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## Introduction

Hello, and welcome to the May 2013 issue of DNA Tribes® Digest. This month's article continues a two-part "big picture" exploration of world genetic relationships using SNP based Multi-Dimensional Scaling (MDS) that began with last month's Digest issue (available for viewing and download at <http://dnatribes.com/dnatribes-digest-2013-04-02.pdf>).<sup>1</sup>

These large scale relationships between regions and continents provide the necessary context to understand the localized relationships between populations. For instance, to understand relationships in a part of the world as complex as South Asia, it is necessary to examine the broader inter-regional relationships with West Asia, Siberia, and East Asia. Also emphasized in this article are South Asian genetic relationships with Oceania that might reflect early coastal and maritime migrations via the Indian Ocean (known to ancient navigators as the "Erythraean Sea").

Best regards,  
Lucas Martin  
DNA Tribes

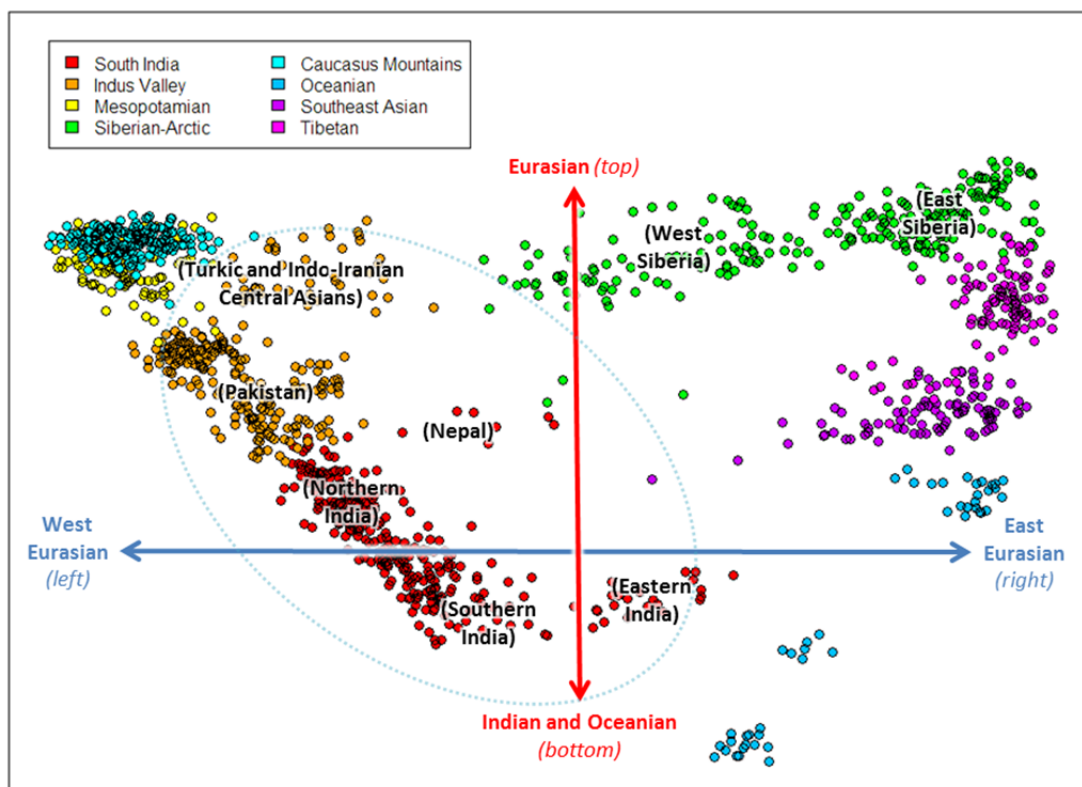
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<sup>1</sup> For more information about DNA Tribes® SNP analysis, see <http://dnatribes.com/snp.html>.

## Visualizing World Genetic Relationships using Multi-Dimensional Scaling (MDS) (Part Two)

### Regional Genetic Relationships in South Asia

To visualize genetic relationships in South Asia, MDS analysis of individuals sampled randomly from the Indus Valley, South India, and neighboring regions<sup>2</sup> identified by *DNA Tribes*® SNP analysis was performed. Results are illustrated in **Figure 1**.



**Figure 1:** MDS plot of individuals randomly sampled from South Asia (circled) and neighboring regions.

**Discussion:** Results in **Figure 1** express two genetic patterns in sampled South Asian individuals. First, the **blue horizontal (left-to-right) axis** expresses the genetic difference between West Eurasian individuals (represented in this plot by Caucasus Mountains and Mesopotamian individuals; to the left of the plot) and East Eurasian individuals (represented in this plot by Southeast Asian, Tibetan, and East Siberian individuals; to the right of the plot).

Along this horizontal axis, sampled South Asians form a genetic continuum that smoothly transitions from West Eurasians (left) and extends towards East Eurasia, with some South Asians reaching approximately midway (Nepal and Southern India) and a few South Asians (from Eastern India)

<sup>2</sup> For more details about these regions, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

reaching to somewhat further towards Eurasia. This gradual transition between West and East Eurasia expressed for South Asians is similar to the horizontal continuum between West Siberia and East Siberia (at the top right of **Figure 1**).<sup>3</sup>

However, these two transitional streams linking West and East Eurasia are generally separate in the graph, with sampled individuals from Central Asia (labeled in **Figure 1**) forming a bridge between West Asia, South Asia, and Siberia.<sup>4</sup> Similarly, a second connecting stream includes some sampled Nepalese individuals that are plotted relatively close to some Tibetan and Southeast Asian individuals (labeled in **Figure 1**).

Second, the **red vertical (top-to-bottom) axis** expresses the genetic distinction between Eurasian (West Asian, Central Asian, and Siberian) individuals (towards the top) and sampled Indian and Oceanian individuals (towards the bottom of the chart). This genetic relationship between Indian and Oceanian populations is expressed based on sampled Melanesian, Papuan, Samoan, and Tongan individuals. If a fuller sampling of SNP genomes from the Indian Ocean becomes available (such as Andamanese, Sumatran, Sundanese, Timorese, and Australian Aboriginal individuals), it might become possible to further clarify the genetic links between South Asia and Oceania.

Similar to MDS analysis, admixture analysis expresses Oceanian and East Eurasian genetic components for some sampled individuals from several local associations in South Asia (see **Table 1**). Based on sampled populations, Oceanian components in South Asia peak in the Dravidian speaking (Malayam<sup>5</sup>) Pulliyar of Southern India (5.8%). Southeast Asian components peak in the Austroasiatic (Munda) speaking Bonda of the eastern state of Orissa (35.7%); this might reflect contacts between Eastern India and Southeast Asia related to the spread of ancestral Munda languages.<sup>6</sup>

Population	Slavic-Baltic	Uralic	Caucasus Mtns.	Indus Valley	South India	Oceanian	Southeast Asian	East Asian	Tibetan	Siberian-Arctic	Other
Bonda Orissa India	0.0%	0.0%	0.0%	0.0%	58.7%	3.2%	<b>35.7%</b>	0.7%	1.4%	0.0%	0.2%
Burusho Pakistan	1.6%	2.7%	6.1%	58.9%	20.0%	0.6%	1.2%	0.2%	2.4%	<b>2.8%</b>	3.4%
Garó [Tibetan cluster]	0.0%	0.0%	0.0%	0.0%	11.7%	0.8%	24.6%	7.8%	54.0%	0.0%	1.0%
Naga [Tibetan cluster]	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.1%	17.4%	82.0%	0.0%	0.2%
Nepal	3.0%	1.6%	1.7%	27.2%	39.1%	0.3%	0.4%	<b>4.2%</b>	<b>17.6%</b>	2.1%	2.8%
Pulliyar India	0.0%	0.0%	0.0%	0.0%	90.7%	<b>5.8%</b>	2.9%	0.0%	0.4%	0.0%	0.2%

**Table 1:** South Asian populations with maximum percentages of Oceanian and East Eurasian genetic components (highlighted in yellow). Garó and Naga percentage are also included; however, these populations are genetically related to the Tibetan cluster rather than the South Asian (Indus Valley and South India) clusters in **Figure 1**.<sup>7</sup>

South Asian maximums for the East Asian (4.2%) and Tibetan (17.6%) components are both expressed for sampled **Nepalese** individuals living in the Himalaya Mountains. This suggests that the

<sup>3</sup> For more detailed analysis of the West Eurasian genetic components in South Asia, see <http://dnatribes.com/dnatribes-digest-2012-11-01.pdf>.

<sup>4</sup> For more discussion about Central Asia, see <http://dnatribes.com/dnatribes-digest-2011-10-01.pdf>.

<sup>5</sup> Similar names appear in several Indian Ocean related cultures, such as Meluhha, Malay, Malacca, and Malagasy.

<sup>6</sup> Para-Munda languages (such as Khasi) have sometimes been proposed for the Bronze Age Harappan Civilization.

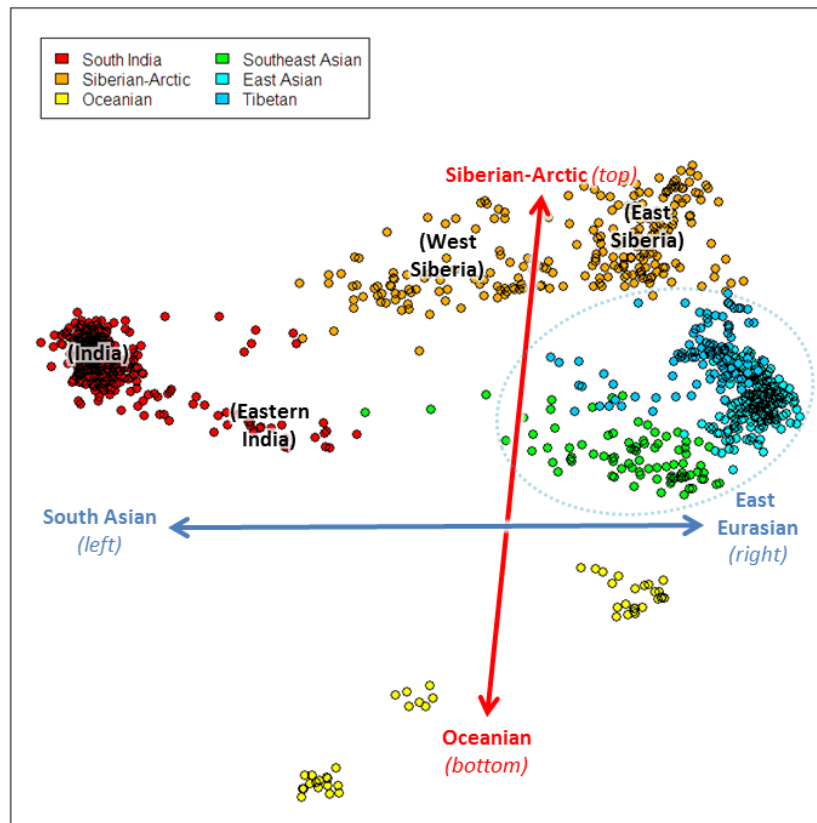
<sup>7</sup> For complete admixture listings as of Feb. 2013, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

northeastern highlands of South Asia have been an important contact point with Tibeto-Burman speaking cultures. Nepal was the location of the early Shakya kingdom, which the Sanskritist Michael Witzel has suggested might have been related to Iron Age Saka (Scythian related) cultures of Central Asia.<sup>8</sup>

In addition, sampled Tibeto-Burman speaking Garo and Naga individuals living in eastern parts of India are primarily related to the Tibetan region (see **Figure 1** and **Table 1**) with some additional South India (11.7%) admixture expressed for sampled Garo (but not for sampled Naga). This might reflect Tibeto-Burman expansions in highland areas near the Tibetan Plateau.

## Regional Genetic Relationships in Asian-Pacific Populations

To visualize Asian-Pacific genetic relationships, MDS analysis of individuals sampled randomly from East Asian, Tibetan, Southeast Asian, and neighboring regions was performed. Results are illustrated in **Figure 2**.



**Figure 2:** MDS plot of individuals randomly sampled from Asian-Pacific (circled) and neighboring regions identified by *DNA Tribes*® SNP analysis.

<sup>8</sup> See <http://www.people.fas.harvard.edu/~witzel/canon.pdf>. Cf. Indo-Scythians and Sistan (Sakistan). It is unknown whether Iron Age Saka and Shakya of South Asia were related to Bronze Age SA.GAZ (Apiru) of West Asia (mentioned in Sumerian records); however, some similar cultural terms appear in both contexts (cf. Kassite *Šuqamuna*; Pali *Shakyamuni*).

**Discussion:** Results in **Figure 2** express two genetic patterns in sampled Asian-Pacific individuals. First, the **blue horizontal (left-to-right) axis** expresses the genetic difference between South Asian (leftmost) and East Eurasian (rightmost) individuals.

As discussed in the previous section of this article, some Siberian and Indian (including Tibeto-Burman speaking Garo and Naga, associated with the Tibetan cluster illustrated in cyan in **Figure 2**) individuals form two separate continua that partly “bridge” the genetic distance between South Asians and East Asians. **Figure 2** shows that at the eastern side of this continuum, some sampled Southeast Asians (displayed as green dots in **Figure 2**) similarly extend leftwards toward South Asia.

Admixture analysis similarly expresses South Asian (Indus Valley and South India) admixture components for some additional Tibetan and Southeast Asian individuals (listed in **Table 2**). Among sampled Tibetans, the largest South Asian components were expressed for Burma (Indus Valley 1.3%; South India 15.1%). Among sampled Southeast Asian populations, South India components peak in Thailand (11.5%). These results suggest contacts between South Asia and the Hindu and Buddhist influenced areas of Southeast Asia (sometimes described as “Greater India”).

Population	Indus Valley	South India	Southeast Asian	East Asian	Tibetan	Other
Burma [Tibetan]	1.3%	15.1%	23.7%	18.6%	38.7%	2.6%
Cambodia [S.E. Asian]	0.6%	3.2%	66.5%	23.8%	2.3%	3.6%
Khmer Cambodia [S.E. Asian]	0.0%	4.4%	53.9%	34.5%	3.8%	3.5%
Malay Singaporean [S.E. Asian]	0.2%	4.5%	67.5%	19.7%	0.7%	7.5%
Thailand [S.E. Asian]	0.6%	11.5%	55.9%	22.7%	2.8%	6.5%

**Table 2:** Asian-Pacific populations with maximum percentages of South Asian (Indus Valley and South India) genetic components (highlighted in yellow).<sup>9</sup>

Second, the **red vertical (top-to-bottom) axis** expresses the genetic continuum between Siberian-Arctic (top) and Oceanian (bottom) individuals. This axis in **Figure 2** expresses a smaller portion of the genetic continuum between Eurasian and Oceanian individuals illustrated in **Figure 1** (discussed in the previous section of this article). In particular, **Figure 2** shows the relative positions of sampled Asian-Pacific individuals within this continuum.

As a group, the most Siberian like Asian-Pacific individuals are sampled individuals from the Tibetan cluster (blue in **Figure 2**), including Mongolic and Tungusic speaking ethnic groups such as Oroqen, Daur, Xibo, Hezhen, and Mongola (admixture components listed in **Table 3**). This might reflect the genetic traces of contacts between Siberia and Northeast Asia, possibly including relationships between early populations speaking Altaic languages (whose relationship is debated by linguists) and nomadic confederacies (such as the Xiongnu, Göktürks, and Mongol states).

Admixture percentages in **Table 3** further reflect the genetic continuity between the East Asian, Tibetan, and Siberian-Arctic clusters, with substantial proportions of multiple ancestral components expressed in each sampled population. As illustrated in **Figure 2**, mainland Asia-Pacific individuals as a group are genetically close to one another, with less “spread” or distance between most points expressed in sampled East Asian and Tibetan (circled in **Figure 2**) than in Siberia or Oceania. However, sampling of additional populations (such as native islanders of Taiwan, the Philippines, the Ryukyu Islands, Okinawa,

<sup>9</sup> For complete admixture listings as of Feb. 2013, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

and Hokkaido, as well as Oceanian populations mentioned in the previous section of this article) might express more locally defined genetic structure in the Pacific Rim of Asia.

Population	East Asian	Tibetan	Siberian-Arctic	Other
Xibo China	38.8%	31.6%	26.4%	3.3%
Oroqen China	18.9%	23.1%	58.0%	0.0%
Mongola China	34.9%	26.0%	38.2%	0.9%
Hezhen China	29.2%	31.3%	39.4%	0.1%
Daur China	28.4%	33.0%	38.5%	0.1%

**Table 3:** Populations related to the Tibetan cluster with maximum percentages of Siberian-Arctic genetic components (highlighted in yellow).<sup>10</sup>

The Asian-Pacific populations with the largest Oceanian percentages expressed (listed in **Table 4**) include not only sampled Malay Singaporeans with ancestral ties to maritime Malay communities of the Indian and Pacific Oceans (4.3% Oceanian), but also more northerly Tibeto-Burman speaking Naxi and Tibetans of highland Asia. This suggests that genetic links between East Asia and Oceania have not been limited to strictly maritime populations, but might have involved a broader continuum of ancestral East Asians.

Further, small percentages of Oceanian components are expressed in some Central Asians, including Kyrgyz (0.9%), Uyghur (0.8%), and Hazara (0.7%). These small percentages might simply express noise or signals of non-Oceanian Asian ancestry not yet characterized by available populations. However, it is noteworthy that a genetic relationship has been identified between present day Oceanians (including Papuans and Melanesians) and the archaic Denisova Cave hominins that lived near the Altai Mountains of Central Asia approximately 41,000 years ago.

As mentioned in the previous section of this article, these Asian-Pacific and Oceanian genetic links (possibly including the genetic traces of Denisovans or other archaic hominin populations in Asia) can be explored in more detail if more samples become available in the future.

Population	South India	Oceanian	Southeast Asian	East Asian	Tibetan	Siberian-Arctic	Other
Malay Singaporean	4.5%	4.3%	67.5%	19.7%	0.7%	0.3%	3.0%
Thailand	11.5%	1.7%	55.9%	22.7%	2.8%	0.6%	4.8%
Vietnam	0.1%	1.4%	32.2%	64.8%	1.1%	0.0%	0.5%
Iban Borneo	0.0%	1.2%	92.7%	6.0%	0.0%	0.0%	0.2%
Naxi China	0.4%	1.2%	3.7%	30.3%	63.6%	0.0%	0.8%
Tibet	0.7%	1.0%	0.0%	4.7%	89.1%	2.7%	1.7%
Kyrgyz	1.5%	0.9%	0.7%	7.2%	16.1%	51.3%	22.3%
Uyghur China	3.5%	0.8%	0.9%	9.2%	17.8%	26.2%	41.5%
Hazara Pakistan	4.8%	0.7%	1.2%	7.4%	10.6%	34.9%	40.6%

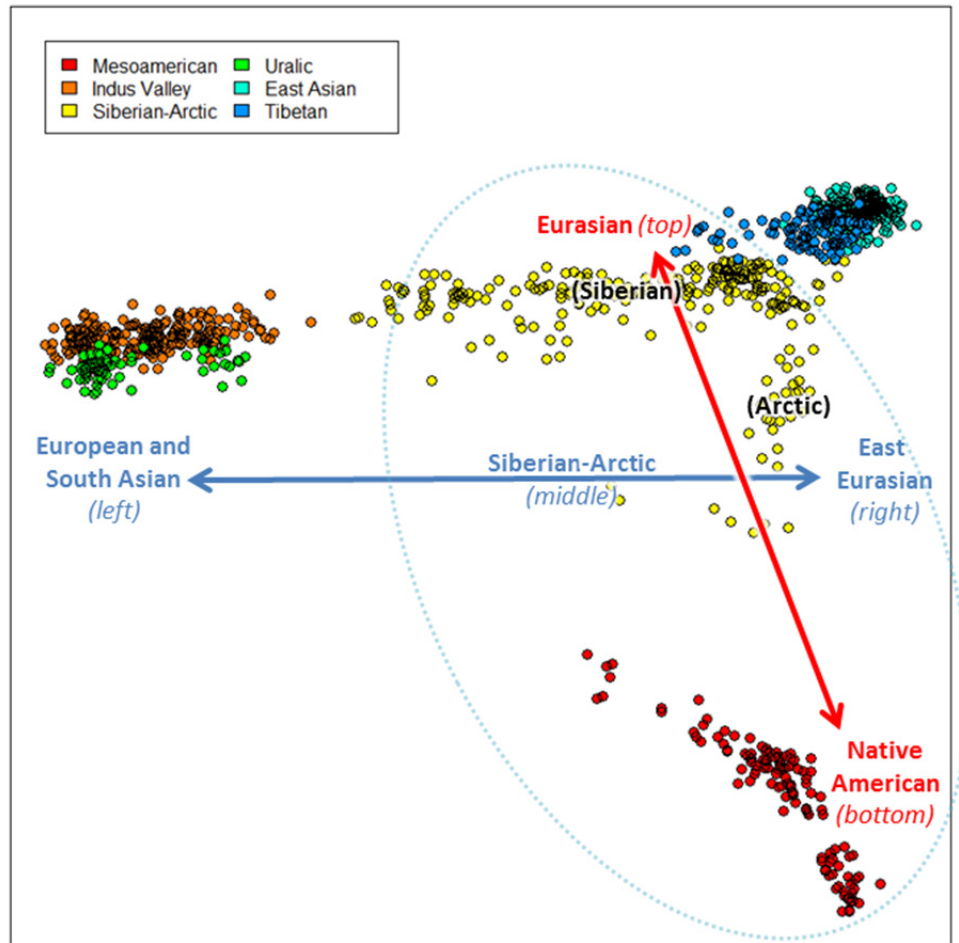
**Table 4:** Sampled Asian-Pacific populations with maximum percentages of Oceanian genetic components (highlighted in yellow).<sup>11</sup>

<sup>10</sup> For complete admixture listings as of Feb. 2013, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

<sup>11</sup> *Ibid.*

## Regional Genetic Relationships in North Asia and Native Americans

To visualize genetic relationships in North Asia and indigenous populations of the Americas, MDS analysis of individuals sampled randomly from Siberian-Arctic, Mesoamerican, and neighboring regions identified by *DNA Tribes*® SNP analysis was performed. Results are illustrated in **Figure 3**.



**Figure 3:** MDS plot of individuals randomly sampled from North Asian and Native American (circled) and neighboring regions identified by *DNA Tribes*® SNP analysis.

**Discussion:** Results in **Figure 3** express two genetic patterns among randomly sampled North Asian and Native American individuals. First, the **blue horizontal (left-to-right) axis** expresses the genetic differences between European and South Asian (left) and East Eurasian (right) individuals.

The left end of this continuum includes the Western Siberian and Central Asian individuals that are most similar to sampled individuals related to the Uralic (green in **Figure 3**) and Indus Valley clusters (orange in **Figure 3**). However, in this graph these two leftmost clusters generally represent the West Eurasian related genetic components of some North Asians, which are not exclusive to Uralic and Indus Valley genetic links.

Admixture percentages in **Table 5** provide a more detailed analysis of West Eurasian and South Asian genetic components in North Asian populations. Results include a variety of European, West Asian, and South Asian genetic components expressed in several ethnic groups:

**European components** (highlighted in yellow in **Table 5**) include Iberian-Italian, Northwest European, Slavic-Baltic, and Uralic percentages. The largest Iberian-Italian percentage is expressed for Hazara (1.4%), a South Asian ethnic group sometimes associated with either medieval Mongols settlers from the period of Genghis Khan or more ancient Kushan (Yuezhi or Tocharian related) populations of Central and South Asia.

The largest Northwest European percentages are expressed for sampled Uyghurs (6.1%), possibly in part descended from early Tocharian speaking populations of the Tarim Basin. Both Iberian-Italian and Northwest genetic components today are associated with populations living far to the west; however, they might reflect genetic traces of early migrations that reached both Europe and Central and South Asia. In particular, both Hazara and Uyghur have possible links with pre-Turkic (Tocharian) populations speaking *centum* Indo-European languages usually associated with the Mediterranean and Western Europe.<sup>12</sup>

Population	Iberian-Italian	Northwest European	Slavic-Baltic	Uralic	East Mediterranean	Mesopotamian	Caucasus Mountains	Indus Valley	South India	Siberian-Arctic	Other
Altai Russian Federation	0.5%	2.2%	0.6%	2.4%	0.5%	0.4%	1.2%	3.2%	1.0%	73.0%	15.1%
Dolgan Russian Federation	0.4%	0.6%	3.2%	2.9%	0.0%	0.0%	1.5%	0.0%	1.1%	89.7%	0.6%
Hazara Pakistan	1.4%	1.2%	1.8%	2.3%	0.9%	5.9%	8.5%	17.8%	4.8%	34.9%	20.6%
Kyrgyz	0.6%	2.2%	1.8%	2.5%	1.6%	1.4%	5.5%	4.7%	1.5%	51.3%	26.9%
Selkup Russian Federation	0.0%	3.8%	3.1%	17.5%	0.0%	0.0%	0.0%	0.2%	0.0%	72.8%	2.7%
Uyghur China	0.3%	6.1%	4.4%	1.5%	0.7%	4.0%	8.6%	14.0%	3.5%	26.2%	30.5%
Uzbek Central Asia	1.0%	3.2%	5.5%	5.6%	2.5%	6.1%	9.2%	17.2%	3.8%	30.0%	15.8%

**Table 5:** Sampled North Asian related populations with maximum percentages of European (highlighted in yellow), West Asian (highlighted in cyan), and South Asian (highlighted in magenta) genetic components.<sup>13</sup>

European genetic components in Siberia also include Slavic-Baltic (largest in sampled Uzbeks at 5.5%) and Uralic percentages (largest in Selkup at 17.5%). These components might express patterns of contact that date to the Iron Age Scythian and Sarmatian migrations, as well as older Bronze Age (Andronovo) and Mesolithic (Keltiminar) links between populations of Eastern Europe, West Siberia, and Central Asia.<sup>14</sup>

**West Asian components** (highlighted in cyan in **Table 5**) include East Mediterranean, Mesopotamian, and Caucasus Mountains percentages. These percentages are all highest for sampled

<sup>12</sup>For more detailed analysis, see <http://dnatribes.com/dnatribes-digest-2012-11-01.pdf> and <http://dnatribes.com/dnatribes-digest-2013-01-02.pdf>.

<sup>13</sup>For complete listings as of Feb. 2013, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

<sup>14</sup>For more analysis of Siberian links in Northern Europe dating to the Mesolithic period, see <http://dnatribes.com/dnatribes-digest-2012-10-01.pdf> and <http://dnatribes.com/dnatribes-digest-2013-01-02.pdf>. For more about European links in Siberia, see <http://dnatribes.com/dnatribes-digest-2009-11-30.pdf>.



Uzbek populations from Central Asia, including: East Mediterranean (2.5%), Mesopotamian (6.1%), and Caucasus Mountains (9.2%). These West Asian genetic components might in part express traces of classical Saka-Scythian populations that integrated elements of the Bronze Age Andronovo cultures with an influx of Iron Age technologies from West Asia. These Iron Age cultures are attested in the Pazyryk burials discovered in the Altai Mountains, which used kurgan mounds and an “animal style” tradition of artwork that derived from the Maykop culture of the third millennium BCE.<sup>15</sup>

The exact cultural relationships between Iron Age Scythian and Sarmatian cultures and later European, Central Asian, South Asian,<sup>16</sup> and Siberian cultures are unclear. However, it is worth noting that Eurasian nomadic confederacies as early as the classical period Xiongnu and Huns included multiple ethnic and linguistic groups.<sup>17</sup>

**South Asian components** (highlighted in magenta in Table 5) include Indus Valley and South India percentages. The highest percentages for both of these components are expressed for sampled Hazara (17.8% Indus Valley and 4.8% South India) living in Afghanistan and Pakistan. As discussed earlier in this section, Hazara are thought to be partly descended from Mongol settlers or possibly earlier Central Asian cultures such as Kushans. However, these results express substantial genetic continuity with neighboring South Asian populations, which might reflect mixture in recent history, but might also reflect traces of Iron Age expansions of Scythians and other South Asian related cultures in the Tarim Basin home of the ancestral Kushans (sometimes suggested as related to modern Hazara).

Conversely, admixture results in **Table 6** list the sampled populations for which the largest percentages of Siberian-Arctic ancestral components are expressed. These include Nganasan (99.4%) of the Taymyr Peninsula in northern Siberia, who speak a locally unique branch of the Uralic languages that are also spoken in northerly parts of Eurasia. High Siberian-Arctic percentages are also expressed for sampled Yukaghir (98.6%), who speak a Paleosiberian language isolate that is sometimes classified as a member of a theoretical Uralic-Yukaghir family.<sup>18</sup> This might reflect a link between Uralic and Paleosiberian languages and early population strata in northern Eurasia.

Population	East Asian	Tibetan	Siberian-Arctic	Other
Nganasan Russian Federation	0.0%	0.5%	99.4%	0.1%
Yukaghir Russian Federation	0.0%	0.3%	98.6%	1.1%
Evenk Russian Federation	0.8%	2.3%	96.9%	0.0%
Yakut Siberia	0.7%	5.0%	93.1%	1.3%
Tuvinians Russian Federation	2.1%	16.3%	80.9%	0.7%
Buryat Russian Federation	4.4%	18.7%	76.5%	0.4%

**Table 6:** Sampled Siberian-Arctic related populations with maximum percentages of local Siberian-Arctic genetic components.<sup>19</sup>

<sup>15</sup> See also <http://dnatribes.com/dnatribes-digest-2012-05-01.pdf>; <http://dnatribes.com/dnatribes-digest-2012-09-01.pdf>; and <http://www.degruyter.com/view/books/9783110266306/9783110266306.77/9783110266306.77.xml>.

<sup>16</sup> Often omitted in discussions of the Iron Age Scythians are the Indo-Scythian and Shakya cultures of South Asia. Present day languages related to ancient Scythian might include Pashto, Yaghnobi, and Ossetian.

<sup>17</sup> Although circular yurts or gers became iconic for Mongolic and Turkic cultures (“all tribes living in felt tents”), the earliest yurt depictions date to the Iron Age, when nomadic *Sakas* (cf. Bronze Age *SA.GAZ*; see note 6) and *Skythoi* (Scythians; cf. *sukkot*) were active in West Asia and several other parts of Eurasia.

<sup>18</sup> For more information, see <http://dnatribes.com/dnatribes-digest-2009-11-30.pdf>.

<sup>19</sup> For complete admixture listings as of Feb 2013, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

Second, the **red vertical (top-to-bottom) axis** expresses the genetic continuum between Eurasian (top) and Native American (bottom) individuals. In particular, Far East Siberian and Arctic (Greenland Inuit) populations are genetically closer to sampled Native Americans from present day Mexico and Central and South America.

Admixture percentages in **Table 7** express these relationships in more detail. In Siberia, Mesoamerican (Native Mexican and Central and South American) percentages are largest for sampled Chukchi (15.8%). However, Mesoamerican percentages are higher for sampled Tunumiit (Inuit) individuals from Eastern Greenland (31.3%). These results are consistent with substantial Native American genetic influence in the most northerly parts of North America, possibly related to early population expansions in the Alaskan and Canadian Arctic.<sup>20</sup>

Population	Siberian-Arctic	Mesoamerican	Other
Yukaghir Russian Federation	98.6%	1.1%	0.3%
Koryak Russian Federation	87.3%	7.1%	5.6%
Chukchi Russian Federation	75.5%	<b>15.8%</b>	8.7%
Eastern Greenland	59.7%	<b>31.3%</b>	9.0%

**Table 7:** Sampled Siberian-Arctic related populations with maximum percentages of Mesoamerican genetic components.<sup>21</sup>

## Conclusion

In summary, Multi-Dimensional Scaling graphs illustrate the genetic continuity among individuals sampled from regions around the world and complement admixture results and other types of autosomal SNP analysis.

MDS analysis of genome data can express many types of relationships between individuals. The MDS graphs in these two Digest articles have been selected to illustrate two kinds of "big picture" genetic relationships that are sometimes overlooked:

- 1) Relationships between individuals from around the world as a whole (Figure 1 in the April 2013 Digest issue<sup>22</sup>); and
- 2) Relationships between individuals randomly sampled from each world region and from neighboring and related world regions (Figures 2-5 in the April 2013 Digest issue<sup>23</sup> and Figures 1-3 in this month's Digest issue).

In particular, the MDS graphs in these two Digest articles have been selected to illustrate large scale or inter-regional relationships and the genetic continuity linking individuals from multiple ethnic groups. These relationships expressed can sometimes cross perceived cultural boundaries, revealing the basic interconnectedness of populations around the world.

<sup>20</sup> For more detailed analysis, see <http://dnatribes.com/dnatribes-digest-2012-12-01.pdf>.

<sup>21</sup> For complete listings as of February 2013, see <http://dnatribes.com/dnatribes-snp-admixture-2013-02-11.pdf>.

<sup>22</sup> See <http://dnatribes.com/dnatribes-digest-2013-04-02.pdf>.

<sup>23</sup> *Ibid.*



## Getting the Most from Your STR Testing

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DNA Tribes® offers several \$24.99 Add-On reports to customize your analysis:

**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.

Once lab testing is complete, Add-On reports can be performed at any time (without the need to submit new DNA samples) by ordering through our secure online checkout at [http://dnatribes.com/order\\_addons.html](http://dnatribes.com/order_addons.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 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.

More information about *DNA Tribes® Europa* is available for \$49.99 at: <http://dnatribes.com/dnatribes-europa.html>

**Confirm or Clarify Your Results with Lab Upgrade:**

For customers who have completed testing with DNA Tribes®, we offer 15-to-21, 15-to-27 and 21-to-27 Marker Upgrade tests. Upgrades include lab testing of additional STR marker systems, allowing a closer comparison of your own DNA to world populations for enhanced match precision and power of exclusion. The incorporation of additional marker systems can confirm or clarify your existing results, and all upgrades includes an update to all Add-On reports previously ordered for your kit.

Upgrades are available through our secure online checkout system at: [http://dnatribes.com/order\\_upgrades.html](http://dnatribes.com/order_upgrades.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. Your personal DNA matches can express recent family genealogy and more ancient genetic relationships among world populations.

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>.