

The Genetic Relationships of the Slavic, Finnish-Ugric and Germanic Populations According to Anthropological and Genetical Data

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Abstract

The calculation of genetic distances of 55 human populations belonging to four great human races considering loci of proteins, enzymes and blood groups, and construction the dendrogram of these populations distinguished some relationship of German, Slavic and Finnish-Ugric populations. So, Russians are close by genetic distances with Poles, Iranians, Komi, Chuvashes, Udmurtians, Nentses and Ossetians. Germans are close with Serbs, Moldavians, Hungarians, Croatians and Czechs. The calculation of genetic distances of 35 Slavic, Finnish and Germanic populations, and constructing the dendrogram confirmed these results. The ancestors of Russians were migrated from places of first differentiation in Asia across the circumpolar area, and before were lived on the North of Siberia. Ancient German populations were migrated in Europe across the South of Siberia, probably by the same way as Hunnu in future time. The investigation of settlements of ancient Caucasoids in Central Asia probably discovered place of living of ancient German populations. The studying of mt DNA of rural Russian population in Yaroslavy region discovered all haplogroups of Russians and even Caucasoids (H, W, I, U, X, T1).

Keywords: Human populations; Genetic relationship; Finnish-Ugric; Slavic; Germanic populations; Genetic distances; Anthropological data

Introduction

Earlier we were made the dendrogram based on the matrix of the calculations of the genetic distances of 55 human populations belonging to four of the major human races according to the loci of proteins, enzymes and blood groups and we were revealed a certain genetic closeness of the Slavic, Finno-Ugric and German populations [1-3].

Russians turned out to be in the subcluster with the Poles, Iranians, Komi, Chuvashes, Udmurtians, Nentses, Ossetians and Azerbaijanians. Some historians think Russians are the descendents of the Rus-Skifian tribes, so their being in this 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 this cluster: the Nentses are evidently a trace of that migration [3,4].

That the Komi, Chuvashes and Udmurtians are in this subcluster may be connected with the fact that around 1000 years ago the tribes of Finnish-Ugric origin—the Merya, Muroma, Meschera and others—became part of the Russian ethnoses. In the works of academican Alekseyeva [5,6] the presence of a Finnish-Ugric anthropological substrata in the Russian populations is shown.

Material and Methods

We were investigated the phenotypes of such human populations as Russian, Evenks, Yakuts, Altaians, Chuckchi, Eskimos and Talyshes in polyacrilamide gel. Methods of those processes are described in Nazarova [7].

The gene frequencies we calculated on computer. The gene frequencies of other human populations we were taken from publish data other authors that were cited in our book “The Genetical Portrait of the People of the World” [8]. The genetic distances of 55 populations of Europe, Asia, America, Africa and Oceania, and of 35 Slave, German and Finnish-Ugric and some other populations we were calculated by method of Cavalli-Sforza and Bodmer [9]. The dendrogram of genetic relationship of those 55 human populations, and of 35 populations of Slaves and others we were constructed by method of Mashurov and Cherkashenko [10] with computer program which was doing by Than H.H.

Results and Discussion

The Germans are in the same subcluster as the Serbs, Moldavians, Hungarians, Croatians, Czechs and Ukrainians [1,11]. This closeness may be explained by the common origin of the ethnoses enumerated and their migration from the first place of differentiation in Asia to Europe by a route other than the ancestors of the Russians who went to Europe via north Siberia. The ancestors of the Germans, and also the current central-European Slavic ethnoses, migrated to Europe from Asia roughly following the same route that the Hunns took earlier. In the works of Sarianidi and the coauthors [12] the discovery of a settlement of ancient Caucasoids in central Asia on the territory of Turkmenia is described. In the opinion of Scherbakov [13] this Caucasoids are the ancestors of the German tribes.

Research on the mitochondrial DNA of the rural Russian population of the Yaroslavy region revealed the presence of practically all haplogroups characteristic of Russians and even Caucasoids as a whole (H,W,I,U,X,T*,T1) [14]. The latest 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 [15], and about 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 and them having the most ancient Runic written language has also been shown [16]. The Finns are in the subcluster with the Swedes, Estonians, Talyshes and Belorussians.

Finnish-Ugric populations

The dendrogram made according to the data on genetic distances computed by us.

As can be seen from the dendrogram in Figure 1, the Poles (2) are in the big subcluster together with the Russians (1), the neighboring branch splits up into several subclusters in which there are the branches of the Serbs (22) and the Germans (2), and further are the branches of the Croatians (23), the Czechs (25), the Ukrainians (18), and the Hungarians (26). In the next neighboring subcluster there are the Swedes (28), the Finns (12), the Estonians (20), and the Belorussians (19). And in the last subcluster of that big cluster there are the Scotch (21) and the Bulgarians (24).

The cluster next to the cluster with the Russians and other Slavic, Germanic and Finnish populations has the branches of the Komi (4), the Chuvashes (5), the Iranians (3), the Ossetians (8), the Nentses (7), and the Urdmurtians (6). So the Finnish-Ugric peoples living in the Volga region and the Ural region now show a genetic closeness to the Ossetians, the descendants of the ancient nomads, the Skifs, and with the Nentses now living in the north of the European part of Russia and Siberia. That closeness could be due to the fact that all these peoples 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 yearlong migration that brought them to their current place of habitation. We first described these processes in works [2-4].

The subclusters containing the branches of the Mongols (16), Altaians (13), Yakuts (15), Mansi (29) and Mari (27) are more distant.

The branches of the Lapps (35) and Africans (33) separates from the common pre Asiatic population much earlier, but the branch of the American Indians (30) splits off earliest of all.

The cluster containing the subclusters of the Slavic-Germanic (Russians, Poles, Serbs, Germans and others) and the Finnish-Ugric (Komi, Chuvashes, Udmurts) as another branch has the subcluster of the Tartars. The subcluster of the Italians (10), Arabs (9), and Evenks (14) split off from the cluster containing the Slavic-Germans and Finnish-Ugric and Tartars even earlier. Already in the book "Anthropology and Ethnography" of Heilborn and Berg, the Evenks are called "Siberian Frenchmen" and their dissimilarity to the rest of the northern mongoloids is stressed.

So 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 supports the conclusions made by us earlier based on matrixes 11 and 55 populations [1-4]. Evidently, in the mid Paleolithic in the Altai region or in the neighboring regions

there was a population ancestral both for the Caucasoids and for the Northern Mongoloids and American Indians.

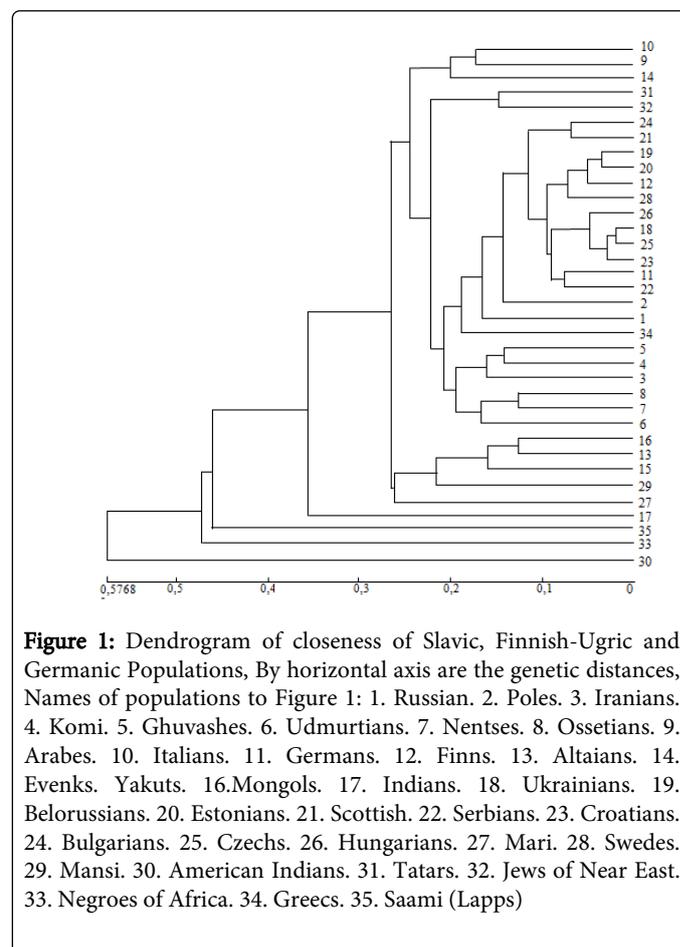


Figure 1: Dendrogram of closeness of Slavic, Finnish-Ugric and Germanic Populations, By horizontal axis are the genetic distances, Names of populations to Figure 1: 1. Russian. 2. Poles. 3. Iranians. 4. Komi. 5. Ghuvashes. 6. Udmurtians. 7. Nentses. 8. Ossetians. 9. Arabes. 10. Italians. 11. Germans. 12. Finns. 13. Altaians. 14. Evenks. 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. Negroes of Africa. 34. Grecs. 35. Saami (Lapps)

The northern Altaians today 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 behind the herds of the ancestors of the American buffalo and the caribou whose ancestral land also is considered southern Siberia. The ancestors of the Indians crossed the Bering Isthmas, which existed in the Paleolithic, to the American continent.

Now are investigated the genetical markers of Y-chromosome of many human populations [17,18]. There were discovered that Slavic populations had precise definite series of such markers that inherited only by man line, because Y-chromosome is inherited only by man line, from father to son. These markers are constant, so there was possible to watch the way of human populations from palaeolithic times to our days. The rare mutations of these markers permit to see the ways of differentiations of populations. So, the Slavic populations had 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 are one branch of big subcluster, and other branch of this subcluster consist of Russians and other Slavic populations, as Poles, Serbs, Croatians, Czechs, Bulgarians, Belorussians, and Germans, Finns, Estonians and Scottish, too.

On the dendrogram of 16 population of Caucasus and some other populations Greeks are in one subcluster with Russians [11]. This fact confirms the data of Malyarchuk [19] indicating on mitochondrial DNA polymorphism data the closeness of the Slavic populations and the populations of Southern Europe. On the dendrogram of 55 human populations Greeks and Mari are in one subcluster [11]. This at the first glance strange union can be explained by the fact that the Mari, who are real Caucasoids, may have been close to some ancient Caucasoids, who migrated to Europe most likely from Asia even thousand years B.C.

I think that there may be the Akheits, representatives of the Crete – Mycenaean civilization, whose descendants are the Greeks.

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 the Baltic states and Scandinavia (Finns, Karelians, Estonians). In the works of the Indian scientist Tilak [20] 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 while. Later the ancestors of the Indians migrated to the south west of the Urals, while the ancestors of the Iranians - east of the Urals.

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 were unearthed in a region of Turkmenia today.

One should keep in mind that the migration of all these tribes which began back in the middle Paleolithic was very long lasting many thousands of years. People went on foot with their families, with their goods and chattels, stopping for a long time in places where food was abundant. And only later were animals which would make the migration a bit easier first domesticated. Some of the tribes went, evidently with the 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. The most ancient stirrups and bits were found in Dnepr region (Ukraine), because there is probably that the domestication of horses took place near 8 thousand years ago in Dnepr region.

Considering the Caucasoid components of the Altaians revealed by us [21] and the identical haplogroups in the mitochondrial DNA of the Altaians and American Indians discovered by other authors [22] it is possible to make the presumption 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. The division of the ancestral population into different clusters, besides for biological reasons, was facilitated, evidently 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.

Russian anthropologist Tomashevich [23], discovered a gradient of distribution of the frequencies of the supra orbital canals of the human skulls. The highest frequency of the supra orbital canals is among Saami, American Indians, and in Yakuts, Evenks, Chuckchi, and Eskimos. And in Kets, Yuragirs, Russians, Mansi, Ossetians and Armenians those frequencies are very close, near 30-38%. Maybe this population had common Asiatic origin.

The biological reasons for the division of human populations were probably the arising and accumulation of mutations. The new mutation may be arising after explosion of volcano Toba at the territoria modern Indonesia 70 thousand years ago. Malyarchuk [19] discovered different sets of mutations of the mitochondrial DNA in the Slavic and Germanic populations in the control region.

Thus, based on the anthropogenetic data we think 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 the northern Mongoloids and American Indians.

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