



DNA Tribes® Digest December 26, 2008  
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## Introduction: Along the First Superhighway

Hello, and welcome to our December 26, 2008 issue of DNA Tribes® Digest. In this issue, we explore genetic relationships along the inland Silk Routes that have connected Europe, Africa, and Asia since ancient times. This allows us to infer paths of gene flow, that is, the ways in which populations of different regions have interacted with their neighbors, and gradually fill in the larger picture of the dynamic, living relationships among peoples living around the world.

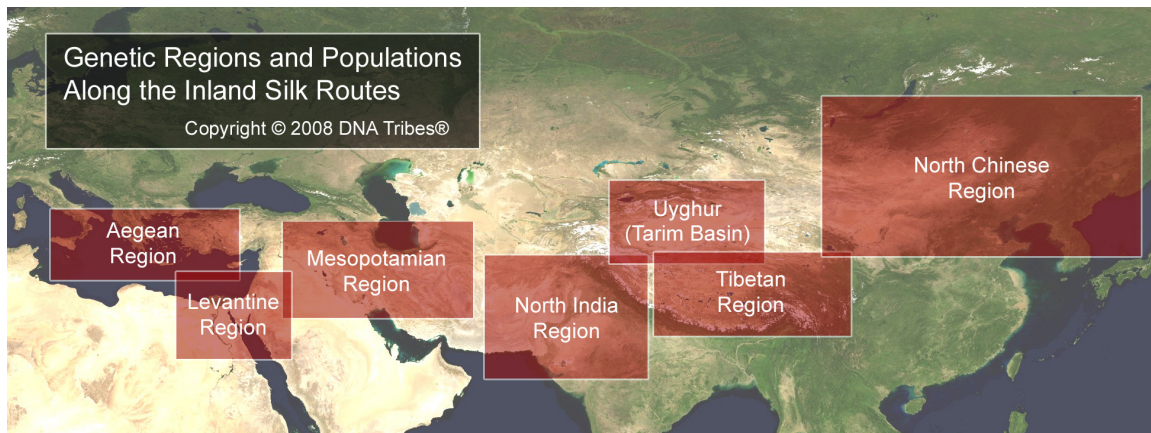
A question that often arises when comparing one person’s DNA to world populations is: How do individuals from a given ethnic group inherit genetic material shared with neighboring or even distant populations? For instance, people of European family origins typically share genetic material with populations in their region of origin and other Europeans, as well as with Near Eastern and in some cases Indian or Central Asian populations. (In contrast, it is substantially less common for people of European family origins to share genetic material with East Asians or American Indians.) How have these particular relationships come to be?

To fully answer this question, it is informative to map the relationships among genetic regions. This provides an empirical foundation for understanding individual ancestry and how this relates to basic underlying genetic relationships among peoples of the world.

Best wishes for a happy and rewarding New Year,  
Lucas Martin  
DNA Tribes

## Patterns of Gene Flow through the Inland Silk Routes

The Silk Routes comprise an ancient trade network that has connected populations of Europe, the Near East, Africa, India, and Asia for thousands of years. In this study, we examined genetic relationships along inland portions of the Silk Routes, beginning with the Aegean genetic region in the west and ending with the North Chinese region in the east. For each region studied, genetic contributions from all other world regions were estimated. Additionally, the Uyghur of the Tarim Basin near the southern fringe of the Altaian genetic region were studied<sup>1</sup>.



**Figure 1:** Genetic regions and populations along the inland Silk Routes explored in this study.

### Birthplace of the West: the Aegean Genetic Region

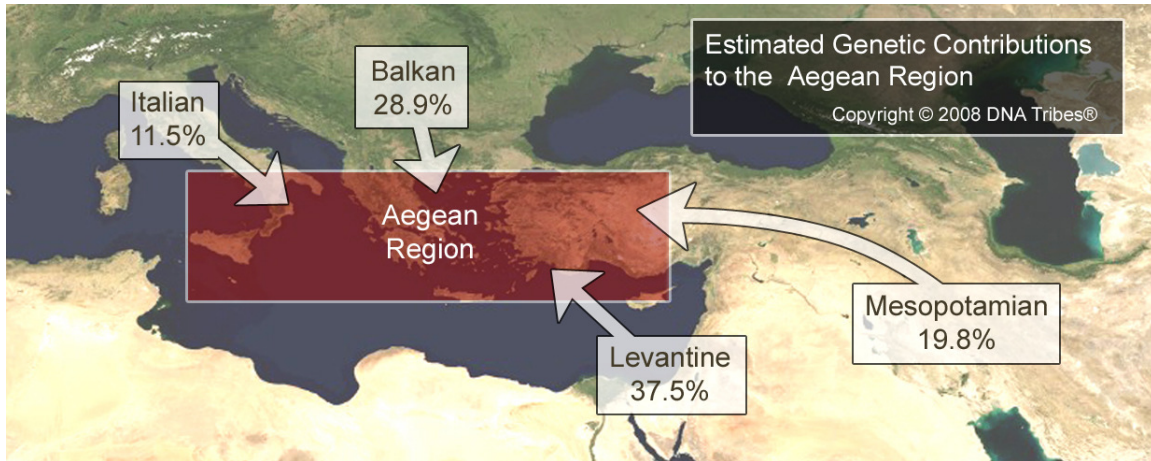
**Background:** The Aegean genetic region characterizes populations surrounding the Aegean Sea, including populations of southern peninsular Italy, Sicily, Greece, and Turkey. This is the place where Western culture emerged, beginning with the Minoan and Mycenaean civilizations and later the city-states of classical Greece such as Athens and Sparta. Although the intellectual, political, and cultural institutions developed here are sometimes described as distinctively Western, the Aegean region has also been a nexus for contacts with neighboring Near Eastern peoples. For instance, according to legend, the Greek alphabet was adapted from an earlier Phoenician alphabet brought to Greek Thebes by Cadmus from Phoenicia (in the Levantine genetic region).<sup>2</sup> More recently, territories of the Greek speaking Byzantine Empire were absorbed by the expanding empire of the Ottoman Turks, who themselves had migrated to Anatolia from their

<sup>1</sup> The Altaian genetic region as a whole was previously studied in the November 28, 2008 issue of DNA Tribes® Digest, available at: <http://www.dnatribes.com/dnatribes-digest-2008-11-28.pdf>.

<sup>2</sup> However, this legendary account of Cadmus bringing the Phoenician alphabet to Thebes before the Trojan War is not born out by archaeological data, which suggest that instead the Phoenician alphabet was introduced to Greece later, several centuries after the Trojan War.

homeland near the Aral Sea through lands of the Mesopotamian genetic region (then controlled by the Seljuk Empire).

**Genetic analysis:** Genetic contributions to the Aegean region from 32 world regions and twelve Europa sub-regions<sup>3</sup> presently identified by DNA Tribes® analysis were estimated. Results are illustrated in **Figure 2** and summarized in **Table 1** below.



**Figure 2:** Estimated genetic contributions to the Aegean genetic region.

<b>Genetic Region</b>	<b>Estimated Contribution</b>
Levantine	37.5%
Balkan	28.9%
Mesopotamian	19.8%
Italian	11.5%
<b>Other</b>	<b>2.3%</b>

**Table 1:** Estimated genetic contributions to the Aegean genetic region.

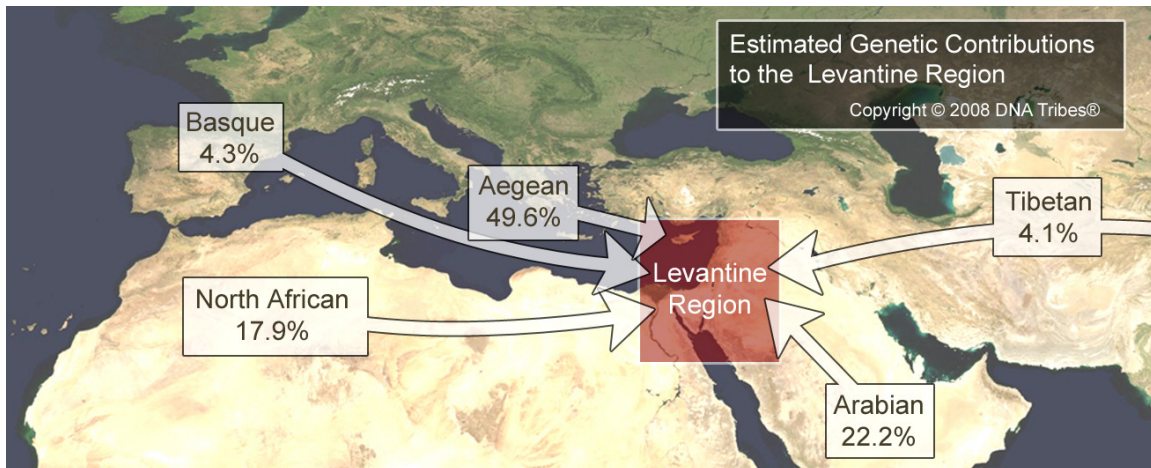
**Discussion:** Results in **Table 1** indicated genetic contributions to the Aegean region from neighboring peoples of both Europe and the Near East. From Europe, Balkan (28.9%) and Italian (11.5%) contributions are observed, and from the Near East, Levantine (37.5%) and Mesopotamian (19.8%) contributions are observed. This is consistent with a history of contacts with neighboring peoples dating to ancient times.

<sup>3</sup> A map illustrating the genetic world regions presently identified by DNA Tribes® analysis can be viewed at: <http://dnatribes.com/populations.html>. A map illustrating Europa sub-regions can be viewed at: <http://dnatribes.com/dnatribes-europa.html>. In this study, all non-European world regions and all Europa sub-regions except each studied region were referenced. European world regions omitted to avoid redundancy were: Eastern European, Mediterranean, and Northwest European. The Greek Europa sub-region was also omitted in the analysis of the Aegean region.

## Eastern Shores of the Mediterranean: the Levantine Genetic Region

**Background:** Levantine genetic patterns characterize populations along the eastern shores of the Mediterranean Sea, including the modern nations of Egypt, Israel, Syria, and Jordan. The Levant (from the French term for eastern) is home to peoples of several cultural traditions and encompasses lands that, together with some lands of the Mesopotamian genetic region to the east, have been described as the Fertile Crescent and the Cradle of Civilization for Europe and the Middle East. Languages spoken in this area today include Hebrew and Arabic, which share linguistic roots with older Afro-Asiatic languages once spoken here such as Egyptian, Phoenician, and Aramaic.

**Genetic analysis:** Genetic contributions to the Levantine region from 32 world regions and thirteen Europa sub-regions presently identified by DNA Tribes® analysis were estimated. Results are illustrated in **Figure 3** and summarized in **Table 2** below.



**Figure 3:** Estimated genetic contributions to the Levantine genetic region.

### Genetic Region Estimated Contribution

Aegean	49.6%
Arabian	22.2%
North African	17.9%
Basque	4.3%
Tibetan	4.1%
<b>Other</b>	<b>2.0%</b>

**Table 2:** Estimated genetic contributions to the Levantine genetic region.

**Discussion:** Results in **Table 2** indicated genetic contributions from several neighboring regions of Europe and the Near East. The largest genetic contribution identified was Aegean (49.6%),

which reciprocates the Levantine contribution to the Aegean identified above, and suggests substantial contacts among populations living in the Eastern Mediterranean. Near Eastern contributions include North African (17.9%) and Arabian (22.2%), which would be consistent with cultural contacts with Afro-Asiatic speaking peoples of western North Africa and the Arabian Peninsula.

Results also show smaller Basque (4.3%) and Tibetan (4.1%) genetic contributions. Although these latter contributions do not necessarily indicate specific contacts with Basques and Tibetans as they exist today, they do suggest the possibility of some gene flow from western European Mediterranean lands and East Asia. The Tibetan contribution might reflect contacts with populations of Transoxiana, perhaps in periods when the Levantine region was in contact with the Turkic world through Mamluks (who at one point ruled Egypt), the Mongol-led invasions of Syria, and the Seljuk and later Ottoman empires<sup>4</sup>. Another possible link with Transoxiana will be seen in our discussion of the Tibetan genetic region below.

## Between the Rivers: the Mesopotamian Genetic Region

**Background:** The Mesopotamian genetic region characterizes populations of the modern nations of Iraq and Iran, and to some extent eastern Anatolian populations of Turkey<sup>5</sup>. Mesopotamian (meaning “the land between the rivers,” the Tigris and Euphrates) lands were a focal point for the Neolithic (agricultural) revolution and include the oldest monumental structures in the world and birthplace of writing. Early civilizations of this region include Sumer, Babylon, and Persia. In fact, the modern name Iraq is thought to derive from Uruk, the name of an ancient Sumerian city mentioned in the *Epic of Gilgamesh*.

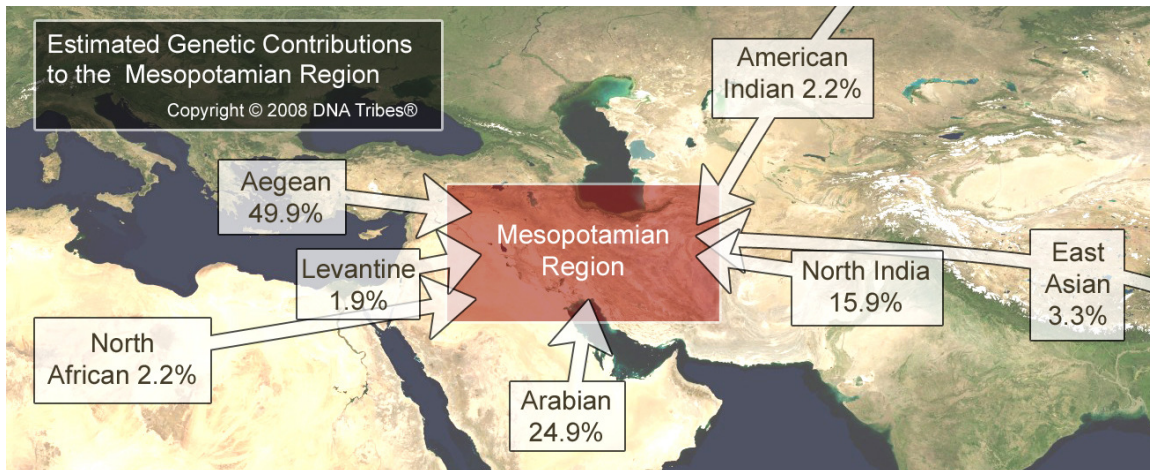
Languages spoken in the Mesopotamian genetic region include Indo-European languages such as Farsi (Persian), Turkic languages such as Turkish and Azerbaijani, and Semitic languages such as Arabic. Persian cultures of Mesopotamian lands trace their origins to the ancient Indo-Iranians thought to have come into contact with cultures of India and the Persian plateau after spreading out from what is today southern Russia and Kazakhstan. Similarly, Turkic cultures trace their origins to Turkic speaking nomads of Inner Asia.<sup>6</sup>

<sup>4</sup> A Tibetan genetic contribution also has been identified for the Russian Europa sub-region. For more information see the November 28, 2008 issue of DNA Tribes® Digest at: <http://www.dnatribes.com/dnatribes-digest-2008-11-28.pdf>.

<sup>5</sup> As with many labels for genetic regions and sub-regions identified by DNA Tribes® analysis, the Mesopotamian genetic region (identified on the basis of shared genetic characteristics) does not correspond exactly with Mesopotamia as usually defined by historians. This is because genetic regions reflect long term patterns of human interaction underlying the formation of cultural and political units, not necessarily determined by the cultural and political units existing in any particular period (including cultural and political units as they exist in the present day). In most parts of the world, human genetic structure is most accurately described in terms of geography rather than linguistic or political boundaries.

<sup>6</sup> Today, Persian and Turkic speaking peoples coexist both in Iran and in Transoxiana to the north and east, and a complete description of these cultures would take into account a long history of mutual contact. Early Persian narratives such as the *Avesta* and *Shahnameh* describe Central Asian lands to the north as *Turan*, a term which has come to be associated with Turkic peoples. However, the people originally called

**Genetic analysis:** Genetic contributions to the Mesopotamian region from 32 world regions and thirteen Europa sub-regions presently identified by DNA Tribes® analysis were estimated. Results are illustrated in **Figure 4** and summarized in **Table 3** below.



**Figure 4:** Estimated genetic contributions to the Mesopotamian genetic region.

<b>Genetic Region</b>	<b>Estimated Contribution</b>
Aegean	49.9%
Arabian	24.9%
North India	15.0%
East Asian	3.3%
American Indian	2.2%
North African	2.0%
Levantine	1.9%
<b>Other</b>	<b>0.8%</b>

**Table 3:** Estimated genetic contributions to the Mesopotamian genetic region.<sup>7</sup>

**Discussion:** Results in **Table 3** indicated genetic contributions to the Mesopotamian region from several regions. These include Aegean (49.9%), Arabian (24.9%), North African (2.0%), and Levantine (1.9%) contributions, which suggest relations to both Indo-European speaking cultures and to Semitic speaking cultures of the Arabian Peninsula and Africa. Also observed was a substantial contribution from North India (15.9%), consistent with contacts with Indo-Aryan

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*Tuirya* during the Avestan age approximately 2500 years ago are thought to have been Persians rather than Turks as they exist today.

<sup>7</sup> Genetic contributions from the Japanese, Malay Archipelago, North Chinese, South Chinese, Southeast Asian, and Tibetan regions were listed as “East Asian.” Genetic contributions from the Amazonian, Andean, Arctic, Athabaskan, Central American, Mayan, Mexican, North Amerindian, Ojibwa, Patagonian, and Salishan regions were listed as “American Indian.”

cultures of India and perhaps with more ancient peoples such as the Elamites of southern Iran, who are sometimes thought to have had linguistic connections with Dravidian cultures of India.

Also identified were smaller East Asian (2.2%) and American Indian (2.2%) contributions, which might reflect more long distance gene flow, mediated by Turkic speaking peoples of Central Asia<sup>8</sup>.

## Land of the Nobles: the North India Genetic Region

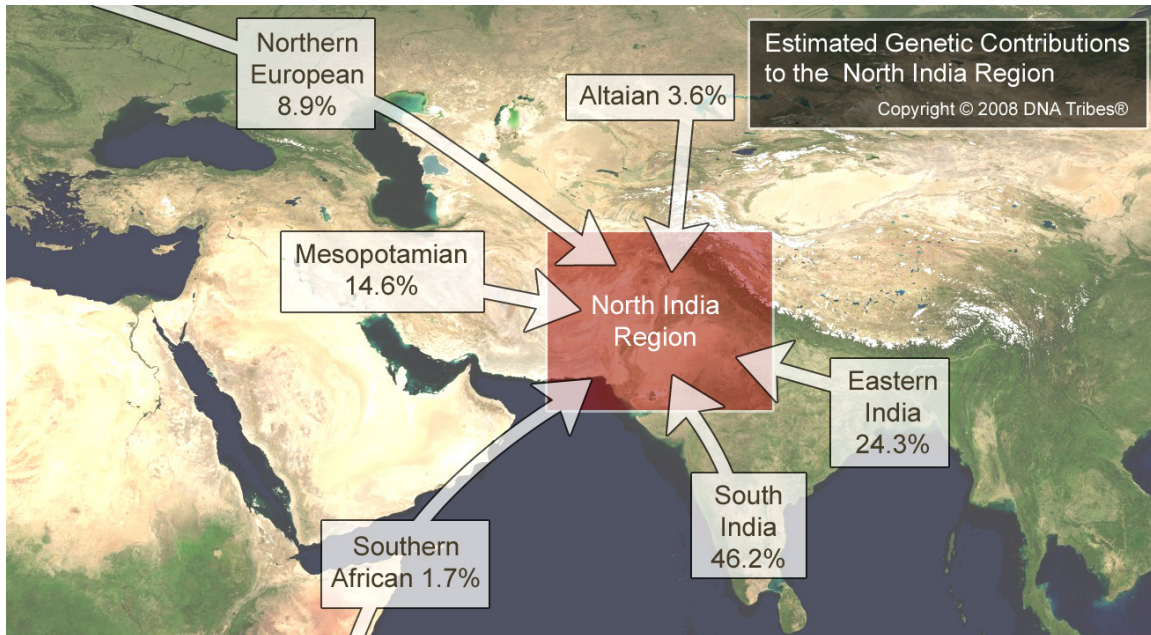
**Background:** The North India genetic region characterizes populations of northern states of India<sup>9</sup> as well as modern Pakistan and (to some extent) Afghanistan. This zone includes lands known as *Aryavarta* (or “Land of the Nobles”) during the Vedic Age beginning approximately 1000 BC. The Vedic peoples of India (who called themselves *Arya* or “nobles”) are thought to have arisen from the interaction of incoming Indo-Iranian cultures originating in the Eurasian steppe (see also the discussion of Mesopotamia above) with the earlier Indus Valley Civilization of India. The history of North India includes periodic contacts with peoples to the north, such as the Kushan Empire originating in the Tarim Basin (whose rulers are thought to have been Indo-Europeans, possibly related to the Tocharians of the same area), and the Mughal Empire (whose rulers were of Turko-Mongol and later Persian origins, with substantial cultural links to Persian cultures).

**Genetic analysis:** Genetic contributions to the North India region from 32 world regions and thirteen Europa sub-regions presently were estimated. Results are illustrated in **Figure 5** and summarized in **Table 4** below.

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<sup>8</sup> Genetic links between American Indians and populations of Eurasia, observed to be strongest in Paleo-Siberian speaking peoples of far eastern Siberia but also present at low levels in other parts of Asia and northern Europe, have been discussed in previous issues of DNA Tribes® Digest. For more information, see: <http://www.dnatribes.com/dnatribes-digest-2008-10-25.pdf> and <http://www.dnatribes.com/dnatribes-digest-2008-11-28.pdf>.

<sup>9</sup> Although India is sometimes described in terms of *jati* or caste, DNA Tribes® analysis indicates that genetic structure among populations of India is substantially geographical. For this reason, a complete empirical description of Indian genetic structure would reference geography in addition to any socio-economic institutions such as caste.



**Figure 5:** Estimated genetic contributions to the North India genetic region.

<b>Genetic Region</b>	<b>Estimated Contribution</b>
South India	46.2%
Eastern India	24.3%
Mesopotamian	14.6%
<i>Celtic</i>	7.3%
<i>Russian</i>	1.6%
<b>Total Northern European</b>	<b>8.9%</b>
Altaian	3.6%
Southern African	1.7%
Other	0.7%

**Table 4:** Estimated genetic contributions to the North India genetic region.

**Discussion:** Results in **Table 4** identified the largest genetic contributions to North India as South Indian (46.2%) and Eastern Indian (24.3%), for a total of 70.5% contribution from genetic regions native to India. In addition, substantial Mesopotamian (14.6%), Northern European (8.9%) and Altaian (3.6%) genetic contributions were also observed, consistent with periodic historical contacts with cultures to the north and west such as Indo-Iranians, Persians, and Turko-Mongols. The connection between northern Europe and the Eurasian steppes will be explored further in our discussion of the Uyghur of the Tarim Basin below.

A smaller genetic contribution from Southern Africa (1.7%) was also identified, suggesting the possibility of some gene flow from populations south of the Sahara Desert, perhaps via the African coast of the Indian Ocean. Today, North India is home to Siddi communities descended from Bantu speaking Africans, including Tanzanians, Kenyans, and



Mozambicans brought to India and Pakistan by Arab and later Portuguese slave traders, as well as free African mercenaries, sailors, and merchants who settled in India. Some Siddis earned reputations as excellent warriors and were sought out by Indian princes as mercenaries.

These results are consistent with substantial genetic continuity with other genetic regions of the Indian Subcontinent in addition to some gene flow from other neighboring regions.

## Heirs of the Tocharians: the Uyghur of the Tarim Basin

**Background:** The Tarim Basin extends across a vast area of what is today western China, at the southern extent of the larger Altaian genetic region.<sup>10</sup> The interior of the Tarim Basin is a desert known as the Taklamakan (sometimes said to mean “you go in and you’ll never come out”), which is one of the world’s largest sandy deserts. However, this forbidding desert was once the Tarim Lake, a vast post-glacial lake that has gradually dwindled to become Lop Nur, a series of scattered sand marshes. In earlier times, the waters of Lop Nur and the Tarim River supported the cultures of the Indo-European speaking Tocharians and later the kingdom of Loulan. Today, Lop Nur is used by the government of China as a test site for nuclear weapons.

Several mummies have been found in the Tarim Basin dating to as early as 1800 BC. Some of these Tarim mummies have been described as having European-like bone structures and in some cases light hair and eyes. Other physical analyses of these mummies have linked them with early civilizations of the Eurasian steppe, the Oxus River and India.

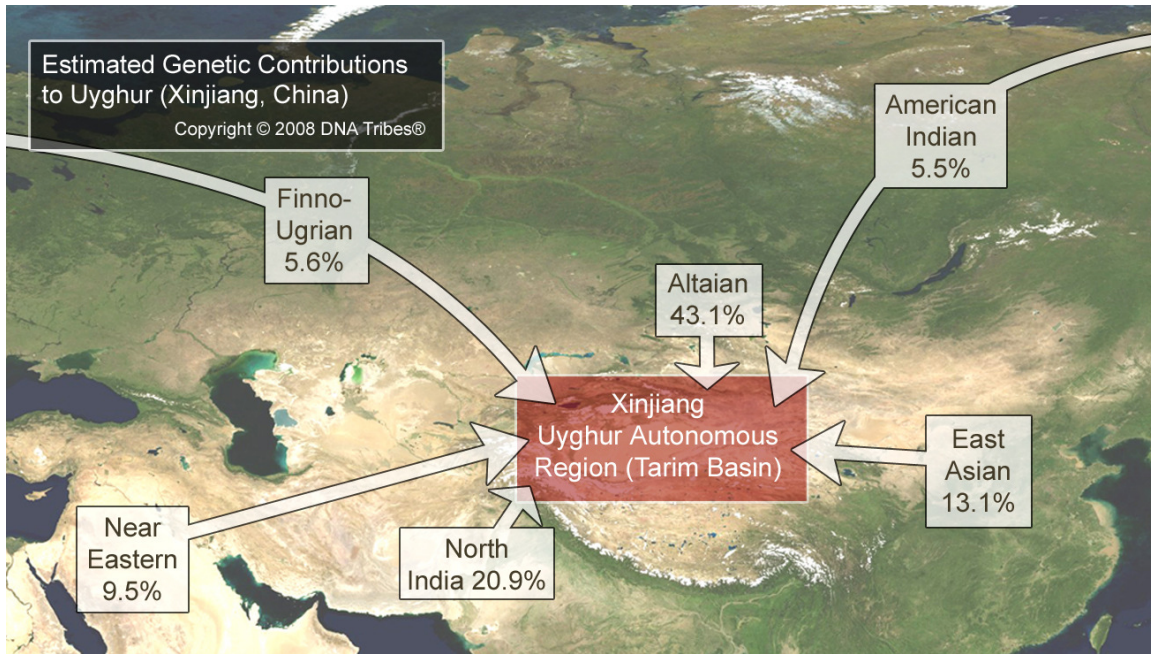
The Tarim Basin is home to the Uyghur or *Tokus-Oguz* (“nine tribes”<sup>11</sup>), a Turkic speaking people from the Altai Mountains to the north. The Uyghur once led the Uyghur Khaganate, an empire of all Altaic tribes established in 744 AD that once extended from the Aral Sea to Mongolia. In 840 AD, the Uyghur Khaganate was conquered by the Yenisei Kyrgyz (described as “of yellow head and red face” in the Chinese historical text *Tang Huiyao*), who burned the Uyghur cities, including the capital in Ordu Baliq near Karakorum in present day Mongolia. Uyghur refugees fled to the south, where they founded smaller states and later established themselves as civil servants in the Mongol Empire.

<sup>10</sup> Genetic characteristics of the Altaian genetic region as a whole are discussed in the November 28, 2008 issue of DNA Tribes® Digest, available at: <http://www.dnatribes.com/dnatribes-digest-2008-11-28.pdf>.

<sup>11</sup> Early Chinese sources describe neighboring peoples as *Tu-Kiu* (“strong” or “powerful”) and later *Tujue*, and early Persian sources such as the *Avesta* describe nomads of Central Asia as *Tuirya* (who are thought to have been Persian speaking). The Indo-European speaking Tocharians of the Tarim Basin were known as *Tocharoi* to the Greeks, who classified them as Scythians. However, the first written use of the term “Turk” to apply specifically to a Turkic speaking people was after 546 AD by the Ashina tribe, who called themselves *Gök türk* (“Blue Turks”).

Although these terms are ascribed with separate etymologies in several languages, the local persistence of phonetically similar ethnonyms among peoples usually thought to be distinct might suggest the possibility that Indo-European speaking populations such as the Tocharians might have been involved in the formation of Turkic populations and cultures (perhaps in a process of genetic and cultural synthesis also involving neighboring proto-Mongolic, Uralic, and/or Paleo-Siberian speaking peoples).

**Genetic analysis:** Genetic contributions to the Uyghur from 32 world regions and thirteen Europa sub-regions were estimated. Results are illustrated in **Figure 6** and summarized in **Table 5** below.



**Figure 6:** Estimated genetic contributions to Uyghur.

Genetic Region	Estimated Contribution
Altaian	43.1%
North India	20.9%
<i>North Chinese</i>	6.2%
<i>South Chinese</i>	3.8%
<i>Japanese</i>	3.1%
<b>Total East Asian</b>	<b>13.1%</b>
<i>Levantine</i>	4.8%
<i>Arabian</i>	4.7%
<b>Total Near Eastern</b>	<b>9.5%</b>
Finno-Ugrian	5.6%
American Indian	5.5%
<b>Other</b>	<b>2.4%</b>

**Table 5:** Estimated genetic contributions to Uyghur.

**Discussion:** Results in **Table 5** identified the greatest genetic contribution as Altaian (43.1%), consistent with Uyghur origins in the Altai Mountains to the north. However, Uyghur also have genetic characteristics that distinguish them from the Altaian genetic region as a whole. The North India genetic contribution of 20.9% might reflect gene flow from peoples of the Indian Subcontinent during periods of contact such as the Kushan Empire, believed to have been led by

Tocharians from the Tarim Basin. East Asian (13.1%) and Near Eastern (9.5%) genetic contributions were also identified, suggesting contact with peoples to the east as well as the west of the Tarim Basin. Also identified were Finno-Ugrian (5.6%) and American Indian (5.5%) contributions, suggesting the possibility of further contacts with Uralic and Paleo-Siberian speaking peoples beyond those that characterize the Altaian genetic region as a whole.

## At the Roof of the World: the Tibetan Genetic Region

**Background:** The Tibetan genetic region characterizes populations of the Tibetan Plateau and nearby, including not only ethnic Tibetans but also Tibeto-Burman speaking Adi people living in the Himalayan hills of northeastern India and (to some extent) Turkic speaking Salar people living in Qinghai province of western China<sup>12</sup>.

Tibetan origins are generally not well understood. However, it is sometimes thought that the Tibetan peoples are descended from nomad cultures that split from the early ancestors of the Han Chinese. Buddhism was first introduced to Tibet as early as the fifth century AD, but was formally established as the official religion of Tibet in the eighth century AD under the guidance of the Indian teacher Padmasambhava. Since that time, Tibetan Buddhism has become influential among peoples of Mongolia and Manchuria (in the North Chinese genetic region) and was an official religion of the Yuan (Mongol) and Qing (Manchu) dynasties of China.

**Genetic analysis:** Genetic contributions to the Tibetan region from 32 world regions and thirteen Europa sub-regions were estimated. Results are illustrated in **Figure 7** and summarized in **Table 6** below.

**Discussion:** Results in **Table 6** indicated the greatest genetic contribution to the Tibetan genetic region from the South Chinese region (72.7%), consistent with an early common origin with the ancestors of Han Chinese. Substantial contributions were also observed from the Eastern India (16.1%), Altaian (5.6%) and North Chinese (3.5%) regions, which might reflect contacts with Indian as well as Turkic and Mongolic peoples. A smaller American Indian contribution of 1.7% was also observed, which might reflect diffusion of American Indian genetic patterns in Asia, perhaps mediated by populations in contact with Paleo-Siberian speaking peoples of far northern and eastern Siberia.

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<sup>12</sup> The Salar of China trace their origins to Oghuz Turks who migrated from near the Aral Sea in Transoxiana during the period of the Mongol Empire and have since intermarried with local Tibetans, Han, and Hui peoples. Interestingly, the east-west connection seen here among the Salar reciprocates the Tibetan genetic contributions observed in some western regions adjacent to Transoxiana. If more data become available for populations living in the zone between the Aral Sea and the Pamir Mountains, it might become possible to clarify these relationships further.

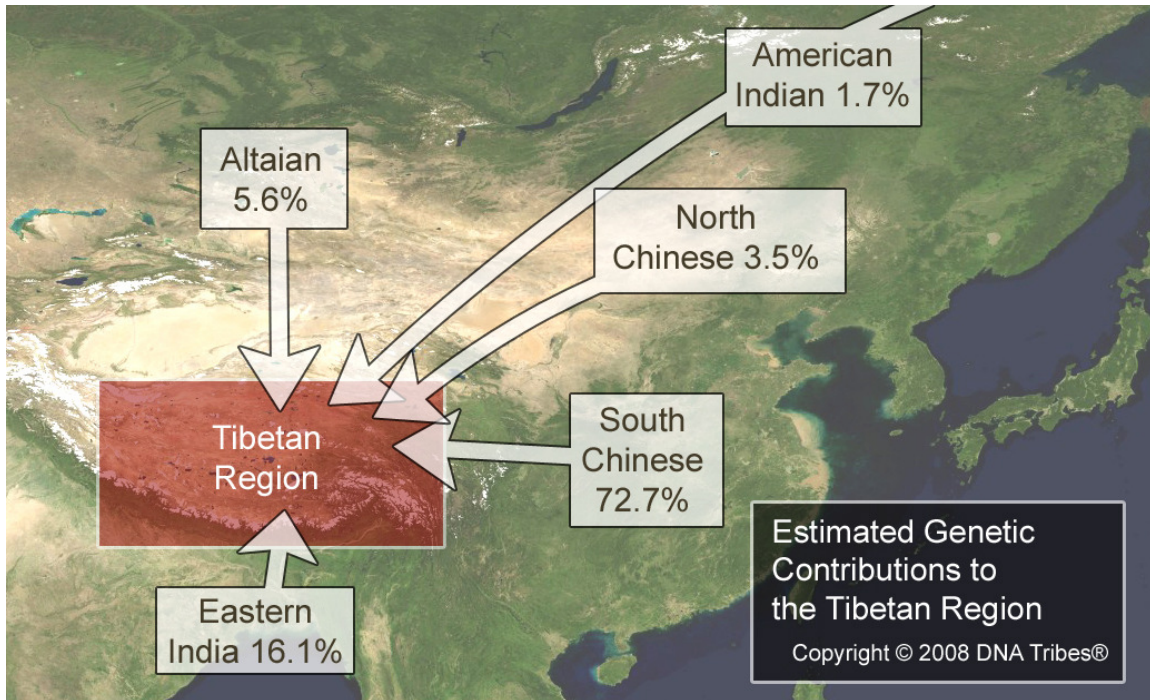


Figure 7: Estimated genetic contributions to the Tibetan genetic region.

Genetic Region	Estimated Contribution
South Chinese	72.7%
Eastern India	16.1%
Altaian	5.6%
North Chinese	3.5%
American Indian	1.7%
<b>Other</b>	<b>0.4%</b>

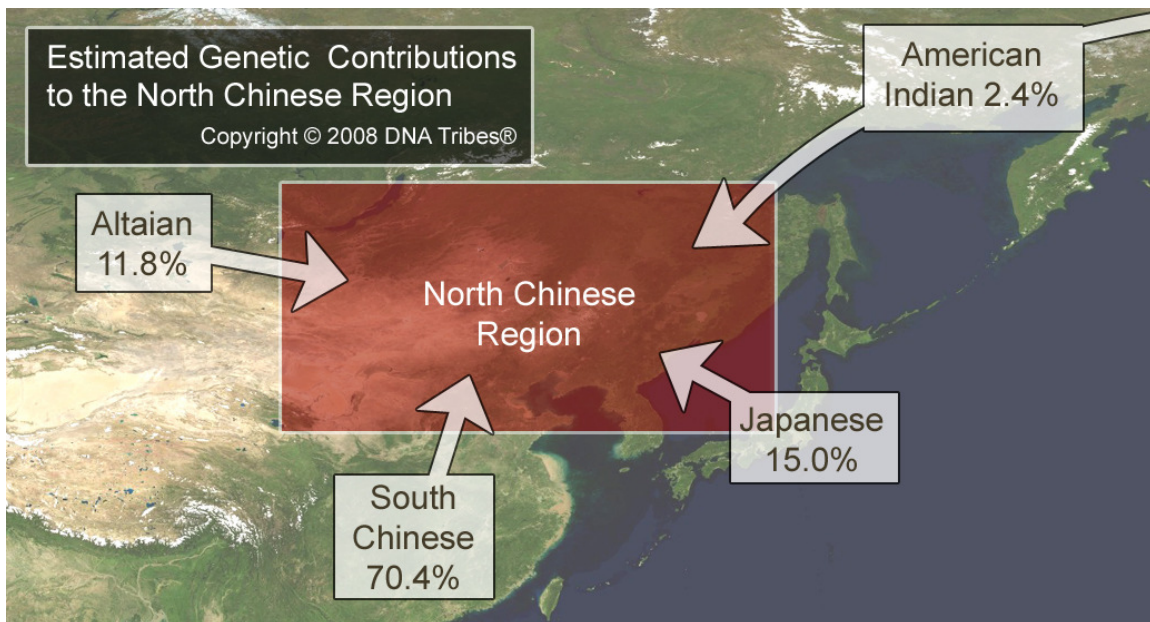
Table 6: Estimated genetic contributions to the Tibetan genetic region.

## All Roads Lead to Cathay: the North Chinese Genetic Region

**Background:** The North Chinese genetic region characterizes Mongolic, Tungusic, Korean, and Sino-Tibetan speaking peoples of Mongolia, Korea, and northern China. The term China is sometimes associated exclusively with the predominant Han ethnic group, named for the culturally influential Han Dynasty. However, modern China is a nation composed of many ethnic groups, and non-Han peoples have played substantial roles in Chinese history since ancient times. The largest contiguous empire in history, the Mongol Empire, was ruled from Mongolia in the North Chinese genetic region and established a *Pax Mongolica* (“Mongol Peace”) that facilitated the exchange of goods and ideas throughout Eurasia. During the time of Marco Polo, Europeans referred to northern China as “Cathay,” from the name of the Khitan people who had ruled the

Liao Dynasty of northern China prior to the Mongol expansion and who are thought to have spoken a proto-Mongolic language. More recently, the last Chinese imperial dynasty was the Qing Dynasty founded by the Manchu Aisin Gioro clan from what is today northeastern China (Manchuria). During the early twentieth century, Imperial Japan was active in parts of Manchuria, at one point colonizing Manchuria but ultimately being driven out of the region by a joint Soviet-Mongolian military force.

**Genetic analysis:** Genetic contributions to the North Chinese region from 32 world regions and thirteen Europa sub-regions were estimated. Results are illustrated in **Figure 8** and summarized in **Table 7** below.



**Figure 8:** Estimated genetic contributions to the North Chinese genetic region.

<b>Genetic Region</b>	<b>Estimated Contribution</b>
South Chinese	70.4%
Japanese	15.0%
Altaian	11.8%
American Indian	2.4%

**Table 7:** Estimated genetic contributions to the North Chinese genetic region.

**Discussion:** Results in **Table 7** indicated a predominant genetic contribution of 70.4% from the South Chinese region. This suggests substantial genetic continuity between the North and South Chinese genetic regions, which might reflect several millennia of cultural and political contacts between these regions. Also observed are Japanese (15.0%) and Altaian (11.8%) genetic contributions, which might reflect contact with populations of the Japanese Archipelago to the east and Turkic peoples to the west, possibly mediated by Mongolic and/or Tungusic peoples. As



is seen elsewhere in populations adjacent to Siberia, a smaller American Indian genetic contribution of 2.4% was also identified. This might reflect a limited diffusion of American Indian genetic characteristics to some parts of Asia, perhaps transmitted by Arctic peoples living near the intersection of Siberia and Alaska.

## **Conclusion**

This study explored genetic relations among several populations spanning three continents. Nevertheless, gene flow was observed between neighboring regions throughout these vast distances. These results might suggest that despite physical separation of populations near the geographical perimeters of Europe, Africa, and Asia, human populations have maintained genetic continuity across great distances through contacts with their geographical neighbors.



## Getting the Most from Your Testing

*Originally published August 29, 2008*

Once your core DNA Tribes® 15-Marker or 21-Marker testing is complete, we offer several options to keep your report current and to customize your analysis to deliver the information you want. (Prices are listed as of November 28, 2008 and are subject to change.)

### Updating Your Analysis:

We incorporate new data in our algorithms on a periodic basis. This includes not only new reference data (our uniquely detailed and comprehensive database now includes 842 reference populations in all inhabited continents around the world), but also refinements to our algorithms and enhanced world region definitions.

New data also allow us to refine our genetic world region definitions. Based on a rigorous mathematical analysis of hundreds of ethnic and national reference samples, world regions express the actual genetic structure we have identified in world populations. These regional definitions both enhance your own analysis, and provide the necessary picture of world genetic structure to put your own results in a global context.

A map illustrating the populations and genetic regions currently identified in our analyses can be viewed at:

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Once lab 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.html>

### Customizing Your Analysis:

DNA Tribes® offers several \$24.99 Add-On reports to customize your analysis for the information you want:

**Extended Match Results:** This is a comprehensive 22-page listing of your DNA match scores for all 871 reference populations in our database. We recommend this Add-On for customers who enjoy combing through lots of information.



**Native American Panel:** This two-page report lists your DNA match scores for all Native American tribal reference populations in our database. This can provide a closer look to complement Parts B and D of core results for customers who have substantial Native American origins.

**African Panel:** This two-page report lists your DNA match scores for all Sub-Saharan African reference populations in our database. This can provide a closer look to complement Parts B and D of core results for customers who have substantial African origins.

**Central Asian Panel:** This two-page report lists your DNA match scores for all Central Asian reference populations in our database, including Turkic populations as well as European Roma (Gypsy) populations. This can provide a closer look to complement Parts B and D of core results for customers who have substantial European, Near Eastern, South Asian, or East Asian origins.

Once lab testing is complete, Add-Ons can be selected at any time of your choice through our secure online checkout at: <http://dnatribes.com/order.html>

#### **DNA Tribes® Europa: A Detailed Comparison to European Sub-Regions:**

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 13 genetic sub-regions of Europe, which is substantially more robust than the individual population matches in Parts B – C of core results and more detailed than the European world regions referenced in Part D of core results.

More information about DNA Tribes® Europa is available at:  
<http://dnatribes.com/dnatribes-europa.html>

#### **Expanding Your Analysis with a 21 Marker Upgrade:**

For customers who have completed 13-marker or 15-marker testing with DNA Tribes®, we now offer a 21 Marker Upgrade. This includes lab testing of additional STR marker systems, which provides a closer comparison of your own DNA to world populations for greater accuracy and power of exclusion. The incorporation of additional marker systems can confirm or clarify your initial 13 or 15-marker results, and includes an update to all Add-Ons previously ordered for your kit.

21 Marker Upgrades are available for \$119.99 through our secure online checkout at:  
<http://dnatribes.com/order.html>





**Researching Your Results:**

Each person's DNA Tribes® results are one of a kind and express their own unique collection of genetic material inherited from both paternal and maternal ancestors. However, human genetic relationships involve a complex hierarchy of relationships, from individual to family to ethnic group to genetic region to global population structure. Detailed information to allow you to interpret your own results in a broader context is available in our Global Survey at:

<http://dnatribes.com/sample-results/dnatribes-global-survey-regional-affinities.pdf>