetic analysis (Li *et al*., 2010; Wells *et al*., 2001; Xu *et al*., 2008), linguistic and archaeological data (Walter, 1998; Hitch, 2009; and Romgard, 2008). There also was some late admixture with Mongolians in this population which can be confirmed by genetic studies (Patterson *et al*., 2012). The Northwestern Chinese sample and the Central Plains sample showed low levels of admixture with western Eurasians during the time of the Silk Road (Iron Age to Medieval). Lee and Zhang (2013) posit that the Great Wall of China was not only a geographical barrier between the peripheral admixed populations and central China but also a physical one preventing the flow of languages, genes, and cultures across it.

Tan *et al.* (2013) analyzed 18 craniofacial traits of 148 Bronze Age skulls from Khotan in Southwestern Xinjiang and later compared them to other contemporaneous crania from around Xinjiang province. They found that Bronze Age crania from around the province showed admixed features from Eastern and Western Eurasian populations. They noted, however, that in the Khotan population two different results were obtained depending on which method they used. Using metric traits as the primary method of assessing ancestry, the crania were classified as closer to the East Asian morphological range. But using a qualitative (non-metric) assessment, the crania appeared to cluster more closely with Western Eurasian crania. They surmised that some Western features, such as a high nasion, are dominant, and therefore in an admixed population a high nasion would be inherited and the appearance of the individual would be skewed towards Western Eurasian, even if the metric analysis indicates the opposite. In the end, the researchers determined that there was more Eastern than Western contribution (between 60-87% Eastern contribution) and that these populations had met and mixed as early as 1,000BC.

Western Eurasia

In populations as far as Anatolia an increased frequency of East Asian morphological palatal traits was observed when comparing a Bronze Age population and an Ottoman population. These traits had not been present in such high frequency in the Bronze Age sample (45%) but increased significantly during the early Ottoman period (87%) starting around 1299 AD. In more modern populations, the frequency of palatine torus decreased to 40%, indicating that this trait was introduced by large migrations from east to west along the Silk routes, probably during the Mongol conquests (Eroglu and Erdal, 2008).

Altay, Mongolia, Southern Siberia

Chikisheva (2008) analyzed a comprehensive cranial series from various graves dating from the 7th Century BC to the 3rd Century AD in Tuva, located northwest of Mongolia near the Altay mountains and east of Kazakhstan. Fifteen craniometrics traits were used to assess the ancestry of these individuals, ranging from vault measurements of cranial length and breadth to facial angles. Admixture was present in this group from before and throughout the Scythian period with hybridization between Western Eurasian and Eastern populations, but there were also many Western Eurasians who were not admixed. The earlier cranial series showed an influx of

Western Eurasian traits, assumed to be from the Western Steppe region while the later series show an increase in East Asian traits, presumably from Northern China. While the male crania showed clearer influences from the East and the West at specific times, the female crania had a much more erratic pattern that was attributed to women being involved in contacts between populations through marriage or the slave trade.

Gokhman and Gromov (2009) analyzed thirteen craniometric measures and six nonmetric traits in crania from an Iron Age (200BC-100 AD) cemetery northwest of Mongolia in the northern Altay mountains. While they found some differences in trait distribution between the sexes the most important measures and indices were roughly the same for males and females. Overall, they observed trait continuity between Bronze Age populations from neighboring Xinjiang and Tuva (see Chikisheva, 2008) and an Iron Age population from Kamenka. Based on nonmetric analysis alone, the Iron Age population was attributed to Indo-Iranian Scythians.

Chikisheva *et al*. (2009) looked at the permanent dentition from a young woman in a Xiongnu burial from the 1st Century BC in North Central Mongolia. By looking at the frequency of distribution of various dental traits by geographic population, the author ascertained that this individual was of Southern Eurasian descent and might have migrated from northwest India. While this represents only one individual, this analysis coupled with artifacts retrieved from her grave indicate the presence of a diverse community living side by side but not mixing under the Xiongnu. This is further supported by one of the few 3DGM craniometric analyses conducted on Xiongnu-era burials in Mongolia: most of the Xiongnu were found to cluster more closely with modern and ancient Chinese samples but at least one of the Xiongnu groups under study showed a closer western Eurasian affinity (Schmidt and Seguchi, 2016) however these were found in a more geographically isolated area of Northern Mongolia.

A previously long-held view that a portion of the Southern Siberian population from the Iron Age who had more gracile facial features might have been of Mediterranean origin is contradicted in a 2008 study by Kozintsev. The theory held that individuals from the Near East might have migrated north to Siberia around or after 2,000 BC. Kozintsev (2008), through craniometric analysis, asserts that these individuals were more likely of Indo-Iranian origin migrating first from Europe and then moving east to Eastern Central Asia during the Bronze Age. In the Iron Age, these individuals returned to Europe and gave rise to the Scythians who emerged on the Central Asian stage around 700 BC (Kozintsev, 2008).

Central Asia

One of the few craniometrics studies on Central Asian populations (Avanesova *et al*., 2010) looked at Bronze Age skeletal remains from Southern Uzbekistan. Eighty-seven individuals were analyzed using 25 linear measurements and 14 cranial indices. Many of these crania had a particular set of traits indicative of a Mediterranean origin: a sharply profiled face, a high narrow nasal aperture, and highly convex nasal bones which would have resulted in a prominent projecting nose. But this population also exhibited traits of unknown origin which suggests that this southern Uzbek population was somewhat admixed as early as the Bronze Age.

Khodzhayov (2008) used linear measurements from traditional craniometrics to study Saka cranial series dating from the 7th Century BC to the 2nd Century BC originating from Kazakhstan near the Pamir Mountains. Through his analysis, he ascertained that the Saka population was admixed with an East Asian component in the lowland areas but there was no East Asian contribution in the highland populations. Generally, there was no admixture in northwestern Central Asia and Kazakhstan where the Saka population was of Eastern Mediterranean origin, but these Saka were different from those of the Eastern Pamir region where there was some admixture with Eastern Asian populations in the Bronze Age through the Iron Age.

It seems therefore that there was already a degree of admixture during the Bronze and Iron Age in populations from south-central and northeastern regions of Central Asia (Abdushelishvili *et al.*, 1968; Avanesova *et al.*, 2010; Chikisheva, 2008; Chikisheva *et al.*, 2009; Gokhman and Gromov, 2009; Keith, 1929; Khodzhayov, 2008; Han, 1994).

AIMS OF THIS RESEARCH

The current study will investigate the craniofacial variation seen in Central Asian populations living during the time of the Silk Road trade. Using 3D geometric morphometric analysis, this research compares the craniofacial morphology of Central Asian populations living along the Silk Road before the opening of the trade routes with those living in the same region at the height or the close of the trade routes. Central Asian populations in this study consist of cranial specimens excavated in Turkmenistan and Eastern Iran, Tajikistan (and Pamirs), Uzbekistan, and Kirghizstan.

Pre-Silk Road populations will encompass the time period at or before 200BC, from the Bronze Age onwards (2nd Millennium BC at the earliest). The later Silk-Road populations will range from 300AD (at the very earliest) to 1600AD. Morphological differences will be assessed through examination of individual craniofacial traits and consideration of the overall shape changes seen in the cranium.

Using morphological analysis this project aims to determine whether cranial and facial variation of local populations were affected by large population migrations along the Silk trading routes. If admixture in the craniofacial traits of Central Asian people is observed and has shown an increase over time, then this is likely due to large migrations that the Silk Road facilitated coming from the East and the West, changing the composition of local populations.

Studying chronological changes in craniofacial morphology of populations living along the trade routes both in urban settings and nomadic communities will help clarify the patterns of admixture in Central Asia for that extended time period. By analyzing craniofacial shape in pre-Silk Road populations and comparing it to later period or Silk Road contemporaneous remains, population-wide changes exhibited over time can be clarified and correlated with the information obtained from genetics, linguistics, and archaeology to offer a holistic explanation of population movement during this important period of history.

RESEARCH QUESTIONS

Question 1: Is evidence of admixture observed in the craniofacial morphology of individuals along the Silk Road trade routes?

The specimens from Central Asia will be analyzed looking for morphological changes that can be identified craniofacially. In this case, admixture is identified in individuals with a mosaic of traits inherited from Eastern and Western Eurasians. Crania are expected to show the most differences in the upper face breadth (frontotemporale and frontomalaretemporale), at points such as the lateral nasal borders (alare) indicating the breadth of the nasal aperture, the shape of the orbital area (dacryon, ectoconchion, inferior and superior orbital borders), the breadth of the mid-face and cranium (zygoorbitale, zygomaxillare, euryon, zygion), the roundedness of the calvarial outline (bregma, lambda, opisthion, opisthocranion), and the extent of nasal projection (glabella, nasion, rhinion, nasospinale). This is because studies have shown that the main differences between European and East Asian crania have been detected in those regions (Abdushelishvili *et al.*, 1968:59-61; Alcade *et al.*, 1998; Ball *et al.*, 2010; Fraser *et al.*, 2003; Le *et al.*, 2002; Scavone *et al.*, 2006,). Because admixed population often present new traits or shapes that can be different from the previous generations (Christensen *et al.,*2014 *:*227), it is impossible to fully predict how other areas of the cranium and face might be affected and where changes may occur. For this reason, although special attention will be paid to the series of traits listed above, morphology of the entire skull must be studied, measured, and described. A spectrum or gradient of craniofacial morphology is expected to be observed ranging from "typical" European craniofacial traits in the western regions to more characteristic East Asian crania further east.

Questions 2: Is there an increase in craniofacial admixture over time?

More admixture (meaning a larger proportion of the population under study can be categorized as admixed) is predicted in Silk Road populations compared to the time prior to the opening of the Silk Roads. Previous studies have indicated craniodental differences in Anatolian populations due to the eastern influx from the Silk Road. Eastern Anatolian collections dating to Byzantine and Ottoman times showed an increase in craniofacial traits more frequently observed in East Asian populations, compared to specimens from the same region from the Bronze Age (Eroglu and Erdal, 2008). Pre Silk Road populations (before 200BC) are thus expected to show a lower proportion of admixture, with most crania from that time-frame fitting within the range of variation of European groups or aligning closely with East Asian groups. The Silk Road populations are expected to mostly fall firmly between the ranges of the European and East

Asian groups, thus presenting significant admixture. The Central Asian specimens from three time-periods will be analyzed looking for changes in the nasal aperture, the mid-face breadth, zygomatic, and orbital regions as well as in cranial breadth. Other studies have shown admixture in certain individuals and populations from that region which may or may not be attributable to the Silk Road migrations. This analysis will help in answering this question.

Question 3: If a pattern of increased admixture is observed in these chronologically-differentiated populations, can these changes be attributed to the Silk Roads?

If admixture in the craniofacial traits of these Central Asian people is observed and shows an increase over time then it is potentially due to large migrations facilitated by the Silk Road from the East and the West. Changes in craniofacial morphology over large periods of time can also be attributed to other factors, including secular changes such as better nutrition and diet that have led to observable growth in the skeleton and the cranium in recent times. Secular changes over time are known to influence craniofacial morphology but they have only been measurable in five features of the cranium: cranial vault height, cranial length, cranial breadth, facial height, and bizygomatic breadth (Jantz and Meadows Jantz, 2000; Wescott and Jantz, 2005). In order to determine if secular changes have affected cranial morphology in this population, each set of chronologically-differentiated cranial series will be analyzed focusing on the differences attributable to secular changes like allometric growth over time.

CONCLUSION

While an argument can be made for studying admixture in Central Asian populations from a genetics perspective, this study will rely purely on morphological analysis taking into consideration information provided by historical accounts, linguistic lineages, archaeological finds and evidence from genetics studies. Modern populations, used most often in genetics studies, have been affected by other movements and migrations and do not always offer an accurate snapshot into a specific time period like the study of bones can. Ancient DNA analysis can be destructive to rare and ill-preserved specimens, leaving them damaged for subsequent research. Ancient crania have often been sitting on dusty museums shelves for decades, handled by numerous people, mixed together, and in some cases the burial context is unknown, all of which make the issues of degradation and contamination large hurdles to overcome. Skeletal data can be used to reconstruct migration patterns by analyzing the frequency of combinations or specific craniofacial traits occurring outside of their ancestral distribution area. Craniofacial traits are genetically determined, and, although the heritability of particular craniofacial traits is still not fully understood, we know that cranial traits do not follow simple patterns of inheritance. One gene does not control one cranial trait. Therefore, identifying the genetic ancestry of someone still does not clarify what skeletal features or traits they may exhibit. Despite the drawbacks of morphological analysis, it is nonetheless an efficacious way to determine population affinities (Chikisheva, 2008; Manica *et al.*, 2010). Furthermore, the purpose of this study is not simply to determine whether admixture occurred or not but to describe how admixture is represented on the craniofacial skeleton paying specific attention to which traits and features are most affected, something only a morphological analysis can do that at this stage.

Chapter 5: Ancestry Estimation and Race Concepts in Physical Anthropology

This chapter will address population assessment methods and ancestry estimation, delineating why they are important to physical anthropologists, and will explain and contextualize the terminology used throughout the next few chapters. The place of race concepts in physical anthropology will also be discussed, detailing the current thinking in the field.

1. ANCESTRY AND POPULATION ASSESSMENT METHODS

Human populations look different from one region to the next, that is, they vary across geographic space, but variation among humans is not a result of different taxonomic lineages, just due to differences in geographic origin. The term ancestry is used when discussing human variation and refers to biological and geographical differences that can be identified genetically and phenotypically and are inherited over one or many generations causing populations to differentiate over periods of time (NMNH, 2009).

In order to explain why human variation occurs, physical anthropologists have looked at population histories to identify whether observed differences stem from evolutionary forces such as drift or gene flow, or from environmental or socio-cultural processes (Tise, 2014). Evolution of the human lineage and migration patterns, past and present, are studied to understand the source of variation among modern humans. A more practical aspect for studying ancestry is to retrieve as much information as possible from skeletal remains, in a bio-archaeology or forensic context, as ancestry is one of the principal components used to describe individuals or populations. The estimation of ancestry is integral to piecing together demographic information of an individual or population under study. The human cranium has traditionally been used as the main focus for the study of human variability, both historically and still today, as it shows the greatest amount of variation of all the skeletal elements (Brace and Hunt, 1990). The estimation of ancestry uses techniques derived from craniometric analysis, as this method was believed to reflect intra and inter-population differences due to genetic, nutritional, and environmental factors (Howells, 1973).

Morphoscopic analysis of the human skull, though it has more recently fallen out of favor, has been used to estimate ancestry through the observation of differences in phenotypic traits (i.e., craniofacial) across geographic distribution patterns. Anthropologists are able to ascertain likely ancestry by analyzing inherited traits that are known to vary in frequency across the world (Kennedy, 1995). It is the differences in the frequency of heritable craniofacial traits that affect the degree to which specific series of features are inherited, across a complex but continuous geographic distribution pattern or cline (Long and Kittles, 2003; Berg and Ta'ala, 2015). However, just because skeletal remains originate from a particular geographic region does not mean that they will necessarily exhibit a specific set of features (White and Folkens, 2000). Livingstone (1962) spoke of clines, not races, indicating that the transition from one population or group to the next involves a gradient of features (increasing or decreasing, broadening or narrowing, lengthening or shortening, in increments, depending on the trait) rather than a distinct demarcation between groups (MacEachern, 2012). “Significant identifying features [of modern human groups from] a given region, then, are stochastically determined and not the products of natural selection.[…] If they are valuable for purposes of identification, they have no coherent adaptive, that is, biological significance. ” (Brace, 1995:171).

Population Assessment Methods

For physical anthropologists interested in human variation, ancestry is one of the pieces of information that is addressed. Ancestry is simply a description of a person's likely geographic range of provenance and carries no social, religious, or political implications. Terms like European, African, or East Asian are used to describe ancestry "because they exclusively refer to a major geographic region of [ancestral] origin, rather than a taxonomic classification engorged with underlying social meaning" (DiGangi and Hefner, 2013:118).

Traditionally, physical anthropologists attempting to assess ancestry from modern human crania have relied on discrete methods. These are considered effective but only for more experienced anthropologists because the features are hard to assess and there are no standardized methods of analysis. Morphoscopic ancestry estimation typically involves analyzing and comparing craniofacial traits, since the human cranium presents the greatest variation between populations of different ancestry (Brace and Hunt, 1990; St Hoyme and Iscan, 1989). The methodology behind morphoscopic analysis is based upon a conflicting paradigm of human biological variation set against the history and sociology of racial concepts (Marks and Synstelien, 2005; Sauer, 1992). By analyzing certain inherited features that are known to vary in frequency across geographic boundaries, anthropologists are able to determine the ancestry of an individual. Facial traits indicative of ancestry are described according to their variation among East Asian, Native American, European, African, Polynesian, Melanesian/Australian (Gill, 1998) and others. When the majority of traits correspond with those found more frequently in one ancestral group this indicates the probable population affinity of that individual (Sauer, 1992). The principal limitation of a purely morphological assessment is that there is no objective criterion on which to base these observations, and the accurate analysis of a feature and subsequent determination of ancestry can only be attained through experience (Hefner, 2009). Another limitation of this method is that it is based on pre-determined fixed categories, while metric assessment consists of quantitative data on a continuous scale (DiGangi and Hefner, 2013).

Metric assessment offers an excellent alternative and has become more widely used in the last few decades. By measuring distances and angles between various cranial and facial landmarks, craniofacial morphology is quantified and compared between individuals and populations. In recent years, metric analysis of craniofacial shape has evolved, and more professionals are using three-dimensional methods to look at skull morphology. The addition of a third plane to analyze subtle changes in shape has revolutionized the field by giving information not as readily available through two-dimensional metric analysis such as facial flatness or volume and a more complete view of facial projection (Shaweesh *et al.*, 2006; Slice and Ross, 2009).The accuracy rate of ancestry estimation methods through metric analysis has been estimated at around 80% for modern North American populations (Giles and Elliot, 1962) but this number varies widely depending on the population or individual being analyzed. One of the main problems in the field of craniometric analysis, as mentioned previously, is that population-specific standards are not always available, and using reference samples from other populations significantly affects the accuracy of the results (Iscan and Steyn, 1999; Kimmerle *et al.*, 2008a). Craniometric analysis, however, is good at determining ancestral origins in groups of disparate geographic origins (Sholts *et al.,* 2011), but a lot of the current work is trying to understand and qualify more subtle differences between groups in a small geographic area. A craniometric study on Bosnian and Croatian populations in the Balkans was able to show that significant differences in craniofacial morphology existed between these long-neighboring populations who had remained isolated from one another due to religious segregation (Ross, 2004). 3D geometric morphometrics has been even more useful at parsing craniofacial variation among populations, comparing ancient and recent cranial samples, and within a small geographic area, such as the Xiongnu in Mongolia or the Pazyryk in southern Siberia (Schmidt, 2012; Schmidt and Evteev, 2014).

While genetic studies are more directly useful in assessing ancestral affinity and relationships between populations, it is important to consider if morphology can be used as proxy for genetic analyses. The correlation between soft and skeletal tissue traits and the genes that control them is still poorly understood (Marks and Synstelien, 2005; Šešelj *et al.*, 2015) but a number of studies have looked at how closely genotype predicts phenotype. Cheverud and Buikstra (1982) assessed the utility of both metric and non-metric skeletal traits in explaining relationships between populations. In effect, they studied the heritability of skeletal traits and found that nonmetric traits were more heritable than metric traits. Other studies have used phenetic analysis of metric traits (such as head length or breadth) to understand the genetic framework, implying a close relationship between the phenotypic traits and their genetic signals (Williams-Blangero and Blangero, 1989).

Human genes and skeletal morphology are known to be influenced by forces of evolutionary change such as drift, natural selection, mutations and migrations (i.e., gene flow). Admixture, as defined by the mating of two geographically distinct populations previously isolated from one another (Rosenboom *et al*., 2016) is the consequence of gene flow. Despite the many adaptive and developmental pressures that influence craniofacial shape, it is the randomly determined processes such as drift and mutations which have been, in evolutionary terms, essential in creating human cranial diversity (Pinhasi and von Cramon-Taubadel, 2009; Zichello, 2014). The difficulty with aligning genetics and morphology in the cranium is that one gene does not necessarily correlate to a single cranial or facial trait. One gene may control a series of traits and if this gene is selected a group of traits that have not been selected for will also be affected (Hlusko, 2004), so we cannot, at this stage, predict what craniofacial morphology an individual would exhibit based on genetic analysis. In one study looking at admixed European and African individuals, less than 10% of the total facial variability observed was due to genetic ancestry variation (Rosenboom *et al.,* 2016). Admixed populations exhibit gene frequencies intermediate between the two ancestral populations but admixture does not affect phenotype morphology in such a linear way: cranial morphology of admixed individuals is not necessarily an intermediate version of the parental morphotypes (Dudzik and Kolatorowicz, 2016: 51-52). In addition, it is important to consider that soft tissue of the face, such as the nose or the brows, may be more susceptible to local adaptation and selection (e.g., diet, climate, and sexual selection) than skeletal traits (Guo *et al.*, 2014; Rosenboom *et al.*, 2016).

Cranial and genetic diversity in modern humans are highest in sub-Saharan Africa and both decrease in tandem with increasing geographical distance from Africa (Manica *et al*., 2007). This observation has led researchers to infer that patterns of cranial variation echo patterns of genetic diversity (Relethford, 1994; Relethford, 2009; Manica *et al*., 2007). Population history strongly affects craniofacial shape diversity (Smith, 2011), so geographically close populations have, in fact, more similar craniofacial morphology than those more distant from one another. However, the great diversity of morphological variation in the skull cannot solely be explained by geographic distance models, and local adaptations based on extreme climatic conditions or shifts in diet that alter the masticatory apparatus are only useful explanations in specific cases (Smith, 2011). Population size and socio-cultural practices can also affect genetic variation, as demonstrated in some Central Asian societies where small population size and strong patrilineal culture led to the maintenance of a high level of paternal genetic diversity (Dulick *et al.*, 2011) but whether these affect craniofacial variation is not known. Cheverud (1988) found that sample sizes need to be above 40 to see phenotype reflecting genotype fairly accurately (i.e., more or less the same degree of variation between craniometric traits and DNA markers) (Tise, 2014).

Konigsberg and Ousley (2009) have demonstrated that for phenotype to be used as a proxy for genotype three conditions are satisfied: the Mahalanobis distance (based on phenotypic traits) is proportional to genetic distance, phenotypic and genetic allometry coefficients are equal, and thus evolutionary models are more easily created because of the close correlation between genotype and skeletal traits (phenotype). In a study by Kohn (1991) heritability was assessed based on cranial morphology, and no significant differences in heritability were found between the facial skeleton and the neurocranium despite the different influences of environment on the neurocranium and splanchnocranium. This was further confirmed in a study by Šešelj *et al.* *(*2015) which found that all cranial and facial traits were heritable to a statistically significant degree (though they differed in extent)and that craniofacial traits from across the skull were all equally useful for identifying population history and reconstructing phylogenies. These studies establish and confirm the validity of using morphology (phenotype), in particular craniofacial morphology, as a proxy for genotype.

2. RACE AND RACE CONCEPTS IN PHYSICAL ANTHROPOLOGY

Race, unlike ancestry, carries heavy cultural and social implications. The American Association of Physical Anthropology (AAPA) published a statement on “Biological Aspects of Race” affirming that all modern human populations are of the same species, *Homo sapiens,* and differences or variation observed across populations are due to hereditary and environmental or socio-environmental factors (AAPA, 1996).

> *"There is great genetic diversity within all human populations. Pure races, in the sense of genetically homogenous populations, do not exist in the human species today, nor is there any evidence that they have ever existed in the past." AAPA (1996:569).*

Although physical anthropologists reached a consensus about the non-existence of biological races when the AAPA issued their statement two decades ago, there is still a gap between the current thinking on the subject and the perceptions of the public at large. Sadly, it is not solely an issue of semantics. The belief in racial classification and what is meant by race among anthropologists across the world varies, and seems to negatively correlate with the level of heterogeneity of a population within a country. A 2004 study by Lieberman *et al.* showed that 70% of physical anthropologists in the US rejected the concept of race, while only 25% did in Poland. But in Poland, the term race was closer in meaning to population (Kaszycka, 2003). Poland, having a far more homogeneous population than that of the US, for them, race was meant to differentiate between individuals from Poland and others from differing geographic and ancestral origins (Kaszycka, 2003). There also exists a significant disconnect between the advances made by the scientific community, specifically in the field of population genetics, and the administrative requirements still in effect in the US. While most physical anthropologists agree that biological races do not exist, census forms, voting ballots, educational and medical questionnaires, among other bureaucratic paperwork, all ask for a person's race as part of basic identifying information. The co-existence of these opposite belief systems creates confusion, especially within the field of forensic anthropology (Brace, 1995). The special case of forensic anthropology will be addressed separately in section 3 of this chapter. Race, within the US context, is an attempt at describing how a person might have been identified, or how the individual might have self-identified while they were alive, the two of which do not always match up (Kennedy, 1995).

So, if race has no biological underpinning, then what is it? Race is a social construct, one that has no basis in biology but is founded on the erroneous idea that humans can be separated out into fixed and unchanging types, or racial groups (Ousley *et al.,* 2018). Race is, therefore, "a culturally constructed label that crudely and imprecisely describes real variation" (Relethford, 2009:20).

Cultural anthropologists deem race a "kind of *ideology*, a way of thinking about, speaking about, and organizing relationships among human groups" (MacEachern, 2012:36). The current race categories in the US (white and black) came out of a particularly fraught historical context of slavery, forming the root of the current system, and grounded in inequality (Hill, 2006). But racial context varies from one place to the next and arises under specific local conditions due to historical and socio-cultural confluences. Racial classifications also vary significantly across countries and over time (MacEachern, 2012), another reason why it is impossible to define races scientifically: they are not universal (Ousley *et al.*, 2018).

Probably the earliest available scientific reference to racial classification is from 1758. Carolus Linnaeus, the father of our current nomenclature system, ascribed human groups to four subspecies based on physical features, character traits, and geographic regions (Linnaeus, 1758). Race concepts in anthropology were rooted in Linnaean taxonomic classification and broadly based on typology, which identified race groups based on features, physical and mental, and character traits (e.g., intelligence) (Quintyn, 2010). It wasn't until the 1950s and 1960s, that important shifts in the understanding of human variation began to occur, moving away from typological interpretations and turning to assessing the impact of evolutionary forces and environmental factors over time (DiGangi and Hefner, 2013; Schmidt, 2012). A seminal paper by Lewontin (1972), demonstrated that genetic variation within a so-called race group (or between individuals within a labelled group) was greater than the genetic variation observed between groups. This changed the way many anthropologists thought about human variation: if there was no reliable way to group or classify humans by race then how could race be a relevant taxonomic unit (Ousley *et al.*, 2018)? Livingstone, Montagu, and Washburn had also come to this conclusion, arguing "that race does not exist because it does not explain the scope of human variation […], it ignores evolutionary forces, and it is imbued with social meaning" (DiGangi and Hefner, 2013:128). The incredible advances within the field of genetics in the last two decades, population genetics in particular, have helped re-shape the views within physical anthropology, moving them once and for all away from racial classification to trying to understand the sources of human variation, looking for evolutionary explanations. Relethford (1994) and others have found that 85% of the total variation observed in humans is among individuals from the same population or group. He also noted that craniometric variation patterned along very similar lines as genetic markers, based on his analysis of 57 landmark distances from the skull. Although only 10-15% of the total variation is observed between populations or groups, it is organized in a way that can tell us about someone's geographic ancestry (Spradley and Weisensee, 2017) as phenotypic distance and geographic distance were found to be closely related, and there is evidence of geographic patterning across the world. The findings from Relethford's efforts indicate that craniofacial morphology has been shaped (for the most part) by neutral evolutionary processes. This has further been confirmed by more recent studies (Guo *et al.,* 2014) using different samples and measurements, 3D methods, and principal components analyses (Roseman and Weaver, 2004; Harvati and Weaver, 2006; von Cramon-Taubadel, 2009; von Cramon-Taubadel, 2011b). Phenotypic variation, in this case craniofacial, has mainly genetic but also environmental components (Tise, 2014) especially for certain features of the face (e.g., the nose) which may be more susceptible to adaptive pressures under specific climatic conditions (Guo *et al.,* 2014).

Major areas of disagreement still remain: on the one hand, there are still anthropologists around the world who have yet to abandon the classification of human populations into races despite what is now known from genetic research (Long and Kittles, 2003). Other anthropologists believe that since all the traits that best reflect discrete biological groups are inherited independently (Ousley et al., 2009) cranial morphology, because it is too variable, cannot be used to identify human variation accurately (Naar *et al*., 2006) and thus morphological analyses of the skull should be abandoned. Mostly though, less fundamental debates are occupying the attention of physical anthropologists, notably around how geographic patterning is structured: whether human variation is primarily clinal or due to a complex set of factors such as founder effects, local migrations, population divisions, and the like (Edgar and Hunley, 2009; Hunley *et al.,* 2009; DiGangi and Hefner, 2013). We have moved into an era where whole genomes can be analyzed and processed, more cheaply and more accurately with every passing year, and it is likely that new technologies and advances in the field will continue to push the current understanding of human variation further in these new directions.

3. FORENSIC ANTHROPOLOGY

The study of human variation is extremely important for the applied discipline of forensic anthropology, and continues to be a major focus of scientific inquiry for professionals in the field (Tise, 2014). The primary undertaking for forensic anthropologists is to construct a biological profile for the individual or set of individuals being examined (Briggs, 1998; White and Folkens, 2000). A biological profile requires, in the first instance, an estimation of ancestry (likely geographic origin), sex, age at death, stature, collecting individuating information, as well as commenting on any trauma, pathology, and oral health (Burns, 1999). In forensic cases, the estimation of ancestry is essential (Spradley and Weisensee, 2017), and must be identified because the estimation of age, sex, and stature, are more accurate if ancestry is known. All anthropological variables are closely connected, and the result of one analysis affects the others. DNA can be employed as a quick and efficient way to identify the sex of an individual, but it is unclear whether an accurate assessment of ancestry in a modern context can be obtained (Chikhi *et al.*, 1998). Ancestral genetic markers do not always relate to the phenotypic characteristics that society considers as representative of a certain ancestry, and in missing person cases or when remains cannot be identified by normal means due to advanced decomposition, it is particularly important that they should align so that families can come forward and claim the remains (Buck and Vidarsdottir, 2004). Anthropological methods are often favored over DNA in cases of extreme decomposition or extensive co-mingling.

Forensic anthropologists work in the medico-legal arena and collect evidence which can be used in a court of law (Byers, 2002). Although most forensic practitioners do not subscribe to the belief that human populations can be or should be classified into racial categories (Sauer, 1992), government entities (e.g., police forces, census collectors, and the judicial circuit) continue to require that individuals fit into a designated racial groups. Police officers need to gather information as quickly as possible about deceased individuals so they can be identified, and a big part of this, in the US at least, is racial identification (Byers, 2002). Despite scientific evidence proving that races among humans have no biological meaning or underpinning, our society is built around socially constructed racial categories and this ideology remains deeply ingrained in the population. When anthropologists are asked to determine the race or ethnicity of human remains, federal and local law enforcement agencies expect a response that fits within the categories available, and are not looking for an academic lecture on evolution and human variation (Kennedy, 1995). “Forensic anthropologists must report their results in terms that are meaningful to their non-anthropological audience, and they have adopted traditional race categories as the most effective way of doing that” (MacEachern, 2012:48). There is a duty, however, to raise awareness among the public about the inexistence of biological races and help to bring about a shift towards identifying individuals based on their likely ancestral origin instead, something which forensic anthropologists have been attempting to do for a long time. By continuing to assert that regional variation exists and is quantifiable, to an extent, but that this observable variation does not mean that typological races exist (Ousley *et al.,* 2018), the message will get eventually through.

4. IMPORTANCE OF DATA IN ANCESTRY DETERMINATION

In the past two decades, software programs such as FORDISC (Ousley and Jantz, 2005), CRANID (Wright, 1992), and 3D-ID (Slice and Ross, 2009), have been used extensively among forensic anthropologists to determine the likely ancestry and sex for unidentified human remains.

Craniofacial measurements (FORDISC and CRANID), or 3D GM landmark data (3D-ID), are collected and entered into the software programs and measurements of an unknown skull are compared to the in-built database of crania. A list of possible and probable ancestral and geographic origins are then given for the skull under analysis, based on discriminant function or regression analyses derived from the measurements of the crania within each database (Wright, 1992). Although these programs are employed frequently, they should not be used at the exclusion of a morphological assessment (Leathers *et al.,* 2002) as the results are heavily dependent on the availability of appropriate comparative samples within the databases.

For both forensic anthropologists looking to identify ancestry and biological anthropologists seeking morphological explanations for human variation, the quality of the analyses hinges on selecting the most appropriate osteological collection for a given question, picking the landmarks or measurements that will best answer the question posed, and using the right comparative samples (or a broad selection of reference populations) from which to derive the best results (DiGangi and Hefner, 2013; Spradley and Weisensee, 2017). For example, in forensics, the standards used to calculate stature are different for individuals of European and African descent, and they are also different for males and females (Trotter and Gleser, 1952). The population sample used to devise regression formulae for stature, however, was from young males who served during the Korean War. The inherent sample bias in this collection will be replicated, to an extent, in the mortality profile of every population examined using it (Bocquet-Appel and Masset, 1982), which can skew results.

Another issue, one that concerns ancestry estimation in particular, is the lack of available population-specific criteria. This can be a problem for populations for whom there is no reference sample, thus the need to contribute more osteological data from around the world and from difficult to access collections, modern and ancient. In the US, more work is needed to be able to clarify "Hispanic" ancestry, as more and more individuals within society identify as such, and in order to derive data and techniques that can aid in ancestry estimation of this growing group (Tise, 2014). Sexual dimorphism in craniofacial measurements, and the lack of diversity in the collections from which measurements are initially taken, are some of the principal limitations associated with determining ancestry.

5. TERMINOLOGY USED IN THIS PAPER

In the following chapters, the terminology employed to discuss, compare, and contrast clusters of individuals is used to describe the range of human variation within this collection. The designated categories (European, East Asian, and Central Asian) are not fixed and unchanging. There is much variation within each group and overlap across the groups. The categories ascribed were simply labelled so that a quantitative analysis could proceed and the results could be explained clearly and succinctly. Outlined below are a series of explanations for the terms used in this analysis.

Group/Population: A group or population, as used in this paper, is defined as a specific skeletal sample within the entire collection studied for this research project. For example, the Central Asian group is meant to encompass all the specimens whose provenance is Central Asia among the entire skeletal collection studied. This does not mean that the Central Asian group in question is necessarily fully representative of all living populations from Central Asia. The European group/population in this context encompasses all the cranial specimens whose provenance is Western, Northern, or Southern Europe (Greece, Italy, Spain, France, UK). The East Asian group/population encompasses all the cranial specimens from China and Mongolia in this collection. Again, none of these collections are necessarily fully representative of all living populations from these regions.

Ancestry: It is the description of someone's probable geographic origin and used when discussing human variation. This is a term that does not hold any social, religious, or political implications. Biogeographical markers are inherited and passed on to subsequent generations, and since craniofacial morphological analysis is a good proxy for genetics, anthropologists are able to determine likely geographic origin, or ancestry, from skeletal specimens.

Ethnic(ity): Ethnicity defines a group of individuals who share national, linguistic, or socio-cultural traditions. Because some ethnic groups might segregate themselves or abide by sets of customs or rules that separate them from other populations, there may be, over time, observable differences that develop within these groups. An example of this is mentioned in chapter 4 where neighboring populations of Bosnians and Croats who remained segregated from each other due to religious traditions for centuries, exhibited, over time, morphological changes in the cranium that made them distinguishable from one another morphometrically (Ross, 2004).

Migration: In this paper, and in biological anthropology as a whole, migration "refers to the movement of peoples, with the end result being the movement, or transfer of genes, in what is called gene flow." (Schmidt, 2012:64).

Admixture: Admixture is defined by the mating of individuals from two geographically distinct populations previously isolated from one another (Rosenboom *et al.*, 2016). It is the consequence of gene flow which involves the exchange of alleles between populations. Genetic studies estimate a 41k year or earlier divergence between European and East Asian populations (Fu *et al.*, 2013; Tateno *et al.,* 2014). Morphological studies, in line with the genetic analyses, also show distinct craniofacial differences between these two groups across time periods (Schmidt *et al.,* 2011; Seguchi *et al.*, 2010; Xing *et al.,* 2013).

Admixed: This term is used in the results and discussion chapters to refer to a specimen from the collection whose craniofacial configuration clusters most closely with the group from Central Asia in this context, and is more distant or distinct from the European or East Asian morphological ranges within this study.

Non-admixed: This term is used in the results and discussion chapters to refer to a particular specimen or set of specimens that have a craniofacial configuration that fits best within the range of variation of the European or the East Asian group only (i.e., a specimen that would most closely cluster with the group from Europe or with the group from East Asia in this collection). This does not imply that Europeans or East Asians are not, nor have never been, admixed, just that the cranial morphology of a given cranium most closely resembles and is characteristic of the groups from either extreme of the Eurasian land mass.

Over the next two chapters, the materials and methods used in the analysis are detailed.

Chapter 6: Materials

MATERIALS USED

For this project, 633 human crania from sites along the Silk Road were selected to represent Europe, East Asia, and the range of variation across Central Asia. Specimens were chosen based on state of preservation and geographical origin. All are adult determined by M3 eruption and spheno-occipital fusion (Buikstra and Ubelaker, 1994). No preference was given to a particular sex with both males and females represented, when possible. While the data collection process is complicated by having to determine sex in each individual within the samples, it is nonetheless important to have an accurate idea of what the entire population in each series might have looked like and how evenly (or not) the sexes were represented in these collections . In some cases, the crania had already been assigned a sex by previous researchers but this depended on the cranial series and a very large number were unspecified.

Crania that had more than half of the facial bones or vault missing were not selected as they would not have provided enough useful data for this project. This significantly decreased the possible number of specimens to choose from.

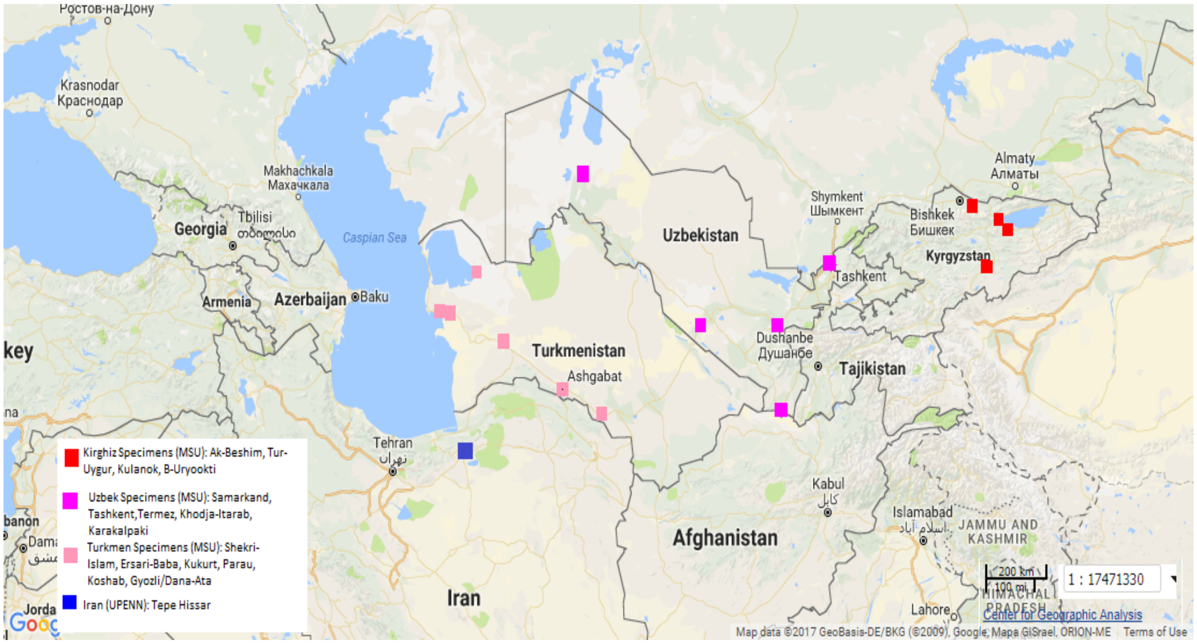
Cranial series from Mongolia and China represent East Asia (Table 6. 1), Turkmenistan, Kirghizstan, the Pamirs, Eastern Iran, Uzbekistan, and Afghanistan represent Central Asia (Table 6.2), and France, Italy, Greece, Germany, Roman Britain represent Europe (Table 6.3). Appendix 1 lists each individual specimen with location, sex, and time-period where available. The series are listed by time period with some collections dating to before 200BC (before the start of the Silk Road), those series that span the Silk Road timeframe (200BC to 1600AD) and those that involve the post-Silk Road period from roughly 1600AD onwards. Some of the collections

(AMNH) do not have information on the exact time period they are from but are dated as modern, from the 18th-20th Century. No radiocarbon dates were available for any of these collections and dates indicated were based on archaeological context or historical records.

Moscow State University Collection (MSU)

The bulk of the Central Asian cranial collection is housed at Moscow State University's (MSU) Department of History and Institute of Anthropology. Close to 500 crania from Turkmenistan, Kazakhstan, Tajikistan, Kirghizstan, the Pamirs, Dagestan, and other regions of Central Asia spanning from the 9th Century BC through the 19th Century were available for analysis. Only some of the series were in a good enough state of preservation to use for this project (Table 6. 1). These crania were collected on various expeditions to Central Asia led by Russian anthropologists in the 19th and 20th Century. Ethnic affiliation in Russia is reported as geographic location. The Kirghizstan sample originated from central, Northeastern, along the border with Kazakhstan, and around the Issyk-Kul lake region of Kirghizstan (see Figure 6.1 for map of collection provenance). Most the crania are listed as being from the 18th Century but there is a question whether the Ak-Beshim specimens could be much older (11th Century). The Uzbekistan collection encompasses three large urban areas: Samarkand (East), Tashkent (Northeast), Termez (Due South on Afghan/Tajik border), and in the autonomous region of Karakalpakia (Northwest region bordered by Kazakhstan and Turkmenistan). The crania from Uzbekistan range from the 6th Century BC to the 16th Century AD, with the majority from the Silk Road period itself. The specimens excavated in Turkmenistan are all from the western side of the country mostly in the north, but the Parau crania are from the south near the Iranian border. These all date from the 1400s until 1800 AD.

Figure 6.1: Map of Central Asian collection provenance



Adapted from http://worldmap.harvard.edu

University of Pennsylvania Collection (UPENN)

To enlarge the pre-Silk Road Central Asian sample, the University of Pennsylvania's Museum of Archaeology and Anthropology hold around 250 crania from Bronze Age (3500BC), Iron Age, and Sassanid Iran (up to 350AD). Most of these are in fragments or too poorly preserved for use in this research, nonetheless some proved very useful (Table 6.1). Tepe Hisssar is located in North Eastern Iran in modern day Damghan the seat of where modern Turkmen still reside in Iran, on the Southeastern shores of the Caspian Sea near the border of Turkmenistan (Figure 6.1). The vast majority of crania are from the Bronze Age around the 1st to 2nd Millennium BC to the

Iron Age, but the collection covers the Sassanid time period also which lasted until about 350AD.

Table 6.1: Central Asian assemblage

GROUP/COLLECTION	**PROVENANCE**	**TIME PERIOD**	**SEX**	**NUMBER**
Iran UPENN	Tepe Hissar NE Iran	Bronze Age to Sassanian (3500BC-350AD)	Unknown	32
			Male	4
Kirghiz MSU	Various, Kyrgyzstan	18th Century	Unknown	7
			Male	27
			Female	27
Uzbek MSU	Samarkand, Uzbekistan	Sogdian (200BC-600AD)	Unknown	11
			Female	3
Uzbek MSU	Tashkent, Uzbekistan	Uzbek Period before 1600 AD	Unknown	6
			Female	2
Uzbek MSU	Termez, Uzbekistan	6th Century BC-12th AD	Unknown	4
Uzbek MSU	Kipchak, KhodjaItarab	11-12th Century AD	Unknown	6
Turkmen MSU	Parau Turkmenistan	15th Century	Unknown	7
Turkmen MSU	Kukurt Turkmenistan	16th Century	Unknown	7
Turkmen MSU	GyozliAta/Dana Ata	15-17th Century	Unknown	4
Turkmen MSU	Koshab Turkmenistan	16th Century	Unknown	7
Turkmen MSU	Ersari-Baba Turkmenistan	19th Century	Unknown	3
Turkmen MSU	Shekhri Islam Turkmenistan	15th Century	Unknown	1
Karakalpaki MSU	AmuDarya Uzbekistan	Probably 16th Century	Unknown	12
Afghan AMNH	Various, Afghanistan		Unknown	2
Turkish AMNH	Assar-Onu, Turkey		Unknown	1
Syrian AMNH	Aleppo, Syria		Unknown	1
TOTAL				**172**

Cambridge University Duckworth Laboratory Collection

The European collection was principally drawn from amongst over 600 crania in the Duckworth Collection at Cambridge University in England. This European sample includes individuals from all over Europe spanning from the Bronze Age through the Medieval period. Most of these collections are catalogued with the specific location of provenance and often by sex, age, and time period (for complete list see Appendix 1, for abridged see Table 6. 2). The largest groups are the Romans from Britain, France, and Italy and the Anglo-Saxons from the 5th-10th Century AD but there are significant contributions from the Bronze Age and late Medieval Europe.

American Museum of Natural History Collection (AMNH)

There is unfortunately very little information about the specimens from East Asia, Europe, and Central Asia in this collection (Tables 6.3, 6.2, and 6.1 respectively). They come from the von Luschan collection (Quigley, 2001) which was purchased in the late 1800s and it is thought that the majority of the crania are from the 18th-19th Century, but this is not certain. Their locality is documented (El-Najjar, 1977) and the preservation state is excellent, so they are a useful addition to the various assemblages. The European assemblage chosen hails from the Mediterranean shores primarily Greece and Italy. The East Asian group consists of a variety of more recent Cantonese individuals from Singapore, the Malay Peninsula, and Canton, as well as Northern and Southeastern Chinese and recent Chinese immigrants to the US. From Central Asia, individuals from Afghanistan, Syria, and Turkey were added to the assemblage. While Syria and Turkey are not, strictly speaking, in Central Asia, the two regions from which the crania were gathered are located along the Silk Road on the Western edge.

Table 6.2: European assemblage

GROUP/COLLECTION	PROVENANCE	TIME PERIOD	SEX	NUMBER
Greek AMNH	Prastos,Peloponnesus		Unknown	10
Greek AMNH	Kastanitsa, Peloponnesus		Unknown	10
Greek AMNH	Crete		Unknown	1
Greek AMNH	Khania, Crete		Unknown	2
Greek AMNH	Candia, Iraklion, Crete		Unknown	7
Italian AMNH	Chiusi		Unknown	2
Italian AMNH	Ostia		Unknown	1
Italian AMNH	Syracuse, Sicily		Unknown	5
Italian AMNH	Pola		Unknown	2
British Cambridge	Various, UK	Bronze Age	Unknown	18
			Male	8
British Cambridge	Various, UK	Iron Age	Unknown	4
British Cambridge	Dorset, UK	LaterIron-EarlyRoman	Unknown	16
British Cambridge	Various, UK	Roman	Male	12
			Female	3
			Unknown	29
Belgian Cambridge	Somerset, UK	Roman-Belgic	Male	1
Saxon Cambridge	Suffolk, UK	Pre-Saxon Germanic	Unknown	8
			Female	2
French Cambridge	Paris and Various		Male	1
			Female	1
			Unknown	6
French Cambridge	Oise, France	Ancient Gaul	Unknown	3
Basque Cambridge	Basque		Unknown	2
Greek Cambridge	Thessaly	Ottoman Rule	Female	1
Italian Cambridge	Italy	Roman	Unknown	5
Italian Cambridge	Paestum, Italy	Greco-Roman	Unknown	1
Italian Cambridge	Perugia, Italy	Etruscan	Male	1
Italian Cambridge	Sardinia	After 1800	Unknown	3
Italian Cambridge	Messina, Sicily	After 1588	Unknown	1
Italian Cambridge	Various, Italy		Unknown	2
Maltan Cambridge	GhainTuffieha Malta	700BC-100AD	Unknown	2
Maltan Cambridge	Bengemma Malta	Phoenician	Unknown	1
Maltan Cambridge	Tel Hor Malta	Bronze/Iron Age	Male	1
Spanish Cambridge	Menorca, Spain		Unknown	2
AngloSaxon Cambridge	Various, UK	5th-10th Century AD	Unknown	22
			Male	4

			Female	2
British Cambridge	Various, UK	Early Medieval	Unknown	6
British Cambridge	Cambridgeshire, UK	Medieval	Unknown	19
TOTAL				**227**

Smithsonian Institute Collection (NMNH)

The Smithsonian Institute, National Museum of Natural History, Anthropology Collections holds a large collection of East Asian, specifically Mongolian crania from Urga (old name for Ulaanbaatar) and Buryatia, where upwards of 200 specimens are available for study (Table 6. 3). The vast majority of these crania were in excellent condition and sex was specified for most. These were collected by Ales Hrdlička in 1912 on one his many expeditions to Northeast Asia. According to Hrdlička, he gathered crania and mandibles from adult remains which had been left to decompose outdoors, as was the Mongolian tradition, where scavengers would deflesh and disarticulate them and leave the skeletal elements behind (Hrdlička, 1942:408).

Table 6.3: East Asian assemblage

GROUP/COLLECTION	PROVENANCE	TIME PERIOD	SEX	NUMBER
Chinese AMNH	North Borneo		Male	7
			Female	2
			Unknown	8
Chinese AMNH	San Francisco	1800-1906	Male	3
			Female	1
			Unknown	2
Chinese AMNH	Canton in Singapore		Unknown	2
Chinese AMNH	Canton in Malay		Male	1
Chinese AMNH	Canton China		Male	2
			Female	1
			Unknown	1
Chinese AMNH	Tientsin		Male	6
			Female	3
			Unknown	1
Chinese AMNH	Tungku		Female	1

			Unknown	2
Mongolian Smithsonian	Urga/Ulan Bator	16th-18th Century	Male	106
			Female	79
			Unknown	6
TOTAL				**234**

Chapter 7: Methods

RESEARCH METHODS

For this project, craniofacial shape was characterized and quantified using three-dimensional geometric morphometrics (3DGM). Traditional linear metric analyses have proved useful in quantifying shapes relative to one another where only qualitative assessments (physical descriptions) had been available in the past. While metric analyses of skeletal elements assess distances and angles between biologically-relevant landmarks, they do not allow for the visualization of the shape under study (Slice and Ross, 2010). Geometric morphometrics is quickly replacing standard linear metric analysis in the field of skeletal morphology because it provides more accurate information about shape than two-dimensional metric assessments. By assigning sets of Cartesian coordinates to each landmark, the specific shape of a skeletal element under study is recorded and can subsequently be compared to other specimens (Adams *et al.*, 2004; Shaweesh *et al.*, 2006; Slice and Ross, 2009). Three-dimensional methods help visualize shapes relative to one another and through specialized software scale the results relative to one another. In addition, unlike traditional methods which cannot accurately analyze crania that have undergone artificial deformation and other shape-changing forces, three-dimensional methods allow for affected areas and landmarks to be virtually reconstructed (Ross and Ubelaker, 2009) which can be extremely useful when studying ancient remains.

In this project, morphological information was collected to obtain three coordinates (x, y, z) for each cranial landmark. Forty-one landmarks (Appendix 2) from a pool of classical craniofacial landmarks have been selected to best characterize differences between European and East Asian crania. These are Type I, II, and III homologous points (O'Higgins, 2000) as depicted in

Appendix 3. Type I landmarks refer to suture intersection points; type II landmarks are associated with biomechanical processes and refer to maximum curvature points which are geometrically determined; and type III landmarks mark the end point of a measure of distance (Slice, 2005: 9). In a study by Ross and Williams (2008) looking at the repeatability of landmarks data collection it was found that landmarks on the craniofacial skeleton that were not at suture-meeting points or associated with muscle attachments had a higher error rate than expected. Landmarks such as euryon and alare for example are essential for ancestry determination and thus care must be used when collecting the data and analyzing it at these particular points (Ross and Williams, 2008). Once the landmarks have been collected, the shape of the specimen can be viewed in 3-D with the help of a software program, in this case *morphologika v2.5* (O'Higgins and Jones, 1998). The data are then subjected to a General Procrustes Analysis (GPA). GPA is a superimposition technique that scales, rotates, and translates all of the landmark configurations so that equivalent landmarks are most closely aligned under a least-squares criterion and all specimens are scaled to a common size, the unit centroid size (Rohlf and Slice, 1990). These homologous landmarks, in turn, can be statistically compared to each other with the help of shape analysis software. The GPA-modified coordinates then undergo a Principal Components Analyses (PCA), a standard multivariate technique for analyzing large multidimensional datasets (Rohlf and Slice, 1990). The advantage of PCA is that it usually explains most of the variation within an entire sample in just a few statistically independent axes.

Three-dimensional methods have been primarily used to better assign taxonomic status to various fossil hominin specimens (Baab, 2008; Baab and McNulty, 2009; Harvati, 2009) and to describe hybridization or admixture between fossil hominin taxa (Harvati *et al.*, 2007; Harvati *et* *al.*, 2010). 3DGM is now becoming more frequently used to identify ancestry and separate individuals by ethnic group based on craniofacial shape differences (Badawi-Fayad and Cabanis, 2007; Ross *et al*., 2004; Slice and Ross, 2009) or to study sexual dimorphism, particularly in the skull (Bigoni *et al.*, 2010; Green and Curnoe, 2009; Kimmerle *et al*., 2008b). According to Bigoni *et al.* (2010) and others (Franklin *et al.*, 2007) one of the main draws of using geometric morphometrics in the field of forensic anthropology is that it "eliminates subjectivity from the evaluation of shape and [allows for] the possibility of an objective proposal of categories for non-metric standards" (Bigoni *et al.*, 2010: 27). Although there seems to be considerable potential for this new method of analysis it has not yet fully replaced standard metric assessments worldwide. This may be due in part to the expense of the equipment, or because of conflicting evidence regarding its effectiveness in "producing biologically significant results" compared to standard metric analysis (Ryan and Kidd, 2009: 258).

DATA AND STATISTICAL ANALYSIS

The coordinates for each skull were collected with a Microscribe G2 digitizer, with each skull stabilized on a table with modeling clay to prevent slippage and moving of the specimen. The coordinates were subjected to Generalized Procrustes Analysis (GPA), to scale, rotate, and translate the landmark configurations, using the freely available software program *morphologika version 2.5* (O'Higgins and Jones, 1998) (http://sites.google.com/site/hymsfme/downloadmorphologica)

The GPA-modified coordinates were then subjected to Principal Components Analyses (PCA), a standard multivariate technique for analyzing large multidimensional datasets. The results are visualized in 3-D on the computer screen through wireframe configurations linking the various landmarks, and these shapes can be compared to one another.

A Multivariate Analysis of Variance (MANOVA) was employed to test for mean shape differences between the three groups: Central Asian, East Asian, and European. This was accomplished using PAST software version 3 (Hammer *et al.,* 2001). One of the multivariate procedures used was a discriminant function analysis which identifies which variables can discriminate between the three populations, looking for significant mean shape differences between groups. The degree of differentiation between each set of two populations was calculated with a Mahalanobis Generalized Distance statistic (D^2) which represents the squared generalized distance of the principal components.

For the second research question which examines whether admixture increases over time, the first part of the analysis required counting those individuals from Central Asia who exhibit craniofacial admixture as well as individuals who did not show any admixture and who are classified as European or East Asian, for each time period. This was based on the data gathered from three discriminant function analyses. The Central Asian population was divided into three main time-differentiated groups: PRE SR (time-period preceding the opening of the Silk Road, SR (time period of the Silk Road, further subdivided into DURING 1 for the early to middle period of Silk Road trade, and DURING 2 for the middle to later period of the trade), and POST SR for the period following the closing of the trade network.

Next, the percentage of individuals showing any admixture was determined in each of the chronologically-differentiated populations. If the percent of admixed individuals overall has not remained the same over time, a more specific analysis will look into how it has changed. A series of Mantel tests were used to determine if admixture has increased over time. The Mantel test is a statistical method that looks at the relationship between two square matrices whose values are represented by distances between points. It tests for the similarity of the matrices using hundreds of permutations of the rows and columns in the matrices to calculate over and over again the correlation between them (Mantel and Valand, 1970). Thirteen horizontal measures of breadth from the mid-facial region and the cranium, as well as the nasal region were compared between the Pre and Early Silk Road groups and the later and Post Silk Road groups. Results will indicate a strong or weak correlation between the data matrices and thus if any significant changes in admixture have occurred in this population over time. If craniofacial changes are seen in the later populations they may be due to admixture and a result of the intense Silk Road migrations.

The third research question looks at whether the craniofacial changes seen in this population could be due to secular changes such as skeletal growth over time. Five pre-Silk Road vertical measurements of the cranium and face were compared to the same measurements from the later Silk Road through a series of Mantel tests to determine whether vertical cranial growth had occurred in this population over time. Admixture, and lack thereof, is determined from results of the first and second research questions. Results will indicate how much of a role the Silk Road migrations played in the craniofacial changes observed in later populations.

To account for intra-observer error in all the measurements, around 9% of the total collection (503 after omitting problematic individuals) were randomly selected to be measured twice: once on the first day of data collection and once at the end of the measurement period. The percent error for each measurement in each individual within this sample was then calculated.

CONCLUSION

In the following chapters the data will be grouped and analyzed according to geographical region and time period. Intra-group and inter-group results will be discussed in the context of the three research questions put forward in chapter 4 and the larger question of the influence of the Silk Road trade routes on Central Asian craniofacial morphology will be addressed.

Chapter 8: Analysis between groups (intergroup comparisons)

In this chapter, the results from intergroup comparisons are presented. These results will determine whether the methods applied here can accurately differentiate among three geographically-differentiated groups or whether the groups are not significantly and statistically different. If the results show that the groups are distinct and that the crania from Central Asia occupy an intermediate position between the crania from Europe and from East Asia, then the case for a distinct Central Asian craniofacial morphology range can be made and admixture can be inferred in this sample population. Intra-observer error will be addressed as will the decision to pool samples by ancestry group solely and not by sex.

PILOT STUDY INDICATES DIFFERENCES BETWEEN GROUPS

A small pilot study was conducted to assess the viability of selecting specific cranial landmarks to distinguish between populations originating from different geographical regions. The crania were selected regardless of sex and age, but all were adults. Forty crania were chosen to represent the European sample with thirty Greek and ten Italian specimens. The East Asian sample was chosen entirely from Chinese populations: from the northeastern region, from the southwestern region, from a city near Beijing, and from Chinese populations in San Francisco, Borneo, and Singapore (AMNH). A Microscribe G2 was used to collect three dimensional data from forty-one facial and neurocranial landmarks (Appendix 2). These specific landmarks were chosen in part because they are able to discriminate the most between European and East Asian individuals in metric and non-metric analyses and through other studies (Abdushelishvili *et al.*, 1968; Alcade *et al.*, 1998; Ball *et al.*, 2010; Fraser *et al.*, 2003; Le *et al.*, 2002; Scavone *et al.*, 2006).

In the first phase of the analysis, only crania from East Asia and from Europe (N=83) were compared in order to determine whether this method of analysis could effectively separate the most geographically distant groups. The coordinates obtained from the landmarks were inputted into *morphologika v2.5*, a shape analysis software program. A Generalized Procrustes Analysis (GPA) was conducted to translate, scale and rotate the points to align them so that they were placed in the same orientation and could be statistically compared to one another.

The newly scaled and aligned data were then subjected to a Principal Components Analysis (PCA). Two outliers were removed from the analysis due missing landmarks (VL1751 from China, and VL2138 from Greece, N=81). This ensured a more accurate interpretation of the results rather than two individuals skewing the entire group. Raw coordinate data were re-run through *morphologika* and a new GPA and PCA were applied to the remaining individuals. The results were visualized in *morphologika's* principal components graph and through its 3D viewer.

The results from the PCA showed that 65% of the variation in the total sample was explained by the first ten principal components (Table 8.1). The first ten principal components were selected based on the results of a scatter plot of PC to eigenvalue where the elbow of the curve represents the maximum number of PCs considered significant for the analysis. Principal components analysis represents an "ordination technique to explore large-scale trends within the data" and thus independent axes are not biologically meaningful on their own (Harvati *et al.*, 2010).

A Multivariate Analysis of Variance (MANOVA) was conducted on the first ten principal component scores obtained through *morphologika* to test for mean shape differences between the East Asian and European groups. This was accomplished using SPSS software version 20. The MANOVA detected significant group differences (Wilk's λ=0.21, F value=26.36, df =10, p<0.0001, Table 8.1). This initial test statistic showed that this method for collecting specific facial and cranial landmarks, given a medium-size sample, is effective in differentiating between East Asian and European individuals. The main differences across all PCs were observed in landmarks relating to mid-facial breadth (Zygomaxillare, Zygoorbitale, Zygion, Inferior maxillary border, Frontomalare temporale, Ectomolare, Alare) and mid-facial projection (Nasion, Rhinion, and Nasospinale) followed by cranial breadth (Euryon)and cranial height (Bregma and Basion or Opisthion) and cranial length (Glabella, Opisthocranion, and Lambda).

Table 8.1: PCs 1-10 percent variance explained for Europe, East Asia, and Central Asia

EUROPE AND EAST ASIA **PC % VARIANCE EXPLAINED** 10 PC = 65% TOTAL VARIATION	**EUROPE, EAST ASIA, CENTRAL ASIA** **PC % VARIANCE EXPLAINED** 10 PC = 75% TOTAL VARIATION
PC 1= 14% PC 2 = 10% PC 3 = 8.0% PC 4 = 6.5% PC 5 = 5.5% PC 6 = 5.0% PC 7 = 4.7% PC 8 = 4.1% PC 9 = 3.7% PC 10 =3.3%	PC 1= 33.3% PC 2 = 8.1% PC 3 = 7.7% PC 4 = 5.8% PC 5 = 4.8% PC 6 = 3.6% PC 7 = 3.4% PC 8 = 2.9% PC 9 = 2.6% PC 10 = 2.4%
MANOVA RESULTS	**MANOVA RESULTS**

Wilk’s λ=0.21 *F* value=26.36 df =10 *p*<0.0001	Wilk’s λ=0.023 *F* value=43 df =20 *p*<0.0001

Through the exact same methodology, the pilot study was repeated and expanded to add in a small very diverse grouping of individuals meant to represent a Central Asian sample (n=8) for a total sample size of 89 individuals. The results from this PCA showed that 75% of the variation in the total sample was explained by the first ten principal components (Table 8.1). A Multivariate Analysis of Variance (MANOVA) was conducted on the first ten principal component scores obtained through *morphologika* to test for mean shape differences among the groups Central Asia, East Asia, and Europe. The MANOVA detected significant group differences (Wilk’s λ=0.023, *F* value=43, df =20, *p*<0.0001, Table 8.1). These test statistics show that the choice of these 41 specific facial and cranial landmarks and the methodology used (3DGM) are effective in differentiating even among a small sample of East Asian, Central Asian, and European individuals.

CURRENT STUDY RESULTS

For the current study, all individuals from the pilot study were added to the total population under analysis (n=627).

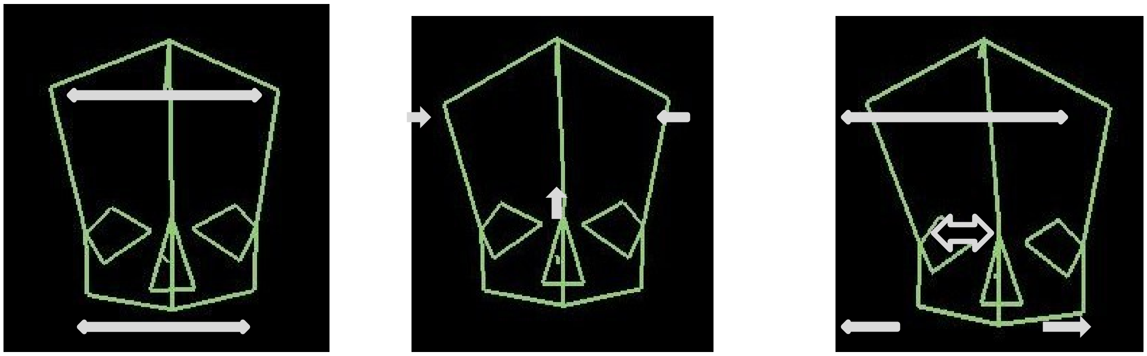
The first goal was to determine whether there were statistically significant differences among all three groups: the Central Asia group, the Europe group, and the East Asia group. The coordinates obtained from the landmarks were input into *morphologika* and a Generalized Procrustes Analysis (GPA) was conducted to translate, scale and rotate the points to align them so they could be compared more easily to one another. The newly scaled and aligned data were then put through a Principal Components Analysis (PCA). In the first phase of this analysis, the entire population sample was used to determine if the methodology was precise enough to differentiate among the groups.

A visual approximation of the crania from Europe and East Asia in the wireframe configuration available on the *morphologika* program showed some differences in shape among the groups. The East Asia sample overall had shorter, more rounded, calvarial outline and a more pronounced curvature from the occipital region to the cranial base (Figure 8.1 b), a broader (8.1a) and flatter midface area (8.1b) than the European group. The facial profile of the East Asia group was much flatter and less anteriorly projecting especially at nasion and glabella, as seen in Figure 8.1b. The sample from Europe was most notable in its calvarial outline which was more posteriorly-projecting. Glabella and nasion were more anteriorly projecting or salient (8.1b), and nasion was more superiorly-positioned in this group (8.1a). The East Asia group had wider bialare breadth and a broader midface with more laterally flaring zygomatics, and larger cranial breadth than the European group (Figure 8.1a). The group from Central Asia had a mosaic of features from the European and East Asian crania and also some traits that were more extreme than either group. The Central Asian group showed the greatest cranial breadth (at Euryon) paired with the most flaring zygomatic arches of all the groups (Fig 8.1a). Nasal breadth is intermediate between European and East Asian, but orbital shape is very different from both groups particularly with a much larger distance between the inner orbit landmarks (Dacryon to Dacryon) (8.1a). In the lateral view (Fig 8.1b) the group from Central Asia exhibited a longer cranial outline than the group from East Asia but not as far posteriorly-projecting as the group from Europe. The calvaria were more rounded and more curved than the European and the East

Asian groups, although closer to the East Asian configuration (8.1b). Nasion was positioned more inferiorly in the Central Asian group than the European group, and was positioned further inferiorly still in the East Asia group (8.1a). The midface region projects further anteriorly in the Central Asia group (than the East Asian) with a more prominent glabella than any other group (8.1b).

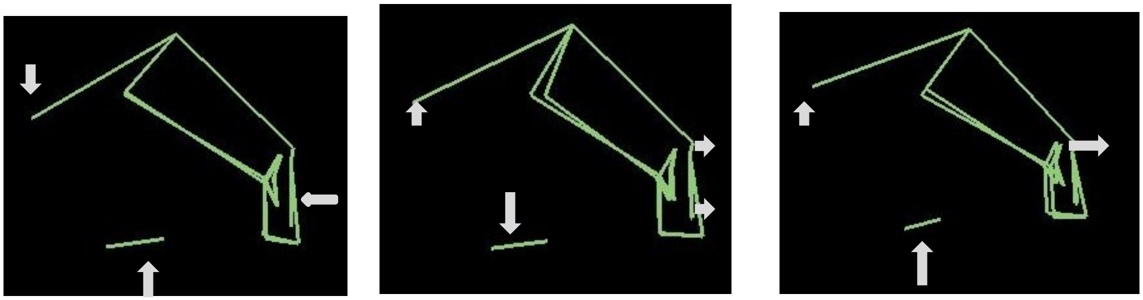
Figure 8.1: PC1/PC2 all groups, wireframe configuration in Morphologika 3D viewer

a. Anterior View



East Asian European Central Asian

b. Lateral View

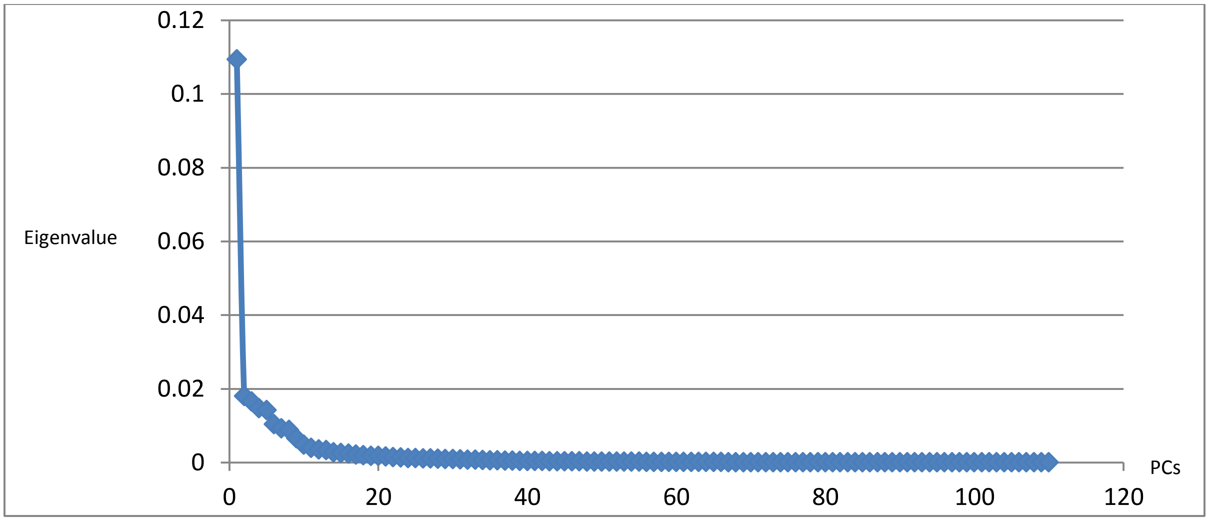


East Asian European Central Asian

Despite these observed differences, only a quantitative analysis could confirm if these differences were significant on a population level.

The results from the PCA showed that 81% of the variation in the total sample was explained by the first ten principal components (PC1=41.7%, PC2=6.8%, PC3=6.3%, PC4=5.6%, PC5=5.4%, PC6=3.9%, PC7=3.5%, PC8=3.3%, PC9=2.5%, PC10=1.8%). The first nine principal components were selected based on the results of a scatter plot of PC to eigenvalue (Figure 8.2), where the elbow of the curve represents the maximum number of PCs considered significant for the analysis. Principal components analysis represents an "ordination technique to explore large-scale trends within the data" and thus independent axes are not biologically meaningful on their own (Harvati *et al.*, 2010).

Figure 8.2: PC to Eigenvalue scatterplot



A Multivariate Analysis of Variance (MANOVA) was conducted on the first nine principal component scores obtained through *morphologika* to test for mean shape differences among the East Asian, European, and Central Asian groups. This was accomplished using PAST software version 3. The MANOVA detected significant group differences (Wilk's $\lambda=0.74$, F value=11.97, df =16, $p<0.0001$). This initial test statistic showed that this method for collecting specific facial and cranial landmarks, given a large-size sample, is effective in differentiating among East Asian, Central Asian, and European individuals. The main differences across all PCs were observed primarily in mid-facial breadth and mid-facial projection (nasal) followed by cranial breadth, and to a much lesser extent cranial height and cranial length.

A Mahalanobis Generalized Distance statistic (D^2) represents the squared generalized distance of the principal components and was used to calculate the degree of differentiation between each set of two populations. A squares distances table was obtained through PAST version 3 and showed that East Asians and Europeans were the furthest apart (most different from each other), followed by Central Asians and Europeans who were a bit closer than the first grouping, and finally Central Asian and East Asians who were closest compared to all other permutations (Table 8.2).

Table 8.2: Mahalanobis square distances (entire sample)

Colors indicate close (red), intermediate (pink), or far (blue) distance relationship between groups

	European	East Asian	Central Asian
European	0	1.18	0.81
East Asian	1.18	0	0.75
Central Asian	0.81	0.75	0

A discriminant function analysis (DFA) identifies which variables can discriminate between the three populations, looking for significant mean shape differences between groups. A discriminant function analysis using cross-validation was conducted on the entire sample of 627 individuals without omitting any data points and using 10PCs which accounted for over 81% of the variance within the sample. Individuals were classified into one of three groups: East Asian, European, or Central Asian.

The results of the DFA showed that Europeans were very poorly classified with only 36% of European individuals classified correctly into the European sample. The other two groups were classified at a much higher level of accuracy (64% East Asian, 87% Central Asian) but the total percent of correct classification was weighed down by the European sample. East Asians were most frequently misclassified as Central Asian (27.5% of the individuals). Europeans were misclassified as Central Asian at a rate of 54%. These results point to the intermediate position of Central Asians between European and East Asian cranial morphology.

Many individuals, mostly from the European group, were missing numerous data points, some crucial to identifying ancestral grouping such as nasal craniometric points (Rhinion, Nasion, Nasospinale, Alare) or from the zygomatic area (zygion or zygomaxillare, ectomolare) and basio-cranial points (Basion and/or Opisthion). Given the importance of these landmarks in accurately identifying or distinguishing population groups, individuals who were missing craniometrics data points from the nasal, zygomaxillary, or basio-occipital regions (173 individuals overall) were omitted from the analysis since they were artificially skewing the results. Additionally, because over one hundred individuals were missing the ectomolare landmarks (Ecm), rather than removing a large sample of specimens from the collection, these landmarks were excluded from the analysis.

A new PCA and MANOVA were conducted from the sample of 454 individuals using 39 landmarks (627 individuals minus the 173 omitted due to missing crucial craniometrics points; 41 landmarks minus Ecm left and right). The broken stick method is generally useful for determining the minimum number of PCs to explain most of the variation within an average sample, but for assessing relatively small differences among modern human populations some studies have suggested selecting enough PCs to explain over 90% of the variance among groups (Roseman and Weaver, 2004; von Cramon-Taubadel, 2009 and 2011b; and Schmidt, 2012). By using 15PCs, which account for over 90% of the total variance in this sample the MANOVA yielded significant differences among all sets of populations (Wilk's $\lambda=0.24$, *F* value=31.73, df1,2 =28,876, $p<0.0001$). Significant differences were found between European and East Asian groups, between European and Central Asian groups, and between East Asian and Central Asian groups (Table 8.3).

Table 8.3 MANOVA and PC % variance for reduced sample

EUROPE, EAST ASIA, CENTRAL ASIA **PC % VARIANCE EXPLAINED** 15 PC >90.7% TOTAL VARIATION
PC 1= 49.43%
PC 2 =8.08%
PC 3 =6.39 %
PC 4 =5.53 %
PC 5 = 5.05%
PC 6 =4.86 %
PC 7 = 2.91%
PC 8 =1.95 %
PC 9 =1.43 %
PC 10 = 1.03%
PC 11=0.93%
PC 12=0.87%
PC 13=0.84%
PC 14=0.73%
PC 15=0.71%

MANOVA RESULTS
Wilk's $\lambda=0.24$
F value=31.73
df =28,876
$p<0.0001$

Statistically significant differences were found among all groups in the pairwise comparisons, with uncorrected p-values as seen in Table 8.4 (statistically significant differences are indicated in red).

Table 8.4 Results of pairwise comparison among the 3 groups

MANOVA using 15 pcs, uncorrected p-values: statistically significant differences are indicated in red.

	European	**EastAsian**	**CentralAsian**
European		1.045E-81	2.099E-40
East Asian	1.04E-81		4.83E-36
Central Asian	2.099E-40	4.83E-36	

A Mahalanobis Generalized Distance statistic (D^2) was used to calculate the degree of differentiation between each set of two populations. A squares distances table was obtained through PAST version 3 and showed, as previously (Table 8.2) that East Asians and Europeans were the furthest apart (most different from each other), followed by Central Asians and Europeans who were closer than the first grouping, and finally Central Asian and East Asians who were closest compared to all other permutations (new analysis in Table 8.5).

Table 8.5: Mahalanobis square distances (reduced sample)

Colors indicate close (red), intermediate (pink), or far (blue) distance relationship between groups

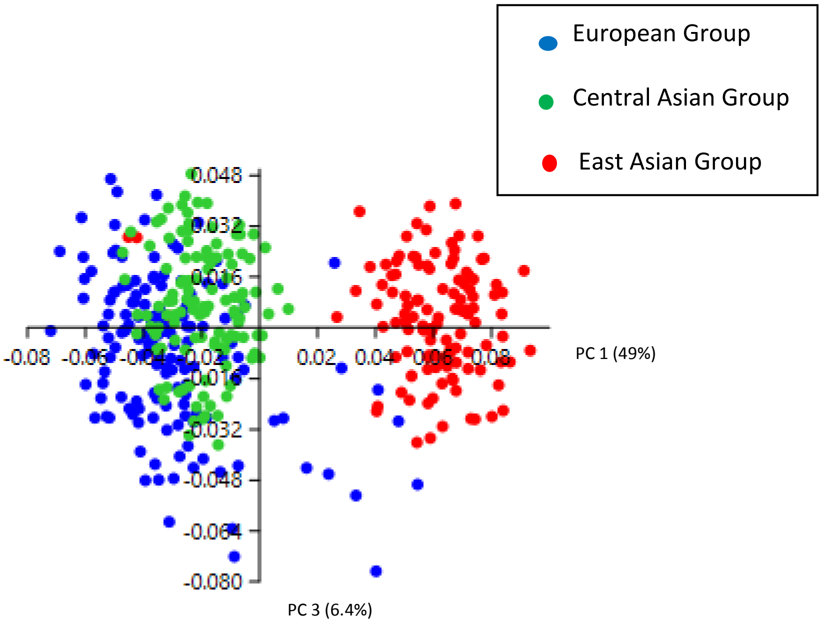
	European	East Asian	Central Asian
European	0	12.05	4.86
East Asian	12.05	0	4.07
Central Asian	4.86	4.07	0

A series of PC graphs highlighting differences among craniofacial shape groups are represented in Figures 8.3 a-f. Shape differences along PC 3 (Fig 8.3a and c) reflect the particularities of the Central Asian group helping distinguish it from the European and East Asian samples: as you move from the positive to the negative areas of the graph along the y axis (PC3, 8.3a) cranial breadth decreases (at Euryon), as does zygomatic flaring (Zygion in particular but all zygomaxillary points). The maximally broad configuration of Euryon is reached in the Central Asian grouping (Fig 8.3f). The same occurs along PC 3 (8.3c) on the x axis moving from negative to positive graph space. Along PC 1 (Fig 8.3a and b) on the x axis from negative to positive, the zygomatics are positioned further inferiorly on the face and retreat posteriorly. Along the same axis and PC, nasal projection decreases and there is an increase in the curvature of the occipital to cranial base region as the occipital plane becomes progressively less posteriorly-projecting. Along PC 2 (8.3c and d) moving from negative to positive along the y axis, mid-facial projection increases and cranial outline lengthens. PC 2 and PC 3 are very important in separating all three population groups from one another (Figs 8.3 c and f) as they seem to primarily affect zygomatic flaring and breadth, mid-facial breadth and height, and mid-facial flattening or projection. Along PC6 (8.3e), as you move towards the negative end of the y axis, projection at glabella increases and cranial breadth narrows.

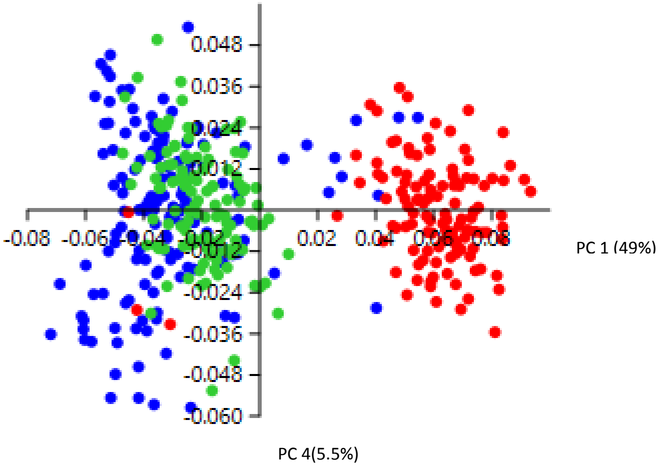
Figure 8.3: PCA of European, East Asian, and Central Asian groups

European group in blue, East Asian group in red, Central Asian group in green.

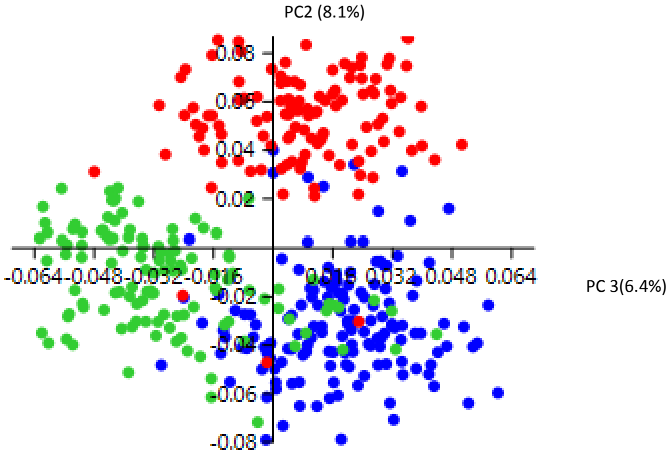
a. PC 1 and PC 3



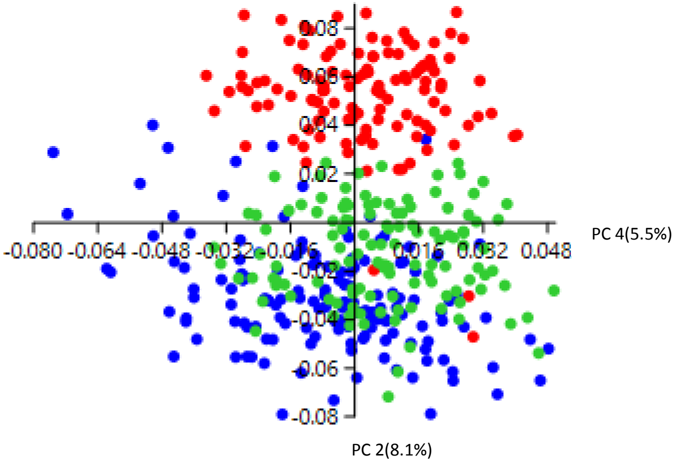
b. PC 1 and PC 4


0.048
0.036
0.024
0.012
-0.08
-0.06
-0.04
-0.02
0.02
0.04
0.06
0.08
-0.012
-0.024
-0.036
-0.048
-0.060
PC 1 (49%)
PC 4(5.5%)

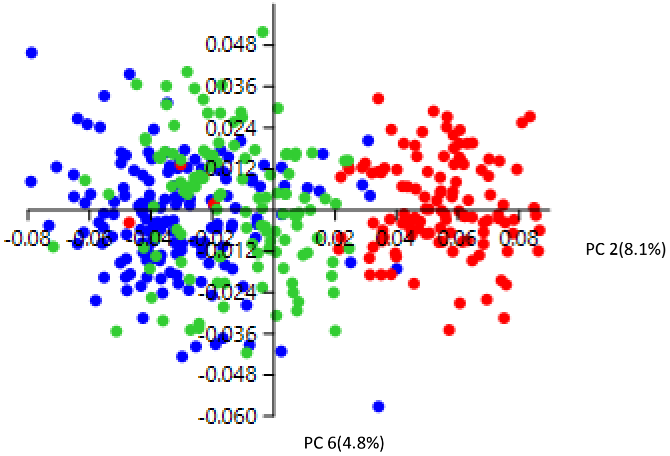
c. PC 3 and PC 2


PC2 (8.1%)
0.08
0.06
0.04
0.02
-0.064
-0.048
-0.032
-0.016
0.016
0.032
0.048
0.064
-0.02
-0.04
-0.06
-0.08
PC 3(6.4%)

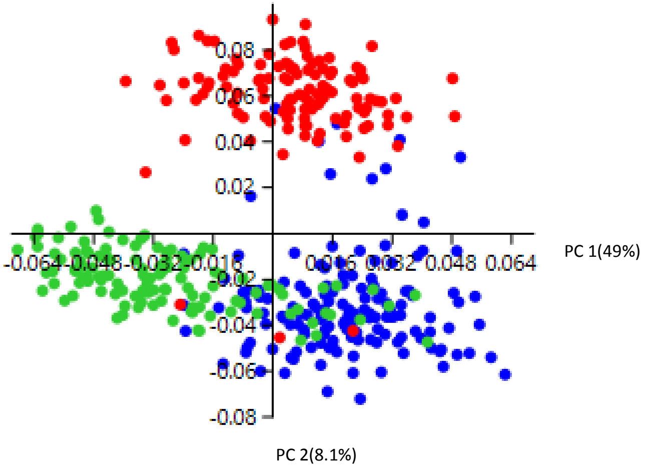
d. PC4 AND PC 2



e. PC2 AND PC6



f. PC 1 and PC 2

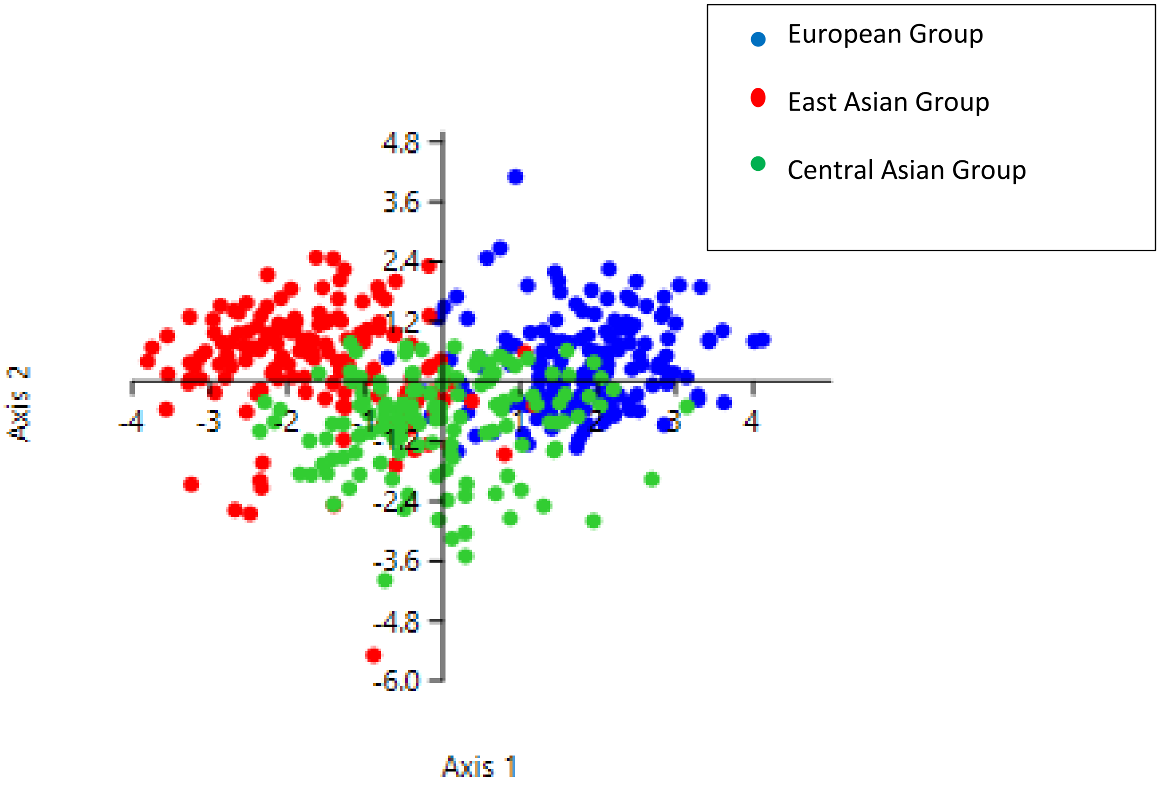


A discriminant function analysis using cross-validation was then conducted on the sample of 454 individuals (173 individuals omitted who had craniometric points missing). Individuals from this sample were classified correctly over 79% of the time. The European group was classified correctly 89% of the time in this sample, and the East Asian group 80%, both much higher than the previous DFA had shown. The Central Asian sample was more frequently misclassified in this scenario at around 70%, although still maintaining a high rate of accuracy. The Central Asian group occupies an intermediate position in between the two populations from East Asia and Europe and as such, more individuals from Central Asia can be classified as strictly East Asian or European compared to the other two populations, as seen in Figure 8.4. There is therefore more extensive overlap between Central Asian and European groups and between

Central Asian and East Asian groups than between European and East Asian groups where a more definite phenotypic division exists.

Figure 8.4: Graph representing 454 individuals, DFA of the three samples

European group in blue 89% correct classification; East Asian group in red 80% correct; and Central Asian group in green 70%.



Although the effects of size as have effectively been removed from the analysis through the GPA, and PCA focuses on analysis of shape, size might be nonetheless an important factor in differentiating across ancestry groups and needs to be investigated. Because all specimens have been scaled to unit centroid size, it is this variable that will be used to determine how much of a factor size plays in differentiating among ancestry groups in this sample.

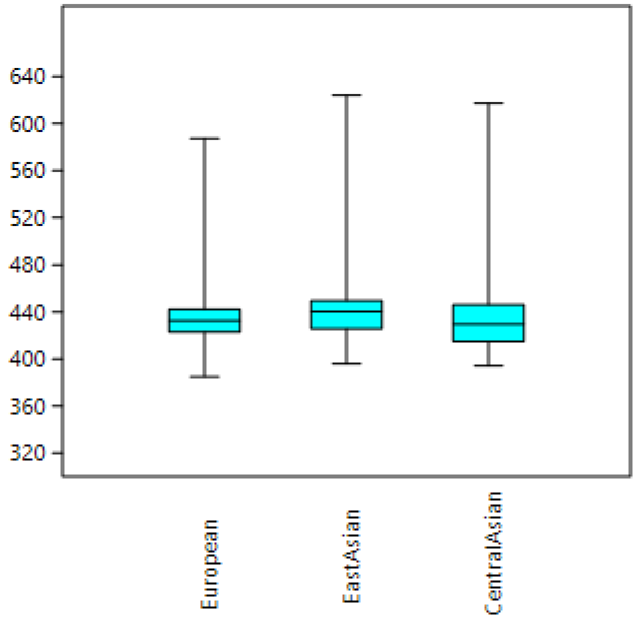
A statistical analysis of each population's centroid size mean to total sample centroid size mean was conducted to determine the standard error and variance for each ancestral group. Results are outlined in Table 8.6. A series of independent group t-tests were then conducted for each set of two populations comparing mean centroid size by ancestral group. No significant differences in mean centroid size among the groups was found (at $p<0.01$).

Table 8.6: Independent group t-tests of mean centroid size by ancestral group

	European Group	East Asian Group	Central Asian Group
N	N=153	N=161	N=140
Mean Centroid Size	432.57	443.04	443.01
Standard Error	1.55	2.39	3.97
Variance	368.733	923.07	2209.6
t-Tests	Europe and East Asia	t=-1.06, p=0.28	Not significant
	Europe and Central Asia	t=0.50, p=0.60	Not significant
	East Asia and CentralAsia	t=1.57, p=0.12	Not significant

The greatest variance in size is observed in the Central Asian sample, but none of the population mean sizes are significantly different from one another as seen in Figure 8.5.

Figure 8.5: Box plot distribution of centroid size by group



To assess the specific impact of size on shape in this cranial collection, a multivariate linear regression of PCs 1 through 15 to log centroid size was undertaken. Statistical significance was set at $p<0.01$. Table 8.7 outlines for which PCs size seems to be a factor. There is a statistically significant relationship between size (centroid size) and PCs 1, 4, 6, and 7 so size seems to play a part in shape analysis for these features. For PCs 2, 3, 5, 8, 9, 10, 11, 12, 13, 14, and 15 no statistically significant relationship was found with size.

Table 8.7: Summary of regression of PC scores (1-15) to centroid size

Statistically significant	PC 1	$r=-0.75$	$p<0.01$
	PC 4	$r=0.17$	$p<0.01$
	PC 6	$r=-0.31$	$p<0.01$
	PC 7	$r=-0.19$	$p<0.01$
Not statistically significant	PC 2	$r=0.11$	$p=0.02$
	PC3	$r=0.07$	$p=0.14$
	PC5	$r=-0.05$	$p=0.31$
	PC8	$r=0.02$	$p=0.57$
	PC9	$r=-0.09$	$p=0.03$
	PC10	$r=0.01$	$p=0.81$
	PC11	$r=-0.02$	$p=0.61$
	PC12	$r=0.02$	$p=0.68$
	PC13	$r=0.07$	$p=0.12$
	PC14	$r=-0.02$	$p=0.59$
	PC15	$r=0.03$	$p=0.56$

A series of DFAs were then conducted to ascertain the importance of size (centroid size) and shape (PCs) in correctly assigning crania to ancestry groups.

A DFA of log centroid size and PC1, PC 4, PC 6, and PC 7 (all PCs statistically significant for size, though PC4 and PC7 have weaker correlations) only classified 61% of the total sample ($n=454$) correctly, much less accurately than the previous DFA which yielded an 80% correct classification overall. The group from Europe and East Asia were only classified correctly 51% and 52% of the time. Size and size-influenced shape variables cannot be considered good predictors of ancestry group membership in this collection.

A DFA of the same cranial sample using PCs 2,3,5, 8,9,10,11,12,13,14, and 15 (all PCs not statistically significant for size) give a 78% correct classification. This result is vastly better than using size components alone and nearly identical to the original classification accuracy rate of over 79% using all 15 PCs (Figure 8.4). The Central Asian group is the most poorly classified here (66%), indicating that size might be a factor in addition to shape for identifying crania from Central Asia in this collection. It could also be that because the Central Asian group is intermediate between the group from Europe and the group from East Asia, that it is most poorly classified regardless of size effects. The East Asia and Central Asia groups are classified with a high level of accuracy (80% and 86% respectively) without accounting for size, so due to differences in shape alone. Size therefore does not play an important part in identifying these two populations and in differentiating them. Figure 8.5 and Table 8.6 show that the greatest variance in cranial size (mean centroid size) in the collection is observed in the Central Asian sample, indicating that there may be inherent allometric effects in this population specifically. Studies have shown that size differences between sexes can be a factor to consider when classifying ancestry groups (Kimmerle *et al*., 2008; Bigoni *et al*., 2010; Green and Curnoe, 2009). It is possible that there is greater variation in cranial size between males and females in this group than in the other samples due to population specificities. Size could, in that case, be a useful variable to further differentiate this population from the others. But, by using all 15 PCs, some of which have a statistically significant relationship with size (PCs 1,4,6,7), all the groups are identified with a high level of accuracy (near 80%) in the DFA, as seen in Figure 8.4. The decision to pool the sexes across this entire collection is discussed in the next section ("sex considerations").

The results from the above analyses point to the largest difference in craniofacial morphology being between the European and the East Asian groups. These results indicate that the chosen methodology and choice of landmarks are sensitive enough to distinguish with near 80% accuracy among individuals from all 3 regions. The results from the PCA and the DFA suggest that the Central Asian group is not only an intermediate between two distant populations, but that the Central Asian sample as a whole forms a clearly defined group. Furthermore, due to the intermediate position of the Central Asia group in the Mahalanobis tables and in the graph representation of the discriminant function analyses as being between the East Asian and European samples, these results support the claim that this Central Asian sample consists of admixed individuals. They exhibit a mosaic of traits from East and West as well as a series of morphological specificities that make them distinguishable as a group, separate from the East Asian and European samples: most individuals in this group are quite distinct in their morphology, as the qualitative analysis showed. Admixture among these populations is identified most precisely by analyzing mid-facial craniometrics landmarks. The nasal and zygo-maxillary craniometric points of crucial importance for identifying Central Asian admixture are Alare, Nasion, Nasospinale, Rhinion, Zygion, Zygomaxillare and Zygoorbitale, Ectomolare, Dacryon and Ectoconchion, as well as cranial breadth (Euryon). However, many individuals in the Central Asian population can be classified squarely into the European or East Asian population range, as seen by the significant overlap among the Central Asian group with the other two ancestral populations.

SEX CONSIDERATIONS

The reasons for identifying the sex of each skull in the sample were explained in the previous chapters (chps 4, 6, 7). Genetic studies have shown differential rates of migration between the sexes, with females migrating outwards more rapidly thus it is possible that differences in admixture levels between males and females could be observed osteologically in these groups.

Under ideal circumstances, both males and females would be represented equally in the populations under study. However, in these samples the number of males exceeded the total number of females by 100 or more (depending on number of omitted individuals due to missing landmarks). Some individuals were not assigned a sex as the cranium alone does not always provide the most accurate way to identify an individual by sex; the pelvic bone is generally preferred (Walrath *et al*., 2004; Williams and Rogers, 2006; Walker, 2008). No associated post-cranial remains were available to complete the analyses in those cases, and in the Duckworth collection (which had the most individuals of unknown sex, totaling 24 out of 189) many crania were not part of a whole population under study but a series of individual crania from various locations and time-frames so there was no opportunity to develop a clear picture of the range of variation within a small regional population across the sexes.

Breaking up each ancestry group into males and females yielded a much smaller sample size on which to run statistical analyses. This was further exacerbated by the need to analyze the Central Asian group by regional and temporal divisions in Chapter 9, yielding small sample sizes even when both sexes and unknowns were included. For example, the UPENN collection (considered mostly from the pre-Silk Road period) which consists of 36 individuals, if divided by sex would be composed of 17 females, 18 males and 1 unknown. Dividing up this group by sex would cause the results to be far less reliable than if dealing with the whole sample. Furthermore, out of the 124 individuals omitted from the analyses due to too many missing landmarks, the vast majority were female which amplified the population size difference between male and female samples even more, specifically in the European group. Finally, by pooling males, females, and unknowns in each sample we are able to analyze and observe the full range of craniofacial morphological variation in each of the three populations, which is an asset when trying to draw broader conclusions about an entire population based on a skeletal sample.

INTRAOBSERVER ERROR

To account for intra-observer error in measuring, approximately 9% of the selected crania were measured twice: once on the first day of data collection and once at the end of the measurement period. The percent error for each individual within this sample was calculated. Conventionally, a 5% or higher error rate is considered unacceptable, and a 3% or less error rate is acceptable (Corner *et al.,* 1992). The total percent error across the entire sample was 2.3% (Cambridge 1.6%, AMNH 2.6%, MSU 2.57%). Intra-observer error increased in individuals with partially eroded or nearly absent landmarks. Lambda, for example when eroded is not easily recognizable. The coefficient of variation (CV) for that specific landmark ranged from 4% to 11% in the MSU collection. The coefficient of variation was calculated by dividing the standard deviation of the data by the mean of the data and multiplying by 100 to obtain a percentage. Similarly points such as Asterion when eroded to the point of invisibility yielded wide ranges (CV=0.3% to 30%) due to the difficulty in accurately collecting assessing and collecting the landmark coordinates. This is one of the main reasons why Asterion was eliminated from the analysis, in addition to it holding no particular importance in discerning amongst the three ancestry groups. On the other hand, intra-observer error decreased overall with time and practice. The last collection to be measured was the Duckworth collection from Cambridge where the intra-observer error was estimated to be 1.6% as opposed to the first collection (AMNH) where it was 2.6%. The percent error calculated in two individuals from the Cambridge collection is shown in Table A4.1, Appendix 4.

In the next section, we will analyze regional and temporal differences seen within the Central Asian group. Does the composition of this population change significantly over time and if so, are these changes attributable to secular changes or do they represent the outcome of the influence of population migrations across the Silk Road? Chapter 9 will present the results of this analysis.

Chapter 9: Analysis within group

In the previous chapter, the results showed that the Central Asia group is admixed as it occupies an intermediate position between the European and East Asian sample populations studied here, and can be differentiated from the other two populations with a fair amount of accuracy (80%) by focusing on the mid-facial region and markers of facial and cranial breadth. The case for admixture and a distinct Central Asian craniofacial morphology has then been put forth, but it is the nature of this admixture and how it changes over time that will be analyzed here. In this chapter, the results from intra-group analyses on the Central Asian population sample are presented.

INTRA GROUP COMPARISON BY TIME PERIOD

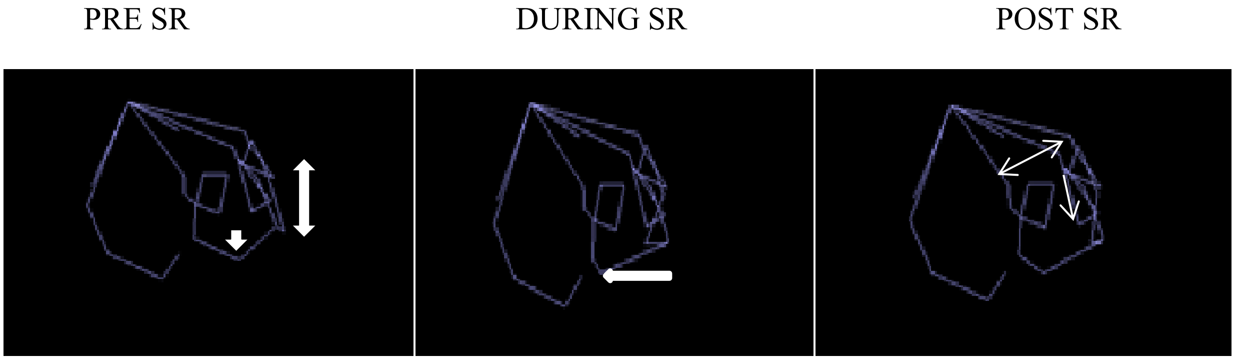
In order to examine how admixture has changed historically along the Silk Road trade routes, a PCA followed by a MANOVA was used to analyze and compare the Pre-Silk Road Central Asian sample (PRE SR) to Central Asian contemporaries of the Silk Road (DURING SR) to the Post-Silk Road Central Asian sample (POST SR), looking for morphological differences in these temporally diverse populations from Central Asia.

A visual approximation of the Central Asian crania across the three time-frames was viewed in the wireframe configuration available on the m*orphologika* program. Figure 9.1(a and b) shows some of the more pronounced differences in shape among the groups. In the PRE SR group, corresponding to the time period before the opening of the Silk Road, individuals on average exhibit a longer mid-face region than the later groups, they have fairly broad but low-lying zygomatics, and a projecting nasal outline (rhinion). The Silk Road group, which spans the longest period of time, was characterized by a shorter mid-face region compared to the PRE and the POST groups and broader more posteriorly-projecting zygomatics with an increase in cranial breadth. The POST Silk Road population still retains the shorter mid-face region but it is longer than in the DURING SR group, the zygomatics are positioned more superiorly and are broader, and the nasal region is slightly less projecting but longer, with a narrowing in the fronto-temporal region, and an increase in cranial breadth.

Figure 9.1: Typical cranial morphology of Central Asian collection by time-period

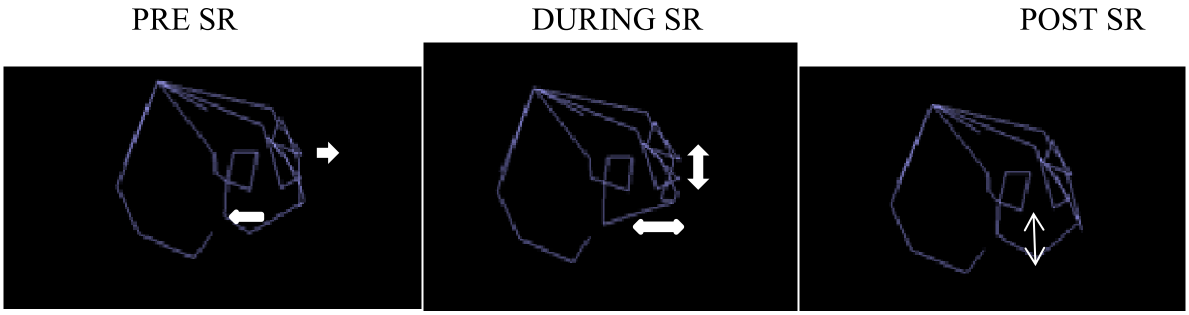
(PC1 and PC2, and PC1 and PC9)

a. PC1 and PC2



PRE SR DURING SR POST SR

b. PC1 and PC9



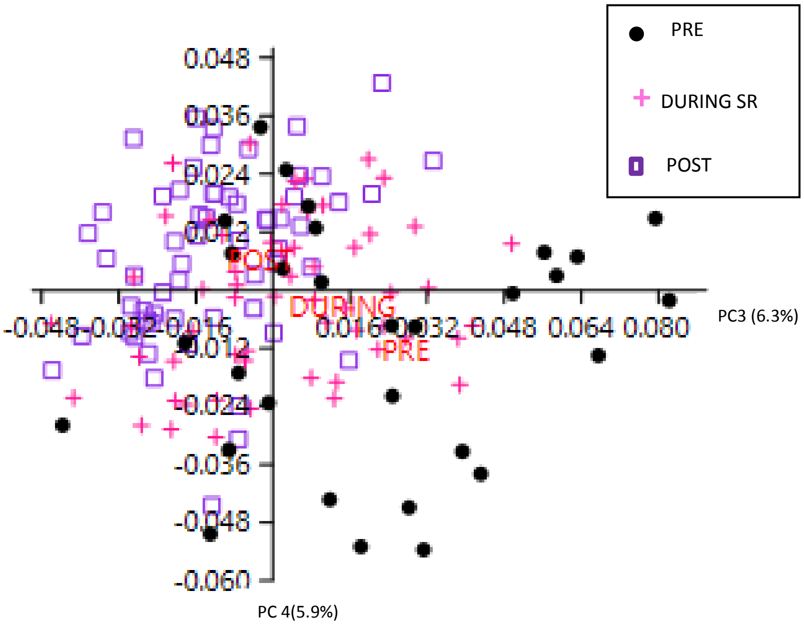
PRE SR DURING SR POST SR

Despite these observed differences, only a quantitative analysis could confirm if these differences were significant on a population level.

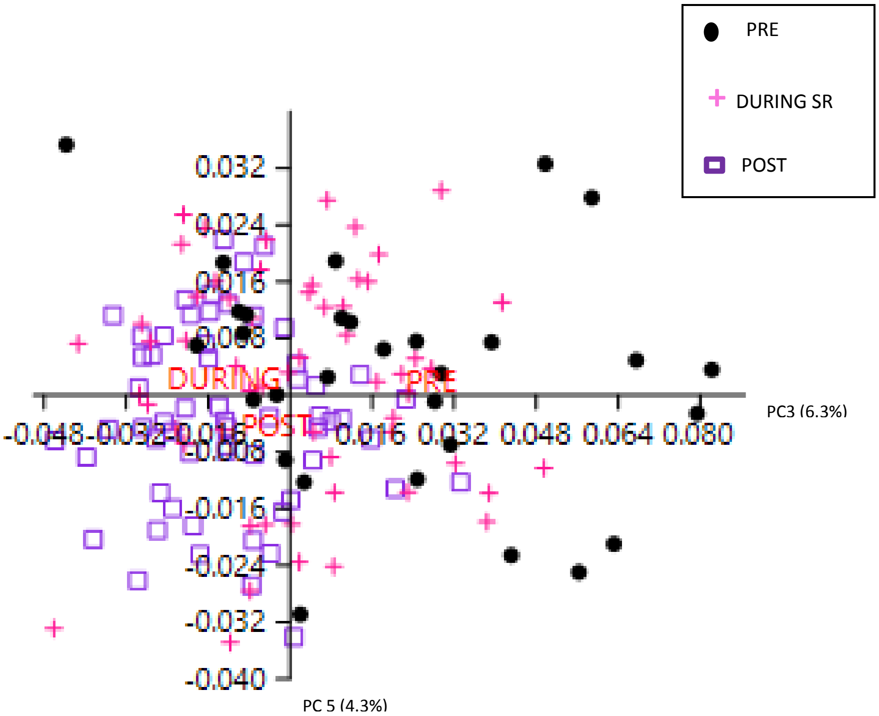
The results from the PCA showed that 89.4% of the variation in the total sample was explained by the first ten principal components (Table 9.2). Figure 9.2a-c show PCA graphs that highlight the differences across the time-differentiated groups. Along PC 3 (Fig 9.2a) on the x axis from positive to negative, cranial breadth increases and nasal projection decreases slightly. PC 4 (Fig 9.2 a and 9.2c) seems to affect mid-facial height which decreases along the y axis from negative to positive (Fig 9.2a), and also decreases along the x axis also from negative to positive in Fig 9.2c. Frontotemporal breadth narrows while cranial breadth and nasal length increase along PC5 (9.2b) as you move along the y axis from positive to negative. The main differences across all PCs were observed primarily in mid-facial breadth landmarks (zygoorbitale, zygomaxillare, dacryon, ectoconchion, zygion, alare) and mid-facial projection (nasion to rhinion) followed by cranial breadth (euryon) and upper facial breadth (frontotemporale).

Figure 9.2: PCA of Central Asian population in three time-frames

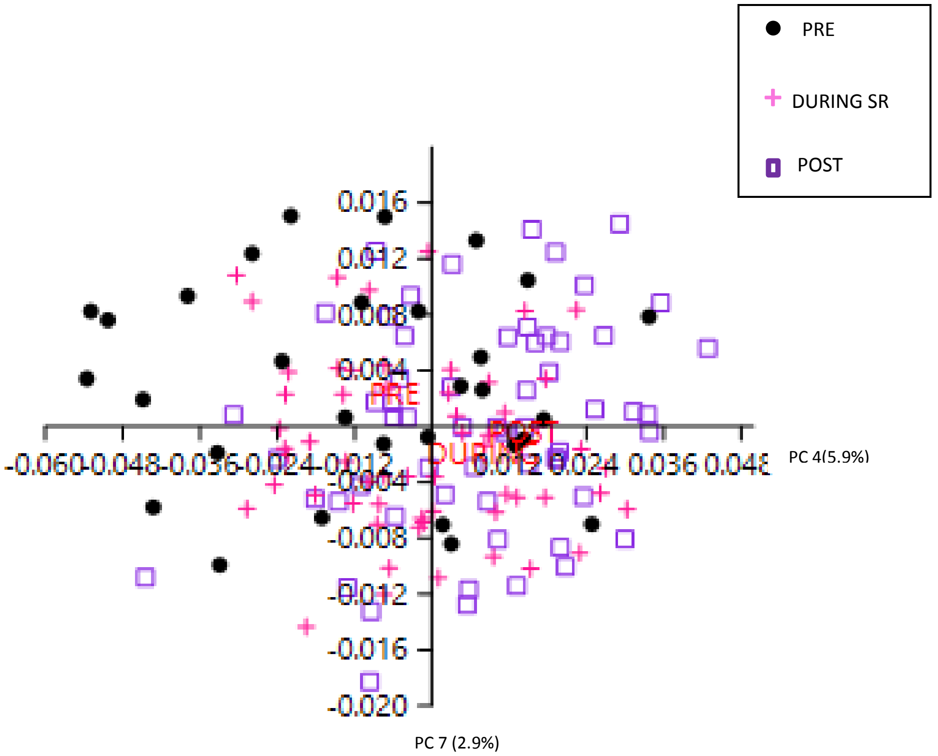
a. PC3 and PC4


PRE
DURING SR
POST
0.048
0.036
0.024
0.012
-0.012
-0.024
-0.036
-0.048
-0.060
-0.048
-0.032
-0.016
0.016
0.032
0.048
0.064
0.080
POST
DURING
PRE
PC3 (6.3%)
PC 4(5.9%)

b. PC3 and PC5


PRE
DURING SR
POST
0.032
0.024
0.016
0.008
-0.008
-0.016
-0.024
-0.032
-0.040
-0.048
-0.032
-0.016
0.016
0.032
0.048
0.064
0.080
DURING
PRE
POST
PC3 (6.3%)
PC 5 (4.3%)

c. PC4 and PC7



A Multivariate Analysis of Variance (MANOVA) was conducted on the first ten principal component scores obtained through *morphologika* to test for mean shape differences among the PRE, DURING, and POST Central Asian groups. This was accomplished using PAST software version 3. The MANOVA detected significant group differences (Wilk's λ= 0.35 with p<0.00002). However this significant difference was observed only between the SR and PRE groups and between the POST and PRE groups. There was no statistically significant difference found between the DURING SR and POST groups among the three. A Mahalanobis generalized squared distance statistical analysis showed that the DURING SR and POST SR groups were much closer to each other than to the PRE group, but there was effectively no statistically significant difference between the DURING SR and POST groups. The Mahalanobis table showed a strong difference and increased distance between the DURING SR and PRE groups and between the POST and PRE groups who were the furthest apart, as seen in Table 9.1.

Table 9.1: Mahalanobis square distances among three time-differentiated Central Asian populations

Colors indicate close (beige), intermediate (pink), or far (blue) distance relationship between groups

	SR	POST SR	PRE SR
SR	**0**	**0.89193**	**7.9373**
POST SR	**0.89193**	**0**	**8.7842**
PRE SR	**7.9373**	**8.7842**	**0**

A new PCA was conducted for the POST and DURING SR groups only (Figure 9.3). The first twenty PCs were used which accounted for 98.06% of the total variance (Table 9.2). A MANOVA was conducted on the 20 PCs and yielded significant differences at this threshold between the DURING SR and the POST groups (Wilk's λ= 0.708 with p<0.0031). In the pairwise comparisons, using p-values with uncorrected significance, the difference and statistical significance between the two groups was certainly weaker than the difference between PRE and POST and PRE and DURING SR but was nonetheless statistically significant.

Table 9.2: PCs 1-20 percent variance and percent cumulative variance explained PRE, DURING, POST

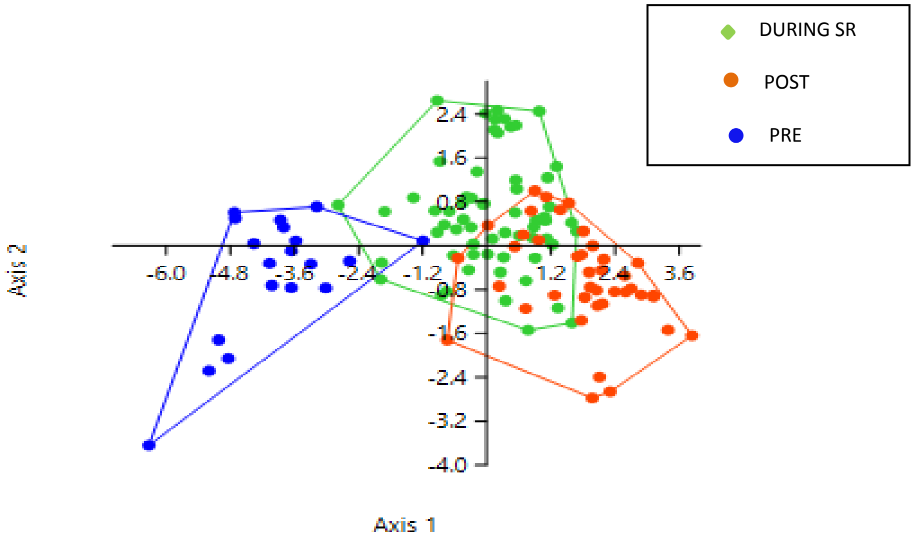
	Eigenvalue	% Variance Explained	% Cumulative Variance Explained
PC 1	0.107416	46.79297	46.79297
PC 2	0.030207	13.15875	59.95172
PC 3	0.014487	6.310756	66.26248
PC 4	0.013697	5.966737	72.22921
PC 5	0.009883	4.305076	76.53429
PC 6	0.007193	3.133502	79.66779

PC 7	0.006745	2.938116	82.60591
PC 8	0.005813	2.532096	85.138
PC 9	0.005125	2.23239	87.37039
PC 10	0.004821	2.100352	89.47075
PC 11	0.004085	1.779495	91.25024
PC 12	0.003757	1.636468	92.88671
PC 13	0.003223	1.404073	94.29078
PC 14	0.002587	1.127124	95.4179
PC 15	0.001427	0.621474	96.03938
PC 16	0.001397	0.60875	96.64813
PC 17	0.001214	0.528695	97.17682
PC 18	0.000847	0.368901	97.54573
PC 19	0.000714	0.311073	97.8568
PC 20	0.000482	0.21004	98.06684

A DFA was then conducted on the entire Central Asian collection (PRE, DURING, AND POST SR) using the first 20PCs which accounted for over 98% of the variance within the sample (Figure 9.3). Individuals were classified into one of three groups: PRE, DURING, or POST with 80% accuracy.

Figure 9.3: DFA graph of Central Asian groups using 20 PCs.

Axis1 represents >91% eigenvalue and Axis 2 >9% eigenvalue.



In this DFA, the group most accurately classified was the PRE group with 94% accurately classified, the POST was the most poorly classified with 75%accurately classified (most frequently misclassified as DURING SR), and the DURING SR sample was classified into the correct membership group at a rate of 79%.

The DURING SR group is the largest (n=68) and most regionally diverse of the three time-differentiated Central Asian groups and is composed of specimens from Turkmenistan, Uzbekistan, and Karakalpakia (an independent region located in north-western Uzbekistan, sandwiched between Turkmenistan and Kazakhstan). It is therefore important to determine if there is a statistically significant difference among these three geographically-differentiated populations or if they can be considered as one for the purposes of our analysis. A MANOVA was conducted and found that there were no statistically significant differences (Wilk's λ= 0.44

but p=0.22, with a statistical significance threshold set at α=0.05) across these three geographically-differentiated groups for this time-period (DURING SR).

The Mahalanobis squared distance analysis in Table 9.3 shows that despite no statistically significant differences, the closest populations might be the crania from Uzbekistan and Turkmenistan overall, followed by those from Turkmenistan and Karakalpakia, and finally slightly further apart are the specimens from Karakalpakia and Uzbekistan.

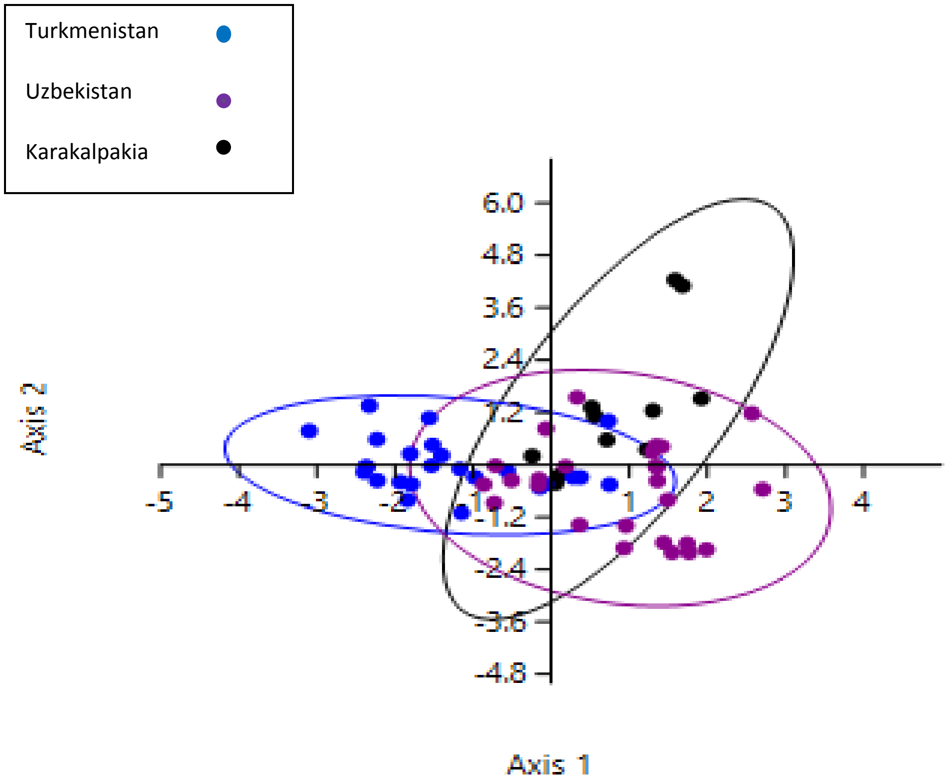
Table 9.3: Mahalanobis of SR groups of different geographic origin

Colors indicate close (red), intermediate (lilac), or far (blue) distance relationship between groups

	Karakalpakia	Turkmenistan	Uzbekistan
Karakalpakia	**0**	3.374	**3.56**
Turkmenistan	3.374	**0**	**2.8078**
Uzbekistan	**3.56**	**2.8078**	**0**

A DFA was conducted to further assess if statistical significance had been achieved to classify these three geographically-differentiated groups correctly. The ranges of these groups are extensively overlapping, as seen in Figure 9.4. While the crania from Karakalpakia were only classified 50% of the time into their correct group, those from Uzbekistan and the Turkmenistan were classified over correctly over 70% of the time. Despite this, statistical significance was not reached for these tests and the results, although potentially correct, could equally be due to chance. The SR group can therefore be considered as one population.

Figure 9.4: DFA graph of DURING SR groups only



A multivariate linear regression of centroid size to PC scores (1-10) was conducted to assess if size was a significant factor in identifying time-period groups in this population. Size was not found to have played a part in the shape differences observed in the three time-differentiated Central Asian groups, as there was no statistically significant relationships between any of the PCs and centroid size with $p<0.05$ (Table 9.4).

Table 9.4: Size analysis and summary of regression of PC scores to log centroid size

Statistics Significance set at p<0.05		**Regression** Significance set at p<0.05		
		PC 1	r= 0.006	p=0.93
R2:	0.0004466	PC 2	r= 0.035	p=0.67
MSE:	0.004084	PC 3	r= 0.051	P=0.54
Wilks´ lambda:	0.9461	PC 4	r= 0.088	p=0.29
F:	0.7805	PC 5	r=0.049	p=0.56
df1:	10	PC 6	r= 0.073	p=0.37
df1:	137	PC 7	r= 0.048	p=0.56
p(regr):	0.6474	PC 8	r=-0.050	p= 0.54
		PC 9	r=-0.066	p=0.43
		PC10	r=-0.019	p=0.82

ADMIXTURE IN THE THREE TIME-PERIODS

As indicated in the previous section, the three time-differentiated groups are statistically significantly different from one another, albeit a much smaller difference between the DURING SR group and the POST group compared to the PRE to POST or PRE to DURING SR groups. Furthermore, it was demonstrated that these differences or changes could not be attributed to geographic affiliation (e.g., Turkmenistan versus Karakalpakia). These craniofacial differences therefore appear to be influenced by time period rather than anything else.

The next step involved counting individuals who did not exhibit any craniofacial admixture and who were classified as part of the European or East Asian groups in each of the three time period samples. The total percentage of individuals showing any admixed traits and thus considered admixed was then calculated in each of the chronologically-differentiated populations.

Three DFAs were conducted here: one for each time-differentiated group (PRE, DURING SR, POST) compared to the entire East Asian and European population samples. Given that across the entire sample 80% of individuals were classified into the correct grouping, it is assumed that the DFAs will provide a very good level of accuracy in assigning an ancestral group to each individual in the sample under consideration. The confusion matrix pinpointed individuals not classified within their own given or assigned group. These individuals accordingly are considered "non-admixed" as they were classified as European or East Asian (and therefore closer to one or the other group) instead of the more recently admixed Central Asians.

A DFA of the PRE group compared to European and East Asian individuals was obtained by using the first 15 PC scores from the PCA analysis which accounted for 84% of the total variance. Out of the 23 individuals in the PRE sample, 16 were assigned to the European group (69%), while 7 were assigned to the Central Asia group (admixed) (30.4%).

Next a DFA of the DURING SR group compared to European and East Asian was obtained by using the first 15PC scores from a PCA analysis which explained 82% of the total variance. Out of the 68 individuals in the Silk Road group only 15 (22%) were classified as non-admixed with 10 classified as European (14.7%) and 5 as East Asian (7.3%).

Finally the last DFA, which looked at the POST SR group and the entirety of the European and East Asian samples, was obtained after conducting a PCA analysis. The first 15PCs which accounted for 84% of the total variance were used in this analysis. Only 7 out of the 61 POST group were classified as non-admixed (11.5%) with 3 of them being squarely within range of the European population (5%) and 4 assigned East Asian ancestry (6.5%).

A list of admixed versus non-admixed tallies per time-period are detailed below in Table 9.5

Table 9.5: Early and late silk road admixed and non-admixed individuals from Central Asian grouping.

Number of Individuals	Provenance	Time-Frame	Number of Admixed	Number of Non-Admixed	Percent Admixed
23	Tepe Hissar	Pre Silk Road	7	16	30.4%
58	Kirghizstan	Post Silk Road	51	7	88 %
13	Samarkand, Uzbekistan	Silk Road (Early)	9	4	70 %
8	Tashkent, Uzbekistan	Silk Road (Mid)	8	0	100%
4	Termez, Uzbekistan	Silk Road (Mid)	3	1	75 %
6	KhodjItarab, Kipchak, Uzbekistan	Silk Road (Mid)	3	3	50 %
7	Parau, Turkmenistan	Silk Road (Mid to Late)	5	2	71.5%
7	Kukurt, Turkmenistan	Silk Road (Late)	4	3	57.2%
4	GyozlAta, Turkmenistan	Silk Road (Mid to Late)	4	0	100%
7	Koshab, Turkmenistan	Silk Road (Late)	7	0	100%
3	Ersari, Turkmenistan	Post Silk Road	3	0	100%
1	Shekri, Turkmenistan	Silk Road (Mid to Late)	1	0	100%
11	Karakalpaki, Uzbekistan	Silk Road (Late)	9	2	82 %
		TOTAL Admixture %:	114	38	75%
				Total PRE admixture %:	30.4%
		Early-Mid Admixture:74%	Mid-Late Admixture: 81%	Total DURING admixture %:	78 %
				Total POST admixture %:	88.5%

ADMIXTURE MANTEL TESTS RESULTS

As observed through visual methods and with DFA, the percent of individuals who can be classified as admixed has fluctuated over time, with the most change between Pre-Silk road trade and thereafter (Table 9.5). Further statistical analyses were used to determine whether admixture in this Central Asian population has increased, decreased, or remained stable over time.

A series of Mantel tests were used to determine if admixture has changed over time (increased, decreased or stayed the same). The Mantel test is a statistical method that looks at the relationship between two square matrices whose values are represented by distances between points. It tests for the similarity of the matrices using hundreds of permutations of the rows and columns in the matrices to calculate over and over again the correlation between them (Mantel and Valand, 1970). Results will indicate a strong or weak correlation between the data matrices and thus if any significant changes have occurred in a population over time.

For the Mantel tests, two matrices are compared at a time, both of which must have the same number of rows, in this case the same number of individuals, in order to proceed. As the PRE SR group was the smallest and consisted of 32 individuals, all MANTEL tests were conducted with 32 individuals per group unless indicated otherwise. The Silk Road group was divided into two subgroups: Early to Mid-Silk Road period (DURING 1)from 200BC to 15th Century and Mid to Late Silk Road (DURING 2) from 15th Century to 16th Century AD, each consisting of 32 individuals (see groupings below Table 9.6). The POST SR group was also divided into two (POST 1 and POST 2) all 18th and 19th Century but since there is no temporal difference between the two subgroups individuals were randomly assigned to one or the other category (KA1 through KA54 Kirghiz for POST 1 and KA55-KA89 Kirghiz plus 3 Ersari-Baba from Turkmenistan for POST 2).

Table 9.6: Group distribution for Mantel tests

MANTEL GROUP	**Provenance**	**Number of Individuals**	**Time Period**
PRE SR	Tepe Hissar	32	3500BC to 350 AD
DURING 1 (Early-MidSR)	Samarkand, Uzbekistan	14	200 BC-600 AD
DURING 1 (Early-MidSR)	Termez, Uzbekistan	4	6th-12th Century AD
DURING 1 (Early-MidSR)	KhodjaItarab, Kipchak, Uzbekistan	6	11-12th Century AD
DURING 1 (Early-MidSR)	Tashkent, Uzbekistan	8	Before 1600 AD
DURING 2 (Mid-LateSR)	Parau, Turkmenistan	7	After 15th Century AD
DURING 2 (Mid-LateSR)	Kukurt, Turkmenistan	7	16th Century AD
DURING 2 (Mid-LateSR)	Gyozli/Dana Ata, Turkmenistan	4	15th-17th Century AD
DURING 2 (Mid-LateSR)	Koshab, Turkmenistan	7	16th Century AD
DURING 2 (Mid-LateSR)	ShekriIslam,Turkmenistan	1	15th Century AD
DURING 2 (Mid-LateSR)	Karakalpakia, AmuDarya	6/12	16th Century AD
POST 1 (After SR)	Kirghizistan	32/61	18TH Century AD
POST 2 (After SR)	Kirghizstan	29/61	18th Century AD
POST 2 (After SR)	Ersari Baba, Turkmenistan	3	19th Century AD

Each set of two groups from above underwent a Mantel test to ascertain whether admixture changed in Central Asian populations over time. Thirteen variables (Table 9.7 below) were used in this analysis which consisted of linear measurements of mid-facial breadth, cranial breadth, nasal projection, and nasal length as these landmarks were shown to best distinguish between Central Asians and Europeans and Central Asians and East Asians as described in chapter 8 (also in Figure 4.1). These distances were all found to increase in admixed individuals from Central Asia compared to non-admixed individuals. These were calculated from the 3D landmark data used to measure the skulls.

Table 9.7: Craniofacial linear measurements used for admixture Mantel test

Linear Measurement	**Craniometric Landmarks involved**
Cranial Breadth (1 measurement)	Euryon Left to Euryon Right
Upper-Facial Breadth (2 measurements)	Frontomalare temporale Left to Right
	Frontotemporale Left to Frontotemporale Right
Mid-Facial Breadth (5 measurements)	Zygomaxillare Left to Zygomaxillare Right
	Zygoorbitale Left to Zygoorbitale Right
	Ectomolare Left to Ectomolare Right
	Inferior Maxillary Border Maximum breadth Left to Right
	Zygion Left to Zygion Right
Nasal Projection (1)	Nasion to Rhinion
Nasal Length (height) (1)	Nasion to Nasospinale
Nasal Breadth (1)	Alare Left to Alare Right
Interorbital breadth (1)	Dacryon Left to Dacryon Right
Outer orbital breadth (1)	Ectoconchion Left to Ectoconchion Right

A summary of the results from the admixture MANTEL tests is provided in Table 9.8 below. Overall, the admixture Mantel tests show there is a statistically significant positive correlation between increased admixture and advancing time in this population.

There is a statistically significant positive correlation between admixture and time period from the pre-Silk Road time frame (Bronze Age to 350AD, PRE) to the early-mid Silk Road time frame (200BC to the 15th Century AD, DURING 1) (Table 9.8). The correlation is positive meaning that as time progresses from the Bronze Age to the early 15th Century there is an increase in admixture seen in this Central Asian population. There is also a statistically significant positive correlation, so an increase in admixture from the Bronze Age/pre-Silk time period (PRE) to the 15th to early 17th century time period (DURING 2). This correlation is slightly less strong here than between the PRE to DURING 1 groups, suggesting a slowing down or decrease of admixture, or gene flow, in the later Silk Road years compared to the earlier years.

This slight decline in gene flow is further emphasized by looking at the early to mid SR years (DURING 1) compared to the later SR years (DURING 2) (Table 9.8): while there is a statistically significant positive correlation between time and admixture here too, it is weaker than in the earlier years (i.e., PRE to DURING 1).

The strongest statistically significant positive correlation between increased admixture and time progression is between the early-mid SR period (DURING 1) and the post SR period (POST 1) (Table 9.8). However, in this MANTEL test, many individuals were omitted due to missing crucial landmarks and thus the strength of this result is tempered by the smaller sample size (>21% smaller than the original sample size of 64). The POST grouping was not divided into two (POST 1 and POST 2) because of time period, but due to MANTEL test constraints which require that the number of rows are equal in both matrices or groupings, thus it is important to consider the POST group as one entity. Since both POST groups are from the same time-frame and regional population (and are of equal sample size) it is best to average the results of the two tests obtained in the PRE vs POST1 and PRE vs POST2 to gain a more accurate picture of the change in admixture over time between the PRE Silk Road and after the closing of the Silk Road. The averaged results yield a correlation which is positive and statistically significant, though the increase in admixture frequency is less pronounced than in the PRE to early period of the Silk Road (Table 9.8). The second strongest increase in admixture is seen between the Silk Road period in its entirety (DURING 1 and 2)and the POST Silk Road period (POST 1 and 2), but as indicated earlier the PRE to early SR period still shows the most change in admixture levels (Table 9.8).

Table 9.8: Mantel admixture over time test results, α=0.05 and N=9999 permutations

TEST GROUP	R CORRELATION	P VALUE	INTERPRETATION
PRE vs DURING 1 (No omissions)	R=-0.0246	p= 0.46	NOT statistically significant result
PRE vs DURING 1 (Ecm omitted due to too many individuals with zero values for Ecm in DURING 1 group and PRE group, missing landmarks)	**R=0.226**	**p=0.049**	**Positive Correlation and Statistically significant**
PRE vs DURING 2 (No omissions)	R= -0.043	p= 0.49	Not statistically significant
PRE vs DURING2 (3individuals from PRE group with zero Ecm values were omitted, 2 from DURING2 with zero Ecm values and one with zero zygion value)	**R= 0.181**	**p= 0.033**	**Positive Correlation and Statistically significant**
PRE vs POST 1 (No omissions)	R= -0.04851	p= 0.55	Not statistically significant
PRE vs POST 1 (Ecm omitted due to too many zero values in PRE group for Ecm breadth)	**R=0.1358**	**p=0.014**	**Positive correlation and statistically significant**
PRE vs POST 2 (No omissions)	**R= 0.2414**	**p= 0.04**	**Positive correlation and statistically significant**
AVERAGE OF PRE vs POST1 and POST 2	**R= 0.1886**	**p=0.027**	**Positive correlation and statistically significant**
DURING 1 vs DURING 2 (No omissions)	R=0.2098	p= 0.11	Not statistically significant
DURING1 vs DURING 2 (omitted 3 individuals from each group with zero values for zygion or ectoconchion)	R= -0.0026	P= 0.47	Not statistically significant
DURING1 vs DURING 2 (3 individuals each as above plus Ecm omitted as numerous DURING1 individuals still have zero values for Ecm)	**R=0.1548**	**p= 0.048**	**Positive correlation and statistically significant**

DURING SR vs POST SR (DURING 1 and DURING 2 vs POST 1 and POST 2, 128 individuals total) No omissions	R=-0.0358	p= 0.58	Not statistically significant
DURING vs POST (Omitted 7 individuals from each group with zero values at Ecm, zygion, or other mid-facial landmarks)	**R= 0.2036**	**p=0.0432**	**Positive correlation and statistically significant**
POST 1 vs POST 2	**NOT RELEVANT AS**	**BOTH GROUPS ARE**	**FROM SAME PERIOD**
DURING 1 vs POST 1 (No omissions)	R=-0.015	p= 0.42	Not statistically significant
DURING 1 vs POST 1 (Omitted all individuals with zero value Zyg, Ec, Ecm, InferiorMaxillary, 7 each from each)	**R=0.59**	**p=0.033**	**Positive correlation and statistically significant**
DURING 2 vs POST 1 (No omissions)	R=0.135	p=0.143	Not statistically significant
DURING 2 vs POST 1 (7 zero value omissions)	R=0.02	p=0.35	Not statistically significant
DURING 2 vs POST 2 (No omissions)	R=-0.096	p=0.73	Not statistically significant
DURING 2 vs POST 2 (3 zero value omissions)	R=-0.096	p=0.87	Not statistically significant

CENTRAL ASIAN CHANGES OVER TIME: SECULAR GROWTH OR OTHER FACTORS?

The following analysis looked at whether craniofacial changes observed over time are due to secular changes such as skeletal growth from improved living conditions, health, and nutrition or if admixture is the more likely driver of change in this population. To determine this, Mantel tests were used to look at how measures of craniofacial growth change over the time span of the Silk Road in this population. Results will indicate a strong or weak correlation between the data matrices and thus if any significant changes in cranial growth have occurred in this Central Asian population from before to after the Silk Road.

For the Mantel tests, two matrices are compared at a time, both of which must have the same number of rows, in this case the same number of individuals, in order to proceed. As the PRE SR group was the smallest and consisted of 32 individuals, all MANTEL tests were conducted with 32 individuals per group unless indicated otherwise. Much like the admixture Mantel tests, the Central Asian population was divided into five time period groups of 32 individuals each: PRE SR, DURING 1, DURING 2, POST 1, and POST 2 (see Table 9.6).

Each set of time-differentiated groups underwent a Mantel test to ascertain whether cranial growth changed in Central Asian populations over time. Five variables (Table 9.9 below) were used in this analysis which consisted of linear measurements of cranial breadth, cranial length, cranial height, mid-facial height, and mid-facial breadth as these landmarks have been shown to best represent secular growth in the skull (Jantz and Meadows Jantz, 2000; Wescott and Jantz, 2005: 231; Kouchi and Koizumi, 1992) (also in Figure 4.1). These distances were all found to increase in individuals from Europe and Asia over time thought to be associated with access to better health and nutrition in these populations (Jantz and Meadows Jantz, 2000; Kouichi and Koizumi, 1992). The linear values were calculated from the 3D landmark data used to measure the skulls.

Table 9.9: Craniofacial linear measurements used for secular growth Mantel tests

Linear Measurement	**Craniometric Landmarks involved**
Cranial Breadth	Euryon Left to Euryon Right
Cranial Vault Length	Glabella to Opisthocranion
Cranial Vault Height	Basion to Bregma
Mid-facial breadth	Zygion Left to Zygion Right
Mid-facial height	Nasion to Prosthion

Results from the cranial growth Mantel tests are summarized in Table 9.10 below. Overall, **there is no evidence whatsoever that advancing time is correlated with cranial growth in this population**. The results show near zero correlation in most matrices, some even show a slight negative correlation, but not any of these results pass the threshold of statistical significance set at α=0.05, with the lowest p-value obtained at 0.2 for the Mantel test between During SR (DURING 1 and 2) and Post SR (POST 1 and 2). These results are categorical in that they demonstrate that there is no statistically significant correlation between secular growth in the cranium in this population in the time-period up to 18th Century in Central Asia. This will be discussed further in the following chapter.

Table 9.10: Mantel cranial growth over time test results , α=0.05 and N=9999 permutations

TEST GROUP	**R CORRELATION**	**P VALUE**	**INTERPRETATION**
PRE vs DURING 1 (No omissions)	R=-0.155	p= 0.98	Negative correlation but NOT statistically significant result
PRE vs DURING 1 (4 individuals each omitted due to zero values)	R=0.012	p=0.378	Near zero correlation and NOT statistically significant result
PRE vs DURING 2 (No omissions)	R= -0.075	p= 0.75	Near zero correlation and NOT statistically significant result
PRE vs DURING2 (4 individuals from each group with zero values omitted)	R= 0.0090	p= 0.4	Zero correlation and NOT statistically significant result

PRE vs POST 1 (No omissions) PRE vs POST 1 (Omitted 4 individuals with zero values)	R= -0.081 R=-0.01	p= 0.86 p=0.5	Near zero correlation and NOT statistically significant result Zero correlation and NOT statistically significant result
PRE vs POST 2	R= -0.057	p= 0.67	Zero correlation and NOT statistically significant result
DURING SR vs POST SR (DURING 1 and DURING 2 vs POST 1 and POST 2, 128 individuals total, No omissions)	R=0.0499	p= 0.2	Near zero correlation and NOT statistically significant result
POST 1 vs POST 2	NOT RELEVANT AS	BOTH GROUPS ARE	FROM SAME PERIOD

Chapter 10: Discussion

In this section, the results obtained from the analyses in chapters 8 and 9 will be discussed further. The three initial research questions laid out in the beginning of this study will be revisited in light of the results from the previous chapters. The data will be considered from a morphological perspective and will be put into a broader context with the information obtained from history, genetic studies, linguistics, and archaeological data.

RESEARCH QUESTIONS: OUTCOMES

Research Question 1: Results and Broader Context

Is admixture observed in the craniofacial morphology of individuals along the Silk Road trade routes?

The results of the analyses conducted in Chapter 8 indicate that the craniofacial morphology of the Central Asian skeletal sample fell between those examined from European and East Asian contexts, part of a statistically significant group distinguishable from those to the east or west, within the broader Eurasian human population. In this framework, they are considered admixed.

A total of 172 specimens from Central Asia were analyzed looking for morphological specificities that could be identified craniofacially through 3D morphometrics. Central Asian admixture was identified as a mosaic of traits inherited from East Asians and Europeans; intermediate in size, breadth, or shape between the two groups. The crania, as expected, showed the most difference in: cranial breadth (Eur); nasal breadth (Al), length (Na to Ns) and nasal projection (Na to Rh); orbit size and inter-orbital breadth (Dc and Ec); mid-facial breadth (Zo, Zm, Zy, Imb, Ecm) and upper facial breadth (Ft and Fmt); and cranial length and outline (B, L, Op, O) (Figure 4.1). This makes sense as the main differences reported between European and East Asian crania have been detected in those regions (Abdushelishvili *et al.*, 1968:59-61; Alcade *et al.*, 1998; Ball *et al.*, 2010; Fraser *et al.*, 2003; Le *et al.*, 2002; Scavone *et al.*, 2006). The PCA and MANOVA conducted on Central Asians, Europeans, and East Asians showed a statistically significant difference among all three groups, which validated the observational analysis and previous work on the subject. The first 10 principal components in this analysis represented over 81% of the variation seen across the three populations. These 10 principal components confirmed that the greatest areas of difference across the three groups were primarily in mid-facial zygomatic breadth measures, nasal projection and breadth, and cranial breadth, and to a much lesser extent cranial length and height.

In addition to the traits that were intermediate between European and East Asian populations, admixed individuals often present new traits or shapes that are different from their ancestral groups. For this reason, although special attention was paid to the series of traits listed above, morphology of the entire skull was studied and measured, yielding the 41 landmarks chosen. The Central Asian group as a whole, though many individuals did not fit into this gross characterization, showed the greatest cranial breadth (Eu to Eu distance), the most flaring or broad zygomatic region (Zy to Zy, Zm to Zm, Zo to Zo), and the greatest inter-orbital breadth (Dacryon to Dacryon) of all groups. The combination of nasal length, breadth, and projection also increased in the Central Asian group.

A Mahalanobis distance statistic was used to calculate the degree of differentiation, or distance, between each set of two populations. The results of this analysis confirmed the intermediate position of the Central Asian group between the European and East Asian groups. In this case, the Central Asian grouping was slightly closer to the East Asian group (0.75) than to the European group (0.81), and the Europeans and East Asians were the furthest apart as expected (Table 8.2). While it is possible that this Central Asian collection as a whole is ancestrally closer to East Asians than Europeans, it is also important to consider the regional makeup of the populations used in this analysis. Over a third (36%) of the individuals from the Central Asian sample were from 18th century Kirghizstan, a country whose longest border is shared with China and which accounts for the eastern half of the Silk Road. Furthermore, because this group represents the post-silk road population and thus a more modern sample it is likely that this group may be closer in morphology to the modern-day Chinese in the East Asian sample. This could skew the Central Asian group in this analysis and would yield a slightly closer relationship between East Asians and Central Asians in the Mahalanobis table. In addition, the East Asian sample was made up of a large contingent from Mongolia, a historically and genetically documented contributor to Central Asian ancestry by way of the Mongol invasions in the 12th Century. This would also help explain the relative closeness of the Central Asian with the East Asian groups as compared to the European group. Nevertheless, these potential factors do not alter the outcome of these analyses which show that overall the Central Asian population under study can be considered as a distinct ancestry group, but with some features from European and East Asian groups as they are more recently admixed than either of the other populations.

The entire analysis was repeated using 39 landmarks on a group totaling 454 specimens, omitting all individuals who had crucial landmarks missing. Individuals who were missing landmarks from the nasal, zygomatic, or basio-cranial region (Rh, Na, Ns, Al, Zy, Zm, Ba, or O) were omitted from this analysis to improve the accuracy of the classification of skulls into their correct ethnic group categories. A discriminant function analysis on the larger sample had shown a particularly poor accuracy rate of classifying European individuals into their correct European group (36% accuracy which is on par with chance). This was thought to be due to the large number of individuals particularly in the European population who were missing these deemed "crucial" landmarks that could identify with fair precision which ancestral group they belonged to. The exclusion of the craniometric point Ectomolare (left and right) was deemed necessary because hundreds of specimens were missing this landmark. Rather than eliminate more individuals and further reducing the sample size, ectomolare left and right were removed.

The results of the DFA on 454 individuals showed that from this entire sample, Europeans were the easiest to classify (89%) or the most easily identifiable from the other two categories and Central Asians were the least identifiable (70%). These results further emphasize the admixed quality of Central Asian ancestry (Fig 8.4). More individuals from Central Asia fell into the range of European or East Asian than the reverse. Central Asian individuals who fit more closely within the European or East Asian cranial morphology range than within the Central Asian grouping can be seen in Figure 8.4. This outcome is not surprising given the geographically intermediate position of Central Asia in between Europe and East Asia, and these results further suggest that Central Asians are an admixed population with some individuals closer to or exhibiting European or East Asian craniofacial morphology. These results only emphasize what is already known about Central Asian admixture.

While it is fair to assume that the first period of potential for admixture in Central Asia corresponds with the inception of the Silk Roads, this would be erroneous. It has been suggested that early interactions between individuals from Western and Eastern Eurasia may have preceded the opening of the Silk Roads by up to 2,000 years. Excavations in eastern Central Asia from the Bronze to Iron ages have revealed fabrics and weavings originating from the Near East (Li, 1999). As early as the Iron Age (1st millennium BC), individuals of different ancestry began arriving and settling more frequently in areas where they were not indigenous. The Tarim basin mummies discovered in western China but bearing European/Near Eastern features and fair hair, dated to 2000 BC (at the earliest) are yet another example of individuals from the West migrating eastward well before the Silk Road trade routes had started (Romgard, 2008; Thornton and Schurr, 2004). Furthermore, there is considerable evidence from historical, linguistic, archaeological, and craniometric studies to suggest that Central Asian people were at least somewhat admixed possibly even as early as the Bronze Age, but certainly in the Iron Age, which would corroborate the results from the first research question indicating that the Central Asian population was and remains admixed.

Four thousand years ago, Indo-European speaking people migrated from the Black Sea and southern Ural mountains spreading across Central Asia and merging with individuals and communities already present in the region. A few hundred years later in a first wave of migration, midway between the 2nd and 1st millennium BC, a large flow of Indo-European speakers migrated as far east as China and west to Europe by way of the Near East, many settling along the way and melding with indigenous communities (Beckwith, 2009:30). Craniometric analyses of southern Uzbek populations from the Bronze Age suggest an admixed craniofacial morphology indicative of Mediterranean origin (high and projecting nasal region) combined with other traits from an unidentified population (Avanesova *et al*, 2010). Other craniometric analyses suggested that Indo-Iranian individuals might have moved from Europe and migrated to Eastern Central Asia during the Bronze Age, but in the Iron Age they returned to Europe and gave rise to the Scythians around 700 BC (Kozintsev, 2008). They established one of the earliest and most expansive overland networks trading wheat and corn between Greece in the West, Persia in the

South, and the Xiongnu further East (Rolle, 1989:110). In the first millennium BC, a second wave of Indo-Europeans, early pastoral nomads of Scythian stock, emigrated eastward. At this junction in time, mostly North Iranian peoples (Scythian origin) inhabited the regions west of the Altay while the Eastern region was inhabited by communities with characteristically East Asian features speaking different languages (Di Cosmo, 2002: 163-166). Craniometric studies on the Saka (Indo-Europeans) dating from the late Bronze to the early Iron Age (7th-2nd BC) confirmed this: little admixture was found in Saka crania from Northwestern Central Asia - they were primarily of Mediterranean or Near Eastern origin- but Saka from the East presented significant admixture with East Asian populations (Khodzhayov, 2008). Cranial analysis of the peoples buried at Tuva (NW Mongolia) matches archaeological information obtained from analyses of funerary constructions and associated artifacts. Before the 6th Century BC, the people of Tuva were culturally and morphologically closer to the East Asian craniofacial morphological range (though still admixed) but around the 2nd Century BC the expansion of the Scythian population eastward brought with it the spread of Indo-European cultures and peoples. The local populations as a result became more admixed with gene flow coming from the West (Chikisheva, 2008). Central Asia in the 2nd and 3rd century BC was controlled by the Scythians in the western and southern regions (Hambly, 1966: 19; Phillips, 1965:54-55).

As there was already a degree of admixture as early as the Bronze and Iron Ages in populations from south-central and northeastern Central Asia (Abdushelishvili *et al.*, 1968; Avanesova *et al.*, 2010; Chikisheva, 2008; Chikisheva *et al.*, 2009; Gokhman and Gromov, 2009; Han, 1994; Keith, 1929; Khodzhayov, 2008) it follows that the Central Asian sample under study here, ranging from Bronze Age western Central Asia to 18th-19th Century eastern Central Asia would also exhibit and retain some level of admixture.

Research Question 2: Results and Broader Context

Is there an increase in craniofacial admixture over time in Central Asian populations?

The results obtained in Chapter 9 suggest that admixture significantly and steadily increased over the time period of the Silk Road in Central Asia.

For this part of the study, the Central Asian collection was analyzed more thoroughly looking for regional and time-driven changes in craniofacial morphology. This population was divided into three broad time-periods (before the SR trade or PRE, during the SR trade or DURING, and after the closing of the trade routes or POST) in order to track the potential effects of the Silk Road trade on craniofacial admixture in the region. A PCA was conducted to assess whether significant morphological differences between the time-differentiated groups existed and if so, where in the skull these differences were most salient.

Over time, this Central Asian population's craniofacial morphology changed subtly: the zygomatic area increased in breadth and height as did the nasal aperture; and cranial breadth increased steadily as did interorbital breadth. A MANOVA using the first ten PC scores showed that these and other changes were significant between the PRE and SR group and between the PRE and POST group. The Mahalanobis squared distance statistic showed that the POST and PRE groups were the furthest apart, followed by the SR and PRE groups. A statistically significant difference between the SR and POST groups was only attained during a follow-up MANOVA using the first 20 PCs which accounted for over 98% of the total variance. The SR group covers the longest time-frame, and most of its sample is weighted towards the tail-end of the Silk Road trade routes (60% from 1400s to 1600s AD, compared to 40% from 200BC to 1100 AD). It would follow then, that the SR group would be closer in morphology to the POST group than it might have been had the sample been more evenly distributed over time. A DFA of the three groups showed much the same result with the POST group most frequently misclassified as belonging to the SR group, but 80% of the SR group was assigned the correct grouping. By using more PCs in the statistical analysis we were able to tease out the smaller differences between the SR and POST groups at a statistically significant level.

The SR group being the largest and most diverse of the three time-differentiated groups with crania from Turkmenistan, Uzbekistan, and Karakalpakia it was important to determine if the changes seen across the group were due to ancestral/geographic differences in craniofacial morphology or if the changes were in fact correlated with time. In comparing the Central Asian group as a whole to East Asian and European groups, a Central Asian craniofacial morphology range emerged, but would this range remain the same when looking at differences among ethnic groups within Central Asia? A PCA and MANOVA were conducted on the SR group which was divided into three groups based on language and location of origin: Turkmenistan, Karakalpakia, and Uzbekistan. No statistically significant difference was found among the crania in these three groups; therefore there is no evidence that local geographic or linguistic affiliation within this Central Asian group during the time of the Silk Road affected craniofacial morphology significantly. These three groups are craniofacially homogenous with regard to morphology. It seems that something else was driving the changes seen over time.

In order to determine the percentage of non-admixed individuals in the Central Asian sample across time, three separate discriminant function analyses were conducted comparing the PRE, DURING, and POST groups to the European and East Asian samples. Individuals whose cranial morphology fell out of the Central Asian range and into the European or East Asian ranges were considered non-admixed. In the PRE group, 69% of the crania fell within the European morphology range, and none within the East Asia morphology range. Only 30.4% of the group was classified as admixed. This result aligns with what we expect of pre Silk Road Central Asian populations dating from the Bronze Age to 200BC: they have a lower level of admixture than subsequent populations.

The PRE SR sample in this study primarily from the Bronze and Iron Ages (but up to Sassanian 350AD) from Tepe Hissar in modern-day northeastern Iran near the Turkmenistan border, in southwestern Central Asia overlaps with the Scythian time period (700 BC onwards) and geographic range. This region was inhabited during some of this period by Scythian populations of Mediterranean or Near-Eastern origin as evidenced by Scythian jewelry found at Tepe Hissar itself (Korbendau *et al.,* 2002:15). As far east as the Kazakh Altay, craniometric analyses on Bronze to early Iron Age populations show that admixture between Western Eurasian and Eastern populations was present from before and throughout the Scythian period, but equally, many Western Eurasians were not admixed at all (Chikisheva, 2008). The Bronze Age sample showed an influx of Western Eurasian traits. Bronze and Iron Age burials across Central Asia reveal an early spread of culture, technology, and art from west to east related to the movements of the early Scythians (as well as the Andronovo culture and the Bactrians) further confirmed by the contemporaneous spread of Indo-European languages in the same direction and genetic studies demonstrating that gene flow moves west to east in the Bronze Age. The presence of a Scythian population at Tepe Hissar would explain why 69% of the PRE cranial sample fell within the European morphological range (non-admixed).

Interestingly, the PRE group did not have any individuals who fell within the East Asian morphological range. This seems to agree with the historical narrative of a mostly European population with some admixture and no East Asian influence west of the Altay: genetic studies have shown that prior to the Bronze Age all individuals belonged to European or Western Eurasian lineages. This also corresponds with historical accounts of Indo-Europeans populating Central Asia early on and evidence of the early Indo-European languages being spoken in the region. However, from about the 6th-5th Centuries BC or the Iron Age, East Eurasian genetic sequences begin to appear in Central Asian populations alongside the Western Eurasian haplotypes (Lalueza-Fox *et al*., 2004). The timing of this eastern influx corresponds with the emergence of the Xiongnu in the region. Another genetic study showed an increase in Northeast Asian and East Asian contribution to European genomes presumably tied to the sweeping conquests of the Xiongnu reaching the eastern borders of Western Europe in the period 1000-400 BC (Hellenthal *et al*., 2014). It is therefore surprising that none of the specimens were categorized as East Asian in the PRE SR group. However, if these specimens are from the earlier period of Tepe Hissar, during the late Bronze/early Iron Age, then there is no reason to expect any significant influx of Eastern individuals migrating westward.

In the DURING SR group, only 22% were categorized as non-admixed. Of those, over 14.7% fell within the European craniofacial range, and 7.3% were classified as East Asian. From the time preceding the Silk Road to the 1600s, admixture as represented in the skull increased by about 48% in this Central Asian population. This leads to a Central Asian population that is 78% or more admixed on average over the entire span of the Silk Road. If you break up the Silk Road by time frame, you begin to see a more precise picture of the evolution of admixture in the region: 74% are admixed in the early to mid-SR period and 81% are admixed in the late SR period. From the early to the mid-late Silk Road period, the percentage of European non-admixed individuals decreased by 14.5% and the percentage of non-admixed East Asians increased by 8%. Similarly, in the POST group, which consisted of individuals who lived after the closing of the trade routes (18th and 19th Centuries) only 11.5% were classified as European or East Asian (non-admixed group). Between the 1600s (late SR) and the 1800 (POST SR) the proportion of admixed individuals increased (7%) in this region, but this is more likely due to group composition differences between the geographically more eastern POST group (95% Kirghizstan, 5% Turkmenistan) and the more western and central late SR group (68% Turkmenistan and 32% Karakalpakia).

In a series of MANTEL tests, conducted to assess craniofacial admixture changes over time in the Central Asian population, the specimens from three time-periods were analyzed looking for changes in the nasal aperture, the mid-face breadth, zygomatic, and orbital regions as well as in cranial breadth. The SR group was subdivided into an early to mid-Silk Road group (DURING 1) and a mid to late-SR group (DURING2) in order to more precisely assess the admixture changes over smaller increments of time. Thirteen linear measurements were selected, representing the traits most strongly associated with regional and temporal differences (see table 9.7).

The results showed an increase in admixture over time at a statistically significant level throughout the collection. The strongest positive correlation between admixture and time was seen from the Bronze Age/Iron Age or PRE SR period to the early-mid Silk Road period (200BC to 1500 AD, DURING 1). This corresponds with the results from the DFAs which show a 44% increase in admixture over an average of 1500 years. These results answer the second research question by indicating that admixture in this Silk Road population increases over time. The Silk Road contemporaneous populations (DURING 1 and 2) were expected to mostly fall firmly between the ranges of the European and East Asian groups, which they do in the discriminant function analyses with 74-81% falling in the Central Asian category (admixed group). The third largest increase in admixture over time was observed between the PRE SR group and the POST groups, so between the Bronze/Iron Ages to the 18th-19th Centuries (the results from PRE to POST 1 and PRE to POST 2 were averaged since the POST SR group was not divided by time-frame due to sample size constraints for the Mantel Test). This result was nearly identical to the increase in admixture seen between the PRE group and the mid-late SR group (R=0.188 for PRE vs POST and R=0.181 PRE to DURING 2, with both p values around 0.03). And the results from these Mantel tests match the DFA results which indicated over 58% increase in admixture from PRE to POST SR groups and a 51% increase in admixture from PRE SR to late SR groups (DURING 2). Therefore, we can say that the most prominent increase in admixture occurs from the PRE SR period to any period thereafter.

The transition from the PRE SR period to the early Silk Road period is poorly documented and fragmentary at best. However, through the paucity of data and complexity of rapidly changing territories, peoples, and empires, a few strong threads of evidence point to what might have happened to local populations and why they might have seen such a large increase in admixture over this time-frame. Genetic studies of Iron Age populations show that gene flow during the later period ran primarily from East Asia to Central Asia due to the Xiongnu expanding their territory westward (Mezzavilla *et al.,* 2014). This would have added a significant measure of admixture into the more western very early Silk Road population. We then jump ahead to the middle of the 6th century AD when the Turks, an admixed group (purported Scythian and Siberian/Altaic, but at the very least European and East Asian) originating from the Eastern Steppe (Millward, 2007:42), defeated the Avars chasing them to the Aral Sea (Sinor, 1997:146). They ruled over most of modern Central Asia and large parts of east and northeast Asia for a few centuries (Millward, 2007:31), significantly contributing to the local population's genetic makeup and morphology. Genetic studies indicate that from 300 AD onwards corresponding to the early SR period in the collection under study, it is the rise of the Turks that explains the common origin of Central Asian people and languages (Comas *et al.,* 1998) and thus establishes a level of admixture in the population higher than it had been in the Bronze or early Iron Ages. The Arab expansion eastward (to Turkmenistan, Afghanistan, and Uzbekistan) and conquest of Merv, the largest city of Central Asia, facilitated trading opportunities which enabled them to settle into the region assimilating with the local populations (Beckwith, 2009: 123, 132) and undoubtedly affecting admixture in the population from Turkmenistan in particular by increasing Near Eastern contribution. But this shifted once again when in the 9th Century the region was ruled by individuals and invaders of Central Asian and Turkic stock, both by now strongly admixed populations.

The second greatest increase in admixture was between the entire population from the Silk Road period (200BC to 1600s) and the POST SR period (18th and 19th Centuries). Though over 10% of the individuals in this sample were omitted due to missing landmarks (14 out of 128 in total) this result is still valid as the sample size from each period still far exceeded that of the other Mantel tests. Because there are significant differences in admixture levels in the DURING SR population itself and it has been split into two subgroups based on time-frame, this test result only indicates that there is a steady increase in admixture over the time-span of the Silk Road and thereafter. Therefore the admixture increase continues from the opening of the Silk Road to after the closing of the Silk Road. More specific information is needed to develop a fuller picture of the shifts in admixture over the centuries that span the Silk Road itself.

A smaller increase in admixture was observed over time between the early-mid SR group (DURING1) and the mid-late SR group (DURING 2), which corroborates with the DFA results showing a 7% increase in admixture in the early-mid SR versus the late SR group. The most rapid increase in admixture occurs between the early-mid SR to the late SR (DURING1 versus DURING 2) over a span of about 200 years thought to correlate with the Mongol invasions from the East. Data from genetic studies point to gene flow from east to west due to the Mongol expansion into Central Asia in the 13th and 14th centuries affecting populations from the East (Uighurs) to the western reaches of Afghanistan (Hazara) and Eastern Turkey, an area that overlaps with the collection studied here. The results of these Mantel tests cannot prove that the observed increase in admixture is caused by an influx of East Asian individuals, but based on previous genetic and craniometric evidence of western Central Asian populations being primarily of European or Near-Eastern origin in the Bronze Age and thereafter, one can postulate that an increase in admixture could be due to an influx from already admixed populations such as the Turks (who invaded the region much earlier) or from a population that is of different descent (admixed or non-admixed). The DFAs showed that admixture increased from the early-mid SR to the mid-late SR: while the percentage of individuals classified as European fell by over 14% during this time period, the percentage of individuals classified as East Asian rose by 8% during this time span. Correlating the results from the MANTEL tests and the DFAs to historical, archaeological, linguistic, and genetic data forms a holistic picture of what likely happened in the region under study. Genetic studies have shown that as a whole, populations along the Silk Road have about the same amount of European ancestry but the migration patterns in the region are complex: there is very little gene flow in the western region but the Eastern gene flow only moved in one direction over time, westward (Mezzavilla *et al.,* 2014). Geneticists have also identified a high frequency male lineage in populations across the region which is attributable to the rapid Mongol expansion through Central Asia (Zerjal *et al*., 2003). Furthermore, Eastern

Central Asian tribes exhibit Y-chromosome diversity that is strongly influenced by the Mongol expansion from the 13th to the 15th Century (Dulick *et al.,* 2011). Based on what we know from history, these early SR populations from Uzbekistan and Turkmenistan in the 12th to the 13th centuries succumbed to unrelenting Mongol attacks ceding all of western and southern Central Asia (Beckwith, 2009:188). They would subsequently be governed by a series of Mongol Khans, descendants of Genghis until the 15th Century when Tamerlane, of Turkic-Mongol origin defeated the Mongols in Central Asia, Iran, and the Caucasus (Chaliand, 2014: 151). It is therefore likely that the admixture increase seen between the early to mid SR period and the late SR period here is due to the Mongol invasion of the region, a migration vector moving east to west, and thus that the increase in admixture is due to an influx of Eastern or Eastern-admixed traits into the population.

These results overall indicate alternating periods of increasing admixture, likely due to foreign groups flowing into the region through the Silk Roads and intermingling with the local populations, periods of slowed admixture where the increase is not as marked; and finally, a stasis, where neither significant increases nor decreases in admixture are observable after the closing of the roads. Interestingly, the admixture levels never really decrease in this cranial collection. As observed in the analyses, in this region once a population undergoes admixture it tends to continue on an upward trend, albeit at a reduced pace, but the population does not seem to revert to a significantly lesser or non-admixed state. One exception that does not agree with the findings here is the case of Eastern Anatolia where craniodental analyses showed an increased frequency of East Asian traits from the Bronze Age (45%) to the early Ottoman period (87%) but in the 20th Century the frequency decreased to 40% (Eroglu and Erdan, 2008). Large migrations along the Silk routes during the Mongol conquests caused an uptick in East Asian contribution which then receded in modern times with the Turkicization of the country under Ataturk (Eroglu and Erdan, 2008). There was a closing in of the country's physical borders and a push of nationalism that led to fewer populations migrating in and out of Turkey. This situation is unique and not the pattern observed for Central Asians in the later years of this sample: the already admixed populations in the region continued to intermingle thus perpetuating the levels of admixture and further reinforcing the Central Asian admixed craniofacial morphology. Significant migrations from Europe and East Asia decreased during this time, thus when comparing the admixture levels of the late SR to POST SR populations they remain about the same.

According to the data obtained in this study and from a thorough review of historical accounts, linguistic, genetic and archaeological data, we can say that the most successful invaders of Central Asia whose impact lingered for centuries were the Scythians in the Bronze to Iron Ages, the Xiongnu in the Iron Age, the Turks in the 3rd to 6th centuries AD, and the Mongols in the 13th and 14th centuries AD. These large groups of individuals migrated along the same routes for centuries creating significant movements across the land that imprinted on the genotype and contributed to the changing craniofacial morphology of Central Asian peoples. A large scale genetic study of mtDNA sequences from across Central Asia confirmed that these populations had all undergone admixture over long periods of time and in great amounts from European and East Asian invaders, the most significant of which correlated with the creation and maintenance of the Silk Road (Comas *et al*., 1998). It was not until the 18th century, however, that these occupying forces' lasting legacy ceased to play as important of a role in the makeup of Central Asian ancestry.

Research Question 3: Results and Broader Context

If craniofacial changes increase over time can these changes be attributed to the Silk Road trade?

The results derived from Chapter 9 indicate it was likely that the changes observed craniofacially in Central Asians were due to admixture increasing between Eastern and Western Eurasian populations in Central Asia as a result of Silk Road migrations over sixteen centuries and not due to secular changes, or other factors.

Craniofacial admixture in this Central Asian population was observed and showed an increase over time, likely due to large migrations from the East and the West facilitated by the Silk Road. However, changes in craniofacial morphology over large periods of time have also been attributed to other evolutionary processes. While genetic drift cannot be entirely ruled out as a factor for the craniofacial changes observed in the Central Asian group, its influence may be reduced when populations under study satisfy a few requirements: the ancestral populations must be large in effective size as well as morphologically and genetically divergent, and the offspring and ancestral populations must be exposed to the same levels of mechanical stress (Martinez-Abadias *et al.,* 2006). In this study, the European and East Asian groups are proxies for the ancestral populations, both of which were large in effective size (Scythian and Xiongnu armies, and large Mongol hordes for example) as well as divergent from each other both genetically (Fu *et al*., 2013; Tateno *et al.,* 2014, estimate a 41k year or earlier divergence between European and East Asian individuals) and morphologically (the results from this study; Schmidt *et al.,* 2011; Seguchi *et al.*, 2010; Xing *et al.,* 2013). It is known that the shift from hunter-gatherer to agriculturalist affected the masticatory apparatus, decreasing mechanical stress, and thus contributing to morphological changes in the mandible specifically (von Cramon-Taubadel, 2011a; Ventresca Miller *et al*., 2014a and 2014b). During the Middle to Late Bronze Age transition, archaeological site analyses from northern Kazakhstan showed a shift in patterns of settlements from agro-pastoralists to mobile pastoralists but this did not correlate with a change in dietary practices as these early Eurasians continued to consume high quantities of dairy and meat (Ventresca Miller *et al.,* 2014a; Ventresca Miller *et al.*, 2014b). Since the earliest population in the current study was from the late Bronze Age, no significant changes in mandibular or maxillary morphology would have occurred in this group, and, therefore, the same level of mechanical stress would be expected across this population.

Smaller populations tend to experience higher genetic drift than large size populations. This evolutionary mechanism is thought to have played a crucial role in the settlement of Eurasia up to 40,000 years ago (Comas *et al.,* 2004), but from the Neolithic onward, its relative importance in explaining resulting human variation in the region decreased (Thomas *et al.,* 2013; Zerjal *et al.,* 2002). As populations grew and expanded, it was migration across and through Central Asia which seems to have played a more important role (Thomas *et al.,* 2013). Genetic studies show that current Central Asian haplotype diversity resulted from the admixture of Eastern and Western Eurasian populations, and that Central Asia represents a "contact zone between two already differentiated groups of peoples" (Comas *et al.,* 2004: 8). In another study, the effects of genetic drift on Central Asian populations (Uighur, Kazakh, Altai, Kirghiz, Turkmen, and Uzbek) were investigated and determined to have been minimal in these populations since at least the 10th Century but probably much earlier (Berkman and Togan, 2009). An exception, are high-altitude populations from Kirghizstan (above 3000m) where low haplotype diversity characteristic of this region is attributed to male-driven founder effects in the settlement of these elevated villages (Perez-Lezaun, 1999). However, none of the crania studied here were from high altitude regions. A single small tribe in eastern Kazakhstan did not show genetic admixture from the Mongol conquests (Tarlykov *et al.,* 2013), thought to be due geographic isolation, but this is the exception rather than the rule as genetic studies have shown that the male lineage in Central Asian populations was strongly influenced by invading Mongols in the 13thcentury (Dulick *et al.,* 2011; Zerjal *et al.,* 2003).

Colonization, or founder effects, require a population to move to a previously uninhabited area and then decrease or significantly reduce in size (i.e., a bottleneck) so that genetic diversity is low (Fix, 1999). These conditions have little historical or genetic basis in the case of Central Asian populations (Heyer *et al.,* 2010). As discussed in chapter 2, historical evidence suggests that local Central Asian populations integrated with the waves of invaders and pledged their allegiance to the ruler of the moment, becoming part of the fabric of the new hierarchy. Genetic evidence further supports this: local Central Asian populations were not replaced by successive invasions of Eastern nomadic groups, instead, their interactions resulted in admixture (Heyer *et al.,* 2010). As such, colonization cannot be used to explain the morphological changes observed in this population over time.

Climatic adaptation, particularly to cold dry air, is known to affect certain craniofacial features such as the shape of the nasal aperture and facial breadth (Betti *et al.,* 2010), two important features under analysis in this study and which have undergone morphological change over time in this population. However, the correlation between temperature and morphology has only been conclusively demonstrated in arctic populations living in extreme environments (e.g., Inuits), not for any other populations (Harvati and Weaver, 2006; Betti et al., 2010). The populations included in this analysis are not from the arctic region and thus no significant climatic adaptations would be expected here. The crania excavated from the highest altitudes in this collection were from Kirghizstan, near Naryn, an ancient Silk Road caravan stop and town, whose elevation is 2,000m. Typically, high altitude craniofacial adaptions have been observed from 3,000-4,500m or higher (Kumar, 2012).

Secular changes, due to improved access to nutritive foods and better health, have led to observable growth in the skeleton and the cranium in recent times and can, therefore, also significantly alter craniofacial morphology over time. Under improved conditions, craniofacial growth has been demonstrated across these linear measures of the cranium: cranial vault height, cranial length, cranial breadth, mid- facial height, and bizygomatic breadth (Jantz and Meadows Jantz, 2000; Wescott and Jantz, 2005).In order to determine if secular changes affected cranial morphology in this population, each set of chronologically-differentiated populations were analyzed through a series of Mantel tests. Five linear measures were obtained for each individual and calculated from the 3D landmark data collected for this study.

While admixture and secular changes are not mutually exclusive, there was no evidence of any correlation positive or negative at a statistically significant level between secular craniofacial changes and time period in this population. Not one of the 8 Mantel tests conducted here led to results of any statistical significance, meaning that even if the correlation was positive or negative or even zero this outcome could be due to chance as much as due to secular effects. Furthermore, all the correlation values obtained were very close to zero, except for one which was the PRE to DURING 1 time-frame (Bronze Age to early-mid SR) which showed a negative correlation R=-0.15 value but the p value in this case was near 1, a far cry from the minimum statistical threshold set at 0.05. Even when omitting individuals in some of the analyses who had missing landmarks and thus zero values for some of the measurements, not a single test yielded a statistically significant outcome.

While these results may seem surprising at the outset since the time-span covered in this entire sample is over 3,000 years and one would expect significant secular change to have occurred at the least between the Bronze Age and 18th Century, the case of Central Asia is a particular one. Studies on secular change have only shown significant increases in growth in craniofacial traits in individuals who lived from the mid-late 1800s through the 20th Century (Jantz and Meadows Jantz, 2000; Kouchi and Koizumi, 1992) in North American and Japanese populations. In the Japanese study, there was no evidence of secular growth in the cranium for pre-historical and historical populations, as it was only observed in the modern population (Kouchi and Koizumi, 1992). Because the Central Asian collection studied here only extends to 18th century with three individuals from the 19th century, it is unlikely that they would show significant secular allometric growth based on North American, European, and Japanese secular growth time-frames .The later populations (POST 1 and POST2) are primarily from Kirghizstan and despite some urban Kirghiz living under the prosperous Khanate of Khokand (in Eastern Uzbekistan), most Kirghiz remained nomadic until much after the Russian invasions of the region in the late 1800s to early 1900s. As mentioned earlier, studies show no significant shift in subsistence strategies or diet over time for nomadic and pastoralist Central Asian populations (i.e., from the Bronze Age onward) (Ventresca Miller *et al*., 2014a and 2014b). Access to nutrition and better health would likely not have been significantly improved for most Kirghiz as their lifestyle did not change much over the years.

It should be noted that relatively more recent admixture can sometimes obscure or mask the details of ancient evolutionary processes, especially when analyzing DNA from living populations (Hunley and Healy, 2011). But, considering the bulk of the genetic evidence (Comas *et al*., 1998; Dulick *et al*., 2011; Hellenthal *et al.,* 2014; Heyer *et al*., 2010; Lalueza-Fox *et al.*, 2004; Mezzavilla *et al*., 2014; Wells *et al*, 2001; Xu *et al.,* 2008; Yang *et al*., 2008; Zerjal *et al*., 2003) in addition to the results from this and other osteological analyses (Chikisheva, 2008; Eroglu and Erdal, 2008; Han, 1994; Khodzhayov, 2008; Lee and Zhang, 2013, Tan *et al.*, 2013) it seems most likely that gene flow (resulting in admixture), or migration, and not drift, natural selection, or secular changes, was the primary evolutionary force at work in the region during the time period of the Silk Road to explain the morphological variation seen craniofacially in this group.

SEX INFLUENCE ON DATA

While it would have been useful to separate the Central Asian population by sex and conduct the analysis accordingly, the decision to pool the sexes prevailed primarily because of the small regional and temporal population sizes.

Craniometric studies have shown mixed results when attempting to identify differing patterns of admixture in males and females. Chikisheva, in a 2008 craniometric study on Bronze and Iron Age populations from the Altay, found that female crania exhibited an erratic pattern of admixture likely because women were more often involved in contacts between populations through marriage or slave trades. Conversely, among male crania clear influences of Eastern and Western traits at specific time-periods were apparent. Gokhman and Gromov's (2009) analysis of Iron Age Altay crania meanwhile found that the most important measures and indices were roughly the same for males and females in their sample though there were some differences in trait distribution between the sexes.

Genetic studies have shown differential migration rates across the sexes with females migrating outwards more rapidly and in larger numbers due to the social structure of some of the nomadic communities. For example, Central Asian highland and lowland pastoral nomads generally have an exogamous patrilineal social structure where women marry outside of the clan or tribe, which means higher rates of female migrations out of the social unit(Perez-Lezaun *et al.*, 1999). But the genetic differences observed between the sexes due to differential migration rates have only been noted in specific communities such as pastoral nomads, a set of circumstances that does not apply to the entire cranial collection under study here. Some crania are presumed to be pastoral nomads: the Kirghiz and some of the Turkmen sample. In this collection, the sample from Kirghizstan is a more modern population that lived after the closing of the Silk Roads in the 18th to 19th centuries and therefore opportunities to interact with foreign traders and merchants would have been greatly reduced and probably non-existent during their lifetime. This is not to say that the women did not marry outside the clan or tribe as was the tradition, but the vast majority, given the historical context, would have married into other local tribes from Central Asia and not into families from distant lands living out of ambulating caravans or living in large urban centers beyond the country's borders. The majority of the Turkmen in this sample were most likely pastoral nomads, but unlike the Kazakh or Kirghiz, there is an endogamous tradition in Turkmen populations and pressure not to marry outside of the group is strong, similar to what is observed in traditional communities across the Near East (Finke, 2014:131). Pastoral nomads from Karakalpakia, however, follow a more typical exogamous structure (Finke, 2014:131) and they would have been the only sample that might have shown differing results between males and females. The sample was so small however (total of 12 individuals) that it seems unlikely that any significant data could have been obtained. The crania from Uzbekistan were excavated from larger ancient towns or cities (Tashkent, Samarkand, Termez) and the mores and traditions of urban dwellers were substantially different from those of the nomadic communities in the steppes.

Ultimately, while a division of the collection by sex would have been ideal, the size of the temporally-differentiated Central Asian samples under those circumstances would not have been large enough to permit an accurate analysis of the data collected.

Chapter 11: Conclusions

FUTURE RESEARCH

This study offers some insight into the migration patterns of populations across Central Asia using the Silk Road overland routes. This is a region of high geographic, demographic, and linguistic complexity with a dense history of rapidly-changing borders and rulers. Large-scale invasions, occupations, and annexations have affected population movements and impacted admixture strongly in Central Asia. Given all these regional and temporal complexities, it was impossible to design a study that would address the entirety of the smaller population shifts. There is therefore a vast opportunity to further study the morphological changes that admixture engenders in historic Central Asian populations.

To start with, a larger cranial sample from Central Asia is needed, one that covers the breadth of time from the Bronze Age to the 20th Century with enough undamaged skulls from each period, and choosing an equal proportion of males and females. Because genetic studies show that there are admixture differences between males and females, and the small craniometrics studies in the broader region seem to indicate similar results, it would be incredibly useful to determine sex in the crania and analyze patterns of admixture accordingly. Because admixture differences according to sex have only been reported in either extremely ancient crania or in pastoral nomads, a larger study encompassing Central Asian populations past and present as well as nomadic and urban groups would yield interesting results.

Because of the major differences seen between urban and nomadic populations, presumably in part due to their differing traditions, but also due to their differing exposure to invading or migrating foreign populations, an expanded study looking at patterns of admixture in urban versus nomadic populations would be of great interest here. Over its history, Central Asian people have moved to urban areas and settled there, but in times of political unrest they have often reverted back to their nomadic roots. During the height of Silk Road, urban areas rose in importance across Central Asia. In cities like Turfan, Kashgar, Samarkand, Merv, Bukhara, and Khotan, migrants and invaders were welcomed and integrated with local dwellers (Wood, 2002:13). In the mid-late Silk Road period, rulers like Tamerlane poured finances into building Central Asian cities, in this case Samarkand, so they would become the cultural heart of Eurasia and model cities for the world (Beckwith, 2009:202-203). This resulted in the Silk Roads themselves shifting to pass through these new cosmopolitan areas where traders from afar lived. Populations residing in these urban centers would have interacted if not intermingled. The expectation is that urbanites from the height of Silk Road period would exhibit slightly more craniofacial admixture over time than nomadic populations. Nomadic pastoralists dominated western Central Asia for hundreds of years and although they frequently moved, they regularly interacted with the salesmen along the routes and traveled to the cities to sell the women of their tribes to urban slave owners (Feltham, 2009).

Since the most pronounced increase in admixture in this study occurred from the Bronze Age to the early and middle Silk Road period, it would be incredibly interesting to redo this analysis on a larger early SR population. By breaking up this lengthy time frame (over 1500 years) into multiple categories we would be able to tease out the relative influence of the successive waves of invaders and their effects on craniofacial morphology. For example: a cranial collection of 60 or more individuals from around 200 BC or at the opening of the Silk Roads would yield information about the Xiongnu and Scythian invasions; a large cranial sample from 300AD-7th

Century AD could assess the impact of the Turkic invasions; a sample from western Central Asia in the 8-10th centuries could shed some light on the extent of Islamic influence in the region; and of course a much bigger sample from the entire region from the 11th to the 15th centuries could ascertain the exact range and influence of the Mongols.

Generally more studies are needed on PRE SR Central Asian populations in particular. There is a lack of material and information on this region's early human interactions and migration patterns which limits our understanding of the evolutionary forces that have shaped Central Asian craniofacial morphology and early genetics. It would also be useful to enlarge the PRE SR cranial sample further east, drawing from Eastern Central Asian populations, and conversely the POST SR sample needs to expand further west. This would give a more accurate picture of cranial admixture over time in the entire Central Asian region. Of course, access to and availability of cranial collections in this entire region is very challenging.

There was a lack of crania from Tajikistan and Kazakhstan from the SR period in this project. Once again, lack of available or accessible collections from those regions limited the analysis. Tajiks, in particular, are interesting because genetic studies have found them to be the most interbred group with the lowest level of genetic diversity in the region compared to all other groups who had quite high levels of genetic diversity (Mezzavilla *et al*., 2014).Exploring the reasons for this difference in terms of craniofacial morphology would be very useful to understanding why some groups become admixed and others less so.

Finally, a region that was not included in this study due to difficulties in accessing collections but a very interesting peculiar case in Central Asia is the population from Xinjiang or the Tarim basin area. Unlike the other regions of Central Asia, there is already a large amount of genetic, historical, archaeological, and linguistic material and information for Tarim Basin populations. There are also a few craniometric studies on the subject mostly from the pre-SR period, but zeroing in on the Silk Road and post Silk Road periods from Xinjiang would really complete the Eastern picture of migration patterns in Central Asia.

Using skeletal samples in any analysis to draw conclusions about the broader populations they stem from necessarily carries a number of limitations. Skeletal collections are just samples, small slices, sometimes quite biased with regard to age or sex, of what the larger population may be and not always fully indicative of the range of morphology seen in the population at large. It is possible that the skeletal collection chosen is an accurate representation of the larger population of the region, but conversely it could be that the particular specimens selected are all outliers when considering an even larger sample. Conclusions and results based on small skeletal samples meant to explain larger population movements should be tempered with caution.

Furthermore, although most of the crania employed in this analysis have detailed provenance, one cannot be certain that a cranium from Uzbekistan is Uzbek, for example. It is possible that some of the crania excavated from the designated locations are not originally from that area but were migrants who moved to and died in that locality. Strontium isotope analysis from bone or tooth enamel can indicate if an individual moved later in life to a new location, or immigrated, as levels of strontium isotopes vary geographically and are absorbed and stored in the human body (Price et al., 2002), but this information was not available for the crania in this collection.

CONCLUSIONS

While migrations through Central Asia to the Near East, Europe, and East Asia were found to have occurred well before the opening of the Silk Roads, these population movements were usually of small groups of individuals, families and communities, moving to new lands for agricultural opportunities. The Silk Road migrations however consisted of frequent large-scale population movements, rapid invasions by warrior factions, with extensive and intensive trade along the way (Han, 1994; Wood, 2002:27). The Scythians, Xiongnu, Turks, Arabs, Seljuks, Mongolians, Chinese, and Europeans from the Mediterranean and Western Europe all used these routes for trade from the late Iron Age onwards. As such, this study sought to assess the influence of the Silk Road trade routes on Central Asian population composition.

This was achieved through craniofacial morphological analysis of populations along the Silk Road from different time periods: a group from before the opening of the trade routes, a group from the early to mid -Silk Road trade period, from the later Silk Road period, and a group representing Central Asians after the closing of the routes. The aim was to identify and qualify craniofacial morphology in this Central Asian population and to track any pattern of changes in these features over time as it related to the Silk Roads. It was also necessary to rule out any other factors such as secular changes that might have played a part in the craniofacial differences observed in this population over time.

The results showed that not only were the Central Asians an admixed population derived from ancestral Europeans and East Asians, but that this admixture created a suite of craniofacial traits that allowed for Central Asian ancestry to be identified with fair accuracy. Furthermore, the results indicated that craniofacial admixture had indeed significantly increased in Central Asia in the early Silk Road period especially, but had also continued to increase steadily over time.

There was a prominent jump in admixture in the mid to late Silk Road period, with a clear east to west movement of people, likely correlated with the Mongol conquests. Secular growth was found to have played no part in the craniofacial changes identified in this population. It was therefore concluded that admixture was indeed the most likely driver of craniofacial change over time in this Central Asian population. Because the Silk Roads provided the conduit along which invading forces and populations moved, it is their physical presence which led to an increase in admixture in the region over time. The Silk Roads were a lifeline to the people of the region and they profited from it for centuries. Had the Silk Roads not been such an important feature in the economic, political, and socio-cultural life of Central Asia, there might have been no reason for large populations to cross these vast and often difficult to navigate lands.

Not only did this study highlight the importance of the Silk Roads as a catalyst for population change and admixture, but it helped provide a more detailed view of the history of the routes and their essential role in the dynamics of the region. Previous research on Central Asia primarily focused on two disparate time periods: genetic studies on migration routes out of Africa into the Near East and archaeological studies of artifacts excavated along the Silk Road. Because of the expansive time-scale of the project at hand, the information gathered from varied sources and the data obtained from this study offer a slightly more continuous picture of the population history and contributes to the growing research on human migration and settlement in the region.

Few studies have addressed admixture in human populations or characterized how hybridization is represented osteologically as most of the research has come from the field of genetics. While they are incredibly informative on a population scale and from a historical perspective, genetic studies cannot identify the range of craniofacial morphological variation from skeletal remains. By quantifying and describing the variability of craniofacial features exhibited by these admixed individuals, this study helped to expand the body of knowledge currently available on Central Asian populations. This data can also be added to forensic craniometric databases to offer a more diverse pool from which anthropologists can draw when attempting to estimate ancestry of unknown remains. Furthermore, the methodology used to identify admixture in this population and track admixture changes over time can also be applied to other admixed groups. As modern populations are rapidly becoming more intermixed this project contributes a small piece of the puzzle on how to define and identify admixture.

Finally, this study has been designed and the results have been analyzed from a holistic point of view, drawing information and context from across the entire spectrum of anthropology which yields a more complete picture of the Central Asian peoples and their life during the Silk Road trade routes.

APPENDICES

Appendix 1: Collection, provenance, time period, and sample size.

Collection	Geographic Region	Provenance	Time Period	Sample size
AMNH	East Asia	North Borneo Chinese	Unknown Modern	17
AMNH	East Asia	San Francisco Chinese	1800-1906	6
AMNH	East Asia	Canton in Singapore	Unknown Modern	2
AMNH	East Asia	Canton in Malay	Unknown Modern	1
AMNH	East Asia	Canton China	Unknown Modern	4
AMNH	East Asia	Tientsin, China	Unknown Modern	10
AMNH	East Asia	Tungku, China	Unknown Modern	3
Smithsonian	East Asia	Urga, Mongolia	16th-18th Century	191
AMNH	Europe	Prastos, Greece	Unknown	10
AMNH	Europe	Kastanitsa, Greece	Unknown	10
AMNH	Europe	Crete, Greece	Unknown	1
AMNH	Europe	Khania, Crete, Greece	Unknown	2
AMNH	Europe	Candia, Iraklion, Greece	Unknown	7
AMNH	Europe	Chiusi, Italy	Unknown	2
AMNH	Europe	Ostia, Italy	Unknown	1
AMNH	Europe	Syracuse, Sicily, Italy	Unknown	5
AMNH	Europe	Pola, Italy	Unknown	2
Cambridge	Europe	Various, UK	Bronze Age	26
Cambridge	Europe	Various, UK	Iron Age	4
Cambridge	Europe	Dorset, UK	LaterIron-EarlyRoman	16
Cambridge	Europe	Various, UK	Roman	44
Cambridge	Europe	Somerset, UK	Roman-Belgic	1
Cambridge	Europe	Suffolk, UK	Pre-Saxon Germanic	10
Cambridge	Europe	Paris and Various France	Unknown	8
Cambridge	Europe	Oise, France	Ancient Gaul	3
Cambridge	Europe	Basque	Unknown	2
Cambridge	Europe	Thessaly	Ottoman Rule	1
Cambridge	Europe	Italy	Roman	5
Cambridge	Europe	Paestum, Italy	Greco-Roman	1
Cambridge	Europe	Perugia, Italy	Etruscan	1

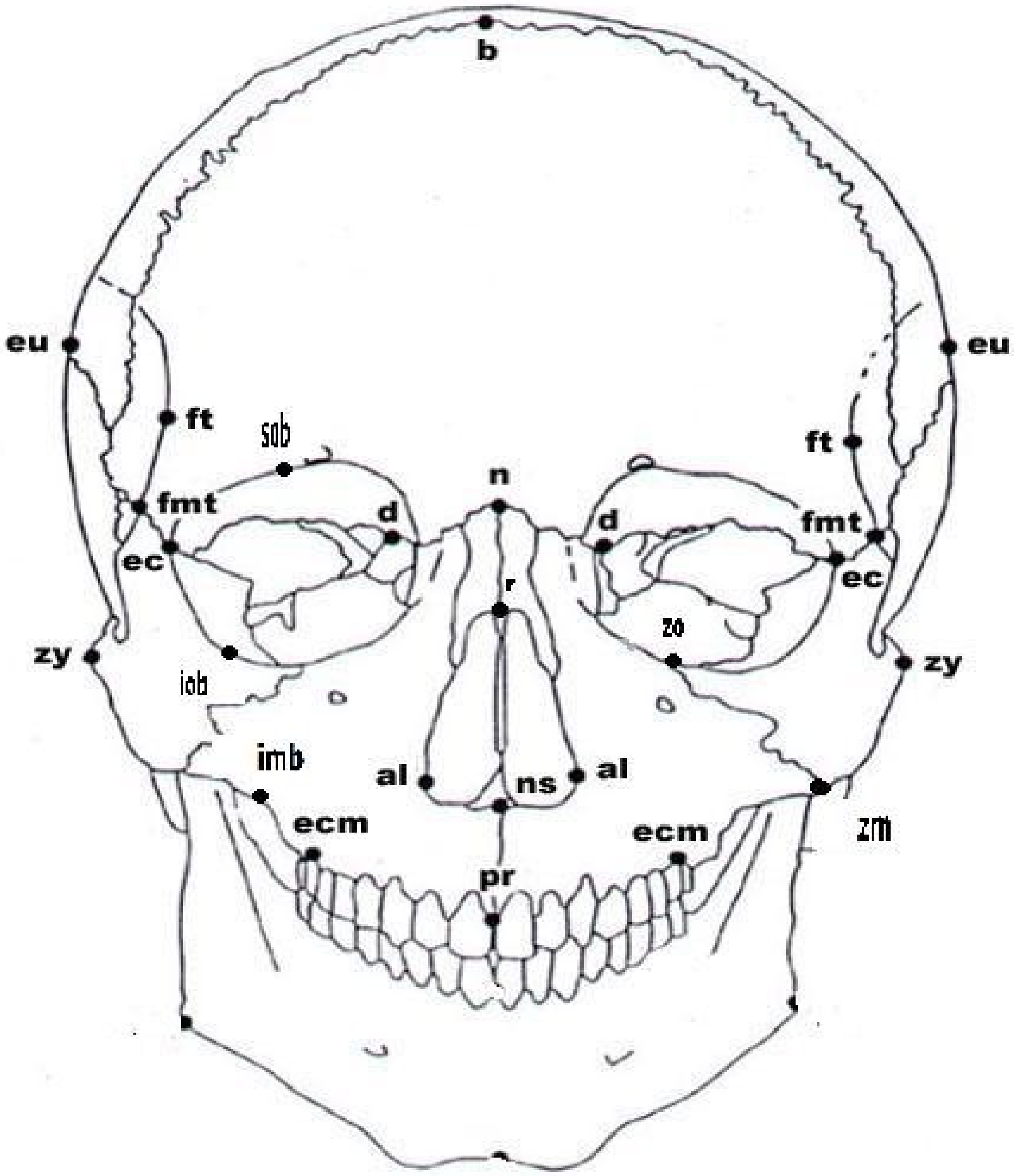
Cambridge	Europe	Sardinia	After 1800	3
Cambridge	Europe	Messina, Sicily	After 1588	1
Cambridge	Europe	Various, Italy	Unknown	2
Cambridge	Europe	GhainTuffieha Malta	700BC-100AD	2
Cambridge	Europe	Bengemma Malta	Phoenician	1
Cambridge	Europe	Tel Hor Malta	Bronze/Iron Age	1
Cambridge	Europe	Menorca, Spain	Unknown	2
Cambridge	Europe	Various, UK	5th-10th Century AD	28
Cambridge	Europe	Various, UK	Early Medieval	6
Cambridge	Europe	Cambridgeshire, UK	Medieval	19
UPENN	Central Asia	Tepe Hissar NE Iran	Bronze Age to Sassanian (3500BC-350AD)	36
MSU	Central Asia	Various, Kyrgyzstan	18th Century	61
MSU	Central Asia	Samarkand, Uzbekistan	Sogdian (200BC-600AD)	14
MSU	Central Asia	Tashkent, Uzbekistan	Uzbek Period before 1600 AD	8
MSU	Central Asia	Termez, Uzbekistan	6th Century BC-12th AD	4
MSU	Central Asia	Kipchak, KhodjaItarab	11-12th Century AD	6
MSU	Central Asia	Parau Turkmen	15th Century	7
MSU	Central Asia	Kukurt Turkmen	16th Century	7
MSU	Central Asia	GyozliAta/Dana Ata	15-17th Century	4
MSU	Central Asia	Koshab Turkmen	16th Century	7
MSU	Central Asia	Ersari-Baba Turkmen	19th Century	3
MSU	Central Asia	Shekhri Islam Turkmen	15th Century	1
MSU	Central Asia	AmuDarya Uzbekistan	Probably 16th Century	12

Appendix 2: Craniofacial landmarks used

Alare*	Al	Euryon *	Eu	Opisthion	O
Alveolon	Alv	Frontomalaretemporale*	Fmt	Opisthocranion	Op
Asterion*	Ast	Frontotemporale*	Ft	Prosthion	Pr
Auriculare*	Au	Glabella	G	Rhinion	Rh
Basion	Ba	Inferior Maxillary Border*	Imb	Superior Orbital Border*	Sob
Bregma	B	Inferior Orbital Border*	Iob	Zygion*	Zy
Dacryon*	D	Lambda	L	Zygomaxillare*	Zm
Ectoconchion*	Ec	Nasion	N	Zygoorbitale*	Zo
Ectomolare*	Ecm	Nasospinale	Ns	* Bilateral Landmark	

Appendix 3: Craniometric points on skull

Frontal View:

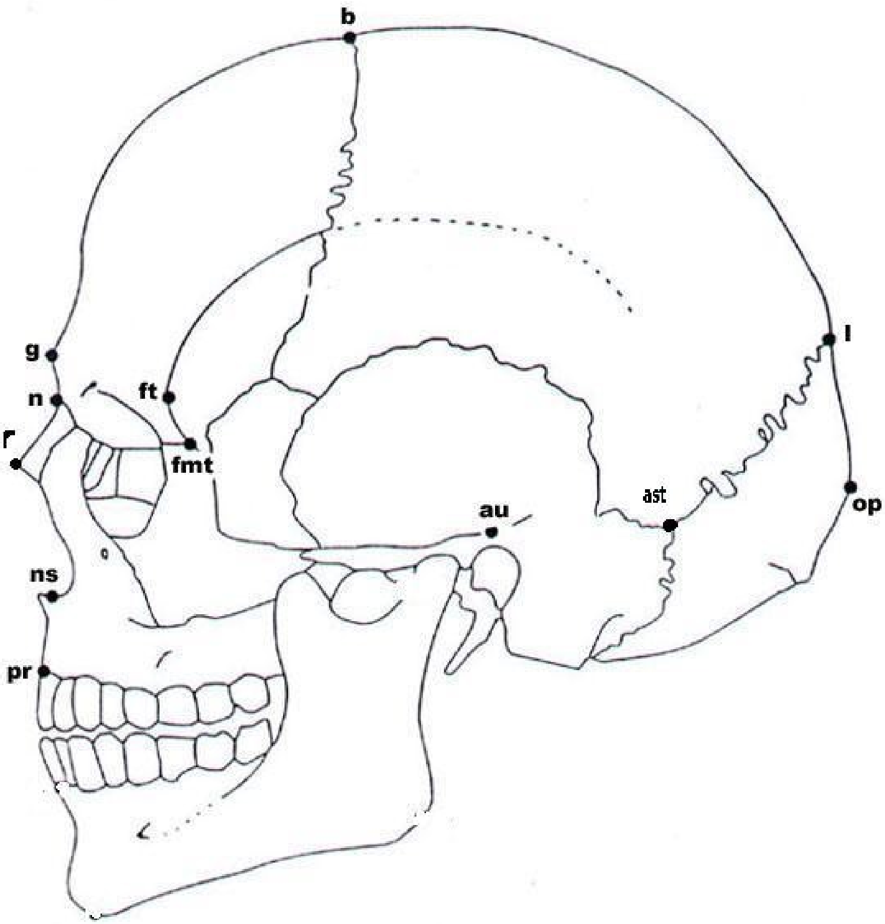


Adapted from Standards by Buikstra and Ubelaker (1994), available from
http://www.cleber.com.br/standard.html

Legend:

b: bregma, eu: euryon, ft: frontotemporale, fmt: frontomalaretemporale, n:nasion, d: Dacryon, ec:Ectoconchion, r:rhinion, zy:zygion, ecm:ectomolare, pr: prosthion, al: alare, ns: nasospinale, iob: inferior orbital border, sob: superior orbital border, imb: inferior maxillary border, zm: zygomaxillare, zo: zygoorbitale.

Lateral View:

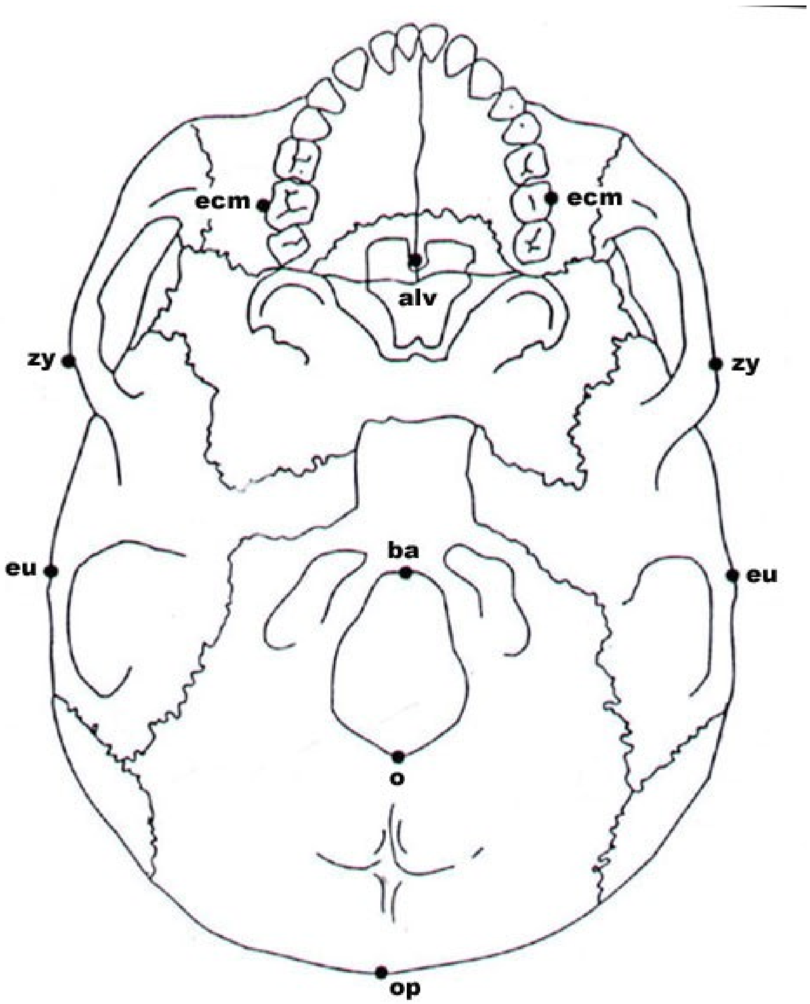


Adapted from Standards by Buikstra and Ubelaker (1994), available from http://www.cleber.com.br/standard.html

Legend:

b: bregma, au: auriculare, ft: frontotemporale, fmt: frontomalaretemporale, n:nasion, r:rhinion, ecm:ectomolare, pr: prosthion, ns: nasospinale, l: lambda, op: opisthocranion, ast: asterion.

Basal View:



Adapted from Standards by Buikstra and Ubelaker (1994), available from http://www.cleber.com.br/standard.html

Legend:

eu: euryon, ecm: ectomolare, alv: alveolon, ba: basion, o: opisthion, op:opisthocranion, zy:zygion.

Appendix 4: Intra-observer error sample calculation

Table A4.1: Intra-observer error calculation, sample of 2 individuals from Cambridge collection

	EU1347					**EU13461**					
Craniometric Pts	X1	X2	Y1	Y2	Z1	X1	X2	Y1	Y2	Z1	Z2
Eur Left	248.812	247.04	-139.1	-138.9	105.33	278.1	277.79	-118	-120.2	134.5	136.6
Eur Right	328.257	316.91	-212.3	-211.9	48.561	281.5	278.74	-235	-229.7	72.29	66.13
Glabella	356.269	353.89	-177.3	-178.2	138.3	357	356.97	-216	-215.9	155.5	155.8
Opisthocranion	263.12	265.85	-114.2	-111.9	19.97	277.4	271.16	-106	-114.3	18.75	18.41
Basion	348.285	348.7	-112.8	-113.7	68.351	364.9	364.73	-151	-151.7	72.78	71.77
Bregma	271.561	272.74	-206.1	-207.5	94.261	250.7	250.61	-193	-194.4	125.2	123.5
Nasion	359.226	359.38	-172	-172.2	137.07	362	362.83	-212	-211.6	151	150.4
Zygomax L	358.524	358.76	-111.1	-111.9	146.25	396.7	396.35	-148	-146.6	145.3	146.4
Zygomax R	406.578	406.05	-159.9	-160.1	91.383	399.1	399.54	-222	-221	90.55	90.94
Zygoorb L	358.832	359.53	-137.6	-138	146.18	382.8	383.49	-175	-175.5	155.2	155.3
Zygoorb R	391.706	391.23	-168.9	-168.2	110.14	384.6	385.35	-222	-221.9	119.1	118.9
Al L	379.653	379.49	-137.2	-138.7	141.54	399.5	400.34	-189	-186.9	144.7	144.1
Al R	392.259	391.54	-151.6	-152.8	126.01	398.7	399.79	-209	-207.8	128.8	128
Prosthion	399.18	400.61	-136.5	-135.5	136.59	418.2	418.31	-197	-195.4	134.1	134.2
EcmL	366.21	367.52	-103.2	-104.3	124.69	0	0	0	0	0	0
Ecm R	397.562	395.53	-136.6	-135.1	87.601	0	0	0	0	0	0
Alv	372.009	372.59	-124.5	-124.1	102.75	388.7	390.16	-171	-169.9	101	102
Aur L	306.651	305.89	-95.55	-96.05	107.49	345	343.49	-106	-104.5	118.4	117.3
Aur R	365.284	365.74	-160.3	-160.1	35.63	345.4	345.11	-200	-199.1	38.74	36.42
Fmt L	323.027	322.83	-139.8	-139.9	150.23	351.7	352.99	-156	-155.9	168.9	170
Fmt R	376.475	374.86	-194.4	-192.2	94.146	354.4	355.73	-240	-239.8	98.48	97
Ns	395.881	395.6	-140.3	-140.4	137.55	412.2	413.12	-200	-198	138.2	137.9
Dacryon L	355.072	354.34	-162.4	-161.1	137.56	365.3	365.3	-197	-196.7	150.1	150.6
Dacryon R	365.998	365.6	-169.5	-170.1	125.87	367.2	367.64	-214	-214.1	135.5	134
Ec L	333.571	333.78	-132.6	-132.2	150.5	364.5	366.15	-156	-155	164.2	163.5
Ec R	385.51	387.36	-182.3	-181.6	96.662	367.6	368.72	-237	-236.3	99.35	99.2
Inf Orbital (max) L	354.308	353.69	-130.8	-129.4	148.57	382.4	381.55	-164	-163.5	159.4	158.8
Inf Orbital (max) R	394.216	394.81	-171.3	-171.1	104.28	384.2	383.71	-232	-231.3	105.3	104.3
Sup Orb (max) L	335.928	335.78	-155.5	-156.1	150.99	355.7	356.09	-178	-176.4	169.7	169.6
Sup Orb(max) R	371.86	374.92	-192.9	-194.4	113.33	358.4	357.97	-241	-237.9	120.3	124.1
Lambda	253.759	254.23	-144.7	-145	23.393	257.6	256.88	-129	-129.1	30.28	31.64
Opisthion	330.832	331.58	-99.43	-100.2	38.392	352.5	352.2	-134	-132.1	44.3	43.56

Inf Maxillary min L	360.515	359.94	-115.3	-114.8	141.49	396.8	396.34	-154	-153.5	142.4	141.3
Inf Maxill min R	399.778	400.71	-155.6	-156.3	96.946	398.9	399.48	-217	-215.8	93.56	94.44
Asterion L	272.847	273.06	-91.63	-92.08	66.561	330.7	329.77	-86.1	-84.96	77.36	77.26
Asterion R	0	0	0	0	0	0	0	0	0	0	0
Rhinion	379.33	378.76	-164	-163.9	146.93	385.5	386.39	-212	-212.4	156.5	156
Ft L	317.895	317.05	-154.7	-155.1	152.79	343	342.72	-164	-164.9	172.3	173.3
Ft R	370.349	370.21	-200.5	-201	101.93	346.5	346.89	-246	-245.7	113	113.2
Zygion L	333.332	334.66	-107.3	-107.3	144.07	370.6	370.19	-131	-131.4	153	153.5
Zyg R	395.819	395.01	-170.7	-171.7	72.879	374.7	376.74	-231	-230.6	69.01	68.95
AVG COLUMN	**343.324**	**343.12**	**-144.7**	**-144.8**	**106.42**	**332.9**	**332.96**	**-170**	**-170**	**109**	**108.7**
% ERROR X,Y,Z	0.00061	0.06%	-4E-04	0.04%	2.1287	4E-05	0.00%	-0	0.25%	0.002	0.19%
% ERROR INDIVIDUAL				**0.13%**					**0.15%**		

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