

Research Article

Genetic Polymorphism of 17 Y-Chromosomal STR Loci in the "On To'rt Uriw" Tribes of Karakalpak Population

Kurganov Sardarkhodja Karimovich*

Laboratory of Forensic Biological Examination of Human DNA, Republican Centre of Forensic Expertise, Tashkent City, Chilonzar district, Chilonzarskiy reg., House 29, Republic of Uzbekistan

*Corresponding author: Kurganov Sardarkhodja Karimovich, Laboratory of Forensic Biological Examination of Human DNA, Republican Centre of Forensic Expertise, Republic of Uzbekistan, Tashkent city, Chilonzar district, Chilonzarskiy reg., House 29, Republic of Uzbekistan; E-mail: sardorbioinformatik@mail.ru

Received: March 09, 2021; Accepted: March 16, 2021; Published: April 01, 2021

Abstract

Haplotypes and allele frequencies for the 17 Y-chromosomal short tandem repeat (Y-STR) loci, DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y GATA H4, DYS437, DYS438 and DYS448 were determined in a sample of "On To'rt Uriw" tribes 100 unrelated Karakalpak males living in the regions of Xojeli (20), Taxiatosh (20), Shimbai (20), Konirat (20) and Moynaq (20) using the Y-filer PCR Amplification Kit (Thermo Fisher Scientific). The gene diversity was 0.9998 (standard error: 0.005). The haplotype diversity calculated from the 17 Y-STR loci was 0.9977 and the discrimination capacity was 0.8890. The DYS385 locus showed the highest gene diversity value (0.8765), while the DYS391 locus showed the lowest gene diversity value (0.5033).

Keywords: DNA analysis, Y chromosome, Population data

Introduction

There have been few reports regarding genetic polymorphisms at the Y-STR loci in Karakalpak population [1-4]. The Karakalpaks are a heterogenous people, their appearance ranging from European to Mongoloid. The Karakalpaks as a whole are divided into two divisions, known as *aris*, the Qon'irat and the On To'rt Uriw. The term On To'rt Uriw, which means fourteen tribes, is somewhat misleading since the On To'rt Uriw are actually composed of just four tribes: the Qitay, Qipshaq, Keneges, and the Man'g'it. Also, The four tribes of the On To'rt Uriw are also divided into clans: the Qitay into 12, the Qipshaq into 13, the Keneges into 8, and the Man'g'it into 4. The difference between a tribe and a clan is defined by matrimonial alliances. The Karakalpaks practice exogamy. It is not possible to marry within one's own clan, but it is possible to marry into another clan within one's own tribe.

The world population of Karakalpaks is probably less than 600,000, making them one of the smallest Turkic groups in Central Asia. About 80% live in the Autonomous Republic of Karakalpakstan, the remainder being mainly located in other parts of Uzbekistan and Kazakhstan. For comparison, the Qazaqs may number up to 14 million worldwide, of which only 8½ million (about 60%) live in Kazakhstan. Surprisingly the Karakalpaks are not the dominant population of Karakalpakstan – they make up less than one third of the population and are just outnumbered by Uzbeks, some of whom have moved into southern Karakalpakstan from other parts of Uzbekistan in recent years. This study aimed to investigate the haplotypes and allele

frequencies for the 17 Y-STR loci in population and establish forensic DNA database.

Materials and Methods

Objects of the Research

The subjects of the study were blood samples and dried saliva on sterile gauze tampons, selected from 100 individuals.

DNA Extraction

Genomic DNA was extracted from peripheral blood and dried saliva samples using the phenol-chloroform-isoamyl alcohol method.

DNA Quantification

After isolation, the quantity of genomic DNA of each sample was determined by quantitative real-time polymerase chain reaction (PCR) using the Quantifiler™ Human Male DNA Quantification kit (Thermo Fisher Scientific), which includes internal positive control to test for the presence of PCR inhibitors in the DNA extracts. Quantitative real-time PCR was performed on 7500 Real-Time PCR System (Applied Biosystems).

PCR Amplification and Detection

To ensure successful amplification, 0.5 ng to 1 ng of DNA was used for each multiplex amplification reaction. All thermal cycling was conducted on Applied Biosystems® GeneAmp® PCR System 9700 thermal cyclers. PCR amplification using Y-filer PCR Amplification

Kurganov Sardarkhodja Karimovich (2021) Genetic Polymorphism of 17 Y-Chromosomal STR Loci in the "On To'rt Urıw" Tribes of Karakalpak Population.

Table 1:

No	B_DYS456	B_DYS389I	B_DYS390	B_DYS389II	G_DYS458	G_DYS19	Y_DYS393	Y_DYS391	Y_DYS439	Y_DYS635	Y_DYS392	R_Y_GATA_H4	R_DYS437	R_DYS438	R_DYS448	G_DYS385
8														0,0108		0,0430
9								0,0753				0,0323		0,0968		0,0376
10								0,6667	0,3118		0,0215	0,0215		0,3656		0,0108
11								0,2258	0,3333		0,5914	0,4409		0,4624		0,1505
12		0,1828					0,2903	0,0323	0,2473		0,0538	0,4301		0,0645		0,1774
13		0,5591				0,0645	0,6129		0,0538		0,1398	0,0753	0,0215			0,2097
14	0,0968	0,2581			0,0215	0,3118	0,0968		0,0538		0,1720		0,6452			0,1452
15	0,5269				0,1075	0,3333					0,0108		0,2151			0,0645
16	0,2473				0,2473	0,2151					0,0108		0,1183			0,0376
17	0,0968				0,3656	0,0753										0,0538
18	0,0323				0,1398										0,0860	0,0376
19			0,0430		0,0860					0,0215					0,2366	0,0054
20					0,0323					0,0645					0,4839	0,0215
21										0,2688					0,0645	0,0054
22			0,0968							0,1505					0,1290	
23			0,2581							0,2903						
24			0,2473							0,1828						
25			0,3441							0,0215						
27			0,0108	0,0215												
28				0,1183												
29				0,3978												
30				0,2258												
31				0,1613												
32				0,0753												
Gene diversity (D)	0,6484	0,5937	0,7506	0,7527	0,7735	0,7436	0,5365	0,5033	0,7326	0,7908	0,6040	0,6201	0,5288	0,6459	0,6891	0,8765

Table 2:

ID	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448
Sample 1_Xojeli	17	13	25	29	16	16	11, 13	13	10	11	23	11	12	14	11	20
Sample 2_Xojeli	15	13	23	32	16	13	15, 17	14A	10	13	22	14	11	13	11	19
Sample 3_Xojeli	15	14	19	30	17	14	13, 13	13	10	13	24	13	11	15	10	19
Sample 4_Xojeli	15	13	25	31	16	15	11, 15	13	11	10	23	11	12	14	11	20
Sample 5_Xojeli	15	13	25	31	16	15	11, 15	13	11	10	23	11	12	14	11	20
Sample 6_Xojeli	15	13	22	29	19	15	9, 16	12	10	12	21	14	11	16	10	18
Sample 7_Xojeli	15	13	24	29	18	14	13, 18	12	10	11	20	14	12	15	11	20
Sample 8_Xojeli	15	12	24	27	17	14	11, 14	12	11	13	23	14	11	15	12	19
Sample 9_Xojeli	16	14	24	30	17	15	11, 14	13	10	11	23	13	12	14	11	18
Sample 10_Xojeli	14	14	23	30	17	14	12, 13	14	10	10	22	14	12	14	10	19
Sample 11_Xojeli	16	14	24	30	17	15	11, 14	13	10	11	23	13	12	14	11	18
Sample 12_Xojeli	15	13	25	29	18	17	12, 12	13	10	10	21	11	11	14	10	22
Sample 13_Xojeli	15	12	23	28	19	15	13, 18	12	10	12	22	11	11	15	9	22
Sample 14_Xojeli	14	13	23	29	17	14	11, 13	14	10	10	22	14	12	14	10	19

Kurganov Sardarkhodja Karimovich (2021) Genetic Polymorphism of 17 Y-Chromosomal STR Loci in the "On To'rt Uriv" Tribes of Karakalpak Population.

Sample 15_Xojeli	16	14	24	29	16	15	12, 15	12	10	14	24	14	13	14	12	18
Sample 16_Xojeli	15	13	25	29	17	17	12, 13	13	10	10	21	11	11	14	10	22
Sample 17_Xojeli	15	13	25	31	15	16	11, 14	13	11	10	24	11	12	14	11	20
Sample 18_Xojeli	15	13	25	29	17	17	12, 12	13	10	10	21	11	11	14	10	21
Sample 19_Xojeli	15	13	25	29	17	17	12, 12	13	10	10	21	11	11	14	10	21
Sample 20_Xojeli	15	14	23	30	15	15	11, 21	14	10	11	21	11	11	14	10	21
Sample 1_Taxiatosh	15	13	22	30	17	14	13, 13	12	10	11	24	11	11	15	9	20
Sample 2_Taxiatosh	18	12	22	29	16	15	13, 13	12	10	11	22	11	11	14	12	20
Sample 3_Taxiatosh	15	12	24	29	20	14	13, 18	12	10	13	19	14	12	16	11	20
Sample 4_Taxiatosh	16	13	23	28	17	14	11, 14	13	11	11	23	13	12	15	12	19
Sample 5_Taxiatosh	15	13	23	29	18	14	12, 18	14	10	10	24	10	12	16	11	19
Sample 6_Taxiatosh	15	13	24	29	17	14	13, 18	12	10	11	20	14	12	15	11	20
Sample 7_Taxiatosh	15	13	25	29	18	16	12, 13	13	10	10	22	11	11	14	10	22
Sample 8_Taxiatosh	15	13	22	30	15	14	13, 13	13	11	13	23	13	11	15	10	20
Sample 9_Taxiatosh	16	14	24	30	17	15	11, 14	13	10	11	23	13	12	14	11	18
Sample 10_Taxiatosh	14	12	23	28	16	14	13, 15	13	10	11	21	11	11	16	10	20
Sample 11_Taxiatosh	16	14	25	32	15	15	11, 12	13	11	10	23	11	14	14	11	18
Sample 12_Taxiatosh	15	13	22	29	18	17	9, 17	12	10	12	21	14	11	16	10	19
Sample 13_Taxiatosh	14	13	22	31	19	14	13, 15	12	10	12	22	11	11	16	10	19
Sample 14_Taxiatosh	14	13	22	31	19	14	13, 15	12	10	12	22	11	11	16	10	19
Sample 15_Taxiatosh	15	13	24	30	20	14	13, 16	12	10	11	21	11	11	15	10	19
Sample 16_Taxiatosh	15	14	24	32	14	16	11, 12	13	9	10	23	11	12	14	11	20
Sample 17_Taxiatosh	16	13	23	29	16	14	12, 14	13	10	11	21	15	12	14	10	19
Sample 18_Taxiatosh	18	13	23	31	16	15	13, 13	12	10	12	22	11	11	16	9	20
Sample 19_Taxiatosh	14	14	23	30	17	14	11, 13	15	10	10	22	16	11	14	11	19
Sample 20_Taxiatosh	16	13	25	29	16	16	11, 14	13	10	11	23	11	12	14	11	20
Sample 1_Shimbai	15	14	23	31	17	14	15.2, 15.2	12	10	12	24	11	11	14	9	21
Sample 2_Shimbai	15	12	25	29	18	16	11, 14	13	11	10	23	11	13	14	11	20
Sample 3_Shimbai	15	13	25	29	18	16	12, 13	13	10	12	21	11	11	14	10	22
Sample 4_Shimbai	14	12	24	27	17	17	11, 14	13	10	12	21	11	12	15	11	20
Sample 5_Shimbai	15	12	23	29	17	13	17.2, 17.2	13	10	12	21	11	9	14	10	20
Sample 6_Shimbai	15	12	23	29	18	15	12, 12	12	10	12	24	12	12	14	11	20
Sample 7_Shimbai	15	13	24	29	18	15	12, 12	13	10	11	21	11	11	14	10	22
Sample 8_Shimbai	15	13	25	29	17	17	12, 12	13	10	10	21	11	11	14	10	22
Sample 9_Shimbai	16	13	25	30	15	15	11, 14	13	11	10	24	11	12	14	11	20
Sample 10_Shimbai	15	13	24	29	19	15	12, 12	13	10	11	21	11	11	14	10	22
Sample 11_Shimbai	16	13	24	32	16	15	11, 15	12	10	10	24	11	12	14	11	20
Sample 12_Shimbai	16	13	24	32	16	15	11, 15	12	10	10	24	11	12	14	11	20
Sample 13_Shimbai	17	13	27	31	15	15	11, 14	13	12	11	23	11	11	14	11	20
Sample 14_Shimbai	15	13	25	31	16	15	11, 15	13	11	10	23	11	12	14	11	20
Sample 15_Shimbai	15	12	23	29	17	13	16, 17	13	10	12	21	11	9	14	10	20
Sample 16_Shimbai	16	14	25	30	16	15	11, 11	13	10	12	21	7	11	14	11	19
Sample 17_Shimbai	18	13	22	31	16	15	13, 13	12	10	12	22	11	11	16	9	20
Sample 18_Shimbai	15	12	24	28	17	16	12, 19	12	10	11	22	13	11	15	10	19
Sample 19_Shimbai	14	14	25	31	16	15	12, 14	13	11	10	23	14	11	14	11	20
Sample 20_Shimbai	15	13	25	31	16	15	11, 15	13	11	10	23	11	12	14	11	20
Sample 1_Konirat	15	13	25	29	18	16	12, 13	13	10	10	21	11	11	14	10	22

Kurganov Sardarkhodja Karimovich (2021) Genetic Polymorphism of 17 Y-Chromosomal STR Loci in the "On To'rt Urıw" Tribes of Karakalpak Population.

Sample 2_Konirat	16	14	23	30	17	14	11, 12	13	11	12	24	14	12	15	12	20
Sample 3_Konirat	15	14	19	30	17	14	13, 13	13	10	14	24	13	11	15	10	19
Sample 4_Konirat	16	13	25	29	17	16	11, 14	13	11	10	23	11	13	14	11	20
Sample 5_Konirat	16	13	25	31	15	17	11, 13	13	10	11	23	11	13	14	11	20
Sample 6_Konirat	15	13	24	28	15	15	13, 17	13	10	11	21	13	12	14	10	18
Sample 7_Konirat	15	12	24	28	19	15	11, 16	12	10	12	20	12	12	15	10	19
Sample 8_Konirat	16	13	25	30	19	16	11, 14	13	11	10	23	11	12	14	11	20
Sample 9_Konirat	15	12	22	28	17	15	12, 15	14	10	11	21	11	10	16	10	22
Sample 10_Konirat	15	14	24	30	18	13	13, 14	13	9	10	21	11	12	14	10	20
Sample 11_Konirat	17	13	23	28	19	13	13, 16	13	10	11	23	16	11	14	11	22
Sample 12_Konirat	16	14	25	32	16	15	11, 14	13	10	10	23	12	11	14	11	20
Sample 13_Konirat	15	14	23	31	17	14	15.2, 15.2	12	10	12	24	11	11	14	9	21
Sample 14_Konirat	15	12	24	28	17	16	12, 19	12	10	11	22	13	11	15	10	19
Sample 15_Konirat	16	13	25	31	17	16	12, 14	13	11	11	24	11	13	14	11	20
Sample 16_Konirat	16	13	23	30	16	13	15, 17	14	11	12	23	14	11	13	11	19
Sample 17_Konirat	15	13	24	29	16	14	13, 17	12	10	12	21	11	11	14	10	20
Sample 18_Konirat	15	13	23	29	17	14	13, 18	12	10	11	20	14	12	15	11	20
Sample 19_Konirat	16	13	25	29	16	15	13, 14	13	10	12	20	11	12	14	11	20
Sample 20_Konirat	17	14	25	32	15	16	11, 14	13	11	10	23	11	12	14	11	21
Sample 1_Moynaq	15	12	24	28	18	14	12.2, 12.2	13	10	12	20	14	12	15	11	20
Sample 2_Moynaq	17	13	23	28	19	13	13, 16	13	10	11	23	16	11	14	11	22
Sample 3_Moynaq	14	13	23	28	15	14	13, 16	12	9	11	21	11	13	15	9	20
Sample 4_Moynaq	15	14	19	30	17	14	13, 14	13	11	14	24	13	11	15	10	19
Sample 5_Moynaq	15	14	19	30	17	14	13, 13	13	10	14	24	13	11	15	10	19
Sample 6_Moynaq	17	13	25	29	16	16	11, 14	13	10	14	23	11	12	14	11	20
Sample 7_Moynaq	17	12	25	29	17	16	10, 14	13	11	11	23	11	12	14	11	21
Sample 8_Moynaq	16	13	23	29	18	14	12, 18	14	10	10	24	10	12	16	11	19
Sample 9_Moynaq	16	13	25	29	17	16	11, 14	13	12	10	23	11	13	14	11	20
Sample 10_Moynaq	15	13	22	28	19	16	9, 17	12	10	11	22	13	11	16	10	18
Sample 11_Moynaq	15	12	23	30	17	15	12, 17	12	10	12	19	13	12	15	10	19
Sample 12_Moynaq	17	13	25	29	16	16	11, 14	13	10	11	23	11	12	14	11	20
Sample 13_Moynaq	16	14	25	32	16	15	11, 14	13	10	10	23	12	11	14	11	20
Sample 14_Moynaq	15	14	24	31	20	15	12, 12	13	9	11	22	11	10	14	10	20
Sample 15_Moynaq	14	14	23	30	16	14	11, 13	14	11	10	22	14	12	14	10	19
Sample 16_Moynaq	17	12	24	29	17	15	12, 14	13	10	12	21	11	11	14	11	20
Sample 17_Moynaq	15	13	24	29	14	14	13, 17	12	10	12	21	11	11	14	10	20
Sample 18_Moynaq	16	13	25	31	17	16	12, 12	13	11	11	24	11	12	14	11	20
Sample 19_Moynaq	17	13	25	29	16	16	11, 14	13	10	11	23	11	12	14	11	20
Sample 20_Moynaq	17	12	25	29	17	16	10, 14	13	11	11	23	11	12	14	11	21

Kit (Thermo Fisher Scientific) was performed as recommended by the manufacturer, although half of the recommended reaction volume (12.5 µl) was used.

Separation and detection of the 17 Y-STR loci were performed using the 3130xl Genetic Analyser (Applied Biosystems) 16-capillary array system and filter set G5. Each sample was prepared by adding 1 mL PCR product to 14 mL of Hi-Di™ formamide and 0.4 mL GeneScan™-500 LIZ™ internal size standard (Thermo Fisher Scientific).

The sample run data were analyzed, together with an allelic ladder and positive and negative controls, using GeneMapper ID-X v3.2 (Applied Biosystems) software.

Statistical Analysis

Comparison information of the sample data was generated using an in-house software program involving DNA-expert macros designed to check for allele sharing across all loci. For all analyses the DYS385

locus was treated as a single haplotype and not two separate alleles. The gene diversity (D) was calculated as $D = \frac{n}{n-1} (1 - \sum p_i^2)$, where p_i is the frequency of the i th haplotype [3]. The discriminatory capacity was determined by dividing the number of different haplotypes by the number of samples in that population. The discrimination capacity (DC) was determined by the formula n/N where n = the number of observed haplotypes divided by the number of samples [1].

Results and Discussion

This population was demonstrated 100 haplotypes, of which 93 were unique. The gene diversity was 0.9998 (standard error: 0.005). The haplotype diversity calculated from the 17 Y-STR loci was 0.9977 and the discrimination capacity was 0.8890. The DYS385 locus showed the highest gene diversity value (0.8765), while the DYS391 locus showed the lowest gene diversity value (0.5033).

Funding

This work was supported by Ministry of Innovation Development of The Republic of Uzbekistan, Grant No. A-2-089+(A-2-056).

References

1. Coble MD, Hill CR, Butler JM (2013) Haplotype data for 23 Y-chromosome markers in four US population groups. *Forensic Sci Int Genet* 7: 66-68. [\[crossref\]](#)
2. Kurganov S, Axmedova D, Filatova V, Muxamedov R, Axmedov B (2018) Genetic Polymorphisms at 17 Y-STR loci in Uzbek Population. *Peer Re J Foren & Gen Sci*.
3. Nei M, Tajima F (1981) DNA polymorphism detectable by restriction endonucleases. *Genetics* 97: 145-163. [\[crossref\]](#)
4. Raphaelle Chaix, Fre'de'ric Austerlitz, Tatyana Kheday, Svetlana Jacquesson, Michael F. Hammer, et al. (2004) The Genetic or Mythical Ancestry of Descent Groups: Lessons from the Y Chromosome. *Am J Hum Genet* 75:1113-1116. [\[crossref\]](#)

Citation:

Kurganov Sardarkhodja Karimovich (2021) Genetic Polymorphism of 17 Y-Chromosomal STR Loci in the "On To'rt Uriv" Tribes of Karakalpak Population. *J Mol Genet* Volume 4(1): 1-5.