

## Report

# Traces of Early Eurasians in the Mansi of Northwest Siberia Revealed by Mitochondrial DNA Analysis

Olga A. Derbeneva,<sup>1</sup> Elena B. Starikovskaya,<sup>1</sup> Douglas C. Wallace,<sup>2</sup> and Rem I. Sukernik<sup>1</sup>

<sup>1</sup>Laboratory of Human Molecular Genetics, Institute of Cytology and Genetics, Siberian Division, Russian Academy of Sciences, Novosibirsk, Russia; and <sup>2</sup>Center for Molecular Medicine, Emory University, Atlanta

The mitochondrial DNA (mtDNA) of 98 Mansi, an ancient group (formerly known as “Vogul”) of Uralic-speaking fishers and hunters on the eastern slope of the northern Ural Mountains, were analyzed for sequence variants by restriction fragment–length polymorphism analysis, control-region sequencing, and sequencing of additional informative sites in the coding region. Although 63.3% of the mtDNA detected in the Mansi falls into western Eurasian lineages (e.g., haplogroups UK, TJ, and HV), the remaining 36.7% encompass a subset of eastern Eurasian lineages (e.g., haplogroups A, C, D, F, G, and M). Among the western Eurasian lineages, subhaplogroup U4 was found at a remarkable frequency of 16.3%, along with lineages U5, U7, and J2. This suggests that the aboriginal populations residing immediately to the east of the Ural Mountains may encompass remnants of the early Upper Paleolithic expansion from the Middle East/southeastern Europe. The added presence of eastern Eurasian mtDNA lineages in the Mansi introduces the possibilities that proto-Eurasians encompassed a range of macrohaplogroup M and N lineages that subsequently became geographically distributed and that the Paleolithic expansion may have reached this part of Siberia before it split into western and eastern human groups.

Analysis of mtDNA diversity in northern European populations has revealed that their overall mtDNA gene pool encompasses all major western Eurasian haplogroups—that is, haplogroups H–K and T–X. Moreover, remarkably high frequencies of haplogroups U and V are found in the Saami, who are thought to be genetically similar to early Upper Paleolithic Europeans (Sajantila et al. 1995; Torroni et al. 1998, 2001; Macaulay et al. 1999; Richards et al. 2000; Finnila et al. 2001; Helgason et al. 2001; Meinila et al. 2001). Likewise, studies of mtDNA diversity in native Siberians residing in northeastern Eurasia have revealed that these populations harbor Asian-specific mtDNA haplogroups A, C, D, G, and Y (Starikovskaya et al. 1998; Schurr et al. 1999). What is unclear is how this striking geographic separation of lineages occurred. Were Europe and Asia settled by totally different migrations out of Africa, or did Eurasian mtDNA diver-

sity start as a continuum that subsequently became geographically stratified?

To address this question, we chose to survey the remnants of the Mansi, a tribal group of sedentary fishers and hunters who, for ages, inhabited the pine-birch boreal forests on the eastern slope of the Ural Mountains, the provisional geographic barrier separating Asia and Europe. The Mansi speak a dialect of the Finno-Ugric language of the Uralic linguistic family, to which the Saami language also belongs (Fedorova et al. 1994).

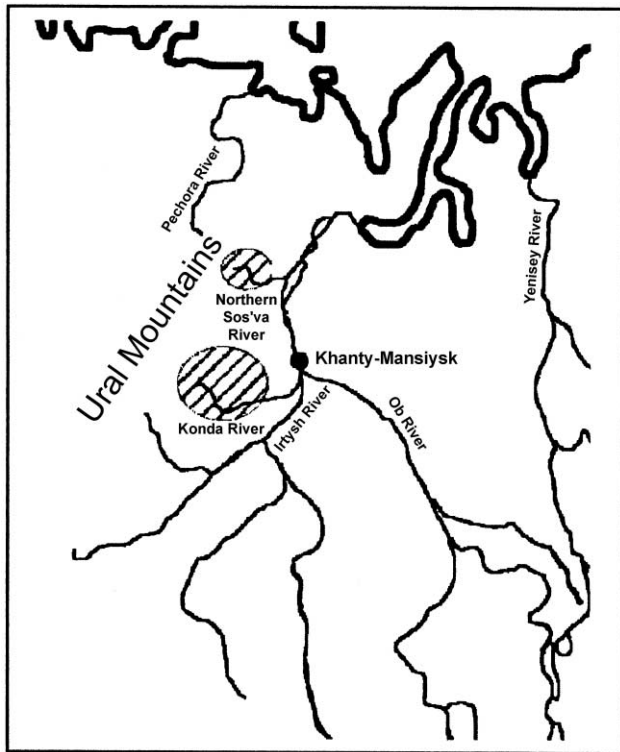
Blood samples were collected from 59 Mansi in the villages of Shaim, Chantarya, Polovinka, and Shugur, which are scattered along the Konda River and its tributaries. An additional 39 samples were collected from the tiny settlements of Shshekurya, Lombovozh, and Sos’va, in the northern Sos’va River/Lyamin River basin (fig. 1).

mtDNA variation was surveyed by digestion with 19 restriction endonucleases, sequencing of hypervariable segments I and II (HVS-I and HVS-II, respectively) of the control region, and sequence detection of diagnostic polymorphic sites at nucleotide positions 7600, 12308, and 12705 (Torroni et al. 1998). The 98 Mansi mtDNA samples proved to be a novel mixture of 63% European mtDNA samples and 37% Asian-Siberian mtDNA sam-

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Address for correspondence and reprints: Dr. Rem I. Sukernik, Laboratory of Human Molecular Genetics, Institute of Cytology and Genetics, 10 Lavrent’ev Avenue, Novosibirsk 630090, Russia. E-mail: sukernik@bionet.nsc.ru

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**Figure 1** A map of northwestern Siberia, indicating the locations of the two Mansi populations sampled.

ples. Of 62 European mtDNA samples, 28 harbored the characteristic 12308G coding-region mutation, indicating that they belong to haplogroup U; of the haplogroup U mtDNA samples, 16 harbored the diagnostic markers of subhaplogroup U4, including the *RsaI*-site gain at nucleotide position 4643 (i.e., 4643 *RsaI*+), 11329 *AluI*+, and the control-region 16356C mutation. An additional four mtDNA samples were assigned to the U5a subcluster, which is characterized by the 16256T and 16270T control-region motif, and five belonged to the U7 subcluster, which is characterized by the 16309G transition and the 16318T transversion. However, the Mansi lacked the U5b1 subcluster defined by the “Saami motif” of 16144C, 16189C, and 16270T control-region variants. Only three mtDNA samples belonged to subhaplogroup K of haplogroup U (tables 1 and 2).

The mtDNA samples that belonged to haplogroup TJ were also well represented in the Mansi and encompassed 7 and 12 mtDNA samples, respectively. The ancestral 4216 *NlaIII*+ and 16126C variants of haplogroup T (fig. 2) were found in the Mansi and also in the Finnish TJ phylogeny (Finnila et al. 2001). Two individuals of sublineage T and one individual of sublineage T1 appeared to have novel mtDNA haplotypes, including a previously undescribed site loss, 13704 *BstNI*-. Haplogroup J was confined to two sublineages, J2 and

the rare J1b1 sublineage. The J2 mtDNA samples were found in 10.2% of the Mansi, even though they are rarely observed in other European populations, including the Saami and Finns (table 2). J1b1 was observed in two individuals.

Haplogroup H, found in >40% of western Europeans, was present in only 14.3% of the Mansi mtDNA samples. Still, several sublineages of haplogroup H were observed, including six mtDNA samples of haplogroup H3, characterized by the 7025 *AluI*-, 14766 *MseI*- coding plus the 16189C and 16356C or 16189C control-region variants. An additional three Mansi mtDNA samples belonged to haplogroup H2, as indicated by the 4769 *AluI*+ variant and an HVS-I sequence identical to the Cambridge reference sequence (Andrews et al. 1999). Two of these three mtDNA samples also had the 8858 *HhaI*+. Finally, five of the haplogroup H mtDNA samples belonged to a unique, previously unreported variant (haplogroup H\*) distinguished by the 16169T and 16184T control-region variants, in HVS-I, and the 73G variant, in HVS-II. Since the 73 site in HVS-II varies among the Mansi haplogroup H mtDNA samples, as well as among the Finnish mtDNA samples and other European mtDNA samples, it appears to be a hyper-variable site (Finnila et al. 2001; Helgason et al. 2001). Therefore, we disregarded the 73 site for phylogenetic reconstruction (fig. 2). Thus, the structure of the haplogroup H mtDNA types in the Mansi is very similar to that in the Finns.

Haplogroup V was found in only one Mansi mtDNA sample. This mtDNA type was characterized by 4577 *NlaIII*-, 14766 *MseI*-, and the 16298C and 72C variants (table 1). Haplogroup V is at its highest frequency, 39.8%, among the Saami and has frequencies of 5.1% among Finns (table 2) and 2.6% among Russians from the Upper Volga River region (Malyarchuk et al. 2001). Hence, this Mansi haplogroup V mtDNA type could be due to gene flow from western Uralic speakers or Russian colonizers.

Among the 36 (37%) Mansi mtDNA samples that belong to traditional Asian haplogroups, 17 Mansi mtDNA samples harbored mtDNA of haplogroup C. One haplogroup C mtDNA type found in four individuals is missing the characteristic 16223T transition, presumably because of a reverse mutation. Eight of the Mansi mtDNA samples belonged to haplogroup D. One of these lacked the classically associated 10394 *DdeI*+/10397 *AluI*+ sites, which characterize macrohaplogroup M (at the RFLP level), which encompasses haplogroups C and D. Sequencing of the segment encompassing this region revealed the expected macrohaplogroup M 10398G and 10400T transitions. However, a 10397G transition was also found that would account for the simultaneous elimination of the adjacent restriction sites. Finally, single mtDNAs of haplogroups G and F and the unclassified M

Table 1

## mtDNA Diversity in the Mansi

Haplogroup	No. of Subjects <sup>a</sup>	RFLP(s) <sup>b</sup>	HVS-I (-16000)	HVS-II
UK:				
U4	1	<b>4643k 11329a 12308g</b>	356 519	73 195 263
	4	<b>4643k 11329a 12308g</b>	356 519	73 195 215 263
	2	<b>4643k 11329a 12308g</b>	311 356 519	73 146 152 195 263
	1	<b>4643k 11329a 12308g</b>	092 311 356 519	73 146 152 195 263
	1	<b>4643k 11329a 12308g</b>	113C 356 362 519	73 195 263
	2	<b>4643k -4685a 11329a 12308g</b>	113C 356 362 519	73 195 263
	1	<b>4643k -4685a 11329a 12308g</b>	113C 239 356 362 519	73 195 263
	1	<b>4643k -4685a 11329a 12308g</b>	113C 189 356 362 519	73 195 263
	1	<b>626e 4643k -11326c 11329a 12308g</b>	189 356 519	73 263
	2	<b>626e 4643k -11326c 11329a 12308g</b>	189 356 519	73 195 263
U5a	1	<b>12308g</b>	192 256 270 311	73 263
	1	<b>-3192c 12308g</b>	129 239 256 270 399	73 150 263
U5a1	2	<b>12308g</b>	114A 192 256 270 294	73 150 263
U7	4	<b>12308g</b>	309 318T 519	73 151 152 263
	1	<b>-1715c 12308g</b>	309 318T 519	73 151 152 263
	3	<b>-322e -9052n 9714e 12308g</b>	224 311 519	73 146 152 263
K				
JT:				
J1b1	2	<b>4216q 10394c -13704t</b>	069 126 145 172 222 261	73 242 263 295
J2	10	<b>4216q 10394c -13704t</b>	069 126 193 301 519	73 152 263 295
T	2	<b>4216q 4914r 13366m 15606a -15925i</b>	126 294 296 304 519	73 263
	2	<b>4216q 4914r -11824a -13259o 13366m -13704t 15606a -15925i</b>	126 294 519	73 194 200 263
T1	1	<b>4216q 4914r -12629b 13366m 15606a -15925i</b>	126 163 186 189 294 519	73 152 195 263
	1	<b>4216q 4914r -8838e -12629b 13366m 15606a -15925i</b>	126 163 186 189 261 294 519	73 152 195 263
	1	<b>4216q 4914r -12629b 13366m -13704t 15606a -15925i</b>	126 163 186 189 294 519	73 152 195 263
HV:				
H*	1	<b>-7025a -14766u</b>	169 184	73 263
	1	<b>-7025a -14766u</b>	169 184	73 152 263
	1	<b>-7025a -14766u</b>	169 184	125 127 263
	2	<b>-7025a -14766u</b>	169 184 311	73 263
H2	1	<b>4769a -7025a -14766u</b>	CRS	204
	2	<b>4769a -7025a -8858f -14766u</b>	CRS	204
H3	1	<b>-7025a -14766u</b>	093 172 189 519	263
	1	<b>-7025a -14766u</b>	189 356 519	263
	1	<b>-7025a -14766u</b>	189 311 356 519	263
	1	<b>-7025a -14766u</b>	189 356 519	73 263
	2	<b>-7025a 8249b -14766u</b>	080 189 356	263
V	1	<b>-4577q -14766u</b>	298	72 263
A	2	<b>663e</b>	039 189 223 290 319 356 362	73 152 235 263
	1	<b>663e</b>	223 227C 230 256 290 311 319	64 73 235 263
F	1	<b>4732k -12406b -12629b</b>	189 232A 249 304 311 519	73 204 248d 263
C	5	<b>10394c 10397a -13259o</b>	223 298 327 519	73 248d 263
	1	<b>10394c 10397a -13259o</b>	223 298 311 327 519	73 189 207 248d 263
	1	<b>-1715c 10394c 10397a -13259o</b>	129 223 298 327 519	73 195 248d 263
	1	<b>-1715c 10394c 10397a -13259o</b>	093 129 223 298 327 519	73 248d 263
	1	<b>10394c 10397a -13259o</b>	086 171 223 298 327 344 357 519	73 248d 263
	3	<b>10394c 10397a -13259o 9bp-ins</b>	086 171 223 298 327 344 357 519	73 248d 263
	1	<b>-1715c 10394c 10397a -13259o</b>	114A 148 223 288 298 327 519	73 248d 263
	4	<b>10394c 10397a -13259o</b>	298 327 519	73 248d 263
D	1	<b>-5176a 10394c 10397a</b>	223 368	125 127 263
	1	<b>-5176a 10394c 10397a</b>	223 362 368	125 127 263
	1	<b>-5176a 10394c 10397a</b>	223 362 368	263
	2	<b>-5176a 10394c 10397a</b>	192 223 261 316 362	73 263
	1	<b>-5176a -5823a 10394c 10397a</b>	223 291 294 362 519	73 152 263
	1	<b>-5176a -10180l 10394c 10397a -15925i</b>	223 319 362	73 239 263 297
	1	<b>-5176a -8838e 12026h (10397 10398 10400 12705)</b>	126 136 189 223 360 362	73 263
G	6	<b>4830n -7598f 10394c 10397a</b>	086 172 223 227 278 362	73 263
M*	1	<b>4164q 5351f 10394c 10397a (12705)</b>	129 189 223 297 298	73 150 199 263

NOTE.—Founding mtDNA types are shown in boldface italic. CRS = Cambridge reference sequence; d = deletion. Mutations relative to CRS [Andrews et al. 1999] are transitions unless the base change is specified.

<sup>a</sup> Comprising 98 subjects overall.

<sup>b</sup> The restriction enzymes are designated by the following single-letter codes appended to nucleotide positions: a = *AluI*; b = *AvaII*; c = *DdeI*; e = *HaeIII*; f = *HbaI*; g = *HinfI*; h = *HpaI*; i = *HpaII*; j = *MboI*; k = *RsaI*; l = *TaqI*; m = *BamHI*; n = *HaeII*; o = *HincII*; q = *NlaIII*; r = *BfaI*; s = *AccI*; t = *BstNI*; u = *MseI*. Underlining of the restriction site implies the simultaneous presence/absence of the linked site that is correlated with a single-nucleotide substitution. 9bp-ins = 9-bp COII/tRNA<sup>Lys</sup> triplication. Additional mutations in the coding region are shown in parentheses and were identified or confirmed by sequencing.

**Table 2****Frequencies (%) of mtDNA Types in the Mansi in Comparison with the Saami and Finns**

HAPLOGROUP	MANSI			SAAMI (N = 176)	FINNS (N = 403)
	Konda River (N = 59)	Northern Sos'va River/ Lyamin River Basin (N = 39)	Total (N = 98)		
U	...	...	...	...	2.5
U2	...	...	...	...	.5
U4	13.6	20.5	16.3	...	.5
U5a	1.7	2.6	2.0	.6	3.2
U5a1	3.4	...	2.0	.6	3.7
U5b	...	...	...	1.7	7.4
U5b1	...	...	...	42.6	8.7
U7	5.1	5.1	5.1	...	.5
U8	...	...	...	...	.7
K	5.1	...	3.1	...	2.5
K2	...	...	...	...	.5
JT:					
J	...	...	...	...	3.0
J1a	...	...	...	...	.5
J1b1	...	5.1	2.0	...	.5
J2	10.2	10.3	10.2	...	.5
T	6.8	...	4.1	...	1.5
T1	...	7.7	3.1	...	.1
H*	3.4	7.7	5.1	...	...
H	...	...	...	1.7	13.1
H1	...	...	...	1.1	2.0
H2	3.4	2.6	3.1	...	10.4
H3	8.5	2.6	6.1	...	7.7
H4	...	...	...	...	2.5
H8	...	...	...	2.8	4.5
V	1.7	...	1.0	39.8	5.5
A	5.1	...	3.1	...	...
F	1.7	...	1.0	...	...
C	15.2	20.5	17.3	...	...
Z	...	...	...	3.4	...
D	6.8	10.3	8.2	5.1	...
G	6.8	5.1	6.1	...	...
M*	1.7	...	1.0	...	...
M	...	...	...	...	2.5
W	...	...	...	.6	9.2
I	...	...	...	...	3.5
X	...	...	...	...	1.0
Other	...	...	...	...	.3

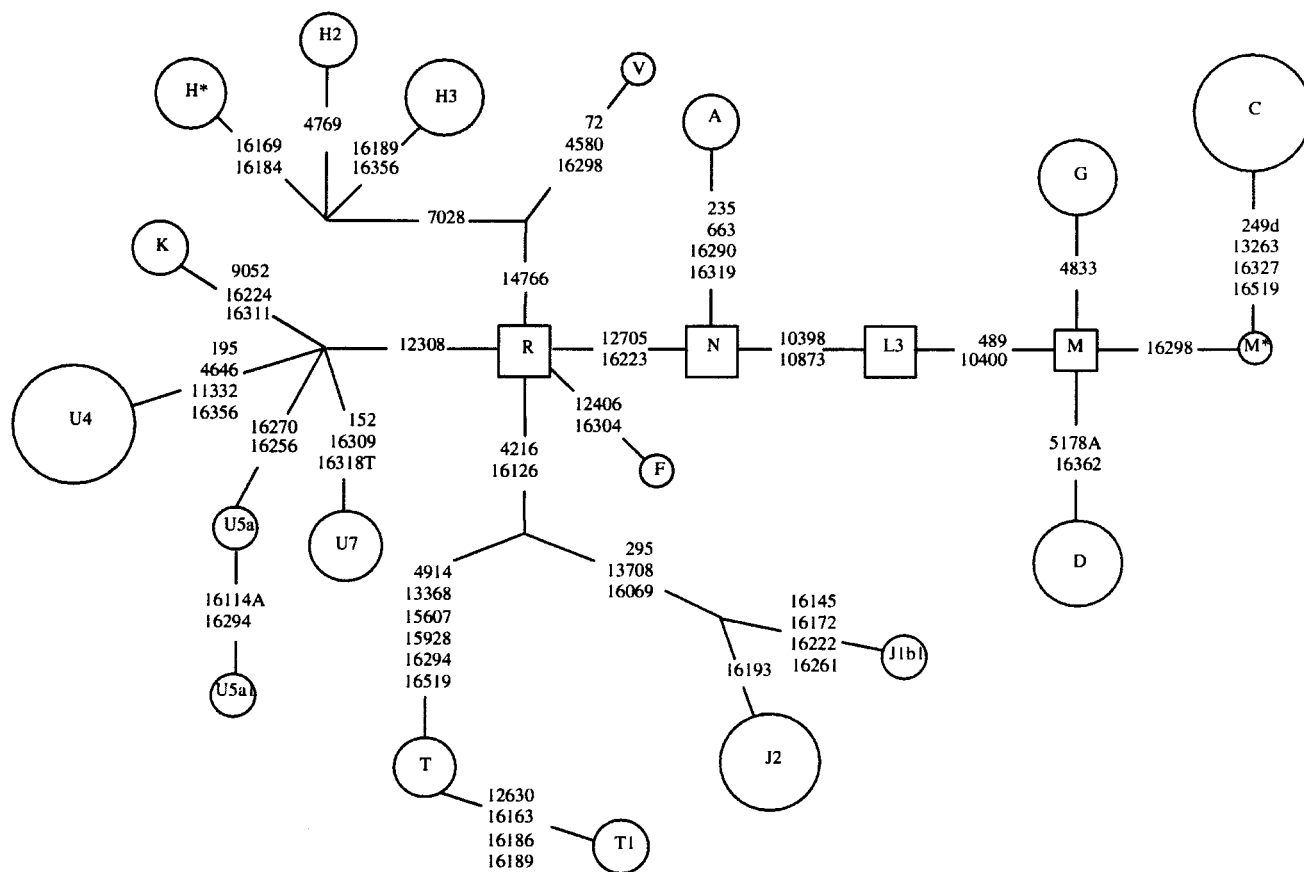
NOTE.—Data for Saami and Finns are from Helgason et al. (2001) and Meinila et al. (2001).

(i.e., M\*) haplogroup were found in the Mansi. These may also be due to recent gene flow.

Thus, this study revealed that the Mansi possess a unique combination of western European and eastern Siberian mtDNA lineages. The novel distribution and subtypes of haplogroup U make it unlikely that this is the result of recent gene flow from modern Europeans. Rather, the Mansi mtDNA pool may contain traces of the ancient proto-Eurasian hunting-gathering populations that originally colonized the trans-Ural region and adjacent part of Siberia. In this regard, the most distinctive feature of the Mansi mtDNA samples is the high frequency (16.3%) of subhaplogroup U4. Neither U4

nor U5 subhaplogroups are common in the Middle East (Macaulay et al. 1999), and subhaplogroup U4 attains its highest frequency (28.9%) in the Ket of the Yenisey River (authors' unpublished data). Hence, subhaplogroup U4 may be indicative of the remnants of Upper Paleolithic populations of Europeans preserved just east of the Ural Mountains.

The presence of subhaplogroup U7 in the Mansi supports the conjecture of its proto-Eurasian origin ~24,000–54,000 years ago (Richards et al. 2000). Subhaplogroup U7 is virtually absent from modern Europeans and is absent or extremely rare in western Uralic-speaking populations, such as the Finns and Saami



**Figure 2** Schematic phylogenetic representation of mtDNA lineages found in the Mansi. The sizes of the circles, which denote lineages, are proportional to the number of sampled individuals. Mutations are transitions unless otherwise specified. Squares denote the phylogenetic position of the roots of the nested haplogroups R, N, L3, and M (Macaulay et al. 1999; Quintana-Murci et al. 1999)

(Helgason et al. 2001; Meinila et al. 2001). However, subhaplogroup U7 is present in the Middle East, although in very low frequencies (Richards et al. 2000). Thus, in the Mansi, subhaplogroup U7 could be a part of Paleolithic dispersals from the Middle East, whose traces have not been erased by subsequent migrations. This conjecture is supported by the presence in the Mansi of subhaplogroup J2, which may indicate a Neolithic phase expansion toward the Ural Mountains.

Although the core of genetic makeup of the Mansi consisted of mtDNA types that apparently were ancient European, 29% of the Mansi mtDNA samples are from three of the four haplogroups that define the migration from Siberia to the Americas (i.e., haplogroups A, C, and D). Such a novel genetic structure could represent the recent amalgamation of western and eastern populations. Alternatively, the Mansi may reflect a more ancient and uniform distribution of mtDNA lineages that subsequently became more specialized as a result of later genetic drift or environmental selection. Whichever

event proves to be the case, it is clear that further surveys of trans-Ural and Siberian mtDNA will yield much information about the genetic history of northern Eurasia and the origins of Uralic-speaking populations.

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