

Analyzing the inner structure of the Y-chromosomal haplogroup N1b

(Jaakko Häkkinen, August 1st, 2009)

1. The aim and data of the study

The aim of this study is to analyze the inner structure of Y-chromosomal haplogroup N1b (former N2), identified by SNP marker P43. It has earlier been proposed that the haplogroup N1b is divided to the lineages N1b-A and N1b-E (Rootsi et al. 2007), and the former yet to clusters N1b-A1 and N1b-A2 (Derenko et al. 2007). These clusters are marked by certain microsatellite (STR) mutations: DYS392 = 14 > 12 for N1b-E and DYS19 = 14 > 15 and DYS 391 = 10 > 11 for N1b-A2, when compared to N1b founder haplotype belonging to cluster N1b-A1.

In Derenko et al. (2007) the median haplotype (formed by the median values of the repeat scores at each microsatellite locus within each haplogroup) is taken as a founder haplotype, but this founder haplotype can also be confirmed by comparing it to the sister lineages N1a and N1c (see Table 3 in the end of study; Rootsi et al. 2007: 210). The founder haplotypes for N1b-A (Table 3) and N1b-E (Table 2) are in *italic*.

I have collected the N1b haplotypes (tested for P43) from the following studies: Xue et al. 2006 (China and Mongolia); Rootsi et al. 2007 (Russia and Siberia); Derenko et al. 2007 (southern and central-eastern Siberia); Lappalainen et al. 2008 (Baltic Sea region); Pimenoff et al. 2008 (north-western Siberia); Balanovsky et al. 2008 (western Russia); Mirabal et al. 2009 (north-eastern Russia and north-western Siberia). In addition I have gathered such N-M231 haplotypes (not tested for N1b-P43 but N1c1-M178 negative), which estimating by their STR -values seem to belong to haplogroup N1b, from Cinnioğlu et al. 2004 (Turkish); Janica et al. 2005 (Polish Tatars); Völgyi et al. 2008 (Hungarians). My estimations were further confirmed when Rootsi et al. 2007 tested the 12 N-M231 haplotypes (15 individuals) from Cinnioğlu et al. 2004, and all but one of them were P43 positive; I similarly excluded the one outlying haplotype on the basis of its STR values. Consequently, in my data there are only 3 haplotypes not yet tested for P43: two Polish Tatars from Janica et al. 2005, and one Hungarian from Völgyi et al. 2008. But as these do not differ at all (the Polish Tatars), or in only two loci (the Hungarian), from the haplotypes found elsewhere, the uncertainty of their N1b status seems to be very low.

The haplotypes are presented by 12 most commonly used STR loci, in numerical order: DYS19, -385a, -385b, 389I, 389b (= II – I), -390, -391, -392, -393, -437, -438, -439. Some studies use less and some more loci, and later in this study I might refer to other markers (not included in the tables) to obtain the higher resolution for certain purposes. In the tables 2 and 3 I present all the N1b haplotypes which differ on the basis of 12 markers and those which do not differ but have been found in the different study and population. In those studies where more markers were applied, there are of course more haplotypes than in my tables.

From this data it is possible to find out more clusters and strata than presented in the earlier studies. I use the term 'lineage' referring to main categories N1b-A and N1b-E as a whole. I use the term 'cluster' denoting to horizontal differentiation: N1b-A2, N1b-A3, N1b-A4 etc. are all clusters branching to the different directions from the founder haplotype of cluster N1b-A1, thus producing the star-like structure for N1b-A lineage. I use the term 'stratum' denoting to vertical differentiation: N1b-E founder haplotype is succeeded by several strata, each of them having gone through the same mutations as the previous stratum, in addition to the very mutation defining the certain stratum. For example, the values of stratum N1b-E6b differ from N1b-E founder haplotype in six loci out of twelve.

I will not use any computing programs, but just calculate the variation simply from the tables by dividing the number of alleles by the number of loci. This, together with the high resolution

structure (great number of clusters or strata) within the lineages N1b-A and N1b-E, is elementary for the understanding of all the N1b expansions.

Unfortunately I found only few haplotypes from the Volga region and northwestern Siberia, both seemingly interesting conglomerate regions between N1b-A and N1b-E clusters: in the former area there seems to prevail an old lineage N1b-E, mostly present in the Uralic (and ex-Uralic, such as northern Russians) populations, and a younger lineage N1b-A, probably entering the area with the Turkic expansion (Chuvashes, Tatars, Bashkirs). In the latter area there seems to prevail an old lineage N1b-A (especially N1b-A1 and its earliest descendant N1b-preE), and younger lineages N1b-E (probably arriving from the west with Ob-Ugric languages) and probably some other N1b-A clusters (arriving from southeast with Samoyedic languages during the Common Era).

Samoyedic expansion center is located north of Altai–Sajan region, so it would be interesting to find out which of the N1b-A subclusters are present in Samoyedic speakers. Especially Nganasans have haplogroup N1b in high frequency (92 %), and it is the only Y-chromosomal haplogroup common to all Samoyedic-speaking peoples (Tambets et al. 2004). I dare to predict on purely geographical basis, that the Samoyedic N1b-A most probably belongs to the same clusters with the Ewenki, which (like Samoyeds) have expanded north near the Yenisei river valley: N1b-A1 and N1b-A6 (DYS385a = 12 > 13).

2. The variation of the N1b lineages

As can be seen from Table 1, the overall variation is higher in the lineage N1b-A than in N1b-E: 33 alleles per 12 loci *versus* 27 alleles per 12 loci. This contradicts the earlier opinions (Mirabal, Underhill & Herrera 2009), and I will return to this question at the end of the study. The variation of N1b-A is highest in southern Siberia, 28 *versus* 18–22 alleles elsewhere. The index of variation in China and Mongolia is high, because there are only 9 loci available, but this may well represent the true variation, because there are certain values in the area not found elsewhere: $DYS389I = 10$ and $DYS437 = 15$. That the variation is highest in the southern populations may be taken as a clue – but not as a proof (cf. Chapter 6) – for southern Siberia–Altai region being the oldest area of N1b.

The variation of N1b-E is highest in the northern Russians (21 alleles) and diminishes towards east (Komi 19, Ob-Ugrians 17), and as the founder haplotype is only present in Mezen Russians, it seems quite clear that this lineage is of European origin.

3. The distribution of the N1b clusters

Almost all of the N1b-A clusters might have originated in southern Siberia–Altai region, the only possible exceptions being N1b-A5 (and its subcluster N1b-A5a) and N1b-K (specific only to the Komi). Still, as N1b-A5 is present not only in the Turkic and Tungusic peoples of China, but also in Turkey, it may have originated in the Altai region, where the Turkic expansion center is located. It seems improbable that N1b-A5 would have arrived at Turkey via China. N1b-K has descended right from the original N1b-A1, but this process may be very late, judging from the low frequency and variation within this Komi-specific lineage. As N1b-A1 is present in a huge area from Russia to southern Siberia–Altai region, N1b-K probably originated in the Komi population in the North-East Europe.

The cluster N1b-A3a has the most interesting distribution: it is present only in the Komi and Siberian Eskimos. Because these haplotypes are connected with two mutations ($DYS392 = 14 > 15$ and $DYS438 = 10 > 11$), which have otherwise only rarely occurred in the N1b-A haplotypes, this cannot be due to chance. This cluster probably was born in the southern Siberia–Altai region, where

its predecessor N1b-A3 is still present. The expansion of this cluster might be quite early (considering the Eskimo), though not very intensive.

N1b-A2 may have originated either in southern Siberia or in north-western Siberia, because N1b-A1 is also present in both areas. N1b-A4 probably also originated in southern Siberia, being otherwise present only in Turkish and southern Russian populations. N1b-A6 is likewise a young lineage, being present only in southern and north-western Siberia, and the same goes with N1b-A7.

The founder haplotype of N1b-A1 is present in a wide area, but the founder haplotype of N1b-E is presented only by one haplotype among the Mezen Russians. All the other N1b-E haplotypes are descendants of the first stratum haplotype N1b-E1, found among the Mansi and Krasnoborsk Russians and separated from the founder haplotype by mutation in DYS19 = 14 > 13. Still, because there are no N1b-A haplotypes in which DYS19 would be 13, there is no reason to question the role of Mezen founder haplotype. It seems likely that a single male – mutated from N1b-preE (present among the Khanty and Khakass) – brought this lineage to northern Russia, and it only slowly grew in number and started to expand.

Stratum N1b-E3b is the first in which there is any considerable variation (in three loci); this probably indicates that this stratum presents the first N1b-cluster expanding to wider area, and included a larger amount of carriers, as well. We may thus label this stratum as ‘the first clearly migratory’ N1b-E lineage, contrary to the earlier ‘sporadically diffusing’ N1b-E lineages. As this cluster is only found among the Khanty, Mansi and southwestern (Priluzski) Komi, it may be connected with some phase in the history of the Uralic languages. This assumption seems to be further confirmed by its ancestral stratum N1b-E2b, being present among the northern (Izhemski) Komi and Tatars (who have later arrived at the Volga bend and acquired the N1b-E lineage from the Finno-Ugrians, because there is no N1b-E in Asia). As we know that the Ob-Ugric languages (Khanty and Mansi) have previously been spoken in the European side of Ural Mountains, it is not too far-fetching to assume that the expansion of stratum N1b-E3b might be connected with the expansion of Ob-Ugric languages. These languages were then adopted by the earlier inhabitants of north-western Siberia, including at least N1b-A clusters N1b-A1 and N1b-preE, which are more numerous than N1b-E in the present-day Ob-Ugric populations.

It is interesting that N1b-E only in the later phases (stratum N1b-E4a) reached the western areas of the Finnic peoples, although it must be borne in mind that the frequency of N1b is very high among Vepsians (18 %; Roots et al. 2007), and it is possible that also some earlier strata will be found among them. It would be curious, if in the Karelians and Vepsians there only were later strata (N1b-E5 and N1b-A6b, respectively) than in the Finns (N1b-E4a) – this would imply that N1b-E expanded straight to Finland and then bounced back towards the east.

4. The structure of N1b lineages

It is interesting that there are at most only three cumulative strata in the N1b-A lineage (N1b-A2 > N1b-A2a > N1b-A2a1), and usually two strata (N1b-A3 > N1b-A3a, N1b-A5 > N1b-A5a, N1b-A7 > N1b-A7a) or only one stratum (N1b-A4, N1b-A6, N1b-K). The only exception in this respect is N1b-preE, which is succeeded by no less than seven strata: N1b-preE > N1b-E > N1b-E1 > N1b-E2a,b > N1b-E3a,b > N1b-E4a,b > N1b-E5 > N1b-E6a,b. At the last stratum (N1b-E6b) there are altogether 8 mutations in 12 loci differentiating it from N1b-A1 founder haplotype: two successive mutations in DYS389-b (16 > 17 > 18) and in DYS392 (14 > 12 > 11), and one mutation in DYS19 (14 > 13), DYS385a (12 > 11), DYS385b (13 > 12), and DYS393 (13 > 12). Compare the haplotypes:

N1b-A1:	14 12 13 13 16 23 10 14 13 14 10 10
N1b-E6b:	<u>13</u> <u>11</u> <u>12</u> 13 <u>18</u> 23 10 <u>11</u> <u>12</u> 14 10 10

This kind of structure, in which a very deep vertical variation is observed, indicates a very deep time span for the lineage N1b-E. Consequently, N1b-preE (descendant of which the N1b-E is) seems to present the oldest diversification and expansion of N1b-A1. All the more shallow N1b-A clusters, where the variation is mostly horizontal (many different one-step-neighbour haplotypes), are probably much later-born (in terms of TMRCA = Time to Most Recent Common Ancestor).

5. Linguistic connections

Here I present some possible connections between the various N1b clusters and the languages. This should not be taken exclusively: there certainly were other haplogroups involved in the linguistic expansions considered here, but in this study I only concentrate on haplogroup N1b.

It is noteworthy that N1b-A lineages are not found in the northern Russian and northern Komi (Izhemski) populations (except the young Komi-specific N1b-K). Thus we may assume that N1b-A clusters in Europe are connected to the Turkic expansion, reaching Europe less than 2 000 years ago. Likewise the Hungarian N1b-A2a (not tested for P43) is most probably connected to Turkic expansion; we know there were Turkic-speaking groups (the Pechenegs, Cumans) in Hungary still in medieval times. As there is no data from the Chuvashes, the speakers of the only survived Bulgar- or Oghur-Turkic language, we cannot reach the Proto-Turkic expansion, but only the Common Turkic expansion, which can be dated to the last centuries of the first millennium AD. In the east the Turkic expansion was a bit earlier, but in the west later.

On the basis of geographical distribution there are altogether four clusters which may be connected to the Turkic expansion: N1b-A1 (central and southern Russians, Priluzski Komi, Ob-Ugrians, southern Siberians, Turkish, Polish Tatars), N1b-A2a (Hungarians, southern Siberians, Turkish, Polish Tatars), N1b-A4 (central and southern Russians, southern Siberians and Turkish), and also N1b-A5 seems to be connected to Turkic expansion (Turkish, Uyghurs).

There seems to be one N1b-E stratum which may be connected to the expansion of the Ob-Ugric languages: N1b-E3a,b (northern Russians, Komi, Mansi, Khanty). The Ob-Ugric expansion from Europe to Siberia has occurred at some time during the first millennium AD, probably at the later end.

There also seem to be two N1b-E stratum which may be connected to the eastern counter-expansion of Finnic languages to the Northern Dvina basin: N1b-E5 (Karelians, northern Russians, Komi) and N1b-E6a,b (Vepsians, northern Russians, Komi). The eastern Finnic expansion from Ladoga–Onega region to the Northern Dvina region (including Pinega and Mezen) has occurred at the turn of the first and second millennia AD, although there may be even earlier, and more southern, Finnic expansions towards the east (Saarikivi 2006). The latest eastern Finnic expansion is, however, the one most probably seen in the genes, as it seems to be connected to massive and sedentary colonisation.

It is also possible that the very early expansion of N1b-preE from southern Siberia to north-eastern Europe (where its descendant N1b-E was born) may be connected with the Pre-Proto-Uralic expansion. The new linguistic time estimations for the expansion of Proto-Uralic are as late as early Bronze Age (ca. 2000 BC in northern Eurasia), and the expansion centre is located in the Kama area between the Volga bend and Ural Mountains (Kallio 2006; Häkkinen 2009). There are typological reasons to locate the Pre-Proto-Uralic area somewhere near southern Siberia (Janhunen 2001; 2007), and from here the language reached the European side of the Ural mountains probably at some time during the fourth millennium BC.

If this is the case, the N1b lineages must have participated also in the Proto-Uralic expansion (along with the other haplogroups not considered here). While this could only be connected with N1b-E (reaching from Finland to north-western Siberia), the clearer picture is yet to be

reconstructed. Especially the N1b haplotypes of the Samoyedic, Volga-Uralic and Volga-Turkic peoples are needed for the more comprehensive scrutiny.

6. Time calculations

I will not use any computing programs but just compare the measure of inner variation between the clusters; after all, the age estimations are based on the variation. As there are several competing views about the age estimations (Lappalainen 2009: 48), it is better to give the data as such, without coding it through any calculation model.

In the previous chapter I sketched the following chronology on the basis of linguistic results:

Expansion	Time estimation	From > to	N1b cluster
Pre-Proto-Uralic	4000–3000 BC	S Siberia > NE Europe	N1b-preE
Proto-Uralic	~ 2000 BC	Kama > west and east	N1b-E?
Ob-Ugric	500–1000 AD	NE Europe > NW Siberia	N1b-E3
Turkic	600–1100 AD	Mongolia > west and east	N1b-A1,A2a,A4,A5
Eastern Finnic	900–1100 AD	Ladoga > N Dvina, Mezen	N1b-E5, -E6

There are two methods for comparing these time estimations with the genetic data: (1) the relative chronology of the cumulative strata, and (2) the inner variation of the clusters. The first method can only be applied to the lineage N1b-E, which fortunately happens to correspond to most of the expansions presented here. There seems to be no contradiction: the oldest expansion is connected to N1b-preE, the second expansion to some early stratum of N1b-E, the third expansion to N1b-E3 and the fourth expansion to N1b-E5 and N1b-E6. Only the Turkic expansion cannot be chronologically related by this method, due to the shallow, star-like structure (variation mainly horizontal) of N1b-A lineage.

The second method is the calculation of the inner variation of the clusters. Here some problems arise, because there are so few haplotypes available – although there are often many haplotypes from the original studies combined together in my tables (if they have originally applied more STR-markers than 12), and there are usually more individuals than haplotypes, this kind of analysis of variation may be called tendencial, at most.

For each expansion I include all the DYS-values found in the certain (expansion-connected) populations at the particular cluster/stratum, and all the DYS-values found in all the populations at all the strata descending from the first stratum. For example, if N1b-E5 is the first stratum connected to eastern Finnic expansion, so also the northern Russians are included if their haplotypes are descendants of the Finnic one. While estimating the time depth of the expansion, naturally all the descending haplotypes must be taken into consideration, whether or not their carriers have gone through the language shift.

For the assumed Pre-Proto-Uralic expansion all the haplotypes beginning from the N1b-preE are included, and for the assumed Proto-Uralic expansion all the haplotypes beginning from N1b-E1 (the first stratum found in Uralic peoples) are included.

Uralic expansions

N1b-preE→E6a,b:	30 alleles per 12 loci (2,50)	Pre-Proto-Uralic
N1b-E1→E6a,b:	27 alleles per 12 loci (2,25)	Proto-Uralic
N1b-E3a,b in Ob-Ugric peoples:	16 alleles per 12 loci (1,33)	Ob-Ugric
N1b-E5 + E6a,b in Finnic peoples and E6a,b in northern Russians:	15 alleles per 12 loci (1,25)	Eastern Finnic

Turkic expansion

N1b-A1 in Turkic peoples:	15 alleles per 12 loci (1,25)
N1b-A2a in Turkic peoples:	14 alleles per 12 loci (1,17)
N1b-A4 in Turkic peoples:	13 alleles per 12 loci (1,08)
N1b-A5 in Turkic peoples:	15 alleles per 12 loci (1,25)

Thus also the results attained by this second method are in pretty good agreement with the linguistic chronology: all those expansions, which supposedly occurred in the last 2 000 years, have the variation between 13–15 alleles per 12 loci, while the oldest expansions, which supposedly occurred at least 4 000 years ago, have the variation double that great. Still, this is not to be taken as any kind of proof for supposed connections, nor any kind of suggestion for absolute time estimations for mutation rate. But as far as there is no contradiction in the relative chronology, it is at least possible to connect certain linguistic expansions with certain genetic clusters.

It would be interesting to find out if there are distributionally similar clusters in the haplogroup N1c-M178 and if their relative measure of variation is similar to those N1b clusters listed here. However, it would be too daring to suppose the absolute measure (alleles per n loci) of variation would be similar, because the frequency of N1c is by far greater than the frequency of N1b, and this leads to greater variation.

7. Discussion

Recently, in the European Journal of Human Genetics, there has emerged a discussion about the origin of N1b (Malyarchuk & Derenko 2009; Mirabal, Underhill & Herrera 2009). The latter writers give a couple of statements in which I have to interfere. First, they say that *"had haplogroup N1b arisen in Siberia, it is likely that high variance estimates would be apparent; however, the Siberian collections included in this work do not possess this said variation (Table 2) despite the large number of Asian Y-chromosomes sampled (N = 140)."*

In their calculations they do not separate N1b-E from N1b-A, so it is obvious that higher variation appears in the area where both of these lineages are present, while lower variation is seen in the area where only one lineage is present. So it is not at all surprising that the variation is highest in the Priluzski Komi, Russians and Mansi, in which all there are present both N1b-A and N1b-E lineages.

So, what is wrong with this? The area of the highest variation cannot tell anything about the place of origin of N1b, because the lineages N1b-A and N1b-E are not dependent on each other. The total N1b variation would be meaningful only if in the particular population/region there was continuity in lineage: if we could follow the mutations step by step from N1b(-A1) founder haplotype to N1b-E haplotypes, we would probably be dealing with the population where N1b-E was born. I shall return to this question later in this chapter.

Practically, all that the total variation alone can really tell, is the region/population in which there have accumulated the largest number of expansive N1b clusters. For example, it has been found only 2 N1b haplotypes in the Finns (Lappalainen 2008), belonging to the lineage N1b-E. But if there were just one more haplotype, belonging to the lineage N1b-A, the variation in the Finns would be much higher, because N1b-A and N1b-E haplotypes differ in so many loci. Therefore the higher variation alone cannot tell the place of origin – neither the place of origin for N1b-E, nor for N1b as a whole. N1b might well have been born in an area which has been the source area, not the target area, of expansions. In such a case the N1b variation in this area of origin could indeed be relatively low.

Consequently, there is no methodological basis to calculate the variation by population, nor by region, but only by lineage. We must separate N1b-A and N1b-E for calculations, and then we

see that the variation in N1b-A is truly higher than in N1b-E: 33 alleles per 12 loci *versus* 27 alleles per 12 loci (see Table 1). Respectively, this should give higher time estimations (TMRCA = Time to Most Recent Common Ancestor) for N1b-A than for N1b-E.

Let us now return to the continuity of lineage. The bridge between N1b-A and N1b-E is a mutation in DYS392 = 14 > 12, and the last N1b-A haplotype which differs from the first N1b-E haplotype only in this respect, is here called N1b-preE (see Table 3). This haplotype is found in the Khanty, and it differs from N1b-A1 founder haplotype by a mutation in DYS389b = 16 > 17. However, this haplotype seems to form a cluster with three one-step-neighbour haplotypes found in the Khakass, in which all we witness the above mentioned value 17. Also the founder haplotype for all N1b (forming the cluster N1b-A1 with all individual one- or two-step-neighbour haplotypes which do not belong to any other subcluster) is present in the Khanty and the Khakass, as well as in the Priluzski Komi, southern Russians, Polish Tatars, and also in Turkey and southern and central Siberia. As N1b-E is only found in European populations and north-western Siberian Ob-Ugric populations (the Khanty and Mansi), there are only two metapopulations in which there occurs a considerable continuity of lineage: the Ob-Ugrians (Khanty and Mansi) and Komi (Priluzski and Izhemski). The mutations are cumulative:

1. N1b-A1 (founder haplotype) – *Khanty, Priluzski Komi*
2. N1b-preE (DYS389b = 16 > 17) – *Khanty*
3. N1b-E (DYS392 = 14 > 12) – *(Mezen Russian)*
4. N1b-E1 (DYS19 = 14 > 13) – *Mansi*
5. N1b-E2b (DYS385b = 13 > 12) – *Izhemski Komi*
6. N1b-E3b (DYS389I = 13 > 14) – *Khanty, Mansi, Priluzski Komi*

The continuity of lineage is nearly perfect (excluding the N1b-E founder haplotype only found in the Mezen Russians) in the Ob-Ugric metapopulation; the first four rows are enough to prove the continuity, but the fifth and sixth row are added to show the presence of early N1b-E strata in all the four subpopulations. Considering the place of origin for N1b-E, it should be kept in mind that the Ob-Ugric languages have spread to Siberia only during the Common Era (indicating also a gene flow to a certain extent), so N1b-E most probably originated in north-eastern Europe.

Even though the vertical variation is deeper in N1b-E than in N1b-A, the former must be descendant of the latter. Therefore N1b-A certainly was born earlier, but the expansion of N1b-E seems to have been earlier than most of the expansions of N1b-A. The oldest expansive N1b-A was probably N1b-preE (found in southern and north-western Siberia), from which the N1b-E mutated, even though this expansion was not extensive migration but probably proceeded only by diffusion of genes in contacts and exogamy.

Another quote from Mirabal, Underhill & Herrera (2009): "*Malyarchuk and Derenko also suggest that N1b-E may have arisen in the Khants, as the proclaimed ancestral modal haplotype for this branch is preceded by a profile present in this group in the figure they have presented. The accumulated variance in the Khants (taking both data from our previous work and from Pimenoff et al. 2008) yields an age estimate of 4.3±2.3 kya for the haplogroup's expansion in the population, a value that is in accordance with the rest of the collections in the region. The conclusion that northwest Siberia may be the birthplace for this branch of haplogroup N1b is undermined by these relatively young TMRCA results. In addition, the Khants and the Mansi are known to have arrived in northwest Siberia only recently during the Soviet era, and represent the expansion from the Uralic range (they both speak Finno-Ugric languages).*"

As I wrote earlier, there is no basis for arguing that overall variation in population could alone prove anything about the place of origin. More important is indeed the continuity of lineage (also pointed out by Malyarchuk and Derenko 2009), which we see in the Ob-Ugric (and to a lesser extent Komi) metapopulation. N1b-E must have been born just once; thus the only continuity of

lineage that matters is that between N1b-preE and N1b-E. It is irrelevant to compare the variation of N1b-A and N1b-E outside this descending lineage, because there cannot be any other bridge from N1b-A to N1b-E than N1b-preE.

Yet the writers are correct in locating the original areas of the Khanty and Mansi in the European side of Ural Mountains, but we have to precisely keep the linguistic and genetic processes separated. Linguistic expansion usually occurs partially by migration and partially by language shift. This means that there is probably a portion of aboriginal north-western Siberian genes in the Khanty and Mansi, even though their languages are western newcomers.

I agree with the writers concerning the European origin of N1b-E, but despite the early expansion of this lineage, it still is a descendant of decisively older N1b-A founder haplotype. The birthplace of N1b is beyond the scope of this study, but the continuity of lineage is still the only valid method for tracking it: we would need to find an N1 haplotype (without P43) similar to the N1b founder haplotype to assess the area of origin. The variation of N1b-A is highest in southern Siberia (see Table 1), but this alone cannot tell much about the place of origin, as demonstrated earlier in this chapter.

Jaakko Häkkinen (M.A, Finno-Ugrian linguistics)
jaakko.hakkinen@helsinki.fi

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TABLE 1: N1b variation by region (alleles per locus)

DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC
N1b-A													
ALL	14 15	11 12 13	12 13 14	10 11 12 13 14	15 16 17	22 23 24	10 11	13 14 15	12 13 14	14 15	10 11	10 11	
S Siberia	14 15	11 12 13	12 ⁴ 13 14	12 13	15 16 17	22 23 24	10 11	14 15	12 ⁴ 13 14	14	10 11 ⁵	10 11	Der Roo
NW Siberia Khanty, Mansi	14	11 12 13	12 13	13	16 17	22 23	10 11	14	13	14	10	10 11	Mir Pim
NE Europe Komi, Russian	14 15 ¹	11 ² 12	12 13 14	13 14	15 ² 16	23 24 ²	10	14 15 ¹	13	14	10 11 ¹	10 11 ¹	Bal Mir
China, Mongolia	---	---	---	10 11	15 16 17	23 24	10	13 14 15	13 14	14 15	10 11	10 11	Xue
Turkey, Hungary*, Pol.Tatar*	14 15	12	13	11 13	15 16 17	23 24	10 11	13 14	13	14	10	10 11	Cin Völ* Jan*
N1b-E													
ALL	13 14 15	11 12	12 13 14	13 14 15	16 17 18 19 21	23 24	10 11	11 12	12 13	14	10	10	
NE Europe Komi, Tatar, Mari, Finn, Russian, Vepsian	13 14 ² 15 ⁶	11 12	12 13 14 ¹	13 15 ¹	17 18 19 ² 21 ²	23 24 ²	10 11 ²	11 ^{1,3} 12	12 13	14	10	10	Bal Mir Der Roo Lap
NW Siberia Khanty, Mansi	13	12	12 13	13 14	16 17 18	23 24	10	12	13	14	10	10	Mir Pim
DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC

1 = Only Komi | 2 = Russian | 3 = Vepsian | 4 = Altaian | 5 = Siberian Eskimo | 6 = Finn | * = P43 not tested

Variation:	Alleles per <i>n</i> loci:
N1b-A (Total)	33 per 12 loci (2,75)
S Siberia	28 per 12 loci (2,33)
NW Siberia	19 per 12 loci (1,58)
NE Europe	22 per 12 loci (1,83)
Komi	19 per 12 loci (1,58)
Russians	18 per 12 loci (1,50)
China, Mongolia	19 per 9 loci (2,11)
Turkey, Hungary	20 per 12 loci (1,67)
N1b-E (Total)	27 per 12 loci (2,17)
NW Siberia	17 per 12 loci (1,42)
NE Europe	25 per 12 loci (2,00)
Komi	19 per 12 loci (1,58)
Russians	21 per 12 loci (1,75)

TABLE 2: N1b-E haplotype clusters (Sources: Bal, Pim, Mir, Roo, Lap)

DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC
N1b-E (founder haplotype)													
Russ.Mezen1	14	12	13	13	17	23	10	12	13	14	10	10	Bal
N1b-E, stratum 1 (DYS19 = 14 > 13)													
Mansi 1	<u>13</u>	12	13	13	17	23	10	12	13	14	10	10	Pim
Russ.Krasn.3	<u>13</u>	12	13	13	17	23	10	12	13	14	10	10	Bal
N1b-E, stratum 2a (DYS389-II = 17 > 18)													
Komi.Izh 17	<u>13</u>	12	13	13	<u>18</u>	23	10	12	13	14	10	10	Mir
Mari	<u>13</u>	12	13	13	<u>18</u>	23	10	12	13	14	10	10	Roo
N1b-E, stratum 2b (DYS385b = 13 > 12)													
Komi.Izh 38,	<u>13</u>	12	<u>12</u>	13	17	23	10	12	13	14	10	10	Mir
Tatar	<u>13</u>	12	<u>12</u>	13	17	23	10	12	13	14	10	10	Roo
N1b-E, stratum 3a (DYS389-II = 17 > 18 or <u>DYS385b = 13 > 12</u>)													
Russ.Mez.2	<u>13</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Bal
Mansi 2	<u>13</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Pim
Komi 1	<u>13</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Roo
Komi.Izh 12,	<u>13</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Mir
Russian	<u>13</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Roo
Komi.Izh 14	<u>13</u>	12	<u>14</u>	13	<u>18</u>	23	10	12	13	14	10	10	Mir
N1b-E, stratum 3b (DYS389-I = 13 > 14)													
Khanty 63	<u>13</u>	12	<u>12</u>	<u>14</u>	17	23	10	12	13	14	10	10	Mir
Khanty 1	<u>13</u>	12	<u>12</u>	<u>14</u>	<u>18</u>	<u>24</u>	10	12	13	14	10	10	Pim
Mansi 3	<u>13</u>	12	<u>12</u>	<u>14</u>	17	23	10	12	13	14	10	10	Pim
Mansi 4	<u>13</u>	12	<u>12</u>	<u>14</u>	<u>16</u>	23	10	12	13	14	10	10	Pim
Komi.Pri 34	<u>13</u>	12	<u>12</u>	<u>15</u>	17	23	10	12	13	14	10	10	Mir
N1b-E, stratum 4a (DYS393 = 13 > 12)													
Finn-2	<u>13</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	<u>12</u>	----	----	----	Lap
Finn-1	<u>15</u>	12	<u>12</u>	13	<u>18</u>	23	10	12	<u>12</u>	----	----	----	Lap
N1b-E, stratum 4b (DYS385a = 12 > 11)													
Russ.Pin.1	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Bal
Russ.Mez.3	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	12	13	14	10	10	Bal
Russ.Mez.4	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	<u>11</u>	12	13	14	10	10	Bal
Russ.Pin.3,9,	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	<u>24</u>	10	12	13	14	10	10	Bal
N1b-E, stratum 5 (DYS393 = 13 > 12 or <u>DYS385a = 12 > 11</u>)													
Russ.Pin.10	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	12	<u>12</u>	14	10	10	Bal
Komi 2	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	12	<u>12</u>	14	10	10	Roo
Karelian	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	12	<u>12</u>	----	----	----	Lap
Russ.Vol.1	<u>14</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	12	<u>12</u>	14	10	10	Bal
Russ.Vol.2	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	<u>11</u>	12	<u>12</u>	14	10	10	Bal
N1b-E, stratum 6a (DYS389-II = 18 > 19)													
Russ.Pin.2,4,	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>19</u>	23	10	12	<u>12</u>	14	10	10	Bal
Russ.Krs.1,2	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>19</u>	23	10	12	<u>12</u>	14	10	10	Bal
Russ.Pin.13	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>21</u>	23	10	12	<u>12</u>	14	10	10	Bal
N1b-E, stratum 6b (DYS392 = 12 > 11)													
Komi.Pri 54	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	<u>11</u>	<u>12</u>	14	10	10	Mir
Vepsian	<u>13</u>	<u>11</u>	<u>12</u>	13	<u>18</u>	23	10	<u>11</u>	<u>12</u>	14	10	10	Roo
DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC

TABLE 3: N1b-A haplotype clusters (Sources: Mir, Bal, Der, Pim, Xue, Roo, Cin, Völ*, Jan*)

DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC
N1a Kazah	14	12	13	13	16	<u>22</u>	10	<u>15</u>	13	14	10	<u>11</u>	Roo
N1c Bashkir	14	12	13	13	16	23	<u>11</u>	14	<u>14</u>	14	10	10	Roo
N1b-A1 (founder haplotype)													
Khakass	14	12	13	13	16	23	10	14	13	14	10	10	Der
Turkey 319	14	---	---	13	16	23	10	14	13	---	---	10	Cin
Khanty10,16,	14	12	13	13	16	23	10	14	13	14	10	10	Mir
Khanty, man.	14	12	13	13	16	23	10	14	13	14	10	10	Pim
Russ.Belgor.	14	12	13	13	16	23	10	14	13	14	10	10	Bal
Ewenk, Altai	14	12	13	13	16	23	10	14	13	14	10	10	Roo
Pol.Tatar 17*	14	12	13	13	16	23	10	14	13	---	---	---	Jan
Buryat	14	12	13	13	16	<u>22</u>	10	14	13	14	10	10	Der
Khakass	14	12	13	13	16	23	10	14	13	14	10	<u>11</u>	Der
Tuva	14	12	13	13	16	23	10	14	13	14	10	<u>11</u>	Roo
Turkey 320	14	---	---	13	16	23	10	14	13	---	---	<u>11</u>	Cin
Turkey 322	14	---	---	13	<u>17</u>	23	10	14	13	---	---	10	Cin
Turkey 323	14	---	---	13	16	23	10	<u>13</u>	13	---	---	10	Cin
Khanty 73	14	12	13	13	16	<u>22</u>	10	14	13	14	10	<u>11</u>	Mir
Komi.Pri 86	<u>15</u>	12	<u>12</u>	13	16	23	10	14	13	14	10	10	Mir
Ewenk	14	12	<u>14</u>	13	16	23	10	14	13	14	10	10	Roo
Russ.Porhov	14	12	<u>14</u>	13	16	<u>24</u>	10	14	13	14	10	10	Bal
Mongol	14	12	13	13	16	<u>24</u>	10	14	13	14	10	10	Der
N1b-A2 (DYS391 = 10 > 11)													
Khanty 48	14	12	13	13	16	23	<u>11</u>	14	13	14	10	10	Mir
Tuva, Khak.	14	12	13	13	16	23	<u>11</u>	14	13	14	10	10	Der
N1b-A2a (DYS19 = 14 > 15)													
Tuva,Tofalar	<u>15</u>	12	13	13	16	23	<u>11</u>	14	13	14	10	10	Der
Turkey 328	<u>15</u>	---	---	13	16	23	<u>11</u>	14	13	---	---	10	Cin
Turkey 329	<u>15</u>	---	---	13	16	23	<u>10</u>	14	13	---	---	10	Cin
Pol.Tatar 42*	<u>15</u>	12	13	13	16	23	<u>10</u>	14	13	---	---	---	Jan
Tofalar	<u>15</u>	<u>13</u>	13	13	16	23	<u>11</u>	14	13	14	10	10	Der
Hungarian*	<u>15</u>	12	13	13	<u>17</u>	23	<u>11</u>	14	<u>14</u>	14	10	10	Völ
N1b-A2a1 (DYS439 = 10 > 11)													
Tuva, Kalm.	<u>15</u>	12	13	13	16	23	<u>11</u>	14	13	14	10	<u>11</u>	Der
Tuva	<u>15</u>	12	13	13	16	23	<u>11</u>	14	13	14	10	<u>11</u>	Roo
Tuva	<u>15</u>	12	13	13	16	23	<u>11</u>	14	<u>14</u>	14	10	<u>11</u>	Der
Tuva	<u>15</u>	12	13	13	16	23	<u>10</u>	14	13	14	10	<u>11</u>	Der
Tuva	<u>15</u>	12	13	13	16	<u>22</u>	<u>11</u>	14	13	14	10	<u>11</u>	Der
Tuva	<u>15</u>	12	13	<u>12</u>	16	23	<u>11</u>	14	13	14	10	<u>11</u>	Der
Tuva	<u>15</u>	12	13	13	<u>17</u>	23	<u>11</u>	14	13	14	10	<u>11</u>	Der
Tuva	<u>15</u>	12	13	13	16	23	<u>11</u>	<u>15</u>	13	14	10	<u>11</u>	Der
N1b-A3 (DYS392 = 14 > 15)													
(*Reconstr.)	14	12	13	13	16	23	10	<u>15</u>	13	14	10	10	----
Altaian	14	12	<u>12</u>	13	16	23	10	<u>15</u>	<u>12</u>	14	10	10	Roo
Khakass	14	12	13	13	<u>15</u>	23	10	<u>15</u>	13	14	10	<u>11</u>	Der
N1b-A3a (DYS438 = 10 > 11)													
Komi.Pri-53	14	12	13	13	16	23	10	<u>15</u>	13	14	<u>11</u>	10	Mir
Komi.Pri-20	14	12	13	13	16	23	10	<u>15</u>	13	14	<u>11</u>	<u>11</u>	Mir
Eskimo	14	12	13	13	16	<u>24</u>	10	<u>15</u>	13	14	<u>11</u>	10	Roo
N1b-A4 (DYS389-II = 16 > 15)													
Kalmyk	14	12	13	13	<u>15</u>	23	10	14	13	14	10	10	Der
Khakass	14	12	13	13	<u>15</u>	23	10	14	13	14	10	<u>11</u>	Der
Russ.Livni	14	12	13	13	<u>15</u>	23	10	14	13	14	10	10	Bal
Kalmyk	14	12	13	13	<u>15</u>	23	10	14	13	14	10	10	Der
Turkey 325	14	---	---	13	<u>15</u>	23	10	14	13	---	---	10	Cin
DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC

DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC
N1b-A5 (DYS389-I = 13 > 11)													
Hezhen 7, 15	---	---	---	<u>11</u>	16	23	10	14	13	14	10	10	Xue
Turkey 326	14	---	---	<u>11</u>	16	23	10	14	13	---	---	10	Cin
Hezhen,Oroq	---	---	---	<u>11</u>	<u>17</u>	23	10	14	13	14	10	10	Xue
Hezhen 17	---	---	---	<u>11</u>	16	23	10	<u>13</u>	<u>14</u>	14	10	10	Xue
N1b-A5a (DYS389-I = 11 > 10)													
Manchu 15	----	----	----	<u>10</u>	16	23	10	14	13	14	10	10	Xue
Uyghur.Ur 1	----	----	----	<u>10</u>	16	23	10	14	13	14	10	<u>11</u>	Xue
Uyghur.Ur23	----	----	----	<u>10</u>	16	<u>24</u>	10	14	13	14	10	10	Xue
Outer mong.	----	----	----	<u>10</u>	<u>15</u>	23	10	14	13	14	10	10	Xue
Oroqen 9	---	---	---	<u>10</u>	<u>17</u>	23	10	<u>15</u>	13	<u>15</u>	<u>11</u>	<u>11</u>	Xue
N1b-A6 (DYS385a = 12 > 13)													
Ewk, Kh,Tof	14	<u>13</u>	13	13	16	23	10	14	13	14	10	10	Der
Khanty	14	<u>13</u>	13	13	16	23	10	14	13	14	10	10	Pim
Khakass	14	<u>13</u>	13	13	16	23	10	14	13	14	10	10	Roo
Khakass	14	<u>13</u>	13	13	16	23	10	14	13	14	10	<u>11</u>	Der
Ewenk	14	<u>13</u>	<u>14</u>	13	16	23	10	14	13	14	10	10	Der
N1b-A7 (DYS385a = 12 > 11)													
Khakass	14	<u>11</u>	13	13	16	23	10	14	13	14	10	10	Der
N1b-A7a (DYS385b = 13 > 12)													
Khanty 42	14	<u>11</u>	<u>12</u>	13	16	23	10	14	13	14	10	10	Mir
Khanty 9,29,	14	<u>11</u>	<u>12</u>	13	<u>17</u>	23	10	14	13	14	10	10	Mir
Russ.Coss.	14	<u>11</u>	<u>12</u>	<u>14</u>	16	<u>24</u>	10	14	13	14	10	10	Bal
N1b-K (DYS389I = 13 > 14)													
Komi.Pri-24,	14	12	13	<u>14</u>	16	23	10	14	13	14	10	10	Mir
Komi.Izh-86	14	12	13	<u>14</u>	16	23	10	14	13	14	<u>11</u>	<u>11</u>	Mir
N1b-preE (DYS389II = 16 > 17)													
Khanty 6,12	14	12	13	13	<u>17</u>	23	10	14	13	14	10	10	Mir
Khakass	14	<u>13</u>	13	13	<u>17</u>	23	10	14	13	14	10	10	Der
Khakass	14	12	13	13	<u>17</u>	<u>22</u>	10	14	13	14	10	10	Der
Khakass	14	12	13	13	<u>17</u>	<u>24</u>	10	14	13	14	10	10	Der
N1b-E (DYS392 = 14 > 12) See Table 2: N1b-E haplotype clusters													
Russ.Mezen1	14	12	13	13	<u>17</u>	23	10	<u>12</u>	13	14	10	10	Bal
DYS →	19	385a	385b	389I	389b	390	391	392	393	437	438	439	SRC

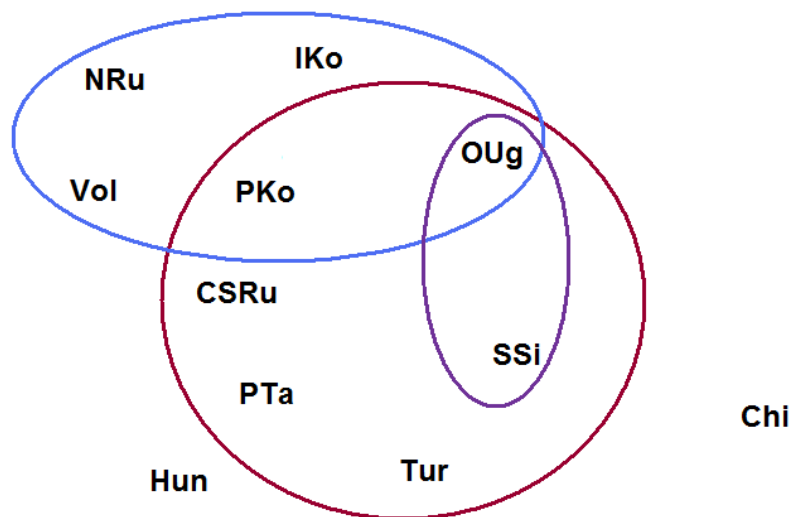
* = P43 not tested.

TABLE 4: Distribution of N1b clusters and subclusters:

	Finnish / Karelian- Vepsian	Russian: North / Ctr-South	Volga: Mari / Tatar	Komi: Izhemski / Priluzski	NW Siber: Ob-Ugric/ Hungarian	S Siberia: Turkic / Mongolic	Turkish / Pol.Tatar	China: Turkic / Tungusic
N1b-A1	-	-/+	-	-/+	+/-	+/+	+/+	-
N1b-A2	-	-	-	-	+/-	+/-	-	-
N1b-A2a	-	-	-	-	-/+	+/-	+/+	-
N1b-A2a1	-	-	-	-	-	+/-	-	-
N1b-A3	-	-	-	-	-	+/-	-	-
N1b-A3a	-	-	-	-/+	-	*+/-	-	-
N1b-A4	-	-/+	-	-	-	+/+	+/-	-
N1b-A5	-	-	-	-	-	-	+/-	-/+
N1b-A5a	-	-	-	-	-	-	-	+/+
N1b-A6	-	-	-	-	+/-	+/-	-	-
N1b-A7	-	-	-	-	-	+/-	-	-
N1b-A7a	-	-/+	-	-	+/-	-	-	-
N1b-K	-	-	-	+/+	-	-	-	-
N1b-preE	-	-	-	-	+/-	+/-	-	-
N1b-E	-	+/-	-	-	-	-	-	-
N1b-E1	-	+/-	-	-	+/-	-	-	-
N1b-E2a	-	-	+/-	+/-	-	-	-	-
N1b-E2b	-	-	-/+	+/-	-	-	-	-
N1b-E3a	-	+/-	-	+/-	+/-	-	-	-
N1b-E3b	-	-	-	-/+	+/-	-	-	-
N1b-E4a	+/-	-	-	-	-	-	-	-
N1b-E4b	-	+/-	-	-	-	-	-	-
N1b-E5	-/+	+/-	-	+	-	-	-	-
N1b-E6a	-	+/-	-	-	-	-	-	-
N1b-E6b	-/+	-	-	-/+	-	-	-	-

* = Not Turkic but Siberian Eskimo.

PICTURE 1: Origin of N1b-E



N1b-A1

N1b-preE

N1b-E

NRu = northern Russians, CSRu = central and southern Russians, IKo = Izhemski Komi, PKo = Priluzski Komi, Vol = Volga (Mari, Tatars), PTa = Polish Tatars, Hun = Hungarians, Tur = Turkish, SSi = southern Siberians, OUg = Ob-Ugrians, Chi = China and Mongolia.