

The Origin of the Baltic-Finns from the Physical Anthropological Point of View

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The author provides a comprehensive analysis of the physical anthropology of the Finns and Saami, comparing them with other Scandinavian peoples and contrasting them genetically with the Mongoloid peoples of Asia, notwithstanding the affinities which link the Finnish language with the Uralic and to a lesser extent the Altaic languages. He concludes that both the Finns and the Saami are genetically Caucasoid or European, and that the Finns especially are closely akin to the other North European peoples of Scandinavia.

Key Words: Finns, Saami, Samoyeds, mitochondrial DNA, nuclear DNA, Y-chromosomal DNA, craniometry, facial index, Caucasoids, Mongoloids.

Introduction

It is impossible to reconstruct the origins of ethnic groups without information about their genetic relationships. This information provides knowledge about inter-population contacts, assists in determining the geographic areas of origins of the populations in question, and sometimes even reveals how long these populations have lived in their present territories. Therefore, these reconstructed genetic relationships can be used to test hypotheses and theories of ethnic origins based on linguistic and/or archeological evidence. In this article, craniometric and nuclear DNA data, as well as the findings of recent studies of mitochondrial DNA and Y-chromosomal DNA variation are used to determine whether the origin of the Baltic-Finns is better explained by the traditional migration theory or by the more recent settlement continuity theory. These two competing theories are reviewed briefly below.

According to the traditional migration theory based primarily on the linguists' family tree model and estimated dates of linguistic divergences, the Finno-Ugrians (the Baltic-Finns and Saami/Lapps) arrived in the Baltic region only about three thousand years ago from the Proto-Uralic homeland in the east (see Häkkinen 1996 for a review). Most researchers locate this homeland in northeastern Europe (Setälä 1926, Korhonen

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1984, Häkkinen 1996), but some in northwestern Siberia (Hajdú 1976, Fodor 1976). Although supported by a minority of the researchers, the Siberian homeland theory is more commonly known than the European one outside the main centers of the uralistic studies.

The Baltic-Finns and Saami are argued to have arrived in their present locations either as a still undifferentiated ethno-linguistic group or as linguistically and ethnically separate people. Supporters of the latter view assume the Saami arrived in Fennoscandia before the Baltic-Finns. The Proto-Baltic-Finns started to separate into different “tribes” with their own languages during the last 2000 years. For example, the separation of the Estonians and Finns would have occurred during the first millennium BC, when the latter moved into Finland (see Häkkinen 1996 for a review).

The continuity theory practically replaced the migration theory in 1980 at the “roots” symposium in Tvärminne, Finland. According to the continuity theory, the Uralic-speakers arrived in the Baltic region either about 6000 years ago with the Typical Comb Ware culture (Meinander 1984, Korhonen 1984), or when the earliest post-Glacial inhabitants of the region arrived about 11,000 years ago (Nuñez 1987, Julku 1995, Wiik 1995, Salo 1996). Supporters of the continuity theory commonly argue that the Uralic-speaking territory extended in the past further west in Central Europe than is traditionally proposed. For example, Kalevi Wiik (this volume) argues that the Finno-Ugric-speaking people lived during the Mesolithic period as far west as the westernmost regions of the North European Plain.

As this article demonstrates, the human biological data (craniometric, nuclear genetic markers, mitochondrial DNA, and Y-chromosomal DNA) supports the continuity theory by showing the Baltic-Finns to have closer genetic affinities with their Scandinavian neighbors than with the eastern Finno-Ugric-speaking populations. Therefore, the genetic ancestors of the Baltic-Finns have lived in the Baltic region more likely for 10,000 years rather than for 3000 years, and more likely arrived from the south than from the east. I will next explain how biological information is used in the reconstruction of the geographic areas of origins of populations and/or ethnic groups.

The Study of Genetic Affinities and Origins

Physical anthropology, the study of human biology, is the

study of human evolution and biological variation. The latter includes the study of age-, sex, and population-related biological variation. In the past, researchers tried to organize the observed population-related variation by dividing humankind into races. This traditional classificatory approach has been largely abandoned because of several factors: disagreements as to the classification criteria and the number of existing races; difficulties in drawing racial boundaries due to the graded distribution pattern of most biological traits; the lack of objectivity on the part of researchers; and wrong-doings performed in the name of race. However, the study of the geographic distribution of visible “racial” traits, such as skin color, nose shape, hair form, etc., was not entirely wasted effort because this information has helped to discover how such variation has emerged as a result of environmental (especially climatic) selection. Since the 1950s, molecular and population genetic studies have had important roles in physical anthropology, especially in the study of evolution and population-related variation. These molecular anthropological studies have greatly increased our understanding of the origin of genetic variation, the inheritance of biological characteristics, and human evolution itself.

Modern research of human population-related biological variation examines how natural selection (for example, climatic selection), migrations (gene flow), genetic drift (the founders’ effect, for example), and mutations effect the genetic structures of populations over generations. Genetic structures of populations can be used to reconstruct their histories and genetic relationships. This reconstruction should ideally be based on different types of biological data because different data reveals information on different aspects and time perspectives of population history. Because all of our biological traits are either direct products of our DNA or results of an interaction between our DNA and the environment, the larger the number of traits studied, the longer segments of DNA are included in analyses. For this reason, I have used craniometric data, allele frequencies of genetic markers found in blood and other tissues (nuclear DNA markers), and the findings of recent mitochondrial DNA and Y-chromosomal DNA studies to reconstruct the origins of the Baltic-Finns.

I have analyzed the craniometric and the nuclear DNA data

through distance analyses. In addition, the craniometric data is analyzed through discriminant function analyses. Inter-population distances provide a great deal of information about population relationships because they are estimations of the degree of genetic relationships. Also, a distance matrix can be used as an input to construct a dendrogram (a “family” tree diagram) or a plot of multidimensional distance coefficients (as is done in this study). These methods exhibit inter-population relationships visually and, therefore, reveal how populations cluster with each other. In general, neighboring populations usually cluster with each other because long-time inter-population gene flow (exchange of genes) has caused them to become genetically similar. Linguistically related populations are often genetically similar (and cluster with each other) because the origin of the linguistic relationship is either a common geographic area of origin or intensive long-term cultural interactions. Linguistic boundaries are often also genetic boundaries, as Barbujani and Sokal (1990) have demonstrated in the case of Europe, because most people do not marry across linguistic and other cultural boundaries. However, we should not automatically assume that the linguistically-related populations always have the same genetic origin or the linguistically distinct populations have separate origins because languages are inherited through cultural transmission. The old assumptions of the Baltic-Finns and other Uralic-speakers’ genetic affinities with the Asian populations are primarily based on the theory that the Uralic-speakers arrived from the east and, therefore, should be genetically distinct from the Indo-Europeans of Europe.

The Old Assumption of the “Mongoloid” Affinities

The widespread assumption that all of the Uralic-speaking people are at least partially “Mongoloid” has its origin in Friedrich Blumenbach’s 200-year-old claim that two Saami (Lapp) skulls and one Finnish skull resembled one Mongol skull. The Mongoloid affinity of the Finno-Ugrians was accepted as scientific truth by those who had actually never seen the people in question because Blumenbach was a prominent scientist of his time and the linguists were looking for the Uralic homeland to be somewhere in the east (Kilpeläinen 1985, Kemiläinen 1985, 1993).

Interpretations of findings of physical anthropologists and

geneticists have been until nowadays strongly influenced by this assumption of eastern affinities of the Finno-Ugrians. For example, Karin Mark (1970) calculated what she calls “Mongolidheitsindex” (Mongoloid-index) from facial features to estimate the proportion of Mongoloid element of Finno-Ugric populations. Also, many prominent geneticists (for example, Guglielmino et al. 1990, Cavalli-Sforza et al. 1994, Piazza et al. 1995) assume that the original homeland of the Uralic people was northwestern Siberia; the ancestral Uralic people were Mongoloids; the Samoyeds are the purest representatives of this ancestral type; ancestors of the Baltic-Finns and the Saami arrived in the west along the Arctic coast and mixed genetically with the Europeans. These researchers (mainly Piazza et al. 1995) consider the Finns, whom they find genetically typical Europeans contrary to this assumption, as an example of a discrepancy between the language and the genes.

These old assumptions are incorrect. In reality, all Finno-Ugrians of Europe (the Baltic-Finns, Saami, Volga-Finns, Permian-Finns, and Hungarians) are phenotypically and genetically typical Europeans. The Ob-Ugrians (Khanty and Mansi) of western Siberia, who are genetically poorly known are phenotypically European-Siberian Mongoloid intermediates. Only the Samoyeds are phenotypically and genetically predominantly Siberian Mongoloids.

The Baltic-Finns and, as a surprise to many people, also the Saami exhibit clearly North European phenotypes. Epicanthic eyefolds, flat faces, coarse straight hair, and other Mongoloid traits are not encountered among them more frequently than among other Europeans (Coon 1939, Brues 1977). Strong cheekbones and flaring zygomatic arches of many Finno-Ugrians, commonly and erroneously assumed to be Mongoloid features, are actually inherited from European Cro-Magnons (Coon 1939, Niskanen 1994b). These two “Paleo-European” features have survived especially well among the Finno-Ugrians of northern Europe because, as the archeological evidence presented by Zvelebil (1986) indicates, the subsistence transition from foraging to farming occurred more recently and with a lesser influx of immigrants in these marginal regions for agriculture than further south. Most other Europeans have been farmers for so many generations (eating soft bread, porridge, etc.) that their cheek bones (which provide attachments for the

masseter muscle) have reduced in size in comparison to other parts of their facial anatomy.

The light coloring of the Baltic-Finns and Saami reflects their long history of inhabiting northern Europe. North Europeans are the lightest colored people of the world because they have lived in northern latitudes the longest. Therefore, natural selection has had the longest time to produce the light skin color adapted to low levels of ultraviolet radiation. The hair and eye colors are predominantly light because the region's first permanent inhabitants' gene pool (the total of all genes of a population) included by chance a large number of alleles (variants of genes) producing light-colored phenotypes. The light-skinned North Asians do not have light-colored hair and eyes because the first permanent inhabitants of East Asia did not have alleles producing color in their gene pool. Natural selection and founders' effect are, therefore, the most important factors behind the distribution of most biological traits. Sexual selection has had far less influence on the geographic distribution of these traits than most people assume. The mate selection among "natural" populations is based more on ability to procure necessities for life, give birth and raise children, and create and maintain alliances between groups and families than on particular physical traits, such as eye color or nasal profile. Due to these reasons, most marriages are arranged in many societies because the mate selection was considered too important to be left to the young in question.

The Degree of Facial Flatness and Frequencies of Eastern Genetic Markers

All human populations are linked to other human populations through at least indirect gene flow. As a result, most biological traits have graded geographical distribution and there have never been pure races. Some human populations are, however, results of an admixture of two or more genetically fairly distinct populations. For example, the Finno-Ugrians of Europe are commonly assumed to have originated from the genetic admixture of European and Siberian populations. To estimate the degree of this assumed admixture, Karin Mark (1970) calculated a *Mongolidheitsindex* (Mongoloid-index) from facial traits of living people. I followed her example and calculated "Mongol-indices" from four indices of facial flatness (DKI, NDI, SII, and SSI) computed from measurements of the

facial skeleton. These measurements and indices are presented in Niskanen (1994b). Table 1 lists sources of the cranial data used. I use the term Mongol-index because the Mongols are among the most flat-faced and, therefore, “Mongoloid-looking” people. At first, I computed index-specific values so that the value indicating the most extreme facial flatness equals 100 and then averaged these values. The higher the Mongol-index, the flatter and, therefore, the more “Mongoloid” the face (Table 2).

Gene-frequency data allows more accurate estimations of genetic admixture than morphological data. Nevanlinna (1978) estimated from nuclear genetic markers (blood groups) that 20-30% of the Finns’ genes originated from the east (Siberia) and the rest originated from the west (Western Europe). He did not provide genetic admixture estimations for other Europeans, which resulted in a common misunderstanding that the Finns are a mixture of Europeans and Asians while their neighbors are “pure” Europeans. As will be pointed out by the “Oriental-indices” discussed below, the 20-30% eastern component of the Finnish gene pool is average for the Europeans.

Guglielmino et al. (1990) estimated from nuclear genetic markers the Finns to be genetically 10.1% Uralic (Samoyeds were used as the Uralic reference population) and 89.9% European, while the Saami were 47.5% Uralic and 52.5% European. Cavalli-Sforza et al. (1994:273) estimated the Saami to be 18% Samoyed (and 82 % European) from genetic distances between the Danes (used as the European reference population), and the Saami (considered as an admixed population), and Samoyeds. However, these very distances reveal that the Saami are genetically further removed from the Samoyeds ($F_{ST} = 857.3$) than the Danes are ($F_{ST} = 828.5$), making it more appropriate to consider the Saami 100% Europeans and the Danes an admixed European-Samoyed population. A recalculation makes the Danes 21.2% Samoyedic (and 78.8% European), while the Saami would be 100% European. Unfortunately, Cavalli-Sforza et al. (1994) did not estimate the Samoyed genetic component of the Finns and other non-Saami Europeans, nor did they provide genetic distances between the Finns and the Samoyeds from which to calculate the Samoyed genetic contribution in the Finnish gene pool.

I used a simple genetic admixture estimation I call the “Oriental-index” to estimate relative western and eastern genetic

<i>Sample</i>	<i>N</i>	<i>Collection</i>
British	90	1,2
Norwegian	55	7
Swedish	96	4,5,6
Finnish	109	1,3,4
Saami	29	3
Mordva	10	3
French	28	1,4
German	28	1,4,5
Austria	61	4,7
Czech	28	1,3,4
Russian	30	1,3,4
Burjat	55	7

Table 1. Cranial samples used in this study. The N figure indicates sample sizes, and the figure for collection refers to collections where the specimens are housed, and or/individuals who provided the data.

1. Department of Palaeontology, British Museum (Natural History), London, U.K.; courtesy of Dr. C.B. Stringer.
2. Duckworth Laboratory, University of Cambridge, Cambridge, U.K.; courtesy of Dr. R. Foley.
3. Department of Anatomy, University of Helsinki, Helsinki, Finland; courtesy of Prof. I. Virtanen.
4. Osteologiska Laboratoriet, Stockholm Universitet, Solna, Sweden; courtesy of Prof. T. Sjøvold.
5. Anatomiska Department, Lunds Universitet, Lund, Sweden; courtesy of Prof. G. Forsberg.
6. Historiska Museet, Lund, Sweden; courtesy of Dr. E. Iregren
7. Provided by Prof. William Howells (Peabody Museum, Harvard University).

I have also used sample means of other populations from Howells (1989). More detailed information about the craniometric data and craniometric measurements used in this study is provided by Niskanen (1994b).

<i>Population</i>	<i>Mongol-index</i>	<i>Oriental-index</i>
Europe (av.)	24.9	22.8
Basque	–	12.4
French	22.4	18.3
German	16.7	19.6
Austria	32.4	20.7
Czech	25.4	16.7
Russia	25.4	21.6
Greek	–	33.4
British	12.9	20.7
Norwegian	28.0	20.5
Swedish	20.4	18.2
Finnish	25.4	25.1
Saami	25.5	42.2
Komi	–	30.1
Mari	–	34.2
Mordvian	39.4	–
Hungarian	–	21.4
Samoyed	–	58.0
Caucasus	–	35.6
Near Eastern	–	32.1
Indian	–	55.40
Mongolian	–	74.9
Buryat	90.0	73.4
Korean	–	78.6
Japanese	69.2	87.5
Ainu	52.0	92.8
South-Chinese	67.8	82.3
Tibetan	–	81.4

Table 2. Mongol- and Oriental-indices. British are pooled Irish, Scottish, and English. The European average Mongol-index is the average of the European populations for which this index is calculated. The European average Oriental-index is the index value calculated using the average allele frequencies of all European populations.

components of Eurasian populations. This index is computed from allele frequencies of six genetic loci (Fy, Esd, Glo1, Hp, P1, Rh) collected from literature (Nevanlinna 1973, Kajanoja 1978, Zubow 1979, Eriksson 1988, Heapost 1993, and Cavalli-Sforza et al. 1994). These genes have clear west-east gradients in Eurasia. First, I calculated allele-specific values (the most eastern value equals 100 and western equals 0) and then averaged them. The resulting Oriental-index is the eastern genetic component in the gene pool. The Mongol- and Oriental-indices are listed in Table 2.

An examination of average Mongol-index values reveals that they increase toward the east. The inhabitants of the British Isles (12.9%) have the sharpest facial profiles and the Buryats (90.0%) of the Lake Baikal region have the flattest faces. The Volga-Finnic-speaking Mordvians (39.4%) and Austrians (32.4%) have the flattest faces in Europe, but the Finns (25.4%) and the Saami (25.5%) are close to the European average (24.9%). The Ainu (52.0%) have the least amount of facial flatness among the Asians, although their faces are considerably flatter than those of European populations. Moderate facial flatness may be an ancient feature of inhabitants of the Pacific coast of Asia because the Polynesians originating from this region are not particularly flat-faced either. It appears that the extreme facial flatness of the classic Mongoloid people originated in the inland of northeastern Asia.

The Oriental-index values also increase toward the east. The Basques are genetically the most western (12.4%) and the Ainu are the most eastern (92.8%). Therefore, the Ainu cannot have an ancient Caucasoid origin, regardless of their relatively sharply profiled faces. The Finns (25.1%) are quite average by European standards (European average is 22.8%) and genetically less eastern than the Greeks (33.4%), Saami (42.2%), Permian-Finnic-speaking Komi (30.1%), and Volga-Finnic-speaking Mari (34.1%). The relatively high Oriental-index of the Saami (42.2%) is much higher than their admixture estimation (18%) based on genetic distances by Cavalli-Sforza et al. (1994), therefore, it is most likely a result of the markers used. The indices of the Komi and Mari have probably increased during the last 1,500 years due to the westward expansion of the Turks. The Samoyeds' Oriental-index (58.0%) reflects their Northwest Asian geographic location and

both western and eastern genetic ancestors.

These indices reveal that the relative eastern components (especially the Oriental-index) increase slowly from the Atlantic to the Ural, but rapidly east of the Urals; the Finns (representing the Baltic-Finns) are typical Europeans; not a single Eurasian population is morphologically and genetically 100% western or eastern; the Mongol- and Oriental indices correspond roughly. This rough correspondence is the result of random genetic drift. According to the fossil evidence, the first permanent inhabitants of Europe had sharply profiled faces and those of East Asia had flat faces. Descendants of these founders inherited these facial features independently from genetic traits used to calculate the Oriental-index values.

It is worth noting that the Finno-Ugrians of easternmost Europe are quite typical Europeans (see Liptak 1980) although they (especially the Komi) are the immediate western neighbors of the Nenets Samoyeds, who exhibit predominantly Mongoloid phenotypes and eastern genetic traits. This finding indicates that the genetic roots and, therefore, areas of origins of all the Finno-Ugrians of Europe were in Europe.

Craniometric Analyses

I used the SAS-package to compute Mahalanobis distances between cranial samples. I used measurement batteries: B39 (35 measurements and 4 indices) and B96 (96 measurements) to calculate Mahalanobis distances and the measurement battery B42 (42 measurements) to extract canonical discriminant function scores. The raw measurements were standardized for size by using W. Howells' c-score method (Howells 1989) and indices were standardized by converting them to z-scores before analyses. Most of the craniometric data used was collected by myself (Niskanen 1994b), although data kindly provided by William Howells is also used. The craniometric samples are listed in Table 1. The Finns represent the Baltic-Finns in these analyses. I have also compared recent European cranial samples with Upper Paleolithic cranial specimens (Cro-Magnon 1, Predmost III, Pavlov I, Obercassel I, Chancelade I, and Cheddar I) through canonical discriminant function analyses.

I used 39 craniofacial measurements and indices (listed in Niskanen 1994a) to calculate Mahalanobis distances between the European cranial samples and the Buryats of the Lake Baikal region (Table 3). These distance-values reveal how similar

(small values) or distant (large values) populations in question are from each other. An examination of these distances reveals that the Finns (and presumably other Finno-Ugrians as well) and the Saami do not possess more similar craniofacial configurations with the Buryats than is typical for the Europeans.

Although 39 craniofacial variables provides accurate information of craniofacial affinities of distantly related populations, a larger number of variables is needed to gain reliable information of population relationships of closely related and, therefore, craniofacially similar populations (Niskanen 1994b). For this reason, I also computed craniometric distances by using 96 craniofacial measurements (listed in Niskanen 1994b) to determine the craniometric relationships of the Europeans (Table 4). Unfortunately, I was unable to include the Norwegians, Austrians, and the Buryats measured by Howells due to lack of measurement values. These distances reveal that the Finns are craniometrically very close to the Swedes and the Russians (mostly from northwestern Russia), and the least distant population from the craniometrically distinct Saami.

I used the multidimensional scaling (MDS) procedure of SAS to construct a two-dimensional picture of the European populations' craniometric relationships. The MDS procedure is a better method than the frequently used tree-diagram because it constructs a kind of map of population relationships. I used the craniometric distances of Table 3 as input because I wanted to include the Norwegians and Austrians. I did not include the Buryats because their inclusions would have pushed all Europeans to the opposite side of the plot, distorting their distances from each other (Niskanen 1994a: Fig.1). Figure 1 (a mirror image of the diagram produced by Proc MDS of SAS) demonstrates that a plot of two dimension coefficients extracted from distances between the European cranial samples places these samples almost exactly where one would place them according to their geographic locations. The Finns are placed between the Swedes and the Russians, and the Swedes are placed between the Norwegians and the Finns. The Saami are placed well apart from other Europeans, but the least apart from the Finns and the Russians.

The craniometric relationships of populations can also be

<i>POP</i>	<i>BRI</i>	<i>NOR</i>	<i>SWE</i>	<i>FIN</i>	<i>SAA</i>	<i>FRE</i>	<i>GER</i>	<i>AUS</i>	<i>CZE</i>	<i>RUS</i>	<i>BUR</i>
BRI	–	69	37	60	149	40	46	93	100	70	511
NOR	69	–	35	64	168	96	101	77	189	103	368
SWE	37	35	–	40	126	65	69	83	138	65	413
FIN	60	64	40	–	98	54	56	72	87	42	369
SAA	149	168	126	98	–	123	107	146	159	91	365
FRE	40	96	65	54	123	–	30	65	48	49	454
GER	46	101	69	56	107	30	–	55	59	41	408
AUS	93	77	83	72	146	65	55	–	92	58	324
CZE	100	189	138	87	159	48	59	92	–	49	477
RUS	70	103	65	42	91	49	41	58	49	–	335
BUR	511	368	413	369	365	454	408	324	477	335	–

TABLE 3. Craniometric (Mahalanobis) distances ($\times 10$) between European populations and the Buryats of the Lake Baikal region computed by using 39 craniofacial measurements and indices. BRI = British (pooled Irish, Scottish, and English), NOR = Norwegians, SWE = Swedish, FIN = Finnish, SAA = Saami, FRE = French, GER = German, AUS = Austria, CZE = Czech, RUS = Russian, and BUR = Buryat. See Niskanen (1994a) for variables and their definitions.

<i>POP</i>	<i>BRI</i>	<i>SWE</i>	<i>FIN</i>	<i>SAA</i>	<i>FRE</i>	<i>GER</i>	<i>CZE</i>	<i>RUS</i>
BRI	–	82	122	317	102	95	175	140
SWE	82	–	96	295	164	151	222	141
FIN	122	96	–	196	185	133	169	96
SAA	317	295	196	–	363	292	334	267
FRE	102	164	185	363	–	103	145	149
GER	95	151	133	292	103	–	119	111
CZE	175	222	169	334	145	119	–	120
RUS	140	141	96	267	149	111	120	–

Table 4. Craniometric (Mahalanobis) distances ($\times 10$) between northern and central European cranial samples calculated from *c*-scores of 96 cranial measurements. BRI = British (pooled English, Scottish, and Irish), SWE = Swedish, FIN = Finnish, SAA = Saami, FRE = French, GER = German, CZE = Czech, and RUS = Russian. See Niskanen (1994b) for variables and their definitions.

examined with the help of the canonical discriminant analyses. Figure 2 presents scores of the first (x-axis) and the second (y-axis) canonical discriminant functions computed using the SPSS-program from c-scores of 42 cranial measurements. The cranial populations are clustered almost as one would expect in light of their geographic relationships. This diagram also demonstrates that the North Europeans (the Finns, Saami, and Swedes) have diverged craniometrically the least from the Cro-Magnons of Europe. This is expected because the transition from hunting to farming occurred both late and without large-scale population movements in Northern Europe. In Southern and Central Europe, this subsistence transition occurred earlier and largely as a result of demic diffusion of farmers of ultimately Near Eastern and/or Balkan extraction. As a result, their cranial configuration has changed more.

These craniometric analyses demonstrate that the Finns (and presumably other Baltic-Finns) and Saami (although they form their own subset within the European set) possess North European craniofacial configuration with more than average amount of Paleo-European (Cro-Magnoid) features. This finding indicates that the Baltic-Finns and Saami (as well as their Scandinavian neighbors) are indigenous people of northern Europe and not recent immigrants from elsewhere (Niskanen 1998).

Genetic Relationships in Light of Nuclear Gene-Frequency Evidence

I used the Chi-Square distance measure of the SPSS-program to calculate genetic distances between populations from the nuclear gene-frequencies. The raw data is collected from literature (Nevanlinna 1973, Kajanoja 1978, Zubow 1979, Eriksson 1988, Heapost 1993, Cavalli-Sforza et al. 1994). The use of this distance measure does not tolerate missing values. For this reason, I had to vary the markers used depending on which populations were compared and, therefore, the distance values computed using different sets of markers are not comparable. In general, the larger the number of genetic markers used, the more reliable the genetic distance.

The Finns and the Estonians represent the Baltic-Finns in these analyses. The Finns represent the Baltic-Finns when large numbers of genetic markers are needed. I had to pool the Mari and the Komi to represent the Finno-Ugrians of the easternmost

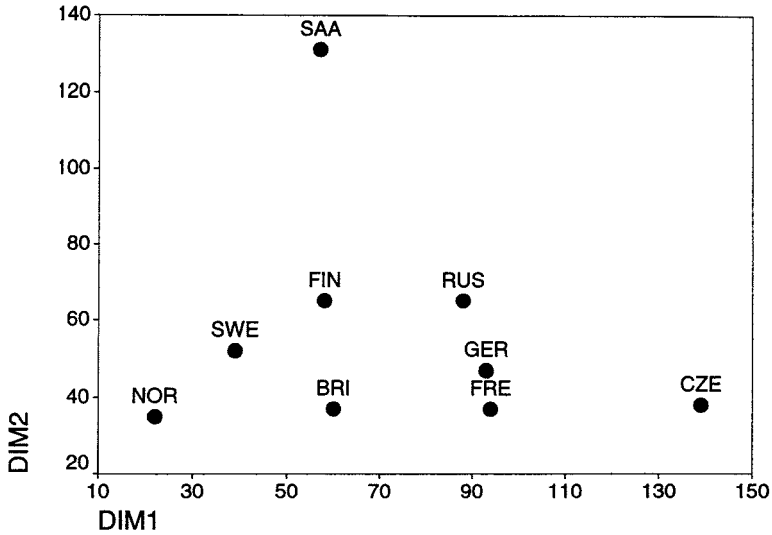


Figure 1. A mirror image of dimension coefficient plot extracted from Mahalanobis distances between the European samples of Table 3 using the MDS-procedure. BRI = British (pooled English, Scottish, and Irish), NOR = Norwegian, SWE = Swedish, FIN = Finnish, SAA = Saami, GER = German, FRE = French, CZE = Czech, and RUS = Russian. Modified from Niskanen (1994a).

Europe (EFU = Eastern Finno-Ugrians) due to insufficient gene-frequency data.

At first, I calculated the genetic Chi-Square distances of European populations from the Finns, Saami, the European average, inhabitants of modern Turkey (Anatolia), Mongols, and Japanese to determine how these populations are placed within the genetic landscape of Eurasia (Table 5). These distances reveal that the Finns are genetically close to their Germanic-speaking neighbors (the Swedes, Germans, and Norwegians), the least distant population from the Saami, and no more distant from the European average than are the Irish and the Basque. Based on the F_{ST} genetic distances presented by Cavalli-Sforza et al. (1994:270), the Finns are genetically a little closer to the Belgians ($F_{ST} = 63$), Germans ($F_{ST} = 77$), and Austrians ($F_{ST} = 77$) than to the Swedes ($F_{ST} = 82$). This difference is a result of Cavalli-Sforza et al. (1994) using a different genetic distance measure and computing distances using a data set including missing values. As Nei and Roychoudhury (1993) have pointed out, inter-group distances can be misleading if the data set from where the distances are computed includes missing values.

The genetic distances to the inhabitants of modern Turkey (Anatolia) indicate that the Finns are just like other North Europeans genetically more distant from the Near Eastern people than are the Central and South Europeans. The genetic distances to the Mongols and the Japanese indicate that the Finns are genetically somewhat less distant to these eastern populations than the Europeans are as an average, but not any closer than other Europeans living along the same longitude (for example, the Greeks and Bulgarians in respect to their distances to the Japanese). Many allele frequencies of the Finns and especially the Saami, which differ from the European averages, and the surprisingly small genetic distance off the Icelanders from the Mongols (which is smaller than that between the Finns and the Mongols) are most likely results of random genetic drift in partially isolated and numerically small population.

The F_{ST} distances (above the diagonal) and Chi-Square distances (below the diagonal) were used to examine the genetic relationships of the Finns with other North European populations more closely (Table 6). These two genetic distance

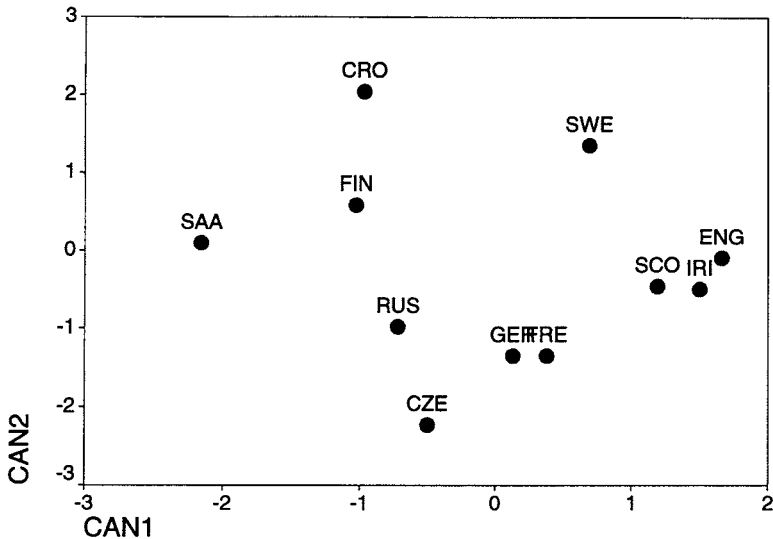


Figure 2. Plot of sample means of the first (CAN1) and the second (CAN2) canonical discriminant function scores computed from c-scores of 42 craniofacial measurements. These two scores explain 70.04% of the total variance. CRO = Cro-Magnons, IRI = Irish, SCO = Scottish, ENG = English, SWE = Swedish, FIN = Finnish, SAA = Saami, GER = German, FRE = French, CZE = Czech, and RUS = Russian. This is the same set of variables than the one used to calculate Mahalanobis distances of Table 3 except that none of the raw measurements were used to compute indices.

measures provide very similar pictures of the inter-population genetic relationships. Based on these distances, the Swedes are the least distant from the Finns. The F_{ST} and Chi-Square distances between the Finns and the Swedes (82 and 156) are, however, considerably larger than the distances of the Swedes to the Norwegians (18 and 84), Danes (36 and 98), Dutch (41 and 118), and English (37 and 123), but about equal to those of the Swedes to the Irish (94 and 192) and Scottish (74 and 157). This finding indicates either that the Baltic Sea has formed a partial restriction of gene flow and, therefore, a genetic boundary, or that the Northwest Europeans and the Northeast Europeans have partly different genetic origins. The relatively large genetic distances between the Finns and other Northwest Europeans could also have resulted from genetic drift, which has altered the Finns' allele frequencies.

The genetic distances of the Finns to the Saami are smaller than those between the Saami and other European, but still very large. This finding indicates that the Finns and the Saami were originally more distant from each other, but have exchanged genes during the more recent history. In other words, it appears that these two Finno-Ugrian-speaking people most likely do not descend from a common ancestral population which lived only 4,000-5,000 years ago. The same conclusion has also been reached in light of the mitochondrial DNA evidence discussed below.

I computed genetic Chi-Square distances between the Irish, Swedes, Finns, Saami, pooled Mari and Komi (EFU = Eastern Finno-Ugrians), Samoyeds (Nenets and Nganasans), and Mongols to estimate the genetic relationships between the Uralic-speaking populations and their non-Uralic-speaking neighbors. Based on these distances (Table 7), the Finns representing the Baltic-Finns are genetically closer to both the Swedes (99) and the Irish (136) than to the pooled Mari and Komi (142). Interestingly, the genetic distance between the Finns and the Irish (136) is not much smaller than the distance between the Irish and the pooled Mari and Komi (159) regardless of the geographic distances between the groups in question.

The genetic distances in Table 7 also reveal that the Finns, Saami, and the pooled Mari and Komi (EFU) to the Samoyeds (Nenets and Nganasans) are not much smaller than those of the

<i>POP</i>	<i>FINNISH</i>	<i>SAAMI</i>	<i>EUROPEAN</i>	<i>ANATOLIAN</i>	<i>MONGOL</i>	<i>JAPANESE</i>
Irish	262	400	176	260	393	501
Scottish	234	315	145	242	389	496
English	196	292	92	207	375	475
Dutch	182	278	100	215	386	481
Danish	171	279	102	221	376	481
Norwegian	166	266	117	229	378	471
Swedish	156	241	143	236	383	474
Finnish	–	225	160	215	363	441
Saami	225	–	280	305	379	454
Icelandic	193	282	149	252	354	466
Belgian	172	282	80	189	374	471
French	203	302	84	176	387	470
German	160	274	60	183	370	464
Austrian	174	296	52	169	376	464
Swiss	179	291	70	181	379	475
Czech	182	316	103	187	376	466
Polish	189	302	129	207	373	458
Russian	208	320	130	206	379	466
Hungarian	172	292	86	176	360	453
Basque	281	368	191	256	435	519
Spanish	233	337	107	162	388	466
Portuguese	222	315	120	189	398	475
Italian	185	304	73	137	372	454
Greek	200	305	145	159	372	433
Bulgarian	202	314	145	150	381	443
Romanian	177	299	108	156	385	455
Yugoslavian	171	292	96	191	375	469

Table 5. The genetic Chi-Square distances (X 10) of the European populations from the Finns, Saami, Europeans' gene-frequency averages (European), Anatolians (inhabitants of the modern Turkey), Mongols, and Japanese. Distances are computed from allele frequencies of the following genetic loci and systems: ABO, ACPI, AKI, ADA, CDE, ESD, FY, GC, GLO1, HLA-A, HLA-B, HP, IGHG, JK, KEL, MNS, PTC, PGD, PGM1, and TF.

<i>POP</i>	<i>IRI</i>	<i>SCO</i>	<i>ENG</i>	<i>DUT</i>	<i>DAN</i>	<i>NOR</i>	<i>SWE</i>	<i>FIN</i>	<i>SAA</i>
IRI	–	29	30	76	68	79	94	223	570
SCO	111	–	27	48	40	58	74	66	447
ENG	123	87	–	17	21	25	37	115	405
DUT	163	124	75	–	9	21	41	123	341
DAN	166	119	73	66	–	19	36	96	334
NOR	170	127	85	81	64	–	18	94	317
SWE	192	157	123	118	98	84	–	82	333
FIN	262	234	196	182	171	166	156	–	210
SAA	340	315	292	278	279	266	241	225	–

Table 6. Genetic FST (above the diagonal) and Chi-Square (below the diagonal) distances between North European populations. The FST distances (x 10,000) are from Cavalli-Sforza et al. (1994:270). The Chi-Square distances (x 10) are computed from allele frequencies of genetic systems and loci listed in Table 4. IRI = Irish, SCO = Scottish, ENG = English, DUT = Dutch, DAN = Danish, NOR = Norwegian, SWE = Swedish, FIN = Finnish, and SAA = Saami.

<i>POP</i>	<i>IRI</i>	<i>SWE</i>	<i>FIN</i>	<i>SAA</i>	<i>EFU</i>	<i>NEN</i>	<i>NGA</i>	<i>MON</i>
IRI	–	116	136	273	159	340	392	338
SWE	116	–	99	236	147	341	400	337
FIN	136	99	–	226	142	302	375	298
SAA	273	236	226	–	248	353	409	339
EFU	159	147	142	248	–	295	365	292
NEN	340	341	302	353	295	–	215	148
NGA	391	400	375	409	365	215	–	248
MON	338	337	298	339	292	148	248	–

Table 7. Chi-Square distances (x10 and rounded up without decimals) between the Irish (IRI), Swedish (SWE), Finnish (FIN), Saami (SAA), pooled Mari and Komi (EFU = Eastern Finno-Ugrians), Nenets Samoyeds (NEN) and Nganasan Samoyeds (NGA), and Mongols (MON). Distances are computed by using allele frequencies of the following genetic systems and loci: ABO, ACPI, ADA, AKI, FY, DI, GLO1, GC, HP, KEL, JK, MNS, P1, PGM1, PGD, SE, TF, CDE, and IGHG.

<i>POP</i>	<i>EST</i>	<i>FIN</i>	<i>SWE</i>	<i>EFU</i>	<i>SAA</i>
EST	–	118	144	146	271
FIN	118	–	116	149	219
SWE	144	116	–	164	236
EFU	146	149	164	–	258
SAA	271	219	236	258	–

Table 8. Chi-Square distances (x10 and rounded up without decimals) between the Estonians (EST), Finns (FIN), Saami (SAA), the pooled Mari and Komi (EFU), and Swedes (SWE). Distances are computed from allele frequencies of the following genetic systems and loci: ABO, DI, FY, GC, HP, KEL, LE, LU, MNS, P1, PTC, CDE, SOD, TF, the subtypes of TF, LW, and UL.

Irish and the Swedes to the Samoyeds. The Samoyeds are also genetically equally distant from the Europeans (both Uralic- and non-Uralic speakers) than are the Mongols. These findings demonstrate clearly European gene pools of even the easternmost Finno-Ugrians and North Asian gene pools of the Samoyeds. It is clear that the ancestors of the Finno-Ugrians and the Samoyeds either diverged a very long time ago from each other (tens of thousands of years ago) or that there never was a common Uralic homeland. A study of the Samoyeds' Y-chromosomal DNA variation by Karafet et al. (1997) supports the idea of distinct genetic and geographic origins for the Samoyeds and other Uralic-speaking populations.

I had to reduce the number of genetic markers used to include the Estonians in the genetic distance analyses. Results presented in Table 8 are, however, similar to those presented above. The Baltic-Finns (the Estonians and Finns) are genetically somewhat closer to the Swedes (144 and 116) than to the pooled Mari and Komi (146 and 149). This finding indicates that the Baltic-Finns and the more eastern Finno-Ugrians do not have recent common ancestors who lived only about 3,000 years ago between the Volga River and the Ural Mountains, as argued in the traditional migration theory. If these groups had a common homeland, they must have diverged from each other over ten thousand years ago instead of 3,000 years ago. The genetic distances presented also demonstrate that the Finns are genetically closer to the Swedes (116) than to the Estonians (118), indicating that the Finns and the Estonians probably diverged from each other (through the migration of the Finns'

ancestors from Estonia) earlier than the traditionally assumed migration date (during the first millennium AD).

The Mitochondrial DNA and Y-Chromosomal DNA Evidence

The mitochondrial DNA (mtDNA) is inherited matrilineally, whereas the Y-chromosomal DNA is inherited patrilineally. This lack of genetic recombination allows reconstructions of maternal lineages (from the mtDNA data) and the paternal lineages (from the Y-chromosomal data) from the DNA sequence differences. This data also provides information about more ancient population history than the nuclear gene frequencies (of blood groups and enzyme polymorphism), which can change markedly through genetic bottlenecks (genetic drift).

The mtDNA studies (Sajantila et al. 1995, Lahermo et al. 1996) reveal that the non-Saami Finno-Ugrians of Europe (the Finns, Karelians, Estonians, Volga-Finns) have the same genetic origin as the non-Uralic-speaking Europeans, and that the Saami represent a unique and ancient sub-group of Europeans that had separated from the other Europeans over 10,000 years ago. Therefore, the Baltic-Finns (the Finns, Karelians, and Estonians) and the Saami do not appear to descend from a common ancestral population that lived as recently as a few thousand years ago. The genetic admixture between the Baltic-Finns and the Saami is also rather recent, but adequate enough to make the Finns and the Karelians the closest genetic relatives of the Saami.

Studies of the mtDNA and Y chromosomal DNA reveal information about ancient population movements and directions. For instance, the distribution and diversity of the mtDNA haplogroup V indicates a population expansion from Southwest Europe starting about 15,000 years ago over the western half of Central Europe and the entire Northwest Europe. The existence of this haplogroup among the Saami, Baltic-Finns, and the Volga-Finns indicates a sizeable ancient West European genetic component in their gene pools. Its frequency is the highest among the Saami (40.9%), Basque (20.0%), and Catalonians (26.7%). It exhibits the greatest amount of diversity among the Iberian populations, suggesting that this region is its most likely area of origins. This diversity is far less among the Saami, indicating that their extremely high

haplogroup V frequencies resulted from founders' effect (Torroni et al. 1998).

While studies of the mtDNA variation indicate strongly the western maternal gene pools of Europe's Finno-Ugrians, the studies of Y-chromosomal DNA variation indicate eastern paternal genetic contribution in their gene pools in addition to the western one. Kittles et al. (1998) noted significant differences in Y chromosome haplotype variation between western and eastern Finland. They thought that the western Finns, characterized by the haplotype B, were of predominantly western ancestry and that the eastern Finns, characterized by the haplotype A, were of Asian ancestry because the haplotype A contains the DYF155S2 deletion found most commonly among Asians. According to Jobling et al. (1996), this deletion is, however, also encountered among the Norwegians and Greeks, and it is the most common in Finland and Mongolia. Therefore, I argue this deletion could have emerged anywhere between Scandinavia and Mongolia, making it a possible genetic marker of a late Ice Age population expansion from the South Russian Plain from where the Northeast Europe and Northwest Asia were colonized after the Last Glacial Maximum.

Zerjal et al. (1997) argued that the C allele on the Y chromosome of some North Europeans and North Asians emerged in Asia and spread to North Europe, where its existence indicates a considerable paternal genetic contribution of North Asians to North European populations, especially the Finno-Ugrians. Villems et al. (1998) discovered that this allele exhibits more variation among Europeans than among Asians and, therefore, they suggested that it originally emerged among Proto-Finno-Ugric populations of Eastern Europe from where it spread to some Siberian populations. I consider this C allele as the genetic marker of the late Ice Age (after the Last Glacial Maximum) population expansion from the South Russian Plain.

A study of Y-chromosomal markers indicate that the Samoyeds are descendants of Paleoasiatic populations which were (linguistically) assimilated by populations who came from southern Siberia (Karafet et al. 1997). This finding explains the phenotypic and genetic distinctness of the Samoyeds from other Uralic-speaking people and similarity with more eastern people, as well as contradicts the assumption that the Samoyeds are genetically the closest to the ancestral Uralic people.

All of this craniometric, nuclear DNA, mtDNA, and Y-chromosomal DNA information indicates that the Finno-Ugrians of Europe originated in Europe, the Baltic-Finns are genetically closer to the Scandinavians than to the Finno-Ugrian people in the east, the Saami form a distinct subset within the Europeans, and the Samoyeds have a distinct genetic origin from other Uralic people. I will next discuss these findings in light of the archeological evidence of population history.

The Genetic Origins and the Archaeological Evidence

Genetic relationships are results of a long history of population events. These events cannot be reconstructed accurately without information about the prehistory and history of the populations in question. In case of northern Eurasia, we have to reconstruct the population events at least since the Last Glacial Maximum (23,000-19,500 BC), after which the entire northern Eurasia was colonized. North Europe was colonized primarily from two of the Last Glacial Maximum refugia areas: the Franco-Cantabria in the west and the South Russian Plain (mainly the Dnieper-Don region). These two refugia areas were separated from each other by a most likely uninhabited isthmus located between the Fennoscandian and Alpine glaciers, although there were some settlements in eastern Austria and western Hungary. West Siberia and Central Asia (except southern Urals) were either uninhabited or sparsely inhabited because West Siberia was almost entirely covered by an enormous inland lake, and the region between the Caspian Sea and the mountains of Central Asia was a dry and inhospitable desert. The upper Yenisey and the Lake Baikal regions were, however, inhabited, as was the entire southeastern half of Siberia (Soffer 1990).

Human settlement started to spread over northern Eurasia when the climate started to ameliorate around 19,500 BC. Groups originating from Franco-Cantabria settled the British Isles and the North European Plain located west of the Vistula River (Creswellian/Hamburg cultures) and the Central European hill region between the Atlantic Ocean and the Carpathian Mountains (Magdalenian culture). Groups originating from the Dnieper-Don region (for example, Swiderian culture) settled the entire northeastern Europe located east of the Oder River and possibly westernmost Siberia

(Dolukhanov 1986, 1993, Soffer 1990, Schild 1996). The mtDNA haplogroup V is the genetic marker of the colonization of Northwest Europe from Franco-Cantabria (Torroni et al. 1998) and the Y-chromosomal C allele is the genetic marker of the colonization of Northeast Europe and West Siberia from the South Russian Plain (Zerjal et al. 1997, Villems et al. 1998).

The Dnieper-Don region of the South Russian Plain is the only candidate for a region from where the entire distribution area of the Uralic languages was settled. The two competing traditional Uralic homelands – the northeastern corner of Europe between the Volga Bend and the Urals and Northwest Siberia – received their first permanent human settlement from this region. Northwest Siberia also received settlers from further east of Siberia. It is, therefore, possible that the late Upper Paleolithic period inhabitants of the entire Northeast Europe and West Siberia spoke ancestral dialects of the Uralic languages (Nuñez 1987, Julku 1995). These groups could have maintained their linguistic affinities through cultural contacts (marriage exogamy, etc.) facilitated by the extensive river network of this huge territory (see Fig. 7 in Nuñez 1987:14).

There is one problem with the idea that the South Russian Plain was the Uralic homeland. According to Mallory (1989), for example, it was possibly settled by Proto-Indo-Europeans already during the Mesolithic period. A solution to this problem could be the late Ice-Age northward displacement of ecological zones and human populations adapted to these zones. The individual group territories became at first stretched in a north-south direction, making the seasonal migrations between the northern and southern parts of hunting territories gradually too long, which resulted in abandonment of the southernmost territories. Groups speaking ancestral dialects to Proto-Indo-Iranian could have expanded into territories being gradually vacated by speakers of Proto-Uralic dialects through the same process, either from the northeastern Balkans or the Kuban region east of the Black Sea.

The earliest post-Last Glacial Maximum inhabitants of the southeastern shores of the Baltic Sea belonged to the Late Upper Paleolithic Swiderian culture (10,800-9700 BP / 9800-8700 cal BC), which descended from the East Gravettian cultures of the South Russian Plain. This culture spread to the Oder River in the west (Schild 1996). If people of the Swiderian

culture spoke a Proto-Uralic language, the Oder River formed the westernmost boundary of the Uralic language at the end of the Paleolithic period.

Whether or not the people of the Swiderian culture were Proto-Uralic-speakers, the most ancient human settlement of the region historically inhabited by the Baltic-Finns belonged to the Early Mesolithic Kunda culture (emerged about 8700 BC), the roots of which are in the Swiderian culture. Finland received her first permanent settlers from the Kunda culture's territory in the south (Estonia) and east (Karelia) about 8500 BC. When these possibly Proto-Uralic-speaking groups arrived in northern Finland around 8000 BC, they met coastal groups, who had arrived in northern Fennoscandia as early as 9000 BC from the ice-free region between the British Isles and Denmark by following the ice-free coast of Norway. At that time, the inland regions of central and northern Scandinavia were still covered by ice (Nuñez 1987, this volume). The coastal people may have become Uralic-speaking Saami as a result of cultural contacts with Proto-Uralic-speaking populations inhabiting inland regions of northern Fennoscandia. This language shift would explain why the Saami are genetically so distinct from Scandinavians and Baltic-Finns, but speak languages that are quite similar to the Baltic-Finnish languages. A similar language change apparently occurred in Western Siberia where the Paleo-Asiatic inhabitants were linguistically assimilated by the Uralic-speakers, giving origins to the Samoyeds.

The introduction of food production changed the linguistic and genetic landscape of the Old World. Colin Renfrew (1987, 1992) has proposed that this subsistence shift was associated with the spread of Indo-European languages from Anatolia over most of Europe. Cavalli-Sforza et al. (1994) have demonstrated with synthetic maps of principal component scores computed from gene-frequency data that there was a population expansion (demic diffusion) from Anatolia into Europe, which made especially Southern- and Central Europeans genetically closer to the Near Eastern populations. The archeological evidence (for example, in Zvelebil 1986) indicates that the spread of farming into northern Europe was slower and took place primarily through cultural diffusion. As a result, North European gene pools received less Near Eastern genes than those of Central- and Southern Europeans and the non-Indo-European languages

survived longer. The early historical period Pictish language of Scotland and the Finno-Ugric languages of northern and eastern Europe represent remnants of indigenous North European languages.

The earliest farming in the East Baltic region dates to the Corded Ware (Battle/Boat Axe) period (3200-2500 cal. BC) (Lang 1998). The spread of this culture over this region must have had a significant impact on the ethnogenesis of the Baltic-Finns. For instance, the Baltic-Finnic protolanguage is thought to have received its Baltic loan words as a result of this event. Central European genes arrived also. Sajantila and Pääbo (1995) have even proposed that the Indo-European-speaking Battle Axe people became linguistically assimilated by the indigenous Uralic-speaking people (Lapps/Saami) in Finland. This theory is based on observations that the Finns are genetically rather linguistically European, while the Saami are very distinct.

Sajantila and Pääbo's (1995) theory has three problems. First, it is unlikely for numerically superior intruders with a more complex social organization to become linguistically assimilated by numerically inferior indigenous people with a simpler social organization. Second, the Estonians and the Livs, living south of the Gulf of Finland, are Finno-Ugrians, although there have never been Lapps in these regions who could have linguistically assimilated the Indo-Europeans. Third, the so-called Lapps who lived in southern and central Finland during the Middle Ages may have been genetically similar to the modern Finns and distinct from the modern Saami of northern Fennoscandia. For these reasons, I consider it more likely that the Battle-Axe people who arrived in Finland spoke a Proto-Baltic-Finnish language (Uralic language influenced by Proto-Baltic languages) and that they were not markedly different genetically from the inhabitants of southern Finland. This theory is supported by archeological evidence from Estonia, indicating the Estonian Corded Ware culture had an indigenous background (Lang 1998). If this was indeed the case, the Baltic-Finnic language phylum and people emerged in Latvia and Estonia around 3200 cal. BC, when local hunter-gatherers came under considerable linguistic and cultural influence of farming populations living further south. The appearance of the Corded Ware culture in Finland would then indicate the arrival of the Baltic-Finns in Finland around 3200 cal. BC.

A recent estimation of the date of genetic divergence of the Estonians and Finns from the mitochondrial DNA data might support this theory. Sajantila et al. (1996) estimated a date of about 3900 (1900 BC) years for the arrival of the Finns in Finland assuming the mutation rate of one substitution in 50 generations and a generation time of 20 years. If the average generation time is 25 years (which is more probable), this date was 4875 cal. BP (2875 cal. BC), which agrees well with the arrival of the Battle Axe (Corded Ware) culture in Finland. However, if the Estonian-Finnish divergence date is based on average mutation rates across the entire nucleotide sequence and the mutation rate is one substitution in 5,000 years (independent of the number of generations), this divergence occurred 10,000 cal. BP (8000 cal. BC) when Finland was first settled. I will return to these dates ahead.

Whether the genetic ancestors of the Finns arrived in Finland 5,000 or 10,000 years ago, the divergence of the Baltic-Finns into different ethnic groups either started or accelerated during the Bronze Age (1500-500 BC). The Scandinavian Bronze culture arrived in the southern and western coastal regions of Finland with Scandinavian immigrants, who had a lasting effect on Finnish gene pools and language. The Finns became genetically similar to the Scandinavians and received Proto-Germanic loan words. These early Scandinavian immigrants were linguistically and genetically assimilated into the indigenous population.

The Middle Ages brought more Scandinavian immigrants into Finland. The Swedish-speaking minority of southern and western coastal regions is descended from the Swedish immigrants who arrived during the years AD 1100-1300. This immigration reduced the Finns' genetic distance from the Swedes (possibly at the expense to that to the Estonians) because there was from the beginning a considerable amount of intermarriage (Virtaranta-Knowles et al. 1991).

The linguistic relationship of the Baltic-Finnish and Saami languages has led to an assumption that the Baltic-Finns and the Saami descend genetically from the same population, and the Baltic-Finns' ancestors diverged from the Saamis' ancestors as a result of fairly recent Baltic and Germanic influences on the first mentioned (see Häkkinen 1996 for a review). However, the Baltic-Finns and Saami are genetically too distant from each

other to have descended from the common ancestral population that lived only about 5,000 years ago. Therefore, it is more likely that ancestors of the Finns and Saami separated from each other at the beginning of the Last Glacial Maximum about 23,000 BP and met each other again in northern Fennoscandia around 8500 BP.

If the above argument is correct, the so-called Lapps who lived in southern and central Finland still during the early historical period and the modern Saami of northern Fennoscandia were genetically distinct from each other. Archeological evidence may support this theory. Matti Huurre (1983) has argued that the southern boundary of the real Saami was located near the north-south midline of Finland. The genetic distinctness of the modern Saami of northern Fennoscandia (for instance, the "Saami-specific motif" in their mtDNA discovered by Sajantila et al. 1995) may have been inherited from the earliest inhabitants of the Arctic coast, who had arrived in the north along the Norwegian coast. These populations, whose ancestral language is unknown, could have become Uralic (more specifically Lappic)-speakers as a result of cultural contacts with Proto-Lappic speaking people arriving from the south. If this was the case, the Lapps of the southern half of Finland would have spoken Lappic (Saami) dialects, but were genetically similar to populations living further south in the East Baltic region. These southern Lapps were also incorporated into the gene pool of northward expanding Finnish populations during the Middle Ages. The reason why their genetic contribution to the gene pool of the Finns is not detectable may be their genetic similarity with the assimilators.

The genetic affinities of the so-called Lapps of the southern half of Finland are key to solving the Finns' origin. Before we know the genetic structure of the so-called Lapps of the southern half of Finland (through extraction of DNA from old bones) we will never be able to determine the origins of the Baltic-Finns and when the Finns arrived in Finland. If the southern Lapps were genetically Saami, the Finns' ancestors probably did not arrive in Finland until about 3200 BC. If these southern Lapps were genetically non-Saami, the Finns' ancestors could have arrived in Finland when the region received its first inhabitants about 10,000 years ago. In light of the available evidence, we can be certain, however, that the Finn's ancestors

arrived in Finland at least 3,000 years earlier than the traditional migration theory would allow.

Conclusion

Whenever the Finns' ancestors arrived in Finland, we cannot deny the European origin of the Baltic-Finns and other Finno-Ugric people based on available physical anthropological and archeological data. The genetic and possibly linguistic ancestors of most of the Finno-Ugric people were very likely the hunter-gatherers who inhabited the periglacial zone located between the Carpathian Mountains and the Volga River during the last glacial maximum. We could say that from a purely physical anthropological point-of-view, the Baltic-Finns are either the easternmost Northwest Europeans or the westernmost Northeast Europeans.

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