
Y-chromosome variation in Basrah population

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ABSTRACT: *DNA profiles of Y-chromosome are useful in forensic science and population genetic. this study conducted a total of 191 unrelated male's analysis of the Y-chromosome verity in different regions of Basrah. This variety was explored by utilizing a system of 17 markers. For a uniparental system, observed the vast majority of haplogroups in the population of Basrah (R1b, J2, E1b1b, G2a, and J1) Originally from the Middle East and later spread to Western Eurasia. In all likelihood, Thirty percent of Y-chromosomes Landings from distant, inaccessible regions. This paper evaluates the level of haplotype diversity, as well as its implication for statistics. The distinctive extent of long geogenetic input observed for the Y-chromosomes seems to Display that gene flow events can mainly involve males in this region.*

KEY WORDS: Basrah population, genetic diversity, Y chromosome, STR, forensic genetics.

INTRODUCTION

Explicitly male is the human Y-chromosome, and the associated Y-STRs situating on the region that is not recombining of the patrilineal inheritance feature of the Y-chromosome, only the succession of fathers is passed on the sons Except for the mutations, they are transmitted unchanged, for paternal lineage analysis, it makes the Y-STR haplotype very useful (Neuhuber et al., 2013; Kayser *et al.*, 2004). Y-STRs are currently commonly used in forensic cases, especially in cases of sexual assault involving high levels of female DNA, and instances of paternity in the alleged father's absence. In population genetics and human evolutionary research, they also play an important role.

MATERIALS AND METHODS

Sample of blood (191) they are collected from unrelated, healthy male volunteers, born and Live in different parts of Basrah, of different ages. DNA was extracted using the gSYNC™ DNA Extraction Kit Quick protocol by the company Geneaid. **Genotyping** of the Y-STR Fifteen Y-STR single-copy loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS438, DYS439, DYS437, DYS448, DYS458, DYS456, DYS635, Y-GATAH4) and a locus for multicopy(DYS385a/b) Amplified with AmpFLSTR® Yfiler™ PCR amplification kit (Applied Biosystems, Foster City, CA, USA) As driven by the manufacturer. The PC

R products were genotyped on an ABI 3500 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) using capillary array electrophoresis. Gene Mapper_RIDX (Applied Biosystems, Foster City, CA, USA) was used for genotyping. All designations are based on similarities to the Yfiler kit's allelic ladder.

Statistical analysis

For the analysis using Microsoft Excel™, YSTR haplotype data was set up, including a Microsatellite Toolkit (Park, 2001).

The essential parameters of molecular diversity were determined utilising the Arlequin software Version 3.1 (Excoffier et al., 2005). Allele and haplotype frequencies were assessed using a simple gene-counting method. The allele frequency of the multicopy locus DYS385 was examined as a blend of two alleles. Quality gene diversity (GD) of every locus and haplotype diversity (HD) was processed.

Prediction of the Y-chromosome haplogroup

The haplotypes of the 191 male YSTRs were sent with identical priors to Whit Athey's Haplogroup Predictor (<http://www.hprg.com/hapest5/index.html>) (Vullo et al., 2015). When based on haplogroups, the most impressive chances have been overcome.

RESULTS AND DISCUSSION

Gene diversity

Gene diversity values for every Y-STR locus are given in Table (1). The lowest GD (0.3547) is found in the DYS392 locus and the highest (0.8461) in the DYS385 locus. The minimum number of alleles (4) is observed in DYS391, DYS439, DYS437, and DYS438, the Maximum number of alleles (9) in the DYS385 locus. For comparison, in a Turkish study on Y-STR loci of Turkey's Cukurova region, the minimum GD (0.5) was recorded in DYS391 and the highest (0.95) in DYS385, while no significant variations were found between these findings and other Data of the haplotype of different Turkish populations (Serin et al., 2011). The lowest value of GD was reported for the Kuwaiti population DYS437 (0.409), while the maximum (0.957) has been found in DYS385. The lowest GD value for the population of Failaka Island has been found in DYS392 (0.236), and the highest (0.976) in DYS385 (Theyab, 2013).

Table 1: Observed numbers of alleles and gene diversity values.

Locus	Sample Size	na*	ne*	h*	I
DYS456	191	6.0000	3.0788	0.6752	1.3221
DYS 3891	191	5.0000	1.9505	0.4873	0.8885
DYS390	191	7.0000	3.2054	0.6880	1.3982
DYS38911	191	7.0000	3.6354	0.7249	1.4963
DYS458	191	7.0000	4.5871	0.7820	1.6776
DYS19	191	8.0000	2.6168	0.6179	1.2462
DYS385	191	9.0000	6.4994	0.8461	1.9477
DYS393	191	6.0000	2.3135	0.5677	1.0564
DYS391	191	4.0000	1.9642	0.4909	0.8443

DYS439	191	4.0000	2.8077	0.6438	1.1692
DYS635	191	8.0000	3.4028	0.7061	1.5142
DYS392	191	7.0000	1.5497	0.3547	0.7958
Y_GATA_H4	191	5.0000	2.3914	0.5818	1.1228
DYS437	191	4.0000	2.1747	0.5402	0.9292
DYS438	191	4.0000	2.8173	0.6450	1.1738
DYS448	191	5.0000	2.5846::	0.6131	1.1916
Mean	191	6.0000	2.9737	0.6228	1.2359
St. Dev		1.6330	1.1988	0.1211	0.3160

na* = Observed number of alleles. ne* = Effective number of alleles. h* = gene diversity .I = Shannon's Information index. Number of polymorphic loci: 16. Percentage of polymorphic loci: 100.00%.

Table (2) Displays the mean number of pairwise differences (MPD) and the mean value of GD for Basrah and neighbouring populations. Iran shows the highest mean value of gene diversity (0.69356) (Haber et al., 2011), while Qatar shows the lowest (0.37274) (Cadenas et al., 2008). Kuwait and Failaka Island share similar GD, with values of 0.62578 and 0.64495, respectively (Theyab, 2013). The mean number of pairwise differences for the Basrah population is calculated at 16.745. The MPD values range from 5.521 for Qatar (Cadenas et al., 2008) to 10.911 for Iran (Haber et al., 2011). The mean numbers of pairwise differences for Kuwait and Failaka Island are 8.951 and 8.775, respectively (Theyab, 2013).

Table 2. Mean numbers of pairwise differences and GD values

Country and city	MPD	Gene diversity	References
Basrah	16.745	0.6228	Current study
Kuwait	8.951859 (+/- 4.153213)	0.62578	Theyab (2013)
Failaka Island	8.775362 (+/- 4.195306)	0.64495	Theyab (2013)
Saudi Arabia	5.276717(+/- 2.563487)	0.47404	Abu Amero et al. (2009).Alshamali et al. (2009)
Iran	10.911554(+/- 4.974798)	0.69356	Haber et al. (2011)
Yemen*	5.942041 (+/- 2.883168)	0.39659	Cadenas et al. (2008)
*Qatar	5.521739 (+/- 2.702610)	0.37274	Cadenas et al. (2008)
United*Arab Emirates	7.121204 (+/- 3.373326)	0.46178	Cadenas et al. (2008)

Allele frequency

Table (3) displays the observed allele frequencies of the 17 YSTR loci. The lowest frequency (0.0052) is seen in allele (1) in DYS3891 and DYS390, allele (2) in DYS19 and DYS393, allele (5) in DYS3891, allele (7) in DYS34, allele (8) in DYS635, and allele (9) in DYS19 and DYS393. The highest frequency was found in allele (3) in the DYS34 locus. The observed alleles in this study for all loci are between alleles (1) and (9), whereas results for the Turkish population have identified the alleles absorbed between (9) and (33) for all loci (Serin et al., 2011). In the current study we have observed no intermediate or null alleles, in contrast with Serin et al.'s (2011) findings for the Turkish population, which have identified a number of intermediate alleles at DYS458 – 12.2, 16.2, 17.2, 18.2, 19.2, and 20.2 –and one null allele at DYS448.

DYS45 6 91	DYS38 0	DYS39 911	DYS38 8	DYS45 8	DYS19 5	DYS38 5	DYS39 3	DYS33 9	DYS43 5	DYS63 5	DYS34 4	Y_GA TA_H 7	DYS43 8	DYS43 8	DYS44 8
0.0471	0.0052	0.0052	0.0105	0.0785	0.0105	0.0105	0.0052	0.0314	0.0942	0.0105	0.0052	0.0157	0.0052	0.2618	0.0681
0.2461	0.1257	0.0262	0.1361	0.1361	0.0052	0.0157	0.0052	0.6492	0.4817	0.0890	0.0262	0.0681	0.6126	0.5026	0.2147
0.4764	0.6806	0.1152	0.3351	0.3351	0.0209	0.0262	0.0314	0.2932	0.3246	0.4817	0.7958	0.5969	0.2670	0.1728	0.5654
0.1832	0.1832	0.4660	0.0157	0.2513	0.0785	0.1571	0.5916	0.0262	0.0995	0.1623	0.0209	0.2147	0.1152	0.0628	0.1257
0.0366	0.0052	0.0942	0.0942	0.0942	0.5497	0.1414	0.2670			0.1309	0.0785	0.1047			0.0262
0.0105		0.0262	0.2827	0.0942	0.2618	0.2042	0.0995			0.0995	0.0681				
			0.4084	0.0105	0.0681	0.1571				0.0209	0.0052				
			0.1204		0.0105	0.1309				0.0052					
			0.0681		0.0052	0.1571	0.0052								

Locus Allele	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 8	Allele 9
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Table 3. Allele frequency

Table (4) shows the minimum and maximum allele frequencies observed in this study. The lowest number of alleles is 4, at: DYS33, with a frequency of 0.5091; DYS439, with a frequency of 0.3562; DYS437, with a frequency of 0.4598, and DYS438, with a frequency of 0.3550. The maximum number of alleles observed is 9, at DYS358, with a frequency of 0.1539. The minimum allele frequency of 0.1111 is observed at DYS385, while the maximum allele frequency of 0.9691 is observed at DYS33, DYS439, DYS437, and DYS438.

Table 4. The minimum and maximum values of allele frequency and ‘The Statistics of Natural Selection’.

Locus	N	K	Obs. F	Min F	Max F	Mean*	SE*	L95*	U95*
DYS456	191	6	0.3248	0.1667	0.9490	0.4622	0.0250	0.2413	0.8421
DYS3891	191	5	0.5127	0.2000	0.9590	0.5290	0.0298	0.2758	0.8990
DYS390	191	7	0.3120	0.1429	0.9391	0.4123	0.0212	0.2171	0.7630
DYS38911	191	7	0.2751	0.1429	0.9391	0.4162	0.0210	0.2191	0.7700
DYS458	191	7	0.2180	0.1429	0.9391	0.4113	0.0224	0.2192	0.7862
DYS19	191	8	0.3821	0.1250	0.9294	0.3710	0.0171	0.1976	0.7012
DYS385	191	9	0.1539	0.1111	0.9197	0.3417	0.0157	0.1863	0.6643
DYS393	191	6	0.4323	0.1667	0.9490	0.4660	0.0278	0.2428	0.8510
DYS33	191	4	0.5091	0.2500	0.9691	0.5989	0.0324	0.3207	0.9486
DYS439	191	4	0.3562	0.2500	0.9691	0.6025	0.0335	0.3251	0.9387
DYS635	191	8	0.2939	0.1250	0.9294	0.3725	0.0187	0.1951	0.7259
DYS34	191	7	0.6453	0.1429	0.9391	0.4110	0.0209	0.2144	0.7691
Y_GATA_H4	191	5	0.4182	0.2000	0.9590	0.5258	0.0299	0.2665	0.8990
DYS437	191	4	0.4598	0.2500	0.9691	0.6018	0.0326	0.3267	0.9387
DYS438	191	4	0.3550	0.2500	0.9691	0.5996	0.0318	0.3198	0.9385
DYS448	191	5	0.3869	0.2000	0.9590	0.5293	0.0308	0.2712	0.8990

These statistics have been calculated using 1,000 simulated samples.

Chromosome STRs Haplotype

The haplotypes found in this study are compared with populations of seven other countries: Tunis (n = 81) (Imen et al., 2007); Germany (n = 88); India (n = 25); China (n = 36); Italy (n = 100) (Manfred et al., 2001); Japan (n = 161) (Hara et al., 2007), and Turkey (n = 245) (Henke et al., 2001) (Table 5).

Table 5. Comparison of haplotypes number in the different population groups.

Population group	Basrah 1	Iraq 2	Tunis 3	German4	Italy 5	China 6	India 7	Turkish
No. of individuals	191	100	105	88	100	36	154	281
No. of haplotypes	161	96	81	77	82	34	125	245

Prediction of the Y-chromosome haplogroup

The results of Y-chromosomal haplogroup predictions, and their probabilities for the Basrah population, are shown in Table (6). The most common haplogroups in Basrah are identified as R1b (20.5%), E1b1b (14.0%), G2a (11.0%), and J1 (10.8%). and 17% are (J2a1b(5%), J2a1h(2%), J2a1xj2a1-bh(4%), J2b(6%).

Kuwait's most prominent haplogroups are J1 (37%), R1a (11%), and E1b1b (7%), while J1 (20%) and E1b1b (17%) are the most common haplogroups in Failaka, (Theyab, 2013).

Y-haplogroup J2b, J2a1 xJ2, and G2a are found a high frequency respectively in Failaka Island (13%) and Kuwait (1%), (3%), and (3%). In this study, haplogroups H and T were found at 10.5% and 0.7%, and in Kuwait at 3% and 4%, respectively, and Failaka Island is not present (Theyab, 2013). The most frequent haplogroups in the Caucasus are F*, G*, and J2: the combined frequency of these three haplogroups ranges from 0.53-1.00. The frequency of haplogroup (I1) in the current study is 1.7, (I2a (xI2a1), 6.5), (I2a1, 2.0), (I2b (xI2b1), 0.4), (I2b1, 1.6), compared with groups of Darginians (0.58), Abkhazians (0.33), and North Ossetians from Ardon (0.32) (Nasidze et al., 2003).

The frequencies of J2 in this study are: 5.0% for J2a1b; 2.0% for J2a1h; 4.5% for J2a1 x J2a1-bh, and 6.5% for J2b. In comparison, the Georgian population from Kazbegi shows a frequency of 0.72 for haplogroup J2 (Wells et al., 2001).

In this study, the frequency of haplogroup G2a is 11.0%. The common Caucasus haplogroup, G, is rare or absent in Europe and among the Turkish and Lebanese populations in terms of other populations (Semino et al., 2000). Yet it is present in Tehran and Isfahan populations (0.1 and 0.2 frequencies, respectively). R1b (20.5%) is the most common haplogroup in Basrah. Haplogroup R1, widespread in Western and Central Europe, is mostly found in the Southern Caucasus (Nasidze et al., 2003).

Table 6. Haplogroup probability.

Haplogroup	Probability %
E1b1a	1.5
E1b1b	14.0
G2a	11.0
G2c	0.3
H	1.5
I1	1.7
I2a (xI2a1)	6.5
I2a1	2.0
I2b (xI2b1)	0.4
I2b1	1.6
J1	10.8
J2a1b	5.0
J2a1h	2.0
J2a1 x J2a1-bh	4.5
J2b	6.5
L	2.0
N	0.3
Q	3.2
R1a	4.0
R1b	20.5
T	0.7

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