



DNA Tribes® Digest October 25, 2008
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Introduction: Turtle Island's Footprints in Asia

Hello, and welcome to the October 2008 issue of DNA Tribes® Digest. Traditional narratives of the Anishnabe (also known as Ojibwa in Canada and Chippewa in the United States) describe the formation of North America on the back of a turtle after a great flood. For this reason, North America is sometimes poetically described as "Turtle Island." This metaphor is apt: like a turtle that can withdraw all limbs into its shell, the North American landmass is geographically isolated by wide oceans and impassable ice. Like the elusive limbs of the turtle, North America has been connected to other continents by extensions of land that have appeared and disappeared periodically.

The most famous of these connections to the outside world is the Bering land bridge. This is the route by which scholars believe the early ancestors of American Indians journeyed from Siberia to Alaska in search of game no earlier than 16,500 years ago. Details of this scholarly theory have recently come under question, and alternate theories have been proposed based on controversial carbon dates in archaeological sites found in both North and South America dated to as old as 40-50 thousand years before present. Other theories propose that early settlers from Asia might have reached North America along the Pacific coast rather than by land. As new data are gathered and analyzed, it is possible that our understanding of North American origins will be substantially revised in the coming years.

All theories aside, DNA Tribes® analysis has identified the greatest genetic division in the world as that between American Indian genetic regions and all other parts of the world, as illustrated in **Figure 1** below:

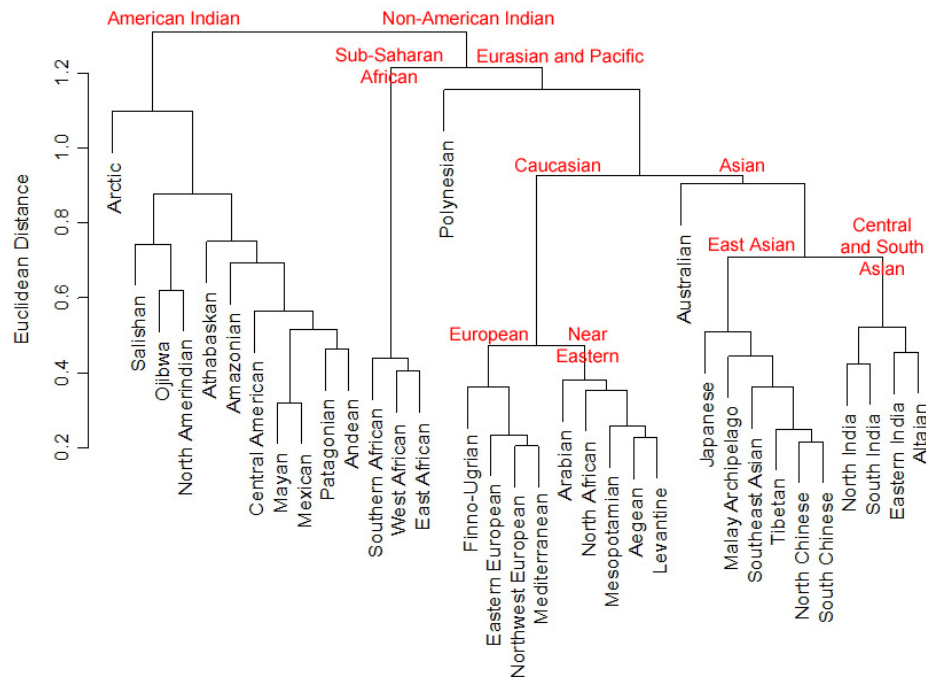
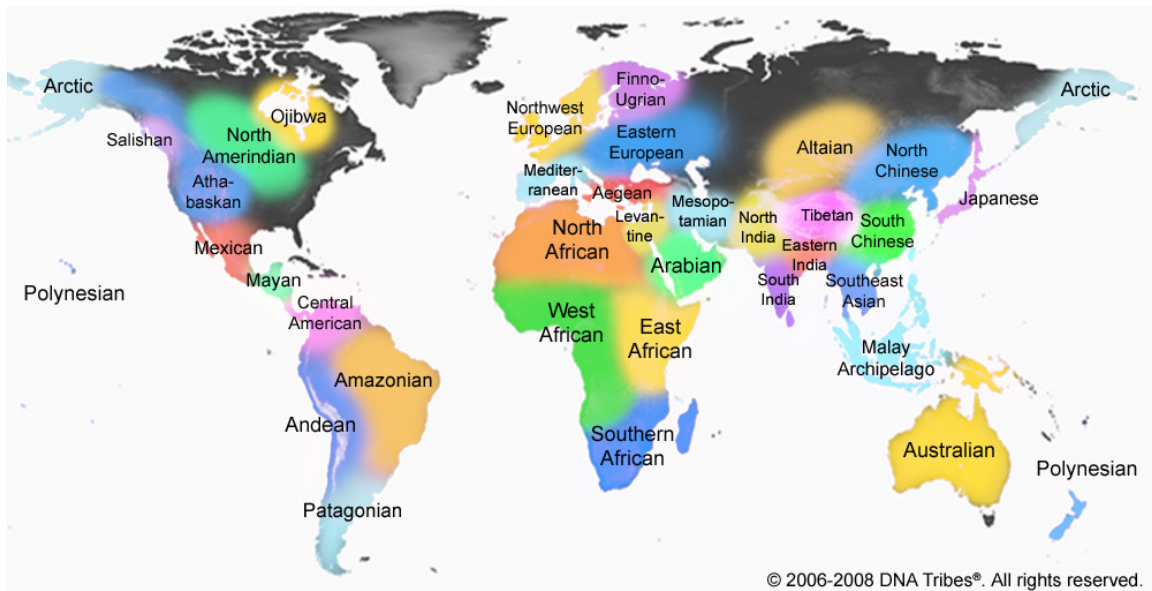


Fig. 1: Neighbor-joining “family tree” diagram of world genetic regions. More closely related regions are joined towards the bottom of the diagram, and more distant relationships are joined towards the top. For more information on this diagram and world genetic structure, see our Global Survey at <http://dnatribes.com/sample-results/dnatribes-global-survey-regional-affinities.pdf>.

This indicates that American Indian populations have developed locally unique genetic characteristics that distinguish them from all other world populations. A proper description of American Indian genetic characteristics begins with recognizing their autochthonous (indigenous or literally, “generated by the earth”) character. All human populations have experienced both major migrations and slower but not less important gene flow with neighboring populations. However, North America (“Turtle Island”) is characterized first and foremost by its uniqueness and relative isolation.

Previously, regional genetic patterns identified by DNA Tribes® analysis in North America had excluded all populations outside of the Americas, even those populations in Siberian regions sometimes thought to be ancestral to American Indians, such as the Altaian and North Chinese regions. However, new data for far eastern Siberia (Chukotka and Kamchatka) have identified for the first time Asian populations sharing North American (Arctic) genetic patterns. The expanded geographical extent identified for the Arctic genetic region is illustrated in **Figure 2** below:



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Fig. 2: Map illustrating genetic regions identified among 872 world reference populations. For more information on this diagram and world genetic structure identified by DNA Tribes® analysis, see our Global Survey at <http://dnatribes.com/sample-results/dnatribes-global-survey-regional-affinities.pdf>.

In this issue's feature article "The Arctic Connection," we will explore this newly identified Arctic connection between far eastern Siberia and North America.

Best regards,
Lucas @ DNATribes.com

The Arctic Connection: Alaska to Siberia

In this study, we investigated genetic relationships between genetic regions of North America and the Arctic genetic region that characterizes some populations of both Alaska and Siberia. First, the genetic regions of Siberia were mapped and described in terms of the language families presenting each region. Second, estimated genetic contributions to the Arctic region were identified. Third, Arctic estimated genetic contributions to all American Indian genetic regions were identified. Finally, a more detailed analysis of genetic contributions to North American genetic regions was performed.

Part One: Genetic Regions and Language Families of Siberia

Siberia is the term for a zone spanning the interior of Eurasia incorporated into the Russian Empire in the past 500 years. However, the singular name for this vast and complex set of territories extending from the Urals to the Pacific Ocean is misleadingly simple, as Siberia encompasses several genetic regions, each with its own history and cultures. **Figure 3** illustrates the genetic regions identified to date by DNA Tribes® analysis within Siberia and lists the language families spoken in each region.

As in most parts of the world, genetic variation in Siberia is most accurately described in terms of geography. Language families such as Turkic are spoken in regions as genetically and geographically distant as the Aegean region of Europe and the Altaian region of South Siberia (named for the Altai Mountains and sometimes thought to be the homeland of Turkic peoples). Conversely, linguistically distinct languages such as Tungusic (Evenki), Sino-Tibetan (Mandarin), and Korean are spoken by populations sharing local genetic characteristics in the North Chinese region. One part of Siberia for which data are not yet available is the northern Urals (historically known as Yugra), where Uralic languages related to Finnish and Estonian are spoken.

However, the only populations of Siberia characterized by North American Indian (Arctic) genetic patterns are found (thus far) in the far eastern Chukotka and Kamchatka peninsulas. Indigenous Siberians in this zone speak languages classified as “Paleosiberian,” unrelated to Turkic and Tungusic languages spoken further west and south in Siberia and thought to predate those other languages in the region. Some linguists have proposed a similarity between Paleosiberian languages and language families of North America including Eskimo-Aleut and Na-Dene (Athabaskan).

Consistent with linguistic descriptions, the Arctic region also stands apart from all other Asian regions on a genetic basis. Specifically, Paleosiberian-speaking Chukchi and Koryaks share Arctic genetic patterns with Eskimo-Aleut-speaking Inupiat and Yupik of Alaska.

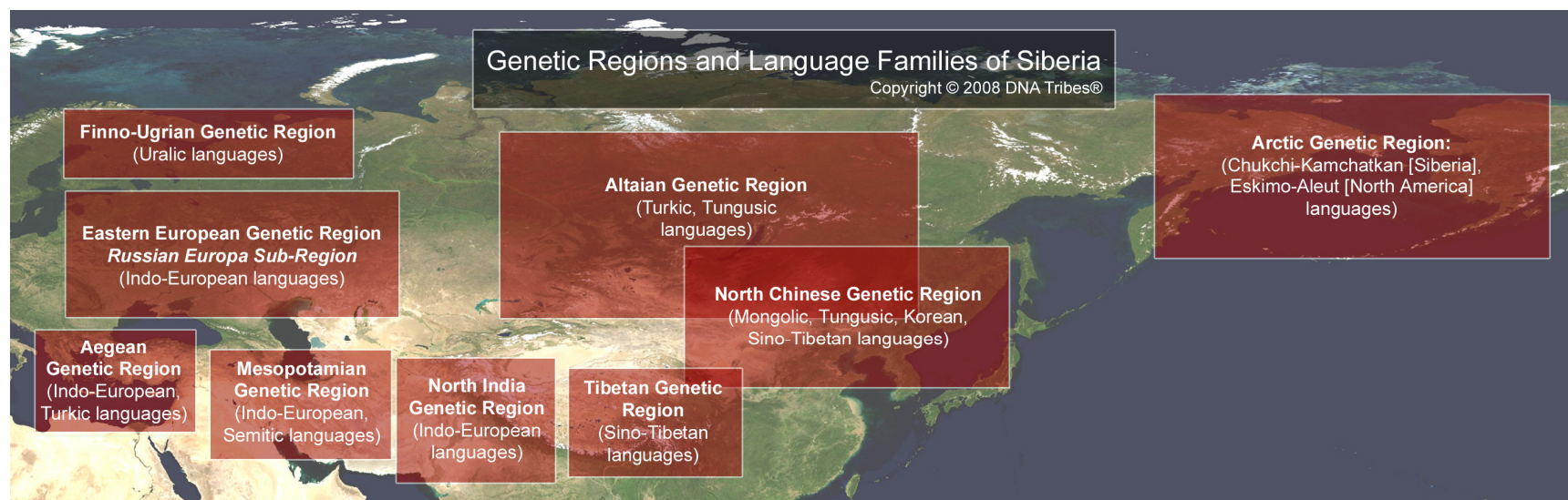


Fig. 3: Map illustrating genetic regions and language families of Siberia proper (the Altaian, North Chinese, and Arctic genetic regions) as well as neighboring genetic regions (the Finno-Ugrian, Eastern European, Aegean, Mesopotamian, North India, and Tibetan genetic regions) that have historically interacted with Siberian peoples.

Part Two: Estimated Genetic Contributions to the Arctic Genetic Region

To explore relations between Arctic populations and genetic regions of Asia and North America further, estimated genetic contributions to the Arctic genetic region were identified based on a comparison to all other world regions¹. These genetic contributions are illustrated in **Figure 4** and listed in **Table 1** below:

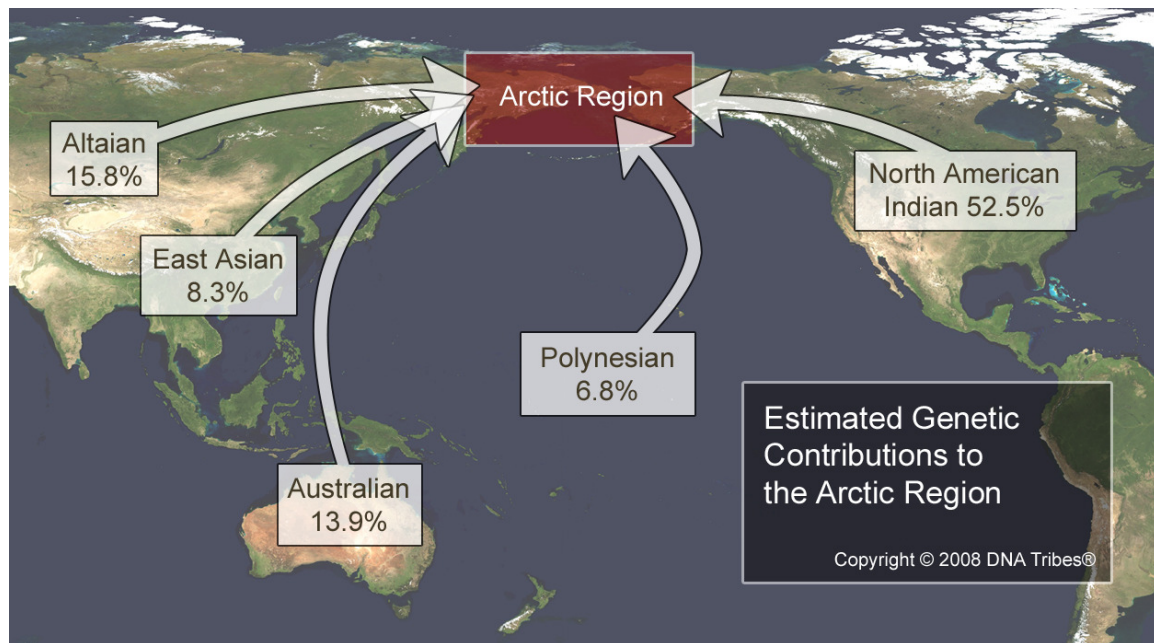


Fig. 4: Estimated genetic contributions to the Arctic genetic region. North American Indian contributions (Salishan, North Amerindian, and Ojibwa) and East Asian contributions (Tibetan, South Chinese, and Southeast Asian) have been mapped together for visual clarity.

¹ As of October 24, 2008, the 36 world regions identified by DNA Tribes® analysis are: Aegean, Altaian, Amazonian, Andean, Arabian, Arctic, Athabaskan, Australian, Central American, East African, Eastern European, Eastern India, Finno-Ugrian, Japanese, Levantine, Malay Archipelago, Mayan, Mediterranean, Mesopotamian, Mestizo, Mexican, North African, North Amerindian, North Chinese, North India, Northwest European, Ojibwa, Patagonian, Polynesian, Salishan, South Chinese, South India, Southeast Asian, Southern African, Tibetan, and West African. A map illustrating these regions can be viewed online at: <http://dnatribes.com/populations.html>. Of these 36 regions, all except the Arctic region were referenced for this analysis.

Genetic Region	Estimated Contribution
Total North American Indian	52.5%
Salishan	26.5%
North Amerindian	19.8%
Ojibwa	6.3%
Altaian	15.8%
Australian	13.9%
Polynesian	6.8%
Total East Asian	8.3%
Tibetan	4.1%
South Chinese	2.6%
Southeast Asian	1.6%
Other	2.7%

Table 1: Estimated genetic contributions to the Arctic genetic region.

Table 1 shows that the largest genetic contribution identified was North American Indian (52.5%). The second largest genetic contribution was from the Altaian genetic region of Siberia. Notably, the total estimated contribution from East Asian genetic regions was comparatively small (8.3%). Less expectedly, substantial genetic contributions from Pacific Ocean regions were also identified: Australian (13.9%) and Polynesian (6.8%). In the case of the Australian contribution, this might reflect a northern extension of an early coastal migration along South Asia identified on the basis of uniparental (Y-DNA and mtDNA) markers. The Polynesian contribution might reflect maritime contacts between Polynesia and the Pacific Coast of North America suggested by observations described in our September issue of DNA Tribes® Digest².

The primary North American Indian genetic contribution identified for the Arctic region may indicate gene flow from Alaska to Siberia. This would reverse the usual scholarly presumption that North American populations have been only a recipient of Asian immigrants and not a source of American Indian emigrants to Asia.

To explore this connection with North America further, a reciprocal analysis was performed as well.

² For more information, see: <http://www.dnatribes.com/dnatribes-digest-2008-09-27.pdf>

Part Three: Estimated Arctic Contributions to American Indians

To further explore relationships between Arctic and American Indian populations, a reciprocal analysis was performed to estimate Arctic genetic contributions to indigenous regions of North, Central, and South America. Results are illustrated in **Figure 5** and listed in **Table 2** below:

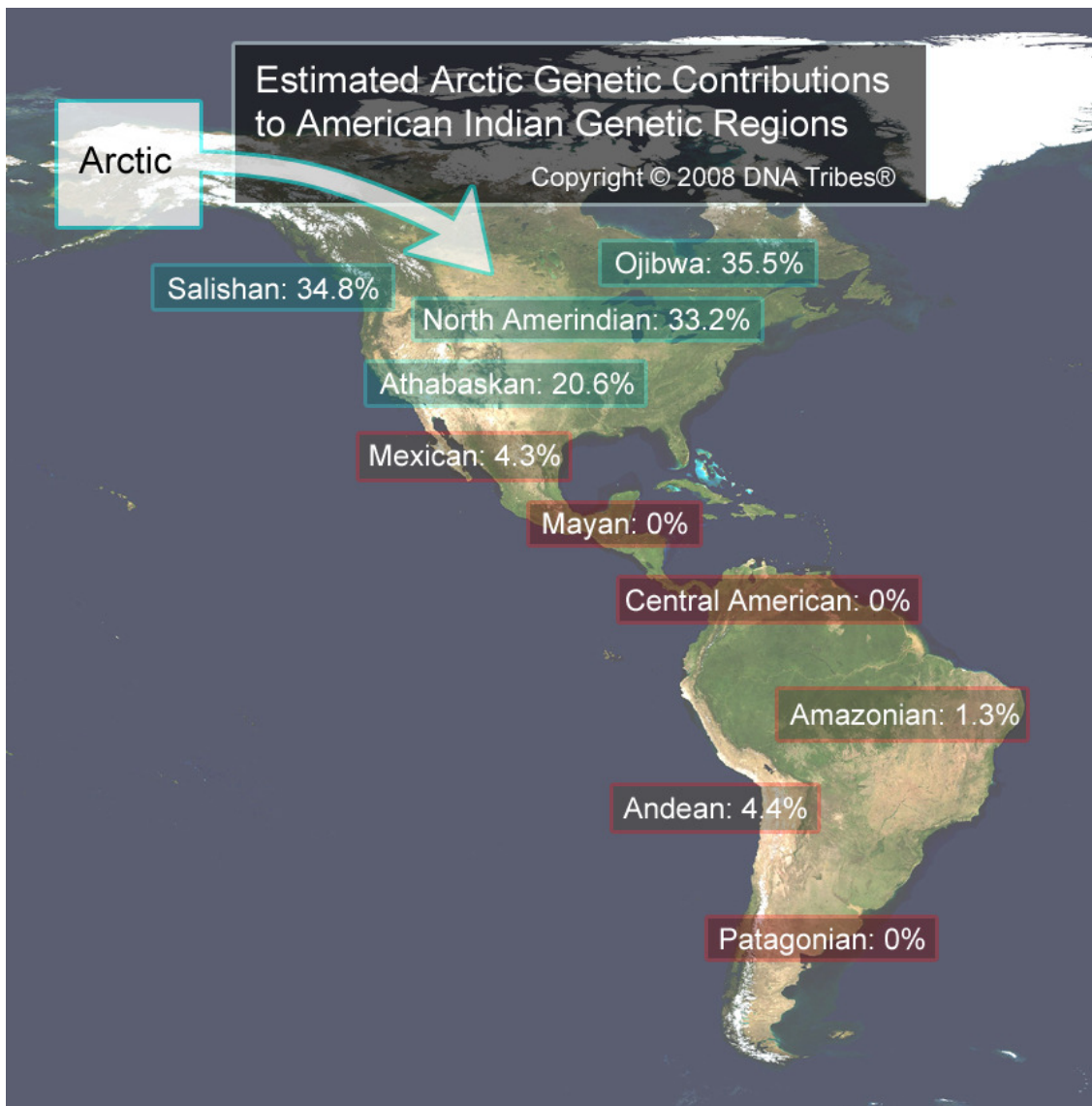


Fig. 5: Estimated genetic contributions from the Arctic region to American Indian genetic regions. Regions for which a greater than 20% Arctic contribution was identified are highlighted in blue. Regions for which less than 20% Arctic contribution was identified are highlighted in red.

Genetic Region	Estimated Arctic Contribution
Ojibwa	35.5%
Salishan	34.8%
North Amerindian	33.2%
Athabaskan	20.6%
Andean	4.4%
Mexican	4.3%
Amazonian	1.3%
Mayan	0.0%
Central American	0.0%
Patagonian	0.0%

Table 2: Estimated Arctic genetic contributions to
American Indian genetic regions.

Among the surveyed American Indian regions, the largest Arctic genetic contributions were observed in North America among the Ojibwa, Salishan, North Amerindian, and Athabaskan genetic regions. These observed contributions are consistent with Arctic gene flow via coastal and/or inland contacts.

Smaller Arctic contributions were also observed for the Andean, Mexican, and Amazonian genetic regions. Of these, the Andean and Mexican regions border the Pacific Ocean, where coastal contacts provide one avenue for gene flow. The smaller 1.3% Arctic contribution identified for the Amazonian genetic region could reflect inland gene flow via the Andean region immediately to the west.

For several American Indian genetic regions (the Mayan, Central American, and Patagonian regions), no Arctic genetic contribution was identified. This could be consistent with earlier settlement for these Central and South American regions than in more northerly regions for which substantial Arctic genetic contributions are identified.

It is noteworthy that among the four North American Indian regions for which an Arctic contribution of more than 20% was identified, the smallest Arctic contribution identified for the Athabaskan region. The Athabaskan genetic region includes speakers of related languages in both the United States Desert Southwest (Navajo and Apache) and Canada and Alaska, and sometimes has been singled out by scholars for a special genetic connection with Alaska due to a hypothetical recent migration to the Desert Southwest. However, these observations indicate that Athabaskan-speakers have experienced less gene flow from the Arctic as compared to other North American Indians surveyed in this study.

None of the surveyed American Indian genetic regions were identified as predominantly Arctic. To examine genetic relationships in North America further, a more detailed and comprehensive analysis of genetic contributions to North American Indian regions of the United States and Canada was performed.

Part Four: Estimated Genetic Contributions to North American Indians

To further explore genetic relationships among North American Indian genetic regions, a more comprehensive analysis was performed that estimated genetic contributions to the Athabaskan, North Amerindian, Ojibwa, and Salishan regions from all 32 other world regions defined by DNA Tribes® analysis.³ Results were mapped and listed in **Figures 6 through 9** and **Tables 3 through 6** below:

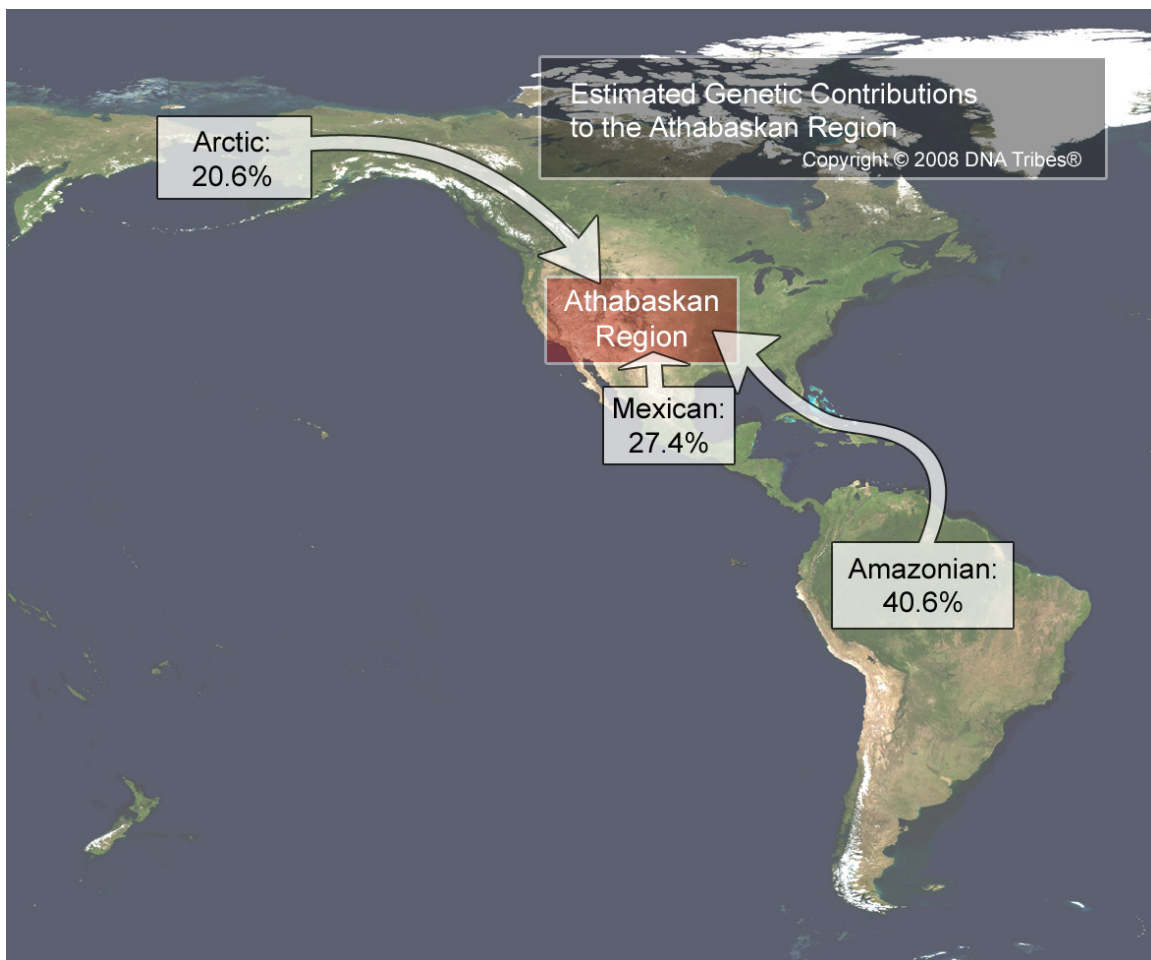


Fig. 6: Estimated world genetic contributions to the Athabaskan genetic region.

³ See <http://dnatribes.com/populations.html>. Of the 36 regions presently identified by DNA Tribes® analysis, all except the Athabaskan, North Amerindian, Ojibwa, and Salishan regions were referenced for this analysis.

World Region	Estimated Genetic Contribution
Amazonian	40.6%
Mexican	27.4%
Arctic	20.6%
Other	11.4%

Table 3: Estimated world genetic contributions to the Athabaskan genetic region.

As discussed in Part Three above, the Athabaskan genetic region includes populations of both the Desert Southwest and Alaska. Nevertheless, the largest genetic contribution identified was from the Amazonian genetic region to the south and east. Although the geographical role of the Caribbean as a possible mediator between North and South American Indians has been given little scholarly attention, one route such gene flow could have taken is along the islands of the Caribbean, beginning in the Antilles and entering North America through Florida. Some traditional narratives of Southeastern United States American Indians mention entry to North America from islands to the east. If controversial radiocarbon dates at archaeological sites in North and South America predating the Last Glacial Maximum are confirmed in the future, the role of the Caribbean as an important population center or refuge during glacial periods might be reconsidered.

The second largest genetic contribution identified for Athabaskans was from the Mexican genetic region. This is unsurprising given the geographical proximity of Southern Athabaskan speakers in the Desert Southwest (Apache and Navajo), and could reflect gene flow from neighboring Pueblo Peoples (some of whom speak Uto-Aztecan languages related to indigenous languages of Mexico), or else older gene flow from the south.

Although genetic data for Muskogean speaking tribal nations of the Southeastern United States (including the Creek, Choctaw, Chickasaw, and Seminole nations) are not available for the present study, some Southeastern traditional narratives describe a migration to the east from Mexico. Also noteworthy are cultural similarities between artifacts of the Moundbuilder cultures of the Southeastern United States and the civilizations of Mesoamerica such as the Aztecs and Mayans.

The third largest genetic contribution identified was Arctic. Although these observations may indicate substantial gene flow from the Arctic, the net Arctic genetic contribution identified here was smaller than contributions identified for the North Amerindian, Ojibwa, and Salishan regions evaluated below.

Of the four North American Indian regions evaluated in Part Four, the neighbor joining tree analysis (see **Figure 1** on page 1) grouped the Athabaskan region in a large “family” that includes all Central and South American Indian regions as well as Mexico. For this reason, the Athabaskan region is best described as a primarily southern American Indian genetic region, as distinguished from the North Amerindians, Ojibwa, and Salishan regions.

It is noteworthy that despite scholarly theories of recent Athabaskan origins in the north, traditional creation narratives of the Navajo are intimately concerned with the Navajo homeland (Dinetah) in the Desert Southwest but make little or no mention of Arctic lands to the north.

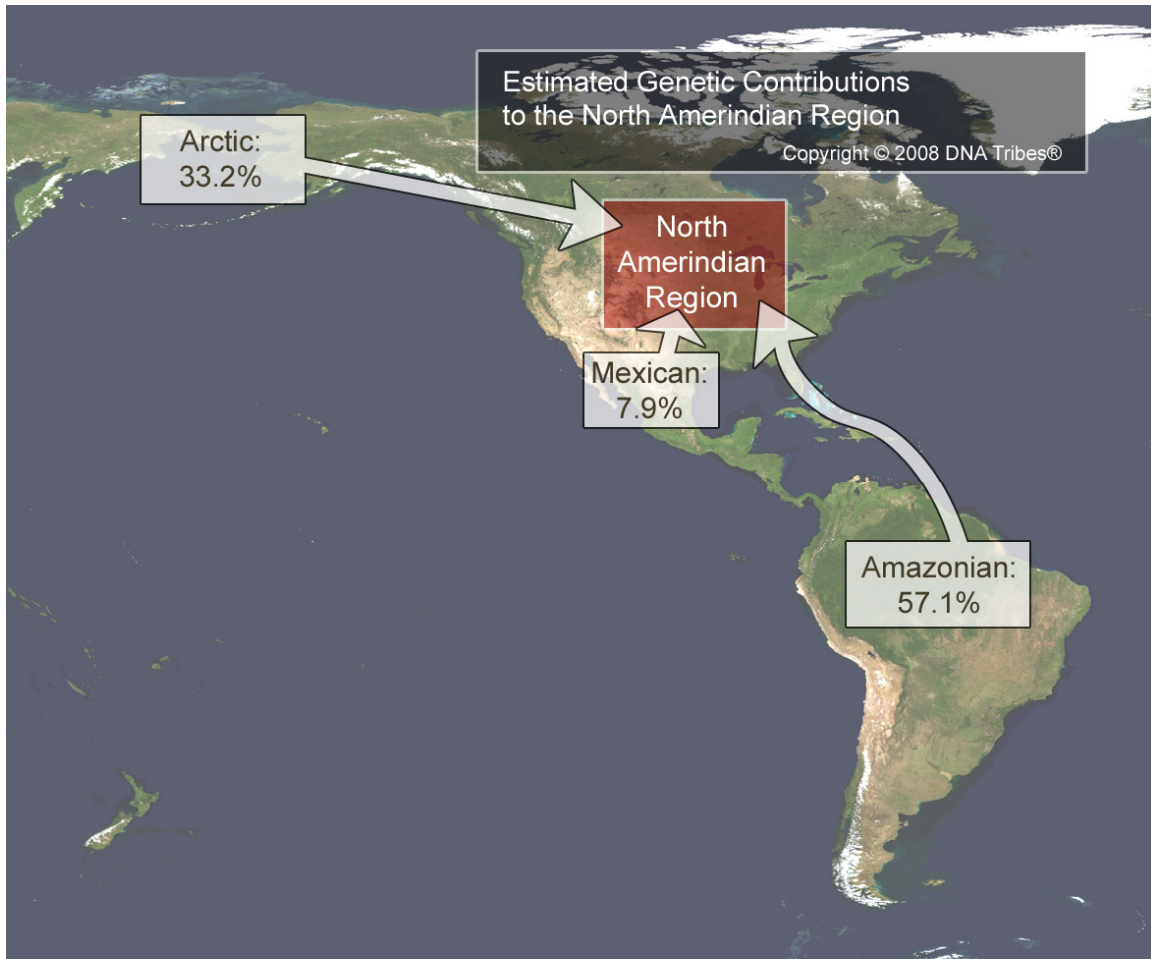


Fig. 7: Estimated world genetic contributions to the North Amerindian genetic region.

World Region	Estimated Genetic Contribution
Amazonian	57.1%
Arctic	33.2%
Mexican	7.9%
Other	1.8%

Table 4: Estimated world genetic contributions to the North Amerindian genetic region.

As with the Athabaskan region, the largest genetic contribution identified for the North Amerindian region was Amazonian (57.1%). As discussed above, one possible route for Amazonian gene flow would be along the Caribbean islands through Florida or other parts of the eastern coasts of North America.

The second largest genetic contribution identified was Arctic (33.2%). Because the North Amerindian as presently identified by DNA Tribes® analysis extends into the Great Plains



of Canada, this gene flow could have taken place along the northern fringes of this part of North America.

The third largest genetic contribution identified was Mexican (7.9%). Although this 7.9% is smaller than the 27.4% Mexican contribution identified for the Athabaskan genetic region, this observation does indicate some gene flow from Mexico. This North Amerindian region contact with Mexico could also be reflected in the geographical extent of Moundbuilder cultures, which have been compared to Mesoamerican tradition and have left artifacts of their civilizations in the form of pyramids, platform mounds, and large effigy mounds as far north as the Great Lakes.

Also noteworthy are connections between the North Amerindian region and eastern populations of North America. The Siouan language family spoken by tribal nations of the Great Plains is related to Catawban languages spoken in Virginia and North Carolina, and some scholars have proposed Siouan origins in the eastern parts of North America more than one thousand years ago prior to westward expansions to their present territories.

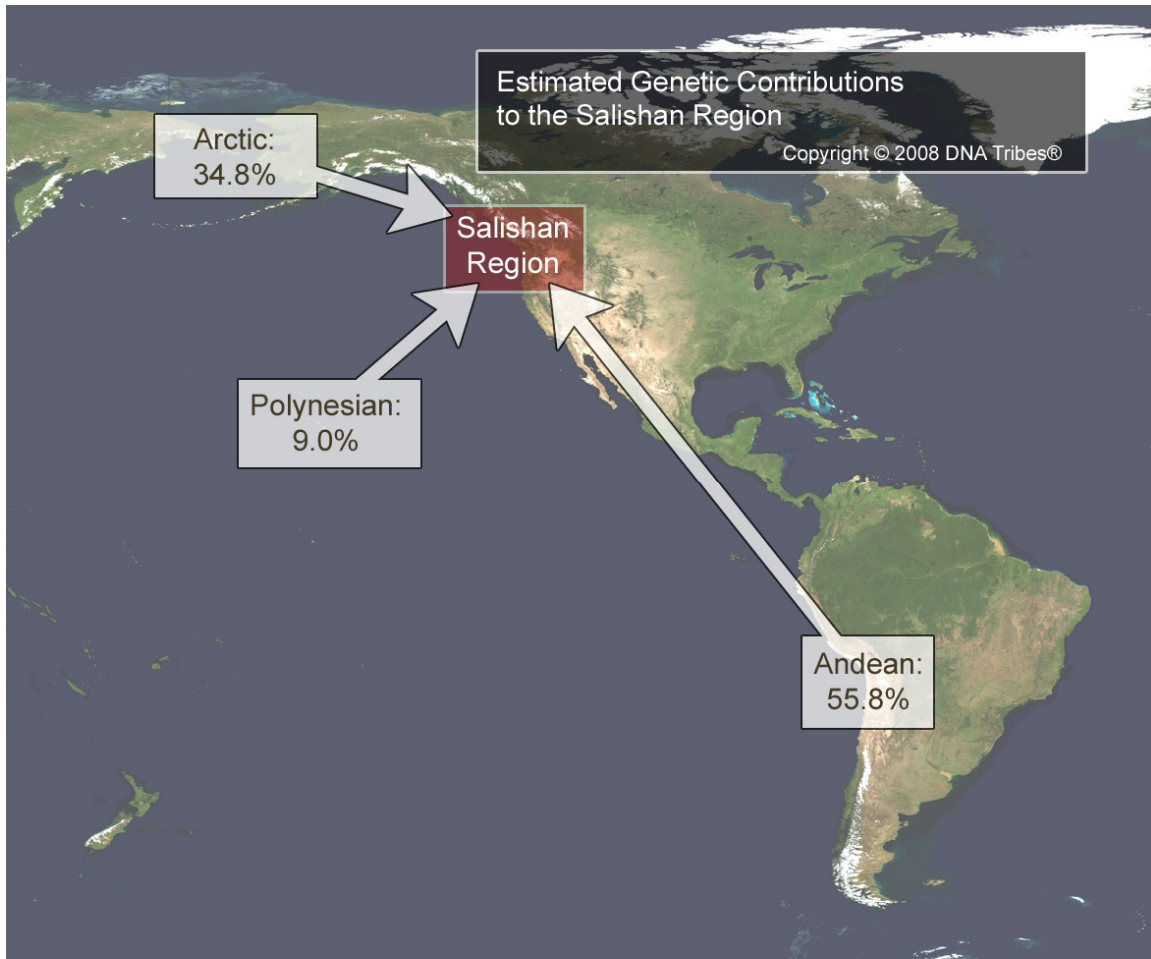


Fig. 8: Estimated world genetic contributions to the Salishan genetic region.

World Region	Estimated Genetic Contribution
Andean	55.8%
Arctic	34.8%
Polynesian	9.0%
Other	0.4%

Table 5: Estimated world genetic contributions to the Salishan genetic region.

The largest genetic contribution identified for the Salishan genetic region was Andean (55.8%). This observation contrasts for the predominantly Amazonian contributions identified for the Athabaskan and North Amerindian genetic regions, and suggests substantially different patterns of gene flow along the Pacific Coast.

The second largest genetic contribution identified was from the Arctic region. This is unsurprising given the Salishan region's location in the Pacific Northwest, adjacent to coastal populations further north and west Alaska.



Less expected was the third largest genetic contribution of 9.0% from the Polynesian genetic region. This reciprocates the Salishan genetic contribution to Polynesians identified in the September 2008 issue of DNA Tribes® Digest.⁴ Although this reciprocal Salishan-Polynesian genetic connection is not explained on the basis of available historical models, it might correspond to cultural similarities in kinship traditions observed between American Indians of the Pacific Northwest and Polynesia.

⁴ Available on the DNA Tribes® website at: <http://www.dnatribes.com/dnatribes-digest-2008-09-27.pdf>

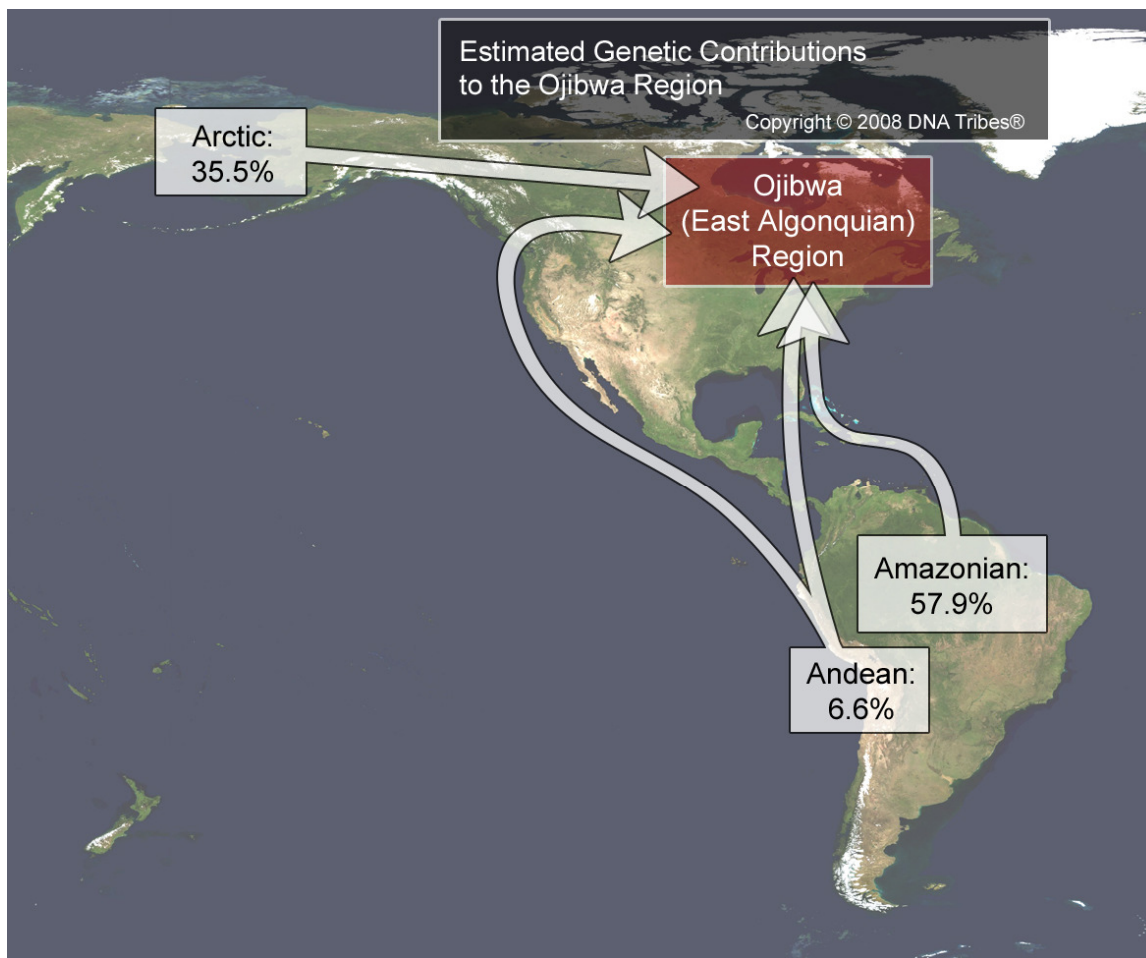


Fig. 9: Estimated world genetic contributions to the Ojibwa genetic region.

World Region	Estimated Genetic Contribution
Amazonian	57.9%
Arctic	35.5%
Andean	6.6%
Other	0.0%

Table 5: Estimated world genetic contributions to the Ojibwa genetic region.

The largest genetic contribution identified for the Ojibwa genetic region was Amazonian (57.9%). This is consistent with the predominant Amazonian contributions identified for the North Amerindian and Athabaskan regions and suggests substantial along eastern parts of North America.

The 35.5% Arctic genetic contribution observed for Ojibwa is consistent with observations for the other three North American Indian regions examined, and is consistent with



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gene flow from points north and west, possible mediated by populations such as the Innu of northeastern Canada.

The 6.6% Andean genetic contribution identified corresponds to the substantially larger (55.8%) Andean contribution identified for the Salishan genetic region. This could reflect Pacific Coast gene flow to eastern Canada mediated by more westerly populations of North America, such as ancestors of present day Northwest Coast tribal nations.

Conclusion

This study identified substantial gene flow between Siberia and North America via the Arctic genetic region. Part One discussed genetic regions identified by DNA Tribes® analysis in Siberia and language families spoken in each region. The Arctic genetic region was identified as specific to Chukchi-Kamchatkan speakers of far eastern Siberia and Eskimo-Aleut speakers of Alaska.

Part Two estimated genetic contributions to the Arctic region, and identified gene flow from North American, Altaian, Australian, Polynesian, and East Asian genetic regions.

Part Three reciprocated this analysis by estimating Arctic genetic contributions to American Indian genetic regions, which identified substantial Arctic contributions to North American Indian populations and (to a significantly lesser degree) to some American Indians of Mexico and South America.

Part Four examined North American Indian regions more closely by estimating world genetic contributions. This analysis identified Amazonian contributions for the Athabaskan, North Amerindian, and Ojibwa regions, suggestive of gene flow along the eastern parts of North America. This contrasted with Andean contributions observed for the Salishan and (to a lesser degree) Ojibwa regions, which suggested independent coastal patterns of gene flow along the Pacific Ocean. Substantial Mexican genetic contributions were observed for the Athabaskan and North Amerindian regions, which might reflect contact with Pueblo Peoples and Moundbuilder peoples of the Southwest and Southeast, respectively. Surprisingly, a Polynesian genetic contribution was identified for the Salishan genetic region, reciprocating the Salishan-Polynesian relationship identified in our September 2008 study of South Seas populations.

As of October 2008, the genetic relationship of American Indians to other world populations remains a subject of controversy. It is likely that the scholarly understanding of American Indian origins will change substantially in the coming decades to incorporate not only new genetic data, but also new archaeological data and as a broader understanding that better synthesizes information about North, Central and South America in a coherent picture.

It is a strange paradox that continents as geographically isolated as the Americas are conventionally described only in terms of migrations. Although evidence of gene flow is often interpreted in terms of migrations, the genetic patterns identified in this study are not inconsistent with slower, long term gene flow or diffusion within the Americas. Many of the genetic processes that shape human populations take place over many centuries or thousands of years, defying the scholarly tendency to describe them in terms of discrete historical events such as invasions and migrations.

As elsewhere in the world, a more objective reference point for understanding North American genetic patterns is provided by geography. The American Indian peoples whose homelands are in the genetic regions identified in DNA Tribes® analysis each retain locally unique genetic characteristics reflecting fundamental geographical patterns. The autochthonous character of these genetic patterns is in keeping with traditional narratives describing emergences or origins in the land itself, which quietly repel scholarly attempts to imagine only migrations from elsewhere for peoples whose roots are in North America.



New Populations for October 25, 2008

We are pleased to announce the addition of several new populations to our database:

New African Populations:

- Botswana (150)

New Central Asian Populations:

- Altaian-Kizhi (80)
- Chukcha (15)
- Evenk (Northeast Siberia) (14)
- Khamnigan Mongol (95)
- Koryak (32)
- Mongol (15)
- Tuva (64)

New East Asian Populations:

- Korea (49)

New European Populations:

- Belgorod, Russia (38)
- Mineralnye Vody, Russia (60)
- Oryol, Russia (72)
- Pskov, Russia (62)
- Saratov, Russia (52)
- Sassari and Orgosolo, Sardinia (125)
- Velikiy Novgorod, Russia (59)

New Latin American Populations:

- Mestizo (Argentina) (565)
- Mestizo (Jalisco, Mexico) (309)
- Mestizo (La Paz and Santa Cruz, Bolivia) (260)
- Mestizo (Puebla, Mexico) (313)
- Mestizo (Yucatan, Mexico) (262)
- Minas Gerais, Brazil (12,000)

New Near Eastern Populations:

- Kuwait (502)

New South Asian Populations:

- Dhimal (West Bengal, India) (66)
- Gond (Ojha) (Madhya Pradesh, India) (89)



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- Gujarat, India (172)
- Kanyakubj (Brahmin) (Madhya Pradesh, India) (110)
- Pakistan (Punjabis, Pushtuns, and Sindis) (155)
- Paliya (West Bengal, India) (107)
- Rajbanshi (West Bengal, India) (91)

Updates:

Previous DNA Tribes customers who would like to update their results to include these new populations and our most up to date algorithms can order using the "Update Your Analysis" option through our secure online checkout at <http://dnatribes.com/order.html>.