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Matrilineal and Patrilineal Genetic Continuity of Two Iron Age Individuals from a Pazyryk Culture Burial

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ABSTRACT In this study, geographic and linguistic distributions of contemporary and ancient matches with the paternal and maternal lineages of two individuals exhumed from the exemplary Pazyryk culture burial site of Ak-Alakha-1 mound I were investigated. Using the shared paternal and maternal haplotypes observed in both ancient individuals, extensive database and literature searches were conducted revealing numerous full matches among contemporary Eurasians, majority of whom speak Altaic Languages. Despite the current focus on the two Pazyryk individuals, a rare glimpse into the ancient migrations was gained through the discovery of paternal and maternal haplotype matches across an immense geography that spans from Yakutia to Turkey. In addition to a vast array of archaeological findings in such Scythian “frozen graves” across Central Asia, accumulating archaeogenetic data are expected to shed light on the anthropology of these otherwise mysterious people.

INTRODUCTION

Scythians were nomadic pastoralists who lived between the 9th and 1st centuries BCE. They inhabited a vast geography spanning the Eurasian Steppe, starting from the Vistula River in Eastern Europe, through the Central Asia, and finally reaching the Tarim Basin in Northwest China. Such a spatial and temporal expanse naturally entailed contacts with numerous other civilizations of the time, which is reflected by the different names attributed to the Scythians in ancient records such as the *Skyth(ai)* by the Greeks, *Saka* by the Persians, *Sai* by the Chinese, *Asgus(ai)* by the Assyrians, and *Ishkigulu* by the Urartians (King and Thompson 1907; Herodotus 1920; Luckenbill 1927; Ercilasun 2008; Durmus 2012).

From the linguistic perspective alone, the ethnonyms associated with the Scythians may perhaps have an Old Turkic and/or Mongolic

root to start with. Briefly, the ancient Persian terminology of *Saka* is reminiscent of the Turkic word *yaqa* for ‘coast, shore or edge’, of course, being an Iranized version of the word with a *y-* to *s-* sound change. Intriguingly, the contemporary Turkic population of Yakuts also call themselves *Sakha*, which is seemingly the Yakut equivalent of the general Turkic word *yaqa* [*y-* to *s-* sound change is typical of the Yakut language, and one of the characteristics that differentiate it from the other Turkic languages] (Kiriscioglu 1994; Stachowski and Menz 2006). The ancient Greek terminology, which has found the most widespread use today, parallels the ancient Persian one. According to Herodotus, the *Skythai* and *Saka* were the same people (Herodotus 1920). Curiously, when the Greek plurality marker *-ai* is removed, the remaining part, *Skyt(h)*, seems to retain the Old Turkic and Mongolic plurality marker *-t*. Hence, the Greek version could be a Grecified version of the originally Turkic-Mongolic *Saqat* or *Saqit* (Ercilasun 2008). Incidentally, the Scythian tribe names

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Targutae, *Skolot* and *Paralat* also end with the sound *-t* and hence could be interpreted as *Türküt*, *Sikülüt* and *Barulat*, in turn being the plural forms of the Turkic tribal names *Türk*, *Çiğil* and *Barula* (Zeki Velidi Togan 1981).

The debate around the population continuity associated with the ancient Scythians is still an unsettled one. Minns could not have been more correct in stating more than a century ago that “*Perhaps no question touching the ethnography of the ancient world has been more disputed than that of the affinities of the Scythians*” (Minns 1913; Kristiansen 1998; Damgaard et al. 2018). Indeed, more than a few different ethnic affinities were proposed for the Scythians, such as Iranian, Uralic-Altaic (proto-Turkic) and Slavonic being the most prominent and persistent ones (Denis 1990; Mallory and Adams 1997; Findley 2004; Beckwith 2009; Cynarski 2018). The most convincing proposal for the ethnic origins of the ancient Scythians remains the possibility that “*They were not a specific people*”, but rather one that comprised a variety of ethnicities “*referred to at variety of times in history, and in several places, none of which was their original homeland*” (Kristiansen 1998).

The Scythian cultural heritage is evident from the legacy of an immense array of artifacts left behind, such as those recovered at numerous kurgan burials across the Eurasian Steppe. At least in the archaeological context, the terms Scythian and Scythic are used interchangeably without a specific linguistic or ethnic connotation to imply a broader display of mounted nomadic characteristics associated with the Scytho-Siberian culture, such as the presence of special weapons, horse gear and of course “the animal style” artwork (Davis-Kimball 1995; Di Cosimo 1999). Among these, the most notable is “the animal style”, the development of which was seemingly influenced by two important progressive steps in human civilization: the emergence of metal processing and progress in animal husbandry. In the Scythian period, “the animal style” had become an integral art form used for decorating everyday objects such as horse gears, jewelry, weapons, mirrors, handled wine jugs, cups, vases, batons, calyptas, appliquéés, shields, plaques, saddlery, belts etc. Furthermore, it was also apparently used as symbols on banners (Roux 1997).

While it was originally thought that the Pontic-Caspian Steppe, situated just above the Black Sea, was the heartland for the Scythian culture, a more recent hypothesis suggested Central Asia as a more likely origin (Bashilov and Yablonsky 2000; Yablonsky 2000). The strongest support for a Central Asiatic origin stems from the discovery of the earliest Scythian kurgan in Tuva from Southern Siberia (Grjaznov 1984). Potential Asiatic origins for “the animal style” artistic traditions also provide further support for the Central/East Asian origin of this culture (Bashilov and Yablonsky 2000). Fortunately, special environmental circumstances associated with the Siberian permafrost provided a unique opportunity for the recovery of highly preserved Scythian human remains and associated organic artifacts, as part of “frozen grave” burials that are dated between 6th and 3rd centuries BCE. Scythian burials, such as those associated with the Pazyryk culture, were found at numerous sites across the Altai Mountains, modern-day Kazakhstan and Mongolia. Along with these unique archaeological findings, an increasing amount of anthropological and archaeogenetic data collectively suggest an admixed genetic and cultural character for the Scythians comprising west and east Eurasian influences (Aleksseev 1986; Voevoda et al. 1998; Voevoda et al. 2000; Clisson et al. 2002; Chikisheva 2003; Lalueza-Fox et al. 2004; Ricaut et al. 2004a; Ricaut et al. 2004b; Pilipenko et al. 2010; Pilipenko et al. 2015; Gubina et al. 2016; Juras et al. 2017; Movsesian and Bakhaldina 2017; Damgaard et al. 2018).

Of particular interest to the current study are the archaeogenetic investigations associated with the exemplary mound 1 from the Ak-Alakha-1 site on the Ukok Plateau in the Altai Republic (Polosmak 1994a; Pilipenko et al. 2015). This typical Pazyryk “frozen grave” was dated around 2268±39 years before present (Bln-4977) (Gersdorff and Parzinger 2000). Initial anthropological findings suggested an undisturbed dual inhumation comprising “a middle-aged European-type man” and “a young European-type woman”, both of whom presumably had a high social status among the Pazyryk elite (Polosmak 1994a). In contrast, recent archaeogenetic investigations revealed somewhat contradicting results since analyses at both the amelogenin gene and Y-chromosome short tandem repeat (Y-STR) loci clearly established that both Scythians were actually males and had paternal and maternal

lineages that are typically associated with eastern Eurasians (Pilipenko et al. 2015). Through the use of mitochondrial, autosomal and Y-chromosomal DNA typing systems, it was possible to not only investigate the potential relationships between the two ancient Scythians but also to gather initial phylogenetic and phylogeographic information on their paternal and maternal lineages (Pilipenko et al. 2015). Archaeogenetic data also helped to establish that the two ancient Scythians had (a) the same mitochondrial hypervariable region 1 (HVR1) profile, hence both had a shared/closely related maternal lineage, (b) possibly the same or a closely related paternal lineage, since the two individuals had a full match across 12 loci at which data was available for both individuals, but (c) the absence of a first-degree kinship due to the exclusions at three out of six autosomal STR loci. The shared mitochondrial HVR1 profile, which was subsequently confirmed elsewhere, corresponded to the east Eurasian haplogroup C (C4a1+16129), which is observed frequently in the gene pool of the Pazyryk people from other burial sites, such as at Ak-Alakha-5, Ala-Gail-2 and Berel', as well as that of contemporary Altaians (Derenko et al. 2003; Derenko et al. 2007; Gubina et al. 2013; Pilipenko et al. 2015; Unterlander et al. 2017). Based on the Y-STR data available, the two Ak-Alakha-1 Scythians had an *in silico* haplogroup assignment of N, which first appeared in southeastern Asia and then expanded in southern Siberia (Rootsi et al. 2007; Pilipenko et al. 2015).

Objectives

Current study aims to investigate the geographical distributions of the ancient and contemporary matches and close genetic variants of the maternal and paternal lineages observed in the two Scythians from the exemplary Ak-Alakha-1 kurgan. An effort is also made to present the contemporary matches of both types of haplotypes in a linguistic context.

METHODOLOGY

Potential matrilineal and patrilineal genetic continuity of the Pazyryk culture population was investigated based on already available archaeogenetic data for two individuals exhumed from the Ak-Alakha-1 Pazyryk burial site (Pilipenko

et al. 2015). Y-STR haplotypes matching with or having only a few allelic variations from that observed in the two Scythians from Ak-Alakha-1 were compiled through searches at the Y-Chromosome STR Haplotype Reference Database (YHRD), Y-Search Utility of the Laboratory of Human Population Genetics, Research Centre of Medical Genetics, Moscow, and literature (Willuweit and Roewer 2015; Chukhryaeva et al. 2016). In cases where the Y-chromosomal SNP based haplogroup assignments were not available, the online 21-haplogroup version of the Whit Athey haplogroup assignment algorithm was used instead (Athey 2006). Median-joining network (M-JN) analysis was carried out with a 17-loci (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y-GATA-H4, DYS437, DYS438, and DYS448) Y-STR dataset that was compiled from the literature and using the Network v.5.0.0.0 software as previously described (Bandelt et al. 1999; Gurkan et al. 2017). mtDNA (HVR1, 16024-16365) haplotypes matching with those observed in the two ancient Scythians were compiled through searches at the EMPOP database and literature (Parson and Dur 2007). Close variants of the PZ1 mtDNA HVR1 haplotype with a single missing or additional mutation were also compiled, albeit only from relevant archaeogenetic studies.

RESULTS

Searches for full 17-loci matches with the Ak-Alakha-1 Y-STR haplotype (PZ1) revealed 15 such haplotypes among the contemporary populations across the Eurasian geography that belonged to: (a) 10 Turkic-speaking individuals from Turkey, Afghanistan and Russia (five Turkish, three Turkmen, one Tatar and one Uzbek), (b) three individuals from the Muslim Hui and Dongxiang minorities in China, (c) one Tajik individual from Afghanistan, and (d) one individual of an unspecified ethnic background from Russia (Table 1a). Notably, the only match between the PZ1 Y-STR haplotype and another ancient DNA sample was that from a 15th century CE Yakut individual, although at only 12 loci that was in common (Crubezy et al. 2010). There were also 75 additional near matches in contemporary populations from various Eurasian ethnicities, each having only a few allelic repeat differences from the 17-loci PZ1 Y-STR haplo-

Table 1a: Matches with and/or close variants of the ancient Ak-Alakha-1 (PZ1) 17-loci Y-STR haplotype*

ID	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	Y-GATA-H4	DYS437	DYS438	DYS448	Hg	Population ID [†]
PZ1 ¹	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N ²	PZ1 (1) [Piliipenko et al. 2015]
1	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N ²	DON (1) [YA003978/YA004178 (GAN)]
2	15	13	23	29	16	14	12, 13	13	10	10	24	13	12	14	10	18	N ²	HUI (2) [YA004121 (XIN); YA003841/YA004065/YA004182 (GAN)] TUR
3	15	13	23	29	16	14	12, 13	13	10	10	24	13	12	14	10	18	N ²	[YA004119 (MAR) (2), YA003668 (CUC) (1), YA004115 (BS) (2)]
4	15	13	23	29	16	14	12, 13	13	10	10	23	14	12	14	10	18	N ²	TUR (2) [YA004115 (BS)]
5	15	13	23	29	16	14	12, 13	13	10	11	24	14	12	14	10	18	N ²	TUR (2) [YA004119 (MAR)]
6	15	13	23	29	16	14	12, 13	13	10	11	24	14	12	14	10	18	N ²	TUR (1) [YA004171 (BandH)]
7	15	13	23	29	16	14	12, 13	13	10	11	25	14	12	14	10	18	N ²	TUR (1) [YA003719/YA003907]
8	15	13	23	30	16	14	12, 13	13	10	10	24	14	12	14	10	18	N ²	TUR (1) [YA003719/YA003907]
9	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N ²	DON (2) [YA003978/YA004178 (GAN)]
10	15	13	23	29	15	14	12, 13	13	10	10	24	14	12	14	10	19	N ²	[YA004116 (CA)]
11	15	13	23	29	16	14	12, 13	13	10	10	23	14	12	14	10	19	N ²	DON (2) [YA003978/YA004178 (GAN)]
12	15	13	23	29	15	14	12, 13	13	10	11	23	14	12	14	10	19	N ²	MAN (1) [YA004169]
13	15	13	23	29	16	14	12, 13	13	10	10	22	14	11	14	10	18	N ²	MAN(1) [YA004169] KHL (1)
14	15	13	23	29	17	14	12, 13	13	10	10	24	14	11	14	10	19	N ²	[YA003670] MON (1) [YA003298/
15	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	19	N ²	YA003909/YA004067/YA004136 (JMC)]
16	15	13	23	29	16	14	12, 13	13	10	11	23	14	12	14	10	19	N ²	HAN (1) [YA003440/YA004082]
17	15	13	23	29	17	14	12, 13	13	10	10	22	14	11	14	10	18	N ²	HUI (1) [YA004065/YA004182 (GAN)]
18	15	13	23	29	17	14	12, 13	13	10	10	24	14	11	14	10	19	N ²	KAZ (1) [YA003979]
19	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	19	N ²	KHL (1) [YA003737 (CMO)] MON (2)
20	15	13	23	28	16	14	12, 13	13	10	10	24	14	11	14	10	18	N ²	[YA004127 (ULA)]
21	15	13	23	28	16	14	12, 13	13	10	10	24	14	11	14	10	19	N ²	KHL (1) [YA003737 (CMO)]
22	15	13	23	28	16	14	12, 14	13	10	10	24	14	11	14	10	19	N ²	UIG (1) [YA003847/YA004122]
23	16	13	23	29	16	14	12, 13	13	10	11	24	14	12	14	10	18	N ²	KHL/BUR/DAR (1) [YA003736] KHL/
24	15	13	23	29	17	14	12, 13	13	10	10	24	14	12	14	10	20	N ²	UUL/BUR (1) [YA003735]
																19	N ²	KHL (1) [YA003670]
																19	N ²	MCH (1) [YA003981] MON (2)
																19	N ²	[YA004127 (ULA)]
																19	N ²	MON (1) [YA004127 (ULA)]
																18	N ²	NHA (1) [YA003756]
																18	N ²	RUS (1) [YA004184]
																19	N ²	RUS (3) [YA003678 (SVE)/ YA004184]

Table 1a: Contd....

ID	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	Y-GATA-H4	DYS437	DYS438	DYS448	Hg	Population ID ¹
25	15	13	23	28	16	14	12, 14	13	10	10	24	14	12	14	10	18	N ²	UIG (1) [YA003847/YA004122]
26	15	13	23	29	17	14	12, 13	13	10	11	24	14	12	14	10	19	N ²	YAK (1) [YA004128]
27	15	13	23	30	16	14	13, 13	13	10	10	24	14	12	14	10	19	N1b	YAK (1) (Karmin et al. 2015)
28	13	13	23	29	17	14	12, 13	13	10	10	24	14	12	14	10	19	N ²	CHU (1) [YA003960]
29	15	13	23	31	16	14	12, 13	13	10	10	24	14	12	14	10	18	N1c1	TAT (1) (Chukhryaeva et al. 2016)
30	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N(xN)	TAT (1) (Chukhryaeva et al. 2016)
31	15	13	23	29	16	14	12, 13	13	10	10	25	14	12	14	10	18	N(xN)	TAT (1) (Chukhryaeva et al. 2016)
32	15	13	23	30	17	14	12, 13	13	10	10	24	14	11	14	10	18	N1b	UKR (1) (Chukhryaeva et al. 2016)
33	16	13	24	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N1	NOG (2) (Chukhryaeva et al. 2016)
34	15	13	23	29	16	14	12, 14	13	10	10	26	14	12	14	10	18	N(xN)	TAT (1) (Chukhryaeva et al. 2016)
35	16	13	23	30	16	13	12, 13	13	10	10	24	14	12	14	10	18	N1b	RUS (1) (Chukhryaeva et al. 2016)
36	15	13	23	29	16	14	12, 13	13	11	10	24	14	12	14	10	19	N1b	KHA (1) (Mirabal et al. 2009)
37	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	19	N1b	KHA (9) (Mirabal et al. 2009)
38	15	13	23	30	16	14	12, 13	13	10	10	24	14	12	14	10	19	N1b	KHA (1) (Mirabal et al. 2009)
39	15	13	23	29	16	14	12, 13	13	10	11	24	14	12	14	10	19	N1b	KHA (1) (Mirabal et al. 2009)
40	15	13	23	30	16	14	12, 13	13	10	10	23	14	12	14	10	19	N1b	KHA (1) (Mirabal et al. 2009)
41	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N-P43	TAJ (1), TMN (3) and UZB (1) (Di Cristofaro et al. 2013)
42	15	13	24	29	16	14	12, 13	13	10	10	24	14	13	14	10	18	N-P43	UZB (1) (Di Cristofaro et al. 2013)
43	15	13	23	30	17	14	12, 13	13	10	10	23	14	12	14	10	18	N-P43	TMN (1) (Di Cristofaro et al. 2013)
44	15	13	23	30	16	14	12, 13	13	10	10	24	14	12	14	10	18	N-P43	TAJ (1) (Di Cristofaro et al. 2013)
45	15	13	23	28	16	14	12, 13	13	10	10	23	14	12	14	10	19	N-P43	MON (1) (Di Cristofaro et al. 2013)
46	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	19	N-P43	MON (1) (Di Cristofaro et al. 2013)
47	15	13	23	29	16	14	12, 13	13	10	10	23	14	12	14	10	19	N-P43	MON (1) (Di Cristofaro et al. 2013)
48	15	13	24	30	16	14	12, 13	13	10	10	25	14	12	14	10	18	N-P43	MON (1) (Di Cristofaro et al. 2013)
49	15	14	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N-P43	MON (1) (Di Cristofaro et al. 2013)
50	15	13	23	29	17	14	12, 13	13	10	10	24	14	12	14	10	19	N1b*	CHL (1) (Dulik et al. 2012)
51	15	13	23	29	17	14	12, 13	13	10	10	24	14	12	14	10	19	N1b*	CHL (2) (Dulik et al. 2012)
52	15	13	23	29	17	14	12, 13	13	10	10	24	14	13	14	10	19	N1b*	CHL (1) (Dulik et al. 2012)
53	15	13	23	29	16	14	12, 13	13	10	10	24	14	12	14	10	18	N2	RUS (1) (Balanovsky et al. 2008)
54	15	13	24	29	16	14	12, 14	13	10	10	24	14	12	14	10	18	N2	RUS (1) (Balanovsky et al. 2008)
55 ¹	-	13	23	29	-	14	12, 13	13	10	10	-	14	-	14	10	-	K(xN), O,P)	aYK (1) (Crubezy et al. 2010)
56	-	13	23	29	-	14	-	13	10	10	-	14	-	-	-	-	N1b	KKP (2) (Balaesque et al. 2015)

Table 1a: Contd....

ID	DYS456	DYS3891	DYS390	DYS3891I	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	Y-GATA-H4	DYS437	DYS438	DYS448	Hg	Population ID ²
57	-	14	23	29	-	14	-	13	10	10	-	14	-	-	-	-	N1c1	KKP (2) (Balaesque et al. 2015)
58	-	13	23	29	-	14	-	14	10	10	-	14	-	-	-	-	N1c1	KKP (1) (Balaesque et al. 2015)
59	-	13	23	29	-	14	-	13	10	11	-	14	-	-	-	-	N1b	TMN (1) (Balaesque et al. 2015)
60	-	13	23	30	-	14	-	12	10	11	-	14	-	-	-	-	N1b	TMN (1) (Balaesque et al. 2015)
61	-	13	23	29	-	14	-	13	10	10	-	15	-	-	-	-	N1b	UZB (1) (Balaesque et al. 2015)
62	-	13	23	29	-	13	-	13	10	10	-	14	-	-	-	-	N1b	TAJ (2) (Balaesque et al. 2015)
63	-	13	23	29	-	14	12,13	13	10	10	-	14	-	14	10	-	N2-A KHA (5)	MAN (9) (Pimenoff et al. 2008)
64	-	13	23	29	-	14	13,13	13	10	10	-	14	-	14	10	-	N2-A KHA (1)	(Pimenoff et al. 2008)
65	-	13	23	29	-	14	-	13	10	10	-	14	-	14	10	-	N*-M231	TUR (4) (Cinnioğlu et al. 2004)
66	-	13	23	29	-	14	-	13	10	10	-	14	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
67	-	13	23	29	-	14	-	13	10	11	-	14	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
68	-	13	23	29	-	14	-	13	10	10	-	13	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
69	-	11	23	27	-	14	-	13	10	10	-	14	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
70	-	13	23	28	-	14	-	13	10	10	-	14	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
71	-	14	23	30	-	14	-	14	10	10	-	13	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
72	-	13	23	29	-	15	-	13	11	10	-	14	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
73	-	13	23	29	-	15	-	13	10	10	-	14	-	14	10	-	N*-M231	TUR (1) (Cinnioğlu et al. 2004)
74	-	13	23	30	-	14	-	13	10	10	-	14	-	14	10	-	N*-M231	TUR (2) (Cinnioğlu et al. 2004)

¹17-loci Y-STR haplotypes matching with the original Scythian haplotype (PZ1) are shown in italics, while those with only a few allelic variations are shown in bold fonts at the differing loci. The only exceptions are haplotypes 55-74 that were typed with different Y-STR systems and have only partial loci overlap with the PZ1 haplotype. Further matches among non-PZ1 haplotypes are: 8 with 44, 9 with 31, 10 with 47, 15 with 37 and 46, 24 with 50. ²Abbreviations for the population ID's (number of samples) (YHRD accession number or reference): PZ1, Ak-Alakha-1 (Pazyryk culture, 4th-3rd centuries BCE) – Ukok Plateau, Altai Republic; aYK (BKH; Balyktakh site, 15th century CE), Khangalassky, Yakutia Republic; DON; Dongxiang – Gansu, China; HUI, Hui – Xinjiang, China (GAN; Gansu; QIN, Qin; QIN, Xinjiang); TUR, Turkish – Turkey (BS, Black Sea; CA: Central Anatolia; MAR: Marmara; CUK: Cukurova; BandH: Turkish expats in Bosnia and Herzegovina); MAN; Eastern Mansi – Ural Republic; KHL, Khalkha – Mongolia (CMO: Central Mongolia; ULA: Ulaanbaatar); MON, Mongolian (IMC: Inner Mongolia, China); HAN, Han – Zhejiang, China; KAZ, Kazakh – Gansu, China; UIG, Uighur – Xinjiang, China; KHL/BUR/DAR, Khalkha, Buryat, Dariganga – Eastern Mongolia; KHL/UUL/BUR, Khalkha, Uuld, Buryat – Gobi, Mongolia; MCH, Manchu – Chengde, China; NHA, Northern Han – Liaoning, China; RUS, Russian – Russian Federation (SVE: Sverdlovsk); YAK, Yakut; CHU, Chuvash; TAT, Tatar; UKR, Ukrainian; NOG, Nogay; TAJ, Tajik; TMN, Turkmen; UZB, Uzbek; CHL, Chelkan; KKP, Karakalpak; KHA, Khanty. ¹ Y-STR haplotypes from ancient DNA samples. ² These haplogroup assignments were made with the Whit Athey Algorithm.

type (Table 1a). Similar searches for full mtDNA HVR1 matches with the Ak-Alakha-1 mtDNA haplotype (PZ1) revealed 145 such haplotypes among contemporary Eurasian populations, plus 15 from among ancient cultures (Table 1b). While close variants of the PZ1 mtDNA haplotype among contemporary populations were too many to be listed in Table 1b, 18 close variants among ancient populations were included.

Figure 1 is a graphical illustration for the geographic distributions of the exact matches between the 17-loci Y-STR and/or mtDNA HVR1 haplotype from Ak-Alakha-1 (PZ1) and those from contemporary and ancient populations. Among the noteworthy observations are: (a) matches between the PZ1 mtDNA haplotype and those from other ancient cultures are seemingly restricted to the Altai mountains and further to the east, although such conclusions could be somewhat biased considering the limitations on the amount of archaeogenetic data currently available, (b) matches between the PZ1 mtDNA haplotype and those from contemporary populations are more widespread and largely concentrated along a diagonal axis running from Yakutia in the northeastern Siberia, through the Central Asia and Caucasus, to Asia Minor; matches observed that are seemingly further away from this axis are still related with the ethnicities along the main axis (for example, Turkic, Mongolic, Tungusic and Uralic) (c) matches between the PZ1 17-loci Y-STR haplotype and those from contemporary populations have a narrower distribution and are mostly restricted to Turkic populations from Afghanistan, Russia and Turkey, although there are also three individuals from the Muslim minorities in China. Turkey is the only country wherein full matches with both the PZ1 17-loci Y-STR and mtDNA HVR1 haplotypes are observed, at least in the same ethnic group, that is, Turkish.

Table 2 provides a summary of the matches between the PZ1 Y-STR (17-loci) and mtDNA (HVR1) haplotypes and those of the contemporary and ancient populations, organized in terms of the language families that each sample is known to be associated with. The majority (66.7%) of the full 17-loci Y-STR matches among the contemporary populations are those from Turkic-speaking ethnicities, while the rest are distributed among ethnicities associated with Indo-European (13.3%), Mongolic (6.7%) and Sino-Tibetan language families (13.3%). The

same trend continues for the close allelic variants of the PZ1 17-loci Y-STR haplotype observed among the contemporary populations with the following breakdown of language families associated with each ethnicity: Turkic (34.6%), Mongolic (28%), Tungusic (1.3%), Uralic (20%), Indo-European (10.7%) and Sino-Tibetan (5.3%). Notably, samples originating from ethnicities associated with the larger Altaic language family also account for 63.9 percent. A total of 145 full matches with the PZ1 mtDNA HVR1 haplotype were observed among the contemporary populations and with the following frequencies based on the language families of the associated ethnicities: Turkic (45.5%), Mongolic (15.2%), Tungusic (16.6%), Koreanic (0.7%), Uralic (9%), Indo-European (9.7%), Caucasian (1.4%), Sino-Tibetan (1.4%) and Afro-Asiatic (0.7%). Samples originating from ethnicities associated with the larger Altaic language family were found to comprise the excess majority with 77.9 percent. There were also 15 full matches between the PZ1 mtDNA haplotype and those originating from ancient cultures with the following breakdown: Pazyryk (20%), Tachtyk (6.7%), Xiongnu (13.3%), Jinggouzi (13.3%) and Yakut (46.7%). Finally, 18 close variants of the PZ1 mtDNA haplotype were also observed among the samples originating from ancient cultures with the following breakdown: Pazyryk (22.2%), Zevakino-Chilikta (5.6%), Xiongnu (22.2%), Jinggouzi (5.6%) and Yakut (44.4%).

Figure 2 depicts the M-JN for the matches and close allelic variants between the PZ1 17-loci Y-STR haplotype and those from contemporary populations. There is again a clear dominance throughout the entire network by the samples associated with the Altaic language family. There are four major star-like descent clusters around the haplotypic ancestral nodes of PZ1/1/30/41/53, 15/37/46, 8/44 and 24/50, wherein ethnicities associated with the Altaic languages are present in every case and often constitute the majority. Figure 3 depicts a phylogenetic network around the PZ1 mtDNA HVR1 haplotype, comprising full and very close variants from various archaeogenetic investigations. In the entire network, the PZ1 haplotype is the most frequent one (17 haplotypes), which is also observed in the remains from Jinggouzi, Tachtyk, Xiongnu and Yakut cultures, as well as other Pazyryk sites. The second most frequent variant (eight haplotypes) is that with only a miss-

Table 1b: Matches with and/or close variants of the ancient Ak-Alakha-1 (PZ1) mtDNA (HVR1) haplotype*

Haplotype ID	mtDNA HVR1 profile	Hg	Population ID [‡]
PZ1 ¹	16093C 16129A 16223T 16298C 16327T	C4a1 / C4a1+16129	PZ1 (2) (Pitipenko et al. 2015) (Unterlander et al. 2017)
1	16093C 16129A 16223T 16298C 16327T	C4a1	YAK (TTS) (2), (USM) (1), (CPC) (1) (Crubezy et al. 2010)
2	16093C 16129A 16223T 16298C 16327T	C4a1	UZB (KHR) (2) (Irwin et al. 2010)
3	16093C 16129A 16223T 16298C 16327T	C4a1	AFG (DNU) (1) (Irwin et al. 2010)
4	16093C 16129A 16223T 16298C 16327T	C4a1	KYR (DKU) (1) (Irwin et al. 2010)
5	16093C 16129A 16223T 16298C 16327T	C4a1	TAJ (12) (Irwin et al. 2010)
6	16093C 16129A 16223T 16298C 16327T	C4a1	RUS (1) (Malyarchuk et al. 2004)
7	16093C 16129A 16223T 16298C 16327T	C4a1	ARB (1) [AFDIL, 2012, unpublished]
8	16093C 16129A 16223T 16298C 16327T	C4a1	KOR (1) (Lee et al. 2006)
9	16093C 16129A 16223T 16298C 16327T	C4a1	EAU (1) [AFDIL, 2013, unpublished]
10	16093C 16129A 16223T 16298C 16327T	C	YAK (5) (Tarskaia and Melton 2006) and (1) (Derenko et al. 2007)
11	16093C 16129A 16223T 16298C 16327T	C4a1+16129+195	TUR (3) (Serin et al. 2016)
12	16093C 16129A 16223T 16298C 16327T	C4a1	BAR (5) (Derenko et al. 2012)
13	16093C 16129A 16223T 16298C 16327T	C	KZJ (1) (Yao et al. 2000)
14	16093C 16129A 16223T 16298C 16327T	C	UIG (1) (Yao et al. 2000)
15	16093C 16129A 16223T 16298C 16327T	C2b1	YUK (5) (Volodko et al. 2008)
16	16093C 16129A 16223T 16298C 16327T	C2b1	CHV (1) (Volodko et al. 2008)
17	16093C 16129A 16223T 16298C 16327T	C*	KHA (3) (Pimenoff et al. 2008)
18	16093C 16129A 16223T 16298C 16327T	C*	MAN (1) (Pimenoff et al. 2008)
19	16093C 16129A 16223T 16298C 16327T	C2b1	NGA (3) (Volodko et al. 2008)
20	16093C 16129A 16223T 16298C 16327T	C	AZE (1) (Richards et al. 2000)
21	16093C 16129A 16223T 16298C 16327T	C	ADG (2) (Macaulay et al. 1999)
22	16093C 16129A 16223T 16298C 16327T	C4	YK1 (1) and YK2 (1) (Crubezy et al. 2010)
23	16093C 16129A 16223T 16298C 16327T	C4	YK3 (4) and YK4 (1) (Keyser et al. 2015)
24	16093C 16129A 16223T 16298C 16327T	C4	PZ2 (1) (Unterlander et al. 2017)
25	16093C 16129A 16223T 16298C 16327T	C4a1+16129	PZ3 (1) (Unterlander et al. 2017)
26	16093C 16129A 16223T 16298C 16327T	C4a1+16129	PZ4 (1) (Unterlander et al. 2017)
27	16093C 16129A 16223T 16298C 16327T	C	TAC (1) (Keyser et al. 2009)
28	16093C 16129A 16223T 16298C 16327T	C	XIO (1) (Keyser-Tracqui et al. 2006)
29	16093C 16129A 16223T 16298C 16327T	C	JIN (2) (Wang et al. 2012)
30	16093C 16129A 16223T 16298C 16327T	C	XBK (1) (Pitipenko et al. 2018)
31	16093C 16129A 16223T 16298C 16327T	C	ALT (6) (Derenko et al. 2003), (2) (Gubina et al. 2013) and ALK (5) (Derenko et al. 2007)
32	16093C 16129A 16223T 16298C 16327T	C	BUR (2) (Derenko et al. 2003), (4) (Starikovskaya et al. 2005) and (5) (Derenko et al. 2007)
33	16093C 16129A 16223T 16298C 16327T	C	TUV (6) (Derenko et al. 2003), (9) (Starikovskaya et al. 2005) and (12) (Gubina et al. 2013)
34	16093C 16129A 16223T 16298C 16327T	C/C4	KZA (1) (Gokcumen et al. 2008) and KZA (4) (Derenko et al. 2012)
35	16093C 16129A 16223T 16298C 16327T	C	HAN (1) (Yao et al. 2002)
36	16093C 16129A 16223T 16298C 16327T	C	EVE (9) (Starikovskaya et al. 2005)
37	16093C 16129A 16223T 16298C 16327T	C	ULC (1) (Starikovskaya et al. 2005)

Table 1b: Contd...

Haplotype ID	mtDNA HVRI profile	Hg	Population ID ^f
38	16093C 16129A 16223T 16298C 16327T	C	MON (1) (Powell et al. 2007), (1) (Derenko et al. 2007) and (2) (Gokumen et al. 2008)
39	16093C 16129A 16223T 16298C 16327T	C	ORO (1) (Powell et al. 2007) and (1) (Kong et al. 2003)
40	16093C 16129A 16223T 16298C 16327T	C	HIM (1) (Powell et al. 2007)
41	16093C 16129A 16223T 16298C 16327T	C	KAL (2) (Derenko et al. 2007)
42	16093C 16129A 16223T 16298C 16327T	C	EYW (13) (Derenko et al. 2007)
43	16093C 16129A 16223T 16298C 16327T 16362C	C	BTG (1) (Gonzalez-Ruiz et al. 2012)
44	16093E 16129A 16223T 16298C 16327T	C	AA5 (1) (Unterlander et al. 2017), YK5 (1) (Crubezy et al. 2010), AAI (1) and VK2 (1) (Gubina et al. 2016)
45	16093E 16129A 16223T 16298C 16327T	C	JIN (1) (Wang et al. 2012), XIO (1) (Keyser-Tracqui et al. 2006) and XBK (2) (Pilipenko et al. 2018)
46	16093C 16129A 16223T 16298C 16327T	C4(C4a1/C4b8/C4+152+16093)	ZEV (1) (Unterlander et al. 2017)
47	16093C 16129A 16223T 16298E 16327T	C4	YK6 (5) (Crubezy et al. 2010) and YK7 (2) (Keyser et al. 2015)
48	16093C 16129A 16213A 16223T 16298C 16327T	C	XIO (1) (Keyser-Tracqui et al. 2003)

^fFull or partial matches with the Pazyryk haplotype (PZ1) are shown in italics fonts, while any additional or missing variations are shown in bold and strike through fonts, respectively. Some mtDNA haplotypes have a wider sequence coverage reported in the literature, but only the data for the HVRI region (16024-16365) are shown herein. Haplotypes IDs provided here are independent of those in Table 1a. Haplotypes 1 through 9 are EMPOP matches. ^gAbbreviations for the population ID's (number of samples) (reference) are the same as those provided in Table 1a, except for the following additional ones: YK1 (No.: 1 site, late 18th century CE) – Khangalassky, Yakutia Republic; YK2 (Bekh Alaas 4 site, 18th century CE) – Churapchinsky, Yakutia Republic; YK3 (Lepsei site, late 17th-18th century CE) – Verkhoyansky, Yakutia Republic; YK4 (Oyogosse Tumula II, late 18th-19th century CE) – Vilyuy, Yakutia Republic; YK5 (Balytakh site, 15th century CE) – Khangalassky, Yakutia Republic; YK6 (Alas Ebe 2, Khangalassky/Jarama 1, Churapchinsky/Ken Ebe 3, Tattinsky (2)/Orto Aryy, Tattinsky; 15th-19th centuries CE), Yakutia Republic; YK7 (Kureleekh, Verkhoyansky/Orto Aryy, Central Yakutia: pre-17th-18th centuries CE), Yakutia Republic; PZ2, Ak-Alakha-5 (Pazyryk culture, 4th-3rd centuries BCE) – Ukok, Altai Republic; PZ3, Ala-Gail-2 (Pazyryk culture, 4th-3rd centuries BCE) – Chuy Valley, Altai Republic; PZ4, Berel' (Pazyryk culture, 4th-3rd centuries BCE) – Bogratsky, Khakassia Republic; BTG, Baga Turgen Gol 1st century CE) – Kazakhstan; TAC, Abakano-Perovo 1 (Tachtyk culture, 1st-4th centuries CE) – Bogratsky, Khakassia Republic; BTG, Baga Turgen Gol Verkh-Kaldzhin-2, mound 1 (Pazyryk culture, 4th-3rd centuries BCE) – Ukok, Altai Republic; ZEV, Zevakino (Zevakino-Chilikta culture, 9th-7th centuries BCE) – Kazakhstan; XIO, Xiongnu (Xiongnu culture, 3rd century BCE - 2nd century CE) – Egin Gol Valley, Mongolia; XBK, Xiongnu (Xiongnu culture, 1st century BCE) – Mongolia, China; KZA, Altaiian Kazakhs – Altai Republic; KZX, Xinjiang Kazakh – Xinjiang, China; YUK, Yukagir – Kolyma River, Yakutia Republic; CHV, Chuvan/Chuvantsi – Chukotka, Russian Federation; NGA, Nganasans – Taymyr Peninsula, Russian Federation; AZE, Azeri – Azerbaijan; ADG, Adygei – Northwest Caucasus; Russia; YAK, Yakut – Yakutia Republic (TYS, Tattinsky; USM, Ust-Maya; CPC, Churapcha); UZB, Uzbek – Uzbekistan (KHR, Khorezm); AFG, Afghani – Uzbekistan (DNU, Denau); KYR, Kyrgyz – Uzbekistan (DKU, Dzhalga-Kudub); TAJ, Tajik – Uzbekistan; ALT, Altaiian; ALK, Altaian-Kizhi; TUV, Tuvan; BUR, Buryat; EVE, Evenki; ULC, Ulchi; ORO, Oroqen; HIM, HAN (JMC: Inner Mongolia, China); KAL, Kalmyk; ARB, Arab – Bahrain; KOR, Korean – South Korea; EAU, East Asian unknown – New York, USA. ¹ mtDNA (HVRI) haplotypes from ancient DNA samples.

Table 2: Distributions of the language families and ethnicities of the individuals bearing full or very close Y-STR (17-loci) and/or mtDNA (HVR1) haplotype matches with those from the Ak-Alakha-1 burial site

<i>Language Family</i>	<i>Population ID †</i>	<i>Ethnicity</i>	<i>Number of Y-STR matches</i>	<i>Number of mtDNA matches</i>
<i>Altaic: Turkic</i>	TUR	Turkish	5 (+9)	3
	AZE	Azeri	-	1
	KAZ / KZJ / KZA	Kazakh	(+1)	6
	UIG	Uighur	(+2)	1
	YAK	Yakut	(+2)	10 (+7 +8)
	CHU	Chuvash	(+1)	-
	TAT	Tatar	1 (+3)	-
	NOG	Nogay	(+2)	-
	TMN	Turkmen	3 (+1)	-
	UZB	Uzbek	1 (+1)	2
	CHL	Chelkan	(+4)	-
	KYR	Kyrgyz	-	1
	ALT	Altaian	-	13
	TUV	Tuvan	-	27
	<i>Altaic: Mongolic</i>	DON	Dongxiang	1 (+4)
MON/KHL		Mongolian/Khalkha	(+15)	4
KHL/BUR/DAR		Khalkha, Buriat, Dariganga	(+1)	-
KHL/UUL/BUR		Khalkha, Uuld, Buryat	(+1)	-
BUR		Buryat	-	11
KAL		Kalmyk	-	2
BAR		Barghuts	-	5
<i>Altaic: Tungusic</i>	MCH	Manchu	(+1)	-
	EVE/EVW	Evenk	-	22
	ULC	Ulch	-	1
	ORO	Oroqen	-	2
<i>Altaic: Koreanic</i>	KOR	Korean	-	1
	MAN	Mansi	(+2)	1
<i>Uralic</i>	KHA	Khanty	(+13)	3
	YUK	Yukaghir*	-	5
	CHV	Chuvantsi	-	1
	NGA	Nganasan	-	3
	RUS	Russian	1 (+6)	1
<i>Indo-European</i>	UKR	Ukrainian	(+1)	-
	TAJ	Tajik	1 (+1)	12
	AFG	Afghan‡	-	1
<i>Caucasian</i>	ADG	Adygei	-	2
	<i>Sino-Tibetan</i>	NHA/HAN/HIM	Han	(+2)
HUI		Hui§	2 (+2)	-
<i>Afro-Asiatic</i>	ARB	Arab	-	1
	<i>Unknown</i>	PAZ	Pazyryk*	-
TAC		Tachtyk*	-	(+1)
ZEV		Zevakino-Chilikta*	-	(+1)
XIO / XBK		Xiongnu*	-	(+2+4)
JIN		Jinggouzi*	-	(+2+1)
EAU		East Asian Unknown	-	1
Total			15 (+75) = 90	145 (+15+18) = 178

†Population ID's as described in Tables 1a and 1b, except for PAZ, which collectively denotes PZ2, PZ3, PZ4, BTG, AA1, AA5 and VK2. The number of full 17-loci Y-STR haplotypes are shown in bold fonts, while those with only a few allelic variations from the PZ1 haplotype are shown in brackets [for example, (+1)]. The number of full mtDNA HVR1 matches are also shown in bold fonts, while those corresponding to ancient DNA samples with full or closely matching haplotypes are shown in bold and plain fonts, respectively, and both in brackets [for example, (+1+1)]. ‡Actual ethnicity and hence the language spoken by this individual is unknown. §Predominantly Chinese-speaking Muslims, Hui's paternal lineages are closer to those of Uighur, Mongolian and Manchu minorities in China (Zhao et al. 2017). *No consensus exists on the precise language family of these ethnicities.

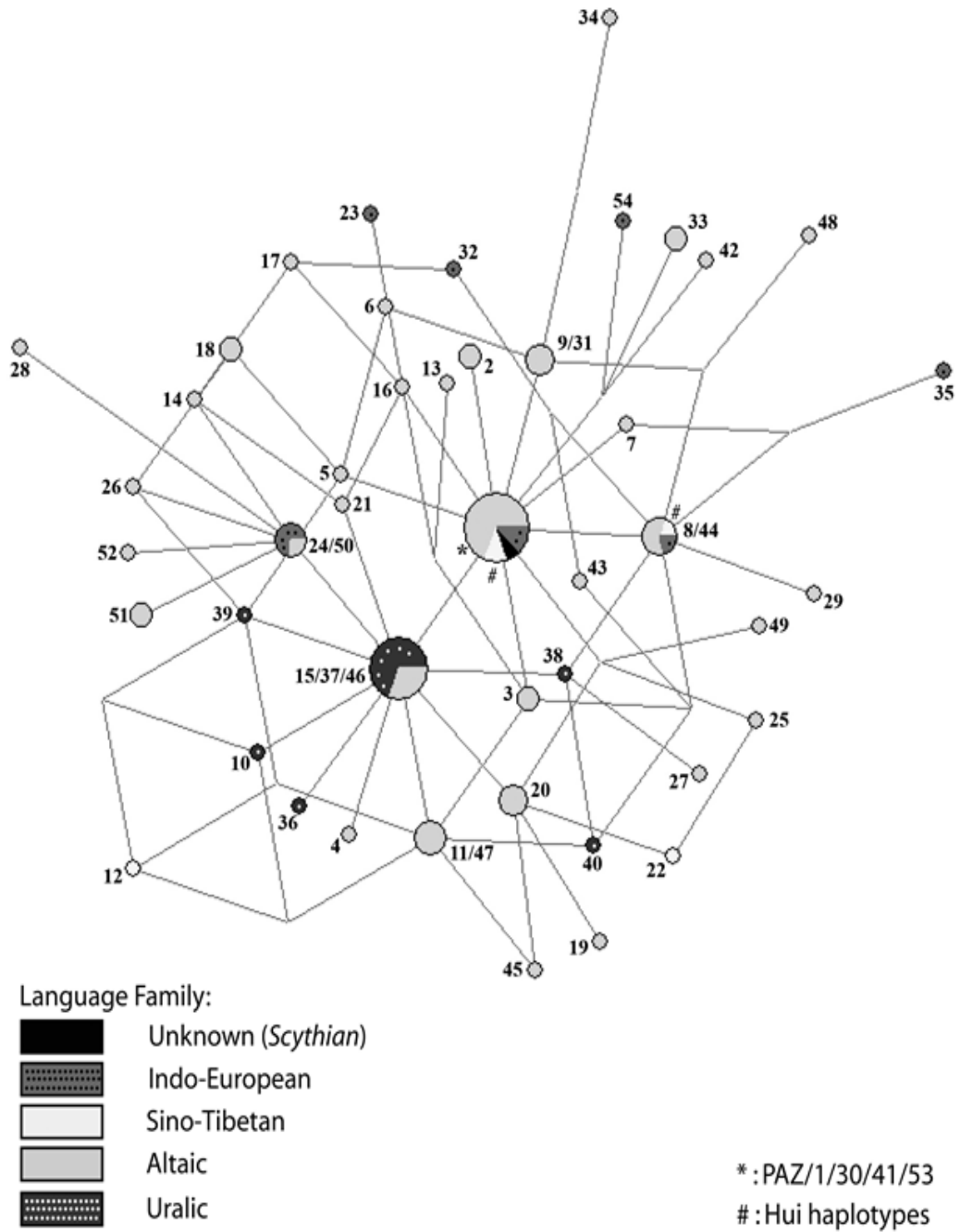


Fig. 2. M-JN analysis of the 17-loci Y-STR haplotypes corresponding to the Scythian haplotype PZ1 from Ak-Alakha-1 burial site and its contemporary matches and close allelic variants (Haplotypes 1 through 54 from Table 1a).

Source: Author

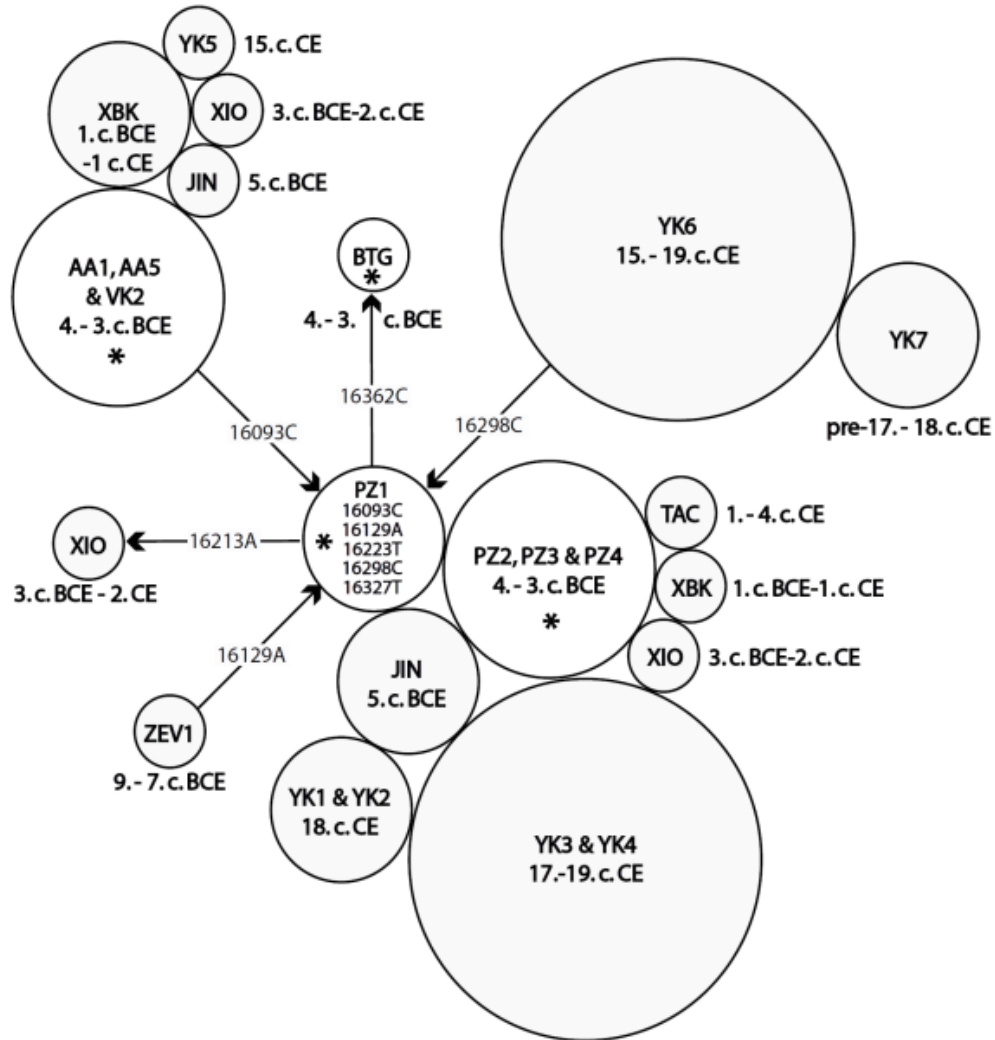


Fig. 3. A phylogenetic network for the ancient PZ1 mtDNA haplotype (HVR1) (haplogroup C) in relation to other fully matching or very closely related (only a single mutation event apart) ancient haplotypes. Each node size is proportional to the number of haplotypes reported (for example, PZ1 was observed in two individuals at Ak-Alakha-1, etc., refer to Table 1b for further details). Abbreviations for population IDs are the same as those in Table 1b. Tangential nodes denote the same HVR1 haplotype, but different populations and/or time periods and/or sites, while the arrows separating two nodes denote a single mutation event. Asterisks denote Pazyryk sample nodes.

Source: Author

ing mutation of 16093C, and it is observed in the remains from Jinggouzi, Xiongnu, Yakut and Pazyryk cultures. The most ancient haplotype in the entire phylogenetic network corresponds to that from the Zevakino-Chilikta culture, and differs from PZ1 by the absence of the 16129A mutation.

DISCUSSION

A recent large-scale archaeogenetic study revealed that different Scythian populations from across the Eurasian Steppe not only shared distinct cultural traditions but also strong genetic connections (Unterlander et al. 2017). This could

be best explained by the presence of a substantial amount of gene flow among the ancient Scythian populations, which would also be consistent with their already known nomadic/semi-nomadic pastoralist lifestyles. Through ancient mitochondrial DNA studies, it was also shown earlier that the Altai Mountains constituted a geographical barrier for the genetic admixture of the east and west Eurasian populations up until the beginning of the Iron Age (Calafell et al. 1996; Comas et al. 1998). The beginning of the Iron Age seemingly coincided with the eastward population expansion from the Pontic-Caspian Steppe in Eastern Europe and a westward expansion of the east Eurasian populations. Indeed, archaeogenetic data on Iron Age nomad samples originating from eastern and western parts of the Eurasian Steppe suggest that the genetic composition of the ancient Scythians could be a mixture of the late Copper Age/Early Bronze Age Yamna culture and East Asian/North Siberian elements (Unterlander et al. 2017). Each ancient Scythian group was also found to bear closer genetic connections with the contemporary populations from the same region, hence indicating substantial population continuity across more than two millennia. For instance, the ancient Pazyryk people were found to share a similar mtDNA gene pool with not only the contemporary Altaians and nearby populations but also with the pre-Iron Age populations from the same region (Gonzalez-Ruiz et al. 2012).

A potential reason for the collapse of the once thriving Pazyryk culture could be attributed to the expansion of the Xiongnu people, who are credited with the formation of the first nomadic empire in Central Asia between the 2nd BCE and 1st CE. Traces of contacts between the Pazyryk and Xiongnu cultures are already evident in many respects, even in the current study, wherein both the Ak-Alakha-1 mtDNA haplotype, as well as its close variant (missing the 16093C mutation) that were observed in other Pazyryk people, were shown to be shared by ancient Xiongnu people from Egyin Gol Valley in Mongolia and Transbaikalia in Buryatia (Fig. 2). Xiongnu are also thought to be genetically and culturally linked with the subsequent Mongolic and Turkic expansions from the same region, which could help further explain the sharing of both the Ak-Alakha-1 mtDNA and Y-STR haplotypes among contemporary populations associated with these two ethnicities (Pilipenko

et al. 2018). In other words, there is an apparent population continuity from the Scythians to the Xiongnu and then onto the Turkic people, possibly because the former two already bore proto-Turkic elements. Following the collapse of the Pazyryk culture, not all members of the community disappeared, but some seemingly formed the basis of a genetic continuity with the contemporary Altaians and other nearby populations in terms of both the paternal and maternal lineages (Dulik et al. 2012; Gonzalez-Ruiz et al. 2012).

As illustrated in Figure 1, both the paternal and maternal lineages belonging to the two Scythians from Ak-Alakha-1 kurgan site exhibit clear signs of reproductive success across almost the entire Eurasian landscape and over two and a half millennia. In agreement with the results from the current study, eastern Scythian lineages were already shown to have a more widespread distribution among the contemporary populations and intriguingly almost exclusively among the Turkic-speaking populations, who are also spread over a substantial part of the Eurasian geography (Unterlander et al. 2017).

It is also noteworthy that a relatively high level of matching was observed in both the maternal and paternal lineages of the two ancient Scythians from Ak-Alakha-1 site and contemporary populations from Anatolia (Tables 1a and b, Fig. 1). This is despite the fact that the Y-chromosomal haplogroup N and mtDNA haplogroup C are today observed at their highest frequencies in both contemporary and ancient east Eurasian populations. As in the case of the Pazyryk culture, there is ample evidence for genetic admixture of the eastern and western paternal and maternal lineages in the contemporary populations from Turkey along with an overall population continuity of the original Anatolian genetic stock (Cinnioglu et al. 2004; Serin et al. 2016). For instance, the overall frequency of the Y-chromosomal haplogroup N (combined N* and N3a) was noted as only four percent across the whole country, where N* was found to account for seventy-five percent of these N lineages (Cinnioglu et al. 2004). That being said, N* alone was also shown to account for up to seven percent in Eastern Black Sea Region in Turkey, while the combined N*/N3a frequency was six percent and ten percent in the Central Anatolia and Aegean Regions, respectively (Cinnioglu et al. 2004). In the meantime, while there is

still relatively limited mtDNA data available from the entire country, mtDNA haplogroup C (C4 and C4a1+16129A) was also observed with a frequency of four percent among the contemporary populations in South and Southeastern Anatolia, where haplogroups C4 and C4a1+16129A accounted for one percent and three percent, respectively (Serin et al. 2016). The substantial presence of the Ak-Alakha-1 mtDNA and Y-STR haplotypes in the contemporary Anatolian populations may be attributed to two major historical events: (a) the less likely being the Scythian invasion of Anatolia around 7th century BCE and settlement for around 30 years near the Aras or Araxes River (Herodotus 1920), and (b) the more likely being the Central Asiatic Turkic migrations into Anatolia from around 11th century CE onwards, keeping in mind the ever growing support for a strong genetic continuity between the ancient eastern Scythians and the proto-Turkic tribes (Unterlander et al. 2017). It should be further emphasized that, the detection in contemporary Anatolian populations of ancient Y-STR and/or mtDNA haplotypes from south Siberian cultures (for example, Xiongnu and Kurgan cultures, etc.) is by no means unprecedented and certainly not limited to those typically associated with East Eurasian populations (that is, Y-chromosomal haplogroup R1a1 and mtDNA haplogroups U4 and T1 are also shared between the both populations) (Keyser-Tracqui et al. 2003; Keyser et al. 2009; Pilipenko et al. 2018). Instead of simply disappearing upon the collapse of the Scythian culture, “the animal style” flourished over an even larger geographical domain, such as through the ethnic traditions of various Turkic peoples. Among the numerous examples are the re-appearance of the ever-popular Scythian symbolism attached with deer and deer antlers in the insignia of the Kok-Turk royal family, as well as ornamental motifs on numerous other artifacts from the associated period (Coruhlu 2014).

Traces of the Scythian influence among other Turkic people, such as those as far as from northeastern Siberia, namely Yakuts or Sakhas, were also previously proposed, but these proposals remain contested (Gogolev 1993; Savinov 2010). Recent archaeogenetic data seem to support a connection between the contemporary Yakuts and ancient Scythians, especially in terms of the Pazyryk culture, because the current model suggests that a demographic expan-

sion of the autochthonous Altaians is more likely to account for the genetic admixture and diversity in Central Asia (Voivod et al. 2003; Gonzalez-Ruiz et al. 2012). Population genetics studies on contemporary Sakhas suggested that they have (a) rather heterogeneous maternal lineages, featuring close affinities with both the autochthonous Northeastern Siberian populations, such as Evenks, who were traditionally Tungusic-speaking reindeer-herders and hunter-gatherers and Southern Siberian Turkic-speaking Tuvans, who had a traditional economy based on semi-nomadic horse and cattle breeding (Pakendorf et al. 2003; Puzyrev et al. 2003), and (b) very homogenous paternal lineages, both geographically and chronologically, possibly due to a population bottleneck or founder effect, with an affinity to those from the Lake Baikal area (Pakendorf et al. 2006; Crubezy et al. 2010). As it can be clearly seen from Table 1b and Figure 1, the Ak-Alakha-1 mtDNA haplotype and its close variants are found abundantly among ancient and contemporary Yakuts. Furthermore, a full match at only the 12 common loci available was also observed between the Y-STR haplotype of Ak-Alakha-1 and a 15th century CE ancient Yakut, which constitutes the only match so far between the Ak-Alakha-1 haplotype and that of an ancient individual from elsewhere. It may also be added that the ornamental edge patterns on the felt hats of both ancient Scythians from Ak-Alakha-1 are also often encountered in diverse Yakut artifacts (Neustroev 1994; Polosmak 1994b; Neustroev 2010). Moreover, closer comparative analyses of the Pazyryk archaeological materials with the contemporary Siberian artifacts suggest that only those belonging to Yakuts have an unusually similar or even identical patterns with those of the Pazyryk culture (Johansen 2008).

Potential connections between the Yakuts and Pazyryk people, the latter of whom are known to have an admixed genetic character comprising both Indo-European and East Asian lineages, may also help raise the veil of secrecy over the previously proposed linguistic ties between the Yakut and Sanskrit languages (Sidorov 1997). Such an indirect link between the Yakuts and Indo-Europeans through the admixed Scythian ancestors could shed light on the inexplicable high frequency of HLA-A1, B17 genotype among the contemporary Yakuts (Fefelova 1990). Major histocompatibility complex HLA-

B17 genotype is associated with a predisposition to ankylosing spondylitis (AS), or the Bekhterev disease, which is encountered with the highest frequencies among Indo-Iranians but almost absent in Mongoloids. Among Yakuts, the *HLA-B17* gene and AS is more common than in any other ethnic groups in modern Yakutia. Among the Yakut patients, gastroduodenal erosive and ulcerative lesions induced by non-steroidal anti-inflammatory drugs are encountered along with AS five times more frequently compared to non-indigenous populations (for example, Russian, etc.) (Fedotov 2011). Interestingly, the older individual from the Ak-Alakha-1 kurgan 1 was also diagnosed with AS (Polosmak 2001; Chikisheva 2003).

In response to aggressive Xiongnu expansion into the Altai region around the 2nd century BCE, some members of the Pazyryk culture may have started moving up North, and eventually reached the Vilyuy River at the beginning of 1st century CE. Notably, there is clear population continuity between the Uralic people such as Khants, Mansis and Nganasans, Paleo-Siberian people such as Yukaghirs and Chuvantsi, and the Pazyryk people even when considering just the two mtDNA and Y-STR haplotypes from the Ak-Alakha-1 mound 1 kurgan (Tables 1a, b, Table 2, Fig. 1). These concepts are also in agreement with the famous Yakut ethnographer Ksenofontov, who suggested that technologies associated with ferrous metallurgy were brought to the Vilyuy Valley at around 1st century CE by the first (proto)Turkic-speaking pioneers (Ksenofontov 1992). Yakut ethnogenesis *per se* possibly involved two major stages, the first being the proto-Turkic epoch through the arrival of Scytho-Siberian culture originating from Southern Siberia, such as that associated with the Pazyryk culture and the second being the proper Turkic epoch.

CONCLUSION

As part of an in-depth case study, extensive searches were carried out in online databases and literature for matches with the paternal and maternal lineages of the two Pazyryk individuals from the Ak-Alakha-1 mound 1 kurgan, which helped reveal a clearer picture of some of the ancient migrations across the Eurasian landscape. While the archaeogenetic data associated with the two ancient Scythians alone certain-

ly can not be considered representative of the whole Pazyryk Culture, let alone that of the highly admixed Scythian populations at large, a rare glimpse into the genetic continuity of the two individuals from a Pazyryk Kurgan that seemingly captured contemporary human imagination was still possible. A major limitation of the current study remains the fact that despite the increasing amount of archaeogenetic data that has become available, there is still unequal data coverage on all the relevant ancient cultures and contemporary populations from across the Eurasian landscape.

RECOMMENDATIONS

Current investigation underscores the need for the generation of more population genetics data that are both spatially and geographically representative so that more authoritative conclusions on potential Scythian population continuity may be drawn.

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