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HUMAN GENETICS

Comparative Characteristics of the Gene Pool of Teleuts Inferred from Y-Chromosomal Marker Data

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Abstract—The gene pool structure of Teleuts was examined and Y-chromosomal haplogroups composition and frequencies were determined. In the gene pool of Teleuts, five haplogroups, C3xM77, N3a, R1b*, R1b3, and R1a1, were identified. Evaluation of the genetic differentiation of the samples examined using analysis of molecular variance (AMOVA) with two marker systems (frequencies of haplogroups and Y-chromosomal microsatellite haplotypes) showed that Bachat Teleuts were equally distant from Southern and Northern Altaians. In Siberian populations, the frequencies and molecular phylogeny of the YSTR haplotypes within Y-chromosomal haplogroup R1a1 were examined. It was demonstrated that Teleuts and Southern Altaians had very close and overlapping profiles of R1a1 haplotypes. Population cluster analysis of the R1a1 YSTR haplotypes showed that Teleuts and Southern Altaians were closer to one another than to all remaining Siberian ethnic groups. Phylogenetic analysis of N3a haplotypes suggested specificity of Teleut haplotypes and their closeness to those of Tomsk Tatars. Teleuts were characterized by extremely high frequency of haplogroup R1b*, distinguished for highly specific profile of YSTR haplotypes and high haplotype diversity. The results of the comparative analysis suggested that the gene pool of Bachat Teleuts was formed on the basis of at least two heterogeneous genetic components, probably associated with ancient Turkic and Samoyedic ethnic components.

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INTRODUCTION

Analysis of human population gene pool structures with the help of marker systems having different natures and characterized by different mechanisms of transmission between the generations is considered to be an effective tool for investigation of basic and applied issues of human genetics. As a rule, large ethnic groups appear to be studied in more details, while small indigenous populations remain rather poorly investigated with the use of modern DNA markers. This situation can be explained by lower medical and applied significance of the latter studies along with more problems in collection of the experimental material. The territory of Siberia is inhabited by a number of small indigenous population groups, including Teleuts. The ancestors of Teleuts are the tribes of the Tele group. In the epoch of ancient Turks, these tribes were settled across the territory of Central Asia, and the ethnic name of Teleuts originates from these groups. According to the ideas of L. P. Potapov, Teleuts played the key role in the ethnogeny of all Altaic groups, both Northern and Southern [1, 2]. In Russian historical sources Teleuts are mentioned under the name of White Kalmyks. In the 17th century, Teleuts were represented by a large Ulus community of nomads from Upper Ob River, which played an important role on the political scene of Southern Siberia. According to classification of Turkic languages, Teleut language is treated as an independent language. Alternatively, it is distinguished as one of southern dialects of the Altaic language, belonging to South–Siberian (east–Turkic) subgroup of the Turkic group of Altaic linguistic family. Until recently, Teleuts, as well as Telenghits, Teleses, Altai-Kizhi, and Maimalars were attributed to Southern Altaians. However, at present, Teleuts are treated by ethnographers as an independent ethnic group. At the same time, linguistic, cultural and ethnic closeness of Teleuts and Southern Altaians raises no doubts.

At present, the total number of Teleuts is 25 people. They mostly live in Kemerovo oblast, as well as in Shebalinskii raion of the Altai Republic, Chumyshskii raion of the Altai Krai, and in Novosibirsk oblast. Teleuts are predominantly rural people: almost 2000 of them live in the settlements of Bekovo, Chelukhoevo, Verkhovskaya, Shanda, Novo-Bachaty, and some others, on the territory of Belovskii raion, Kemerovo oblast. Based on the main distribution of Teleut uluses on the shores of Bol'shoi and Malyi Bachat rivers of the Ob River basin, in the branches of the Kuznetskii Alatau highlands, this group is called as "Bachat Teleuts" [3, 4].

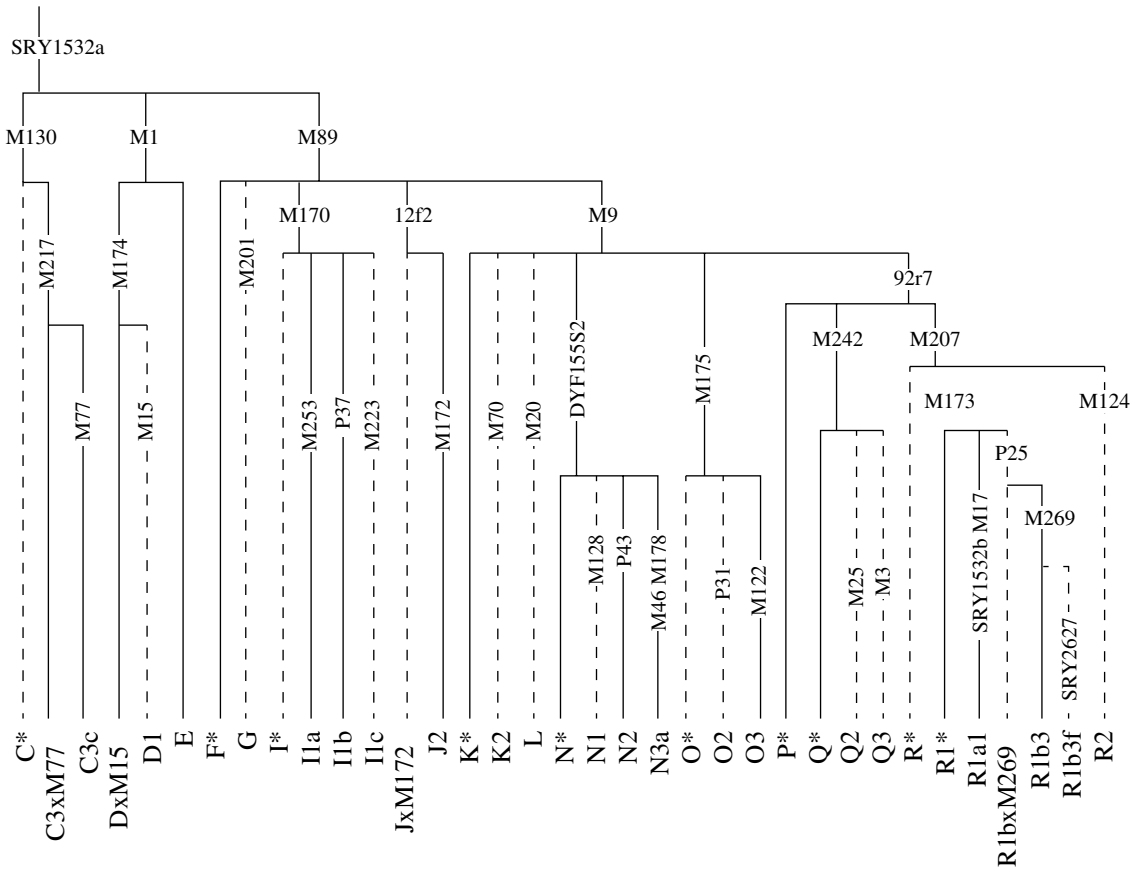

Fig. 1. Phylogenetic tree of Y-chromosomal haplogroups used in the study.

Recent studies of the Bachat Teleut demographic structure revealed current negative dynamics, i.e., increasing disproportion in the sex ratio, age structure close to regressive type, the mortality exceeding the birth rate, the absence of simple generation substitution, and shifts in generations overlapping. As a result of these negative demographic processes, depopulation of Teleut ethnos takes place. Furthermore, the population of Bachat Teleuts is characterized by intermarriage, predominantly with Russians [5].

The present study was focused on comparative characteristic of the gene pool structures of Teleuts, Southern Altaians, and other indigenous populations of Southern Siberia using two marker systems from nonrecombining part of Y- chromosome. This work is a continuation of earlier started project devoted to the investigation of Y-chromosomal gene pool of the indigenous population of Siberia.

MATERIALS AND METHODS

Total DNA for the analysis was isolated from peripheral blood lymphocytes using standard methods [6]. A population sample of Bachat Teleuts comprising 35 individuals was examined. The sample was formed from the inhabitants of the settlement of Belovo and the settlements of the Belovskii raion, Kemerovo oblast, Bekovo, Chelukhoevo, Verkhovskaya, Shanda, Novo-Bachaty, and some others.

In this study, Y-chromosomal haplogroup composition and structure was examined using two systems of genetic markers, biallelic loci, mostly represented by SNP, and microsatellites (YSTR). Nomenclature of haplogroups, determined based on genotyping of biallelic markers, is given in accordance with that of the Y-Chromosome Consortium [7]. Individual STR haplotype of each sample was determined through genotyping of the set of microsatellite markers.

Biallelic markers. Identification of haplogroups, composing the gene pool of Teleuts, was performed using a set of 37 biallelic loci from nonrecombining part of Y-chromosome: *SRY1532, YAP (M1), 92R7, DYF155S2, 12f2, M3 (DYS199), M9, M15, M17, M20, M25, M46 (Tat), M70, M77, M89, M122, M124, M128,M130 (RPS4Y), M170, M172, M173, M174, M175, M178, M201, M207, M217, M223, M242, M253, M269, SRY2627, P25, P31, P37*, and *P43* (Fig. 1). Genotyping was carried out using polymerase chain reaction, followed by the analysis of DNA fragment with the help of different methods, as described earlier [8–10]. Most of the primer sequences, except for

Table 1. Distribution of Y-chromosomal haplogroups among Southern Altaians and Teleuts

Haplogroup	Frequency, % (*N*)	
	Teleuts (*N* = 35)	Southern Altaians (*N* = 96)
C3xM77	5.71 (2)	2.08 (2)
C3c	–	1.04 (1)
DxM15	–	6.25 (6)
E	–	1.04 (1)
F*	–	4.17 (4)
I1a	–	1.04 (1)
I1b	–	1.04 (1)
J2	–	4.17 (4)
K*	–	1.04 (1)
N*	–	5.21 (5)
N2	–	4.17 (4)
N3a	28.57 (10)	2.08 (2)
O3	–	7.29 (7)
P*	–	1.04 (1)
Q*	–	4.17 (4)
R1b*	31.43 (11)	–
R1a1	31.43 (11)	53.12 (51)
R1b3	2.86 (1)	1.04 (1)
H	0.7378 ± 0.0306	0.6941 ± 0.0518
H YSTR	0.9311 ± 0.0252	0.9554 ± 0.0123

Note: *H*, gene diversity over the haplogroups; *H* YSTR, gene diversity over microsatellite haplogroups.

specially mentioned changed variants, were described in the work on haplogroup nomenclature system [7].

Microsatellite markers. Analysis of STR haplotypes was carried out using seven microsatellite markers from nonrecombining part of Y-chromosome (*DYS3891, DYS389II, DYS390, DYS391, DYS392, DYS393*, and *DYS394* (*DYS19*)). Fluorescent-labeled primers (HEX, FAM, and TET dyes used) were produced at Perkin-Elmer Oligo Factory (Weiterstadt, Germany). Genotyping of microsatellite markers was performed as described earlier [11, 12]. Conformity of the DNA fragment sizes of the loci examined with the numbers of tandem repeats represented was confirmed by sequencing of PCR products of all STR markers in some of the samples examined. Sequencing was performed from reverse primers, which were not fluorescence labeled. Allele nomenclature agrees with the generally accepted (for DYS389) without scoring the three-copy number TCTG repeat [13, 14].

Statistical methods. Genetic relationships among the populations were analyze using factor analysis and multidimensional scaling. Factor analysis was conducted using the method of principal components, and the rotation varimax normalized was applied [15]. Graph construction and analysis were conducted using STATISTICA 6.0 (StatSoft, United States) software package. In the populations examined, genetic diversity equivalent to the expected heterozygosity for diploid data was valuated using the formula suggested by Nei [16]. Population genetic differentiation was estimated using analysis of molecular variance (AMOVA) [17]. Using the F_{st} coefficient, 10000 permutations of the initial data was performed. Statistical significance of interpopulation differences at the haplogroup and YSTR haplotype frequencies was evaluating using the exact test for population differentiation (the number of Markov chain steps was equal to 10000, the number of steps, not taken into consideration was 1000, the significance level was equal to 0.05). The matrices of Slatkin's pairwise distances (F_{st}) were calculated using 100 permutations of the initial data. The calculations were performed in the ARLEQUIN 2.000 software package (http:anthro.unige.ch/arlequin) [18]. Median networks of Y-chromosomal haplotypes were constructed in the Network v. 4.2.0.1 software program (Fluxus Technology) (www.fluxus-engineering.com), using the median network method of Bandelt with sequential use of the RM (reduced median) and MJ (median-joining) algorithms [19, 20] (the ε parameter was taken as equal to 0). To consider the differences in mutation rates upon the networks constructions, each STR locus was given a weight, proportional to its variability within the haplogroups examined (DYS19 : DYS389I : DYS389II DYS390 : DYS391 : DYS392 : DYS393 = 5 : 2 : 5 : 2 : 2 : 10 : 10). Population phylogenetic trees were constructed using neighbor-joining algorithm [21] in the PHYLIP software package [22].

RESULTS AND DISCUSSION

Frequencies of Y-Chromosomal Haplogroups in Teleuts

Analysis of the allele distributions of the biallelic markers chosen in 35 individuals presenting the sample of Bachat Teleuts revealed the presence of five haplogroups: C3xM77, N3a, R1b*, R1a1, and R1b3 (Table 1). The gene pool structure of Teleuts was found to be remarkably different from the earlier examined gene pool of Southern Altaians [10]. First, Teleuts lack most of rare haplogroups (C3c, E, I1a, I1b, K*, and P*), found in Southern Altaians, as well as some rather frequent lineages (J2, N*, N2, O3, and Q*). These findings can be explained by rather small Teleut sample size examined. Second, in Teleuts the frequency of haplogroup N3a reaches almost 30%, while in Southern Altaians only sporadic chromosomes belong to this haplogroup. Third, in Teleuts haplogroup R1b* is found with the frequency similar to that of the R1a1 lineage. At the same time, earlier analysis of three population samples of Southern Altaians showed the absence of R1b* in this population. The similarity of two ethinc groups compared lies in the fact that four haplogroups of Teleuts (except R1b*) are shared by Southern Altaians. Moreover, haplogroups

C3xM77 and R1b3 are found in the latter ethnic group with similarly low frequencies. The most frequent Y-chromosome variant in both groups is haplogroup R1a1. However, in Teleuts its frequency is about 20% lower than in Southern Altaians. In the latter group the frequency of haplogroup R1a1 constitutes more than 53%. The next frequent lineage (O3) is nearly seven times more rare. At the same time, in Teleuts three lineages (N3a, R1b*, and R1a1) are detected with almost equal frequencies (about 30%). As a result, genetic diversity of Teleuts relative to haplogroups is higher than that in Southern Altaians. On the contrary, the index of genetic diversity relative to microsatellite haplotypes is somewhat higher in Southern Altaians (Table 1).

Genetic Relationships Among the Populations

Pooled genotyping data for Teleuts and six samples of Altaians examined earlier [10] were analyzed by factor analysis with the help of the method of principal components. It was demonstrated that the Teleut sample examined was almost equally distant from Southern and Northern Altaians, albeit not occupying the intermediate position between these samples (Fig. 2). Individual samples of Southern (the settlement of Beshpel'tir and the settlement of Kulada) and Northern (the city of Gorno-Altaisk and the settlement of Turochak) Altaians appeared to be more close to one another than to Teleuts. The first PC, explaining 62.81% of data variability most effectively differentiated the samples of Teleuts and Southern Altaians. Multidimensional scaling of Slatkin's F_{st} distance matrices over the YSTR haplotype frequencies revealed rather similar pattern of relationships between the ethnic groups. The plot obtained only brought close one of Southern Altaian sample to Teleuts. Thus, the data obtained disagree with the ethnographic and linguistic data on the closeness of Teleuts to Southern Altaians.

Genetic Differentiation of the Populations

Genetic differentiation of the population samples was evaluated using analysis of molecular variance (AMOVA) [17], which was performed with two marker systems. Specifically, the level of differentiation was evaluated at the haplogroup frequencies (Table 1), as well as at the YSTR haplotypes of Y-chromosome (Table 2). Analysis of the population genetic structure includes computation of the proportions of variance on account of the differences within and among the groups at different hierarchical levels. Computations were performed using the genotyping data for Northern and Southern Altaians described earlier [10]. In case that the samples tested were distributed into three groups, of Northern Altaians, Southern Altaians, and Teleuts, analysis of haplogroup and YSTR haplotype frequencies identified the proportion intergroup differences equal to 8.11 and 9.92%, respectively. The differences between the populations within the groups of Altaians

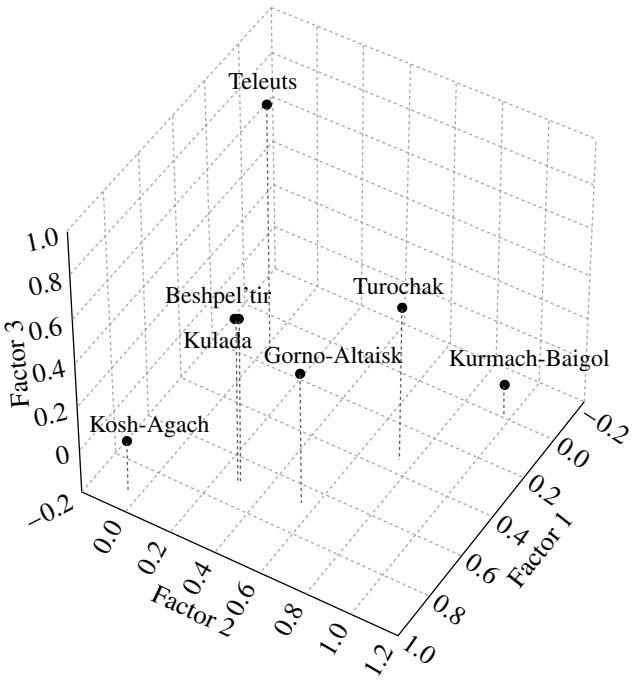

Fig. 2. Positions of Teleut and Altaian populations in the space of three principal components in terms of Y-chromosomal haplogroup frequencies.

accounted for 3.53 and 2.82% of variation. The proportion of total intrapopulation variation constituted 88.37 and 87.26%, respectively. It should be noted that until recently, Teleuts were attributed to the group of Southern Altaians. On the other hand, substantial differentiation between Northern and Southern Altaians was established long ago. At the same time, the values of intergroup (interethnic) differentiation for the three groups chosen were slightly higher than the values obtained upon comparison of only Northern and Southern Altaians (5.02%, for haplogroups, and 8.97% for YSTR haplotypes) [10]. Then, analogous calculations were performed, comparing of only Southern Altaians and Teleuts. The proportion of interpopulation differences relative to haplogroups was somewhat higher (11.85%), while the value of this index relative to haplotypes was slightly lower (8.82%), and the proportion of intrapopulation variation constituted 86.78 and 88.7%, respectively. Thus, analysis of the gene pool structure at the level of haplogroups showed that Teleuts were more different from Southern Altaians (two fold higher F_{st} values), than Southern Altaians from Northern Altaians. Analysis of molecular variance of Y-chromosomal microsatellite haplotypes showed nearly equal differentiation between these three groups.

Phylogenetic Analysis of Haplogroup R1a1 in Teleuts

Phylogenetic analysis of haplogroup R1a1 with the use of seven YSTR markers allowed establishment of its detailed structure via construction of the haplotype

Table 2. Distribution of YSTR haplotypes among Teleuts

Haplotype	DYS 19	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	Haplogroup	*N*
1	15	10	15	23	10	11	14	C3xM77	2
2	14	10	18	23	10	14	14	N3a	7
3	14	10	17	23	10	14	14	N3a	1
4	14	11	16	23	10	14	13	N3a	1
5	15	11	16	23	11	14	14	N3a	1
6	14	10	17	22	11	13	13	R1b*	4
7	15	10	17	22	11	13	13	R1b*	3
8	14	10	17	22	11	14	13	R1b*	1
9	15	10	17	22	12	14	13	R1b*	1
10	15	11	17	22	11	13	13	R1b*	1
11	16	10	17	23	11	13	13	R1b*	1
12	16	11	17	25	11	11	13	R1a1	5
13	16	11	18	24	11	11	13	R1a1	1
14	16	12	17	24	11	11	13	R1a1	1
15	16	12	17	25	11	11	13	R1a1	1
16	17	11	17	26	11	11	13	R1a1	1
17	17	11	18	25	11	11	13	R1a1	1
18	18	12	17	25	11	11	13	R1a1	1
19	14	10	17	24	11	13	12	R1b3	1

tree with the help of the method of median networks (Fig. 1). The computations were performed using personal data (56 samples of Southern Altaians and 14 samples of Northern Altaians [10]), as well as the literature data available on YSTR haplotypes of haplogroup R1a1 (21 Teleuts and 35 Southern Altaians [23]). The data were adjusted to unify designation of haplotypes at the *DYS389* locus. Genotypes for additional YSTR markers (other than seven markers genotyped for the purposes of present investigation) were not included into the analysis. The circle sizes (tree nods) correspond to the number of identified samples belonging to a certain haplotype. The branch length between the nodes corresponds to the number of mutational steps between the haplotypes. The names of the mutated loci are shown along the branches. The nod color corresponds to the ethnicity of the individuals comprising the sample.

In Teleuts, a total of 15 haplotypes were identified, and ten of these were shared with Southern Altaians, differing only in haplotype frequencies. This finding points to similarity of internal haplotype structure of haplogroup R1aq1 in these two ethnic groups. Two haplotypes were also shared with Northern Altaians, and one haplotype, exclusively with Northern Altaians. The most frequent haplotype of Teleuts (11 out of 33 samples) is one mutational step apart from that in Southern Altaians, and is the third most frequent haplotype in the latter group. The most frequent in Southern Altaians founder haplotype is the second most frequent in Teleuts.

To perform a comparative analysis of the genetic relationships between Siberian populations carrying haplogroup R1a1 in their gene pools, a data base was constructed. This database contained information on the haplotype frequencies and structure in Siberian populations, which in addition to the populations mentioned also included the literature data on this haplogroup (22 Shors, 18 Khakassians, 15 Tuvinians, 7 Sojots, and 7 Evenks [23]), as well as personal unpublished data on other populations (46 Tuvinians, 16 Khanty, 15 Tomsk Tatars, and 5 Evenks). Base on the R1a1 haplotype distributions among different populations, using ARLEQUIN 2000 software program, a matrix of genetic distances was constructed (Slatkin's F_{st}). Based on this matrix, population genetic tree was constructed with the help of the NEIGHBOR software program (Fig. 4). Two different Teleut samples were close to one another, and so were two samples of Southern Altaians, who formed one cluster with Teleuts. On the plot, Teleuts and Southern Altaians were closer to one another than all other populations to them, and between each other. This noteworthy finding once again points to very close genetic relatedness of the most frequent gene pool components of these two ethnic groups, marked by haplogroup R1a1.

These results explain the substantial differences in the estimates of genetic differentiation of Teleuts and Southern Altaians respective to the frequencies of haplogroups and YSTR haplotypes. In these ethnic groups, the haplogroup compositions and ratio display remark-

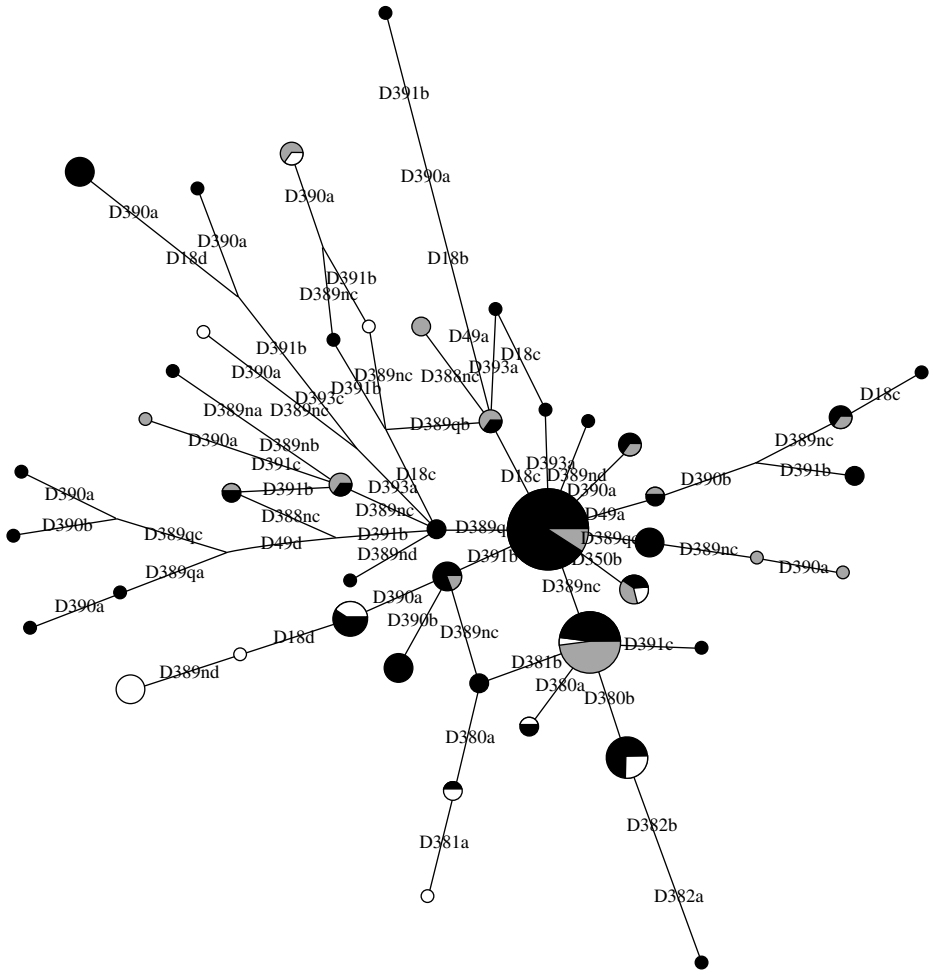

Fig. 3. Median network of the R1a1 YSTR haplotypes in Teleuts and Altaians. The circle sizes (tree nods) correspond to the number of identified samples belonging to a certain haplotype. The nod color corresponds to the ethnicity of the individuals comprising the sample. Teleuts are designated by gray color; Southern Alatians are designated by black color, and Northern Altaians, by white color.

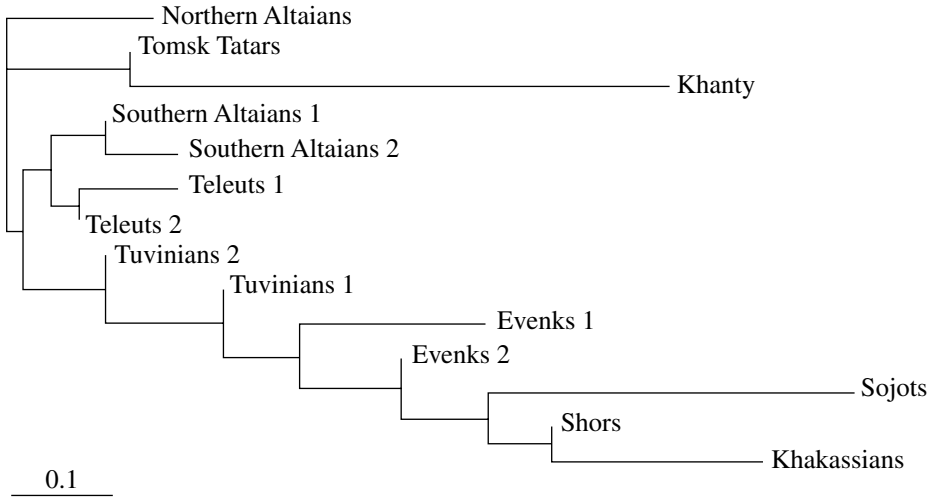

Fig.4. Dendrogram of genetic relationships between different Siberian ethnic groups based on genetic distances for YSTR haplotypes of haplogroup R1a1.

able differences, while internal molecular structure of the most frequent lineage is rather similar.

Phylogenetic Analysis of Haplogroups R1b and N3a in Teleuts*

Although Teleuts and Southern Altaians are as close to one another, as no one else among Siberian ethnic groups, in terms of R1a1 structure, the results of factor analysis, AMOVA, and multidimensional scaling revealed substantial differences between these two groups upon the analysis of the whole Y-chromosomal pool. From here it follows that relative to the two other main haplogroups of Teleuts (R1b* and N3a), substantial haplotype diversity should be expected. For haplogroup R1b* no interethnic matches were found, since this haplogroup was not identified in the samples of Southern Altaians. The finding that R1b* constituted more than 30% in the gene pool of Teleuts was surprising. This haplogroup is absent from Northern Altaians. Furthermore, our data for other ethnic groups, along with the literature data indicated that the frequency of R1b* varied from 2 to 3% in all populations examined, and it was absent in most of the populations studied so far. This lineage is usually identified upon analysis of the large samples consisting of hundreds individual specimens. Unfortunately, until recently, cogenotyping of the P25 and M269 Y-chromosomal markers was not performed, and from ample literature data the presence of relatively high frequencies of R1b* in some populations cannot be excluded. However, it is evident that Bachat Teleuts are currently characterized by the world peak frequency of haplogroup R1b*. This finding is supported by tribal composition of Teleuts. Specifically, the carriers of this haplogroup are the individuals belonging to Ashkyshtyms, who are treated by Potapov as Teleuts by descent [2].

Haplogroup R1b* first attracts attention as it is ancestral to R1b3 lineage, which is widely distributed in Europe, especially in Western Europe, where it is a major components of male gene pools of different populations. It is suggested that settlement of the R1b3 carriers and the formation of current distribution range of the haplogroup of interest was associated with mostly eastward re-colonization of Europe following the last glacial maximum from the Iberian refugium. The time and place of origin of haplogroup R1b* is still doubtful. It is suggested that the haplogroup arose on the territory of Europe and penetrated Southern Siberia with some early migrations across Eurasian steppes. Alternatively, the haplogroup could arise in Central Asia and serves as the link between the Q and R clades.

After genotyping of biallelic markers and attribution of the specimens in the sample of Bachat Teleuts to different haplogroups, it was suggested that the high frequency of R1b* lineage could be explained by a recent founder effect. As a consequence, haplotype diversity within this group was expected to be low. However, YSTR markers showed that 11 specimens attributed to R1b* belonged to six different haplotypes. A median network for R1b* haplotypes was constructed similarly to that for R1a1, using genotyping data available, which included personal (10 Tuvianians, one Tomsk Tatar, and one Kyrghyz) and literature (seven Hazaras, six Turks, four Nakhi, three Uigurs, one Mongol, one Japanese, and one Chinese [24, 25]) data. The tree constructed (Fig. 5) showed that Teleuts were characterized by very specific haplotype profiles. Moreover, these haplotypes were located close to the network center, being probably close to the founder haplotype of this haplogroup. The Teleut haplotypes do not form the starlike phylogeny with the prevalence of a single haplotype. On the contrary, the distance between extreme variants constitute seven mutational steps. Obviously, high frequency of haplogroup R1b* in Bachat Teleuts is not the consequence of the gene drift. To maintain such high level of haplotype diversity, the population should be characterized by substantial effective population size along with the high proportion of the R1b* carriers during several hundred years. The remaining ethnic groups formed the peripheral parts of median network. The closest to Teleut haplotypes are those of Hazaras from Pakistan. Hazaras represent the ethnic group of Mongoloid origin, which was formed rather recently as a result of Mongol conquests. Hazaras consider themselves to be direct descendants of Mongols, and even Chingisides. Identification of the world maximum of the presumptive haplotype of Chingis Khan and its direct male-line descendants (belonging to haplogroup C3xM48) in this population confirms this proposal [26]. Interestingly, Tuvinians, who are most geographically close to Teleuts, are characterized by absolutely different R1b* haplotype profile with the prevalence of one haplotype, found in six out of ten samples tested. It can be thus suggested that haplogroup R1b* has Central Asian origin.

Similar calculations performed for haplogroup N3a revealed completely different situation. Teleuts demonstrated the presence of only four haplotypes, one of which accounted for seven out of ten samples examined (haplotype 2, Table 2). One more haplotype stood aside from the first one by a single mutational step. The two haplotypes mentioned were unique and were not detected in other ethnic groups. These data suggest a founder effect in recent genetic history of the Bachat Teleut population. Indeed, Bachat Teleuts are mostly represented by the members of the *Merkit* tribe, which is second most frequent (10.9%) in Teleuts. On the other hand, in Altaians the members of this tribe account for only 0.16% of the population [5]. The two remaining Teleut haplotypes were also detected in Buryats and Tuvinians. Two haplotypes of Southern and two haplotypes of Northern Altaians were distant from Teleut haplotypes. Two Teleut-specific haplotypes were closest to the three haplotypes identified in Tomsk Tatars.

Phylogenetic cluster analysis of Slatkin's F_{st} distance matrix for the N3a YSTR haplotype frequencies revealed a remarkable difference of Teleuts from the

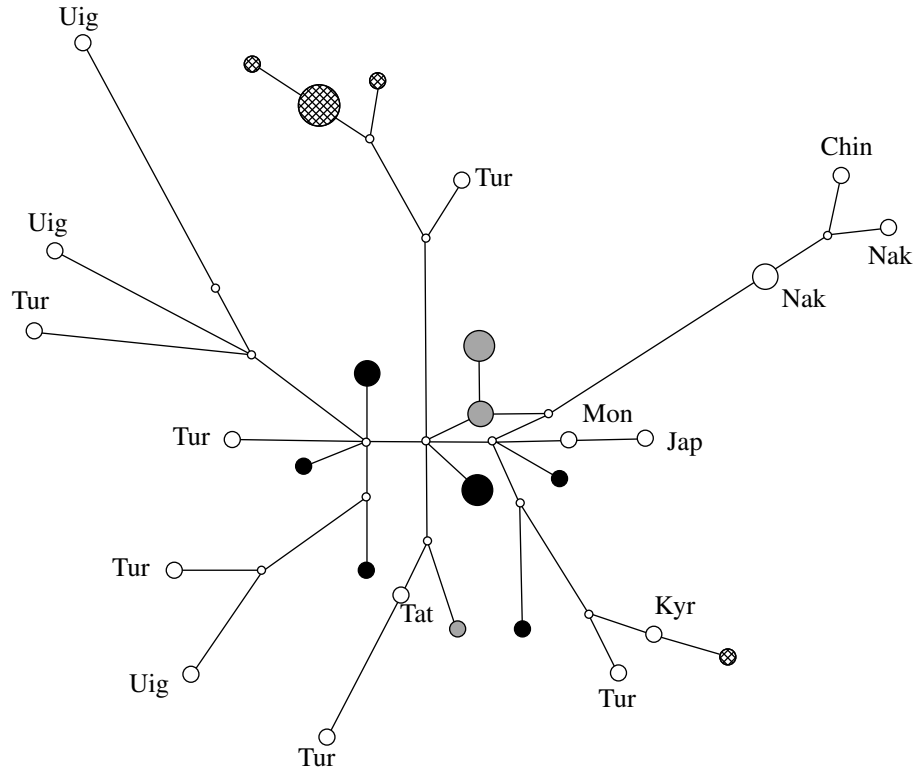

Fig. 5. Median network of the R1b* YSTR haplotypes. The sizes of the network nodes correspond to the number of identified samples belonging to a certain haplotype. Teleuts are designated by black color, and Hazaras, by gray color. Tuvinians are hatched. Tur, Turks; Uig, Uigurs; Nak, Nakhi; Mon, Mongol; Tat, Tatar; Kyr, Kyrghyz; Jap, Japanese; and Chin, Chinese [24, 25].

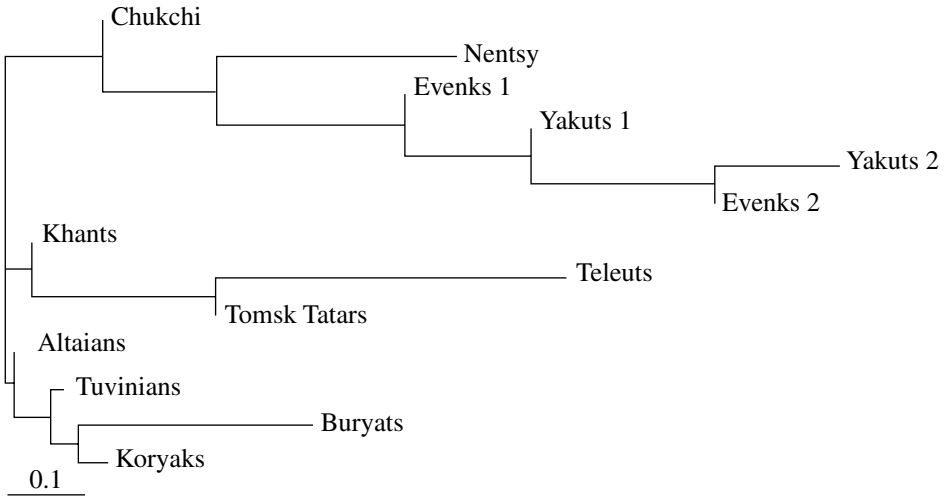

Fig. 6. Dendrogram of genetic relationships between different Siberian ethnic groups based on genetic distances for YSTR haplotypes of haplogroup N3a.

other Siberian ethnic groups along with their closeness to Tomsk Tatars, with which they formed a single cluster. Haplotypes of Altaians and Tuvinians formed another population cluster, and they were closer to the haplotypes of Khanty and Tomsk Tatars, than to those of Teleuts (Fig. 6).

The closeness of Teleuts to Tomsk Tatars in terms of one of the haplogroups was not surprising. It is known that in addition to Eushtas and Chats, the so-called Tomsk Teleuts (Kalmakas) were among the main components participated in the formation of Teleuts. Tomsk Teleuts constituted one Teleut volost of Tomsk okrug.

The settlements were located to the south from Tomsk, along the Iskitim River, the left tributary of Tom' River. In 1897, the population of the settlements constituted 713 persons. On the other hand, an important component of the formation of Teleuts from Kemerovo oblast was represented by different local Turkic-speaking ethnic groups. They were related to the groups living in the Middle and Tomsk Ob region, and inhabited these territories long before the arrival of Teleuts from Dzungaria and Altai. There are the data that Ashkyshtyms, one of these Turkic groups, were one of the main components of ethnogeny of Bachat Teleuts [27].

In general, the results of the present study suggest that the gene pool of Bachat Teleuts was formed based on at least two heterogeneous genetic components. The first component, marked by haplogroup R1a1, brings Teleuts very close to Southern Altaians. Being one of most typical to Southern Siberian Turks, this genetic component is thought to be present in Y-chromosomal gene pool of the ancestors of Teleuts for a long time. This component can be conditionally designated as ancient Turkic. It seems likely, that the second component, associated with haplogroup N3a, reflects the contribution of local ethnic groups. This component is thought to be rather recently acquired by Teleuts. It is suggested that in the gene pools of the local ethnic groups mentioned the appearance of the genetic component of interest was associated with fact that early Turkic migrants assimilated even more ancient Samoyedic and possibly Ugric groups. The situation with extremely high frequency of haplogroup R1b* is less clear. It can be suggested that this haplogroup (along with R1a1) was initially present in the gene pool of ancient Turks and Teleuts. Southern Altaians lost this haplogroup as a result of genetic drift. Alternatively, R1b*, similarly to N3a, was acquired by Teleuts rather recently. In our view, the first scenario seems more probable.

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