GENETIC POLYMORPHISMS IN 15 STR LOCI IN THE TURKISH POPULATION LIVING IN ISTANBUL PROVINCE

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ABSTRACT

Objective: Short tandem repeats (STRs) are short sequences of nucleotides that are repeated and distributed all over the genome. These polymorphisms enable investigation of the forensic, ancestral lineage and evolutionary studies in human population. Owing to the historical migration and ethnic groups, it is very valuable to evaluate genetic distances in Turkey. The aim of the present study is to examine the STR data of Istanbul and compare the genetic distances and allele frequency with the previously published data of 27 countries from Europe, Asia, America, Africa and Middle East.

Material and Method: Peripheral blood samples were obtained from 400 healthy individuals. DNA samples were amplified using a commercial kit. Multiplex STR-PCR (Applied Biosystems, Foster City, CA, USA) was used

and the amplicons were evaluated on an ABI 3130 Genetic Analyzer.

Results: Among all loci, D21S11 and D18S51 were the most polymorphic loci. The power of discrimination (PD) ranged from 0.8329 (TPOX) to 0.9722 (D18S51). The combined PD and probability of exclusion (PE) were found to be >0.99999999 and 0.99999671, respectively.

Conclusion: In this study, six STR markers were selected to compare the genetic distances and allele frequency of the present results with the results of twenty-seven studies which were published previously. This study indicates that the population in Turkey is an intermediate between Europe, Middle East and Central Asia.

Keywords: Human genetics, polymorphism, population genetics, short tandem repeat.

İSTANBUL'DA YAŞAYAN TÜRK NÜFUSUNDA 15 STR LOKUSUNDA GENETİK POLİMORFİZMLER

ÖZET

Amaç: Kısa ardışık tekrarlar (STR), tekrarlanan ve genomun her yerine dağılan kısa nükleotid dizileridir. Bu polimorfizmler, insan popülasyonunda adli tıp, ata soyları ve evrim çalışmalarının araştırılmasını sağlar. Tarihsel göç ve etnik gruplar nedeniyle Türkiye'deki genetik mesafelerin değerlendirilmesi çok değerlidir. Bu çalışmanın amacı, İstanbul'un STR verilerini incelemek ve aynı zamanda, Avrupa, Asya, Amerika, Afrika ve Orta Doğu'dan 27 ülkenin daha önce yayınlanmış verilerini kullanarak genetik mesafeleri ve alel frekansını karşılaştırmaktır.

Materyal ve Metot: Dörtyüz sağlıklı kişiden periferik kan örnekleri toplandı. DNA örnekleri ticari bir kit kullanılarak çoğaltıldı. Multiplex STR-PCR (Applied Biosystems, Foster City, CA, USA) yöntemi kullanıldı ve amplikonlar ABI 3130 Genetic Analyzer'da değerlendirildi.

Bulgular: D21S11 ve D18S51 lokusları hepsinin içinde en polimorfik lokuslardı. Ayrımcılık gücü 0,8329 (TPOX) ile 0,9722 (D18S51) arasındaydı. Birleşik ayrımcılık gücü ve dışlama olasılığı sırasıyla >0,99999999 ve 0,99999671 idi.

Sonuç: Bu çalışmada, mevcut sonuçların genetik mesafeleri ve allel frekansı açısından altı STR belirteci seçildi ve daha önce yayınlanmış yirmi yedi çalışmanın verileri ile karşılaştırıldı. Sonuçlar Türkiye'deki nüfusun Avrupa, Orta Doğu ve Orta Asya arasında bir ara bölge olduğunu göstermektedir.

Anahtar kelimeler: İnsan genetiği, polimorfizm, popülasyon genetiği, kısa tandem tekrar.

INTRODUCTION

Turkey is located in the Southeastern Europe and Western Asia, and the region of Anatolia constitutes a significant portion of the territory where many important civilizations, states, communities and empires had existed and had been established. Some groups of these communities have continued to inhabit in different parts of the modern Turkey, particularly in Istanbul and these communities contributed to the ethnic variety of the population of Istanbul. Throughout history, the land of Istanbul has acted both as a barrier and a bridge, and it has become a site of historical, political and cultural interaction between Europe and Asia. Due to the historical migration and the wide variety of the ethnic groups in Istanbul, it is highly valuable to evaluate genetic distances. Turkey has a complex population structure with a heterogeneous gene pool. STR are short sequences of nucleotides directly adjacent to each other (generally 2–6 base pair long) that are repeated and distributed all over the genome.

Genetic data have been widely used to reconstitute; population history, revealing the origins of human populations, migration patterns, and linguistic relationships. Highly variable nuclear microsatellite markers show Mendelian inheritance and are more preferred for the studies of population genetic structure, parentage and relatedness, genetic diversity and recent population history. Nuclear STR loci are used in variety of fields for a variety of purposes, such as forensic serology, forensic identification of biological material, and paternity identification. It has also been shown that significant allele frequency differences exist between ethnic groups and the frequency distribution of a certain STR can be population-specific.[1,2]

The analysis of STR polymorphisms by PCR-based technique has become one of the most widely used method for forensic identification of biological material, paternity identification, and population genetics for evolutionary studies. The multiplex STR-PCR is a fast method to perform typing more than one STR region at a time.

The aim of the present study is to examine the STR data of Istanbul in Turkey and compare the genetic distances and allele frequency with the previously published data of 27 countries from Europe, Asia, America, Africa and Middle East. Therefore, 15 STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPOX, D18S51, D5S818 and FGA) were investigated in the population of Istanbul and the data were compared to determine genetic distances between Turkey and other 27 countries. Six STRs were selected and were compared to characterize the genetic relationship between Turkish, European and Asian populations.

MATERIAL AND METHOD

Population Selection and Sample Collection

In the present study, blood samples of 400 unrelated healthy Turkish individuals living in Istanbul Province (177 females, 223 males) were analyzed. Information

Table 1. The populations which were compared with the Turkish population		
Population	**Abbreviation**	**Reference**
Turkey	TR	this study
Greece	GR	Sánchez-Diz et al., 2008
Italy	IT	Brisighelli et al., 2009
Sweden	SE	Montelius et al., 2008
Serbia	RS	Novkovic et al., 2010
United States	USA	Butler et al., 2003
Syria	SY	Abdin et al., 2003
Iraq	IQ	Barni et al., 2007
Iran	IR	Alshamalia et al., 2005
Saudi Arabia	SA	Alshamalia et al., 2005
Dubai	Dub	Alshamalia et al., 2005
Yemen	YE	Alshamalia et al., 2005
Tunisia	TN	Mahfoudh-Lahiani et al., 2006
Morocco	MA	Abdin et al., 2003
Egypt	EG	Coudray et al., 2007
Afghanistan	AF	Berti et al., 2005
Uzbek, living in Afghanistan	AFUZ	Di Cristofaro et al., 2012
Turkmen, living in Afghanistan	AFTM	Di Cristofaro et al., 2012
Tadjik, living in Afghanistan	AFTJ	Di Cristofaro et al., 2012
Hazaran, living in Afghanistan	AFHZ	Di Cristofaro et al., 2012
Pakistan	PK	Rakha et al., 2009
Kashmiri Muslim, living in Pakistan	PKKas	Rakha et al., 2008
Lotha Naga tribal, living in India	INLo	Mastana et al., 2007
Chinese, living in Singapore	SGCN	Yong et al., 2004
Malay, living in Singapore	SGMY	Yong et al., 2004
Japan	JP	Hashiyada et al., 2003
Philippines	PH	De Ungria et al., 2005
Brazil	BR	Grattapaglia et al., 2001

STR data of 27 studies published previously (from Europe, Asia, Middle East and Africa) and STR data of this recent study belonging to Istanbul were compared.

related to the ethnic origins of the volunteers could not be obtained. This is a limitation of the study. The median age in the subject group was 46.3 (min.21, max.91 y) years. All subjects volunteered to participate in the study and were informed about the study. Written informed consent was obtained from all subjects. The procedures were carefully explained to all volunteers. The study was performed according to the amended Declaration of Helsinki and approved by the Clinical Research Ethics Committee of Haliç University (17.03.2011, 2011-03/02). This study was supported by the Scientific Research Fund of Haliç University.

STR-PCR Analysis

DNA analyses of the samples were conducted in the Department of Medical Biology, in Istanbul Faculty of Medicine. The chimerism laboratory is a laboratory accredited by EFI (European federation of Immunogenetics) and is included in a quality control program named EPT Chimerism. Quality control tests are performed with 20 samples yearly. Genomic DNA was isolated from peripheral blood leukocytes by three-methylamine bromide salts precipitation/denaturation method.[3] PCR amplifications of 15 STR loci were performed using AmpFlSTR Identifier STR kit (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's instructions.[4] The PCR products were separated using a reference ladder and 4–capillary electrophoresis system on an ABI 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). The alleles' size and discriminations were accomplished using the GeneMapper Software (Version3.1).

Statistical Calculations

Exact Hardy–Weinberg p-values, expected heterozygosity (He) and observed heterozygosity (Ho) were calculated using the Arlequin ver. 3.11 software package.[5] The power of discrimination (PD), probability of exclusion (PE) and polymorphism information content (PIC) were calculated with the Powerstats v1.2 software package (Promega Corp). D3S1358, D16S539, D18S51, TH01, VWA and FGA data from 27 populations were compared with the Turkish population (Table 1). The common Six STR loci were compared in common with other population studies.

Genetic distances between Turkey and other populations were accomplished by Gendist program using Nei's Genetic Distance model on PHYLIP software platform.[6,7] Neighbor-joining tree was constructed by POPTREE.[8] Locus by locus computation of the unbiased estimate of the exact p-value of the probability test was calculated by Arlequin ver. 3.11 software package.[5]

RESULTS

The allelic frequencies observed for each of the 15 STR loci in Table 2 and various statistical parameters such as H_o, observed heterozygosity; H_e, expected heterozygosity; PD, power of discrimination; PIC, polymorphic information content; PE, probability of exclusion is shown in Table 3. D21S11 and D18S51 were found to be the most diverse loci, with 17 and 16 alleles, respectively, whereas only seven alleles were observed in D7S820 and D3S1358. Deviations from Hardy–Weinberg equilibrium was detected at loci CSF1PO (p:0.0178), D16S539 (p:0.0201) and D19S433 (p:0.0001). However, after applying the Bonferroni correction (0.05/15=0.003), only D19S433 remained significant. The H_e ranged from 0.6512

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
5						0.00500									
6						0.30625						0.00125			
7			0.01750			0.16500						0.00500		0.00500	
8	0.015		0.20375	0.00250		0.12625	0.14250	0.02875				0.52500		0.01125	
9	0.0175		0.09500	0.02000		0.20625	0.08250	0.15250		0.00250		0.10875		0.04625	
9.3						0.17625									
10	0.07375		0.25500	0.27750		0.01375	0.06125	0.09500		0.00125		0.08750	0.00625	0.10125	
11	0.06375		0.25750	0.31625		0.00125	0.30000	0.29375		0.01250		0.23375	0.01625	0.30625	
12	0.09625		0.14125	0.30250			0.28875	0.28125		0.08750		0.03375	0.12750	0.33125	
12.2										0.01375					
13	0.29000		0.03000	0.06625	0.00750		0.09125	0.13000		0.24500	0.00750	0.00500	0.15125	0.18625	
13.2										0.02875			0.00500		
14	0.24125			0.01375	0.06750		0.03250	0.01750		0.28750	0.10375		0.18000	0.01000	
14.2										0.04500			0.00875		
15	0.15000			0.00125	0.24125		0.00125	0.00125	0.00125	0.13500	0.08625		0.11875	0.00250	
15.2										0.07000					
16	0.04750				0.28750				0.03250	0.03250	0.22250		0.13250		
16.2										0.02750					
17	0.00500				0.22500				0.20625	0.00250	0.32375		0.10375		
17.2										0.00875					
18					0.16125				0.09875		0.17250		0.06000		0.00375
19					0.01000				0.13375		0.07500		0.05125		0.04000
20									0.13875		0.00875		0.02000		0.09625
21									0.03500				0.00625		0.17250
22									0.03750				0.01125		0.16875
23									0.13625						0.17750
24									0.09750				0.00125		0.15500
25		0.00125							0.06750						0.11875
26		0.00375							0.01375						0.05125
27		0.01125							0.00125						0.01375
28		0.14125													0.00125
29		0.25875													0.00125
29.2		0.00250													
30		0.19875													
30.2		0.02750													
31		0.04875													
31.2		0.10250													
32		0.01250													
32.2		0.13125													
33		0.00625													
33.2		0.04000													
34		0.00125													
34.2		0.01250													
35		0.00125													

Table 2. Allele frequencies of 15 STR loci of Turkish population (n=400)

The observed allele frequencies of 15 STR loci for Istanbul. At each locus, a different number of alleles was observed with frequencies.

Table 3. Statistics for 15 autosomal loci in Turkish population															
	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
H_o	0.8225	0.8175	0.7775	0.6825	0.7625	0.7900	0.7875	0.7425	0.8450	0.8025	0.7775	0.6250	0.8300	0.7275	0.8375
H_e	0.8146	0.8406	0.7980	0.7274	0.7788	0.7901	0.7874	0.7853	0.8752	0.8225	0.7930	0.6512	0.8799	0.7501	0.8595
PD	0.9335	0.9565	0.9287	0.8756	0.9146	0.9210	0.9260	0.9172	0.9696	0.9368	0.9272	0.8329	0.9722	0.8992	0.9615
PIC	0.7900	0.8224	0.7666	0.6760	0.7419	0.7574	0.7563	0.7524	0.8613	0.8004	0.7632	0.6051	0.8666	0.7084	0.8420
PE	0.6414	0.6367	0.5580	0.4017	0.5314	0.5852	0.5761	0.4970	0.6850	0.6037	0.5580	0.3220	0.6559	0.4721	0.6704
p	0.1540	0.1640	0.2656	0.0178*	0.4059	0.2494	0.6568	0.0201*	0.0775	0.0001*	0.3625	0.4170	0.0510	0.9152	0.5170

H_o: Observed heterozygosity, H_e: expected heterozygosity, PD: power of discrimination, PIC: polymorphic information content, PE: probability of exclusion, *p*: Hardy–Weinberg equilibrium exact test, *: Bonferroni correction (0.05/15=0.003).

(TPOX) to 0.8799 (D18S51). The PD ranged from 0.8329 (TPOX) to 0.9722 (D18S51). The combined PD and PE were >0.99999999 and 0.99999671, respectively.

TH01, D3S1358, D16S539, D18S51, VWA and FGA loci data were selected and compared between African, European, American and Asian populations. In comparison with the Turkish population, the shortest genetic distance was observed in the Italian (0.0054) and Greek (0.0081) populations, while the longest genetic distance was observed in the Philippines (0.1144) and Japanese (0.1121) populations in this study. Genetic distances between the Turkish population and the other 27 populations are shown in Table 4. The positions on the constructed Neighbor-joining tree belonging to the populations studied, are consistent with their geographical positions (Figure).

DISCUSSION

The allele frequencies in our population samples were compared with previous studies and the researchers found that the Turkish genome structure had an admixture of Middle Eastern and European population structure.[9-16]

The allele frequencies in our population sample were compared with previous studies. All of the 15 STR loci had been previously studied by Yavuz et al. in a population of 500 individuals.[9] No significant differences were observed compared to our data.
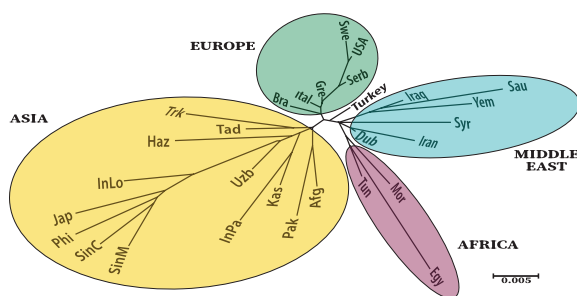
Figure. Neighbor-Joining Tree based on STR data. Neighbor-Joining Tree showing Istanbul and 27 populations. The tree was constructed using allele frequency data of 6 STR loci for all populations.

Two other studies, the first one conducted on 116 individuals from Ağrı-Van districts, Eastern Anatolia, and the second one conducted on 198 university students, were investigated.[17,18] Cakır et al. found all loci in Hardy-Weinberg equilibrium excluding D5S818, and Akbasak et al. found all loci in Hardy-Weinberg equilibrium excluding D16S539.[17,18] However, the loci CSF1PO, D16S539 and D19S433 were not found to be in Hardy-Weinberg equilibrium in our study. Another study conducted by Tug et al. comparing two regions in Turkey (Bolu and Duzce) showed that these two populations revealed significant differences in terms of D19S433, D3S1358 and D21S11.[19] Baransel et al. studied allele frequencies for 13 STRs loci in a Western Anatolia population and they found that the locus with the highest PD was D18S51 (0.966).[20] Similar to the results of Baransel et al., we found that D18S51 had the highest PD value (0.9722). Thus, population studies could be an indicative guide for forensic science. Bozman et al. studied Southeastern Anatolia Region of Turkey, and they showed that the Southeastern Anatolia population had close genetic affinities with other regional populations from Turkey, along with those from an apparent genetic continuum extending from the Near East to Southeastern Europe.[21]

In the study conducted by Cantürk et al., the most informative STR locus was found to be D12S391 for WTR, MAR[excIST], SEA, BS, MED, AEG and IST data sets, and D2S1338 for EA and CA (Middle Anatolia) data sets.[22] On the other hand, the locus D2S1338 was not found to be significant in our study.

The tree graphically represents genetic distance among 27 populations. The analysis indicates that the Turkish population is more closely related to the European and Middle Eastern populations rather than the Central Asian population. Although the language and other cultural features are closely related to Central Asia, the genetic contribution of the Central Asian populations is interestingly lower than expected. These results particularly indicate the importance of population studies in regions where migration occur. Economic, political and social factors as well as migration changes have affected genetic data throughout history.

Table 4. Genetic distances between 27 populations

	TR	GR	IT	SE	RS	USA	SY	IQ	IR	SA	Dub	YE	TN	MA	EG	AF	AFUZ	AFTM	AFTJ	PK	AFHZ	PKKas	INLo	SGCN	SGMY	JP	PH	BR
TR	0.0000																											
GR	0.0081	0.0000																										
IT	0.0054	0.0056	0.0000																									
SE	0.0397	0.0243	0.0271	0.0000																								
RS	0.0178	0.0094	0.0135	0.0113	0.0000																							
USA	0.0291	0.0177	0.0202	0.0074	0.0119	0.0000																						
SY	0.0120	0.0207	0.0202	0.0662	0.0315	0.0577	0.0000																					
IQ	0.0326	0.0368	0.0331	0.0794	0.0599	0.0637	0.0424	0.0000																				
IR	0.0243	0.0359	0.0226	0.0625	0.0433	0.0578	0.0308	0.0453	0.0000																			
SA	0.0279	0.0356	0.0269	0.0684	0.0498	0.0588	0.0476	0.0161	0.0483	0.0000																		
Dub	0.0170	0.0284	0.0245	0.0664	0.0426	0.0525	0.0259	0.0209	0.0238	0.0267	0.0000																	
YE	0.0364	0.0494	0.0382	0.1002	0.0711	0.0812	0.0577	0.0283	0.0424	0.0272	0.0296	0.0000																
TN	0.0271	0.0360	0.0269	0.0639	0.0396	0.0548	0.0342	0.0430	0.0367	0.0377	0.0152	0.0390	0.0000															
MA	0.0249	0.0178	0.0222	0.0496	0.0270	0.0425	0.0277	0.0388	0.0390	0.0497	0.0209	0.0556	0.0174	0.0000														
EG	0.0376	0.0452	0.0417	0.0940	0.0658	0.0847	0.0410	0.0444	0.0444	0.0632	0.0384	0.0518	0.0474	0.0363	0.0000													
AF	0.0149	0.0257	0.0179	0.0418	0.0312	0.0345	0.0253	0.0387	0.0340	0.0342	0.0212	0.0542	0.0264	0.0363	0.0620	0.0000												
AFUZ	0.0217	0.0349	0.0289	0.0764	0.0488	0.0605	0.0223	0.0425	0.0320	0.0501	0.0139	0.0404	0.0174	0.0263	0.0478	0.0154	0.0000											
AFTM	0.0146	0.0255	0.0243	0.0620	0.0357	0.0486	0.0256	0.0406	0.0270	0.0497	0.0175	0.0286	0.0318	0.0325	0.0318	0.0321	0.0209	0.0000										
AFTJ	0.0213	0.0241	0.0274	0.0531	0.0288	0.0493	0.0181	0.0478	0.0428	0.0533	0.0264	0.0514	0.0264	0.0215	0.0491	0.0233	0.0157	0.0205	0.0000									
PK	0.0378	0.0406	0.0275	0.0364	0.0373	0.0326	0.0574	0.0764	0.0427	0.0642	0.0457	0.0690	0.0331	0.0468	0.0980	0.0238	0.0351	0.0512	0.0377	0.0000								
AFHZ	0.0405	0.0527	0.0452	0.0743	0.0569	0.0639	0.0468	0.0443	0.0449	0.0494	0.0259	0.0535	0.0330	0.0446	0.0826	0.0212	0.0188	0.0427	0.0273	0.0375	0.0000							
PKKas	0.0241	0.0393	0.0371	0.0823	0.0469	0.0602	0.0299	0.0838	0.0446	0.0794	0.0371	0.0604	0.0459	0.0514	0.0752	0.0378	0.0218	0.0224	0.0326	0.0493	0.0511	0.0000						
INLo	0.0643	0.1030	0.0828	0.1374	0.1070	0.1222	0.0697	0.1123	0.0587	0.1052	0.0580	0.0842	0.0683	0.1041	0.0967	0.0477	0.0348	0.0512	0.0637	0.0748	0.0490	0.0377	0.0000					
SGCN	0.0886	0.1067	0.0973	0.1594	0.1209	0.1492	0.0835	0.1172	0.0825	0.1310	0.0798	0.0764	0.0707	0.0802	0.0854	0.0896	0.0463	0.0613	0.0468	0.0915	0.0596	0.0675	0.0591	0.0000				
SGMY	0.0750	0.0997	0.0919	0.1608	0.1161	0.1427	0.0663	0.1163	0.0742	0.1305	0.0700	0.0817	0.0702	0.0829	0.0758	0.0738	0.0344	0.0547	0.0510	0.0999	0.0574	0.0474	0.0346	0.0170	0.0000			
JP	0.1121	0.1493	0.1396	0.2039	0.1612	0.2005	0.0890	0.1546	0.1065	0.1679	0.1060	0.1336	0.1258	0.1424	0.1349	0.0978	0.0677	0.0860	0.0688	0.1316	0.0795	0.0793	0.0410	0.0441	0.0409	0.0000		
PH	0.1144	0.1362	0.1253	0.1925	0.1661	0.1833	0.1160	0.0994	0.0865	0.1309	0.0945	0.0830	0.1182	0.1198	0.0929	0.1096	0.0809	0.0864	0.0916	0.1474	0.0848	0.1237	0.0858	0.0444	0.0514	0.0729	0.0000	
BR	0.0163	0.0161	0.0126	0.0203	0.0155	0.0173	0.0272	0.0446	0.0279	0.0450	0.0235	0.0599	0.0235	0.0217	0.0515	0.0101	0.0218	0.0288	0.0197	0.0183	0.0323	0.0393	0.0664	0.0882	0.0801	0.1177	0.1143	0.0000

Note: Current study (TR), Greece (GR), Italy (IT), Sweden (SE), Serbia (RS), United States (USA), Syria (SY), Iraq (IQ), Iran (IR),Saudi Arabia (SA), Dubai (Dub), Yemen (YE), Tunisia (TN), Morocco (MA), Egypt (EG), Afghanistan (AF), Uzbek-living in Afghanistan (AFUZ), Turkmen- living in Afghanistan (AFTM), Tadjik-living in Afghanistan (AFTJ), Pakistan (PK), Hazaran- living in Afghanistan (AFHZ), Kashmiri Muslim-living in Pakistan (PKKas), Lotha Naga tribal-living in India (INLo), Chinese-living in Singapore (SGCN), Malay-living in Singapore (SGMY), Japan (JP), Philippines (PH), Brazil (BR)

In this study, STR data were compared with the results of 27 populations to investigate the origins of the current population of Turkey.[23-41] TH01, D3S1358, D16S539, D18S51, VWA and FGA loci data were selected and compared among the African, European, American and Asian populations. The Turkish population presented the shortest genetic distance with the Italian and Greek populations and the longest genetic distance with the Philippines and Japanese populations in this study.

The use of multiplex STR-PCR analysis is a simple and effective approach to evaluate the ancestral origin. Although population samples from Istanbul indicate a challenge in terms of patterns of admixture, we estimate that larger sample sizes and multi-center studies may provide relevant information about the population in Istanbul and ancestral knowledge.

CONCLUSION

Data of 15 STR loci in the population of Istanbul were analyzed and compared the genetic distances and allele frequency of common six STR loci with the previously published data of 27 countries. Genetic distances between Turkey and other populations were accomplished by Gendist program using Nei's Genetic Distance model on PHYLIP software platform. The shortest genetic distance was observed in the Italian and Greek populations, while the longest genetic distance was observed in the Philippines and Japanese populations in this study

*The authors declare that there are no conflicts of interest.

GENETIC POLYMORPHISMS IN 15 STR LOCI IN THE TURKISVH POPULATION LIVING IN ISTANBUL PROVINCE

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