A Comparative Analysis of Chinese Historical Sources and Y-DNA Studies with Regard to the Early and Medieval Turkic Peoples

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Abstract

In the past 10 years, geneticists have investigated the genetic variation of modern Turkic populations as well as ancient DNA of the Xiongnu and others. The accumulated findings of these surveys, however, have not been adequately noted by specialists in Inner Asian history. In order to fill this gap, we conducted a comparative analysis of textual information and genetic survey data on the early and medieval Turkic peoples. First, we examined the information on the origins, identity, and physiognomy of the early and medieval Turkic peoples contained in the Chinese Standard Histories (*zhengshi* 正史). We then discussed how the findings of genetic surveys complement the textual information. Both Chinese histories and modern DNA studies indicate that the early and medieval Turkic peoples were made up of heterogeneous populations. The Turkicisation of central and western Eurasia was not the product of migrations involving a homogeneous entity, but that of language diffusion.

Keywords

Turkic peoples – Chinese Standard Histories – Y-DNA haplogroup – Turkicization – physiognomy

Introduction

In the past 10–15 years, geneticists have traced the genetic origins of various human populations by studying their paternally inherited Y-chromosomes and maternally inherited mitochondrial DNA.¹ In the process, geneticists have also investigated the genetic variation of modern Inner Asian populations (Wells *et al.* 2001; Zerjal *et al.* 2002), as well as ancient DNA extracted from the remains of the Xiongnu and the Sakhas (Yakuts), among others, as will be discussed below.² The accumulated findings of these genetic surveys, however, have not been adequately noted by specialists in Inner Asian history.³ This article aims to fill this gap by conducting a comparative analysis of textual information and genetic survey data on the early and medieval Turkic peoples. First, we will examine the information on the origins, identity and physiognomy of the early and medieval Turkic peoples contained in the Chinese Standard Histories (*zhengshi* 正史).⁴ We will then demonstrate in detail how the findings of genetic surveys on the ancient and modern Turkic peoples corroborate or complement the textual information. The conclusions of this article are as follows: both medieval Chinese histories and modern DNA studies point to the fact that the early and medieval Turkic peoples were made up of heterogeneous and somatically dissimilar populations. The Turkicization of central and western Eurasia in the past two millennia was not the product of migrations involving a single, homogeneous Turkic entity, but that of multiple waves of language diffusion involving both Turkic and Turkicized peoples.

1 For introductory studies, see Underhill & Kivisild (2007); Oppenheimer (2012).

2 The term 'Inner Asia' is used in this article to refer to the Mongolian and Kazakh steppes, while 'Central Asia' is used for the interior region stretching from the Caspian Sea in the west to Xinjiang, China, in the east and from Kazakhstan in the north to Afghanistan in the south.

3 At the same time, it is also true that geneticists' interpretations of DNA data on Inner Asian populations are often impaired by their limited knowledge of Inner Asian history and the languages needed to study it and, on rare occasions, are influenced by biases. Therefore, although we have used genetic survey data from numerous genetic studies in this work, we do not necessarily agree with the interpretations suggested in these studies.

4 The Standard Histories (*zhengshi* 正史), also known as the Twenty-Four Histories, are a collection of official Chinese annals covering the period from antiquity to the Ming Dynasty in the seventeenth century.

The Origins, Identity, and Physiognomy of the Early and Medieval Turkic Peoples according to Chinese Histories⁵

The Xiongnu

The Xiongnu were the first nomadic empire-builders in Inner Asian history. Historians have been unable to confirm whether or not the Xiongnu were a Turkic people.⁶ According to some fragmentary information on the Xiongnu language that can be found in the Chinese histories, the Xiongnu were Turkic and not Mongolic. The mid sixth-century work *Weishu* relates that the language of the Gaoche (高車), a Turkic people who established a nomadic state in modern-day Xinjiang in the late fifth century AD, and that of the Xiongnu were roughly the same with some differences.⁷ In addition, the mid seventh-century work *Beishi* recounts that the language of the Yuwen Xiongnu, a Xiongnu tribe active during the Sixteen Kingdoms Period (304–439 AD) in northern China, was quite different from that of the Xianbei, a Mongolic or Para-Mongolic people (*Beishi* 98.3270). However, the linguistic affiliation of the Xiongnu may remain open to speculation even though some of the Xiongnu remnants later may have taken part in the formation and development of various Turkic nomadic confederations. Concerning the origin of the Xiongnu, the *Shiji* by Sima Qian (司馬遷, d. 86 BC) relates that they were descended from Chun Wei (淳維) (*Shiji* 110.2879), a legendary figure from the ancient Xia (夏) Dynasty, thus attributing a Xia origin to the Xiongnu. Such an explanation is of no scientific value in determining the origin of the Xiongnu. Yet it does suggest that the physiognomy of the Xiongnu was not too different from that of Sima Qian's own Han (漢) Chinese population, who also considered themselves descendants of the Xia. However, the Jie (羯), 'a separate branch of the Xiongnu (匈奴別部)', who founded the Later Zhao Dynasty (319–351 AD), appear to have possessed West Eurasian physiognomy, that is, 'deep-set eyes', 'high nose bridges' and 'heavy facial hair'. The *Jinshu* relates that when the Later Zhao Dynasty was overthrown, the Han Chinese rebel leader Ran Min massacred about 200,000 Jie, or those with 'high nose bridges' and 'heavy beard (高鼻多須)' (*Jinshu* 107.2792). Moreover, the *Jinshu* records the following conversation between a Jie notable and a Han Chinese official:

5 We are not concerned with modern theories of ethnicity or identity in this study. Our main concern is demonstrating how the historical Turkic peoples were identified by their contemporary historians.

6 For a detailed study of the Xiongnu affiliations, see Golden (1992: 57–9); Kim (2016: 7).

7 '其語略與匈奴同而時有小異' (*Weishu* 103.2307).

Sun Zhen, the chamberlain (詹事) of the crown prince, asked the minister (侍中) Cui Yue, 'I suffer from eye diseases. What is the remedy for it?' Yue, who had always been informal towards Zhen, teased him saying, 'if [you] urinate in the middle [of the eye], it will be cured'. 'How can you urinate in the eye?' Zhen asked. 'Your eyes are dented. You can urinate in the middle', Yue said. Zhen harboured hatred and reported this to [Crown Prince] [Shi] Xuan (石宣). Xuan was the most 'barbarian' (*hu* 胡)-looking among the princes. His eyes were deep. Hearing this, he became very angry. He killed Yue and his son.⁸

The Dingling or Tiele

Unlike for the Xiongnu, historians know with certainty that the Dingling (丁零), a nomadic people who inhabited present-day northern Mongolia during the Xiongnu period, were a Turkic people. Chinese histories are unanimous in depicting them as the ancestors of the Tiele (鐵勒), a group of Turkic tribes that became one of the dominant nomadic powers in the Mongolian steppes after the disintegration of the Xiongnu empire (*Weishu*, 103.2307; *Beishi*, 98.3270). According to the *Shiji*, Maodun (冒頓, r. 209–174 BC), who founded the Xiongnu empire in the late third century BC, subdued the Dingling (*Shiji* 110.2893), along with the Donghu (東胡), the Yuezhi (or Rouzhi 月氏) (*Shiji* 110.2889–90) and the Qirghiz (Gekun 鬲昆) (*Shiji* 110.2893). The Dingling are mentioned again in the Chinese histories as Han allies who, along with the Wusun (烏孫) and the Wuhuan (烏桓), raided the weakened Xiongnu during the first century BC (*Hanshu* 94a.3787–88).

The Dingling outlived the Xiongnu and re-appear as the Gaoche, or Tiele, in the medieval Chinese histories. As to the origin of the Gaoche, or Tiele, the *Weishu* and the *Beishi* describe them as 'the remnants of the ancient Chidi (古赤狄之餘種)' (*Weishu* 103.2307; *Beishi* 98.3270.), while the *Suishu* (c. 630s AD) and the *Jiu Tangshu* (c. 940s AD) merely describe them as 'the descendants of the Xiongnu (匈奴之苗裔)' or 'a separate stock of the Xiongnu (匈奴別種)' (*Suishu* 84.1879–80; *Jiu Tangshu* 199b.5343). The latter two histories also describe the Tiele as a large and widespread group of tribes that inhabited not only the Mongolian steppes but also the Kazakh steppes. Some of them include Uighur (Huihe 回紇 or Weihe 韋紇), Syr Tarduš (Xueyantuo 薛延陀),

8 '太子詹事孫珍問侍中崔約曰：「吾患目疾，何方療之？」約素狎珍，戲之曰：「溺中則愈。」珍曰：「目何可溺？」約曰：「卿目眊眊，正耐溺中。」珍恨之，以白宣。宣諸子中最胡狀，目深，聞之大怒，誅約父子。珍有寵于宣，頗預朝政，自誅約之後，公卿已下憚之側目' (*Jinshu* 106.2776). The Jie may have spoken a Yeniseian language. See Vovin (2000: 92–103).

Bayegu (拔也古), Hun (渾), Tuva (Doubo 都播), Quriqan (Guligan 骨利幹) and Alan (阿蘭), among others (*Suishu* 84.1880). Some of these Tiele tribes listed in the Chinese histories seem to have been non-Turkic-speaking groups. For instance, the mid eleventh-century work *Xin Tangshu* writes that the language of the Bayegu was somewhat different from that of the Tiele (言語少異) (*Xin Tangshu* 217b.6140). Furthermore, the Alans were an ancient Iranic people known to classical writers from the first centuries AD. Regarding the Tiele, the *Suishu* also notes that 'their custom was similar to that of the Tujue (Kök Türks) (其俗大抵與突厥同)', but that the two differed in their marriage and burial customs.⁹ Importantly, the Chinese histories do not make any particular mention of the physiognomy of the Tiele.

The Kök Türks

The nomadic people who spread the Turkic language and the name *Türk* beyond the Mongolian steppes were the Kök Türks (*Tujue* 突厥 in Chinese) led by the Ashina clan. Importantly, Chinese histories do not describe them as descending from the Dingling or as belonging to the Tiele confederation.¹⁰ The *Zhoushu* (c. 630s AD), for instance, describes them as 'a separate tribe of the Xiongnu (匈奴之別種)' (*Zhoushu* 50.907) or ascribes their origin to the Suo state (*suo guo* 索國) located to the north of the Xiongnu (*Zhoushu* 50.908). The *Suishu* recounts that the Kök Türks are descended from 'the mixed barbarians (*za hu* 雜胡) of Pingliang (平涼)'¹¹ (*Suishu* 84.1863). Interestingly, the *Zhoushu* also relates that the Ashina clan was related to the Qirghiz (Qigu 契骨) (*Zhoushu* 50.908), who are described in the *Xin Tangshu* as possessing 'red hair' and 'blue eyes' (*Xin Tangshu* 217b.6147). However, as to their physiognomy, the Kök Türks differed from the Qirghiz. According to the *Jiu Tangshu*, an Ashina commander named Ashina Simo (阿史那思摩) was not given a high military post by the Ashina rulers because of his Sogdian (*huren* 胡人) physiognomy:¹²

Simo was a relative of Xieli. Because his face was like that of the 'barbarian' (*huren* 胡人) and not like that of the Tujue, Shibi [Khagan] and Chuluo [Khagan] were doubtful of his being one of the Ashina. Thus although he always held the title of Jiabi tele[i] (夾畢特勒) during Chuluo

9 The Tujue (Kök Türks) cremated their dead, while the Tiele buried them (*Suishu* 84.1880).

10 For a detailed study of the Kök Türk founding legends, see Sinor (1982).

11 Pingliang was located in present-day Gansu Province, China.

12 *Hu* (胡) denoted the Sogdians in Tang China.

and Xieli's time, he could not become a *shad* (she 設) in command of the army till the end ...¹³

It should be noted that the seventh-century Tang historian Yan Shigu (顏師古), who added a commentary to the *Hanshu* (c. 80s AD), describes the Wusun (烏孫) as follows:

The Wusun have the weirdest appearance among all the Rong (戎) of the Western Region (西域). Today's Hu (胡) people, being blue-eyed and red-bearded, and having the appearance of macaques, were originally their progeny.¹⁴

However, no comparable depiction of the Kōk Türks or Tiele is found in the official Chinese histories.¹⁵

The Kōk Türks became divided into Eastern Türks and Western Türks in the late sixth century (583 AD). The Western Türks, centred in the Kazakh steppes, developed into an autonomous tribal confederation that included some tribes not found among their eastern counterpart, such as the Qarluq (Geluolu 歌邏祿), the Chuyue (處月),¹⁶ the Türgesh (Tuqishi 突騎施),¹⁷ and perhaps the Khazars (Hesa 曷薩).¹⁸ These tribes, which would outlive the Ashina clan and

13 '思摩者，頡利族人也。始畢、處羅以其貌似胡人，不類突厥，疑非阿史那族類，故歷處羅，頡利世，常為夾畢特勒，終不得典兵為設' (*Jiu Tangshu* 194a.5163). Perhaps this is reminiscent of the Kazakh view of non-Inner Asian physiognomy. Ármín Vámbéry, the Hungarian Turkologist, who travelled in Central Asia in the mid nineteenth century, writes that '[the Kazakhs] compassionate all whose faces have not the pure Mongol conformation. According to their aesthetic views, that race stands at the very zenith for beauty ...' (Vámbéry 1865: 421).

14 '烏孫於西域諸戎其形最異。今之胡人，青眼赤髭鬚，狀類獼猴者，本其種也' *Hanshu*, 96b.3901. The same passage is written in the *Tongdian* 通典 [Comprehensive statutes], a universal administrative history. See Du You 杜佑. *Tong dian* 通典 [Comprehensive statutes], chapter 192. <https://zh.wikisource.org/zh-hant/%E9%80%9A%E5%85%B8/%E5%8D%B7192> (accessed 14 July 2017).

15 Perhaps the physiognomy of the Kōk Türks is well manifested in the stone head of Kül Tegin, an Ashina general of the Second Türk Khaghanate. According to the Russian anthropologist Oshanin, the Kōk Türks spread the 'Mongoloid' phenotype to Central Asia (Oshanin 1964: 20).

16 The *Jiu Tangshu* lists the Qarluq and Chuyue among the tribes of the Western Türks (*Jiu Tangshu* 194b.5179; *Xin Tangshu* 217b.6143).

17 For instance, in the *Jiu Tangshu* (194b.5190), Wuzhile[i] (烏質勒), a Türgesh chief, is described as being from 'a separate stock of the Western Türks (西突厥之別種)'.

18 The Khazars are referred to as 'Tujue Hesa (突厥曷薩)' in the *Xin Tangshu* (221b.6247). Thus, the Khazars may well have been an offshoot of the Western Türks.

the Eastern Türks and play an important role in medieval Central Asian history, had probably incorporated some indigenous, non-Turkic elements of the Kazakh steppes. The *Jiu Tangshu* (194b.5179) writes that the language of the Western Türks was 'slightly different' from that of their eastern counterpart.

Interestingly, the Chinese histories refer to some obscure nomadic tribes residing beyond northern Mongolia as Tujue, i.e., Kök Türk. These include such tribes as the Muma Tujue (木馬突厥) [Wooden-horse Türk], the Xianyu Tujue (鮮于突厥) and the Niuti Tujue (牛蹄突厥) [Ox-hoof Türk], who resided to the east of the Qirghiz.¹⁹ However, not much is known about them and as to why they were designated as Tujue.²⁰ According to the *Xin Tangshu* (217b.6148), the Doubo (都播), an ancestral tribe of modern Tuvinians, constituted one of the three Muma Tujue tribes, who 'mourn their dead like the Kök Türks'.²¹

The Uighurs

One of the major Tiele tribes that were subdued and ruled by the Kök Türks was the Uighur (Huihe 回紇), who allied with the Qarluq, a Western Türk tribe, and the Basmil, another Tiele tribe, and overthrew the Second Türk Khaghanate in 745 AD. As to the origin and identity of the Uighurs, the Chinese histories describe them as descending from the Xiongnu and previously belonging to the Tiele (*Jiu Tangshu* 195.5195). Importantly, they do not associate or identify the Uighurs with the Kök Türks. For instance, whereas the Shatuo tribe is referred to as 'a separate tribe of the Western Tujue' in the *Xin Tangshu* (218.6153), no such mention is made regarding the origin of the Uighurs. In fact, the Uighurs themselves viewed the Kök Türks as aliens,²² just as the latter had not regarded the Uighurs and Tiele (referred to as Toquz Oghuz in the Orkhon inscriptions) as Türks.²³

19 For the Muma Tujue, see *Xin Tangshu* (217b.6148). For the Xianyu Tujue and Niuti Tujue, see *Xin Wudaishi* (73.907).

20 It is not clear whether or not these Tujue tribes were indeed Kök Türks. Denis Sinor suggests that they were the Kök Türks 'living outside the Türk state' or '[not belonging] to the ruling stratum of the Türk state' (Sinor 1985: 152–7).

21 '送葬哭泣，與突厥同' (*Xin Tangshu*, 217b.6144).

22 For instance, in their official inscriptions, the Uighurs (Uyğur) use the term *Türük* only for the Kök Türks, whom they consider to be their enemies and oppressors. See Tekin (1983: 46 (text), 49 (trans.)); see lines 9–10 (north side) of the Šine-Usu inscription (Moriyasu *et al.* 2009: 11 (text), 24 (trans.)).

23 For instance, see lines 11–14 (east side) of the Kül Tegin inscription translated in Silay (1996: 4).

The Qirghiz

The Qirghiz, who destroyed the Uighur Khaganate in 840 AD, were centred in the upper Yenisei region, not in the Mongolian steppes. According to the *You yang za zu*, written by Duan Chengshi in the ninth century AD, the Qirghiz regarded themselves as progenies of a god and a cow:²⁴

The Jiankun (堅昆) [Qirghiz] tribe, [unlike the Türks], is not of wolf descent. Their ancestors were born in a cave located to the north of the Quman Mountain. They themselves say that in the ancient times there was a god who mated with a cow in that cave. The people's hair is yellow, eyes are green, and beards are red.

The Qirghiz are distinguished from the Uighurs and other Tiele tribes in Chinese histories. The *Xin Tangshu*, which provides detailed information on the Qirghiz and the Tiele tribes, does not include the former among the latter (*Xin Tangshu* 217b.6139–6145). In addition, while the *Xin Tangshu* states that 'their language and script were identical to those of the Uighurs (其文字言語，與回鶻正同)' (*Xin Tangshu* 217b.6148), it also notes the peculiar physical phenotype of the Qirghiz. The *Xin Tangshu* relates: 'The people are all tall and big and have red hair, white faces, and green eyes (人皆長大，赤髮、皙面、綠瞳)' (*Xin Tangshu*, 217b.6147).²⁵ According to the *Xin Tangshu*, their neighbouring tribe named Boma (駁馬) or Bila (弊剌) resembled the Qirghiz, although their language was different (*Xin Tangshu* 217b.6146). This may imply that the Qirghiz were originally a non-Turkic people²⁶ who became Turkicized during the Kōk Türk period at least partly through inter-tribal marriages. The *Xin Tangshu* relates that 'the Kōk Türks sent women as wives for the [Qirghiz]

24 '堅昆部落非狼種，其先所生之窟在曲漫山北。自謂上代有神與牯牛交於此窟。其人髮黃，目綠，赤髭髯。' Duan Chengshi 段成式. *You yang za zu* 酉陽雜俎 [Miscellany of Youyang], chapter 4. <https://archive.org/stream/06047413.cn#page/n120/mode/2up> (accessed 16 July 2017).

25 Gardizī, a mid eleventh-century Persian historian and geographer, also writes in his work that the Qirghiz were characterised by their 'reddishness of hair and whiteness of skin' because they were originally Slavs (*Saqlāb*). See 'Abd al-Hayy ibn Zāḥḥāk Gardizī (1984: 557): for an English translation of this text, see Martineez (1982: 126).

26 On the origin of the Qirghiz, see Golden (1992: 177–8). While Golden acknowledges that the Qirghiz may have been a 'Turkicised' people, Michael R. Drompp (1999: 399–400) refutes this idea and argues that whether the Qirghiz were 'originally' a Turkic people or a 'Turkicised' people would never be determined. However, genetic studies show that the Qirghiz were most likely a non-Turkic people by origin.

chiefs (突厥以女妻其酋豪)' (*Xin Tangshu*, 217b.6149). In the case of Are (阿熱), the Qirghiz ruler who destroyed the Uighur Khaganate, his wife was a Qarluq woman, while his mother was a Türgesh (*Xin Tangshu* 217b.6149). In addition, the *Xin Tangshu* relates that the Qirghiz 'intermixed with the Dingling (其種雜丁零)' (*Xin Tangshu* 217b.6146–47). At any rate, the (red-haired) Qirghiz 'found dark hair ominous (以黑髮為不祥)' and 'regarded those with black eyes as descending from [Li] Ling (李陵)', a Chinese general who had defected to the Xiongnu.²⁷

The Önggüt and the Naiman

From the collapse of the Uighur Khaganate in the mid ninth century AD to the rise of the Mongols in the early thirteenth century AD, the nomadic peoples of the Mongolian steppes remained largely divided and were loosely controlled by the Khitan Liao (907–1125 AD) and the Jurchen Jin (1115–1234 AD). During this period, there was an increase of Mongolic elements in the Mongolian steppes (Golden 1992: 284). The Turkic tribes that were still present in the Mongolian steppes at the turn of the thirteenth century included the Önggüt and the Naiman. The Önggüt were probably descended from the Chuyue, the above-mentioned Western Tujue tribe. The *Yuanshi* states that the chief of the Önggüt, Alawusi Tijihuli (阿剌兀思剔吉忽裏), who submitted to Chinggis Khan in 1203, was 'a descendant of the Shatuo-yanmen (沙陀雁門之後)' (*Yuanshi* 118.2923). In turn, the *Xin Tangshu* relates that the Shatuo (沙陀) were 'a progeny of the Chuyue, a separate tribe of the Western Tujue (西突厥別部處月種也)' ('Alā' al-Dīn 'Aṭā Malik Juvaynī 1958: vol. 1, 55–6).²⁸ The origin of the Naiman is not well documented. However, one may speculate that the Naiman were an offshoot of the Uighurs. The name of the Naiman ruler before their defeat by Chinggis Khan was Inanch Bilgä Bügü Khan according to Rashīd al-Dīn Hamadānī (1247–1318) (Rashīd al-Dīn Faḡlallāh Hamadānī 1988: vol. 1, 97–98; Rashiduddin Fazlullah 1998–99: vol. 1, 69). In fact, Bügü Khan was the legendary founder of the Uighurs, who was born of two parent-trees.²⁹ Inanch Bilgä Bügü Khan was named after the Uighur progenitor Bügü Khan maybe because the Naiman also viewed the latter as their ancestor.

27 '以黑髮為不祥。黑瞳者，必曰陵苗裔也。' (*Xin Tangshu* 217b.6147).

28 According to the *Xin Tangshu* (218.6153), the Chuyue acquired the name 'Shatuo Türk' after residing near a great desert called Shatuo.

29 See 'Alā' al-Dīn 'Aṭā Malik Juvaynī (1958: vol. 1, 55–57): A similar legend of Bügü Khan was also recorded by Yu Ji in the *Gaochang wang shi xun bei* 高昌王世勳碑 [The monumental inscription of the king of Gaochang]: see Su Tianjue (1965: vol. 2, 259). For a detailed

In addition, the Naiman used the Uighur script, which was later adopted by the Mongols.³⁰ Perhaps their relatedness was one of the reasons why the Naiman and the Uighur tribes had special ties in the Uzbek Khanate of Khiva (1511–1804 AD). In the *Firdaws al-Iqbāl*, a history of the Qunghrat Uzbek Dynasty (1804–1920 AD), the two are described as friend (*dūst*) tribes (Shīr Muḥammad Mirāb Mūnīs & Muḥammad Rīzā Mirāb Āgahī 1988: 103).³¹ As to the physiognomy of the Önggüt and the Naiman, Rashīd al-Dīn relates that the former ‘resembled the Mongols (*bi-mughūl mānand*)’ (Rashīd al-Dīn Faẓlallāh Hamadānī 1988: Vol. 1, 99; Rashiduddin Fazlullah 1998–99: Vol. 1, 70) and that the girls (*dukhtarān*) of the latter were ‘renowned for their beauty and comeliness (*bi-ḥusn va jamāl mashhūr bāshand*)’ (Rashīd al-Dīn Faẓlallāh Hamadānī 1988: Vol. 1, 99; Rashiduddin Fazlullah 1998–99: Vol. 1, 70).

The Qipchaq

The Qipchaq were a Turkic group that formed the dominant nomadic confederation in the Qipchaq Steppe (Kazakh and Black Sea steppes) from the mid eleventh century to the early thirteenth century AD. After being conquered by the Mongols, some of them served the Chinggisids as auxiliary forces in the Yuan Dynasty (1271–1368 AD). The Chinese histories do not provide substantial information on the Turkic tribes of the Qipchaq Steppe but the *Yuanshi* (c. 1370s AD) offers interesting information on the origin of the Qipchaq clan Ölberli³² in the biography (*liezhuan* 列傳) of the Yuan general Tutuha (土土哈):

Tuotuoha's ancestors were originally the tribe of the Andahan Mountain, by the Zhelian River, north of Wuping. At first Quchu migrated to the north-west, to the mountain called Yüliboli, by which they named their

discussion of the Qocho Uighur foundation myths involving a parent-tree, see Okada (1987: 197–201).

30 After defeating the Naiman, Chinggis Khan hired Tatatonga 塔塔統阿, who was an Uighur scholar (傳) serving the Naiman khan, to teach his sons in the Uighur script (*Yuanshi* 124.3048).

31 According to Yuri Bregel, the Naiman and Uighur tribes in Khiva were regarded as sharing ‘common ancestors’ and were ‘related with marriage’: see Shīr Muḥammad Mirāb Mūnīs & Muḥammad Rīzā Mirāb Āgahī (1999: 548 n107). Abū al-Ghāzī Bahādur Khan (r. 1644–63), the Chinggisid ruler of the Uzbek Khanate of Khiva, also notes their friendly relations in his work: see Aboul-Ghāzī Béhādur Khān (1970: 185 (text), 195 (trans.)).

32 Both Omeljan Pritsak (1982: 336–9) and Peter Golden (1988: 22) support a Mongolic origin of the Ölberli clan.

clan, and they called their state Qinchā (Qipchaq). Its territory is 30,000 *li* away from China. The summer nights are extremely short. The sun rises as soon as it sets. Quchū begat Suomona. Suomona begat Yinasi. They were kings of the Qinchā from generation to generation.³³

Concerning the physiognomy of the Qipchaq tribe, the *Zizhi tongjian houbian* [Later compilation to the comprehensive mirror to aid in government], a seventeenth-century continuation of Sima Guang's *Zizhi tongjian* by Xu Qianxue, states that they had 'blue eyes and red hair' (青目赤髮).³⁴

The Muslim Depiction of Turkic Peoples

From the eleventh century onwards, Islamic Central Asia and the Qipchaq Steppe replaced the Mongolian steppes and eastern Inner Asia as the main regions for the activities of the Turkic nomads. Unlike Chinese historians, who reserved *Tuǰue* (*Türk* in Turkic) for the Kōk Türks, Muslim writers used the term *Turk* broadly to denote not only the Turkic-speaking peoples, but also other non-Turkic peoples. However, like Chinese historians, Muslim writers in general depict the 'Turks' as possessing East Asian physiognomy. For instance, Sharaf al-Zamān Ṭāhir Marvazī describes them as being 'short, with small eyes, nostrils, and mouths' (1942: 53–4, 156).³⁵ Similarly, Ṭabarī (d. 923) depicts the 'Turks' as being 'full-faced with small eyes' (1987: 21). In his *Qābūs-nāma*, the eleventh-century Ziyarid ruler Kai Kā'ūs also describes the 'Turks' as possessing 'a large head (*sar-i buzurg*), a broad face (*rūy-i pahn*), narrow eyes (*chashmhā-i tang*), and a flat nose (*bīnī-i pakhch*), and displeasing lips and teeth (*lab va dandān na nikū*)' (Kai Kā'ūs ibn Iskandar 1951a: 103; 1951b: 64). The Arab historian and geographer al-Mas'ūdī (896–956) writes that the Oghuz Turks³⁶ residing in

33 '土土哈，其先本武平北折連川按答罕山部族，自曲出徙居西北玉裡伯裡山，因為氏，號其國曰欽察。其地去中國三萬餘里，夏夜極短，日暫沒即出。曲出生唆末納，唆末納生亦納思，世為欽察國王' (*Yuanshi* 128.3131).

34 Xu Qianxue 徐乾學, *Zizhi tongjian houbian* 資治通鑑後編, chapter 141: http://skqs.guoxuedashi.com/wen_562r/1559.html (accessed 16 July 2017). However, E. Bretschneider (1876: 174, n301) argues that the Qipchaqs are confused with the Russians here. According to the Russian anthropologist L.V. Oshanin (1964: 24, 32), the 'Mongoloid' phenotype, characteristic of modern Kazakhs and Qirghiz, prevails among the skulls of the Qipchaq and Pecheneg nomads found in the kurgans in eastern Ukraine.

35 An Arabic geographical manuscript states that the Uighurs (Toquz Oghuz), the people of China, and the Turks resembled each other in facial appearance: see Frye (1949: 92–3).

36 The Oghuz were a nomadic group that inhabited the Aral Sea and Caspian Sea steppes during the ninth and tenth centuries AD.

Yengi-kent, a town near the mouth of the Syr Darya, 'are distinguished from other Turks by their valour, their slanted eyes, and the smallness of their stature' (*wa hum ashadd al-Turk ba'san wa aqşaruhum wa aşgharuhum a'yunan wa fi al-Turk man huwa aqşar min hā'ulā'*) (al-Mas'ūdī 1962–: Vol. 1, 212).³⁷ However, Muslim writers later differentiated the Oghuz Turks from other Turks in terms of physiognomy. Rashīd al-Dīn writes that 'because of the climate their features gradually changed into those of Tajiks. Since they were not Tajiks, the Tajik peoples called them *turkmān*, i.e. Turk-like (*Turk-mānand*)' (Rashīd al-Dīn Faẓlallāh Hamadānī 1988: Vol. 1, 35–6; Rashiduddin Fazlullah 1998–99: Vol. 1, 31). Ḥāfiẓ Tanīsh Mīr Muḥammad Bukhārī (d. c. 1549) also relates that after the Oghuz came to Transoxiana and Iran, their 'Turkic face did not remain as it was' (1983: fol. 17a (text), Vol. 1, 61 (trans.)). Abū al-Ghāzī Bahadur Khan similarly writes that 'their chin started to become narrow, their eyes started to become large, their faces started to become small, and their noses started to become big' after five or six generations (Abu-l-Gazi 1958: 42 (text), 57 (trans.); Ebūlgazī Bahadır Han 1975: 57–8). As a matter of fact, the mixed nature of the Ottomans, belonging to the Oghuz Turkic group, is noted by the Ottoman historian Muṣṭafā 'Ālī (1541–1600). In his *Kūnhū'l-aḥbār*, he remarks that the Ottoman elites of the sixteenth century were of mostly of non-Turkic origin: 'Most of the inhabitants of Rum are of confused ethnic origin. Among its notables there are few whose lineage does not go back to a convert to Islam ...' (*Ekser-i sükkān-i vilāyet-i Rūm meclis-i muḥteliṭ ul-mefhūm olub ā'yānında az kimsene bulunur ki nesebi bir müslüm-i cedīde muntehī olmaya*) (Fleischer 1986: 254; Muṣṭafā 'Ālī, *Kūnhū'l-aḥbār* 1860–68: Vol. 1, 16).

In sum, the official Chinese histories, which provide substantial information on the origins, identity and physiognomy of the early and medieval Turkic-speaking peoples, do not describe the latter, including the Tiele, the Qirghiz, and the Kōk Türks, among others, as having a single origin. Neither do they describe the early and medieval Turkic peoples as sharing a common (Turkic) identity. Furthermore, the Chinese histories depict the Turkic peoples as possessing Inner Asian phenotypic traits in general with a number of exceptions (see Table 1).

In the following section, we will discuss how genetic surveys corroborate or complement the Chinese historical records on the origins, identity, and physiognomy of the early and medieval Turkic peoples.

37 The stone heads of the Seljuk princes kept at the New York Metropolitan Museum of Art show that the Oghuz possessed Inner Asian physiognomy. For images of the Seljuk stone heads, see Canby *et al.* (2016: 44–46, 50).

TABLE 1 *The Turkic peoples as described in the Chinese and Muslim sources*

	Their origin	Their physiognomy	Their possible (modern) descendants
Xiongnu	Descendants of Chun Wei from the Xia Dynasty	(Not differentiated from that of Han Chinese)	Various Turkic peoples and Mongols
Jie Xiongnu	A separate branch of the Xiongnu	Described as possessing 'deep-set eyes', 'high nose bridges' and 'heavy facial hair'	
Dingling/ Tiele	The remnants of the ancient Chidi; The descendants of the Xiongnu; A separate stock of the Xiongnu	(Not differentiated from that of Han Chinese)	Various Turkic peoples, including Sakhas, Tuvinians, Western Yugurs and Buryats, among others
Kök Türks	A separate tribe of the Xiongnu; The Suo state located to the north of the Xiongnu; The mixed barbarians of Pingliang	Non-Sogdian (<i>huren</i> 胡人) looking	Various Turkic peoples, including Tuvinians
Uighurs	Tiele (non-Kök Türks); The descendants of the Xiongnu	(Not differentiated from that of Han Chinese)	Western Yugurs and Xinjiang Uighurs, among others
Yenisei Qirghiz	(Non-Tiele); (Non-Kök Türks)	Described as being 'tall and big' and as having 'red hair', 'white faces' and 'green eyes'	Tien Shan Qirghiz, Khakass and southern Altaians, among others
Önggüt	A separate tribe of the Western Tujue (Türks)	Described as 'resembling the Mongols'	Kazakhs and Mongols, among others
Qipchaq	The tribe of the Andahan Mountain, north of Wuping (Ölberli Qipchaq)	Described as possessing 'blue eyes and red hair' (in a 17th-century source)	Kazakhs, Uzbeks, and Crimean and Volga Tatars, among others
'Turks' in Muslim sources	Descendants of Japheth, son of Noah	Described as being 'short, with small eyes, nostrils, and mouths' or 'full-faced with small eyes'	Various Inner Eurasian peoples

Genetic Surveys on the Turkic Peoples

The Genetic Variation of Modern Turkic Populations

The Y chromosome is one of the two gender-determining chromosomes that makes a person male. It is inherited from a man by his sons, who then pass it on to their sons largely intact throughout time³⁸ until it develops a mutation. When a mutation, which is a permanent structural alteration in the DNA sequence, occurs, a man with that mutation will then pass it along to all of his male descendants. Over time, such mutations accumulate, which allow us to trace relatedness in groups of people.

The male group or patrilineal lineage that shares a certain mutation is called a Y-DNA haplogroup (see Figure 1). In other words, a haplogroup is a population descended from a common ancestor who had and passed on a specific mutation. Population geneticists have categorised human Y-DNA into over 20 major groups, with many sub-groups,³⁹ to which all males belong.

FIGURE 1
Simplified Y-DNA haplogroup tree.

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- 38 Every person has 22 matching pairs of chromosomes, but the 23rd pair, the x and y gender chromosomes, are unmatched and they determine one's maleness (xy) or femaleness (xx). A large portion of the Y chromosome does not exchange material with the x chromosome.
- 39 A Y-DNA haplogroup is defined by the presence of one or more Y-DNA mutations called Single Nucleotide Polymorphism, or SNP. For instance, haplogroup C is defined by a mutation named M216 and others. The Y Chromosome Consortium (YCC), a scholarship group formed to standardize haplogroup nomenclature, named Y-DNA haplogroups using the capital letters A through T and their subclades using numbers and lower case letters. When a new SNP is discovered and tested, a new haplogroup subclade is determined. For the most up-to-date version of the Y-DNA haplogroup nomenclature and Y-SNP tree, see <http://www.isogg.org/tree>. For introductory studies of the Y-chromosome DNA haplogroups, see Y Chromosome Consortium (2002); Hammer & Zegura (2002); Karafet *et al.* (2008); Chiaroni *et al.* (2009).

MAP 1 Dominant Y-DNA haplogroups in different world regions.

In general, different populations show different Y-chromosome DNA haplogroup compositions and frequencies.⁴⁰ For instance, the most common Y-chromosome haplogroups among the Arabic-speaking peoples are haplogroups J and E. The most common Y-chromosome haplogroups among Africans, western Europeans and East Asians are haplogroup E, haplogroup R1b and haplogroup O, respectively. Among the Native Americans and the Inuit people, haplogroup Q prevails. Haplogroup C2 (formerly known as C3) is most characteristic to Mongolic, Turkic and Tungusic, that is, the 'Altaic'-speaking populations (see Map 1).

Interestingly, the dominant Y-DNA haplogroups among various modern Turkic populations are not uniform, and neither are their haplogroup compositions.⁴¹ While they may share certain haplogroups, the frequencies of these haplogroups vary in general. This means that various Turkic populations, including the Sakhas (inhabiting northeastern Siberia), the Tuvinians (residing

40 For the origins of modern human populations based on the study of Y-chromosomes, see Underhill *et al.* (2001); Jobling & Tyler-Smith (2003).

41 This study is concerned with the Y-chromosome DNA, i.e., the paternal ancestry, not the mitochondrial DNA, i.e., the maternal ancestry, of the Turkic peoples. One should note that Turkic peoples can be differentiated more readily by their Y-chromosome DNA than by their mitochondrial DNA. For instance, the Turkic Tuvinians and Sojots and the Mongolic Buryats are not very distinguishable from each other when it comes to their maternal ancestry since they all share similar mitochondrial DNA haplogroups. See Derenko *et al.* (2003: table 3).

MAP 2 *Turkic peoples and their dominant Y-DNA haplogroups.*

in the Sayan Mountains region), the Altaians (various groups residing in the Russian Altai Mountains region), the Volga Tatars (residing in the Volga-Ural region), the Xinjiang Uighurs and the Uzbeks (inhabiting the Central Asian oasis regions), the Kazakhs (inhabiting the Central Asian steppe region), the Turkmen (residing in the Karakum Desert region), the Azeris (residing in the Caucasus region) and the Turks (inhabiting Anatolia and the Balkans), are not made up of homogeneous patrilineal lineages (see Map 2 and Table 2).⁴²

42 Contemporary states in Inner Eurasia cannot readily use genetics to make nationalist claims since DNA analysis challenges nationalist paradigms that tend to emphasise the autochthonous development or homogeneity of a nation. For instance, mainstream Kazakh scholarship emphasises the lineal descent of the Kazakhs from the Indo-European pastoralists who resided in the Kazakh Steppe in the Bronze Age (characterised by haplogroup R1a1), while downplaying the later Mongol contribution to the ethnic makeup of the Kazakhs. However, DNA analysis shows that the most prevalent Y-DNA haplogroups among the Kazakhs are haplogroups C2 and O, among others, that they share with the Mongols and eastern Inner Asian Turkic peoples. Importantly, it is unlikely that the Turkic-speaking Central and Inner Asian states will make 'pan-Turkic' claims using genetics since DNA analysis points to their heterogeneity, not their homogeneity. At the same time, the main author of this article suspects that the collection and presentation of genetic data can be influenced by historical or political claims although this suspicion cannot be proven. Interestingly, according to the DNA data of the Manchus provided in some Chinese studies, the presence of Y-DNA haplogroup O2b, which appears at high frequency among the Japanese and Koreans but is virtually absent among the Han Chinese, is rather minimal among the Manchus. However, O2b reaches 27~34% among the Manchus in the Japanese and Korean DNA surveys. For the Manchu Y-DNA haplogroups, see Katoh *et al.* (2005: table 1); Jin *et al.* (2010: table 4).

TABLE 2 *The Y-DNA haplogroups of modern Turkic peoples*

	Their Y-DNA haplogroups (percentage)	Their possible most recent ancestral groups
Sakhas	N (89~94%); C2 (2.1~3.6%)	Quriqan (Tiele)
Tuvinians	N (42.2~45.1%); C2 (16.1~26.5%); Q (4.9~13.9%); R1a1 (7.8~12.3%)	Muma Tujue (Türks) Tiele
Khakass	N (50%); R1a1 (35.2%); Q (4%); C (1.1%)	Yenisei Qirghiz, among others
Southern Altaians (Altai-Kizhi)	R1a1 (50%); C2 (20%); Q (16.7%); N (4.2%)	Yenisei Qirghiz, among others
Tien Shan Qirghiz (Kyrgyz)	R1a1 (over 60%); C2 (12~20%); O (0~15%); N (0~4.5%)	Yenisei Qirghiz, among others
Western Yugurs	C2 (21.2~30%); D (19.2%); O3 (34.6%); Q (15%); R1a1 (1.9~7%)	Ancient Uighurs, among others
Kazakhs	C2 (59.7~78%); O (11~26%)	Qipchaqs and Mongols, among others
Argyn	G1 (57.7%)	
Qipchaq (Karakypshak)	R1b (63.6%)	
Naiman	C2 (63%); O3 (61.2%)	
Karakalpaks	C2 (31.5%); G (26%); R1a1 (9.26%); N (7.4%) among the On Tört Uruw grouping; R1a1 (29.6%); N (22.2%); C2 (20.4%); Q (11.1%) among the Qonghrat grouping	Qipchaqs and Mongols, among others
Xinjiang Uighurs	R1a1 (21~28.6%); J (18.4~27%); O3 (12.2~17%); C2 (6.1~18%); N (0~4.1%)	Ancient Uighurs and Bronze Age Indo-European pastoralists, among others
Uzbeks	R1a1 (17.6~32%); J (5.9~21.4%); C2 (7~18%, 41.2%); O3 (0~12%); N (0~5.9%)	Various Turkic and Iranic groups, and Shibanid Uzbeks, among others
Volga Tatars	R1a1 (20.8~34.1%); N (23.1~28.3%); I (4~13.2%); J (15.1%); C (1.6~5.7%)	Various Turkic, Slavic, and Uralic groups
Chuvashes	R1a1 (29.5~31.6%); N (27~28%); J (15.9%); I (11.4%); C (0~1.3%)	Various Turkic, Slavic, and Uralic groups
Bashkirs	N (3~65%); R1a1 (9~48%); R1b (0~84%); C (0~17%); J (0~8%); I (0~2%)	Various Turkic, Slavic, and Uralic groups

TABLE 2 *The Y-DNA haplogroups of modern Turkic peoples (cont.)*

	Their Y-DNA haplogroups (percentage)	Their possible most recent ancestral groups
Turkmens	Q (33.8~42.6%); J (14.3~17.6%); R1a1 (14.5~16.2%); L (4~5.8%); G (4~5.7%); E (4.3~5.4%); N and O (2.9~9.45%); C (0~1.35%) among the Turkmens in Afghanistan and northern Iran Q (73%); H (7%); R1b (5%); R1a1 (4%); G2 (4%); N (2~4%); J (2~4%); C2 (1~2%) among the Turkmens in Karakalpakstan (I) R1a1 (72.5%); N (3.9%) among the Turkmens in Karakalpakstan (II) L (57%); J (13%); Q (13%); E (10%); N (3%) among the Afshar Turkmen villagers in Turkey	Oghuz/Turkmens, among others
Azeris	J (31%); G (18%); E (6%) among the Azeris in Azerbaijan J (27.2%); R1a1 (19.0%); R1b (17.5%); E (11.1%); G (8%); T (7.9%); Q (4.8%); N (1.6%) among the Azeris in northeastern Iran	Oghuz/Turkmens and various indigenous groups
Turks	J (33.5%); R1b (15.86%); E (11.3%); G (10.9%); R1a1 (6.9%); I (5.3%); L (4.2%); N (3.8%); Q (1.9%); C (1.3%); O (0.2%)	Oghuz/Turkmens and various indigenous groups

The Sakhas, formerly known as Yakuts, are the easternmost as well as northernmost Turkic people in the world. They were originally a horse-riding people from the western Baikal region.⁴³ It is believed that the Sakhas descend from the Quriqan (Tokarev 1962: 107; Golden 1992: 143–4, 415), which was a Tiele tribe (see *Jiu Tangshu* 199b.5343). According to recent genetic surveys, the most

43 The funerary rituals of the pre-modern Sakhas were similar to those of the Turkic peoples of the western Baikal region and of the ancient Xiongnu (Crubézy *et al.* 2010: 8, 9–10).

typical Y-chromosome haplogroups of the Sakhas and their frequencies are as follows: N1c1 (89~94%) and C2 (2.1~3.6%) (Pakendorf *et al.* 2006: 346, table 6: N-TatC corresponds to N1c1; Kharkov *et al.* 2008: 200, table 1: N3a corresponds to N1c1). Haplogroup N1c1 is widespread among the Uralic peoples and Turkic peoples. Haplogroup N originated in East Asia and approximately 8000–10,000 years ago spread from Siberia into eastern/northern Europe (Hong Shi *et al.* 2013). It is present in northeastern Europe at high frequency: 70.9% and 41.3% among eastern Finns and western Finns, respectively (Lappalainen *et al.* 2008: table 1), and 43% and 17% in northern Russia and central Russia, respectively (Balanovsky *et al.* 2008: 242, table 2). C2 is the major haplogroup of the Mongols, Kazakhs, and Evenks, who belong to the proposed Altaic language family (for the Evenks, see Pakendorf *et al.* 2007: 1017, table 5: C-M217 and its subclades C-M48 and C-M86 correspond to C2; for the Mongols and Kazakhs, see Wells *et al.* 2001: 10245, table 1: M130 and M48 correspond to haplogroup C2; Zerjal *et al.* 2002: 474, table 3: haplogroups 10 and 36 correspond to haplogroup C2).

In northwestern Mongolia and the Sayan Mountains region, now reside the Tuvinians. Perhaps, they are the descendants of the Tiele and/or Muma Tujue (Türks), one of whose three tribes was Doubo (Tuva). The major Y-chromosome haplogroups of the Tuvinians and their frequencies are as follows: N subclades N1c1 and N1b (42.2~45.1%), C2 (16.1~26.5%), Q (4.9~13.9%), and R1a1 (7.8~12.3%) (Gubina *et al.* 2013: 339, table 3; see Kharkov *et al.* 2013: 1239. C3 in this article corresponds to C2). The frequencies of each haplogroup may vary depending on the surveys with different samples, but the above two recent surveys show that haplogroups N and C2 are the most prevalent paternal lineages among the Tuvinians. Haplogroups N and C2 are also the main paternal clans among the Buryats (see Kharkov *et al.* 2014: 183, table 1), who are the neighbouring Mongolic people of the Tuvinians.⁴⁴ Haplogroup Q, which is found across Eurasia, is present at significant frequency among the Turkmens, two Siberian peoples (Yeniseian Kets and Uralic Selkups at 93.7% and 66.4%, respectively) (Tambets *et al.* 2004: 667, table 3), and the Native Americans (at over 90%).⁴⁵ Haplogroup R1a1, more specifically, its subclade R1a1a1b2 (defined by mutation Z93), is the genetic marker of the Indo-European pastoralists, who migrated from modern-day Ukraine to modern-day Iran, India, the Kazakh

44 However, the two groups possess different subclades of N and C2, which means that they have distinct paternal origins.

45 According to genetic studies, the Native Americans descend from a migrant group from the Altai Mountains region. See e.g. Dulik *et al.* (2012: 229–46; Malyarchuk *et al.* 2011: 583–8).

steppes, the Tarim Basin, the Altai Mountains region, the Yenisei River region, and western Mongolia during the Bronze Age.⁴⁶

Naturally, R1a1, more specifically, its subclade R1a1a1b2 (R1a-Z93), occurs at high frequency among the Turkic peoples now residing in the Yenisei River and the Altai Mountains regions in Russia. Compared to the Tuvians, the Khakass (whose name was created by the Soviets from Xiajiasi (黠戛斯), a Chinese name for Qirghiz, since they were regarded as descending from the Qirghiz) have noticeably higher percentages of R1a1 (35.2%) and much lower percentages of haplogroups C (1.1%) and Q (4%). However, N is also the most prevalent haplogroup (50%) of the Khakass (Gubina *et al.* 2013: 339, table 3; Shi *et al.* 2013: table 3). As for the Altaians, the Altai-Kizhi (southern Altaians)⁴⁷ are characterised by a high percentage of R1a1 (50%) and low to moderate percentages of C2 (20%), Q (16.7%) and N (4.2%) (Dulik *et al.* 2012: 234, table 2). The major differences between the Khakass and the southern Altaians are the lower frequency of haplogroup N (in another study, haplogroup N is found at high frequency (32%) among the Altaians in general: see Gubina *et al.* 2013: 329, 339) and the higher frequencies of haplogroups C2 and Q among the latter.

The descent of the Qirghiz (Kyrgyz) of the Tien Shan Mountains region (Kyrgyzstan) from the Yenisei Qirghiz is debated among historians.⁴⁸ However, among the modern Turkic peoples, the former have the highest percentage of R1a1 (over 60%). Since the West Eurasian physiognomy of the Yenisei Qirghiz recorded in the *Xin Tangshu* was in all likelihood a reflection of their Eurasian Indo-European marker R1a1a1b2 (R1a-Z93), one may conjecture that the Tien Shan Qirghiz (Kyrgyz) received their R1a1 marker from the Yenisei Qirghiz.⁴⁹ That is, the former are descended from the latter. The other Y-chromosome

46 On this point, see Semino *et al.* (2000: 1156: M17 or Eu19 in this article corresponds to R1a1); Zerjal *et al.* (2002: 477–8, table 3: haplogroup 3 corresponds to haplogroup R1a1); Keyser *et al.* (2009: 406–9); Li *et al.* (2010: 9–10).

47 The Altaians have been divided into northern and southern groups based on linguistic, cultural and anthropological traits. According to genetic research, the northern Altaians are closer to Yeniseian, Ugric and Samoyedic speakers, while the southern Altaians are closer to their neighbouring Turkic groups. The southern Altaians and the Tien Shan Qirghiz (Kyrgyz) share recent common ancestry with each other. The northern Altaians in general exhibit relatively higher frequencies of haplogroups N and Q and lower frequencies of C2 and R1a1 in comparison to the southern Altaians. See Dulik *et al.* (2012: 234).

48 On this issue, see Golden (1992: 404–6). For a study that acknowledges their connection, see Bernshtam (1962: 119–28).

49 According to a major study of haplogroup R1a1, the Kyrgyz mostly carry the R1a1 subclade R1a-Z2125, a subgroup of R1a-Z93 that is rare among the Khakass. See Underhill *et al.* (2014:

haplogroups found among the Qirghiz (Kyrgyz) are C2 (12~20%), O (0~15%) and N (0~4.5%).⁵⁰ The lack of haplogroup Q among the Qirghiz (Kyrgyz) mostly distinguishes them from the Altaians.

The Western Yugurs residing in Gansu Province, China, are descended from the remnants of the ancient Uighurs (Golden 1992: 409). Their major Y-chromosome haplogroups are C2 (21.2~30%), D (19.2%), O3 (34.6%), and Q (15%).⁵¹ Haplogroup D is the genetic marker of the Tibetans (Shi *et al.* 2008: 5, table 2), while haplogroup O3 is that of East Asians (Xue *et al.* 2005: table 1). Haplogroup O3 is also found among various Mongolic and Turkic groups at moderate frequency.⁵² The low frequency of haplogroup R1a1 (1.9~7%) among the Western Yugurs differentiates them from the Qirghiz (Kyrgyz) and the Altaians.

Haplogroup C2 (formerly known as C3) reaches its highest frequency among the Kazakhs (66~73.7% among the Kazakhs of Kazakhstan,⁵³ 75.47% among the Kazakhs of Xinjiang (Zhong *et al.* 2010: figure 1), 78% among the Kazakhs of Karakalpakstan (Balaesque *et al.* 2015: supplementary figure 1) and 59.7% among the Kazakhs of the Altai Republic in Russia (Dulik *et al.* 2011, 2–3, tables 1 & 2)), whose ancestors include the Qipchaqs and other Turkic groups, and the Mongols, among others. However, some Kazakh tribes, divided into the Senior Horde (*Ulu Jüz*), the Middle Horde (*Orta Jüz*), and the Lesser or Junior Horde (*Kishi Jüz*), have their own representative Y-chromosome haplogroups. Among the Naiman, belonging to the Middle Horde, haplogroups C2 and O3 are the most common.⁵⁴ Among the Argyn, another Middle Horde tribe, haplogroup

table S4). This means that if the Khakass are the true descendants of the Yenisei Qirghiz, the Kyrgyz may not be the direct descendants of the latter.

- 50 See Wells *et al.* (2001: 10245, table 1: M17, M130, M46, M175 and 122, and M48 correspond to haplogroup R1a1, C2, N1c1, O, and C2b1b1, respectively); Zerjal *et al.* (2002 474, table 3: haplogroups 3, 10, 13, 16, and 36 correspond to haplogroups R1a1, C2, O3, N1c1, and C2b1a2, respectively); Balaesque *et al.* (2015: supplementary figure 1); Di Cristofaro *et al.* (2013: figure S7).
- 51 See Zhou *et al.* (2008: 202, figure 2); Xu & Wen (2017: 69).
- 52 For the Mongols, see e.g. Katoh *et al.* (2005: 66, table 1). For the Kazakhs, see e.g. Dulik *et al.* (2011: 2–3, tables 1 & 2).
- 53 Wells *et al.* (2001: 10245, table 1: M130 and M48 correspond to haplogroup C2); Zerjal *et al.* (2002: 474, table 3: haplogroups 10 and 36 correspond to haplogroup C2).
- 54 For haplogroup C2, see Zhabagin *et al.* (2017: table S1). For haplogroup O, see Sabitov (2013: 35). A survey shows that haplogroup O3 accounts for over 50% of the tested samples. See haplotypes 1–41, which make up 61.2% of all tested haplotypes in Tarlykov *et al.* (2013: 21, table 2). An online haplogroup predictor has been used to determine the haplogroup of the given Naiman haplotypes.

G1-M285, which is believed to have originated in West Iran,⁵⁵ is found at high frequency (57.7%). The Qipchaq (Karakypshak) tribe, another Middle Horde tribe, is characterised by the R1b subclade R1b1a1a1 (R1b-M73) (63.6%).⁵⁶ This is a rare haplogroup that appears at moderate to high frequency only among this Kazakh tribe and some Turkic groups of the Altai Mountains region (35.3% among the Kumandin: Dulik *et al.* 2012: 234, table 2), among others. In general, the Kazakhs are characterised by a high frequency of haplogroup C2 and a low frequency of haplogroup R1a1, which differentiates them from the Qirghiz (Kyrgyz) and the southern Altaians. The Karakalpaks, a Qipchaq Turkic-speaking people residing in western Uzbekistan, exhibit a set of haplogroups similar to those of the Kazakhs with relatively lower frequency of haplogroup C2 and higher frequency of haplogroups N and R1a1: C2 (31.5%), G (26%), R1a1 (9.26%), and N1b and N1c1 (7.4%) among the On Tört Uruw grouping; R1a1 (29.6%), N1b and N1c1 (22.2%), C2 (20.4%), and Q (11.1%) among the Qonghrat grouping (Balaresque *et al.* 2015: supplementary figure 1).

Compared to those of Inner Asian nomadic origins, the Turkic peoples who descend from both the nomadic and sedentary populations of the Central Asian oasis regions, i.e. Transoxiana and the Tarim Basin (which roughly correspond to modern-day Uzbekistan and southern Xinjiang, respectively), have more diverse sets of representative haplogroups. The Xinjiang Uighurs, who descend from both the ancient Indo-Europeans and the ancient Turkic Uighurs (Golden 1992: 409), exhibit haplogroups R1a1 (21~28.6%), J (18.4~27%), O3 (12.2~17%), C2 (6.1~18%), and N (0~4.1%).⁵⁷ The modern Uzbeks, who also descend from the ancient Indo-European (Iranic) populations and various Inner Asian nomadic peoples (Golden 1992: 407), including the Shibanid Uzbeks,⁵⁸ exhibit a set of haplogroups similar to those of the Xinjiang Uighurs: R1a1

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- 55 Haplogroup G, mostly its subclade G2, is found at low frequencies in Europe, North Africa, the Middle East and South Asia, and at high frequency in the Caucasus region. G1 is mainly found in Iran and Kazakhstan. For a detailed study of haplogroup G1-M285, see Balanovsky *et al.* (2015).
 - 56 Sabitov (2013: 35). A different subclade of R1b, haplogroup R1b1a1a2 (R1b-M269), is the genetic marker of Western Europeans, reaching 85.4% among the Irish people. For its distribution among different European populations, see Balaresque *et al.* (2010: table 1).
 - 57 Zhou *et al.* (2008: 202, figure 2). See Wells *et al.* (2001: 10245, table 1: M17, M130, M46, M172, M175 and 122, and M48 correspond to haplogroups R1a1, C2, N1c1, J, O, and C2b1b1, respectively); and see Zerjal *et al.* (2002: 474, table 3: haplogroups 3, 9, 10, 13, 16, and 36 correspond to haplogroups R1a1, J, C2, O3, N1c1, and C2b1b1, respectively).
 - 58 The Shibanid Uzbeks were a Turkic nomadic people who conquered the Turkic and sedentary Iranic populations of Transoxiana at the turn of the sixteenth century. Importantly, the Shibanid Uzbeks and the Kazakhs were one and the same people inhabiting the

(17.6~32%), J (5.9~21.4%), C2 (7~18%, 41.2%⁵⁹), O3 (0~12%) and N (0~5.9%).⁶⁰ Haplogroup J is a patrilineal lineage originating in the Middle East and probably reached Central Asia with Neolithic farmers from the Middle East.⁶¹ As to haplogroup R1a1 among the modern-day Uzbeks and Xinjiang Uighurs, the extent to which it originated from the Bronze Age Indo-European pastoralists and from the Turkic and Turkicized Inner Asian nomadic groups, respectively, remains open to speculation. Haplogroups O3, C2, and N were in all likelihood brought to Transoxiana by various Turkic and Mongolic peoples.⁶²

The Qipchaq Turkic-speaking Volga Tatars and the Oghuric Turkic-speaking Chuvashes inhabiting the Volga-Ural region are characterised by high frequencies of haplogroups R1a1 (20.8~34.1% and 29.5~31.6%, respectively) and N (both N1c1 and N1b subclades) (23.1~28.3% and 27~28%, respectively) according to some surveys. Haplogroups J (15.1% and 15.9%, respectively), I (4~13.2% and 11.4%, respectively), and C (1.6~5.7% and 0~1.3%, respectively) are also found among the Volga Tatars and the Chuvashes (Trofimova *et al.* 2015: table 1; Tambets *et al.* 2004: 667, table 3). The Bashkirs, another Qipchaq Turkic-speaking people of the Volga-Ural region, are also characterised by the high presence of haplogroups N1c1 (3~65%) and R1a1 (9~48%). R1b subclades R1b1a1a1 (R1b-M73) (0~55%) and R1b1a1a2 (R1b-M269) (0~84%),⁶³ C (0~17%), J (0~8%), and I (0~2%) also make up the genetic composition of the Bashkirs.⁶⁴

Kazakh Steppe prior to their division in the sixteenth century. On this point, see Lee (2016: 121–39).

- 59 This high frequency of C2 is found among an Uzbek group residing in Afghanistan. We are inclined to think that this group is descended from the nomadic Uzbeks from the Qipchaq Steppe (Haber *et al.* 2012: table S4).
- 60 See Wells *et al.* (2001: 10245, table 1: M17, M130, M46, M172, M175 and 122, and M48 correspond to haplogroups R1a1, C2, N1c1, J, O, and C2b1b1, respectively); Zerjal *et al.* (2002: 474, table 3: haplogroups 3, 9, 10, 13, 16, and 36 correspond to haplogroups R1a1, J, C2, O3, N1c1, and C2b1b1, respectively); Haber *et al.* (2012: table S4). According to another recent survey, the Uzbeks of Afghanistan exhibit R1a1 (29%), J (18%), Q (8.6%), C (4%), N (4%), R1b1a1a1 (3%), R2 (3%) and O (2.3%); see Di Cristofaro *et al.* (2013: figure S7).
- 61 Zerjal *et al.* (2002: 476–7: haplogroup 9 in corresponds to haplogroup J). On the spread of haplogroup J to Europe from the Neolithic period, see Semino *et al.* (2004).
- 62 The higher frequency of haplogroup O3 among the Xinjiang Uighurs may reflect the contribution of Han Chinese.
- 63 As mentioned above, R1b-M269 is the genetic marker of Western Europeans, whereas R1b-M73 is a lineage found at moderate to high frequency only among some Turkic groups in Inner Eurasia.
- 64 The frequency of each haplogroup varies depending on geographic regions. R1b1a1a1 (R1b-M73) is found at high frequency (55% and 19%) in Abzelilovsky District and Burzyansky District, respectively, but elsewhere it is virtually absent (Lobov 2009: 15, table 5; Trofimova

However, it is difficult to assess the extent of the Turkic and non-Turkic genetic contributions to these groups with the given data. In the surveys discussed above, haplogroup R1a1 has not been classified into its subclade R1a1a1b1a (R1a-Z282), which prevails among East Slavs, and subclade R1a1a1b2 (R1a-Z93), which spread across Eurasia by the Bronze Age Indo-European (Iranic) pastoralists and is carried by various modern-day Turkic groups.⁶⁵ One should also note that haplogroup N, found among the Turkic peoples of the Volga-Ural region and Central Asia, has 'a common Siberian genetic background of Finno-Ugric and Turkic tribes' (Khusnutdinova *et al.* 2008: 378).

Unlike the Turkic peoples of Kazakhstan, Tatarstan and Bashkortostan, who speak the Qipchaq Turkic language, the Turkmens, the Azeris and the Anatolian Turks speak the Oghuz Turkic languages. The Turkmens descend from the Oghuz, a Turkic nomadic group that inhabited the Aral Sea and Caspian Sea steppes during the ninth and tenth centuries AD.⁶⁶ The founders of the Seljuk and Ottoman empires belonged to this Turkic group. According to DNA testing of the Turkmens living in (Jawzjan) Afghanistan and northern Iran, they belong to haplogroups Q (33.8~42.6%), J (14.3~17.6%), R1a1 (14.5~16.2%), L (4~5.8%),⁶⁷ G (4~5.7%), N and O (2.9~9.45%), E (4.3~5.4%),

et al. 2015: table 1). The Y-chromosomes of the Crimean Tatars have not been studied in detail. However, according to a survey, the Crimean Tatars residing in Uzbekistan exhibit haplogroups I (5%), J (14%), R1a1 (32%), C (9%) and O (10%) (Wells *et al.* 2001: 10245, table 1: M17, M130, M46, M172, M175 and 122, and M48 correspond to haplogroup R1a1, C2, N1c1, J, O and C2b1b1, respectively). According to Brian Glyn Williams (2001), most Crimean Tatars of today descend from indigenous sedentary elements. While the nomadic Tatars were closer to the Kazakhs in terms of physiognomy and spoke a Qipchaq Turkic dialect, the sedentary elements in the Crimea, who descend from ancient Goths, Greeks, Italians, Armenians and Alans, among others, exhibit West Eurasian physiognomy and speak a mixed Turkic or an Oghuz Turkic dialect like the Turks of Anatolia. According to another study, some Tatars of Mokhshi, the present-day Narovchat village in Penza Region, belong to haplogroups J, L and Q (Sabitov & Akchurin 2014: 5–13). Haplogroup L is mainly concentrated in South Asia.

- 65 As a matter of fact, according to the study of R1a1 by Underhill *et al.*, the Tatars of Bashkortostan and the Chuvashes do not carry R1a1a1b2 (R1a-Z93) at all. Concerning the Tatars of Tatarstan, 64% of their R1a1 belong to R1a1a1b1a (R1a-Z282). See Underhill *et al.* (2014: table S4). This implies that the source population of the Tatar and Chuvash R1a1 is East Slavs.
- 66 It has been suggested that the Turkmens were formed from the Turkic groups who inter-mixed with the Iranic peoples of Central Asia. See Barthold (1962: 80–81); Agadzhanov & Karryev (1978: 171).
- 67 Haplogroup L is a South Asian lineage, found at significant frequencies in South Asia, but at low frequencies in the Middle East, Europe and Central Asia. For its frequency in India and elsewhere, see Sengupta *et al.* (2006: tables 5, 6 & 7).

and C (0–1.35%) (Grugni *et al.* 2012: 7, table 1; Di Cristofaro *et al.* 2013: 5–7, figure S7). While one may attribute Inner Asian origin to haplogroups Q, N, C, and O, it is difficult to determine to what extent haplogroup R1a1 (R1a-Z93) is from Inner Asia, since it is also carried by Iranic-speaking peoples such as modern Iranians (Persians) (4.5–20.3%) (Grugni *et al.* 2012: 7, table 1) and Pashtuns (51.2–56.3%) (Di Cristofaro *et al.* 2013: 5–7, figure S7; Haber *et al.* 2012: table S4).⁶⁸ At any rate, haplogroup Q also dominates the gene pool of the Turkmens living in Uzbekistan (Karakalpakstan). More specifically, the Turkmens mostly belonging to the Yomud tribe exhibit haplogroups Q (73%), H (7%),⁶⁹ R1b1a1a1 (R1b-M73) (5%), R1a1 (4%), G2 (4%), N (2–4%), J (2–4%), and C2 (1–2%) (Skhalyakho *et al.* 2016: 88). Therefore, one may assume that haplogroup Q is the most prevalent lineage among the Turkmens.⁷⁰

Finally, the Turks of the Republic of Turkey, a successor state to the Ottoman empire, show the highest haplogroup diversity according to an extensive survey of Anatolian Turkish Y-chromosome variation. Their major haplogroups are those common in the Near East and Europe (Cinnioğlu *et al.* 2004: 130, figure 2): J (33.5%), R1b (15.86%, including R1b-M73, which makes up 0.76% of the Turkish R1b) (Cinnioğlu *et al.* 2004: 130), E (11.3%), G (10.9%), R1a1 (6.9%), I (5.3%) and L (4.2%). Haplogroups I, more specifically its subclade I2 (formerly I1b), is most common in the Balkans, reaching its highest incidences among the Croats and Bosnians.⁷¹ Importantly, haplogroups N (3.8%), Q (1.9%), C (1.3%), and O (0.2%), which must have come from or via Central and Inner Asia, make up less than 10% of the total population (Cinnioğlu *et al.* 2004: 135).⁷² The

68 One should note that among the Turkmen tribes, the Tekke, for instance, are of (captive) Iranian origin. See Golden (1992: 400).

69 Haplogroup H is a South Asian lineage, found at significant frequencies in South Asia.

70 Interestingly, another survey reveals that the Turkmens living in Karakalpakstan are characterised by high presence of haplogroup R1a1 (72.5%) and minimal or non-existence of haplogroups N (3.9%) and Q (0%) (Balaesque *et al.* 2015: supplementary figure 1). A survey of the Afshar Turkmen villagers in Turkey offers a different picture of the Turkmen haplogroups. They are as follows: L (57%), J (13%), Q (13%), E (10%) and N (3%) (Gökçümen 2008: 125–9). In another Turkish village, the frequency of haplogroup N is 23% (Gökçümen 2008: 134).

71 The most common Turkish I subclade is I2 (formerly I1b) (Cinnioğlu *et al.* 2004: 134). For the frequencies of I2 in the Balkans, see Rootsi *et al.* (2004: 130, table 1).

72 According to the study of R1a1 by Underhill *et al.*, about 57% and 43% of the Turkish R1a1 belong to R1a1a1b2 (R1a-Z93) and R1a1a1b1a (R1a-Z282), respectively. See Underhill *et al.* (2014: table S4). One should note that many of the Turkish men belonging to R1a1a1b2 (R1a-Z93), as well as haplogroup J, may be of Central Asian origin. Then the Central and Inner Asian contribution to the modern Turkish gene pool may be greater than suggested in Cinnioğlu *et al.*'s study. According to an admixture analysis of modern-day Anatolian Turks, Central Asian male contribution to the Turkish gene pool is 13% (see Berkman &

Y-chromosome haplogroup composition of another Oghuz Turkic-speaking nation, the Azeris, is somewhat similar to that of the Anatolian Turks: J (31%), G (mostly G2) (18%), and E (6%) (Nasidze *et al.* 2003: table 2). The same holds true for that of the Azeris of northeastern Iran: J (27.2%), R1a1 (19.0%), R1b (17.5%), E (11.1%), G2 (8%), T (7.9%),⁷³ Q (4.8%), and N (1.6%) (Grugni *et al.* 2012: table 1).

In sum, although they share certain haplogroups, modern Turkic populations exhibit dissimilar sets of Y-chromosome haplogroups with different representative haplogroups. The most prevalent haplogroups among different Turkic peoples are as follows: (1) N1c1 among the Sakhas residing in northeastern Siberia; (2) N (both N1b and N1c1), C2, Q, and R1a1 among the Tuvinians residing in the Sayan Mountains region; (3) R1a1 and C2 among the southern Altaians and the Qirghiz (Kyrgyz) from the Altai Mountains and the Tien Shan Mountains regions, respectively; (4) N and R1a1 among the Khakass from the Yenisei River regions; (5) R1a1 (mainly R1a-Z282), N, R1b (mainly R1b-M269), J, and I among the Turkic peoples of the Volga-Ural region; (6) R1a1, J, O3, and C2 among the Xinjiang Uighurs and the Uzbeks residing in the Central Asian oasis regions; (7) C2, O3, and G1 among the Kazakhs residing in the Inner Asian steppes; (8) Q, J, and R1a1 among various Turkmen groups; (9) J, R1b (R1b-M269), E, and G2 among the Turks and the Azeris residing in Anatolia and the Caucasus region, respectively. Such diversity implies that the Turkic peoples living in different regions have heterogeneous paternal origins and that they include linguistically Turkicised indigenous elements. This also indicates that the Turkicisation of many areas of Eurasia did not necessarily involve mass migrations of Turkic peoples.

Analysis of Ancient DNA

Importantly, studies of ancient DNA extracted from human skeletal remains reveal that the early and medieval Turkic-speaking peoples also possessed diverse sets of haplogroups. DNA analysis of the remains of 62 specimens excavated from a Xiongnu elite cemetery in the Egin Gol valley reveals that the Xiongnu possessed haplogroups N1c1, Q, and C (Petkovski 2006: 114, 138–40).⁷⁴

Togan 2009: 2344–5). A study of autosomal chromosomes shows that Central Asian contribution ranges from 9% to 15% (see Hodoğlugil & Mahley 2012: 138–9).

73 Haplogroup T is a rare but geographically widespread lineage observed in the Middle East, Europe, India and East Africa.

74 For haplogroup N1c1, see Keyser-Tracqui *et al.* (2004: 326). Analysis of the mitochondrial DNA, which is maternally inherited, shows that the Xiongnu remains from this Egin Gol necropolis consist mainly of Asian lineages (89%). West Eurasian lineages make

According to the DNA study of three human remains from another Xiongnu cemetery in Duurlig Nars in northeastern Mongolia, one specimen belonged to haplogroup C and the other to haplogroup R1a1 (Kim *et al.* 2010).⁷⁵ Interestingly, the Chinese geneticists who studied the DNA in the human remains from the pre-Xiongnu and Xiongnu periods conclude that haplogroup Q was the major Xiongnu lineage: four male samples from the Eastern Zhou period (770–221 BC) buried in Pengyang, China, carry haplogroup Q (Zhao *et al.* 2010: 218). However, the authors do not clearly state that these samples were Xiongnu. Another Chinese study found only haplogroup Q among the human remains from Barköl, Xinjiang, China. The authors of this Chinese study suggest that the Xiongnu spoke a Yeniseian language, since haplogroup Q is mostly found in Yeniseian and Native American peoples (Kang *et al.* 2013).⁷⁶ If the samples studied by the Chinese geneticists are indeed Xiongnu remains, it appears that haplogroups C and Q were the most common Xiongnu patrilineal lineages.

While it may be safe to assume that haplogroup R1a1 was not a major Xiongnu lineage, it probably constituted the majority of the nomads residing in the Altai Mountains during the Bronze Age. A study of 14 human specimens excavated in the westernmost Mongolian Altai Mountains shows that the Bronze Age nomads of the Altai Mountains belonged to haplogroups R1a1a1b2 (R1a-Z93) (44.45%), Q subclade Q1a2a1-L54 (44.45%) and C (11.12%) (Hollard *et al.* 2014: 201, table 1).⁷⁷

One should note here that the above-discussed genetic makeup of the Xiongnu and their neighbouring Altaian nomads, who were probably incorporated into the Xiongnu confederation, corroborates the Xiongnu phenotypical characteristics depicted in Chinese histories. It is likely that the Inner Asian-looking Xiongnu mostly belonged to Y-chromosome haplogroups C2, Q, and N, while the West Eurasian-looking Jie probably belonged to Y-chromosome

up the rest (11%) (Keyser-Tracqui *et al.* (2003: 258). However, according to a more recent study of ancient human remains from central Mongolia, the Xiongnu population in central Mongolia possessed a higher frequency of western mitochondrial DNA haplotypes (37.5%) than the Xiongnu from the Egyin Gol necropolis (Rogers 2016: 78).

- 75 Kwang-Ho Lee, one of the main Korean authors of this work, commented in an interview that the carrier of haplogroup R1a1 was a slave buried with his Xiongnu master. The same author also revealed in another work published in Korean that haplogroups C (30%) and O (33.3%) are the two major lineages to which the Xiongnu skeletons he studied belong (Lee 2006: 129).
- 76 The Kets, who speak a Yeniseian language, exhibit the highest frequency of haplogroup Q (93.7%) in Eurasia (Tambets *et al.* 2004: 667, table 3).
- 77 Analysis of mitochondrial DNA shows that the ancient Altaian samples carried both West and East Eurasian matrilineal lineages (Hollard *et al.* 2014: 203).

haplogroup R1a1. Alternatively, if the Jie, 'a separate branch of the Xiongnu', who founded the Later Zhao Dynasty (319–351 AD), were indeed a Yeniseian-speaking people, they may have been carriers of haplogroup Q and resembled modern-day Kets of Siberia.

During the Bronze Age and early Iron Age, the Yenisei River region was inhabited by Indo-Europeans. The DNA study of 26 ancient human specimens from the Krasnoyarsk area dated from the middle of the second millennium BC to the fourth century AD shows that the Yenisei pastoralists mostly belonged to haplogroup R1a1 (Keyser *et al.* 2009: 401, table 3). The high frequency of R1a1 among the modern-day Qirghiz (Kyrgyz) and Altaians may thus prove that they are descended from the Yenisei Qirghiz. In addition, this may explain the reason why medieval Chinese histories depict the Qirghiz as possessing West Eurasian physiognomy.⁷⁸

The medieval Sakhas were characterised by haplogroup N1c1 like their modern descendants. The analysis of the Y-chromosome DNA extracted from 58 mummified frozen bodies dating from the fifteenth to the nineteenth centuries shows that haplogroup N1c1 accounts for 61% of the Sakha male samples (38% of the samples were unidentifiable. See Crubézy *et al.* 2010: 2). This indicates that the Turkic nomads inhabiting the west Baikal region⁷⁹ around the fifteenth century and earlier were also characterised by haplogroup N, perhaps like modern-day Tuvinians. If the Sakhas are indeed descended from the Quriqan, a Tiele tribe, it may be that the official Chinese histories differentiated between the Yenisei Qirghiz and the Dingling/Tiele because the two were distinct peoples, perhaps characterised by haplogroup R1a1 and haplogroup N, respectively.⁸⁰

78 In turn, the Inner Asian physiognomy of the modern-day Qirghiz (Tien Shan Kyrgyz) may be explained by their moderate frequency of Y-chromosome haplogroups C2 (about 20%) and N and their high frequencies of East Eurasian mitochondrial DNA haplogroups (over 70%). The same may hold true for the modern Khakass, who are also considered to be the descendants of the Yenisei Qirghiz. As discussed above, they exhibit high frequencies of Y-chromosome haplogroup N (about 50%) and East Asian mitochondrial DNA haplogroups (75.8%). For the Qirghiz, see Comas *et al.* (2004: 498, table 1); for the Khakass, see Zakharov *et al.* (2004: 24, tables 1 & 2).

79 It has even been suggested that the Sakhas left their original area of settlement in the Baikal region due to Mongol pressure: see Pakendorf *et al.* (2006: 350).

80 As high as 50% of the medieval Magyars belonged to haplogroup N1c1, according to a Hungarian study of the DNA extracted from tenth-century Magyar skeletons. Although the Magyars were Ugric not Turkic, the fact that they were carriers of N1c1 shows that N1c1 was one of the major Y-chromosome haplogroups of the horse-riding peoples of the Eurasian steppes. For the Magyar N1c1, see Csányi *et al.* (2008: 526).

The Y-chromosomes of the Kōk Türks have not been studied. After the collapse of the Second Türk Khaganate in 745 CE, the Kōk Türks became dispersed and it is difficult to identify their modern descendants. If they were indeed descended from the Saka (*Suo*) or related to the Qirghiz, as the *Zhoushu* states (*Zhoushu* 50.908), the Ashina may have belonged to the R1a1 lineage. Instead, if the Kōk Türks were related to the Muma Tujue (Türks), the former may have been genetically close to the ancestors of modern Tuvinians and characterised by high frequencies of haplogroups N, C2 and Q. As a matter of fact, Chinese geneticists tested the DNA extracted from the remains of a Yuan nobleman, who was probably an Önggüt prince. The Y-chromosome haplogroup of this person was Q (Cui *et al.* 2015: 3, 5–8). Since the Önggüt were probably descended from the Western Türks through the Shatuo tribe, as discussed above, one may speculate that haplogroup Q was one of the Y-chromosome haplogroups carried by the Western Türks.

Like the Kōk Türks, the Y-chromosomes of the Tiele or the ancient Uighurs have not been tested. Yet we may perhaps infer their genetic markers from the DNA testing of the medieval Sakhas, modern-day Western Yugurs, Naimans and Buryats. As discussed above, the Western Yugurs and Naimans are the descendants of the ancient Uighurs and are characterised by moderate to high frequencies of haplogroups C2, O3, and Q and by the absence, or a low frequency, of haplogroup R1a1. The Buryats are viewed by some historians as (at least partly) descending from the Quriqan (e.g. Tokarev 1962: 106–7), a Tiele tribe, like the Sakhas, and are characterised by the high frequencies of haplogroups C2 (40%) and N (48%) (Kharkov *et al.* 2014: 183, table 1). If the Western Yugurs, Naimans, Sakhas, and Buryats, along with the Tuvinians, are the modern descendants of the medieval Tiele, one may assume that the Tiele (or at least the Tiele who resided in Mongolia) were carriers of haplogroups C2, N, O3, and Q, among others.

The mitochondrial DNA extracted from the remains of the Qipchaqs (Cumanians) has been tested by Hungarian geneticists. Interestingly, their study reveals that the Qipchaqs possessed West Eurasian mitochondrial DNA lineages, even though analysis of their skulls shows that the Qipchaq specimens possessed Inner Asian physiognomy (Bogácsi-Szabó *et al.* 2005: 642, 658). The Y-chromosomes of the Qipchaq specimens were not tested in this study. However, the Y-chromosome haplogroup of the medieval Qipchaqs may be inferred from those of their modern descendants among the Kazakhs. As discussed above, the Qipchaq (Karakypshak) tribe belonging to the Kazakh Middle Horde is characterised by a high frequency of R1b1a1a1 (R1b-M73) (Sabitov 2013: 35). This may be the reason why the *Zizhi tongjian houbian* described the medieval Qipchaqs (Qincha 欽察) as possessing ‘blue eyes and

red hair' (*Zizhi tongjian houbian*, chapter 141). Alternatively, we may assume that the modern descendants of the Qipchaqs are the western Kazakhs, belonging to the Lesser Horde, who are characterised by a high frequency of C2 subclade C2b1b1 (formerly known as C3c1). This haplogroup may explain why the Qipchaq crania excavated from the kurgans (burial mounds) of eastern Ukraine possess Inner Asian physiognomy (Oshanin 1964: 24, 32).

The major Y-chromosome haplogroups of the medieval Turkmens may also be inferred from those of their modern descendants, which are haplogroups Q, R1a1, J and N, among others. The presence of haplogroups R1a1 and J among the Turkmens may explain the reason why the medieval Turkmens were described as having lost their original Turkic physiognomy and as becoming Tajik-looking, i.e., sedentary Iranian-looking, by Muslim writers. At the same time, haplogroups Q and N may explain why al-Mas'ūdī wrote that the Oghuz Turks residing in Yengi-kent had 'slanted eyes' and 'diminutive stature' (al-Mas'ūdī 1962–: Vol. 1:212).

In sum, like the modern-day Turkic peoples, the Xiongnu (who had haplogroups C2, Q, N and R1a1), the Sakhas (characterised by haplogroup N), the Yenisei Qirghiz (characterised by haplogroup R1a1), the Tiele (who had haplogroups C2, N, O3, and Q, among others), the Turkmens (who had haplogroups Q, J, R1a1 and N), and the Qipchaqs (who probably had haplogroup R1b1a1a1 (R1b-M73) and C2, among others) possessed different representative haplogroups and exhibited dissimilar haplogroup compositions. It is therefore likely that the early and medieval Turkic peoples themselves did not form a homogeneous entity and that some of them, non-Turkic by origin, had become Turkicised at some point in history. Accordingly, one may also suggest that many of the modern Turkic-speaking populations, who exhibit more diverse haplogroup compositions, are not direct descendants of the early Turkic peoples (Table 3).

On a final note, one should remember that medieval Chinese historians did not classify the Inner Asian tribes into Turkic-speaking and Mongolic-speaking groups. Likewise, Muslim writers generally viewed the Mongols and other non-Turkic Inner Asian tribes as a branch of Turks. Genetic studies corroborate the fact that drawing a clear line between the historical Mongolic peoples and the Turkic peoples is unrealistic, since the two shared such haplogroups as C2, N, Q, O3 and even R1a1. The geneticists who analysed the DNA of the Xiongnu specimens from the Egyin Gol necropolis and that of modern Mongolians suggest that 'the impact of the succession of Turkic and Mongolian confederations on the territory of the current Mongolia was a cultural or linguistic process rather than a migratory and/or genetic one' (Keyser-Tracqui *et al.* 2006: 279). Similarly, a comparative study of the autosomal DNA of the Mongols and the Tsaatan, a Turkic people residing in northern Mongolia, also concludes that

TABLE 3 *The Y-DNA haplogroups of early and medieval Turkic peoples*

	Ancient DNA	The Y-DNA haplogroups of their possible modern descendants
Xiongnu	C2, N, Q, and R1a1, among others	
Sakha	N	
Dingling/Tiele/Uighurs		C2, N, O3, Q, among others (if their modern descendants are Western Yugurs, Naimans, Tuvinians, Sakhas, and Buryats, among others)
Kök Türks		R1a1 (if they were related to Yenisei Qirghiz) Q, among others (if their descendants were Önggüt) N and C2, among others (if their descendants are/were Tuvinians/Muma Tujue (Türks))
Yenisei Qirghiz	R1a1 (the Yenisei Indo-European pastoralists)	R1a1 (Tien Shan Qirghiz)
Önggüt	Q, among others	
Naiman		C3 and O3, among others
Qipchaqs		R1b, among others (if their modern descendants are the Kazakh Kypshak tribe) C2, among others (if their modern descendants are the Kazakhs)
Turkmens		Q, J, R1a1, and N, among others

the two, along with the Sakhas, form the same cluster and are genetically distinct from other world populations (Brissenden *et al.* 2015: 82). Finally, an extensive study of the genetic legacy of the Turkic nomads across Eurasia based on autosomal DNA analysis reveals that the source populations for the Turkic nomads who spread ‘Asian genes’ to non-Turkic peoples were (the ancestors of modern-day) Tuvinians, Mongols and Buryats, despite the fact that the latter two are Mongolic (Yunusbayev *et al.* 2015).⁸¹ In sum, one should note that the early eastern Turkic peoples were in all likelihood genetically closer to their

81 Russian physical anthropologists have already noted that the Xiongnu and Kök Türks, among others, spread the ‘Mongoloid’ phenotype to Central Asia and beyond: see Oshanin (1964: 16–25).

neighbouring Mongolic peoples than to various later Turkic peoples of central and western Eurasia.

Conclusion

In this article, we conducted a comparative analysis of textual information provided in Chinese histories and genetic survey data on the origins, identity and physiognomy of the early and medieval Turkic peoples. As discussed above, the official Chinese histories do not view the Turkic peoples such as the Tiele/Uighur, Kōk Türks (Tujue) and Qirghiz as belonging to a single uniform entity called 'Turks'. Instead, they describe them as forming separate identities. The Chinese histories also depict the Turkic-speaking peoples as typically possessing East/Inner Asian physiognomy, as well as occasionally having West Eurasian physiognomy. DNA studies corroborate such characterisation of the Turkic peoples.⁸² While it is true that insufficient amounts of ancient DNA samples have been studied, one may still infer from the given genetic data that the early and medieval Turkic peoples possessed dissimilar sets of Y-chromosome haplogroups with different representative haplogroups, some of which were of West Eurasian origin. This means that the various Turkic peoples did not have a common patrilineal origin or uniform physiognomy. Notably, the Xiongnu themselves, whether they were a Turkic-speaking entity or not, were a hybrid

82 We are not arguing that certain Y-DNA haplogroups necessarily correlate to certain physiognomies. Y chromosome is simply one of the two gender-determining chromosomes. For instance, we are aware that even though both indigenous Australians and modern-day Mongols are characterised by a high frequency of haplogroup C, the two groups do not share common phenotypes. The physical traits of a certain people can change due to the influence of the environment in the long term and its intermixture with other ethnic groups. However, a correlation can be observed between certain Y-DNA haplogroups and certain phenotypes during the formative period of the Turkic peoples in eastern Inner Eurasia. In general, prior to their intermixture with indigenous peoples of eastern Inner Asia, the carriers of West Eurasian Y-DNA haplogroups (such as R1a1 and R1b) possessed West Eurasian physiognomy, whereas the carriers of East/Inner Eurasian Y-DNA haplogroups possessed East/Inner Eurasian physiognomy. It should be noted that, while a medieval Turkic-speaking group possessing both West Eurasian Y-DNA haplogroups and East Eurasian mitochondrial haplogroups as the result of intermixture could have exhibited 'Inner Asian' physiognomy, like modern-day Qirghiz and Altaians, it is highly unlikely that the peoples (not individuals) described as being 'blue-eyed and red-haired' in the Chinese histories were carriers of East/Inner Eurasian Y-DNA haplogroups.

people composed of carriers of both East and Inner Eurasian haplogroups C2, N, and Q and West Eurasian haplogroup R1a1.

The analysis of genetic survey data on the Turkic peoples also allows us to speculate on the Turkic *Urheimat*. We suggest that it was a geographical region where the carriers of haplogroups C2, N, Q and R1a1 could intermix, since these haplogroups are carried by various past and modern-day Turkic peoples in eastern Inner Asia and the Xiongnu. It has been suggested that the early Turkic peoples probably had contact with Indo-European, Uralic, Yeniseian, and Mongolic groups in their formative period (Golden 2006: 139). As non-linguists, we are unqualified to discuss the origin of the Turkic languages. However, drawing on the findings of DNA studies, we are inclined to think that certain similarities that exist between the Turkic languages and the Mongolic, Tungusic and Uralic languages are at least partly associated with haplogroups C2 and N, among others. More specifically, we conjecture that the Turkic languages came into existence as a result of the fusion of Uralic groups (characterized by a high frequency of haplogroup N subclades) and Proto-Mongolic groups (characterized by a high frequency of haplogroup C2) who also merged with other linguistic groups, including Yeniseian speakers (characterized by a high frequency of haplogroup Q like the Kets) and Indo-European speakers (characterized by a high frequency of haplogroups R1a1).⁸³ The best candidate for the Turkic *Urheimat* would then be northern and western Mongolia and Tuva, where all these haplogroups could have intermingled, rather than eastern and southern Mongolia or the Yenisei River and the Altai Mountains regions in Russia.⁸⁴

Finally, we suggest that the Turkicisation of central and western Eurasia was the product of multiple processes of language diffusion⁸⁵ that involved not

83 It is unlikely that the early Turkic speakers were characterised by a high frequency of haplogroup R1a1a1b2 (R1a-Z93), since the earliest carriers of this haplogroup in South Siberia and Central Asia were Indo-European speakers. It was the carriers of haplogroup R1a1a1b2 who also spread the Indo-European language to South Asia and Iran. Therefore, one may assume that an R1a1a1b2 dominant group were not the earliest Turkic speakers.

84 For a discussion of the Turkic *Urheimat*, see Golden (2006: 138–40).

85 This also implies that conquest and empire-building activities by various Turkic peoples did not play a significant role in the diffusion of genes. The prevalence of indigenous Y-DNA haplogroups among the Turkic populations in central and western Inner Eurasia, as shown in this work, clearly indicates this phenomenon. As a matter of fact, even the Mongol empire, which is the most successful Inner Asian nomadic empire in history, did not diffuse haplogroup C2, the most common Mongol lineage, widely throughout its realm. The famous Y-Chromosome haplotype dubbed ‘star cluster’, which is associated with Chinggis Khan’s lineage, is also found at a noticeable frequency only among some

only originally Turkic-speaking groups, but also Turkicised (Indo-European) groups. That is, the earliest Turkic groups first Turkicised some non-Turkic groups residing in Mongolia and beyond. Then both Turkic and 'Turkicised' groups Turkicised non-Turkic tribes (who were mostly carriers of haplogroups R1a1) residing in the Kazakh steppes and beyond. Through multiple processes, including the Mongol conquest, the members of the extended Turkic entity spread the Turkic languages across Eurasia. They Turkicised various non-Turkic peoples of central and western Eurasia, including those in the Central Asian oases (who were carriers of haplogroups R1a1 and J, among others). Importantly, the Turkmens, who were themselves made up of both original Turkic and Turkicised elements (carriers of haplogroups Q, J, R1a1 and N, among others), reached Anatolia and Turkicised the local populations carrying haplogroups J, R1b, G, E, R1a1 and T, among others, who have now become 'Turks'.

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References

- Beishi* = Li Yanshou (2003).
Hanshu = Ban Gu (1962).
Jinshu = Fang Xuanling (1974).
Jiu Tangshu = Liu Xu (2002).
Shiji = Sima Qian (2003).
Suishu = Wei Zheng (2008).
Weishu = Wei Shou (2003).
Xin Tangshu = Ouyang Xiu & Song Qi (2003).
Xin Wudaishi = Ouyang Xiu (1974).
Yuanshi = Song Lian (2005).
Zhoushu = Linghu Defen (2003).
Zizhi tongjian houbian = Xu Qianxue (N.D.)

peoples of nomadic origin. For this haplotype, see Zerjal *et al.* (2003: 717–21). In all likelihood, the same may hold true for the Kök Türk empire.

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