Prediction of the Y-Chromosome Haplogroups Within a Recently Settled Turkish Population in Sarajevo, Bosnia and Herzegovina

Serkan Doğan[1], Gülşen Doğan[1], Adna Ašić[1], Larisa Bešić[1], Biljana Klimenta[2], Mirsada Hukić[1,3], Yusuf Turan[1,4], Dragan Primorac[5,6,7,8] and Damir Marjanović[1,9]

[1] International Burch University, Department of Genetics and Bioengineering, Sarajevo, Bosnia and Herzegovina

[2] Health Centre, Sarajevo, Bosnia and Herzegovina

[3] Academy of Sciences and Arts of Bosnia and Herzegovina, Department of Medical Science, Sarajevo, Bosnia and Herzegovina

[4] Balikesir University, Faculty of Arts and Sciences, Department of Biology, Balikesir, Turkey

[5] University of Split, School of Medicine and Department of Forensic Science, Split, Croatia

[6] University of Osijek, School of Medicine, Osijek, Croatia

[7] University Park, Penn State University, Eberly College of Science, PA, USA

[8] University of New Haven, New Haven, CT, USA

[9] Institute for Anthropological Research, Zagreb, Croatia

ABSTRACT

Analysis of Y-chromosome haplogroup distribution is widely used when investigating geographical clustering of different populations, which is why it plays an important role in population genetics, human migration patterns and even in forensic investigations. Individual determination of these haplogroups is mostly based on the analysis of single nucleotide polymorphism (SNP) markers located in the non-recombining part of Y-chromosome (NRY). On the other hand, the number of forensic and anthropology studies investigating short tandem repeats on the Y-chromosome (Y-STRs) increases rapidly every year. During the last few years, these markers have been successfully used as haplogroup prediction methods, which is why they have been used in this study. Previously obtained Y-STR haplotypes (23 loci) from 100 unrelated Turkish males recently settled in Sarajevo were used for the determination of haplogroups via 'Whit Athey's Haplogroup Predictor' software. The Bayesian probability of 90 of the studied haplotypes is greater than 92.2% and ranges from 51.4% to 84.3% for the remaining 10 haplotypes. A distribution of 17 different haplogroups was found, with the Y-haplogroup J2a being most prevalent, having been found in 26% of all the samples, whereas R1b, G2a and R1a were less prevalent, covering a range of 10% to 15% of all the samples. Together, these four haplogroups account for 63% of all Y-chromosomes. Eleven haplogroups (E1b1b, G1, I1, I2a, I2b, J1, J2b, L, Q, R2, and T) range from 2% to 5%, while E1b1a and N are found in 1% of all samples. Obtained results indicate that a large majority of the Turkish paternal line belongs to West Asia, Europe Caucasus, Western Europe, Northeast Europe, Middle East, Russia, Anatolia, and Black Sea Y-chromosome lineages. As the distribution of Y-chromosome haplogroups is consistent with the previously published data for the Turkish population residing in Turkey, it was concluded that the analyzed population could also be recognized as a representative sample of the Turkish population residing in Turkey.

Key words: Y-STRs, Y-SNPs, Y-chromosome, haplotypes, haplogroup predictor, Turkish population

Introduction

The Y-chromosomal non-recombining segment (NRY) provides essential information for human population studies[1]. It serves as an exceptionally effective tool in historical and demographic studies, which is used by anthropologists and geneticists for those purposes[2]. Y-chromosomal short tandem repeats (Y-STRs) are investigated more and more each year. However, in order to determine their applicability in forensic and anthropological research, an even higher number of diverse populations should be studied[3]. The application of these markers ranges from paternity testing and male kinship analysis to evolutionary and human migration studies[4].

Biallelic markers located on the NRY determine lineages that are referred to as haplogroups, and are defined as a group or a family of Y-chromosomes which are ancestrally related[5–7]. The usage of Y-STRs enables determination of male contributions by estimating Y-chromosome admixtures. Because of the low effective population size[8], as well as the high reproductive variability of male individuals[9], the higher susceptibility of the Y-chromosome to genetic drift compared to mtDNA, X-chromosome, and autosomal chromosomes needs to be considered. Therefore, in order to determine admixture estimates for males, methods that assess the impact of genetic drift should be preferred. Furthermore, Y-chromosome haplogroups are of increasing significance in the latest studies. However, determining them by the application of single nucleotide polymorphisms (SNPs) can be costly, which is why the prediction of haplogroups by using Y-STRs is the method of choice[10].

In this study, major Y-chromosome haplogroup frequencies were estimated from the collected Y-STR data via Whit Athey's Haplogroup Predictor, which is based on a Bayesian-allele-frequency approach. The program calculates the probability of a Y-STR haplotype which can be found within a haplogroup[11]. Y-STR data of 100 Turkish individuals residing in Sarajevo as a representative sample of the Turkish population were used to estimate the frequency of major Y-chromosome haplogroups. The aim of the study was to provide the haplogroup prediction and distributions in the Turkish population.

Materials and Methods

Haplotype data, based on 23 Y-chromosomal STR loci typed using PowerPlex Y23 system, obtained from 100 unrelated Turkish males residing in Sarajevo, Bosnia and Herzegovina (B&H)[12], was used for the prediction of Y-chromosome haplogroups. Geographic origin of individuals tested in this research is represented in Figure 1 and it shows that examined persons are originating from different parts of Turkey, making this population truly representative sample of Turkish population. Prediction of Y-chromosome haplogroups from Y-STR values was performed using Whit Athey's Haplogroup Predictor Program v.5, which is based on a Bayesian-allele-frequency approach[11]. Twenty three Y-STR markers were an input and the Bayesian probability for each haplogroup was estimated as an output. The Y-haplogroup nomenclature used in this research is in accordance with the recommendations of the Y-Chromosome Consortium[7].

Results and Discussion

The previous genetic analysis of 100 Turkish male DNA samples yielded 100 different haplotypes, that is, all profiles appeared only once[12]. That population was analyzed in the present study. Y-chromosome haplogroups of Turkish population residing in Sarajevo, B&H, were predicted from Y-STR data by the use of Haplogroup Predictor program. The Y-haplogroup distribution in the study population is illustrated (Figure 2). A more detailed insight into the results of the study is demonstrated via sublineage frequencies within the main Y-chromosome haplogroups (Figure 3). Seventeen different haplogroups were found (Figure 2). Four of them, namely J2a, R1b, G2a, and R1a, occurred at high frequencies (>10%). These four haplogroups alone account for 63% of all Y-chromosome haplogroups in the study population. The remaining 13 haplogroups, namely E1b1a, E1b1b, G1, I1, I2a, I2b, J1, J2b, L, N, Q, R2, and T, were present in low frequencies, representing 1–5% of all haplogroups. The Bayesian probability of accurate haplogroup prediction for 90 haplotypes was greater than 92.2%, and that of the remaining 10 haplotypes ranged from 51.4 to 84.3% (Table 1). Additionally, haplotypes which were used in the research and predicted haplogroups are illustrated (Table 1).
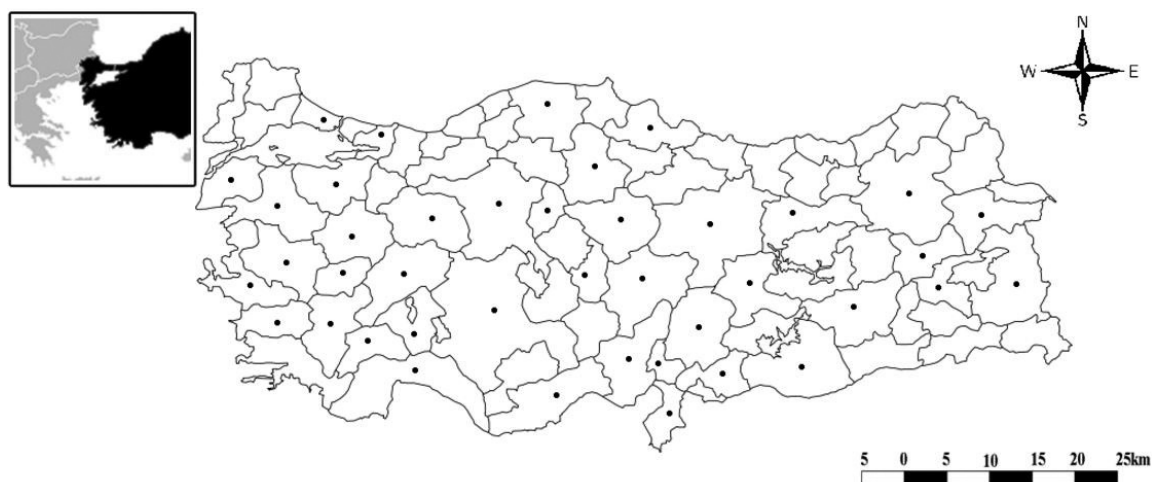

Fig. 1. City locations of birth places of donors from Turkey are marked by full circles in the city area.
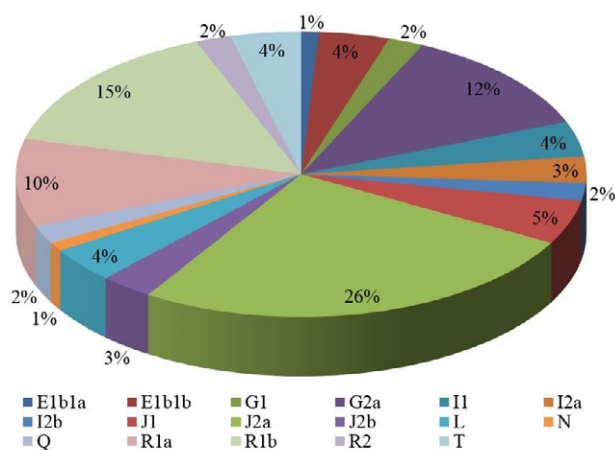
Fig. 2. Schematic representation of Y-haplogroup frequencies in the Turkish population residing in Sarajevo, B&H.
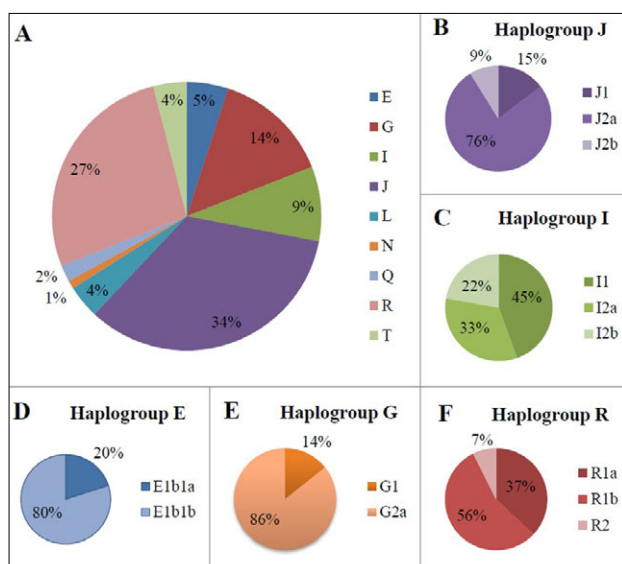

Fig. 3. Frequencies of the main Y chromosome haplogroups found in the Turkish population residing in Bosnia and Herzegovina (A), and frequencies of the sublineages of the haplogroups J (B), I (C), E (D), G (E), and R (F).

Haplogroup J2 represents 29% of all, with its first sublineage haplogroup J2a having the highest Y-lineage prevalence of 26% and its second sublineage, J2b, accounting for the remaining 3%. Previous research on Y-chromosome haplogroups suggested that the J haplogroup originates from the Middle East, and that it was introduced in the European gene pool by migrations during and after Neolithic period[13]. This haplogroup is referred to as the haplogroup of »Early Farmers« who survived the Last Glacial Maximum in Asia and Africa and brought farming to the European continent 10,000–9,000 years ago[14]. Its two sublineages J1 and J2 can be identified by transversion mutations M267 and M172, respectively. In the general

Turkish population, the frequency of J2 haplogroup was found to be 24% with an even distribution throughout the country[15].

This points to the fact that the current results are in accordance with the previous study of Turkish populations in Turkey. Apart from its prevalence in the Turkish population, J2 haplogroup is present in high frequency in many neighboring countries, such as Iraq, Lebanon, Syria, Armenia, and Georgia. Within Europe, this haplogroup is present in Italy and the Balkan countries[16,17].

Haplogroup R1b, which originated in West Asia[18], was the second most frequent haplogroup in the study population, with a prevalence of 15%. Furthermore, R1a accounts for 10%, thus making R1 widely spread in the investigated population with a frequency of 25%. A previous study of Turkish population in Turkey yielded similar results, as it demonstrated that R1 accounted for 21.6%[15]. In Western Europe, R1b is the most frequent Y-haplogroup, with an occurrence of 70%. On the other hand, R1a haplogroup demonstrates a trend of increased frequency from west to east, with the highest frequencies in the populations of Eastern Europe, namely Polish (56.4%), Hungarian (60%), and Ukrainian (54%)[19]. Such observations are expected if the latest findings on this topic are considered. Primorac *et al* (2011) stated that R haplogroup came from Asia into Eurasia region before J2 haplogroup, that is, approximately 15,000–10,000 years ago during Mesolithic time.

G2a is the third most frequently found haplogroup in the Turkish population with a frequency of 12%. This sublineage is mostly expanded to the Anatolian, Caucasus and European regions during the upper Paleolithic era[11,15]. Additionally, G1 accounted for 2%, thus making G present in 14% of the study population. In a previous investigation of Turkish population residing in Turkey, G1 and G2a haplogroups together were accounting for 10.9% of all haplogroups[15]. This haplogroup was also observed in the neighboring countries, since G-M201 lineages accounted for ~30% in Georgia[19] and the north Caucasus[20]. It was also present in Southeast Europe, the Mediterranean[19], and Iraq[21]. G2-P15 lineages were observed in the Middle East with a maximum of 19% in the Druze population[22], as well as in Southern Europe with an average of 5% in Italy and Greece[23].

When Turkish population residing in Sarajevo, B&H is compared with native Bosnian-Herzegovinian population, numerous differences can be observed. In the study of representative population in B&H[13], the most frequent haplogroups were haplogroup I with an average frequency of 48.7%, followed by haplogroups E (approximately 15%) and R (around 14%). The first difference between these two populations is much higher prevalence of the dominant haplogroups in Bosnian-Herzegovinian population than it is the case with Turkish population. The second difference is the structure of haplogroups themselves. Haplogroups E, I and R are characteristic for the countries of the Balkan region and, therefore, suggest that Bosnian-Herzegovinian population is genetically diverse from Turkish population.

TABLE 1
Y-STR HAPLOTYPES, PREDICTIONS OF Y-HAPLOGROUP AND PROBABILITY IN TURKISH POPULATION (TP)
(N=100) RESIDING IN BOSNIA AND HERZEGOVINA

Haplo-type	576	389 I	448	389 II	19	391	481	549	533	438	437	570	635	390	439	392	643	393	458	385	456	H4	Prediction	Probability	N
Y001	18	13	19	29	14	10	22	11	12	12	16	17	25	24	13	13	10	12	16	11.14	15	12	R1b	100	1
Y002	18	12	21	28	14	10	22	12	12	9	14	16	24	23	11	11	9	12	18	13.17	13	11	J2a	99.9	1
Y003	20	13	19	29	14	11	22	12	12	12	15	16	23	24	12	13	10	12	15	11.14	16	12	R1b	100	1
Y004	15	12	20	30	13	11	27	12	11	10	14	17	22	23	14	11	9	12	18.2	12.19	15	10	J2a	59.4	1
Y005	16	12	20	28	14	10	25	12	11	10	16	20	21	23	12	11	12	13	16	14.14	14	11	I1	100	1
Y006	17	13	19	29	14	10	24	14	11	11	14	16	22	22	12	15	12	13	18	13.13	15	10	Q	66.7	1
Y007	20	12	20	29	15	11	21	12	9	10	16	18	21	22	12	11	11	14	17	13.14	15	13	G2a	100	1
Y008	16	13	21	29	14	9	22	13	12	9	14	18	21	23	12	11	10	12	13	13.16	16	12	J2a	100	1
Y009	15	13	19	29	14	11	22	13	11	10	14	17	22	23	12	13	10	14	17	14.16	17	11	T	99.9	1
Y010	17	14	20	30	14	10	22	11	10	9	15	16	22	24	12	11	10	12	20	14.17	15	12	J2a	100	1
Y011	18	13	20	30	14	10	22	12	12	10	14	18	21	23	13	11	12	13	16	16.20	15	14	E1b1b	100	1
Y012	17	13	20	29	15	11	23	11	12	11	14	18	23	25	11	11	10	13	16	11.15	18	13	R1a	100	1
Y013	16	13	20	30	14	10	25	12	12	10	16	15	21	23	12	14	11	12	16	17.18	15	11	L	100	1
Y014	17	14	19	32	15	11	26	12	12	10	14	20	21	23	13	12	12	14	16	14.14	13	11	I2b	97.4	1
Y015	17	13	19	29	14	11	24	11	12	12	15	19	24	24	13	13	10	12	16	12.14	15	13	R1b	100	1
Y016	17	14	21	31	15	10	22	12	12	10	14	20	21	24	13	11	12	13	16	16.18	17	12	E1b1b	100	1
Y017	18	13	21	29	15	10	23	12	11	9	14	16	21	23	12	11	10	12	15	12.16	14	13	J2a	100	1
Y018	17	12	21	29	15.16	9	21	11	11	10	16	18	21	23	11	11	11	14	19	12.14	15	12	G2a	100	1
Y019	18	14	20	31	16	10	23	11	12	11	14	18	23	25	12	11	10	13	15	11.14	16	13	R1a	100	1
Y020	17	14	20	31	14	10	27	12	11	10	14	17	21	22	11	11	9	12	17.2	14.14	15	11	J1	100	1
Y021	19	12	21	28	14	10	22	12	11	9	14	16	21	24	11	11	9	12	22	13.16	15	11	J2a	100	1
Y022	18	13	20	31	14	10	23	13	11	9	16	15	21	25	11	11	9	12	18	13.14	15	12	J2a	100	1
Y023	15	12	22	29	15	10	24	12	10	9	14	22	21	24	11	12	11	13	16	14.15	15	11	G2a	76.4	1
Y024	18	13	19	30	15.16	10	21	11	10	10	16	22	22	22	11	11	11	13	15	14.14	14	11	G2a	98.2	1
Y025	18	14	20	31	14	11	23	12	12	11	14	18	23	23	10	11	10	13	15	11.14	16	11	R1a	100	1
Y026	17	13	20	31	14	10	24	15	11	10	14	20	21	23	10	11	9	12	18.2	13.18	15	11	J1	96.8	1
Y027	15	13	21	31	12	10	22	12	11	9	14	17	21	22	11	11	8	12	15	13.15	15	11	J2a	100	1
Y028	16	12	19	27	14	10	22	13	11	11	15	16	23	24	13	14	10	12	18	11.15	15	13	R1b	100	1
Y029	15	13	21	29	15	11	23	12	12	9	13	16	21	23	11	11	11	12	15	13.18	16	12	J2a	100	1
Y030	17	14	19	29	14	10	25	12	11	11	14	21	27	23	11	10	10	14	16	13.20	16	12	R2	100	1
Y031	19	12	20	29	16	11	23	12	12	11	14	19	23	25	10	11	10	13	16	11.14	16	13	R1a	100	1
Y032	17	12	21	28	13	10	22	12	11	9	14	16	21	23	11	11	9	12	17	14.18	15	11	J2a	100	1
Y033	17	14	20	31	14	11	23	11	11	9	15	16	22	23	10	11	10	12	16	14.17	16	11	J2a	100	1
Y034	16	12	20	28	15	10	24	13	10	10	15	18	22	24	11	12	12	13	17	13.16	13	10	G1	99.3	1
Y035	16	14	19	30	14	11	23	13	12	12	15	17	24	24	12	13	10	12	15	11.14	16	11	R1b	100	1
Y036	18	13	19	29	14	10	22	13	12	12	15	17	23	24	12	13	7	12	16	12.15	16	12	R1b	100	1
Y037	15	12	22	28	15	10	21	12	10	11	16	19	21	21	11	11	12	14	16	13.15	15	11	G2a	100	1
Y038	16	13	19	30	15	10	24	12	12	10	16	15	21	23	12	13	11	11	15	13.16	15	10	L	100	1
Y039	17	13	20	30	15	10	25	11	11	10	15	20	21	24	11	11	12	14	18	12.13	13	11	I2a	99.4	1
Y040	18	13	20	29	16	10	22	13	10	10	16	17	21	24	11	11	10	12	16	12.16	17	12	J2a	92.2	1
Y041	19	13	18	30	14	10	21	12	12	10	12	17	25	23	10	14	10	13	17	12.13	15	12	R1b	77.5	1
Y042	15	12	23	29	16	10	21	12	10	10	16	18	20	21	11	11	12	13	17	13.15	15	11	G2a	100	1
Y043	16	14	19	31	14	10	23	14	11	9	14	18	21	23	11	13	10	13	16	13.16	15	11	T	100	1
Y044	18	14	21	31	14	11	22	12	12	9	15	18	21	23	12	11	8	13	13	13.16	15	11	J2a	100	1
Y045	19	12	19	29	15	10	22	11	11	10	15	17	19	23	13	12	12	12	17	12.16	15	12	L	79.7	1
Y046	19	11	19	27	14	11	23	13	12	12	15	17	26	24	13	13	10	12	16	12.15	15	12	R1b	100	1
Y047	19	13	20	31	14	10	23	13	14	9	15	15	24	23	11	11	10	12	16	13.14	17	10	J2a	100	1
Y048	16	13	21	29	15	10	23	13	11	9	14	16	22	23	12	11	10	12	15	12.16	15	13	J2a	100	1
Y049	18	13	21	29	15	9	22	13	12	9	14	18	21	23	12	11	10	12	14	13.16	15	11	J2a	100	1

TABLE 1 Continued

Haplo-type	576	389 I	448	389 II	19	391	481	549	533	438	437	570	635	390	439	392	643	393	458	385	456	H4	Pre-diction	Prob-ability	N
Y050	15	11	21	27	15	10	21	11	11	10	16	17	20	22	12	10	11	14	17	15.16	15	12	G2a	100	1
Y051	16	13	21	28	15	9	22	12	12	9	14	17	21	22	11	10	10	13	13	13.16	15	11	J2a	100	1
Y052	19	13	18	31	15	10	26	13	11	10	14	19	20	23	10	11	10	12	18.2	12.17	17	12	J1	97.9	1
Y053	16	13	20	31	15	11	23	12	12	11	14	17	23	25	10	11	10	15	17	11.14	15	13	R1a	100	1
Y054	19	13	19	28	15	11	22	13	12	12	15	17	24	25	13	13	10	12	16	11.13	15	13	R1b	100	1
Y055	18	12	20	29	13	10	26	12	11	10	14	17	21	25	12	11	10	12	18.2	12.19	15	10	J1	99.9	1
Y056	16	13	20	29	15	10	22	12	11	9	14	16	23	22	12	11	8	13	17	13.14	17	11	J2a	100	1
Y057	19	15	18	31	14	11	22	12	13	12	15	17	24	23	11	13	11	12	16	11.14	16	12	R1b	100	1
Y058	16	13	20	31	13	10	23	13	11	9	14	14	21	23	11	13	11	12	14	15.17	15	12	T	99.1	1
Y059	18	13	19	29	14	10	25	12	11	10	14	18	20	23	11	11	9	12	18.2	12.17	15	11	J1	100	1
Y060	16	13	21	32	15	10	22	12	12	9	13	19	20	23	11	11	11	12	16	13.16	15	12	J2a	100	1
Y061	20	14	20	31	14	10	22	12	11	9	15	17	24	23	11	11	10	12	17	14.14	15	11	J2a	100	1
Y062	18	13	19	31	16	10	31	11	13	10	15	18	23	24	13	11	10	13	17	14.16	15	11	I2a	100	1
Y063	15	13	20	29	15	9	22	12	12	9	14	17	22	24	11	11	11	12	14	13.16	16	12	J2a	100	1
Y064	17	13	19	30	14	11	22	14	12	12	15	16	23	24	12	13	10	12	16	11.14	15	12	R1b	100	1
Y065	19	12	20	29	15	11	21	12	9	10	16	18	21	22	12	11	11	14	17	13.14	15	13	G2a	100	1
Y066	19	12	21	28	15	10	22	12	9	10	16	18	20	22	12	11	12	13	20	12.14	15	11	G2a	100	1
Y067	18	14	18	30	15	10	23	12	13	11	14	16	24	24	13	13	10	13	11	12.14	15	11	R1b	99.9	1
Y068	18	13	20	32	16	10	21	12	12	11	14	17	23	25	10	11	10	13	15	11.14	15	13	R1a	100	1
Y069	18	13	20	31	15	11	23	12	11	11	14	19	24	25	10	11	10	13	16	11.15	15	13	R1a	100	1
Y070	17	14	20	30	14	10	22	10	11	9	15	17	21	23	12	11	12	12	16	13.15	14	12	J2a	100	1
Y071	16	14	21	30	15	9	21	13	12	9	14	19	21	23	10	11	10	13	14	13.16	15	13	J2a	100	1
Y072	17	13	19	30	13	10	26	10	12	10	14	18	22	23	12	11	13	13	17	14.15	17	11	E1b1b	51.4	1
Y073	14	13	21	29	14	11	22	12	10	10	16	16	21	23	11	12	11	14	17	15.16	14	10	G1	95	1
Y074	19	14	19	30	13	10	24	12	12	11	15	17	24	22	11	15	12	13	18	12.15	15	11	Q	66.6	1
Y075	16	14	20	31	15	10	26	12	12	10	14	17	21	23	11	12	12	14	16	15.15	15	11	I2b	100	1
Y076	17	12	24	29	15	10	21	11	10	10	16	17	21	21	11	11	12	15	19	13.14	17	11	G2a	100	1
Y077	16	12	19	28	14	10	25	12	11	10	16	19	22	23	11	11	12	13	15	13.14	14	11	I1	100	1
Y078	18	13	19	31	17	10	23	12	12	11	14	19	24	25	10	11	10	13	15	12.14	15	13	R1a	100	1
Y079	18	12	22	29	15	10	21	11	10	10	16	17	22	21	11	11	12	14	18	13.15	15	12	G2a	100	1
Y080	16	13	19	29	14	10	21	12	12	11	14	17	24	23	10	14	10	13	16	12.13	15	12	R1b	80.4	1
Y081	18	12	18	28	15	10	22	12	11	9	14	15	20	23	11	11	9	12	18	15.16	13	11	J2b	93.5	1
Y082	17	13	20	29	15	11	25	12	12	10	15	17	21	25	11	11	12	12	16	12.13	16	10	I2a	100	1
Y083	17	13	19	30	14	11	21	13	12	10	14	16	24	23	10	14	12	13	17	13.13	15	12	N	97.1	1
Y084	17	14	19	31	13	10	26	12	12	9	15	18	21	22	11	13	12	13	16	13.15	18	10	T	100	1
Y085	16	13	20	29	14	10	22	13	11	9	16	15	21	25	11	11	9	12	18	14.15	15	12	J2a	100	1
Y086	16	13	19	29	14	10	22	14	12	12	15	18	25	24	12	13	10	12	15	11.13	15	13	R1b	100	1
Y087	16	12	19	28	15	10	23	14	12	9	16	17	22	24	14	11	9	12	17	15.17	13	11	J2b	100	1
Y088	19	14	21	30	15	9	21	11	11	9	14	16	25	22	11	11	10	12	16	13.20	15	11	J2a	100	1
Y089	17	13	20	30	15	10	22	13	12	12	15	17	24	23	12	13	10	12	15	11.14	15	12	R1b	100	1
Y090	18	14	19	31	15	10	25	12	12	9	14	19	21	22	11	11	9	12	17	16.18	16	12	E1b1a	84.3	1
Y091	18	13	19	29	15	10	24	12	11	9	14	18	21	23	12	12	9	12	16	15.19	14	12	J2b	79.7	1

TABLE 1 Continued

Y092	18	14	20	30	16	11	23	12	12	12	14	18	23	26	10	11	10	13	15	11.14	16	12	R1a	100	1
Y093	15	12	20	28	14	10	24	12	12	10	16	19	21	22	11	11	12	13	15	14.14	15	11	I1	100	1
Y094	17	13	20	30	15	11	23	12	12	11	14	19	23	25	10	11	11	13	15	12.14	16	12	R1a	100	1
Y095	15	12	22	29	16	10	19	11	10	10	16	17	21	22	11	11	11	13	17	13.15	16	10	G2a	100	1
Y096	16	13	18	30	16	10	26	13	11	11	15	18	24	23	11	10	13	14	17	11.17	15	11	R2	99.2	1
Y097	18	14	20	30	14	10	22	13	11	9	15	15	24	23	12	11	10	12	17	12.15	16	9	J2a	100	1
Y098	15	14	19	31	16	10	24	13	12	10	16	15	22	23	12	15	11	11	19	12.16	15	11	L	100	1
Y099	17	13	20	29	14	10	25	12	11	10	16	21	23	22	10	11	11	13	17	13.14	13	11	I1	100	1
Y100	18	13	20	32	13	10	24	12	10	10	14	18	23	24	13	11	12	13	18	17.18	15	11	E1b1b	100	1

In light of the presented results as well as their accordance with the previous studies, it can be concluded that the Turkish population residing in Sarajevo, B&H is of marked resemblance to the Turkish population living in Turkey and, therefore, can be considered a representative sample of Turkish population. When taking the distribution of its haplogroups into consideration, particularly since the haplogroup with the highest frequency accounts for only 26% of all haplogroups observed, it can be concluded that the Turkish population is significantly heterogenous. Since Y-chromosome haplogroups can be used for the purposes of tracing history and migrations, this study provides an insight into the origins of the Turkish population. The presence of R1b haplogroup implies that the region of modern Turkey has been inhabited as far as during Mesolithic time, while the presence of J2 haplogroup implies that farming during the Neolithic time intensively took place in this area. However, haplogroup I with all its sublineages accounts for only 9% of all haplogroups identified in the Turkish population. Based on the aforementioned analyses of the heterogeneity of the Turkish population, it is clear that Y-chromosomal SNPs represent an important tool for tracing history and discovering migration patterns that shaped modern population. It is also important to note that, in addition to the results provided with this study, another study of Turkish population, possibly with a larger study cohort, would definitely provide interesting results and perhaps even new discoveries.

REFERENCES

1. KARAFET TM, MENDEZ FL, MEILERMAN MB, UNDERHILL PA, ZEGURA SL, HAMMER MF, Genome Res, 18 (2008) 305. DOI: 10.1101/gr.7172008. — 2. CAVALLI-SFORZA LL, MENOZZI P AND PIAZZA A, The History and Geography of Human Genes (Princeton University Press, New Jersey, 1994). — 3. TURRINA S, ATZEI R, AND LEO DD, Int. Congress Ser 1288 (2006) 265 — 4. BUTLER JM, J Forensic Sci, 15 (2003) 91. — 5. BERKMAN CC, & TOGAN I, Disc. App. Math., 157 (2009) 2341. — 6. DE KNIJFF P, Am J Hum Genet, 67 (2000) 1055. DOI: 10.1016/S0002-9297(07)62935-8 — 7. Y CHROMOSOME CONSORTIUM, Genome Res, 12 (2002) 339. — 8. JOBLING M, HURLES M, & TYLER-SMITH C, Human evolutionary genetics: origins, peoples & disease (Garland Science, 2013). — 9. CABALLERO A, Genetics, 139 (1995) 1007. — 10. ATHEY TW, Journal of Genetic Genealogy, 1 (2005) 1. — 11. ATHEY TW, Journal of Genetic Genealogy, 2 (2006) 34. DOI: 10.4236/ojgen.2014.44027 — 12. DOGAN S, PRIMORAC D, MARJANOVIĆ D, Croat Med J, 55 (2014) 530. DOI: 10.3325/cmj.2014.55.530 — 13. MARJANOVIC D, FORNARINO S, MONTAGNA S, PRIMORAC D, HADZISELIMOVIC R, VIDOVIC S, Ann Hum Gen, 69 (2005) 757. — 14. PRIMORAC D, MARJANOVIĆ D, RUDAN P, VILLEMS R, & UNDERHILL PA, Croat Med J, 52 (2011) 225. — 15. CINNIOĞLU C, KING R, KIVISILD T, KALFOĞLU E, ATASOY S, CAVALLERI GL, ... & UNDERHILL PA, Hum Gen, 114 (2004) 127. — 16. BAMSHAD M, KIVISILD T, WATKINS WS, DIXON ME, RICKER CE, RAO BB, ... & JORDE LB, Genome Res, 11 (2001) 994. — 17. KIVISILD T, ROOTSI S, METSPALU M, MASTANA S, KALDMA K, PARIK J, ... & VILLEMS R., Am J Hum Genet, 72 (2003) 313. — 18. MYRES NM, ROOTSI S, LIN AA, JÄRVE M, KING RJ, KUTUEV I, ... & UNDERHILL PA, Eur J Hum Genet, 19 (2011) 95. DOI: 10.1038/ejhg.2010.146. — 19. SEMINO O, PASSARINO G, OEFNER PJ, LIN AA, ARBUZOVA S, BECKMAN LE, ... & UNDERHILL PA, Science, 290 (2000) 1155. — 20. NASIDZE I, QUINQUE D, OZTURK M, BENDUKIDZE N, & STONEKING M., Ann Hum Gen, 69 (2005) 401. — 21. AL-ZAHERY N, SEMINO O, BENUZZI G, MAGRI C, PASSARINO G, TORRONI A, & SANTACHIARA-BENERECETTI AS, Mol Phylogenet Evol, 28 (2003) 458. — 22. HAMMER MF, REDD AJ, WOOD ET, BONNER MR, JARJANAZI H, KARAFET T, ... & BONNÉ-TAMIR B, Proceedings of the National Academy of Sciences, 97 (2000) 6769. — 23. DI GIACOMO F, LUCA F, ANAGNOU N, CIAVARELLA G, CORBO RM, CRESTA M, ... & NOVELLETTO A, Mol Phylogenet Evol, 28 (2003) 387.

S. Doğan

International Burch University, Department of Genetics and Bioengineering, Francuske revolucije bb, Ilidža 71210, Sarajevo, Bosnia and Herzegovina
e-mail: serkan.dogan@ibu.edu.ba

PREDVIĐANJE HAPLOGRUPA Y-KROMOSOMA UNUTAR NEDAVNO USELJENE TURSKE POPU-LACIJE U SARAJEVU (BIH)

S A Ž E T A K

Analiza distribucije haplogrupe Y-kromosoma se naširoko koristi prilikom istrage geografskih skupina različitih populacija, zbog čega ona ima važnu ulogu u populacijskoj genetici, obrascima migracija ljudi pa čak i u forenzičkim istragama. Pojedinačno određivanje tih haplogroupa uglavnom se temelji na analizi markera polimorfizma jednostrukog nukleotida (SNP) koji se nalazi dijela Y kromosoma (NRY) koji se ne spaja. S druge strane, svake godine se naglo povećava broj forenzičkih i antropoloških studija koje su istraživale kratke tandemska ponavljanja na Y-kromosomu (Y-STR). Tijekom posljednjih nekoliko godina, ovi markeri su se uspješno koristili kao metoda predviđanja haplogroupa, zbog čega su korišteni u ovom istraživanju. Prethodno dobiveni Y-STR haplotipovi (23 loci), od 100 nesrodnih turskih muškaraca koji su nedavno doselili u Sarajevo, su korišteni za određivanje haplogroupa pomoću softwarea »Whit Athey's haplogroup predictor«. Bayesovska vjerojatnost od 90 istraživanih haplotipova je veća od 92,2%, a kreće se od 51,4% do 84,3% za preostalih 10 haplotipova. Pronađen je distribucija od 17 različitih haplogroupa, od kojih je Y-haplogroupa J2a najviše rasprostranjena, a pronađena je u 26% svih uzoraka. Y-haplogrupe R1b, G2a i R1a su manje rasprostranjen, a pokrivaju raspon od 10% do 15% svih uzoraka. Zajedno, ove četiri haplogroupe čine 63% svih Y kromosoma. Jedanaest haplogroups (E1b1b, G1, I1, I2a, I2b, J1, J2B, L, Q, R2 i T) u rasponu od 2% do 5%, dok E1b1a i N se nalaze u 1% svih uzoraka. Dobiveni rezultati ukazuju na to da je velika većina turske očinske linije pripada lozi Y-kromosoma zapadne Azije, europskog Kavkazu, zapadne Europi, sjeveroistoka Europe, Bliskog istoka, Rusije, Anadolije i Crnog mora. Kako je raspodjela haplogroupa Y-kromosoma u skladu s ranije objavljenim podacima za tursko stanovništva koji žive u Turskoj, zaključeno je da analizirane populacije također mogu biti prepoznate kao reprezentativni uzorak turskog stanovništva koji žive u Turskoj.