



DNA Tribes® Digest October 1, 2011
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Introduction

Hello, and welcome to the October 2011 issue of DNA Tribes® Digest. This month’s issue features two articles, one based on STR analysis and one based on SNP analysis.

The first article, “STR Analysis of the Salishan Region,” explores indigenous genetic relationships of the North American Pacific Northwest based on autosomal STR data. The second article, “SNP Analysis of Siberia and Central Asia,” explores possible traces of the Central Asian Oxus and Tarim Civilizations based on autosomal SNP data.

Best regards,
Lucas Martin
DNA Tribes

STR Analysis of the Salishan Region

Background

The Salishan genetic region characterizes indigenous populations of the coastal Pacific Northwest of North America. In particular, this region includes Coast Salish speaking First Nations of present day British Columbia, Canada (see map in **Figure 1**).

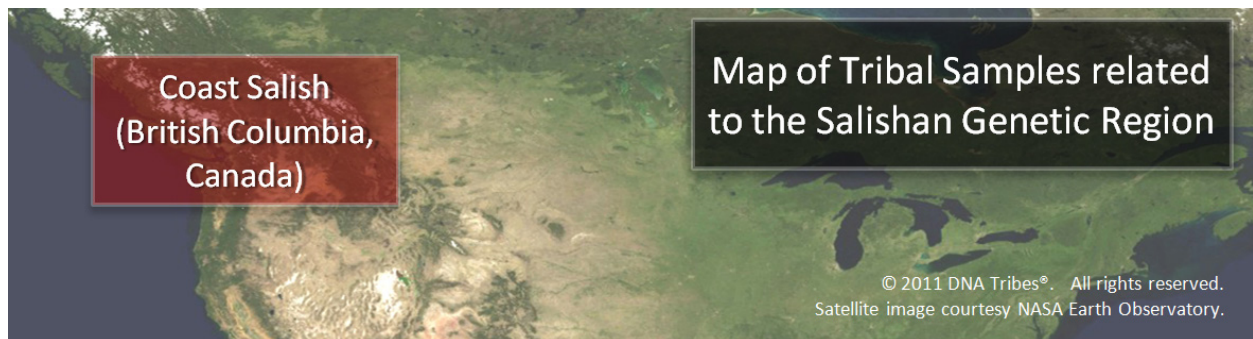


Figure 1: Map of the Salishan genetic region and associated tribal samples in our database.

These coastal territories of North America are located at one corner of the vast Pacific Ocean, linking the Americas by sea with the Pacific Rim of East Asia. Because of its relatively mild oceanic climate and ecological richness of fish, game, and plant life, indigenous peoples of the coastal Pacific Northwest enjoyed some of the highest population densities in North America prior to European contact.

Native communities here established networks of decentralized but complex small scale societies. These communities were often linked by local waterways and spoke a variety of languages, including not only Salishan languages but also Chinook, Haida, Tlingit, Tsimshian, and many others. One custom shared by several cultures in this area is the potlatch, a traditional festival based on gift-giving.

The remarkable cultural and linguistic diversity of the Pacific Northwest also characterized indigenous communities living in the neighboring territories of present day California, where over 300 dialects were spoken. This local linguistic diversity suggests that the Pacific Coast of North America might be home to some of the oldest indigenous populations in the Americas.

Genetic Analysis

Genetic contributions to the Salishan world region were identified based on autosomal STR data.¹ Results are summarized in **Table 1** and illustrated in **Figure 2**.

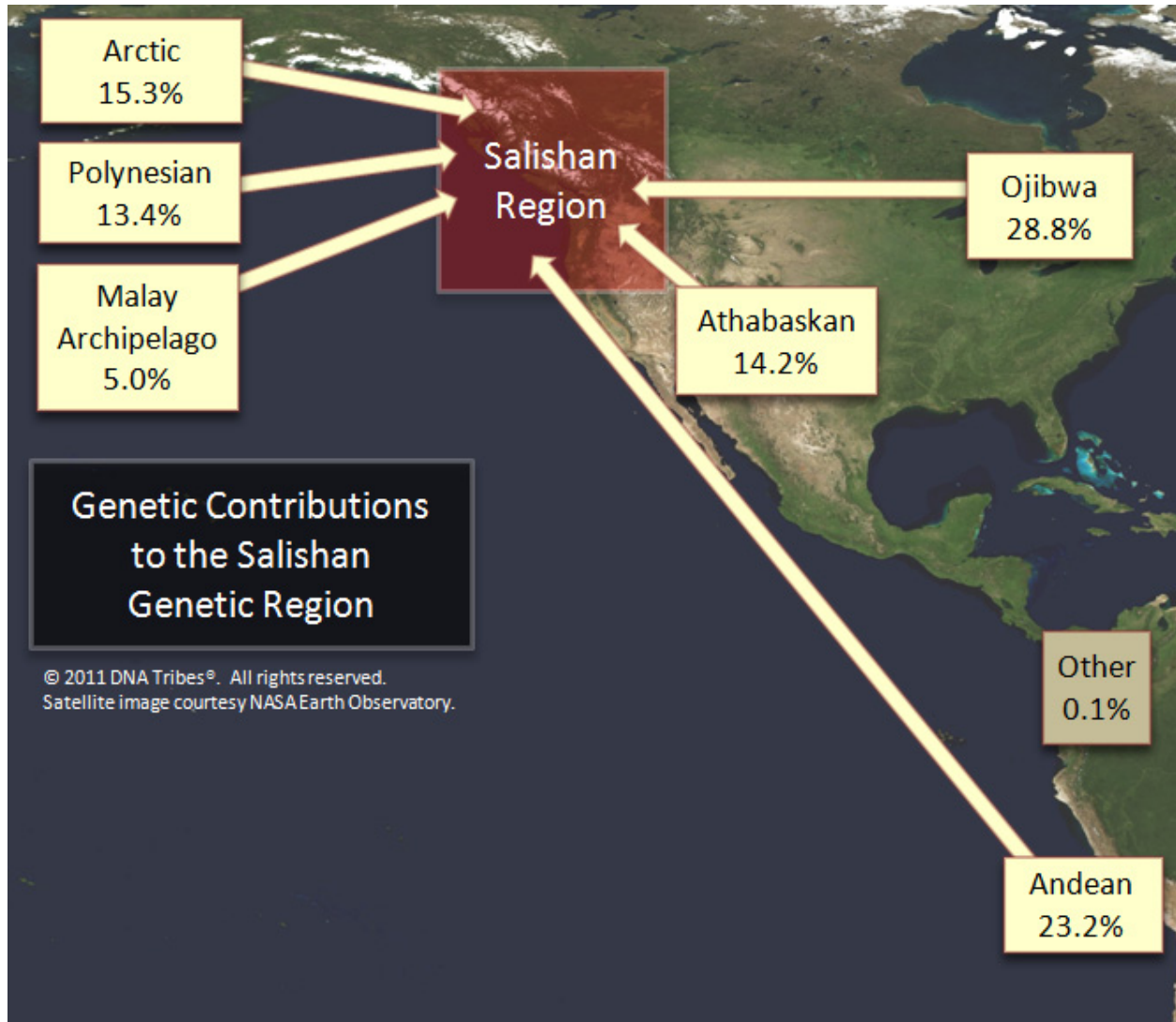


Figure 2: Genetic analysis of the Salishan genetic region based on autosomal STR markers.

¹ A map illustrating the genetic world regions presently identified by DNA Tribes® analysis can be viewed at <http://dnatribes.com/populations.html>.

Discussion: Results indicate genetic links with several world regions, including Native North American regions, as well as regions of South America and the Pacific Ocean.

Native North American links include Ojibwa (28.8%), Arctic (15.3%), and Athabaskan (14.2%), for a total of 58.3% contribution from other North American regions. Results also indicate an additional 23.2% contribution from the Andean region that includes indigenous populations of the western coast of South America.² This Andean genetic link suggests maritime contacts along the Pacific Ocean, possibly associated with early settlement of the Americas and later patterns of interaction.³

In addition, results indicated genetic links with two more distant regions of the Pacific Rim: Polynesian (13.4%) and Malay Archipelago (5.0%). These results suggest the possibility of genetic maritime contacts with Asia and Oceania, possibly along the chain of islands and coastal lands surrounding the Pacific Ocean.

Based on available data, these genetic links with Polynesian and Malay Archipelago populations are specific to Pacific Northwest populations. Notably, these Salishan links with Asian and Pacific regions are distinguished from the Arctic and Far East Siberian genetic links that generally distinguish indigenous North Americans from South American populations.⁴

World Region	Genetic Contribution
Ojibwa	28.8%
Andean	23.2%
Arctic	15.3%
Athabaskan	14.2%
Polynesian	13.4%
Malay Archipelago	5.0%
Other	0.1%

Table 1: Genetic contributions to the Salishan region.

² For more information about indigenous regions of South America, see <http://dnatribes.com/dnatribes-digest-2009-05-30.pdf>.

³ In more recent times, Haida cultures are thought to have engaged in raids over considerable distances.

⁴ See “The Arctic Connection” (page 8) at <http://dnatribes.com/dnatribes-digest-2008-10-25.pdf>.



Getting the Most from Your STR Testing

Once your 15, 21, or 27 Marker Kit STR testing is complete, we offer several options to keep your report current and customize your genetic analysis for the information you want. (*Prices are listed as of October 1, 2011 and are subject to change.*)

Updating Your Analysis:

DNA Tribes® analysis is updated on a periodic basis to include new reference data as well as refinements to our match algorithms and world regions analysis. (A map illustrating current populations and genetic regions is available at <http://dnatribes.com/populations.html>.)

After your testing is complete, your analysis can be updated at any times of your choice for \$24.99 through our secure online checkout at http://dnatribes.com/order_addons.html.

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African Panel: A listing of your DNA match scores for all individual Sub-Saharan African populations in our database.

Central Asian Panel: A listing of your DNA match scores for individual native Central Asian and Siberian populations in our database, also including Roma (European Gypsy) match scores.

East Asian Panel: A listing of your DNA match scores for East Asian populations in our database, including all individual Chinese, Japanese, Korean, and Southeast Asian populations.

Middle Eastern Panel: A listing of your DNA match scores for Middle Eastern populations in our database, including all individual Arab, Berber, Caucasus, Jewish, Persian, and Turkish populations.

Native American Panel: A listing of your DNA match scores for all individual Native American populations in our database.

South Asian Panel: A listing of your DNA match scores for South Asian populations in our database, including all individual populations of Bangladesh, India, Nepal, Pakistan, and Sri Lanka.

Extended Match Results: A comprehensive listing of your DNA match scores for all individual populations in our database.

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DNA Tribes® Europa provides the most detailed and complete analysis of European autosomal genetic structure available. DNA Tribes® Europa provides your DNA match scores for 17 genetic sub-regions of Europe, which is substantially more robust than the individual population matches in Parts B – C of reports and more detailed than the European world regions referenced in Part D of core results.

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Upgrades are available through our secure online checkout system at:
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A library of articles based on DNA Tribes® original ongoing research and analysis of world genetic structure is available free at <http://dnatribes.com/library.html>.

SNP Analysis of Siberia and Central Asia: Traces of the Oxus and Tarim Civilizations

Background

DNA Tribes® SNP is a geographical analysis based on autosomal SNP markers that complements DNA Tribes® STR based 15 Marker, 21 Marker, and 27 Marker Kit tests.⁵ *DNA Tribes® SNP* currently identifies seven continental zones based on our database of SNP samples (see **Figure 3**).

This article will explore genetic links in the Siberia and Central Asia, which has been an ancient meeting place between the civilizations of several continents and home to the mysterious oasis and river based civilizations of the Oxus and Tarim Basin.

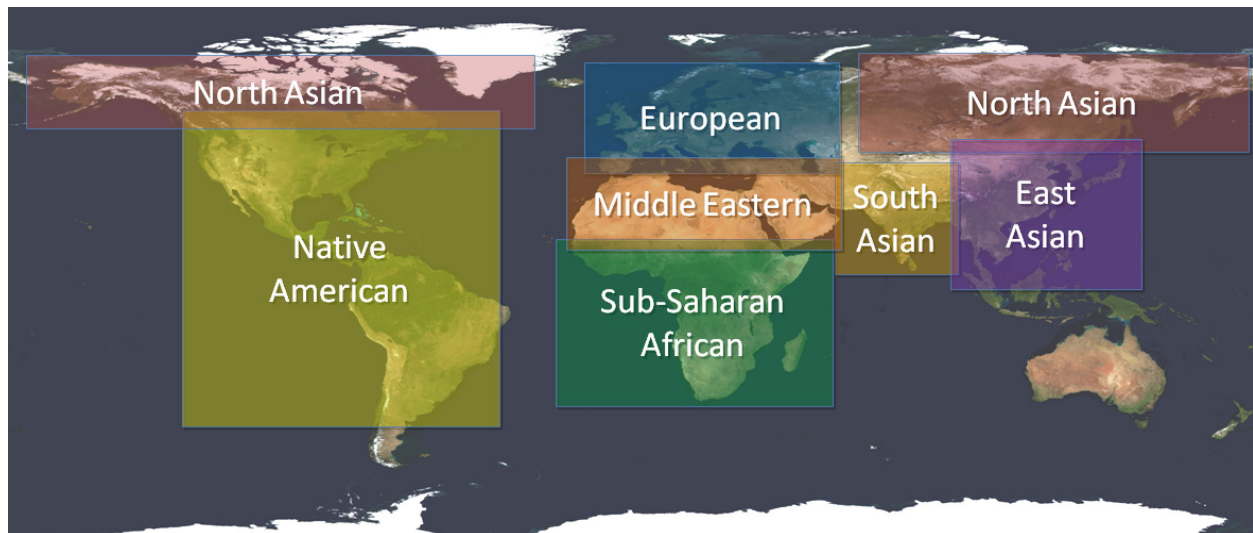


Figure 3: Map of continental zones identified by *DNA Tribes® SNP* analysis.

⁵ For more information about *DNA Tribes® SNP* analysis, see <http://dnatribes.com/snp.html>. For more information about DNA Tribes® STR based 15, 21, and 27 Marker Kit tests, see <http://dnatribes.com/index.html>.

Genetic Analysis

SNP admixture analysis was performed based on seven continental zones for several populations of Siberia and Central Asia. Results are summarized in **Table 2** and illustrated in **Figures 4** and **5**.

Population	North Asian	European	Middle Eastern	South Asian	East Asian	Native Amer.	Sub-Sah. African
Altai (Siberia)	58.5%	12.2%	0.0%	9.7%	17.4%	1.9%	0.2%
Burusho (Pakistan)	1.5%	8.1%	1.0%	86.8%	1.6%	0.9%	0.0%
Buryat (Siberia)	71.2%	0.0%	0.3%	2.9%	25.3%	0.0%	0.2%
Chuvash (European Russia)	22.1%	71.1%	0.0%	5.3%	0.0%	1.4%	0.0%
Dargin (Caucasus)	0.0%	41.9%	31.2%	27.0%	0.0%	0.0%	0.0%
Dolgan (Siberia)	88.7%	7.8%	0.0%	3.3%	0.0%	0.0%	0.2%
Hazara (Pakistan)	24.2%	12.1%	10.4%	29.8%	23.2%	0.2%	0.0%
Ket (Siberia)	76.2%	19.0%	0.0%	1.1%	0.0%	3.6%	0.0%
Kyrgyz (Central Asia)	39.2%	13.3%	4.6%	13.8%	28.7%	0.5%	0.0%
Mongola (China)	33.8%	0.0%	0.6%	0.0%	65.1%	0.5%	0.0%
Monguor (Tu) (China)	13.2%	0.9%	0.0%	3.7%	80.6%	0.8%	0.8%
Selkup (Siberia)	67.3%	28.3%	0.0%	1.4%	0.0%	3.1%	0.0%
Tuvan (Siberia)	77.8%	2.5%	1.2%	1.7%	16.9%	0.0%	0.0%
Uyghur (China)	19.6%	17.0%	8.3%	25.6%	28.2%	1.4%	0.0%
Uzbek (Central Asia)	22.2%	21.8%	12.8%	27.4%	15.3%	0.6%	0.0%

Table 2: Table listing regional admixture components of Siberian and Central Asian populations based on the continental zones currently identified by DNA Tribes® SNP analysis. Central Asian populations near the ancient Oxus and Tarim Basin civilizations are highlighted in red.

Discussion: Results in **Table 2** and **Figure 4** indicated North Asian and European admixture in most surveyed populations. North Asian admixture was highest in Siberian populations, including Turkic speaking Dolgans (88.7%); Yeniseian speaking Kets (76.2%); and Uralic speaking Selkups (67.3%). European admixture was highest in Turkic speaking Chuvashes (71.1%); Nakh-Daghestanian speaking Dargins (41.9%); and Uralic speaking Selkups (28.3%).

These Central Asian and Siberian populations speak multiple languages, the product of cultural expansions from multiple directions. These expansions are thought to include the Mesolithic era spread of Uralic languages (possibly from near the Ural Mountains); the Bronze Age spread of Indo-European languages (possibly from near the Black Sea); and the Migration Period and medieval spread of Turkic languages (possibly from near Mongolia).

Despite this variety of languages, most surveyed populations share North Asian and European genetic characteristics, which characterize cultures living near the Siberian taiga and Eurasian steppe. This continues further south into Central Asian populations, such as Uzbeks, Uyghur, and Kyrgyz. However, Central Asian populations are characterized by another pattern of genetic links, possibly inherited from the ancient oasis civilizations of the Oxus and Tarim Basin, which will be explored next in this article.

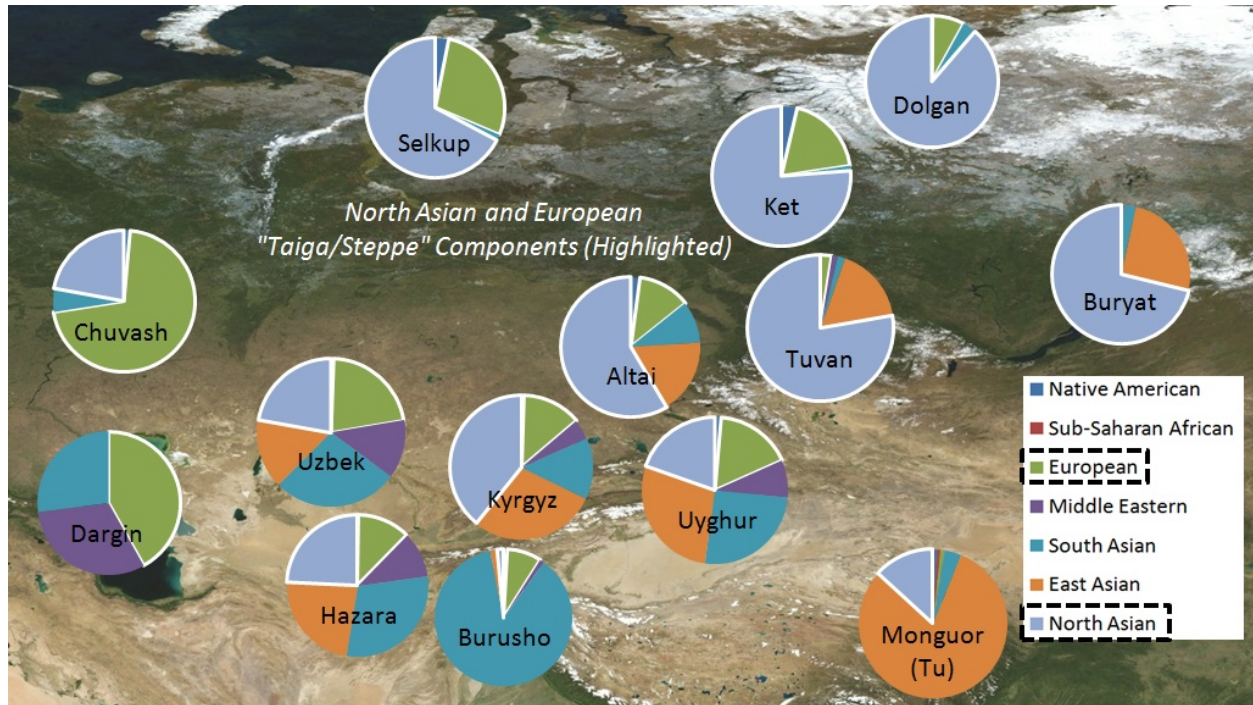


Figure 4: Map illustrating regional admixture components of Siberian and Central Asian populations based on the continental zones currently identified by *DNA Tribes*® SNP analysis. The highlighted North Asian and European components note possible links with taiga (northern forest) and steppe populations.

During the Bronze Age, agricultural communities of the Oxus Civilization or BMAC⁶ emerged between the Caspian Sea and Hindu Kush Mountains. Also during this period, early settlements were established in the neighboring Tarim Basin, in present day Western China (see map in **Figure 5**).

The languages first spoken by these Central Asian oasis-river cultures remain unknown. However, some scholars have suggested an early link between Alarodian languages (related to ancient Hurro-Urartian and modern Nakh-Daghestanian) and cultures living near Khwarezm and the Caspian (Khvalyn) Sea.⁷

In classical antiquity, these Silk Route crossroads were a meeting point for several cultures and languages, by then including speakers of Indic (Prakrit) and Scythian (Saka) languages linked to neighboring civilizations of South Asia and Eurasian steppe cultures. In addition, the Tarim Basin was home to the “Tocharian” languages, Tocharian A (Arsi or Turfanian) and Tocharian B (Kucuban), whose connections with surrounding cultures are more enigmatic.

Despite geographical proximity to eastern (“satem”) Indo-European languages of Asia, the Tocharian languages were more similar to “centum” Indo-European languages more common far to the west. Possible explanations for these unusual features include an early proto-Tocharian migration from

⁶ BMAC stands for Bactria-Margiana Archaeological Complex.

⁷ Several ethnonyms and toponyms near the BMAC (Avar, Khvalisy; Khvalyn, Khwarezm, Khorasan) resemble the ancient name of the Hurrians (*hurwohe* or *hurrohe*, possibly from an older Hurrian-Subarian ethnonym *huvwur*) and related toponyms (such as *Khabor*). See *Hurrians and Subarians* by I. Gelb, p. 14; and *The Hurrians* by G. Wilhelm.

Europe, prior to the expansion of the eastern “satem” group of languages. However, the circumstances of such an extraordinary journey across Asia are unknown.⁸

In later antiquity, Tocharian speaking cultures are thought to be related to the Yuezhi and Kushans that appeared in Chinese and Indian history as early patrons of Buddhist culture. Visual traces of these early Silk Road societies can be seen in artwork preserved in the Kizil Caves (near Kucha in the Tarim Basin) and the Gandhara (Greco-Buddhist) artistic style that blended traditions of the East and West. In time, these Tocharian cultures of Central Asia were replaced by Xiongnu and later Turkic speaking societies expanding from present day Mongolia.

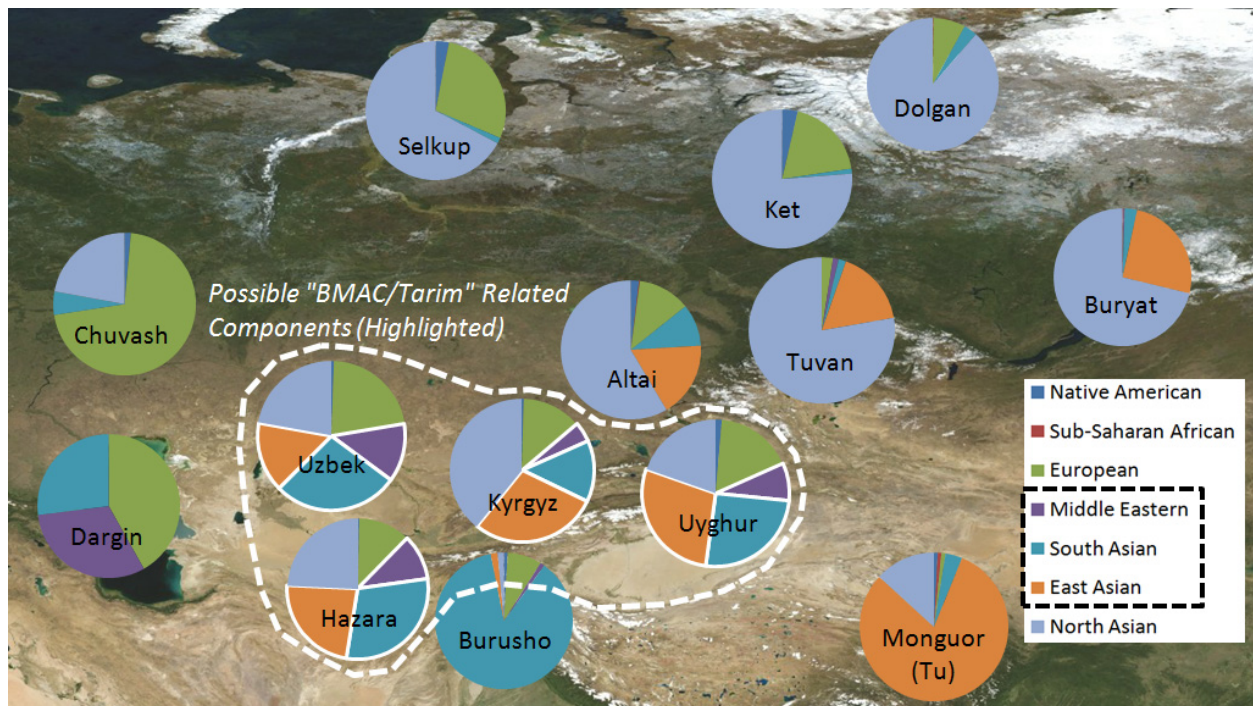


Figure 5: Map highlighting the Middle Eastern, South Asian, and East Asian genetic components that distinguish Central Asian populations. These might express traces of local populations linked to the ancient oasis and river based civilizations of the BMAC and Tarim Basin.

Nevertheless, the relationships (if any) between historically attested Tocharian speaking societies and the more ancient founders of the Oxus (BMAC) and Tarim Basin civilizations are unknown. However, clues to the origins of those early agricultural settlements can perhaps be found among modern populations of Central Asia, including present day Uzbeks, Hazaras, Kyrgyz, and Uyghurs (highlighted in **Table 2** and **Figure 5**).

In **Figure 5**, three genetic components are highlighted that distinguish Central Asians from their Siberian neighbors: Middle Eastern, South Asian, and East Asian. The Middle Eastern component is found in Uzbek (12.8%); Hazara (10.4%); Uyghur (8.3%); and Kyrgyz (4.6%) populations, but is

⁸ One archaeological link to the Tocharian languages that has been proposed is the Afanasevo culture, which appeared north of the Tarim Basin around 2500-2000 BCE. This period is not long after the decline of the “Old European” Cucuteni-Trypillian civilization near the Black Sea.

substantially lower in surrounding populations. This Middle Eastern admixture might express links with neighboring populations of Southwest Asia, perhaps via contacts near the Caspian Sea.

South Asian admixture also was identified in the Central Asian populations, including Hazara (29.8%); Uzbek (27.4%); Uyghur (25.6%); and Kyrgyz (13.8%). However, lower levels of South Asian admixture were also identified in even more distant populations, including: Altai (9.7%); Monguor (3.7%); and Dolgan (3.3%). These links suggest the possibility of early BMAC and Tarim Basin contacts with South Asia (attested in archaeological evidence of trade between the BMAC and Indus Valley Civilization). Further, the South Asian links in more remote parts of Siberia and China suggest wide ranging (and perhaps ancient) contacts between North and South Asia.⁹

A third component that distinguished Central Asians from their Siberian neighbors was a higher ratio of East Asian admixture relative to North Asian admixture¹⁰, for instance: Uyghur (1.4 to 1 East Asian to North Asian ratio); Hazara (1 to 1 ratio); Kyrgyz (1 to 1.4 ratio); and Uzbek (1 to 1.5 ratio).¹¹

This suggests that East Asian admixture in Central Asia might (to some degree) express contacts that predate the historical expansions of North Asian related Xiongnu and Turkic populations from Mongolia. For instance, one pre-Mongolian link between Central and East Asia might have been Tibeto-Burman and related cultures living near the southern oases of the Tarim Basin and neighboring lands of the Qinghai-Tibetan Plateau and Gansu Corridor.¹²

In summary, modern Central Asian populations are characterized by Middle Eastern, South Asian, and East Asian admixture that might (to some extent) date to early cultures of the Oxus and Tarim Basin. This suggests the possibility of early links between the sedentary Oxus and Tarim Basin populations with civilizations of West Asia, India, and China, perhaps more ancient than the better known connections with nomadic Scythian and Turkic societies.

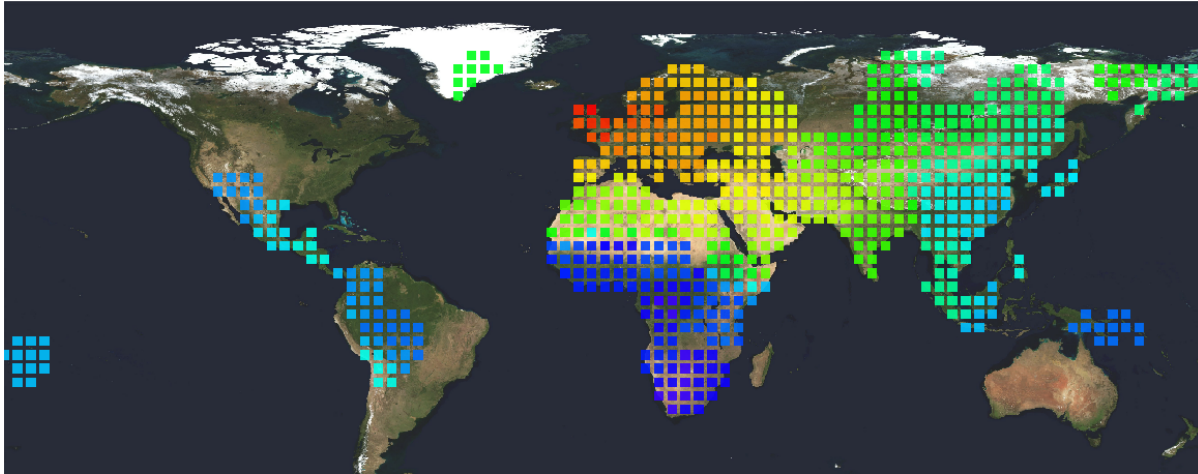
⁹ South Asian admixture was identified in modern populations near the ancient Andronovo horizon (2300-1000 BCE), which linked pastoralist-metallurgist societies of West Siberia with Central Asia (and thus South Asia). However, older contacts have also been proposed between the Central Asian Keltiminar culture (5500-3500 BCE) and West Siberian taiga cultures (possibly related to Proto-Uralic languages). See Early Contacts between Uralic and Indo-European: Linguistic and Archaeological Considerations pp. 265-288, available at <http://tiedekirja.fi/>.

¹⁰ East Asian admixture was also found in other populations of Siberia (such as Buryats, Altai, and Tuvans), but with a greater preponderance of North Asian admixture (see **Table 2**).

¹¹ In contrast, the ratio of East Asian to North Asian admixture was lower for Siberian populations, for instance: Buryat (1 to 2.8 ratio); Altai (1 to 3.4); and Tuvan (1 to 4.6). For a listing of admixture levels, see **Table 2**.

¹² During the time when Xiongnu were expanding from near Mongolia, a group of “Small Yuezhi” family groups leaving the Tarim Basin moved south to join Tibeto-Burman speaking Qiang cultures (perhaps due to previous inter-cultural links or alliances). Early Tibetan connections were also suggested by archaeologists studying the Yanbulaq cemetery near the eastern Tarim Basin. See The Tarim Mummies by J. P. Mallory and V. Mair, p. 141. More ancient Tibetan contacts near Central Asia have also been proposed, including at Mehrgahr before 4300 BCE and the “Northern Neolithic” after 3200 BCE. See The Indus Civilization by Gregory Possehl, pp. 35-36.

DNA Tribes® SNP Ordering Information



DNA Tribes® SNP analysis can be performed based on genome data from any of several SNP microarray based tests. More information and sample reports are available at <http://dnatribes.com/snp.html>.

An update to your personal DNA Tribes® SNP report can also be ordered at the above link.