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Announcement of Population Data

Allelic and haplotypic frequencies at 11 Y-STR loci in Buryats from South-East Siberia

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Abstract

We have obtained Y-STR haplotypes in 12 loci (DYS19, DYS385, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439) from 215 Buryat males. We have found that one haplotype (15-11,18-13-28-23-10-11-14-14-10-12) comprises more than 30% of Y chromosomes in this population while another haplotype (14-11,13-14-30-23-10-14-14-14-10-10) comprises additional 14% of chromosomes. The population under study seems to be very homogenous as far as Y chromosome is regarded and the most frequent haplotype seems to be the modal haplotype for Buryats.

Keywords: Buryats; Y-STR; Y chromosome

Population: Buryat samples ($n = 215$) were collected in the villages of the Buryat Republic (Dzhida, Bichursk, Ivolga, Kyakhta, Tunka, Kizhinga, Khorinsk, Zakamensk, Eravna, Selenga, Barguzin and Kabansk districts), Chita (Aginsk district) and Irkutsk (Alarsk, Bayandaevsk, Bokhan, Nukutsk, Olkhon, Ust-Orda, Osa and Ekhirit-Balagansk districts) regions, thus encompassing all territories inhabited by modern Buryats (Fig. 1). Only a few samples were chosen from each locality, limiting the probability of sampling relatives. All of these individuals were paternally and maternally unrelated and originated from the area considered for this study. All samples were collected with approval of an appropriate ethical committee as well as with informed consent.

DNA extraction: The whole blood was obtained by venipuncture and collected into EDTA vacutainer tubes. DNA was extracted by following the standard phenol–chloroform extraction method [1]. The quantity of recovered DNA for most samples was determined using the Quantiblot™ system (Applied Biosystems, Foster City, CA, USA).

PCR amplification: PowerPlex Y® amplification system (Promega) was used to amplify 12 Y-STR loci: DYS19, DYS385, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439. Aliquots of DNA samples were diluted at the 1:30 ratio and 1 μL of each dilution was added to the amplification reaction prepared according to the manufacturer's protocol with one exception, i.e. Taq polymerase manufactured by Promega was used instead of AmpliTaq Gold. Cycling conditions

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Table 1
Allele frequencies at 11 Y-STR loci investigated in Buryats ($n = 215$)

Allele	Abs. freq.	Rel. freq.
DYS19		
13	1	0.005
14	48	0.223
15	128	0.595
16	28	0.130
17	8	0.037
18	2	0.009
	LD = 0.5800 ± 0.0293	
DYS389I		
12	9	0.042
13	158	0.735
14	48	0.223
	LD = 0.4103 ± 0.0329	
DYS389II		
27	1	0.005
28	121	0.563
29	45	0.209
30	40	0.186
31	8	0.037
	LD = 0.6063 ± 0.0263	
DYS390		
22	4	0.019
23	161	0.749
24	34	0.158
25	16	0.074
	LD = 0.4103 ± 0.0372	
DYS391		
9	17	0.079
10	185	0.860
11	11	0.051
12	2	0.009
	LD = 0.2518 ± 0.0377	
DYS392		
10	4	0.019
11	162	0.753
12	1	0.005
13	6	0.028
14	42	0.195
	LD = 0.3948 ± 0.0353	
DYS393		
11	1	0.005
12	6	0.028
13	42	0.195
14	165	0.767
15	1	0.005
	LD = 0.3738 ± 0.0349	
DYS437		
13	1	0.005
14	199	0.926
15	8	0.037
16	7	0.033
	LD = 0.1415 ± 0.0320	
DYS438		
9	3	0.014
10	190	0.884
11	19	0.088
13	3	0.014
	LD = 0.2118 ± 0.0356	
DYS439		
10	66	0.307
11	21	0.098
12	96	0.447
13	30	0.140
14	2	0.009
	LD = 0.6805 ± 0.0182	

Haplotype	Abs. freq.	Rel. freq.
DYS385		
10,14	1	0.005
10,19	2	0.009
11,11	1	0.005
11,13	39	0.181
11,14	8	0.037
11,15	3	0.014
11,17	5	0.023
11,18	106	0.493
11,19	6	0.028
12,12	19	0.088
12,13	9	0.042
12,14	1	0.005
12,15	2	0.009
12,19	5	0.023
13,13	1	0.005
13,15	1	0.005
13,16	2	0.009
13,17	2	0.009
13,18	1	0.005
14,14	1	0.005
	LD = 0.7138 ± 0.0283	

Explanations: abs. freq., absolute frequency; rel. freq., relative frequency; LD, locus diversity.

Table 2
Sixty-five distinct Y-STR haplotypes revealed by the analysis of 215 Buryat Y chromosomes

Abs. freq.	Rel. freq.	DYS 19	DYS 385	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439
69	0.321	15	11,18	13	28	23	10	11	14	14	10	12
30	0.140	14	11,13	14	30	23	10	14	14	14	10	10
19	0.088	15	11,18	13	28	23	10	11	14	14	10	13
7	0.033	16	12,12	13	29	24	9	11	13	14	10	11
4	0.019	17	12,12	13	29	24	10	11	14	14	10	10
4	0.019	15	11,17	13	28	23	10	11	14	14	10	12
3	0.014	16	12,13	13	29	24	9	11	13	14	10	11
3	0.014	15	11,19	13	28	23	10	11	14	14	10	12
3	0.014	15	11,18	13	28	24	10	11	14	14	10	12
2	0.009	15	11,18	13	28	23	10	11	14	14	9	12
2	0.009	14	11,13	14	30	23	10	14	13	14	10	10
2	0.009	15	11,18	13	28	23	10	11	13	14	10	12
2	0.009	14	13,16	13	29	24	10	11	12	15	10	11
2	0.009	18	12,12	13	29	25	10	11	13	14	10	10
2	0.009	14	11,13	14	29	23	10	14	14	14	10	10
2	0.009	15	11,19	13	28	23	10	11	14	14	10	13
2	0.009	15	12,13	13	29	25	10	11	13	14	10	10
2	0.009	16	10,19	14	29	23	9	13	14	14	13	12
2	0.009	14	12,19	12	29	23	10	10	14	16	11	10
2	0.009	15	12,15	13	28	24	9	11	13	15	11	12
2	0.009	15	11,18	14	29	23	10	11	14	14	10	12
2	0.009	14	12,19	12	28	23	10	10	14	16	11	10
2	0.009	15	11,18	13	28	23	11	11	14	14	10	13
2	0.009	14	11,13	14	31	23	10	14	14	14	10	10
2	0.009	16	11,14	13	29	25	11	11	13	14	11	10
2	0.009	15	12,12	14	31	24	9	11	13	14	10	11
1	0.005	15	11,18	13	28	22	10	11	14	14	10	13
1	0.005	13	13,17	14	29	23	10	12	13	16	10	13
1	0.005	17	12,13	13	29	25	10	11	13	14	10	10
1	0.005	15	11,17	13	29	23	10	11	14	14	10	13
1	0.005	15	12,14	13	29	24	10	11	13	14	11	11
1	0.005	16	11,14	14	31	24	11	11	13	14	11	10
1	0.005	15	11,18	13	28	23	10	11	13	14	10	14
1	0.005	15	11,18	13	28	23	10	11	14	14	10	14
1	0.005	14	11,13	14	30	23	10	13	14	14	10	10
1	0.005	16	13,13	12	28	24	10	13	12	13	10	12
1	0.005	16	12,13	13	29	25	10	11	13	14	10	10
1	0.005	15	11,18	13	29	23	10	11	14	14	10	12
1	0.005	17	12,12	13	29	24	10	11	13	14	10	10
1	0.005	14	11,18	13	28	23	10	11	14	14	10	13
1	0.005	15	11,11	13	28	22	10	14	12	15	10	11
1	0.005	14	12,13	13	29	22	10	14	13	14	10	10
1	0.005	14	11,14	13	29	24	10	13	13	15	13	13
1	0.005	17	11,15	13	31	25	11	11	14	14	11	11
1	0.005	15	11,15	13	30	25	11	11	13	14	11	10
1	0.005	15	11,14	14	31	23	11	11	13	14	10	10
1	0.005	16	11,15	13	30	25	11	11	13	14	11	10
1	0.005	15	11,18	13	28	24	10	11	14	14	10	13
1	0.005	16	13,18	13	30	24	10	13	12	15	9	10
1	0.005	14	11,13	14	30	23	10	14	15	14	10	10
1	0.005	16	10,14	13	29	25	10	11	13	14	11	11
1	0.005	16	11,14	13	29	25	10	11	13	14	11	11
1	0.005	16	12,12	13	29	24	10	11	14	14	10	11
1	0.005	16	12,12	12	28	25	9	11	13	14	10	11
1	0.005	16	12,12	13	29	24	10	11	14	14	10	10
1	0.005	15	12,19	13	28	23	10	11	14	14	10	12

Table 2 (*Continued*)

Abs. freq.	Rel. freq.	DYS 19	DYS 385	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439
1	0.005	16	11,14	13	30	25	12	11	13	14	11	10
1	0.005	15	13,17	12	27	23	10	14	12	16	11	12
1	0.005	15	11,19	13	28	23	11	11	14	14	10	12
1	0.005	14	13,15	12	28	24	10	14	11	15	11	13
1	0.005	16	11,18	13	29	23	11	11	14	14	10	12
1	0.005	17	11,14	13	29	24	12	11	13	14	11	10
1	0.005	16	12,13	13	30	25	10	11	13	14	10	10
1	0.005	15	11,13	14	30	23	10	14	14	14	10	10
1	0.005	16	14,14	12	31	22	10	11	14	16	10	12

Explanations: abs. freq., absolute haplotype frequency; rel. freq., relative haplotype frequency.

were set according to the PowerPlex Y kit manufacturer's suggestions.

Electrophoresis and typing: Products of amplification were electrophoresed using ABI3100 Genetic Analyzer with an appropriate filter set prepared on the basis of the relevant PowerPlex® Matrix Standards provided by Promega [2]. Fifty-centimeter capillaries and POP-6 polymer were used for optimal resolution. One microliter of each sample was mixed with 9 μL of deionized formamide (Applied Biosystems) and 0.5 μL of Internal Lane Standard 60–600 (Promega). Electrophoresis results were analyzed using Genscan Version 3.7 and Genotyper Version 3.7 software (Applied Biosystems). Y Power Typer macro (Promega) was used to assign allelic names. Alleles were designated according to the recommendations of the DNA commission of the International Society of Forensic Genetics [3].

Quality: Allelic ladders and control DNA samples provided with the PowerPlex Y kit were used. YHRD quality control exercises passed successfully by the laboratory.

Results: See Tables 1 and 2.

Statistical analysis: Population statistics and FST values were calculated using Arlequin software (Version 2.000) [4]. MDS analysis was performed using STATISTICA Version 7.1 (StatSoft) [5].

Additional data access: Additional data available from corresponding author.

Comments: The Buryats, numbering approximately 436,000, are the largest ethnic minority group in Siberia and are mainly concentrated in the Buryat Republic in central southern part of Siberia border to Mongolia and China. The Buryat language belongs to the Mongolic branch of the Altaic family, and the ancestors of modern Buryats could have been both Mongolic tribes and Tungusic and Turkic nomads who expanded into Baikal region from Central Asia in Neolithic times [6].

Haplotype diversity of the Buryat sample investigated ($n = 215$) was 0.8691 ± 0.0186. The most frequent haplotypes were: 15-11,18-13-28-23-10-11-14-14-10-12 (32.1%), 14-11,13-14-30-23-10-14-14-14-10-10 (14%) and 15-11,18-13-28-23-10-11-14-14-10-13 (8.8%) (order of loci: DYS19, DYS385, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439). The first the third most frequent haplotypes are one-step neighbors and the only difference between them is at DYS439 locus. We have used the minimal haplotype portions of the three most frequent haplotypes (i.e. DYS19, DYS385, DYS389I,

Fig. 1. A map of East Asia. The region where samples were collected is bordered by a thick black line and shaded in gray.

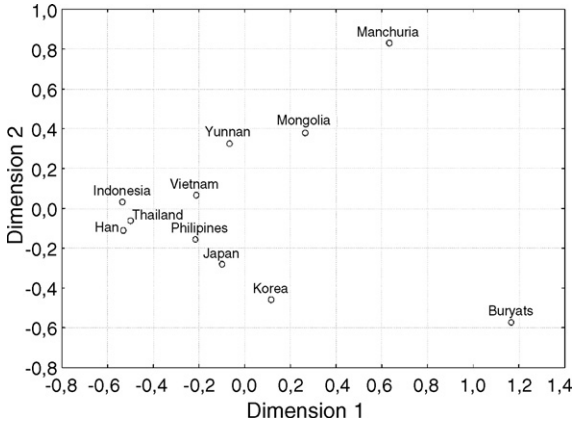

Fig. 2. MDS plot of FST pairwise differences for "minimal Y-STR haplotype" in 11 Asian populations, including Siberian Buryats (denoted in the plot as "Buryats") and 10 Asian populations from Kwak et al. [8].

DYS389II, DYS390, DYS391, DYS392 and DYS393) to scan the YHRD database (Version 16 [7]) for similar haplotypes. It turned out that the most frequent Buryat minimal haplotype (identical for the first and the third most frequent haplotypes in our sample) is not present in the database even though the database contains 42 samples from Mongolia described as Buryats. Thus, the haplotype may represent a modal haplotype for Buryats living in Siberia. Among the most frequent minimal haplotype's one-step neighbors one was found in Vietnamese population (15-11,18-13-29-23-10-11-14, frequency 2/209) but this haplotype turned out to be 10-10 in DYS438 and DYS439 loci so it was not a one-step neighbor if the extended set of loci was regarded. The second one-step neighbor of the Buryats' most frequent minimal haplotype present in the YHRD was 15-11,19-13-28-23-10-11-14, detected in the population of Mongolian Khalks (1/39). The minimal haplotype part of the second most frequent haplotype in Buryats turned out to be present in 10 population samples from Eurasia, including Tatars from Poland (2/124), Turks from Central Anatolia (2/110), Finns (5/399), Buryats (1/42) and Khalks (1/39) from Mongolia, populations of Moscow (1/85), Novogorod (1/50), Vladivostok (1/148) in Russia, Taraz in Kazakhstan (2/175) and population of Sweden (1/405).

Our Buryat sample was compared for ''minimal haplotype'' with other populations of East and South-East Asia, including Buryats from Mongolia, by means of AMOVA analysis based on pairwise FST comparisons. We have used Asian Y-STR data available from literature [8]. The degree if interpopulation variability was 11.16% when Siberian Buryats were included into the dataset while it was equal to 4.78% when the calculations were performed without Siberian Buryats Y-STR data. MDS analysis of the populations under investigation shows significant distance between Siberian Buryats and other Asian populations (Fig. 2).

Homogeneity seems to be the main characteristic of the Buryat population regarding Y-STRs under study. Locus and haplotype diversity indices are lower than usually reported for the loci under study [9–11]. Such a homogeneity was not observed when studying mtDNA diversity from the same subjects [12,13]. This paper follows the guidelines of publication of population data in Forensic Science International [14].

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