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Introduction

Hello, and welcome to the July 2014 issue of DNA Tribes[®] Digest. This month's article features an in depth exploration of how ancestral relationships between world populations are expressed by admixture percentages of **five continental cores** identified by the new DNA Tribes[®] SNP Update.

Best regards, Lucas Martin DNA Tribes

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Five Continent Core Components in 44 World Regions

Background: Deep Ancestry Expressed in Five Isolated Clusters

The new DNA Tribes® SNP update features two new forms of admixture analysis. Last month's Digest article (available at <u>http://dnatribes.com/dnatribes-digest-2014-06-02.pdf</u>) introduced the new 44 cluster analysis of world genetic structure. This month's article focuses on how deeper genomic relationships between populations are expressed by percentages of five continent cores (illustrated in **Figure 1**).

The continental cores are a select group of five more isolated clusters (out of the 44 total world clusters) that are representative of major segments of world genetic structure:

- Basque (core Mediterranean)
- Mesoamerican (core North Eurasian and Native American)
- Dravidian-South India (core Central Eurasian)
- Mbuti-Aka (core Sub-Saharan African)
- South Chinese (core Asian-Pacific)



Figure 1: Map of five continent cores identified in the Summer 2014 *DNA Tribes[®] SNP* Update. Each core cluster is representative of a major segment of world genetic structure (listed in parentheses).

Average percentages of these five continental components for individuals from the world populations sampled in our SNP database are listed at <u>http://dnatribes.com/dnatribes-snp-admixture-2014-06-03.pdf</u>. This month's Digest article further explores how these continent core percentages vary between the 44 world clusters identified by the new DNA Tribes[®] SNP Update, **expressing genetic traces of the early human migrations that populated the African, Eurasian, and American continents**.

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Five Core Components in African Regions

 Table 1 and Figure 2 show the percentages of five continent cores expressed in the African clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.



Figure 2: Percentages of five continent cores expressed in African genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.¹

Within Africa, **Aka-Mbuti (core Sub-Saharan African)** percentages are highest (expectedly) in the Aka-Mbuti-Hadza (92.9%) and Khoisan (90.0%) clusters and lowest in the Red Sea Yemen-Egypt (14.5%) and Berber-North African (21.5%) clusters. Notably, these components are lowest near the Nile River and Sahara Desert, which have been important contact points for migrations between Africa and Eurasia.

Conversely, **Basque (core Mediterranean)** percentages in Africa are highest in the Berber-North African (57.1%) and Red Sea Yemen-Egypt (56.5%) clusters, in which Basque is the highest core component expressed. Basque percentages are also relatively high in the Horn of Africa (31.9%) cluster, perhaps also due to early contacts between African and Eurasian populations via the Red Sea and Arabian Peninsula (perhaps including **Basal Eurasian** expansions predicted by recent models of

¹ More information about the new SNP update is available at <u>http://dnatribes.com/snp.html</u>.



human population history).² In contrast, Basque percentages are lowest (but not absent) in the Aka-Mbuti-Hadza (2.2%) and Khoisan (3.2%) clusters.

This suggests that, although small amounts of gene flow from ancestral Mediterranean related populations might have shaped these remote clusters, Aka-Mbuti-Hadza and Khoisan populations represent the living Africans that have been least affected by Mediterranean related expansions (possibly in part related to First Farmers expanding in Africa and Eurasia from the Fertile Crescent).³

Surprisingly, substantial **Dravidian-South India (core Central Eurasian)** percentages are expressed in several African clusters. Dravidian percentages are highest in Red Sea Yemen-Egypt (27.4%) and Horn of Africa (20.9%) clusters, suggesting that gene flow related to the Indian **Subcontinent (possibly related to expansions originating near West Asia)** has helped shape African genetic structure. As with Basque (core Mediterranean) components, Dravidian percentages are lowest but not absent in Khoisan (2.4%) and Aka-Mbuti-Hadza (3.7%) clusters. These traditional hunter-gatherer Khoisan and Aka-Mbuti-Hadza populations might represent the modern Africans least affected by these Eurasian related migrations.

Traces of another unexpected Eurasian component, **South Chinese (core Asian-Pacific)**, are also expressed at low levels in some parts of Africa. South Chinese percentages are highest in Omotic-Ari Ethiopia (3.5%) and West African (2.9%) clusters and lowest in Red Sea Yemen-Egypt (0.6%) and Aka-Mbuti-Hadza (0.7%) populations. This pattern contrasts with the distribution of Basque and Dravidian core components in Africa, which might reflect different or more ancient expansions (possibly including Eastern Non-Africans or early archaic hominin expansions pre-dating the Paleolithic Out of Africa migrations).⁴

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Aka-Mbuti-Hadza	<mark>92.9%</mark>	2.2%	3.7%	0.7%	0.5%
Bantu-Southern African	84.1%	4.6%	8.8%	1.9%	0.5%
Berber-North African	21.5%	<u>57.1%</u>	19.7%	0.9%	0.9%
Horn of Africa	44.8%	31.9%	20.9%	1.5%	0.8%
Khoisan	92.0%	3.2%	2.4%	0.9%	<u>1.6%</u>
Nilotic	72.4%	10.2%	14.3%	2.9%	0.3%
Omotic-Ari Ethiopia	62.7%	16.7%	16.6%	<u>3.5%</u>	0.5%
Red Sea Yemen-Egypt	14.5%	56.5%	<mark>27.4%</mark>	0.6%	1.0%
West African	79.2%	5.9%	11.7%	2.9%	0.3%

Table 1: Percentages of five continent cores expressed in African genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

² More discussion of Mediterranean related components in the Horn of Africa is included in these Digest articles: <u>http://dnatribes.com/dnatribes-digest-2014-05-01.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2014-03-01.pdf</u>. ³ For more discussion of First Farmers in Africa and Eurasia, see <u>http://dnatribes.com/dnatribes-digest-2014-03-01.pdf</u>. <u>01.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2013-08-01.pdf</u>.

⁴ More discussion of ancestral Eastern Non-Africans and possible archaic components linking African and Asian-Pacific populations is included at <u>http://dnatribes.com/dnatribes-digest-2014-03-01.pdf</u>.



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Finally, relatively little trace of the **Mesoamerican (core North Eurasian and Native American)** component is expressed in Africa, except for small percentages in Khoisan (1.6%) and Red Sea Yemen-Egypt (1.0%) populations. This might reflect small traces of **Ancestral North Eurasian (ANE)** expansions that primarily affected the Middle East and Europe but reached some parts of Africa (possibly via indirect migrations). **If so, the ANE links with Africa might have involved West Asian related populations living near both the Nile Valley and locations associated with ancestral Khoisan populations (possibly prior to Khoisan migrations into Southern Africa).⁵**

Five Core Components in European Regions

Table 2 and **Figure 3** show the percentages of five continent cores expressed in the European clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.



Figure 3: Percentages of five continent cores expressed in European genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.⁶

Within Europe, **Aka-Mbuti (core Sub-Saharan African)** percentages are highest in the Sephardic Sicilian (6.1)%, Ashkenazi Jewish (5.0%), Spanish-Portuguese (4.2%), and Aegean-Balkan-Italian (3.1%) clusters, all associated with Mediterranean related cultures, including both Afro-Asiatic speaking (Hebraic and Phoenician) and Indo-European speaking societies (in particular the expansionary Greco-Romans) of the ancient Mediterranean.

In contrast, Aka-Mbuti percentages in Europe are lowest in the Finnish (1.4%) and Basque (1.6%) clusters, both associated with geographically isolated cultures speaking non-Indo-European languages near the Baltic Sea (Finnish) and Pyrenees Mountains (Basque). This suggests that within Europe, Aka-Mbuti components might in part reflect contacts with expansionary

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⁵ More discussion of ANE migrations in Eurasia is included at <u>http://dnatribes.com/dnatribes-digest-2014-02-01.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2014-04-02.pdf</u>.

⁶ More information about the new SNP update is available at <u>http://dnatribes.com/snp.html</u>.





maritime cultures active in the ancient Mediterranean, linking Iron Age Near Eastern, European, and African societies.⁷

A somewhat different Atlantic European distribution is expressed for Basque (core Mediterranean) percentages, which are highest (expectedly) in Basque (84.4%), Spanish-Portuguese (73.9%), and NW European (72.0%) clusters. Basque percentages are lowest in North and East European clusters, including Mari-Chuvash (48.3%), Tatar-Chuvash (54.4%), and Finnish (65.0%). Nevertheless, Basque is the highest component expressed for all European clusters. This suggests that Basque percentages reflect a predominant ancestral component in Europe, which is also found at substantial levels throughout the Middle East and Central Eurasia (as the next sections of this article will discuss).

Surprisingly, **Dravidian-South India (core Central Eurasian)** percentages are also expressed for all studied European clusters. These percentages are highest in Ashkenazi Jewish (25.0%), Sephardic-Sicilian (25.0%), Balto-Slavic (23.3%), and Tatar-Chuvash (23.2%) clusters. Dravidian percentages are lowest for Basque (11.6%) and Spanish-Portuguese (18.8%) clusters. Although further study is needed, these unexpected links might in part reflect Ancestral North Eurasian (ANE) components found throughout the Middle East and Europe, perhaps related to steppe migrations linking the Middle East and Europe with Central Asia during early periods (such as the Bronze Age and Iron Age).⁸

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Aegean-Balkan-Italian	3.1%	71.3%	22.4%	0.4%	2.7%
Ashkenazi Jewish	5.0%	67.7%	<mark>25.0%</mark>	0.3%	2.0%
Balto-Slavic	1.7%	67.6%	23.3%	0.7%	6.7%
Basque	1.6%	<mark>84.4%</mark>	11.6%	0.7%	1.6%
Central European	2.0%	69.8%	22.5%	0.4%	5.3%
Finnish	1.4%	65.0%	22.5%	2.9%	8.2%
Mari-Chuvash	1.7%	48.3%	23.0%	<mark>15.1%</mark>	<mark>11.9%</mark>
NW Europe	1.9%	72.0%	21.2%	0.1%	4.8%
Sephardic-Sicilian	<mark>6.1%</mark>	67.3%	<mark>25.0%</mark>	0.3%	1.2%
Spanish-Portuguese	4.2%	<u>73.9%</u>	18.8%	0.4%	2.8%
Tatar-Chuvash	2.0%	54.4%	23.2%	10.8%	9.6%

Table 2: Percentages of five continent cores expressed in European genetic clusters identified by the

 Summer 2014 DNA Tribes[®] SNP Update.

⁷ For more discussion of African and Middle Eastern genetic components in Europe, possibly related to East Mediterranean expansions dating in part to the Neolithic period, see <u>http://dnatribes.com/dnatribes-digest-2014-04-02.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2014-03-01.pdf</u>.

⁸ For more discussion of Ancestral North Eurasian (ANE) populations identified by recent ancient DNA recovered from Paleolithic Siberians and Mesolithic Northern Europeans, see <u>http://dnatribes.com/dnatribes-digest-2014-01-03.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2014-02-01.pdf</u>.





In contrast to the wide distribution of Dravidian components, **South Chinese (core Asian-Pacific)** percentages are found in only some European clusters, including Mari-Chuvash (15.1%), Tatar-Chuvash (10.8%), and Finnish (2.9%) populations. Because of this limited distribution in Uralic and Turkic speaking populations of Northeastern Europe, these components might reflect more specific migrations between Europe and Asia, such as the **Seima-Turbino Phenomenon** and medieval Turko-Mongol expansions.⁹

A different pattern is expressed for **Mesoamerican (core North Eurasian and Native American)** percentages, which are found at low levels in all studied European clusters. Like South Chinese components, Mesoamerican percentages are highest in Mari-Chuvash (11.9%), Tatar-Chuvash (9.6%), and Finnish (8.2%) populations. However, small Mesoamerican percentages are found even in Sephardic-Sicilian (1.2%), Basque (1.6%), and Ashkenazi Jewish (2.0%) clusters. This wide, low level distribution might reflect an ancient expansion that reached all parts of Europe, such as **Ancestral North Eurasian (ANE)** expansions (possibly also related to the Dravidian-South India core component discussed in this section).

Five Core Components in West Asian Regions

Table 3 and **Figure 4** show the percentages of five continent cores expressed in the West Asian clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Azeri-Kurdish-Persian-Turkey	5.0%	57.4%	34.3%	1.1%	2.2%
Bedouin-Gulf Arabs	9.4%	61.4%	27.8%	0.7%	0.8%
Central Asian	3.0%	41.4%	<mark>36.0%</mark>	<mark>13.2%</mark>	<mark>6.4%</mark>
Daghestan-North Caucasus	3.0%	57.8%	33.8%	0.6%	4.8%
Lebanese-Cyprus East Mediterranean	6.7%	<mark>63.0%</mark>	28.8%	0.3%	1.1%
Mideastern Jewish	5.1%	59.9%	33.5%	0.3%	1.3%
Pontic West Caucasus	3.6%	58.1%	32.8%	2.2%	3.3%
Red Sea Yemen-Egypt	14.5%	56.5%	27.4%	0.6%	1.0%

 Table 3: Percentages of five continent cores expressed in West Asian genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

As in Europe (see previous section), **Dravidian-South India (core Central Eurasian)** percentages are found throughout West Asia. These are highest in the Central Asian (36.0%) and Azeri-Kurdish-Persian-Turkey (34.3%) clusters, but also substantial in the Red Sea Yemen-Egypt (27.4%) and Bedouin-Gulf Arabs (27.8%) clusters. This might reflect traces of widespread Eurasian expansions that helped shape both European and Middle Eastern genetic structure, perhaps including ANE expansions discussed earlier in this article.

However, **South Chinese (core Asian-Pacific)** components are found only in some West Asian clusters, including: Central Asian (13.2%), Pontic West Caucasus (2.2%), and Azeri-Kurdish-Persian-

⁹ For more discussion, see <u>http://dnatribes.com/dnatribes-digest-2013-06-01.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2013-10-01.pdf</u>.



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Turkey (1.1%) clusters. Similar to Europe, these might reflect specific traces of medieval Turko-Mongol expansions.

More elusively, **Mesoamerican (core North Eurasian and Native American)** percentages are found at low levels in most parts of West Asia, with the highest percentages in the Central Asian (6.4%) and Daghestan-North Caucasus (4.8%) clusters and the lowest percentages in Bedouin-Gulf Arabs (0.8%) and Red Sea Yemen-Egypt (1.0%) clusters. These small components might in part reflect traces of Ancestral North Eurasian (ANE) expansions, which might have entered the Middle East near the Caspian Sea (ancient Khorasan) with early steppe migrations (such as the Hurro-Urartian expansions during the Middle Bronze Age).¹⁰



Figure 4: Percentages of five continent cores expressed in West Asian genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.¹

¹⁰ For more information, see <u>http://dnatribes.com/dnatribes-digest-2012-11-01.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2012-09-01.pdf</u>.



Five Core Components in Indian Subcontinent Regions

Table 4 and **Figure 5** show the percentages of five continent cores expressed in the Indian Subcontinent clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

Within the Indian Subcontinent, **Aka-Mbuti (core Sub-Saharan African)** percentages are highest in the Kalash-Balochi (4.6%), Kannadi-Kurumba (2.4%), and Burusho-Punjabi-Sindhi (2.3%) clusters, located in the West and Northwest of the Indian Subcontinent (nearest the Arabian Sea). In contrast, Aka-Mbuti components are lowest in the more geographically isolated Northeast India (1.1%), Dravidian-South India (1.2%), and Tribal India (1.3%) clusters, which are all associated with non-Indo-European languages (**Tibeto-Burman, Dravidian, and Munda**, respectively).

Intriguingly, this suggests that within South Asia, Aka-Mbuti components might in part reflect **Indo-European expansions, possibly involving early West Asian contacts with areas near Africa** (such as the Arabian Peninsula).¹¹



Figure 5: Percentages of five continent cores expressed in Indian Subcontinent genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.¹²

Similarly, **Basque (core Mediterranean)** components are highest in northwestern clusters of the Indian Subcontinent associated with Indo-European speaking cultures, including: Kalash-Balochi (39.0%), Burusho-Punjabi-Sindhi (30.6%), and Gangetic North-Central India (16.6%) populations. Basque components are smaller (although not absent) in the Tribal India (1.0%), Northeast India

¹¹ For more discussion about early African links with the Indian Subcontinent (possibly related to maritime contacts of the Harappan Civilization), see <u>http://dnatribes.com/dnatribes-digest-2013-10-01.pdf</u>. ¹² More information about the new SNP update is available at <u>http://dnatribes.com/snp.html</u>.

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(2.2%), Kannadi-Kurumba (3.6%), and Dravidian-South India (4.8%) clusters, associated with other language families.

As expected, **Dravidian-South India (core Central Eurasian)** components are highest in the Dravidian cluster (89.5%), with the other highest percentages in Kanadi-Kurumba (88.4%) and Tribal India (81.0%) populations. Dravidian percentages are lowest at the outskirts of the Indian Subcontinent, including the Northeast India (26.4%) and Kalash-Balochi (53.6%) clusters.

Nevertheless, as discussed in other sections of this article, Dravidian core components are found not only in the Indian Subcontinent, but also in distant parts of the Middle East, Europe, and Siberia. This suggests the Dravidian component might reflect traces of more ancient population expansions in Eurasia, not restricted to any present day language or culture within South Asia.

South Chinese (core Asian-Pacific) components reach local maxima in the Tibeto-Burman speaking Northeast India (67.4%) and Munda speaking Tribal India (16.1%) clusters, with the lowest percentages in Indo-European speaking Kalash-Balochi (0.1%) and Burusho-Punjabi-Sindhi (1.8%) populations. These components might reflect specific traces of Asian related expansions in the north and east of the Indian Subcontinent.¹³

A somewhat different, northerly distribution is expressed for **Mesoamerican (core North Eurasian)** percentages, which are highest in the Burusho-Punjab-Sindhi (3.6%), Northeast India (2.9%), and Kalash-Balochi (2.7%) clusters and lowest in interior Tribal India (0.6%) and Dravidian (1.1%) populations. This might reflect multiple expansions of partly Ancestral North Eurasian (ANE) populations in India, possibly including both Indo-European and Tibeto-Burman speaking cultures.

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Burusho-Punjab-Sindhi	2.3%	30.6%	61.6%	1.8%	<mark>3.6%</mark>
Dravidian South India	1.2%	4.8%	<u>89.5%</u>	3.3%	1.1%
Gangetic North-Central India	1.6%	16.6%	77.4%	2.1%	2.3%
Kalash-Balochi	<mark>4.6%</mark>	<mark>39.0%</mark>	53.6%	0.1%	2.7%
Kannadi-Kurumba South India	2.4%	3.6%	88.4%	4.4%	1.3%
Northeast India	1.1%	2.2%	26.4%	<mark>67.4%</mark>	2.9%
Tribal India	1.3%	1.0%	81.0%	16.1%	0.6%

Table 4: Percentages of five continent cores expressed in Indian Subcontinent genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

Five Core Components in North Eurasian Regions

Table 5 and **Figure 6** show the percentages of five continent cores expressed in the North Eurasian (Northeast European and Siberian) clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

Throughout North Eurasia, **Aka-Mbuti (core Sub-Saharan African)** percentages are generally low, reaching a local maximum in Central Asia (3.0%), which might reflect contacts with Middle Eastern populations linked to the Arabian Peninsula and Africa (such as medieval Muslim expansions or more ancient Harappan contacts with the Fertile Crescent).

¹³ See <u>http://dnatribes.com/dnatribes-digest-2013-10-01.pdf</u>.

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However, substantial **Basque (core Mediterranean)** components are found in several parts of North Eurasia, with the highest percentages expressed in Tatar-Chuvash (54.4%), Mari-Chuvash (48.3%), Central Asian (41.4%), and West Siberian (24.9%) clusters located near the outskirts of Europe and the Middle East. Lower but substantial percentages are also expressed even in distant parts of North Eurasia, including Tibetan (1.5%), Japan-North China (1.9%), and Koryak-Chukchi (3.7%) populations.

This suggests pervasive and probably ancient patterns of contact linking even distant parts of North Eurasia with the Mediterranean world, perhaps including **Upper Paleolithic Gravettian expansions** (possibly related to Dené-Caucasian languages),¹⁴ as well as later Bronze and Iron Age steppe cultures (such as the **Andronovo culture horizon and classical Scythian-Sarmatian cultures**) and historical Silk Route trade links between Mediterranean and Asian-Pacific cultures.



Figure 6: Percentages of five continent cores expressed in North Eurasian genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.¹⁵

Less expectedly, substantial **Dravidian-South India (core Central Eurasian)** components are found in several North Eurasian clusters, including: Central Asian (36.0%), West Siberian (24.3%), and Tatar-Chuvash (23.2%). Dravidian components are found at low but substantial percentages even in more distant North Eurasian clusters, including: Japan-North China (4.6%), Tibetan (8.2%), and Koryak-Chukchi (10.5%).

This wide distribution suggests that ancestral Dravidian related populations (possibly rooted in early populations living in the Indian Subcontinent, but not necessarily speaking Dravidian languages) played a role in shaping the genetic structure of large parts of Eurasia. For instance, this might have included an early South Asian branch of Eastern Non-African (ENA) populations during **Paleolithic "Out of Africa" expansions**, or perhaps Cro-Magnon related populations that ranged between Central Asia, Europe, and (in the Mesolithic period) the Indian Subcontinent.¹⁶

Also found throughout North Eurasian clusters are South Chinese (core Asian-Pacific) percentages. These are highest in Japan-North China (86.3%), Tibetan (83.6%), and Buryat-Mongol

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¹⁴ More discussion at <u>http://dnatribes.com/dnatribes-digest-2014-01-03.pdf</u>.

¹⁵ More information about the new SNP update is available at <u>http://dnatribes.com/snp.html</u>.

¹⁶ For more discussion, see <u>http://dnatribes.com/dnatribes-digest-2014-02-01.pdf</u>.



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(64.1%) populations and lowest in Tatar-Chuvash (10.8%), Central Asian (13.2%), and Mari-Chuvash (15.1%). This distribution is generally geographical, with the highest amounts in the area to the east of Lake Baikal and the lowest percentages further west and south. Although these expansions probably began early in prehistory with early expansions such as the **Seima-Turbino Phenomenon** (possibly associated with Uralic languages),¹⁷ medieval **Turko-Mongol expansions** likely played an important role in spreading South Chinese core components throughout North Eurasia.¹⁸

At the outer periphery of North Eurasia, another less expected genetic component is expressed at substantial levels: **Mesoamerican (core North Eurasian and Native American)**. Percentages of this component are highest in Koryak-Chukchi (32.9%), North Siberian (16.3%), and Yeniseian (16.3%) clusters, all associated with hunting-fishing specialized cultures, in some cases speaking Paleosiberian languages not related to present day Mongol or Turkic.¹⁹ This suggests that Mesoamerican genomic ancestry outside of the Americas might reflect traces of **Paleolithic and Mesolithic hunting-fishing cultures that once had a wider range prior to the emergence of farming and pastoralist (animal herding) cultures in the Neolithic period.²⁰**

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Buryat-Mongol	1.2%	10.5%	11.5%	64.1%	12.8%
Central Asian	<u>3.0%</u>	41.4%	<mark>36.0%</mark>	13.2%	6.4%
Japan-North China	0.6%	1.9%	4.6%	<mark>86.3%</mark>	6.6%
Koryak-Chukchi Beringian	1.1%	3.7%	10.5%	51.8%	<mark>32.9%</mark>
Mari-Chuvash	1.7%	48.3%	23.0%	15.1%	11.9%
North Siberian	1.4%	6.8%	12.2%	63.3%	16.3%
Tatar-Chuvash	2.0%	<u>54.4%</u>	23.2%	10.8%	9.6%
Tibetan	1.2%	1.5%	8.2%	83.6%	5.5%
West Siberian	1.4%	24.9%	24.3%	40.0%	9.3%
Yeniseian	1.5%	21.7%	18.2%	42.4%	16.3%

 Table 5: Percentages of five continent cores expressed in North Eurasian genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

¹⁷ See http://dnatribes.com/dnatribes-digest-2013-06-01.pdf.

¹⁸ Notably, the Paleolithic Mal'ta genome did not express Asian-Pacific related genetic components, suggesting that Chinese related expansions in Siberia took place during later periods. For more information, see http://dnatribes.com/dnatribes-digest-2014-01-03.pdf.

¹⁹ For more detailed discussion, see <u>http://dnatribes.com/dnatribes-digest-2009-11-30.pdf</u>.

²⁰ For discussion of ancient DNA evidence consistent with Mesoamerican related ancestry in Paleolithic Siberians, see <u>http://dnatribes.com/dnatribes-digest-2014-01-03.pdf</u>, <u>http://dnatribes.com/dnatribes-digest-2014-02-01.pdf</u>.



Five Core Components in Asian-Pacific Regions

 Table 6 and Figure 7 show the percentages of five continent cores expressed in the Asian-Pacific clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Japan-North China	0.6%	1.9%	4.6%	86.3%	<mark>6.6%</mark>
South China	0.7%	0.3%	2.2%	<u>95.1%</u>	1.7%
Malay-SE Asian	1.4%	<mark>2.0%</mark>	17.5%	78.4%	0.8%
Polynesian	3.0%	1.7%	18.5%	76.6%	0.3%
Melanesian	<mark>8.8%</mark>	1.5%	<u>51.1%</u>	36.6%	2.0%

 Table 6: Percentages of five continent cores expressed in Asian-Pacific genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

Among Asian-Pacific clusters, **Aka-Mbuti (core Sub-Saharan African)** components are expressed primarily in Oceanian and Pacific clusters, including: Melanesian (8.8%), Polynesian (3.0%), and Malay-SE Asian (1.4%) populations. Notably, the highest percentages are in the Melanesian cluster, in which archaic Denisovan related ancestry has been identified based on new ancient DNA evidence. For this reason, one possibility is that genomic components shared between Sub-Saharan African and Oceanian populations might reflect either very early Out of Africa migrations, or else traces of archaic hominins that came in contact with early Homo sapiens in both African and Pacific environments.²¹

Basque (core Mediterranean) components are expressed only at low levels in Asian-Pacific clusters, with the highest percentages in Malay-SE Asian (2.0%) and Japan-North China (1.9%) populations. One intriguing question raised by this distribution is whether Basque related ancestry in Asia entered Oceania through a northern migration route originating in North Asia, or else through a southern or maritime migration route originating in the Indian Subcontinent.²²

Larger percentages of **Dravidian-South India (core Central Eurasian)** components are expressed in Asian-Pacific clusters, including: Melanesian (51.1%), Polynesian (18.5%), and Malay-SE Asian (17.5%) populations. The lowest Dravidian percentages are expressed in South China (2.2%) and Japan-North China (4.6%). This distribution suggests that **Dravidian related ancestry may reflect an older layer of Asian-Pacific genetic structure**, possibly predating the expansions of Chinese related populations since the Neolithic period.²³

As expected, **South Chinese (core Asian-Pacific)** components are highest in South China (95.1%), Japan-North China (86.3%), and Malay-SE Asian (78.4%) and lowest in the Melanesian cluster (36.6%). This might reflect the traces of Neolithic expansions from near present day China and related Austronesian expansions south into Island Southeast Asia.²⁴

The highest percentages of **Mesoamerican (core North Eurasian and Native American)** components in Asian-Pacific clusters are expressed in Japan-North China (6.6%) and (surprisingly)

²¹ For more discussion, see <u>http://dnatribes.com/dnatribes-digest-2014-03-01.pdf</u>.

²² More discussion at <u>http://dnatribes.com/dnatribes-digest-2013-06-01.pdf</u>.

²³ For more discussion, see <u>http://dnatribes.com/dnatribes-digest-2014-01-03.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2013-10-01.pdf</u>.

²⁴ See <u>http://dnatribes.com/dnatribes-digest-2013-06-01.pdf</u>.





Melanesian (2.0%) populations. Mesoamerican components in Japan-North China might reflect traces of Paleolithic Siberian hunting-fishing populations related to Ancestral North Eurasians (ANE), such as the ancient Mal'ta individual (discussed earlier in this article). However, traces of this component in Melanesians are harder to account for, but might somehow relate to the small percentage of Oceanian ancestry (4%) identified for the Mal'ta genome from near Lake Baikal.²⁵



Figure 7: Percentages of five continent cores expressed in Asian-Pacific genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.¹

²⁵ See <u>http://dnatribes.com/dnatribes-digest-2014-01-03.pdf</u>.



Five Core Components in Native American Regions

Lastly, **Table 7** and **Figure 8** show the percentages of five continent cores expressed in the Native American clusters among the 44 world clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.



Figure 8: Percentages of five continent cores expressed in Native American genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.¹

Among Native American clusters, **Mesoamerican (core North Eurasian and Native American)** percentages are highest (as expected) in the Mesoamerican cluster (96.8%). In particular, **ancient DNA evidence from western Montana has shown that the present day Mesoamerican component is related to the Paleoindian Clovis culture**.²⁶ All other components are highest in the Greenland cluster (shown in **Table 7**). This suggests that Greenland Inuit populations have been less genetically isolated from Eurasian expansions than indigenous populations of living in southerly locations of the Desert Southwest, Central America, and South America.²⁷

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Greenland	<u>1.0%</u>	<mark>11.9%</mark>	<mark>11.8%</mark>	<mark>29.8%</mark>	45.6%
Mesoamerican	0.3%	1.2%	0.5%	1.2%	<u>96.8%</u>

 Table 7: Percentages of five continent cores expressed in Native American genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.

 ²⁶ For more information, see <u>http://www.nature.com/nature/journal/v506/n7487/full/nature13025.html</u>.
 ²⁷ More detailed discussion of multiple waves of ancestry in the Americas is included at <u>http://dnatribes.com/dnatribes-digest-2014-02-01.pdf</u> and <u>http://dnatribes.com/dnatribes-digest-2012-12-01.pdf</u>.



Conclusion: Five Core Components in 44 World Regions

In summary, admixture analysis using five continental cores expresses deep relationships between world populations (shown in **Table 8** and **Figure 9**). Although further research is needed to clarify the underlying population histories expressed by these components, some possible processes related to each core component are listed below:

- Basque: *East Mediterranean First Farmers.*
- Mesoamerican: *Paleolithic North Eurasian Hunters.*
- Dravidian-South India: *Early Eurasian Hunter-Fishers and Pastoralists*.
- Mbuti-Aka: *African Hunter-Gatherers*.
- South Chinese: *Chinese Neolithic Agriculturalists.*

Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Aegean-Balkan-Italian	3.1%	71.3%	22.4%	0.4%	2.7%
Aka-Mbuti-Hadza	92.9%	2.2%	3.7%	0.7%	0.5%
Ashkenazi Jewish	5.0%	67.7%	25.0%	0.3%	2.0%
Azeri-Kurdish-Persian-Turkey	5.0%	57.4%	34.3%	1.1%	2.2%
Balto-Slavic	1.7%	67.6%	23.3%	0.7%	6.7%
Bantu-Southern African	84.1%	4.6%	8.8%	1.9%	0.5%
Basque	1.6%	84.4%	11.6%	0.7%	1.6%
Bedouin-Gulf Arabs	9.4%	61.4%	27.8%	0.7%	0.8%
Berber-North African	21.5%	57.1%	19.7%	0.9%	0.9%
Burusho-Punjab-Sindhi	2.3%	30.6%	61.6%	1.8%	3.6%
Buryat-Mongol	1.2%	10.5%	11.5%	64.1%	12.8%
Central Asian	3.0%	41.4%	36.0%	13.2%	6.4%
Central European	2.0%	69.8%	22.5%	0.4%	5.3%
Daghestan-North Caucasus	3.0%	57.8%	33.8%	0.6%	4.8%
Dravidian South India	1.2%	4.8%	89.5%	3.3%	1.1%
Finnish	1.4%	65.0%	22.5%	2.9%	8.2%
Gangetic North-Central India	1.6%	16.6%	77.4%	2.1%	2.3%
Greenland	1.0%	11.9%	11.8%	29.8%	45.6%
Horn of Africa	44.8%	31.9%	20.9%	1.5%	0.8%
Japan-North China	0.6%	1.9%	4.6%	86.3%	6.6%
Kalash-Balochi	4.6%	39.0%	53.6%	0.1%	2.7%
Kannadi-Kurumba South India	2.4%	3.6%	88.4%	4.4%	1.3%
Khoisan	92.0%	3.2%	2.4%	0.9%	1.6%
Korvak-Chukchi Beringian	1 1%	3 7%	10.5%	51.8%	32.9%

 Table 8: Percentages of five continent cores expressed in 44 world genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update (*continued next page*).

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Cluster	Aka-Mbuti	Basque	Dravidian- South India	South Chinese	Mesoamerican
Lebanese-Cyprus East Mediterranean	6.7%	63.0%	28.8%	0.3%	1.1%
Malay-SE Asian	1.4%	2.0%	17.5%	78.4%	0.8%
Mari-Chuvash	1.7%	48.3%	23.0%	15.1%	11.9%
Melanesian	8.8%	1.5%	51.1%	36.6%	2.0%
Mesoamerican	0.3%	1.2%	0.5%	1.2%	96.8%
Mideastern Jewish	5.1%	59.9%	33.5%	0.3%	1.3%
Nilotic	72.4%	10.2%	14.3%	2.9%	0.3%
North Siberian	1.4%	6.8%	12.2%	63.3%	16.3%
Northeast India	1.1%	2.2%	26.4%	67.4%	2.9%
NW Europe	1.9%	72.0%	21.2%	0.1%	4.8%
Omotic-Ari Ethiopia	62.7%	16.7%	16.6%	3.5%	0.5%
Polynesian	3.0%	1.7%	18.5%	76.6%	0.3%
Pontic West Caucasus	3.6%	58.1%	32.8%	2.2%	3.3%
Red Sea Yemen-Egypt	14.5%	56.5%	27.4%	0.6%	1.0%
Sephardic-Sicilian	6.1%	67.3%	25.0%	0.3%	1.2%
South China	0.7%	0.3%	2.2%	95.1%	1.7%
Spanish-Portuguese	4.2%	73.9%	18.8%	0.4%	2.8%
Tatar-Chuvash	2.0%	54.4%	23.2%	10.8%	9.6%
Tibetan	1.2%	1.5%	8.2%	83.6%	5.5%
Tribal India	1.3%	1.0%	81.0%	16.1%	0.6%
West African	79.2%	5.9%	11.7%	2.9%	0.3%
West Siberian	1.4%	24.9%	24.3%	40.0%	9.3%
Yeniseian	1.5%	21.7%	18.2%	42.4%	16.3%

 Table 8 (continued): Percentages of five continent cores expressed in 44 world genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.



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Figure 9: Percentages of five continent cores expressed in 44 world genetic clusters identified by the Summer 2014 DNA Tribes[®] SNP Update.²⁸

²⁸ More information about the new SNP update is available at <u>http://dnatribes.com/snp.html</u>.

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DNA Tribes[®] SNP Update for Summer 2014

We are pleased to announce a new update for *DNA Tribes[®] SNP* analysis. This includes:

- New Populations
- Updated Admixture Analysis
- Updated MDS Analysis
- Enhanced Population Admixture (Best Fits for Your Genome Composition)
- New Population Admixture (*Alternative Iterative Fits for Your Genome Composition*)
- Enhanced World Region Grid (*Best Fits for Your Genome Composition*)
- Enhanced Population Similarity (Best Fits for Your Genome Composition)
- Updated Admixture Tables

New Caucasus Mountains Populations:

- Azerbaijan
- Imer Georgia
- Kabardin
- Laz Georgia
- Tabasaran

New Diasporic Populations:

- Jewish Algeria
- Jewish France
- Jewish Italy
- Jewish Kurdistan
- Jewish Libya
- Jewish Syria
- Jewish Tunisia

New European Populations:

- Abruzzo, Italy
- Agrigento, Sicily
- Central Greece
- Central Sicily
- Croatia
- Kursk, Russia
- Moldavia
- Oryol, Russia
- Smolensk, Russia
- Sweden (*new samples*)
- Tatar Russian Federation
- Thessaly, Greece
- Voronezh, Russia
- Western Sicily

Updated Admixture Analysis based on DNA Tribes® proprietary analysis of world population structure, based on five continental cores and 44 detailed regional clusters:

Continental Core	Percentage
Basque	75.3%
Dravidian South India	17.5%
Mesoamerican	6.6%
Aka-Mbuti-Hadza	0.6%
South China	0.0%

Regional Cluster	Percentage
NW Europe	44.2%
Balto-Slavic	29.8%
Central European	10.4%
Finnish	7.3%
Basque	5.7%
Aegean-Balkan-Italian	2.8%



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Updated Multi-Dimensional Scaling (MDS) to visualize your genotype's position among continent cores and genetic clusters:



Enhanced Population Admixture (Best Fit for Your Genome Composition) based on the combination of populations that best fits your genome's ancestral composition:

Population (Native Only)	Percentage
Ireland	66.5%
Estonia	17.5%
Lithuania	16.0%

Population (Native and Global)	Percentage
Ireland	66.5%
Estonia	17.5%
Lithuania	16.0%



Enhanced Population Admixture (Alternative Iterative Fits) illustrating several alternative combinations of populations that fit your genome's ancestral composition:



Enhanced World Grid Genome Fit Map showing the geographical distribution of your combination of 44 ancestral components on a shaded world map:



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Enhanced Population Genome Fit Rankings individually listing the countries and ethnic groups in our SNP database where your combination of 44 ancestral components fits best:



Updated World Admixture Tables (including average five continent core and 44 region cluster percentages for samples populations in our SNP database) are available at <u>http://dnatribes.com/dnatribes-snp-admixture-2014-06-03.pdf</u>.

Update Your Personal SNP Analysis New SNP analysis orders (Sale Price \$39.99 *with submitted grandparent information form*) and SNP updates (\$19.99) be ordered at <u>http://dnatribes.com/snp.html</u>.