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Introduction: Inferring Networks of Gene Flow

Hello, and welcome to the November 26, 2008 issue of DNA Tribes® Digest. In this issue's feature article, "Genetic Relationships in Northern Europe," we will explore a part of the world that is perhaps more familiar: Europe. This is a bit of a change from the past two issues, where we looked at peoples and places (Oceanian peoples and American Indians) whose origins are less fully known to historians and the only speculatively described by scholars.

Nevertheless, the apparent familiarity of Europe can be misleading: the origins of peoples such as the Celtic, Germanic, Fenno-Scandinavians, Baltic, and Slavic tribes were mysterious even to the most learned writers of the Greek and Roman worlds. Many histories of these northern peoples have been elaborated: sometimes on the basis of indigenous oral narratives remolded in Biblical and Greco-Roman frameworks, sometimes making sure to conform to contemporary political realities. Sometimes relationships with neighbors were emphasized or downplayed, and other times they were simply forgotten or never noted. All said, the historical narratives we are left with are colorful and engaging, heroic or pathetic (depending on the storyteller's intent), but something less than complete or objective.

What is sometimes easy to overlook is that human populations are living systems composed of hundreds, thousands, and today billions of people interacting in complex ways over the course of many thousands of years. History can give us bits and pieces of information to help



make sense of genetic patterns, but more often than not, what we are observing is much older and deeper than any history. What we are seeing is the cumulative outcome of two kinds of processes: first, gene flow between populations (whether by historically notable migrations and invasions or by slower, quieter gene flow over many generations); and second, local genetic characteristics generated within populations by internal processes such as mutation and genetic drift.

Human populations are dynamic and interconnected rather than static or isolated. Part of what makes each Europa sub-region unique is its characteristic relationships with neighboring regions. For instance, substantial two-way gene flow is observed between the Celtic and Norse Europa sub-regions. If one were to exclude the Celtic genetic contribution to the Norse sub-region (or vice-versa), one no longer would be describing Norse peoples as they actually exist. As the understanding of human genetic relationships matures in the coming decades, empirical descriptions of these web-like networks of gene flow might shed light and add quantified detail to the more literary descriptions of ancestry and national origins.

Have a safe and happy Thanksgiving Holiday,
Lucas Martin
DNA Tribes

Genetic Relationships in Northern Europe

In this study, we examined northern European genetic relationships by identifying the estimated genetic contributions to each of six Europa sub-regions: the Russian, Finno-Ugrian, Polish, Germanic, Norse, and Celtic sub-regions. As illustrated in **Figure 1** below, these genetic sub-regions only sometimes correspond to present-day national or ethnic boundaries within Europe. These genetic patterns are most accurately described as geographical zones, each reflecting underlying patterns of human interactions dating back several thousand years and substantially more ancient than the comparatively recent formation of modern European nationalities.

However, we first examined genetic characteristics of the Altaian genetic region of Siberia, which includes the territories of the easternmost Indo-European-speaking peoples known to history: the Tocharians of the Tarim Basin in the present day People's Republic of China. Our study then proceeded westward through the lands of the ancient Scythians and finally reaching the British Isles.

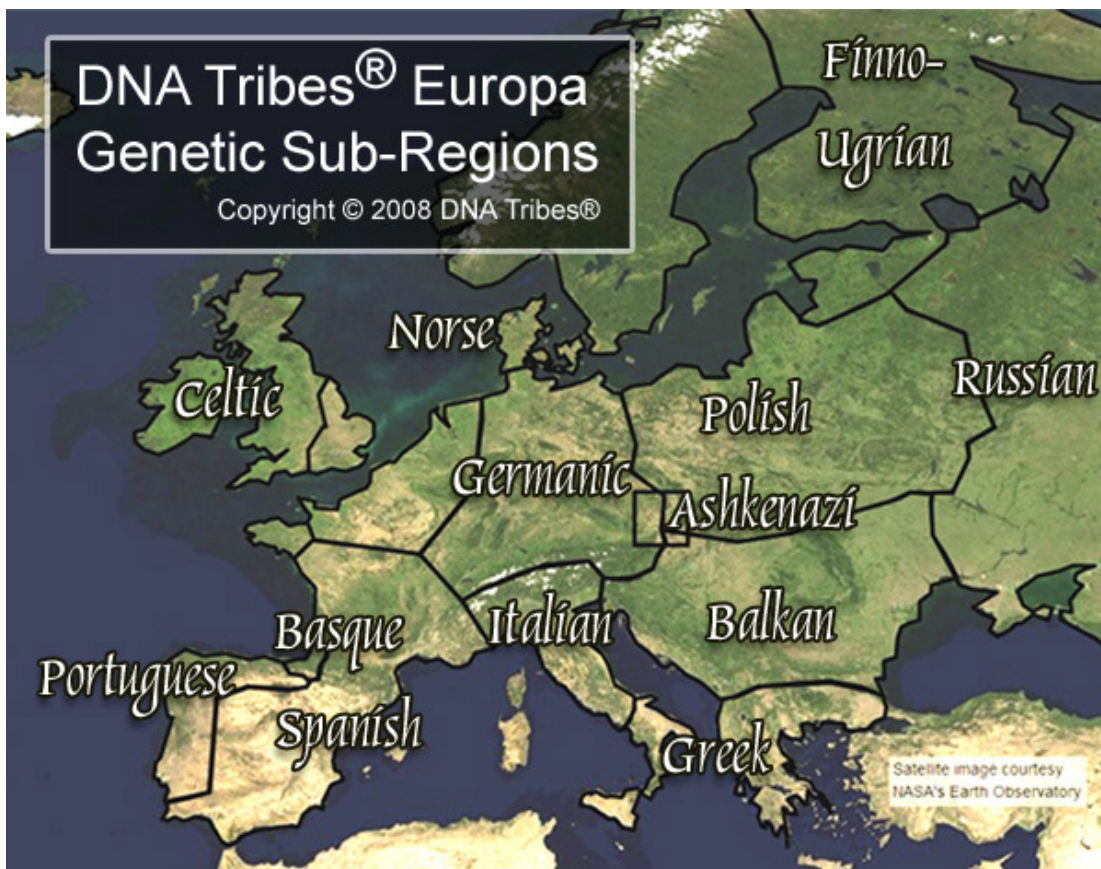


Figure 1: Genetic sub-regions of Europe presently identified by DNA Tribes® Europa analysis.

Where Earth Meets Sky: The Altaian Genetic Region

Background: The Altaian genetic region is named for the Altai or “Golden” Mountains of southern Siberia, located near the intersection of Europe, Asia, and the Arctic fringes of Siberia that periodically connect to North America. The Altaian zone of Eurasia is inhabited primarily by Turkic-speaking peoples, and is genetically distinct from the nearby North Chinese region, where Mongolic, Tungusic, Korean, and Sino-Tibetan languages are spoken.

In the past, the Altaian zone has also been home to Indo-European speaking peoples such as the Tocharians of the Tarim Basin (in what is presently the Xinjiang Uyghur Autonomous Region of the People’s Republic of China). Individuals with European-like light hair or eyes can be found to this day among the peoples of this region. Further to the east in present day Mongolia (part of the North Chinese genetic region), people of Genghis Khan’s clan Borjigin were known for their red hair, said to have been inherited from a tall, long-bearded, red-haired and green-eyed stranger, likely from these Altaian lands to the west.

Genetic analysis: Genetic contributions to the Russian Europa sub-region from 31 world regions and thirteen Europa sub-regions presently identified by DNA Tribes® analysis were identified.¹ Results are illustrated in **Figure 2** and summarized in **Table 1** below.

Discussion: Results indicate that, consistent with its geographical location adjacent to the Gobi Desert and Manchuria, the largest genetic contribution to the Altaian region is North Chinese (38.0%). However, substantial genetic contributions from Northern Europe (a total of 30.1%) are observed, along with a substantial American Indian contribution of (15.9%). These European and American Indian contributions distinguish the Altaian region from other regions of Asia, and suggest that Altaian peoples can be described as Asian only in a general sense, retaining substantial connections to non-Asian regions.

The observed 30.1% Northern European genetic contribution might reflect historical contacts with Russians, Scythians, and Tocharians. This also likely reflects gene flow from earlier pre-historic peoples of Europe roaming the steppe lands of Asia such as the Kurgan peoples, who left impressive burial monuments in a zone extending from Eastern Europe to the Altai Mountains. Another possible source of gene flow from Northern Europe is contact with Uralian-speaking peoples of northwestern Siberia, as will be discussed below in our analysis of genetic contributions to the Finno-Ugrian genetic region.

¹ A map illustrating the genetic world regions can be viewed at: <http://dnatribes.com/populations.html>. In this study, all non-European world regions and all Europa sub-regions except each studied region were referenced. European world regions omitted to avoid redundancy were: Aegean, Eastern European, Mediterranean, and Northwest European.

The thirteen Europa sub-regions presently identified by *DNA Tribes® Europa* analysis and referenced in this study were: Ashkenazi, Balkan, Basque, Celtic, Finno-Ugrian, Germanic, Greek, Italian, Norse, Polish, Portuguese, Russian, and Spanish. More information about *DNA Tribes® Europa* analysis is available at: <http://dnatribes.com/dnatribes-europa.html>.

Genetic contributions from the Arctic, Amazonian, Andean, Athabaskan, Central American, Mayan, Mexican, North Amerindian, Ojibwa, Patagonian, and Salishan regions were listed as “American Indian.”

The smaller but substantial American Indian genetic contribution (15.9%) observed might reflect gene flow from the Americas through the Arctic genetic region that connects Alaska with far eastern Siberia.²

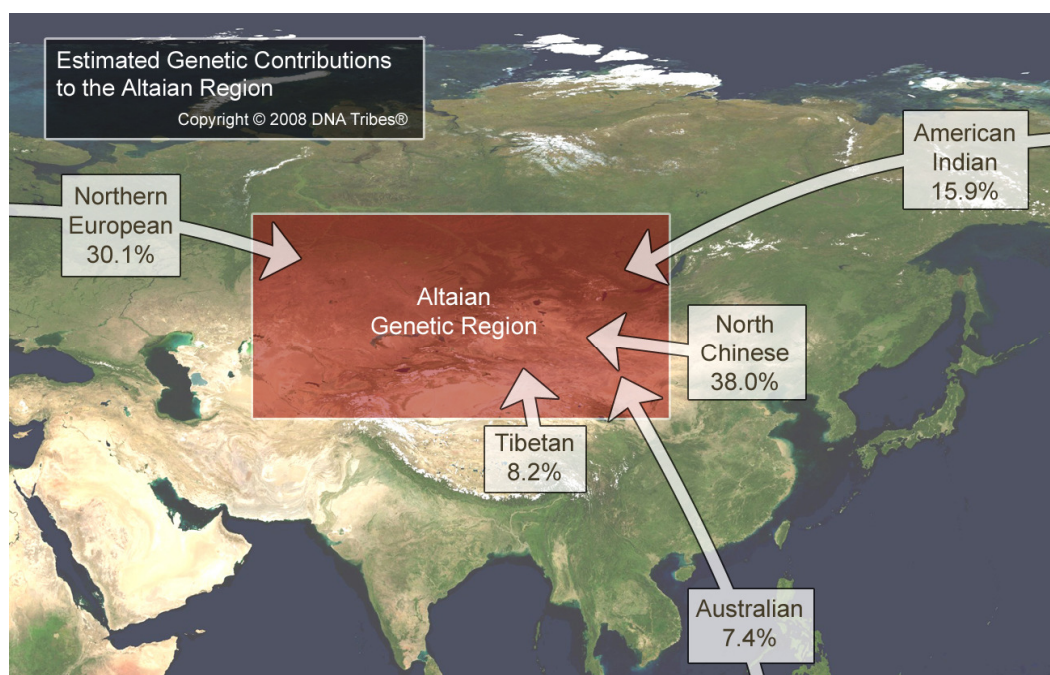


Figure 2: Estimated genetic contributions to the Altaian genetic region.

Genetic Region	Estimated Contribution
North Chinese	38.0%
Norse	16.5%
Russian	7.5%
Finno-Ugrian	6.1%
Total Northern European	30.1%
American Indian	15.9%
Tibetan	8.2%
Australian	7.4%
Other	0.4%

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

² For more information, see "The Arctic Connection: Alaska to Siberia" in the October 25, 2008 issue of DNA Tribes® Digest, available online at: <http://www.dnatribes.com/dnatribes-digest-2008-10-25.pdf>.

Also noteworthy is a link between the Ket language of the Siberia and Na-Dene languages of North America recently proposed in 2008 by the linguist Edward Vajda. For more information about this proposed linguistic link, see: <http://www.uaf.edu/anlc/dy.html>. Although linguists have interpreted this connection as a remnant of migrations from Siberia to North America, observations made on the basis of genetic data might suggest an alternative possibility of gene flow from North America to Siberia.

Smaller genetic contributions were also observed from the Tibetan region (8.2%) immediately to the south of the Tarim Basin, as well as from the Australian region (7.4%). This Australian contribution recalls the similar Pacific Ocean contributions observed further east in the Arctic region,³ possibly reflecting early migrations from the coasts of Southern Asia before the expansion of East Asian peoples. Alternatively, this Australian contribution could reflect early contact with populations of India.⁴

Legacy of the Scythians: The Russian Europa Sub-Region

Background: The Russian Europa sub-region includes the lands of the ancient Scythian tribes, now inhabited primarily by East Slavic-speaking peoples. Peoples of this zone have interacted in historical times with peoples such as the northern Varangian (Scandinavian⁵) Rus' Khaganate, the eastern Kipchak (Turkic) Golden Horde (*Altin Ordu*), indigenous peoples of the Ural Mountains, and numerous other neighboring peoples.

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

Discussion: The largest genetic contributions to the Russian Europa sub-region were identified as Polish (75.6%) and Balkan (13.3%), for a total estimated contribution of 88.9% from predominantly Slavic-speaking sub-regions. These observations are consistent with the expansion of the East Slavs primarily from the vicinity of modern Poland and Belarus. Both Polish and Belarusian populations share genetic characteristics of the Polish genetic sub-region identified by DNA Tribes® Europa analysis, as will be discussed later.

Substantial Tibetan (5.1%), Altaian (3.5%), and American Indian (2.5%) genetic contributions were also identified. These observations likely reflect a long history of settlements and Russian interactions with Turkic and Uralic peoples to the east and north, whose territories have included parts of modern day Russia. More specifically, the Altaian contribution likely reflects contact with Turkic peoples such as the Khazars of the Khazar Khaganate and later the Kipchaks of the Golden Horde, as well as more ancient interactions of the ancient Scythians.

The American Indian and Tibetan contributions observed might reflect interactions with northern parts of Eurasia not yet fully represented among the available data. As discussed above, the Arctic genetic region of Alaska and far eastern Siberia is predominantly affiliated with American Indian genetic regions. American Indian genetic contributions are also observed in the Altaian genetic region. Geographically intermediate populations, such as peoples of the Ural

³ *Ibid.*

⁴ For more information about genetic connections between India and Australia, see "Exploring Ancestry in the South Seas" in the September 27, 2008 issue of DNA Tribes® Digest, available at: <http://www.dnatribes.com/dnatribes-digest-2008-09-27.pdf>

⁵ Although the founders of the Rus' Khaganate were Norsemen (known to Turkic peoples to the south as "sea kings"), the territories of the early Rus' state were also inhabited by Baltic, Slavic, and Finnic peoples.

Mountains and more eastern parts of northern Siberia also might have served as intermediaries for the American Indian gene flow to Russia suggested by these results.

Similarly, the Tibetan genetic contribution identified might reflect gene flow through an historically important part of the Turkic world for which few genetic data are presently available: the zone between the Aral Sea and Hindu Kush range of the Pamir Mountains known to European historians as Transoxiana (meaning “[the land] beyond the Oxus [River]”).⁶

As more data for this part of Europe become available, it might become possible to describe genetic structure within the Russian zone in greater detail.

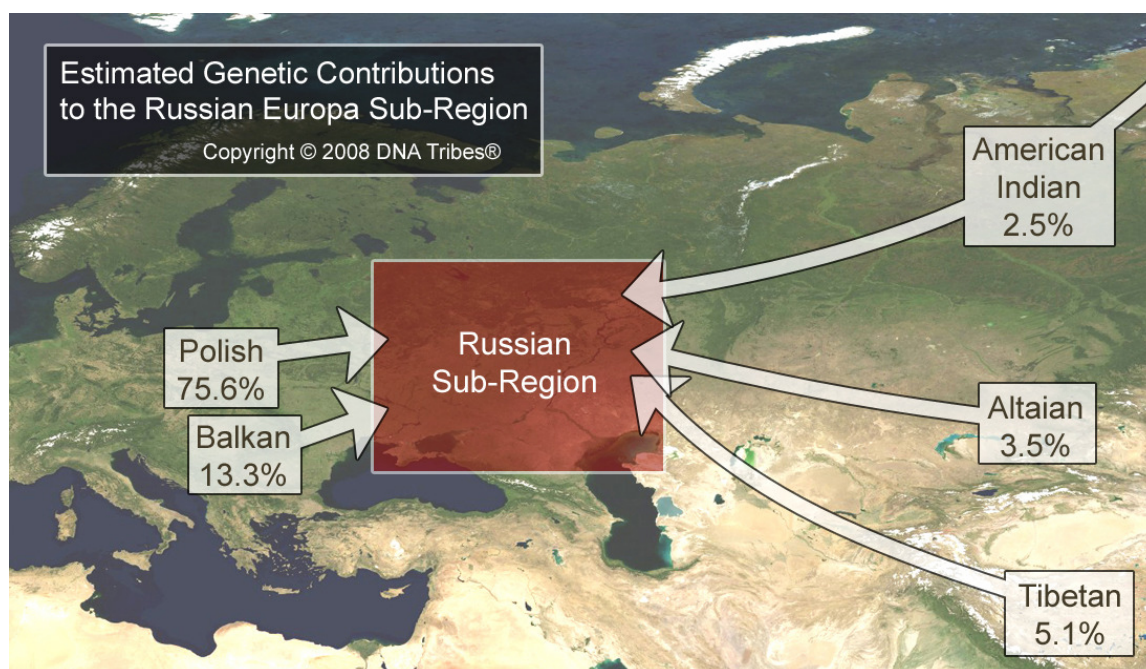


Figure 3: Estimated genetic contributions to the Russian Europa Sub-Region.

Genetic Region	Estimated Contribution
Polish	75.6%
Balkan	13.3%
Tibetan	5.1%
Altaian	3.5%
American Indian	2.5%

Table 2: Estimated genetic contributions to the Russian Europa Sub-Region.

⁶ Notably, the Oghuz Turks originated near the Aral Sea and founded the Seljuk and Turkish (Ottoman) Empires whose domains extended to the Mesopotamian, Aegean, and Levantine genetic regions. As with the term “Siberia,” the use of general and potentially misleading labels such as “Central Asia” obscures the actual historical and genetic complexity in this part of the world.

Western Peoples of the Taiga: The Finno-Ugrian Europa Sub-Region

Background: The Finno-Ugrian Europa sub-region characterizes indigenous Uralic-speaking peoples of the northern Baltic coast, such as the Finns and Estonians, and also Slavic-speaking peoples of some neighboring districts of Russia, such as Pskov. Other Uralic-speakers include the Sami of northern Scandinavia and the Ugriic and Samoyedic peoples in the zone surrounding the Ural Mountains, for whom data are not presently available. These Uralic-speaking peoples represent the westernmost Eurasian cultures of the circumpolar taiga zone. Other circumpolar cultures include peoples of the Arctic genetic region of far eastern Siberia and Alaska, who share genetic patterns characteristics primarily with North American Indians, but also with Asian and Pacific peoples.⁷

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

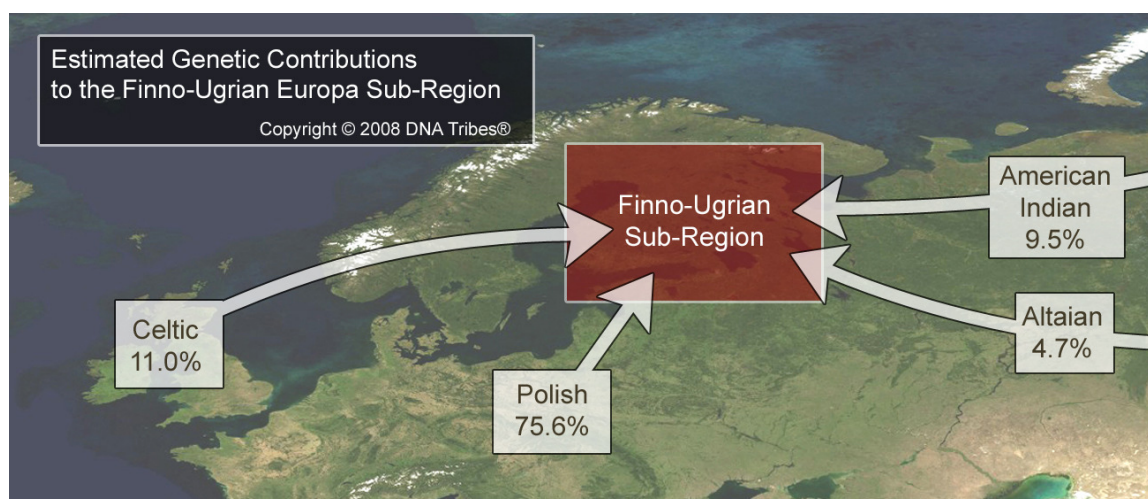


Figure 4: Estimated genetic contributions to the Finno-Ugrian Europa Sub-Region.

Genetic Region	Estimated Contribution
Polish	73.7%
Celtic	11.0%
American Indian	9.5%
Altaiian	4.7%
Other	1.0%

Table 3: Estimated genetic contributions to the Finno-Ugrian Europa Sub-Region.

⁷ For more information, see “The Arctic Connection: Alaska to Siberia” in the October 25, 2008 issue of DNA Tribes® Digest, available online at: <http://www.dnatribes.com/dnatribes-digest-2008-10-25.pdf>

Discussion: The largest genetic contributions identified were from the European Polish (73.7%) and Celtic (11.0%) genetic regions (for a total of 84.7%). This indicates that Finno-Ugrian peoples of Europe are primarily European in origin. The Celtic genetic contribution might suggest an ancient source of gene flow from northwestern Europe pre-dating more recent contacts with Germanic-speaking Scandinavians.

Substantial genetic American Indian (9.5%) and Altaian (4.7%) contributions were also identified. These observations likely reflect contact with other circumpolar peoples to the east in Siberia, including speakers of related Ugric and Samoyedic languages near the Ural Mountains. As discussed above, the substantial American Indian genetic contribution might suggest gene flow from North America, perhaps mediated by Paleo-Siberian-speaking peoples of far eastern Siberia.

Birthplace of the Slavs: The Polish Europa Sub-Region

Background: The Polish genetic sub-region of Europe includes the territories of present day Poland and Belarus. This zone European zone is sometimes considered to be the homeland of the early Slavic peoples, expanded from here to the Balkan and Russian sub-regions. The name Belarus or "White Russia," refers to the medieval state of Kievan Rus', which was founded by Varangian traders from Scandinavia and the Baltic to the north. The Polish genetic sub-region also includes territories that were later part of the Polish-Lithuanian Commonwealth, which was composed of both Baltic and Slavic peoples and known for its religious tolerance and a political ideal of "Golden Liberty," in which the freely elected king's power was limited by a powerful class of nobles (*szlachta*).

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

Discussion: Consistent with its geographical location, results indicate substantial genetic contributions to the Polish genetic sub-region from sub-regions to the west (Germanic 38.5%), east (Russian 26.4%), south (Balkan 23.2%), and north (Finno-Ugrian 11.7%). These observations suggest substantial interactions with neighboring peoples not limited to Slavic-speakers but also including Germanic and Finno-Ugrian peoples.

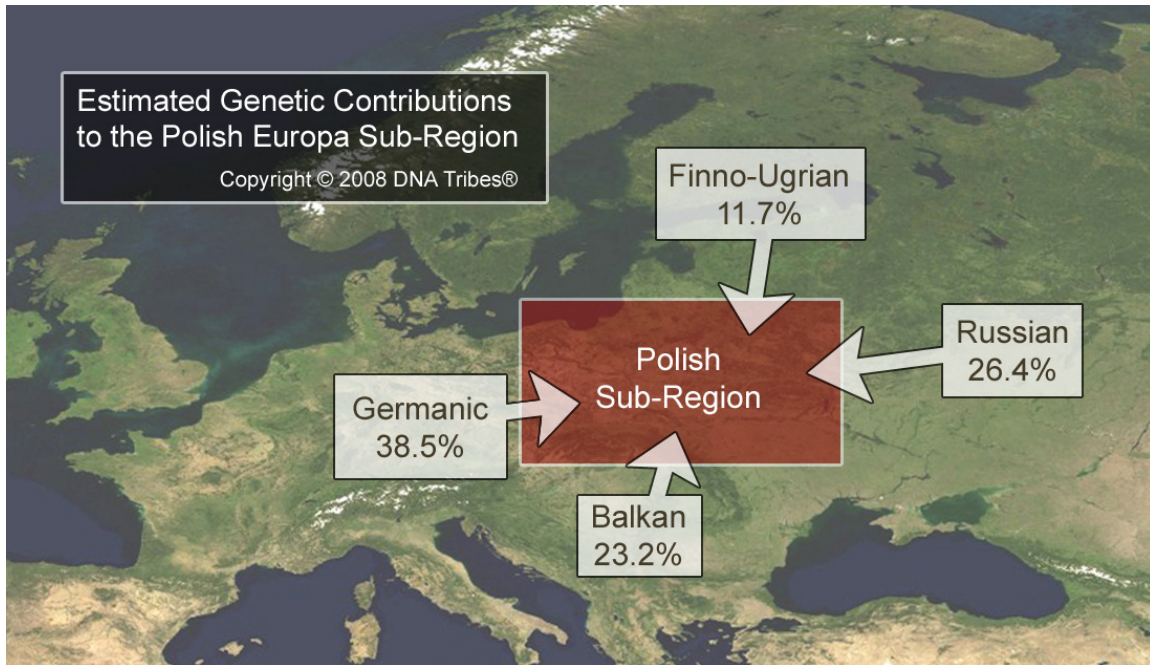


Figure 5: Estimated genetic contributions to the Polish Europa Sub-Region.

Genetic Region	Estimated Contribution
Germanic	38.5%
Russian	26.4%
Balkan	23.2%
Finno-Ugrian	11.7%
Other	0.2%

Table 4: Estimated genetic contributions to the Polish Europa Sub-Region.

Old Europe: The Balkan Europa Sub-Region

Background: The Balkan genetic sub-region includes the first Neolithic (agricultural age) settlements in Europe. This part of Europe is presently home to peoples of several ethnic and cultural groups, including South Slavs, Magyars (Hungarians), Romanians, and others, and includes territories of the Byzantine, Ottoman, and Habsburg (Austrian) empires in historical times.

Genetic analysis: Genetic contributions to the Polish Europa sub-region from 32 world regions and twelve Europa sub-regions were identified. Results are illustrated in **Figure 6** and summarized in **Table 5** below.

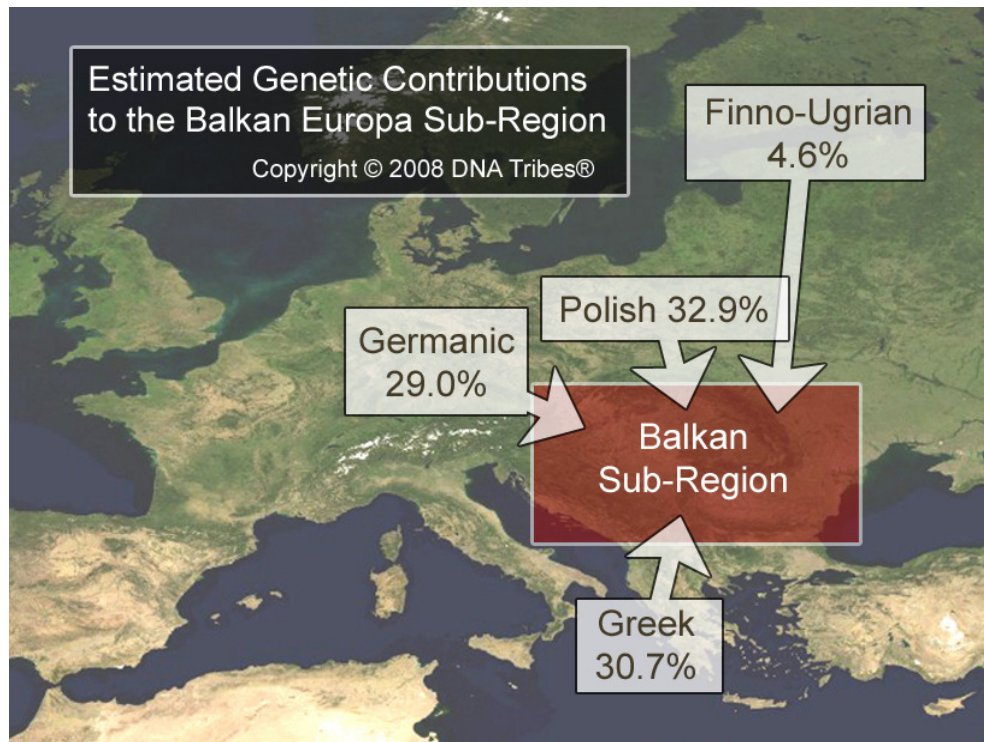


Figure 6: Estimated genetic contributions to the Balkan Europa Sub-Region.

Genetic Region	Estimated Contribution
Polish	32.9%
Greek	30.7%
Germanic	29.0%
Finno-Ugrian	4.6%
Other	2.8%

Table 5: Estimated genetic contributions to the Balkan Europa Sub-Region.

Discussion: Consistent with central location of the Balkan sub-region, results in **Table 5** indicate genetic contributions from several adjacent sub-regions of Europe. Notably, these observed genetic contributions are substantially consistent across modern Balkan populations despite differences in ethnic and/or linguistic affiliations. Because the Balkans have been continuously inhabited for thousands of years, it is unlikely that a given genetic contribution reflects any single event recorded by historians. Nevertheless, some historical events can be identified that correspond to genetic contributions observed here.

For instance, the observed Polish genetic contribution corresponds to the expansion of Slavic peoples from north of the Balkan region. The observed Greek genetic contribution corresponds to historical contacts with Thracians and later, with the Byzantine and Ottoman empires. The Germanic genetic contribution might correspond to the expansion Germanic peoples in the *Drang nach Osten* (“Drive to the East”) during the Middle Ages and later with the

Habsburg Empire. The smaller Finno-Ugrian genetic contribution corresponds to contact with Uralic-speaking Magyars. These historical correspondences are perhaps best described as recent examples of underlying geographical relationships rather than complete explanations of the genetic patterns observed among modern peoples.

At the Heart of Central Europe: The Germanic Europa Sub-Region

Background: The Germanic sub-region includes populations of present-day Germany and Austria, historically involved in the formation of numerous kingdoms and empires in historical times. These include the Carolingian Empire, Holy Roman Empire, Habsburg Empire, German Empire (including the Kingdom of Prussia, whose territories extend eastwards into modern Poland), and, more recently, East Germany and West Germany. The Germanic peoples of this region are thought to have expanded from southern Scandinavia and northern Germany before coming into contact with the Roman Empire. Although this part of Europe is primarily inhabited by Germanic-speaking populations, since ancient times it has been in contact with Italians, Wends, Sorbs, Prussians, Slovenes, Croats, Magyars, and numerous other neighboring peoples.

Genetic analysis: Genetic contributions to the Germanic Europa sub-region from 32 world regions and twelve Europa sub-regions were identified. Results are illustrated in **Figure7** and summarized in **Table 6** below.

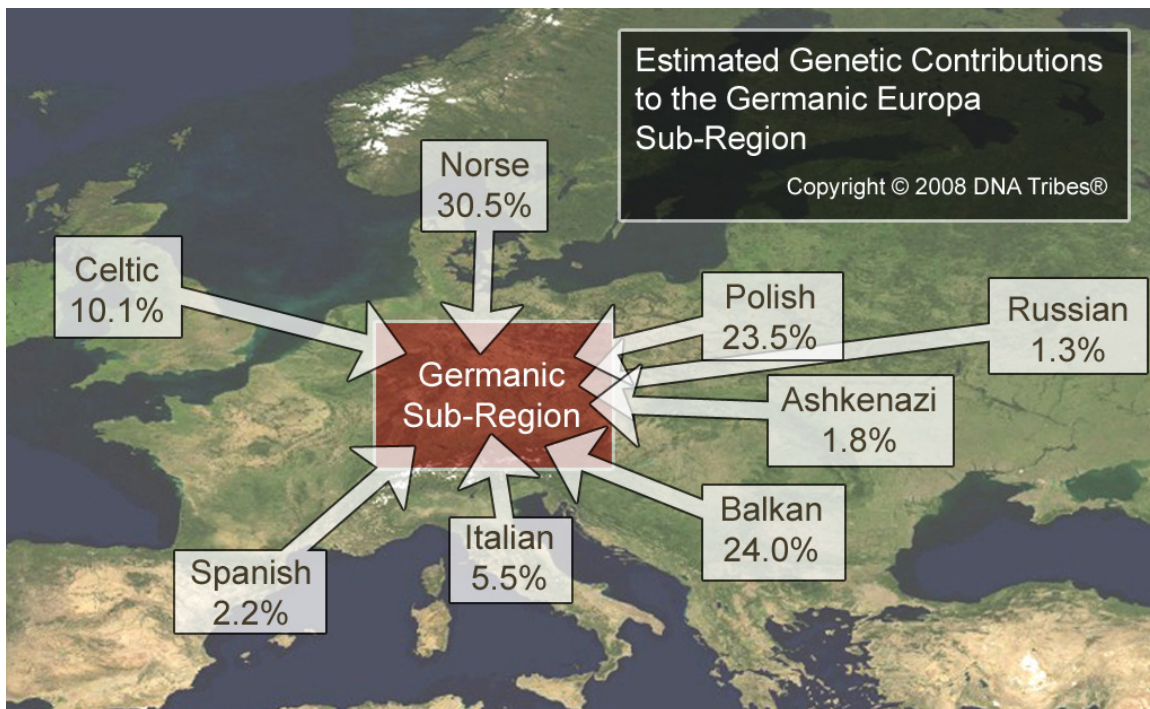


Figure 7: Estimated genetic contributions to the Germanic Europa Sub-Region.

Genetic Region	Estimated Contribution
Norse	30.5%
Balkan	24.0%
Polish	23.5%
Celtic	10.1%
Italian	5.5%
Spanish	2.2%
Ashkenazi	1.8%
Russian	1.3%
Other	1.2%

Table 6: Estimated genetic contributions to the Germanic Europa Sub-Region.

Discussion: The largest genetic contribution to the Germanic sub-region identified was Norse (30.5%), consistent with an early expansion of Germanic peoples from southern Scandinavia and northern Germany. However, substantial genetic contributions were also identified from several neighboring sub-regions of Europe. As with the Balkan region discussed above, these contributions might represent gene flow associated with not only known historical contacts, but also unrecorded ancient events as well as long term geographical gene-flow among neighboring peoples. For instance, the Balkan contribution might reflect to some degree contacts among peoples of the Habsburg Empire, and the Polish contribution might reflect contacts with Prussians to the east of modern Germany. Uniquely among northern Europa sub-regions surveyed in this study, an Ashkenazi genetic contribution of 1.8% was identified, which might reflect intermarriage between Jewish and non-Jewish communities in this part of Europe.

Peoples of the North Sea: The Norse Europa Sub-Region

Background: The Norse sub-region of Europe includes modern Scandinavia as well as populations surrounding the North Sea, including peoples of the Low Countries and (to some extent) England, northern France, and northern Germany.

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

Discussion: The largest genetic contribution to the Norse Europa sub-region was identified as Celtic (58.1%). This is consistent with the proximity of the Norse lands to the North Sea and English Channel and suggests extensive gene flow from peoples of the British Isles. This might reflect both early gene flow along the coasts of western and northern Europe, as well as more recent historical contacts including Viking settlements in England, Scotland, and Ireland. A substantial genetic contribution from the Germanic sub-region to the south (40.1%), where related Germanic tongues are spoken, was also identified. Notably, a smaller contribution of 1.8% from the Altaian genetic region was also identified, reciprocating the Norse contribution identified in

the Altaian region. This might reflect some gene flow from the interior of Asia mediated by early Uralic-speaking peoples of Siberia and Scandinavia.

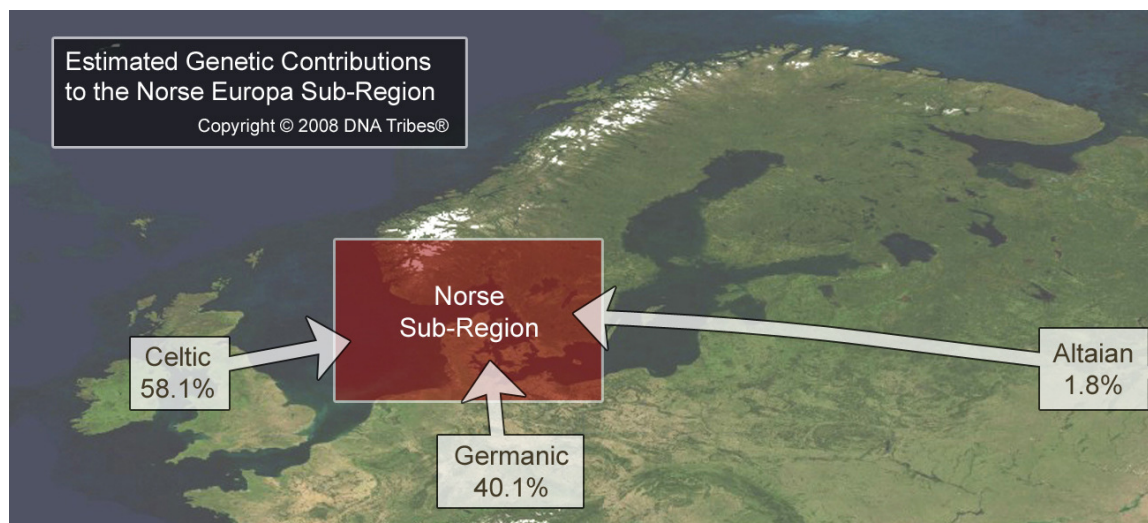


Figure 8: Estimated genetic contributions to the Norse Europa Sub-Region.

Genetic Region	Estimated Contribution
Celtic	58.1%
Germanic	40.1%
Altaian	1.8%

Table 7: Estimated genetic contributions to the Norse Europa Sub-Region.

Isles of the Setting Sun: The Celtic Europa Sub-Region

Background: The Celtic British Isles include some of the westernmost lands of northern Europe (aside from Iceland). Accessible only by sea, the Celtic sub-region is geographically isolated from most of Europe. Traditional narratives of the Celtic peoples such as the Irish *Lebor Gabála Éirenn* or Book of Invasions, although semi-mythical in substance and presentation, describe several waves of migrations from the Iberian Peninsula (where related Celtiberian peoples lived in the era of the Roman Empire) as well as the far north. More recently, the British Isles have been invaded and settled by Normans and Vikings of the Norse genetic region.

Celtic legends also describe journeys to islands far to the west, such as the mythical *Tír na nÓg* (“Land of Eternal Youth”) and *Mag Mell* (“Plain of Joy”), reflecting the Celtic sub-region’s maritime orientation and location at the ends of the (known) earth. Not incidentally, it is from the coastal Northwest European world region (which includes the more local Celtic and

Norse sub-regions) that North America was settled in the past 500 years, bringing the many sea voyage legends of these lands to historical fruition.⁸

Genetic analysis: Genetic contributions to the Celtic Europa sub-region from 32 world regions and twelve Europa sub-regions were identified. Results are illustrated in **Figure 9** and summarized in **Table 8** below.

Discussion: The largest genetic contribution identified for the Celtic sub-region was Norse (83.8%). Genetic contributions from the Iberian Portuguese (6.2%) and Spanish (5.7%) sub-regions were also identified. These observations are consistent with historical descriptions of contacts with seagoing Scandinavian peoples as well as with the Iberian Peninsula.

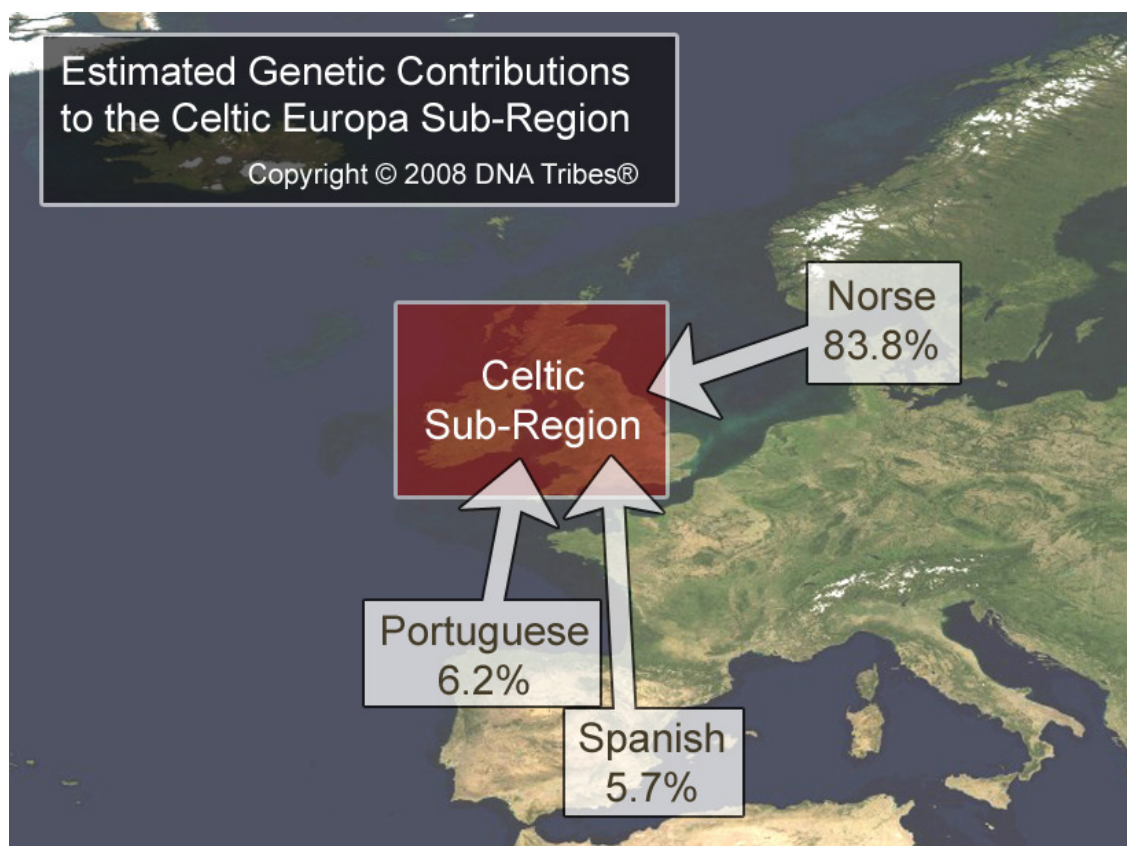


Figure 9: Estimated genetic contributions to the Celtic Europa Sub-Region.

⁸ For more information, see “Who are the Americans?” in our August 2008 issue of DNA Tribes® Digest, available online at: <http://www.dnatribes.com/dnatribes-digest-2008-08-29.pdf>.

Genetic Region	Estimated Contribution
Norse	83.8%
Portuguese	6.2%
Spanish	5.7%
Other	4.3%

Table 8: Estimated genetic contributions to the Celtic Europa Sub-Region.

Conclusion

The results of this study indicate that genetic contributions to sub-regions throughout Europe are primarily from neighboring peoples, reflecting the primarily geographical nature of human genetic structure. In some eastern and northern sub-regions, substantial Asian and American Indian genetic contributions were observed, suggesting some gene flow across continental borders. In many cases, observed genetic contributions between regions corresponded with events and contacts known to history. However, these correspondences likely reflect only historically identifiable examples of underlying geographical relationships rather than sufficient or complete explanations of the genetic patterns observed today.



Getting the Most from Your Testing

Originally published August 29, 2008

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

Updating Your Analysis:

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

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

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

<http://dnatribes.com/populations.html>

Our current analyses now include a frequency-based match analysis as well as U.S. patent-pending DNA Tribes® TribeScore system that measures how well your own DNA fits in a population compared to members of that ethnic group or region. This unique scoring system provides the information you need to see how well your genetic fit is around the globe, providing detailed information about your genetic relationships to hundreds of populations.

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

Customizing Your Analysis:

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

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



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

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

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

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

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

DNA Tribes® Europa provides the most detailed and complete analysis of European autosomal genetic structure available. DNA Tribes® Europa provides your DNA match scores for 13 genetic sub-regions of Europe, which is substantially more robust than the individual population matches in Parts B – C of core results and more detailed than the European world regions referenced in Part D of core results.

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

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

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



Researching Your Results:

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

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