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Population Data for 17 Y-STRs in Samples from Southeastern Anatolia Region of Turkey

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ABSTRACT In this study, Y chromosome short tandem repeats (Y-STR) haplotype data were obtained for 86 individuals from the Southeastern Anatolia region of Turkey. Allele frequencies were determined for 17 Y-STRs and haplotypes were obtained. The highest gene diversity was observed at DYS385 (0.95) while the lowest was at DYS437 (0.44). A total of 79 different haplotypes were identified, of which 74 were unique. The haplotype diversity for all loci and discrimination capacity were calculated as 0.9959 ± 0.0029 and 0.92, respectively. Haplotype data for different neighbouring populations obtained from Y-Chromosome Haplotype Reference Database (YHRD) were used for comparison. The result of the Analysis of Molecular Variance (AMOVA) indicated that there is no significant genetic distance between Southeastern Anatolia population and neighbouring populations at all. Armenian, Rasht (Iran-Gilaki) and Izeh (Iran-Bakthiari) populations were found to be closest to our population, while Syria and Iraq populations were more distant.

INTRODUCTION

Anatolia (Asian part of the present day Turkey) has been occupied by modern humans since the lower Paleolithic times (Kuhn 2002). It has acted as a bridge between Balkans and the Near East for numerous movements of modern humans throughout the history. Anatolia has been shaped by trade, wars and migrations throughout its history resulting to a very diverse population. Anatolia was populated by various civilizations such as Hattians, the Hurries, the Hittites, the Phrygians, the Lydians, the Urartians, the Medes, the Romans, the Sassanids, the Byzantines, the Seljuk Turks and the Ottomans (Tambets et al. 2000). Southeastern Anatolia Region is in between Eastern Anatolia and Mediterranean Regions and has a border with Syria and Iraq (Fig.1). Southeastern Anatolia Region is localized in so called "Upper Mesopotamia" which is widely considered as the cradle of civilization.

Analyzing the distribution of genetic variation within and among populations has long been used to gain insight into the demographic history of humans. Y chromosome, the only haploid chromosome in the human genome, is characterized by holoandric transmission and has a low rate of parallel and recurrent mutations. Thus polymorphisms of Y chromosome are valuable in reconstruction of paternal lineages thousands and thousands years backwards. Y-STRs are commonly used to distinguish lineages and to provide information about lineage relationships (Lowery et al. 2013; Tarlykov et al. 2013).

Different molecular markers, such as proteins (Brega et al. 1998), mitochondrial DNA (Mergen et al. 2004; Ottoni et al. 2011) and Y chromosomal markers (Cinnioglu et al. 2004) were used in the earlier studies to compare Anatolian population with European and Asian populations. Several studies focusing on Y-STR profiling in Anatolia (Nasidze et al. 2003; Cinnioglu et al. 2004; Rustamov et al. 2004; Donbak et al. 2006; Alakoc et al. 2010; Serin et al. 2011) were published previously. Genetic information on the Southeastern Anatolia Region particularly in relation to Y chromosome-linked markers is scarce. No study for Y-STR profiling of Southeastern Anatolia population has been carried out yet.

The objective of the present study was to create a Y-STR haplotype database for Southeastern Anatolia population and to explore genetic relationships of the population with neighbouring populations.

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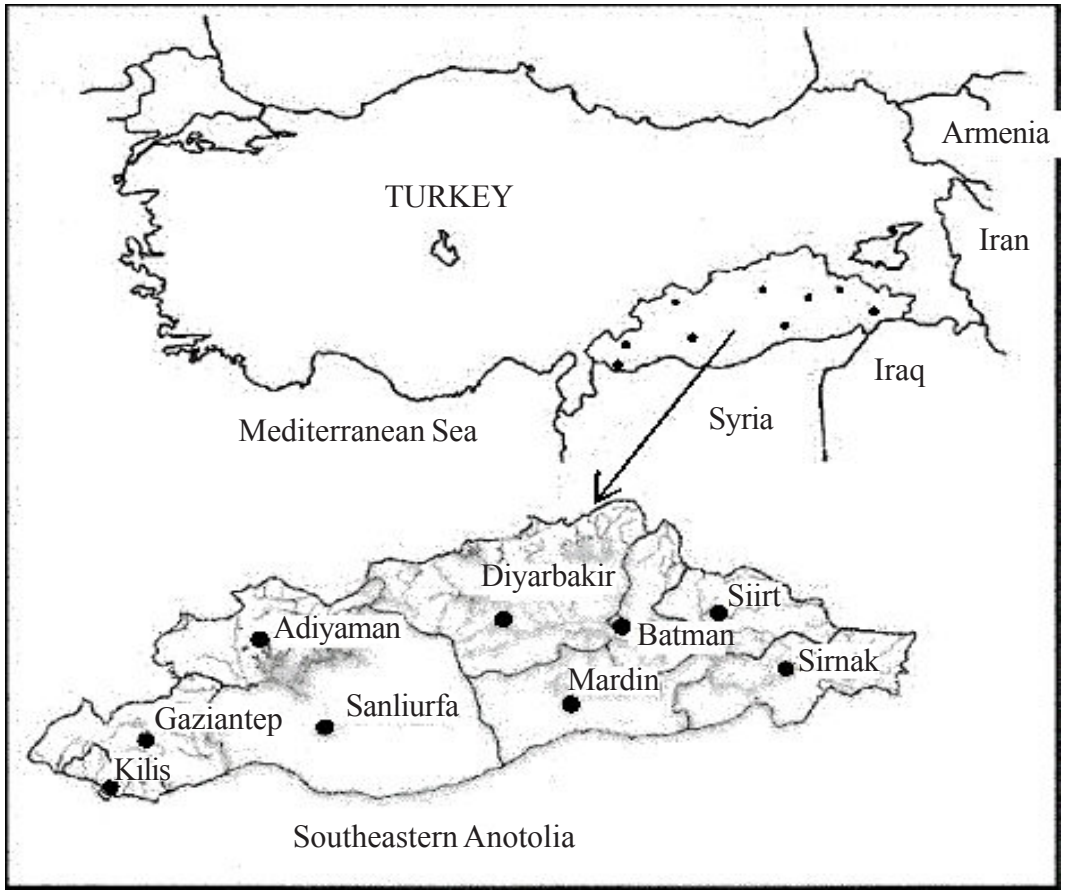

Fig. 1. Map of the Southeastern Anatolia Region of Turkey

MATERIALS AND METHODS

Study Population

A total of 86 males from the Southeastern Anatolia region of Turkey were included in this study. The individuals were paternally unrelated, they had different surnames and they defined themselves as belonging to a paternal lineage residing in the area from at least three generations. Samples were collected in all provinces of the region; Gaziantep (n=14), Kilis (n=5), Adiyaman (n=7), Mardin (n=13), Diyarbakir (n=14), Sanliurfa (n=17), Batman (n=4), Siirt (n=2) and Sirnak (n=10). Blood samples were collected using standart procedures in ethylenediaminetetraacetic acid (EDTA) coated tubes. The written informed consent was obtained from all participants.

Total genomic deoxyribonucleic acid (DNA) was isolated from peripheral blood samples by using a standard salting-out procedure (Miller et al. 1988). DNA samples were quantified spectrophotometrically and purity was assessed by electrophoresis in 1% agarose gels and the DNA was stored at -80 °C.

Genotyping

DNA samples were amplified by using the commercially available AmpFlSTR Yfiler Polymerase Chain Reaction (PCR) kit (Applied Biosystems, FosterCity, CA, USA) following the manufacturer's recommendations. Y-STR loci amplified by the kit were; DYS19, DYS385a/b, DYS389 I/II, DYS390, DYS391, DYS392, DYS393, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439,

Table 1: Allele frequencies and gene diversities of the 17 Y-STR loci in population sample from Southeastern Anatolia

Allele	*DYS19*	*DYS389I*	*DYS389II*	*DYS390*	*DYS391*	*DYS392*	*DYS393*	*DYS438*	*DYS439*	*DYS437*	*DYS448*	*DYS456*	*DYS458*	*DYS635*	*GATAH4*	*Genotype*	*DYS385*
9					0.035			0.337	0.012						0.081	11, 13	0.012
10					0.570	0.012		0.395	0.116						0.047	11, 14	0.128
11		0.012			0.349	0.721	0.023	0.128	0.442						0.395	11, 15	0.047
12		0.244			0.047	0.023	0.535	0.128	0.372						0.267	12, 12	0.012
13	0.151	0.593				0.140	0.360	0.012	0.058			0.012			0.209	12, 14	0.023
14	0.500	0.151				0.070	0.058			0.709		0.140	0.058			12, 15	0.023
15	0.291					0.023	0.023			0.233		0.663	0.140			12, 16	0.070
16	0.047					0.012				0.058		0.128	0.244			12, 17	0.047
17	0.012											0.058	0.209			12, 18	0.035
17.2													0.035			12, 19	0.035
18													0.128			13, 13	0.023
18.2													0.070			13, 14	0.035
19											0.302		0.035			13, 15	0.070
19.2													0.070			13, 16	0.035
20											0.453		0.012	0.058		13, 17	0.023
21				0.035							0.186			0.430		13, 18	0.070
22				0.151							0.035			0.233		13, 19	0.023
23				0.453										0.233		14, 13	0.012
24				0.244							0.023			0.047		14, 15	0.047
25				0.116												14, 16	0.012
26																14, 17	0.023
27			0.047													15, 15	0.012
28			0.058													15, 16	0.012
29			0.407													15, 17	0.023
30			0.326													15, 18	0.023
31			0.105													16, 16	0.012
32			0.058													16, 17	0.070
																17, 17	0.023
																17, 18	0.023
GD[1]	0.64	0.56	0.71	0.70	0.55	0.45	0.58	0.70	0.65	0.44	0.67	0.52	0.84	0.70	0.72		0.95

[1] Gene diversity

DYS448, DYS456, DYS458, DYS635/Y GATA C4 and YGATA H4.

PCR products were separeted by capillary electrophoresis on an ABI PRISM® 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) and typing was done by "Gene Mapper Software v. 3.2" (Applied Biosystems). Allele designations were determined by comparison of the sample fragments with those of allelic ladders provided within the kit.

Statistical Analysis

Arlequin software v.3.5 (Excoffier and Lischer 2010) was used to calculate allele and haplotype frequencies, gene diversities (GD) and haplotype diversity (HD). The discrimination capacity (DC) was also determined as DC=h/n where h is the number of different haplotypes observed in the population (Nei 1987).

Population pairwise genetic distances (R_{ST}) were calculated by using AMOVA with 10.000 permutations using an online tool of the YHRD and genetic distances were also used to generate Multi-Dimensional Scaling (MDS) plots. For the population comparison, previously published haplotype data present in YHRD were used. Population samples with the number of haplotypes were as follows; Armenian population (n=100), Azerbaijan population (n=72), Ishafan Iranian population (n=48) and Tehran, Iranian population (n=80) (Nasidze et al. 2003), Iraq Kurds population (n=126) and Syria (Syrian) population (n=113) (YHRD), Izeh, Iran (Bakthiari) population (n=50) and Rasht, Iran (Gilaki) population (n=47) (Roewer et al. 2009), Cukurova, Turkey population (n=249) (Serin et al. 2011). Due to the limited data for other populations, analysis was performed on a minimal European Y-STR haplotype comprising nine loci: DYS19, DYS389I, DYS389II, DYS385ab, DYS390, DYS391, DYS392 and DYS393.

RESULTS

Seventeen Y-STR loci were genotyped in a population of Southeastern Anatolia region of Turkey. A total of 79 different Y-STR haplotypes were observed in 86 individuals. The majority of the haplotypes were unique (74/79), while 2 haplotypes were shared by three individuals and 3 were shared by two individuals. The overall haplotype diversity (HD) was calculated as

Table 2: Pairwise genetic distance matrix based on Φ_{ST} values between Southeastern Anatolia population and neighbouring populations

	Southeastern Anatolia	*Armenia*	*Azerbaijan*	*Iraq*	*Isfahan, Iran*	*Izeh, Iran*	*Rasht, Iran*	*Syria*	*Tehran, Iran*	*Cukurova, Turkey*
Southeastern Anatolia	-	0.5345	0.3755	0.1665	0.2215	0.6890	0.6690	0.0882	0.3110	0.0749
Armenia	-0.0025	-	0.8072	0.9301	0.8803	0.9674	0.9821	0.0874	0.2538	0.4887
Azerbaijan	0.0000	-0.0065	-	0.8418	0.8715	0.4405	0.7936	0.0727	0.1988	0.9422
Iraq	0.0052	-0.0064	-0.0064	-	0.8442	0.5952	0.9230	0.0153	0.0657	0.8586
Isfahan, Iran	0.0057	-0.0097	-0.0108	-0.0086	-	0.5353	0.8905	0.1072	0.3916	0.7870
Izeh, Iran	-0.0063	-0.0115	-0.0013	-0.0042	-0.0044	-	0.9227	0.2449	0.3885	0.2805
Rasht, Iran	-0.0066	-0.0131	-0.0097	-0.0104	-0.0142	-0.0148	-	0.1409	0.3902	0.8458
Syria	0.0091	0.0086	0.0121	0.0176	0.0113	0.0040	0.0095	-	0.7163	0.0028
Tehran, Iran	0.0015	0.0026	0.0058	0.0128	-0.0008	-0.0006	-0.0012	-0.0049	-	0.0227
Cukurova, Turkey	0.0086	-0.0011	-0.0064	-0.0035	-0.0064	0.0024	-0.0074	0.0205	0.0156	-

*p values were shown above and Φ_{ST} values below the diagonal. The level of significance is $p<0.05$.

0.9959 ± 0.0029 with a discrimination capacity (DC) of 0.92. The haplotypes were submitted to the Y-Chromosome Haplotype Reference Database (YHRD) under the accession number YA003727 and the population was defined as "Southeastern Anatolia, Turkey [Turkish]".

The allele frequencies and gene diversity values of 17 Y-STR loci for the Southeastern Anatolia population were given in Table 1. Allele frequencies ranged from 0.012 (at more than one locus) to 0.721 (at DYS392 locus, allele 11) in the population. The highest and the lowest locus gene diversity was observed at DYS385 (0.95) and DYS437 (0.44), respectively. The average gene diversity value was calculated as 0.65. Intermediate variant alleles (17.2, 18.2 and 19.2) have been found at DYS458 locus with the second highest GD value (0.84). The frequency of DYS458 variant alleles was % 16.3 in total.

The haplotypes observed in Southeastern Anatolia population were compared with the haplotypes of different neighbouring populations by using data from YHRD database. The AMOVA pairwise distances based on R_{ST} values between populations were calculated and shown in Table 2.

The genetic distances between the Southeastern Anatolia population and neighbouring populations ranged from -0.0066 to 0.0091, all of them were found as non-significant ($p>0.05$). However, Armenian population and two Iran populations (Rasht and Izeh) were found to be much closer than Cukurova (eastern Mediterranean region of Turkey) population which is the geographically closest neighbour.

MDS plot was also generated by using pairwise R_{ST} values to visualize genetic relationships between population samples (Fig. 2). Armenian, Rasht, Iran (Gilaki) and Izeh, Iran (Bakthiari) populations were found to be closely related to our population in both dimensions, while Syria, Cukurova (Turkey), Isfahan (Iran) and Iraq populations were much distant.

DISCUSSION

Y-STR profiling has been considered as the marker of choice for population genetic studies. Previous population genetic studies based on Y chromosome variations mainly focused on the general population of Turkey (Cinnioglu et al. 2004) with only a few samples from the Southeastern Anatolia region or other different

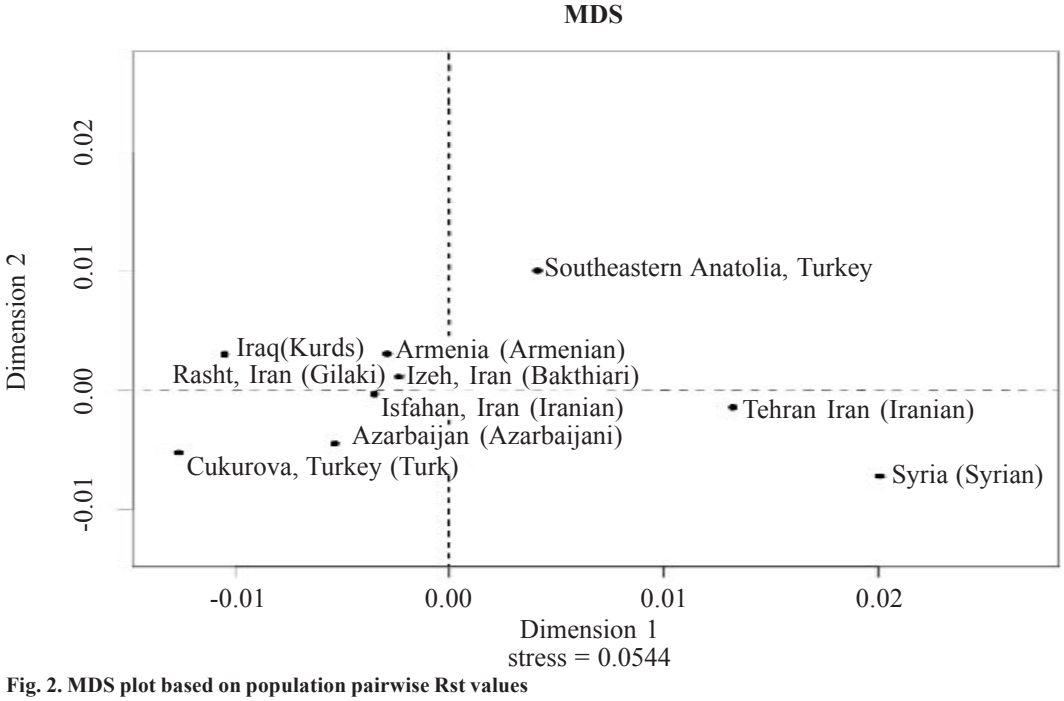

Fig. 2. MDS plot based on population pairwise Rst values

sub-populations such as Cukurova (Serin et al. 2011), Central Anatolia (Alakoc et al. 2010) and Mediterranean population (Donbak et al. 2006). This study presents the first population data for 17 Y-STR loci in the Southeastern Anatolia population.

The Anatolian Peninsula is an important geographic link between the Middle East, Asia and Europe. Due to numerous gene flow, admixture and local differentiation processes spanning from the late Pleistocene to the present day, this region manifests an elaborate genetic constitution (Cavalli-Sforza et al. 1994). Previous studies suggested that Anatolia had a stepping stone position between Asian and European populations and that is closer to the European populations (Calafell et al. 1996; Comas et al. 1998; Cinnioglu et al. 2004). The Asian genetic contribution in the Anatolian gene pool has been attempted to be quantified in many studies. Cinnioglu et al. (2004) determined the Central Asian contribution as lower than 9% by comparing the frequencies of Asian specific Y-chromosomal haplogroups C and O3 in Asia and Anatolia.

Y-STR haplotype analysis revealed a very high haplotype diversity (0.9959) in Southeastern Anatolia population, similar to populations from Cukurova (Serin et al. 2011) and Meditterrenaen regions (Donbak et al. 2006) of Turkey. Due to having experienced many migrations and hosted various civilizations throughout the history, the Upper Mesopotamia is expected to have a high haplotype diversity. In concordance with the results of the previous studies from Turkey, DYS385 was the most informative marker with a gene diversity value of 0.95. Intermediate alleles were observed in DYS458 locus in our population as in the Cukurova population. It has been reported that these alleles were most frequently found in Northern and the Eastern Africa and Caucasus (Grskovis et al. 2010; Myres et al. 2007; Ferri et al. 2008) and less common in Europe (YHRD). These variants occur at low frequencies but increase the discrimination power of DNA evidence and therefore become a useful tool for better understanding regional Y chromosome variations and recent migrations.

The sample size does not confirm the quality of population sampling in population genetics (Roewer 2003; Willuweit and Roewer 2007). Having different population specific haplotypes and resulting high value of haplotype diversity is the confirmation of sampling quality. However, large sample size provides opportunity to identify the rare alleles such as variants at DYS458 locus.

Due to the lack of 17 Y-STR data for several populations in YHRD, European minimal haplotype set consisting of nine loci with high levels of variability in worldwide populations was used for AMOVA pair-wise distances based on R_{ST} values between Southeastern Anatolia population and ten neighbouring populations. Non-significant values for genetic distances were obtained between our population and all neighbouring populations. However, among the compared populations the closest populations were Armenian population and two Iran populations (Rasht and Izeh). These populations were found to be much closer than even another Turkish population from Cukurova (geographically closest to our population). As the MDS plot clearly shows, Syria and Iraq (Kurds) populations were also found more distant than others. But still no significant genetic distance was found between our population and these populations. Donbak et al. (2006) previously reported that several Y-STR haplotypes were found to be shared between Mediterrenean population, Syria and Iraq populations.

A previous comparative study of Human Leukocyte Antigen (HLA) alleles and haplotypes in Turkish population revealed that Turks, Kurds, Armenians, Iranians, Jews, Lebanese and other Mediterranean groups share a common ancestry: the older "Mediterranean subsratum" (Arnaiz-Villena et al. 2001). This might be due to the fact that Turks, Kurds and Armenians have been living in the area for many millenia. Lowery et al. (2013) analyzed the Armenian population sub-structure by 17 Y-STR loci and reported that the genetic affinites of the Armenian groups to the Middle East and Anatolia are greater than to Europe. The present study also confirmed a close genetic relationship between these populations.

Due to the lack of recombination, Y-STR profiling has the advantage of having greater sensitivity to detect incidents in the demographic histories of populations. By providing the first data on Y-STR variations in Southeastern Anatolia population, this study has an impact on better understanding of the events contributed to current genetic composition of the population, as well as on male identification in fo-

rensic crime cases and parentage testing in the population.

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REFERENCES

Alakoc YD, Gokcumen O, Tug A, Gultekin T, Gulec E, Schurr TG 2010. Y-chromosome and autosomal STR diversity in four proximate settlements in Central Anatolia. *Forensic Sci Int Genet*, 4(5): 135-137.

Arnaiz-Villena A, Karin M, Bendikuze N, Gomez-Casado E, Moscoso J et al. 2001. HLA alleles and haplotypes in the Turkish population: Relatedness to Kurds, Armenians and other Mediterraneans. *Tissue Antigens,* 57: 308-317.

Brega A, Scacchi R, Cuccia M, Kirdar B, Peloso G, Corbo RM 1998. Study of 15 protein polymorphisms in a sample of the Turkish population. *Hum Biol*, 70(4): 715-728.

Calafell F, Underhill P, Tolun A, Angelicheva D, Kalaydjieva L 1996. From Asia to Europe: Mitochondrial DNA sequence variability in Bulgarians and Turks. *Ann Hum Genet*, 60(1): 35-49.

Cavalli-Sforza LL, Menozzi P, Piazza A 1994. *The History and Geography of Human Genes*. Princeton: Princeton University Press.

Comas D, Calafell F, Mateu E, Pérez-Lezaun A, Bosch E et al. 1998. Trading genes along the silk road: mtDNA sequences and the origin of central Asian populations. *Am J Hum Genet,* 63(6): 1824-1838.

Cinnioglu C, King R, Kivisild T, Kalfoðlu E, Atasoy S et al. 2004. Excavating Y-chromosome haplotype strata in Anatolia. *Hum Genet*, 114(2): 127-148.

Donbak L, Bajanowski T, Brinkmann B, Hohoff C 2006. Y-STR haplotypes in populations from the Eastern Mediterranean region of Turkey. *Int J Legal Med,* 120(6): 395-396.

Excoffier L, Lischer HE 2010. Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Mol Ecol Resour*, 10(3): 564-567.

Ferri G, Robino C, Alù M, Luiselli D, Tofanelli S, Caciagli L et al. 2008. Molecular characterization and population genetics of the DYS458.2 allelic variant. *Forensic Sci International Genet,* 1(Supple 1): 203–205.

Grskovic B, Mrsic G, Vrdoljak A, Merkas S, Andelinovic S 2010. Population genetic analysis of haplotypes based on 17 short tandem repeat loci on Y chromosome in population sample from eastern Croatia. *Croat Med J*, 51: 202–208.

Kuhn SL 2002. Paleolithic archeology in Turkey. *Evol Anthropol*, 11: 198-210.

Lowery RK, Herrera K, Uribe G, Reguiero M, Herrera RJ 2013. Sub-population structure evident in forensic Y-STR profiles from Armenian geographical groups. *Leg Med (Tokyo)*, 15(2): 85-90.

Mergen H, Oner R, Oner C 2004. Mitochondrial DNA sequence variation in the Anatolian Peninsula (Turkey). *J Genet*, 83(1): 39-47.

Miller SA, Dykes DD, Polesky HF 1988. A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Res,* 16(3): 1215.

Myres NM, Ekins JE, Lin AA, Cavalli-Sforza LL, Woodward SR, Underhill PA 2007. Y-chromosome short tandem repeat DYS458.2 non-consensus alleles occur independently in both binary haplogroups J1-M267 and R1b3-M405. *Croat Med J,* 48: 450–459.

Nasidze I, Schädlich H, Stoneking M 2003. Haplotypes from the Caucasus, Turkey and Iran for nine Y-STR loci. *Forensic Sci Int,* 137(1): 85-93.

Nei M 1987. *Molecular Evolutionary Genetics*. New York: Columbia Univ. Press.

Ottoni C, Ricaut FX, Vanderheyden N, Brucato N, Waelkens M et al. 2011. Mitochondrial analysis of a Byzantine population reveals the differential impact of multiple historical events in South Anatolia. *Eur J Hum Genet*, 19(5): 571-576.

Roewer L 2003. The Y-Short Tandem Repeat Haplotype Reference database (YHRD) and male population stratification in Europe-impact on forensic genetics. *Forensic Sci Rev*, 15(2): 164-170.

Roewer L, Willuweit S, Stoneking M, Nasidze I 2009. A Y-STR database of Iranian and Azerbaijanian minority populations. *Forensic Sci Int Genet,* 4(1): 53-55.

Rustamov A, Gümüþ G, Karabulut HG, Elhan AH, Kadikiran A, Bökesoy I 2004. Y-STR polymorphism in Central Anatolian Region of Turkey. *Forensic Sci Int*, 139(2-3): 227-230.

Serin A, Canan H, Alper B, Sertdemir Y 2011. Haplotype frequencies of 17 Y-chromosomal short tandem repeat loci from the Cukurova region of Turkey. *Croat Med J*, 52(6): 703-708.

Tambets K, Kivisild T, Metspalu E, Parik J, Kaldma K et al. 2000. The topology of the maternal lineages of the Anatolian and Trans-Caucasus populations and the peopling of Europe: some preliminary considerations. In: C Renfrew, K Boyle (Eds.): *Archaeogenetics: DNA and the Population Prehistory of Europe: Preliminary Conclusions.* Series of Monographs of the McDonald Institute for Archeological Research. Cambridge: Cambridge University, pp. 219-235.

Tarlykov PV, Zholdybayeva EV, Akilzhanova AR, Nurkina ZM, Sabitov ZM et al. 2013. Mitochondrial and Y-chromosomal profile of the Kazakh population from East Kazakhstan. *Croat Med J*, 54(1): 17-24.

Willuweit S, Roewer L 2007. International Forensic Y Chromosome User Group, Y chromosome haplotype reference database (YHRD): Update. *Forensic Sci Int Genet*, 1(2): 83-87.

Y Chromosome Reference Database YHRD 2013. From <http://www.yhrd.org> (Retrieved March 15, 2013).