

A possible scenario explaining the phylogeographic pattern of hg N1b is that the subclusters N1b-A and N1b-E might have diverged from a common ancestor anywhere in Siberia approximately 15 ky ago (with upper bound of divergence time, T_D , between these subclusters estimated (according to Zhivotovsky⁹) as 14.7 ± 5.9 ky). According to STR variation, expansion of Northwest Siberian/Uralic/Northeast European branch, N1b-E, may have occurred approximately 7 kya and the expansion of South Siberian branch N1b-A about 5 kya. Divergence time between South Siberian and Northwest Siberian/Uralic N1b-A haplotypes is 4 ky ($T_D = 4.0 \pm 1.0$ ky), so this suggests that expansion of N1b-A lineages in Northwest Siberia and Urals (about 3 kya) might have occurred right after their migrations from South Siberia. Future studies of Y-chromosome variation using a combined STR-SNP approach may enable a better definition of geographic origin of N1b-P43 mutation.

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Boris Malyarchuk¹ and Miroslava Derenko¹

¹Genetics Laboratory, Institute of Biological Problems of the North, Russian Academy of Sciences, Magadan, Russia
E-mail: malyarchuk@ibpn.ru

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Reply to B Malyarchuk and M Derenko: a need for further investigation of Uralic and Siberian populations in the search for haplogroup N1b's origins

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Malyarchuk and Derenko (see accompanying letter) have expanded on our previous work¹ by including northwest² and south³ Siberian samples in Time to Most Recent Common Ancestor (TMRCA) calculations under haplogroup N1b (P43) (The Russian Pomor populations⁴ the authors claim to have newly included in their analyses were already included in our TMRCA calculations¹). We have taken the liberty of reanalyzing the data published in the aforementioned articles along with the results from the publications already investigated in our previously published work¹ using a population based as opposed to a regionally based approach to compliment Malyarchuk and Derenko's findings.

It should be noted that the results presented by Malyarchuk and Derenko should be tempered given that all claims made are based solely on TMRCA estimates. Although TMRCA estimates provide a signal of demographic expansion dating to the last recognizable bottleneck, determination of high frequency and/or diversity areas are particularly pertinent. In addition, these estimates (TMRCA) are subject to large standard errors, can be affected by founder population size and may also reflect gene flow within the same lineage. Insights from archaeology, linguistics and other lines of evidence besides molecular clocks may be worth considering. It should also be noted that STR haplotypes generally coalesce to more recent times than those ascertained by TMRCA as a result of lineage extinctions that are not always possible to detect.⁵

Overall, age of accumulated Y-chromosome short tandem repeat (Y-STR) variation of 12.1 ± 4.4 kilo years ago (kya) as per Malyarchuk and Derenko's analyses is in close agreement

with our estimate yielding 11.5 ± 3.1 kya, when all individuals from the regions analyzed (European, Uralic and Siberian) are pooled (Table 1). Malyarchuk and Derenko explain that data attained in their analyses suggests that the subset of Y-chromosomes belonging to haplogroup N1b-E (European branch) may have arisen earlier than N1b-A (Asian branch), as the former attains older age estimates (6.8 ± 2.6 kya) than the latter (4.8 ± 1.7 kya). Our analyses yield similar ages to the ones reported by Malyarchuk and Derenko for Europeans and Siberians/Mongolians (Table 1), and also indicate that Y-STR variance and accumulated age estimates in a population-by-population basis are higher in European collections, ranging from 0.083 in the Mezen (3.0 ± 2.1 kya) to 0.598 in the Other Slavs (exhibiting a bipartite structure including both Asian (6.0 ± 3.7 kya) and European (7.0 ± 3.6 kya) core haplotypes) than in Asian groups, which fluctuate from 0.046 in the South Siberian Tuvinians (1.7 ± 0.7 kya) to 0.292 in the northwest Siberian Mansi (9.7 ± 4.4 kya) (Table 2). Therefore, our results are in support of Malyarchuk and Derenko's findings, but in disagreement with the traditional view that branch N1b-A is older than N1b-E.⁶

The highest overall accumulated Y-STR variance and age estimates are achieved in the Komi from Priluzski (0.611 and 12.9 ± 4.1 kya, respectively), as previously indicated.¹ Meanwhile, with the exemption of the Mansi from northwest Siberia, all Asian populations exhibit accumulated

ages of 6.3 Kya or less (Table 2). These results, along with the overall homogeneity (low Y-STR variance values as compared with the European or Uralic groups included in this study) throughout northwest and south Siberia and Mongolia are not suggestive of these regions as the cradle for haplogroup N1b. Generally, populations within Siberia are highly stratified, exhibiting pronounced levels of differentiation between them^{8,9} and 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 ($N = 140$).

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 work¹ and from Pimenoff *et al.*²) 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

Table 1 Time to most recent common ancestor (TMRCA) for haplogroup N1b (P43)

Population (region)	N	Network shape	TMRCA ^a (kya)
Europeans	29	Bipartite star	11.9 ± 4.6 (6.0 ± 3.7 and 7.7 ± 3.8) ^b
Uralic	16	Bipartite star	12.8 ± 5.0 (5.0 ± 3.6 and 6.6 ± 4.4) ^b
Siberians/Mongolians	140	Bipartite star	4.9 ± 1.7 (6.9 ± 3.3 and 3.5 ± 1.6) ^b
All	185	Star-like	11.5 ± 3.1

Abbreviation: kya, kilo years ago.

^aA mutation rate of 0.00069 mutations per locus per generation was used to estimate time.

^bSubclustering of haplotypes led to separate time estimates for each branch.

Table 2 Haplotype variance and time to most recent common ancestor (TMRCA) for haplogroup N1b (P43)

Population (region)	N	Haplotype variance	Network shape	TMRCA ^a (kya)	References
Komi Izhemski (Uralic)	9	0.181	Star-like	6.7 ± 4.2	1
Komi Priluzski (Uralic)	7	0.611	Star-like	12.9 ± 4.1	1
Mezen (Slavic)	4	0.083	Star-like	3.0 ± 2.1	4
Pinega (Slavic)	15	0.163	Star-like	5.6 ± 2.9	4
Other Slavs ^b	10	0.598	Bipartite Star	16.3 ± 5.8 (6.0 ± 3.7 and 7.0 ± 3.6) ^c	3,4
Hezhen (Siberian)	8	0.077	Star-like	3.0 ± 1.8	7
Khakassian (Siberian)	21	0.056	Star-like	6.3 ± 5.2	3
Tuviniian (Siberian)	25	0.046	Star-like	1.7 ± 0.7	3
Mansi (Siberian)	15	0.292	Star-like	9.7 ± 4.4	2
Khanty (Siberian)	28	0.129	Star-like	4.3 ± 2.3	1,2
Other Siberians/Mongolians ^d	43	0.059	Star-like	2.2 ± 1.2	3,7

Abbreviation: kya, kilo years ago.

^aA mutation rate of 0.00069 mutations per locus per generation was used to estimate time.

^bKrasnoborsk, Vologda, Belgorod, Cossacs, Livni, Porhov.

^cSubclustering of haplotypes led to separate time estimates for each branch.

^dUyghur, Oroqen, Outer Mongolian, Shors, Kalmyks, Tofalars, Altaian, Buryats, Evenks.

expansion from the Uralic range¹⁰ (they both speak Finno-Ugric languages^{11,12}).

The higher variance and age estimates (Tables 1 and 2) for both European and Uralic populations as compared to the Siberian groups lend support to our previous statement suggesting that N1b may have arisen in the Uralic range or in an area/region proximal to it; however, a much more exhaustive investigative effort must be conducted to trace the origins of N1b and its branches N1b-A and N1b-E.

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Sheyla Mirabal^{1,2}, Peter A Underhill³ and Rene J Herrera^{1,2}

¹Department of Molecular and Human Genetics, College of Medicine, Florida International University, Miami, FL, USA

²Department of Biological Sciences,

Florida International University, Miami, FL, USA; ;

³Department of Psychiatry and Behavioral Sciences, Stanford University School of Medicine, Stanford, CA, USA

E-mail: herrerar@fiu.edu

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