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Original Research Article

Y-chromosomal STR variation in Kurds and Arabs population in Iraqi Kurdistan

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ABSTRACT

Background: The Iraqi Kurdistan local population involves more than eight gatherings of tenants. The Muslim Kurds make up most of the population and after that the Yezidi Kurds. Alternate gatherings incorporate Armenians, Assyrian, Chaldea, Syriacs, and little minority of Arab and Turkmen individuals.
Methods: A total of 36 unrelated males from the two population groups in Iraqi Kurdistan: Kurds and Arabs were analyzed for eight Y-chromosome STRs (DYS19, DYS392, DYS437, DYS448, DYS456, DYS458, DYS635 and Y-GATA-H4). Total DNA from blood cells was extracted using DNA extraction Kit.
Results: A number of genetic parameters such as mean number of alleles, allele frequency, gene diversity, polymorphic information content (PIC), and genetic distance were calculated using Power Marker V3.25 software. The DYS458 had the highest diversity (GD: 0.883), while loci DYS456 and Y-GATA-H4 had the lowest (GD: 0.574). The Dendrogram separated the populations into two main clades, the Kurd group and the Arab group except in one case only from the whole population.
Conclusions: This study confirms the discriminating power of high-resolution Y-STR typing and provides first primary dataset on Iraqi Kurdistan samples. The comparison of Kurdish and Arab datasets reveals an interesting overall picture of isolation of Kurdish group. The primers DYS19, DYS448, DYS458, and DYS635 can be considered the best for their high PIC power.

Keywords: Genetic diversity, Kurds and Arabs population and Iraqi Kurdistan, Y-chromosome STRs

INTRODUCTION

The Kurds are one of the indigenous peoples of the Mesopotamian plains and the highlands in what are now south-eastern Turkey, north-eastern Syria, northern Iraq, north-western Iran and south-western Armenia. They are Indo-European talking group.[1] The Iraqi Kurdistan local population involves more than eight gatherings of tenants. The Muslim Kurds make up most of the population and after that the Yezidi Kurds. Alternate gatherings incorporate Armenians, Assyrian, Chaldea, Syriacs, and little minority of Arab and Turkmen individuals.

DNA can be used to study human evolution. Besides, information from DNA typing is important for medico-legal matters with polymorphisms leading to more biological studies.[2] Since the STR markers are important for human identification purposes, the number of repeats can be highly variable among individuals and can be used for identification purposes.[3]

Chromosome Y microsatellites or STRs seem to be ideal markers to delineate differences between human populations for several reasons:

- They are transmitted in uniparental (paternal) fashion without recombination,
- They are very sensitive for genetic drift, and
- They allow a simple highly informative haplotype construction.

Also, for forensic applications this ability to differentiate distinct Y-chromosomes makes Y-STR's an advantageous addition to the well characterized autosomal STRs.[4-6] Only a few genetic studies have been carried out on Kurdish groups.

Previous genetic studies of classical markers indicated an overall genetic similarity of Kurds with other Middle Eastern populations.[7] Comas et al, studied mtDNA HV1 sequence variability among Kurmanji-speaking Kurds living in Georgia (Caucasus), and found close European affinities for Kurdish mtDNA lineages.[8]

Richards and his co-workers studied mtDNA HV1 sequence variability among 53 Kurds from Eastern Turkey and found that some mtDNA haplotypes found in Kurdish samples presumably originated in Europe, and were associated with back-migrations from Europe to the Near East.[9]

Wells and his colleagues investigated Y-chromosome SNP haplogroup distributions among Central Asian groups, including a group of Kurmanji-speaking Kurds living in Turkmenistan, but no specific conclusions were made regarding the history of the Kurdish group.[10] Nebel and his co-workers studied Y-chromosome SNP and short tandem repeat (STR) loci among different groups from the middle East, including a group of 95 Kurds from northern Iraq, and found close affinities for the Kurdish group to other Middle Eastern groups.[11] Finally, Nasidze and his co-workers studied three Kurdish groups: Zazaki and Kurmanji speakers from Turkey, and Kurmanji speakers from Georgia.[1]

The first aim of this study was to apply a number of microsatellite marker set for the genetic characterization of Kurds and Arabs population in Duhok province.

The second aim was to study a number of genetic parameters within population such as mean number of alleles, allele frequency, and gene diversity, polymorphic information content (PIC), genetic distance and phylogenetic tree and to select the most informative primers for further population genetic studies.

METHODS

A total of 36 blood samples from unrelated males of two ethnic groups who live in Duhok province/Kurdistan Region of Iraqi, the Kurds and Arabs were collected. Genealogical information of the donors was also collected. The DNA was extracted from the whole blood samples using DNA extraction Kit according to the instructions provided by the supplier company (Product # AV1002 AccuVis Bio's leaflet). Eight STR primers were used in this study, namely: DYS19, DYS392, DYS437, DYS448, DYS456, DYS458, DYS635 and Y-GATA-H4.

The PCR cycle parameters were as follows; one cycle of initial denaturation at 94˚C for 5min; then 38 cycles of denaturation at 94˚C for 60sec, annealing at 50˚C (DYS19); 51˚C (DYS392 and Y-GATA-H4); 55˚C (DYS448); 57˚C (DYS635); 58˚C (DYS437and DYS456); 62˚C (DYS458) for 30sec and extension at 72˚C for 1min; and followed by one cycle of final extension two at 72˚C for 7min.

The amplified products were run firstly on 1.5% agarose gel for fast and easy detection of successful amplifications. Then PCR products electrophoresed in 8% polyacrylamide gel. 100bp ladder DNA marker was run with PCR products for sizing of the bands and the DNA bands were visualized by silver staining.[12]

The resulting microsatellite data were analyzed using the power marker V3.25 software and TreeViewX was used for the construction of phylogenetic tree. The genetic relationships were estimated with Nei's (1972) standard genetic distance (SD).[13]

RESULTS

Basic parameters of molecular diversity and population genetic structure, including mean number of alleles, allele frequency, gene diversity, polymorphic information content, genetic distance was calculated using the software power marker V3.25.

The total number of alleles scored in both populations was 88 alleles. Allele sizes ranged between 115bp to 321bp (Table 1 and Table 2).

The number of alleles per locus varied from 3 alleles in the Kurds population at locus DYS 437 and DYS448 to 10 alleles in both populations at DYS 458 locus with an average of 5.125 alleles per locus (Table 3).

While for Arabs population, the number of alleles per locus ranged from 4 at DYS19, DYS392 and Y-GATA-H4 to DYS458 with average of 5.875 alleles per locus.

The results of this study revealed a range of allele frequency which varied from 0.222 in DYS458 to 0.611 in DYS456 with mean of 0.370 in the Kurds population (Table 4). In Arab population the range of allele frequency ranged from 0.167 in DYS458 to 0.556 in DYS 437 and Y-GATA-H4 with mean of 0.346 (Table 5).

In order to obtain reliable data analysis, the value of availability (number of observed alleles per number of individuals sampled) was determined. This value was found to be high in the both populations Kurds and Arabs with an average of 1.000.

Gene diversity is a way for populations to fit with changing environments. The gene diversity in Kurds population varied from 0.574 in DYS456 to 0.883 in DYS458 with mean of 0.739, which can be considered as a high.

In Arabs population the gene diversity ranged from 0.574 in Y-GATA-H4 to 0.883 in DYS 458 with mean of 0.748 which is higher than Kurds population.

Table 1: The Allele's size of Kurds population.

Primer	DYS 19	DYS 392	DYS 437	DYS 448	DYS 456	DYS 458	DYS 635	Y GATA H4
1	192	255	185	297	161	129	157	142
2	192	255	181	285	161	129	167	142
3	188	255	181	291	153	139	155	134
4	188	255	181	291	153	115	167	134
5	184	261	185	285	153	135	171	138
6	180	258	181	297	157	141	167	130
7	180	267	181	285	157	135	159	130
8	184	261	181	291	153	131	171	138
9	180	255	177	297	153	143	151	134
10	180	258	181	291	153	119	155	134
11	176	261	185	285	153	125	167	138
12	???	258	177	291	153	125	167	138
13	???	???	177	297	149	???	167	132
14	???	258	185	291	153	127	167	138
15	180	258	185	297	153	127	163	138
16	184	258	177	297	153	131	167	138
17	180	255	177	297	149	127	151	142
18	180	258	177	297	149	127	155	130
Means	183.2	258.0	180.8	292.3	153.7	122.5	162.4	136.1

Table 2: The allele's size of Arabs population.

Primer	DYS 19	DYS 392	DYS 437	DYS 448	DYS 456	DYS 458	DYS 635	Y GATA H4
1	204	273	185	303	145	131	163	142
2	208	264	185	309	149	129	153	138
3	200	262	181	315	149	137	159	138
4	200	270	181	309	153	127	163	146
5	196	285	181	321	149	143	157	142
6	204	261	181	321	149	143	157	138
7	196	258	177	321	149	145	157	142
8	196	267	181	303	153	137	147	138
9	200	267	185	303	145	119	159	138
10	196	261	185	315	151	125	155	134
11	200	261	185	303	137	119	155	142
12	196	261	185	309	141	133	157	138
13	196	258	185	309	141	139	151	138
14	200	261	189	315	141	115	153	142
15	196	261	189	315	145	139	151	138
16	200	258	189	309	145	115	151	138
17	200	258	185	309	145	115	151	142
18	196	258	185	313	149	137	145	138
Means	199.1	262.1	184.1	311.2	146.4	130.4	154.7	139.6

In this study the PIC was calculated for each marker as a relative measure of informativeness and ranged from 0.533 in DYS456 which can be considered as the least informative to 0.872 in DYS458 that has been considered the most informative primer (Table 4 and Table 5).

In the present study, the genetic distance in the Kurds population varied from 0.33 to 1.00 (Table 6) and the same in the Arabs population from 0.33 to 1 (Table 7).

Phylogenetic analysis results are shown in Figure 1. The Dendrogram separated the populations into two main clades, Kurd group and Arab group except only one case: a person (No.4) who was supposed to be a Kurd, clustered with the Arab group.

Table 3: A summary of the number of alleles per each population revealed by eight STR microsatellite loci.

Primer	Groups		Total
	Kurd	Arab	
DYS19	5	4	9
DYS 392	4	6	10
DYS 437	3	4	7
DYS 448	3	5	8
DYS 456	4	6	10
DYS 458	10	10	20
DYS 635	7	8	15
Y GATA H4	5	4	9
Total	41	47	88
Average	5.125	5.875	5.5

Table 4: Allele frequency, availability, gene diversity, and PIC in the Kurds population.

Marker	allele. frequency	Availability	Gene diversity	PIC
DYS 19	0.389	1.000	0.765	0.735
DYS 392	0.389	1.000	0.704	0.652
DYS 437	0.389	1.000	0.660	0.586
DYS 448	0.444	1.000	0.642	0.568
DYS 456	0.611	1.000	0.574	0.533
DYS 458	0.222	1.000	0.883	0.872
DYS 635	0.444	1.000	0.741	0.714
YGATA H4	0.389	1.000	0.741	0.700
Mean	0.370	1.000	0.739	0.700

Table 5: Allele frequency, availability, gene diversity, and PIC in the Arabs population.

Marker	Allele frequency	Availability	Gene diversity	PIC
DYS 19	0.444	1.000	0.636	0.565
DYS 392	0.389	1.000	0.716	0.671
DYS 437	0.556	1.000	0.611	0.558
DYS 448	0.333	1.000	0.759	0.719
DYS 456	0.333	1.000	0.765	0.730
DYS 458	0.167	1.000	0.883	0.871
DYS 635	0.222	1.000	0.846	0.827
Y-GATA-H4	0.556	1.000	0.574	0.500
MEAN	0.346	1.000	0.748	0.709

Table 6: The genetic distance within Kurds population.

K	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0.00	0.44	0.89	0.89	0.89	0.89	1.00	1.00	0.78	1.00	0.89	1.00	0.89	0.89	0.78	0.89	0.67	0.89
2	0.44	0.00	0.78	0.67	0.89	0.78	0.78	0.89	0.89	0.89	0.78	0.89	0.89	0.89	1.00	0.89	0.78	1.00
3	0.89	0.78	0.00	0.33	0.89	0.89	0.89	0.67	0.67	0.44	0.89	0.78	1.00	0.78	0.89	0.89	0.89	0.89
4	0.89	0.67	0.33	0.00	0.89	0.78	0.89	0.67	0.67	0.56	0.78	0.67	0.89	0.67	0.89	0.78	0.89	1.00
5	0.89	0.89	0.89	0.89	0.00	1.00	0.78	0.44	0.89	0.89	0.44	0.78	1.00	0.67	0.67	0.67	1.00	1.00
6	0.89	0.78	0.89	0.78	1.00	0.00	0.56	0.89	0.78	0.67	0.89	0.78	0.78	0.78	0.67	0.67	0.78	0.56
7	1.00	0.78	0.89	0.89	0.78	0.56	0.00	0.89	0.89	0.78	0.89	1.00	1.00	1.00	0.89	1.00	0.89	0.78
8	1.00	0.89	0.67	0.67	0.44	0.89	0.89	0.00	0.89	0.67	0.67	0.67	1.00	0.67	0.78	0.56	1.00	1.00
9	0.78	0.89	0.67	0.67	0.89	0.78	0.89	0.89	0.00	0.67	0.89	0.78	0.78	0.89	0.67	0.67	0.44	0.67
10	1.00	0.89	0.44	0.56	0.89	0.67	0.78	0.67	0.67	0.00	0.89	0.67	1.00	0.67	0.67	0.78	0.89	0.67
11	0.89	0.78	0.89	0.78	0.44	0.89	0.89	0.67	0.89	0.89	0.00	0.56	0.89	0.56	0.67	0.67	1.00	1.00
12	1.00	0.89	0.78	0.67	0.78	0.78	1.00	0.67	0.78	0.67	0.56	0.00	0.67	0.33	0.67	0.44	0.89	0.78
13	0.89	0.89	1.00	0.89	1.00	0.78	1.00	1.00	0.78	1.00	0.89	0.67	0.00	0.78	0.89	0.67	0.67	0.67
14	0.89	0.89	0.78	0.67	0.67	0.78	1.00	0.67	0.89	0.67	0.56	0.33	0.78	0.00	0.44	0.56	0.89	0.78
15	0.78	1.00	0.89	0.89	0.67	0.67	0.89	0.78	0.67	0.67	0.67	0.67	0.89	0.44	0.00	0.56	0.67	0.56
16	0.89	0.89	0.89	0.78	0.67	0.67	1.00	0.56	0.67	0.78	0.67	0.44	0.67	0.56	0.56	0.00	0.78	0.67
17	0.67	0.78	0.89	0.89	1.00	0.78	0.89	1.00	0.44	0.89	1.00	0.89	0.67	0.89	0.67	0.78	0.00	0.44
18	0.89	1.00	0.89	1.00	1.00	0.56	0.78	1.00	0.67	0.67	1.00	0.78	0.67	0.78	0.56	0.67	0.44	0.00

DISCUSSION

The average number of Allele in Arab population (5.875) was higher than that of Kurds population (5.125). The

mean number of alleles per locus scored in this study showed to be smaller than those published in fact sheet of National Institute of Standards and Technology (NIST) USA with an average of 9 alleles per locus.[14] Another study by Imad and his colleagues (2013) showed a range of 3 to 7 alleles per locus with an average of 5 alleles which is very close to the results of this study.[15] Similar results also have been reported by Peng and his co-workers (2008) and Park and his colleagues (2012) who used the majority of these markers.[16,17] High number of alleles per each population suggests high amount of genetic diversity in the population.

Table 7: The genetic distance within Arabs population.

A	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0.00	0.78	1.00	0.89	0.78	0.89	0.89	0.89	0.67	0.89	0.67	0.89	0.89	0.89	0.89	0.89	0.67	0.89
2	0.78	0.00	0.78	0.89	0.78	0.78	0.89	0.89	0.78	0.89	0.89	0.67	0.67	0.89	0.89	0.78	0.78	0.67
3	1.00	0.78	0.00	0.78	0.89	0.56	0.89	0.67	0.67	0.78	0.78	0.78	0.89	0.67	0.67	0.78	0.89	0.67
4	0.89	0.89	0.78	0.00	1.00	0.89	1.00	0.78	0.89	1.00	0.89	0.89	0.89	0.89	1.00	0.78	0.78	1.00
5	0.78	0.78	0.89	1.00	0.00	0.56	0.33	0.89	0.78	0.78	0.78	0.67	0.67	0.89	0.89	0.89	0.67	0.56
6	0.89	0.78	0.56	0.89	0.56	0.00	0.67	0.78	0.89	0.89	0.89	0.67	0.89	0.89	0.78	0.89	1.00	0.78
7	0.89	0.89	0.89	1.00	0.33	0.67	0.00	0.89	0.78	0.89	0.89	0.78	0.78	0.89	0.89	0.89	0.78	0.67
8	0.89	0.89	0.67	0.78	0.89	0.78	0.89	0.00	0.89	0.89	0.89	0.78	0.78	1.00	0.78	0.89	1.00	0.67
9	0.67	0.78	0.67	0.89	0.78	0.89	0.78	0.89	0.00	0.89	0.56	0.78	0.78	0.89	0.78	0.67	0.67	0.78
10	0.89	0.89	0.78	1.00	0.78	0.89	0.89	0.89	0.89	0.00	0.67	0.67	0.78	0.78	0.67	1.00	0.89	0.78
11	0.67	0.89	0.78	0.89	0.78	0.89	0.89	0.89	0.56	0.67	0.00	0.78	0.89	0.67	0.89	0.89	0.67	0.89
12	0.89	0.67	0.78	0.89	0.67	0.67	0.78	0.78	0.78	0.67	0.78	0.00	0.44	0.78	0.67	0.78	0.78	0.67
13	0.89	0.67	0.89	0.89	0.67	0.89	0.78	0.78	0.78	0.78	0.89	0.44	0.00	0.89	0.56	0.56	0.56	0.56
14	0.89	0.89	0.67	0.89	0.89	0.89	0.89	1.00	0.89	0.78	0.67	0.78	0.89	0.00	0.67	0.67	0.67	1.00
15	0.89	0.89	0.67	1.00	0.89	0.78	0.89	0.78	0.78	0.67	0.89	0.67	0.56	0.67	0.00	0.56	0.78	0.78
16	0.89	0.78	0.78	0.78	0.89	0.89	0.89	0.89	0.67	1.00	0.89	0.78	0.56	0.67	0.56	0.00	0.33	0.78
17	0.67	0.78	0.89	0.78	0.67	1.00	0.78	1.00	0.67	0.89	0.67	0.78	0.56	0.67	0.78	0.33	0.00	0.78
18	0.89	0.67	0.67	1.00	0.56	0.78	0.67	0.67	0.78	0.78	0.89	0.67	0.56	1.00	0.78	0.78	0.78	0.00

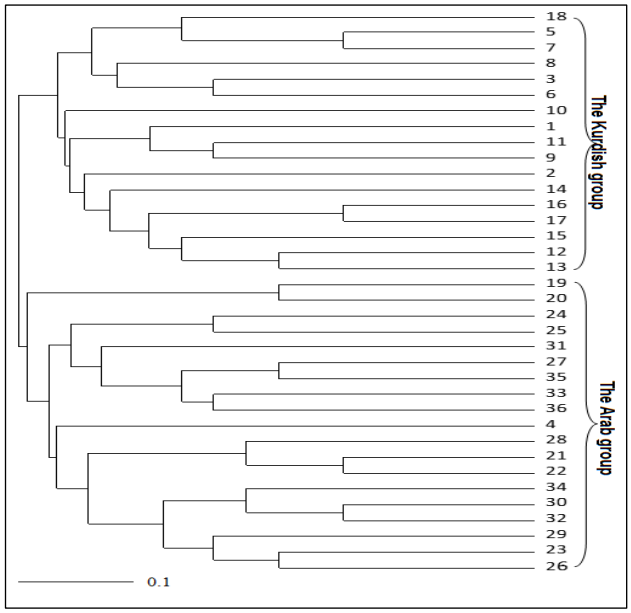

Figure 1: Dendrogram for the genetic relationship of Kurd and Arab populations.

The polymorphic information content (PIC) in the both populations are highly polymorphic because all values in all loci are greater than 0.5. Following the criteria of Botstein et al. (1984), all the markers were observed to be highly informative (PIC>0.5).[18] Which also suggested high utility of these markers for population assignment and genome mapping studies in addition to genetic diversity analysis.

These results indicate the presence of a high genetic diversity at the investigated Y chromosome loci in both populations, however the variance in Arab population was higher than those in the Kurds population. The genetic distance in both populations indicates the existence of great genetic distance between the studied populations.

Phylogenetic tree was constricted to determine the genetic differentiation. The neighbour-joining method was used to obtain the Dendrogram which separated the populations into two main clades, Kurd group and Arab group except only one case: a person (No.4) who was supposed to be a Kurd, clustered with the Arab group. This may be due to the recent migrations.

The molecular genetic evidence related to the origins of the Kurds is very limited. Nevertheless, we find some scattered papers. The Kurds are considered an ancient

autochthonous or native population.[19,20] Who may even be the descendants of the shepherds who first inhabited the high lands during the Neolithic period.[8,21] Although Kurdistan came under the successive control of various conquerors, including the Romans, Byzantines, Armenians, Arabs, Persian, Ottoman Turks and Iraqis.[18] They are the only western Asian group that remained relatively unmixed by the influx of invaders, because they were protected by inhospitable mountainous homeland .[20] On the basis of mtDNA polymorphisms, the Kurds were counted to be more closely related to Europeans than to middle Easterners.[8] These evidences are in agreement with the results of this study by using Y-STR markers and showed that the Kurds population was formed from a clad significantly different from the Arabs population. To study the origins and relationships of the Kurdish-speaking groups, Nasidze, (2005) used eleven Y chromosome bi-allelic markers, nine Y-STR loci and mtDNA HV1 sequences to analyze three Kurds groups: Zazaki and Kurmanji speakers from Turkey, and Kurmanji speakers from Georgia.

They compared their results with published data from other Kurds groups as well as groups from Europe, Caucasia, and West and Central Asian. They found that Kurds groups are most similar genetically to other West Asian groups, and most distant from Central Asian groups, for both mtDNA and the Y-chromosome. They found that the Kurds groups show a closer relationship with European groups than with Caucasian groups based on mtDNA, in contrast to the data based on the Y-chromosome, these indicate some differences in their maternal and paternal histories. The genetic data of their results also do not support the hypothesis of the origin of the Zazaki-speaking group living in northern Iran; genetically they are more similar to other Kurds groups.[1]

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