

Full Length Research Paper

The closeness of the Finnish Ugric, Slav and Germanic populations according to anthropological and genetical data

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The computation of genetic distances of 55 human populations belonging to four great human races, based on proteic, enzymatic and blood group loci, and the construction of a dendrogram for these populations, distinguished some relationship among German, Slavic and Finnish-Ugric populations. According to the results, Russians cluster together with Poles, Iranians, Komi, Chuvashes, Udmurtians, Nentses and Ossetians; Germans cluster together with Serbs, Moldavians, Hungarians, Croats and Czechs; and Greeks are in closeness with Slavic populations. Common migrations of these populations from places of first differentiation in Asia were identified. In Europe, German populations migrated differently than ancestors of Russians, which migrated into Europe across the North of Siberia. The ancestors of Germans probably migrated in the same way than Hunnu. Settlements of ancient Caucasoids in Central Asia are currently under investigation. Haplogroups H, W, I, U, X and T1, defined by mitochondrial DNA, of the rural Russian population in the Yaroslavl region corresponded to that of Russians and Caucasoids. Additionally, the last decoding of petroglyphs in the Baikal region discovered the presence of ancestors of Caucasoids in Siberia in paleolithic.

Key words: Human populations, genetic closeness, finnish-ugric, slave, Germanic populations, genetic distances, anthropological data.

INTRODUCTION

Monophyletic origin of humanity is admitted now by biggest part of scientists. Both anthropological and genetical studies indicate that all human populations and races originated from a single common root (Alekseev, 1974; Cavalli-Sforza, 1997). The investigations of mitochondrial DNA polymorphism even permitted to suggest that all human branches (races in European literature) originated from one woman lived in Africa near 200 000 years ago (Cann et al., 1987). Though it is later turned out that the common ancestral mother of mankind must have existed much earlier (Kruger and Vogel, 1989), the data concerning the polymorphism of the mt DNA confirmed the common origin of mankind.

In the course of research concerning the polymorphisms of blood groups, serum proteins and red cell enzymes it became obvious that human races and populations differ in the level of polymorphisms of these loci (Mourant et al., 1976; Nei and Roychoudhury, 1974). In last work there were calculated the genetic distances between the major human races basing on genetic loci encoding serum proteins and red cell enzyme

groups, and blood groups. It was assumed that the divergence of African branch (race) from the common tree of Caucasoids and Mongoloids took place around 110 000 years ago. However, the differentiation in Caucasoids and Mongoloids took place only about 50 000 - 40 000 years ago (Nei, 1978).

We suggested on basis of discovering Caucasoid gene frequencies in Altaians (Nazarova and Kusnetsova, 1993) and the same haplogroups of mt DNA (A,B,C,D) in Altaians and American Indians (Sukernik et al., 1996) the paleoasiatic origin of Caucasoids, North Mongoloids and American Indians from one ancient populations inhabited in South Siberia region near 50 000 - 40 000 years ago (Nazarova, 1999, 2000, 2005, 2008).

According to previous studies, Slavic, Finno-Ugric and German populations have certain genetic closeness, based on a dendrogram on genetic distances of 55 human populations belonging to four of the major human races, and with proteic, enzymatic and blood-group loci (Nazarova, 2008). Russians cluster together with Poles, Iranians, Komi, Chuvashes, Udmurtians, Nentses, Osse-

tians and Azerbaijanians. There is evidence by some historians that Russians are the descendents of the Rus-Skifian tribes thus; their being in a cluster with other descendents of the Skifians-the Iranians and the Ossetians-is understandable.

The Paleolithic migration of the ancestors of the Russians from the center of Asia, Southern Siberia, across the north of Siberia to the north of Europe explains why the Nentses are in the same cluster: the Nentses are evidently a trace of that migration (Nazarova, 1999, 2000, 2005).

Around 1,000 years ago, the tribes of Finnish-Ugric origin-the Merya, Muroma, Meschera and others—became part of the Russian ethnos, fact that can explain the clustering of the Komi together with the Chuvaches and Udmurtians. Alekseyeva (1954, 1973) reports the presence of a Finnish-Ugric anthropological substratum in the Russian populations.

METHODS

The phenotypes of human populations such as Russian, Evenks, Yakuts, Altaians, Chuckchi, Eskimos and Talyshes were investigated in polyacrilamide gels. Methods and experimental procedures are described in detail in Nazarova (1989). Nazarova, 2008). 7-10 ml of blood from the veins was centrifuged in order to separate the plasma from the blood cells; the plasma and separated erythrocytes were immediately frozen. Electrophoresis of the proteins was done after returning to Moscow. The electrophoresis was carried out in a vertical block of polyacrilamide gel, following – in some modifications – the method described by Gahne et al. (1977).

The haptoglobin was stained with a solution containing 1 ml 30% H₂O₂ in 30 ml 10% CH COOH. The group specific component (GC), transferrin (TF), and albumin (ALB) were stained with Coomassie-Blue. We investigated 28 alleles of 12 proteic, enzymatic and blood-group loci. These loci are: AB0, Rh, Hp, Gc, Tf, GLO I, Es D, PGM I, ACP, AK, ADA, 6-PGD. The gene frequencies were calculated on computer with standard program, statistical procedure is described by Lee (1978).

Gene frequencies for other human populations were taken from published data from other authors that were cited in(Nazarova and Alkhutov 1999.Nazarova, 2009) Genetic distances of 55 populations from Europe, Asia, America, Africa and Oceania, and of 35 Slave, German and Finnish-Ugric and some other populations were calculated following Cavalli-Sforza and Bodmer (1971). The dendrogram of genetic relationships of those 55 human populations, and of 35 populations of Slavs and others were constructed by the method of Mashurov and Cherkashenko (1987).

RESULTS AND DISCUSSION

The Germans clustered together with the Serbs, Moldovans, Hungarians, Croations, Czechs and Ukrainians (Nazarova, 2008). This closeness may be explained by the common origin of these ethnic groups and by their migration from the first place of differentiation in Asia to Europe by a route different than that of the ancestors of the Russians, who entered Europe via north Siberia. The ancestors of the Germans, and also the current central - European Slavic ethnic groups, migrated to Europe from

Asia roughly following the same route that the Hunns. The study by Russian scientists in book” Near the Sources of Civilizations” (2004) describes the discovery of a settlement of ancient Caucasoids in central Asia on the territory of Turkmenia. According to Scherbakov (2000) they are the ancestors of the German tribes. Research on the mitochondrial DNA of the rural Russian population of the Yaroslav region reveal the presence of practically all haplogroups characteristic of Russians and even Caucasoids as a whole (H,W,I,U,X,T*,T1) (Nazarova et al., 2007). Moreover, the recent deciphering of the hieroglyphs in the Baikal region indicates that the ancestors both of the Shumers and of the Japanese were there in the Paleolithic (Kifishin and Kikeshev, 2005), and the presence in this region of the most ancient written language. The presence of the ancestors of the Russians in almost all Eurasia in the Paleolithic, those with the most ancient runic written language, has also been shown (Chudinov, 2006).

The Finns clustered together with the Swedes, Estonians, Talyshes and Belorussians. The matrix of the genetic distances of 35 Slavic, Germanic and Finnish-Ugric populations is shown in Table 1. The dendrogram based on the data given in Table 1 corresponds to that of 55 populations (Figure 1), and with the conclusions made from the matrix. As can be seen from the dendrogram in figure 1, the Poles (2) were in the big subcluster together with the Russians (1), the neighboring branch splitted up into several subclusters in which there were the branches of the Serbs (22) and the Germans (2), and further were the branches of the Croations (23), the Czechs (25), the Ukrainians (18), and the Hungarians (26). In the next neighboring subcluster, there were the Swedes (28), the Finns (12), the Estonians (20), and the Belorussians (19). The last subcluster of the big cluster gets together the Scots (21) and the Bulgarians (24).

The cluster next to that with the Russians and other Slavic, Germanic and Finnish populations had the branches of the Komi (4), the Chuvaches (5), the Iranians (3), the Ossetians (8), the Nentses (7), and the Udmurtians (6). So, the Finnish-Ugric people living in the Volga region and the Ural region showed a genetic closeness to the Ossetians, the descendents of the ancient nomads, the Skifs, and the Nentses now living in the north of the European part of Russia and Siberia. That closeness can be due to the fact that all these people were originally ancient ancestral Asiatic populations who inhabited southern Siberia (the Altai and the neighboring regions) in the Paleolithic and then went on a many thousand year long migration that brought them to their current place of living. These processes were first described in Nazarova (1999, 2000 and 2005). The subclusters containing the branches of the Mongols (16), Altaians (13), Yakuts (15), Mansi (29) and Mari (27) were more distant. The branches of the Lapps (35) and Africans (33) separated from the common pre Asiatic population much earlier, but the branch of the American

Table 1. Matrix of genetic distances between Slavs and other human populations. Population identification: 1. Russians; 2. Poles; 3. Iranians; 4. Komi; 5. Ghuvashes; 6. Udmurtians; 7. Nentses; 8. Ossetians; 9. Arabs; 10. Italians; 11. Germans; 12. Finns; 13. Altaians; 14. Evenks; 15. Yakuts; 16. Mongols; 17. Indians; 18. Ukrainians; 19. Belorussians; 20. Estonians; 21. Scottish; 22. Serbians; 23. Croatians; 24. Bulgarians; 25. Czechs; 26. Hungarians; 27. Mari; 28. Swedes; 29. Mansi; 30. American Indians; 31. Tatars; 32. Jews of Near East; 33. African Negroes; 34. Greeks; and 35. Saami (Lapps).

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35. Saami (Lapps)	0.38710 ±0.05587	0.46035 ±0.05953	0.40471 ±0.05682	0.32513 ±0.05218	0.40068 ±0.05566	0.36861 ±0.05483	0.37814 ±0.05538	0.46091 ±0.05956	0.41196 ±0.05719	0.35582 ±0.05408	0.43152 ±0.05817	0.39818 ±0.05647	0.31477 ±0.0515	0.40745 ±0.05696	0.3938 ±0.05624	0.41203 ±0.0572	0.53367 ±0.06255	0.34111 ±0.05319	0.2879 ±0.04964	0.35584 ±0.05409	0.38955 ±0.05601	0.43193 ±0.05819	0.35154 ±0.05383	0.51084 ±0.06167	0.42868 ±0.05803	0.44006 ±0.05859	0.38875 ±0.05596	0.43749 ±0.05846	0.34915 ±0.05368	0.67134 ±0.06678	0.39332 ±0.05621	0.45444 ±0.05926	0.46977 ±0.05995	0.38102 ±0.05554		35. Лопари
	1. Русские	2. Поляки	3. Иранцы	4. Коми	5. Чувашаи	6. Удмурты	7. Ненцы	8. Осетины	9. Арабы	10. Итальянцы	11. Немцы	12. Финны	13. Алтайцы	14. Эвенки	15. Якуты	16. Монголы	17. Индийцы	18. Украинцы	19. Белорусы	20. Эстонцы	21. Шотландцы	22. Сербы	23. Хорваты	24. Болгары	25. Чехи	26. Венгры	27. Марийцы	28. Шведы	29. Манси	30. Индейцы Америки	31. Татары	32. Евреи Ближнего Востока	33. Негры Африки	34. Греки	35. Лопари	

Indians (30) splitted off earliest.

There was a cluster containing the subclusters of the Slavic-Germanic (Russians, Poles, Serbs, Germans and others) and the Finnish-Ugric (Komi, Chuvashes, Udmurts) and another branch had the subcluster of the Tartars. The subcluster of the Italians (10), Arabs (9), and Evenks (14) splitted off from the cluster containing the Slavic-Germans and Finnish-Ugric and Tatars even earlier. The Evenks are called "Siberian Frenchmen" by Heilborn and Berg (1913) and their dissimilarity to the rest of the northern mongoloids is well established. Thus, the matrix of genetic distances of 35 human populations containing the Slavs, Germans and Finno-Ugrics, and also the Saami and American Indians on the whole supported the conclusions of previous studies, based on matrixes 7 and 55 populations (Nazarova, 2008, 1999, 2000, 2005). Evidently, in the mid Paleolithic in the Altai region or in the neighboring regions, an ancestral population, both for the Caucasoids and for the Northern Mongoloids and American Indians, was present. The actual northern Altaians are direct descendants of this ancestral population. The ancestors of the American Indians, the first to separate from this Asiatic ancestral population, migrated across Siberia to the north-east of it, moving, perhaps be-

hind the herds of the ancestors of the American buffalo and the caribou whose ancestral land is also southern Siberia. The ancestors of the Indians crossed the Bering Isthmas, which existed in the Paleolithic, towards the American continent.

The genetic markers of the Y- chromosome of many human populations indicate that Slavs have a precise and defined series of such markers, male-inherited only, transmitted from father to son (Size, 2001; Wallace, 2002). These markers are constant, so it is possible to track the way of human populations from Paleolithic times to our days. The rare mutations of these allow to distinguish the manner in which populations differentiated. The Slavic populations had the haplogroup R 1a1.

In the Paleolithic, the ancestors of the Northern Mongoloids migrated from southern Siberia to its north, finally settling where they live now. The Evenks, Nganasans, and the Yakuts are now living in Siberia as well as the Nentses who moved toward the north-east of Europe. The ancestors of the Caucasoids (Russians) went, evidently, also from the south of Siberia to its north, and further via the circumpolar zone crossed to the north of Europe. That was also probably the route of migration of the Saami now living in the north of Europe Finland, the Kola

Peninsula, Norway and Sweden).

On the dendrogram at Figure 1, Greeks represented one branch of a big subcluster, and another branch of this subcluster consisted of Russians and other Slavic populations, as Poles, Serbs, Croatians, Czechs, Bulgarians, Belorussians, as well as Germans, Finns, Estonians and Scottish. On the dendrogram of 16 populations of Caucasus and some other populations, Greeks are in one subcluster with Russians (Nazarova and Alkhutov, 2005). This fact confirmed the data of Malyarchuk (1997), indicating that mitochondrial DNA polymorphism are close to the Slavik populations and the populations of Southern Europe. On the dendrogram of 55 human populations Greeks and Mari are in one subcluster (Nazarova, 2005). This at first glance strange union can be explained by the fact that the Mari, who are real Caucasoids, may have been closed to some ancient Caucasoids, who migrated to Europe most likely from Asia even a thousand year B. C. -the Akheits, representatives of the Crete - Mycenaean civilization, whose descendants are the Greeks.

The forming of ancient Caucasoids on territory of Asia was suggested and data of molecular genetics. The sequence of mitochondrial DNA of Neandertal man discovered in Germany in 1856,

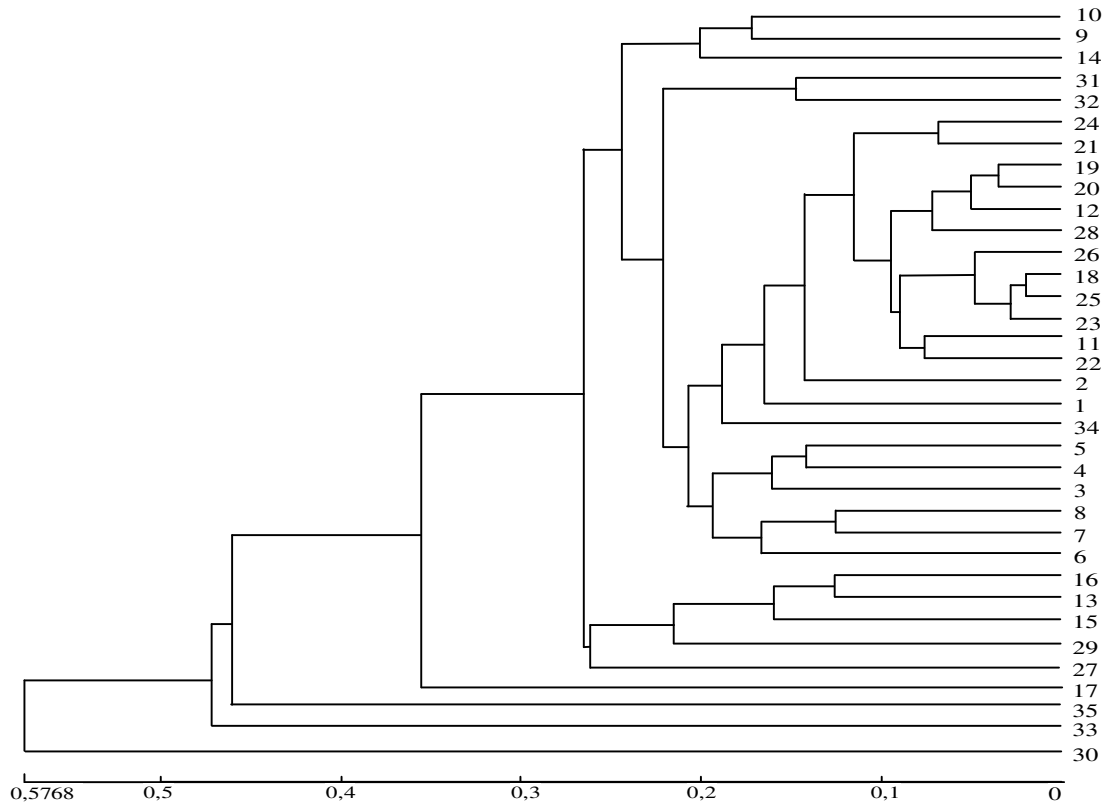


Figure 1. Dendrogram based on genetic distances (horizontal axis) among Slavic, Finnish-Ugric and Germanic Populations. Population identification: 1. Russians; 2. Poles; 3. Iranians; 4. Komi; 5. Ghuvashes; 6. Udmurtians; 7. Nentses; 8. Ossetians; 9. Arabs; 10. Italians; 11. Germans; 12. Finns; 13. Altaians; 14. Evenks; 15. Yakuts; 16. Mongols; 17. Indians; 18. Ukrainians; 19. Belorussians; 20. Estonians; 21. Scottish; 22. Serbians; 23. Croatians; 24. Bulgarians; 25. Czechs; 26. Hungarians; 27. Mari; 28. Swedes; 29. Mansi; 30. American Indians; 31. Tatars; 32. Jews of Near East; 33. African Negroes; 34. Greeks; and 35. Saami (Lapps).

turned out so far from the sequence of modern human mitochondrial DNA that origin of Kromanions from European Neandertal men is no probable (Krings et al., 1997).

The other branch of the Caucasoids, the Finnish-Ugric tribes, most likely went from Asia to Europe somewhat more south across the Urals and settled in the Volga region, the Kama region and the Ural region and further on, in a significant part of European Russia (Merya, Muroma who later became part of the Russian ethnos), and finally in the Baltic states and Scandinavia (Finns, Karelians, Estonians). In a dermatoglyphic research of the Finnish-Ugric populations, the Finnish-Ugric peoples present the same components as those that formed the anthropological appearance of the population of northern Eurasia (Khit and Dolinova, 2000).

In the works of Tilak (2002) it is shown, through the analysis of epic works of the Caucasoids of Asia, that the ancestors of the Indians and Iranians also inhabited the circumpolar zone for a certain period. Later, the ancestors of the Indians migrated to the South across west of the Urals, while the ancestors of the Iranians migrated to the South across east of Urals.

The ancestors of the Germanic tribes, in the opinion of Kurovsky are the Skifian tribes of Asia. So it is likely that the ancestors of the Germans migrated to Europe not across the north, but across the south of Siberia, and further across Middle Asia, where remainders of the civilization of the Caucasoids are unearthed in a region of Turkmenia today ("Near the Sources of Civilizations" et al., 2004; Scherbakov, 2000).

One should keep in mind that the migration of all these tribes which began back in the middle Paleolithic was very long lasting. People walked along with their families, their goods and chattels, stopping for long times in places where food was abundant, and only later they domesticated animals which would make migration a bit easier. Some of the tribes walked along ancestors of the large horned cattle. We discovered the presence of antigen V in the large horned cattle in southern Asia and in the Estonian red breed of cows (Mashurov et al., 1998).

The domestication of horses took place just 8 thousand years ago in the Dnepr region where the most ancient stirrups and bits were found. Considering the Caucasoid components of the Altaians revealed by us and the iden-

GENETIC RELATIONSHIP BETWEEN FINNO-UGRIC

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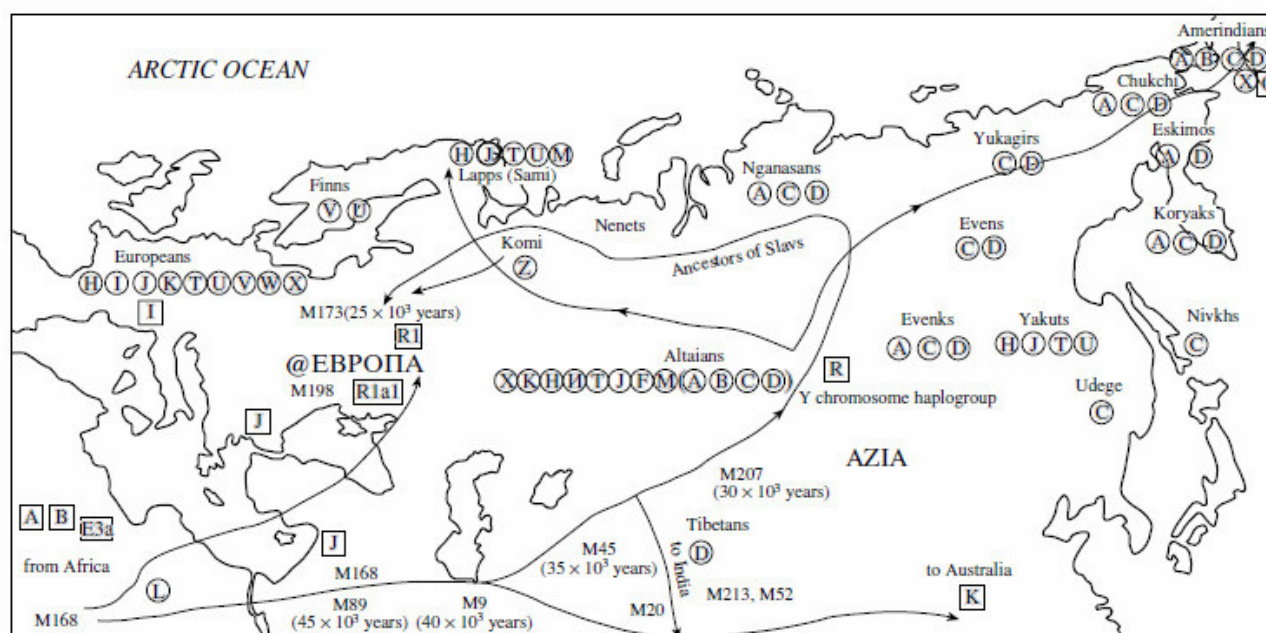


Figure 2. The diagram of migrations of prehistoric human populations marked with mtDNA and Y chromosome haplogroups. Latin letters in circles indicate mtDNA haplogroups; symbols in rectangles, Y chromosome haplogroups. Letter M with numbers indicates the probable place of the appearance of a one nucleotide polymorphism (snip) in the Y chromosome, the time of its appearance (years ago) is indicated in parentheses. The data on the geographic distributions of mtDNA and Y chromosome haplogroups have been summarize from studies published by different authors.

tity in mitochondrial DNA haplogroups between the Altaians and American Indians discovered by other authors (Sukernik, Shurr, Starikovskaya, Wallace, 1996; Brown et al., 1998), it is possible to assume that there was an ancestral population in southern Siberia and in the neighboring regions in the Paleolithic that gradually split into a number of branches which migrated in different directions and gave rise both to the ancestors of the American Indians and the northern Mongoloids as well as the Caucasoids. At the same time as the ancestors of the northern Mongoloids splitted into different branches, the ancestors of the Finns splitted off from the ancestors of the Slavic and Germanic populations. The division of the ancestral population into different clusters, besides by biological reasons, was facilitated by the division of the Nostratic ancestral language into families - Indo-European and Finnish-Ugric, the group of languages of the ancestors of the American Indians and then the splitting up of the language groups into separate languages.

According to Tomashevich (1988), a gradient of distribution of the frequencies of the supra orbital canals of the human skulls exists. The highest frequency of the supra orbital canals is among Saami, American Indians, and in Yakuts, Evenks, Chuckchi, and Eskimos. And in Kets, Yukagirs, Russians, Mansi, Ossetians and Armenians these frequencies are very close, near 30 - 38%, maybe confirming their common Asiatic origin.

The biological reason for the division of human populations was the arising and accumulation of mutations. Malyarchuk (1997) discovered different sets of mutations of the mitochondrial DNA in the Slavic and Germanic populations in the control region.

Figure 2 shows a probable way of migrations of ancient human populations marked with haplogroups of mitochondrial DNA and Y-chromosome, from Paleolithic. Data of mt DNA and Y-chromosome there were taken by author from many published works of different scientists. After this ancient migration human populations had arrived to modern place of their habitation.

Thus, based on the anthropogenetic data we suppose that the Caucasoids today-the Slavs, Finns and Germanic populations are from the same ancestral population inhabiting a region of Southern Siberia in the middle of the Paleolithic as that of northern Mongoloids and American Indians.

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