Iraqi Journal of Biotechnology, April 2019, Vol. 18, No. 1, 67-76

Estimation of Allele and Haplotype Frequencies for 17 YSTR Markers in the Diyala Arab Population

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Received: January 22, 2019 **/ Accepted:** April 10, 2019

Abstract: In this study, 17 Y chromosome –Short tandem Repeat (Y-STR) sites were (DYS635, DYS437, DYS448, DYS456, DYS458). YGATA H4 DYS1919, DYS38911, DYS90, DYS391, DYS392, DYS393, DYS438, DYS439 and DYS385 a / b) were analyzed in 110members of the Diyala Arab population. According to measures of genetic diversity the highest diversity was observed at loci DYS385a/b= (0.933), DYS458=(0.8 30) Low gene diversity (0.253). Therefore, these loci should be considered the most diverse and polymorphic for forensic testing that can be used to distinguish between male relatives. Genetic diversity values ranged from 0.253 to 0.933. The Diyala Arab populations is largely heterogeneous and a total of 78 different haplotypes were observed, there were 55 (0.009091) uniques haplotypes and 23 haplotype were shared between individuals. Haplotype diversity was 0.9990 and Discrimination capacity (DC) (0.705128).

Keywords: Haplotype, Y chromosome, population structure, Gene Diversity, Diyala populations.

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Introduction:

Human origin and migrations is an active topic in the field of anthropology and molecular genetics (1, 2). Separate genetic profiles can be constructed using standard marker sets for the autosomal chromosomes one through 22), Y-chromosome, and mitochondrial DNA. The types of genetic marker currently used in forensic genetic practice are length polymorphisms called short tandem repeats (STRs). STRs used forensically typically have a simple or more complex tetranucleotide repeat structure. The markers are highly polymorphic, with between 15 and more than 100 alleles observed at a locus, giving these markers, taken together, high power to discriminate between individuals (3).

In 1997, an effort was made to standardize the nomenclature for STR alleles, based on the number of repeated motifs or overall length polymorphism size (4, 5). That same year, the Federal Bureau of Investigation (FBI) announced a core of 13 autosomal STR loci required for the National DNA Index System (NDIS), a subset of the U.S. National Combined DNA Index System (CODIS). These markers were chosen to be highly informative, easily amplified using PCR, and on different chromosomes or opposite ends of the same chromosome so they are almost genetically unlinked (6).

A DNA analysis of markers located on the Y chromosome is valuable in certain cases, particularly in sexual assault cases, in which evidence often contains a mixture of DNA from both a female victim and a male perpetrator. The forensic community has agreed on a core set of 17 Y-STR (Y-chromosome short__tandem__repeat) markers, named the minimal haplotype DNA Y-chromosome(unique) segment (DYS) (DYS19, DYS389 I, DYS389 II, DYS390, DYS391, DYS392, DYS393 and DYS385ab) to use in routine Y-STR analysis(7).

The routine Y-STR analysis is based on multiplex amplification of the minimal haplotype loci as well as the loci recommended by **Scientific Working Group on DNA Analysis Methods** (SWGDAM) (DYS439 and DYS439). The amplified fragments are then size separated using Capillary electrophoresis (CE). (8, 9).

Highly variable regions within the DNA termed Short Tandem Repeats (STRs) are widely used for characterizing population structure and estimating human genetic diversity (10,11).

Such DNA-based data also provide leads in disease susceptibility studies, paternity and individual identification. Population genetic analyses utilizing such variable markers have identified bidirectional human migration through the Middle East, linking movement through Africa, Asia and Europe (12,13).

The Y chromosome is less variable than the other chromosomes. Many markers are thus needed to obtain a high degree of discrimination between unrelated males (14,15).

Research in DNA technologies has helped law enforcement agencies such as the police in the investigation of crimes such as murder, attempted murder, physical assault, and sexual assault. Sexual assault such as rape is one of the most violent crimes and is a serious problem which is faced by many countries (16).

The Y-chromosome haplotype is commonly constructed using STR markers. As the Y-chromosome is subjected to rapid genetic drift, haplotypes can be used to study the geographical distribution of ethnic groups (17). The Y-chromosome contains the largest non-recombining section within the human genome, providing informative haplotypes for genetic analyses of populations (18). The main source of information about Y-STR is the website YHRD.org. In practice, the frequency of the Y-STR profile in question can be estimated by referencing databases with large numbers of Y-STR profiles and counting the number of matching profiles within the population of interest. This provides an estimate of the profile probability for the Y-haplotype. One of these databases is the Y Chromosome Haplotype Reference Database (YHRD) (19). Following the guidelines of the International Society of Forensic Genetics (ISFG) for the publication of genetic population data, submissions to YHRD are required to consist at least 17 Y-STR markers (including the eight-marker minimal Y-haplotype: DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385).

It contains a description of the Y-STR loci used in forensic analysis, mutation rates, and the biggest global database available (more than 194,000 sampled individuals to this date).

Moreover, one of the *f*-estimating methods is implemented on the website, and its estimates are freely available. The only drawback is that, since many researchers publish anonymously on the website and do not want their data to be globally known, the haplotypes in the database are not accessible. For a haplotype H, an expert can only access the number of occurrences of H in the database, by subpopulation, and the f-estimate mentioned earlier (19).

Materials and Methods:

Collection of samples:

In this study, a buccal swab was collected from unrelated individuals living in Diyala (Arab Iraqi samples). All samples were DNA extraction in laboratory Al-Nahrain University in forensic DNA center research and training (3).

Genomic DNA extraction method:

DNA was extracted from buccal samples using organic extraction method (manual method), Organic extraction metho**d** was done according to the manufacturer protocol(20).

Estimate quantification of DNA:

The quantity of DNA was determined according to methods described by quantifier Y Human male quantification kit (21,22).

Amplification Y chromosome STR by using AmpFSTR^{R} Y Filer kit:

A commercial kit Y filer™ PCR amplification kit (Applied Biosystems, Foster City, CA) that amplifies 17 Y-STR loci: DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390 DYS439, DYS392, DYS393, DYS385a and DYS385b and a segment of the amelogenin gene was used.

Allele frequency:

The allele frequency of the multicopy locus DYS385a/b was analyzed as a combination of both alleles (16,23)

Allele frequencies for Y-Chromosomal STR were calculated by direct counting therefore:

Allele frequencies = Total no. of alleles / Total no. of samples

Haplotype frequency:

Haplotype frequency means of each haplotype of the sample found with any sample size. Haplotype Frequency was calculated by using the Excel program by using filter .

Gene diversity:

Gene diversity (GD) was calculated for each Y-STR according to the formula supplied by (24,25):

$$HD = \frac{N}{N-1}(1-\sum x^{2})$$

Where *n* is the sample size and *x* the relative allele frequency. Gene diversity among populations occurs if there are differences in allele frequencies between those populations

Haplotype diversity:

Haplotype Diversity (HD) was calculated using the same equation as calculating gene diversity using haplotype frequencies instead of allele frequencies (25).

Discrimination Capacity:

Discrimination Capacity (DC) was calculated using the following formula (25):

$$Discrimination\ Capacity = \frac{Number\ of\ unique\ hap.}{Number\ of\ hap.}$$

Y-STR Haplotype Reference Database:

The largest and most widely used forensic and general population genetics Y-STR database, known as the Y-STR Haplotype Reference Database (YHRD), was created by Willuweit and Roewer (19).

Results and Discussion:

Samples collected for the purpose to we will work were collected (Y-STR) of the provinces of Diyala Iraq of Arab Individuals lives in included the central governorates

Allele, Genotype frequencies and Gene Diversity for Diyala of Iraq males (n=110).

The GD value for DYS385 a/b among Diyala males was 0.933 (Table 1). Gene diversity values for Diyala of Iraq males ranges from 0.830 to 0.253. The highest GD value for a single-copy locus was 0.830 (DYS458). The lowest GD value was 0.253 (DYS392). DYS448, DYS458 and DYS635 have 8, 7 and 7 total number of alleles respectively (Table 1) with the genetic diversity of 0.631 0.830 and 0.693 respectively.

Loci which exhibited lower polymorphisms were DYS391, DYS38911, and DYS3891and DYS437 have a total number of 4 alleles with genetic diversity 0.482, 0.603, 0.588 and 0.567 respectively. DYS456, DYS19, DYS393, DYS439 and R-Y-GATA-H4 have 5 total numbers of alleles with 0.635, 0.603, 0.639, 0.560 and 0.578 genetic diversity.

All Y-STR loci showed a unimodal distribution modal distribution with one frequent allele and with less frequent adjacent alleles, differing by one repeat unit from the most frequent allele. Therefore, the distribution of chromosome Y STR alleles appears to be in accordance with the often proposed step-wise mutation model whereby new alleles of an STR-locus descend from the ancestral allele by deletions or expansions of one repeat unit (26).

The Allele Frequency data obtained from the present study was Similar found in other studies (27,28). Across the regions, the most frequent allele differs for nearly all loci.

Y-STR-haplotype and haplotype frequency:

In this study 110 haplotypes, each with 17 alleles were analyzed by using excel. The analysis measures the haplotype and haplotype frequency The observed number of haplotype and Haplotype frequency of any individual tabulated in Table (2). We identified 110 different haplotypes in our study sample; 55 (70.52%) were unique haplotype, 23 were (29.48.18%) were replicated haplotype among more individuals.

The highest haplotype was in sample 8 at frequency 0.072 (haplotype replicated 8 times), while the low haplotype number frequency (of haplotype 0.009), DC of the 17 Y-STR Yfiler 0.705 while HD was (0.999) in 17 Y-STR.

Table (1): Allele, Genotype frequencies and Gene Diversity for Al-Anbarl of Iraq males (n=112).

Allele	**DYS456**	**DYS3891**	**DYS390**	**DYS38911**	**DYS458**	**DYS19**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**R-Y-GATA-H4**	**DYS437**	**DYS438**	**DYS448**	**Genotype**	**DYS385ab**
6																11.13	0.018
7																11.14	0.027
8														0.018		11.15	0.009
9								0.055						0.209		11.19	0.036
10								0.564	0.027		0.018	0.036		0.582		12.12	0.018
11		0.009					0.036	0.300	0.600		0.864	0.600		0.173		12.13	0.018
12		0.136				0.009	0.527	0.082	0.282		0.027	0.218		0.009		12.14	0.027
13	0.027	0.691			0.009	0.173	0.255		0.064		0.036	0.136	0.018	0.009		12. 19	0.027
14	0.391	0.164			0.018	0.573	0.145		0.027		0.027	0.009	0.591			12.20	0.073
15	0.455				0.209	0.209	0.036				0.027		0.273			13.13	0.027
16	0.100				0.155	0.036							0.118		0.018	13.14	0.009
17	0.027				0.109										0.018	13.15	0.036
18					0.191										0.018	13.16	0.027
19					0.236										0.182	13.18	0.082
20					0.073					0.073					0.564	13.19	0.209
21			0.045							0.500					0.145	13.20	0.045
22			0.073							0.182					0.045	14.15	0.027
23			0.527							0.136					0.009	14.16	0.036
24			0.255							0.073						14.17	0.018
25			0.091													14.19	0.018
26			0.009							0.018						15.15	0.009
27										0.018						15.16	0.009
28				0.018												15.17	0.064
29				0.400												15.18	0.018
30				0.482												16.16	0.018
31				0.100												16.18	0.036
32																17.17	0.009
33																17.18	0.009
34																18.18	0.027
																18.19	0.009
sum freq.	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		1.000
N	110	110	110	110	110	110	110	110	110	110	110	110	110	110	110		110
NA	5	4	6	4	7	5	5	4	5	7	6	5	4	6	8	30	
G.D	0.635	0.482	0.647	0.603	0.830	0.603	0.639	0.588	0.560	0.693	0.253	0.578	0.567	0.593	0.631		0.933

***N=number of samples; NA= number of Alleles of each locus; GD = gene Diversity**

Table (2): Haplotype frequency in Diyala Arab of Iraq.

ID	DYS456	DYS389I	DYS 390	DYS389II	DYS458	DYS19	DYS385ab	DYS393	DYS391	DYS439	DYS635	DYS392	GATAH4	DYS437	DYS438	DYS448	N	Ferq.
H1	15	13	23	29	15	14	12,20	12	10	11	21	11	13	15	9	19	8	0.072727
H2	14	13	23	31	18	14	13,19	12	10	11	21	11	11	14	10	20	1	0.009091
H3	14	13	23	29	19	14	13,18	12	10	11	21	11	11	14	10	20	2	0.018182
H4	14	13	23	30	19	14	13,19	12	11	11	21	11	11	14	10	20	2	0.018182
H5	14	13	24	30	16	14	13,13	12	10	11	24	11	12	16	9	21	2	0.018182
H6	14	13	23	29	18	14	13,19	12	12	11	21	11	11	14	10	20	2	0.018182
H7	16	13	25	30	16	13	16,18	13	10	13	20	11	12	14	10	20	1	0.009091
H8	14	13	23	30	18	14	13,19	12	11	11	21	11	11	14	10	20	1	0.009091
H9	17	13	24	30	15	13	16,18	13	10	14	24	12	12	14	10	20	2	0.018182
H10	14	13	25	29	18	14	13,16	13	9	13	23	13	11	15	11	18	2	0.018182
H11	15	14	24	30	16	14	15,16	11	9	11	23	14	11	16	11	19	1	0.009091
H12	14	14	23	30	15	14	15,15	12	10	12	20	11	12	15	9	21	1	0.009091
H13	14	14	23	30	17	14	13,19	12	12	11	21	11	11	14	10	20	1	0.009091
H14	14	13	23	29	18	14	13,19	12	12	12	21	11	11	14	10	19	1	0.009091
H15	15	12	21	29	16	16	13,15	15	10	11	21	11	12	16	10	22	1	0.009091
H16	15	12	21	30	15	15	13,15	15	10	12	22	11	11	16	9	22	2	0.018182
H17	14	13	24	30	20	14	13,18	12	10	11	20	11	11	14	10	21	1	0.009091
H18	14	13	24	30	17	14	13,13	12	10	11	24	11	12	16	9	21	1	0.009091
H19	17	13	24	30	15	13	16,18	14	11	12	21	11	12	14	10	20	1	0.009091
H20	15	12	22	29	18	15	12,14	14	10	11	22	11	11	16	10	21	1	0.009091
H21	15	12	22	28	19	15	13,14	14	10	13	21	11	11	16	10	22	1	0.009091
H22	16	12	21	29	18	16	13,16	15	11	11	21	11	11	16	10	23	1	0.009091
H23	16	12	24	30	16	13	16,16	13	10	11	21	11	12	14	10	21	1	0.009091
H24	14	12	24	30	18	13	15,18	14	10	12	22	11	11	15	10	20	2	0.018182
H25	15	13	24	29	14	15	12,13	13	10	13	27	13	12	13	11	17	2	0.018182
H26	15	13	23	30	16	14	17,18	13	10	11	20	11	11	14	8	20	1	0.009091
H27	14	13	23	30	19	14	11,19	12	12	11	21	11	11	14	10	20	1	0.009091
H28	15	14	25	31	17	15	11,13	13	10	10	23	11	13	14	11	20	1	0.009091
H29	16	14	22	30	17	13	14,17	13	10	12	22	15	10	14	11	19	1	0.009091
H30	15	14	23	30	16	14	15,17	12	10	12	23	11	12	15	9	20	1	0.009091
H31	16	13	23	31	18	14	14,16	12	10	12	21	11	11	15	9	19	1	0.009091
H32	16	13	24	29	15	15	11,14	12	11	12	23	14	12	15	12	19	1	0.009091
H33	16	13	24	28	18	14	12,14	12	11	12	23	14	13	15	13	19	1	0.009091
H34	15	13	23	29	16	15	14,15	12	10	11	22	11	12	15	9	21	2	0.018182
H35	15	13	25	30	16	13	14,17	12	10	12	22	11	11	16	9	20	1	0.009091
H36	15	13	25	30	15	16	11,15	13	11	10	23	11	12	14	11	20	1	0.009091
H37	15	14	23	30	15	16	14,15	14	10	11	21	12	11	15	8	20	1	0.009091
H38	15	14	23	30	20	14	11,19	12	9	12	21	11	11	14	11	21	3	0.027273
H39	15	13	24	30	17	14	18,18	13	11	11	20	11	13	14	10	20	2	0.018182
H40	15	13	24	31	15	13	15,17	14	10	11	23	11	12	16	9	19	1	0.009091
H41	14	13	23	29	19	14	13,18	12	10	11	21	11	12	14	10	20	2	0.018182
H42	14	13	23	29	19	14	13,18	12	11	11	21	11	11	14	10	20	1	0.009091
H43	15	13	25	31	15	15	11,14	13	11	11	23	11	12	14	11	20	1	0.009091
H44	16	14	25	30	16	15	12,14	13	11	10	24	11	12	14	11	20	1	0.009091
H45	14	12	24	30	18	13	15,17	14	10	12	22	11	11	15	10	20	3	0.027273
H46	13	14	22	30	19	14	13,19	12	11	11	21	11	11	14	10	20	2	0.018182
H47	13	14	22	30	18	14	13,19	12	11	11	22	11	11	14	10	20	1	0.009091
H48	14	13	23	30	19	15	13,19	11	11	12	21	11	11	14	10	20	3	0.027273
H49	15	13	23	29	19	14	13,18	12	10	11	23	11	11	14	10	20	1	0.009091
H50	15	13	23	29	15	14	14,16	13	10	11	24	11	11	15	9	21	1	0.009091
H51	15	13	23	29	20	14	13,19	12	11	11	22	11	11	14	10	20	1	0.009091
H52	15	13	23	29	19	14	13,19	12	11	11	21	11	11	14	10	20	1	0.009091
H53	15	13	23	29	20	14	13,18	13	10	14	23	11	11	14	10	21	1	0.009091

ID	**DYS456**	**DYS389I**	**DYS 390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385ab**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**GATAH4**	**DYS437**	**DYS438**	**DYS448**	**N**	**Ferq.**
H54	15	13	21	31	17	15	13,15	13	11	12	22	11	10	16	10	22	1	0.009091
H55	15	11	23	29	19	14	12,19	12	10	13	21	11	11	14	10	20	1	0.009091
H56	14	13	23	30	18	14	13,19	12	10	11	21	11	11	14	10	20	1	0.009091
H57	14	12	24	30	18	13	15,17	14	10	11	22	11	11	15	10	20	2	0.018182
H58	14	13	23	29	19	14	13,19	12	11	11	21	11	11	14	10	20	2	0.018182
H59	14	13	23	29	19	14	13,20	12	11	11	21	11	11	14	10	20	1	0.009091
H60	14	13	23	29	19	14	13,19	12	12	12	21	11	11	14	10	19	1	0.009091
H61	14	13	23	29	19	14	13,19	12	12	11	23	11	11	14	10	20	1	0.009091
H62	14	13	23	29	19	15	13,19	12	12	11	21	11	11	14	10	20	1	0.009091
H63	15	13	26	31	13(NEW Aelle)	15	11,14	13	11	11	23	11	13	14	11	20	1	0.009091
H64	15	13	22	29	17	13	14,16	13	10	12	22	15	10	14	11	20	2	0.018182
H65	15	13	24	30	17	14	18,19	13	11	11	20	11	13	14	10	20	1	0.009091
H66	14	13	23	30	19	14	14,19	12	11	12	21	11	11	14	10	20	2	0.018182
H67	15	12	23	31	17	15	13,18	12	10	11	20	11	11	14	10	20	1	0.009091
H68	15	13	24	29	16	15	12,12	14	10	11	21	11	11	15	10	16	2	0.018182
H69	15	13	24	30	18	14	18,18	13	11	11	21	11	14	14	10	20	1	0.009091
H70	15	14	23	29	16	14	13,20	14	10	11	26	10	11	14	11	19	2	0.018182
H71	16	14	24	31	16	13	16,16	13	10	12	24	11	11	14	10	19	1	0.009091
H72	14	13	23	30	20	14	13,20	12	11	11	21	11	11	14	10	20	1	0.009091
H73	14	13	23	30	20	14	12,19	12	11	11	21	11	11	14	10	21	1	0.009091
H74	16	13	25	31	17	12	17,17	13	10	12	21	11	11	14	10	20	1	0.009091
H75	15	14	23	30	15	14	12,19	12	10	11	21	11	13	15	9	19	1	0.009091
H76	16	13	23	30	15	14	13,20	13	10	12	21	11	12	15	9	21	1	0.009091
H77	15	13	25	31	15	15	11,13	13	11	11	23	11	12	14	11	20	1	0.009091
H78	14	13	23	30	19	13	13,19	12	12	11	22	11	11	14	10	20	1	0.009091

Y-STR Haplotype Reference Database (YHRD):

The largest and most widely used forensic and general population genetics Y-STR database, known as the Y-STR Haplotype Reference Database (YHRD), YHRD is one of the most important Y-STR data analysis sites in the world. Populations from the Y-chromosome Haplotype Reference Database (YHRD) were chosen and compared to haplotype from the present study (referred to as the "present study") (www.yhrd.org) The Genetic distance was identified using the Population genetic distances (FST) calculated by using Analysis of molecular variance (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, analysis of molecular variance (AMOVA and MDS) tool available at the YHRD website (http://www.yhrd.org).

The result MDS plot Figure (1) and Fst test AMOVA Table (3) shows the genetic relative between the Arabian population of present study with population from United Arab Emirates ,Tunisia ,Saudi Arabia ,Kuwait, Algeria ,Bahrain ,Iran, Egypt ,Jordan ,Morocco ,Sudan, Yemen , Libya and Lebanon .The Iraq Arab population YSTR haplotype Studied in present study relative genetic relationship with Bahrain Fst(0.045) then Yemen Fst(0.0497) and Libya Fst(0.0439), While the most distant genetic relationship countries from Iraq were

Algeria Fst (0.2343), Sudan Fst(0.286) and Tunisia Fst (0.2005). Triki-Fendri *et al.* (28) used Y-STR data to support the relationship between the degree of genetic diversity and geographical location (29, 30, and 31). Genetic relatedness was seen between the Kuwaiti population and Arabian Peninsula populations (Yemen, Saudi Arabia and the UAE) (32, 33, 34) reflecting the close geographical location of the groups (35, 36, 37).

Table (3): Fst (AMOVA) results using 17 loci within different Arab populations.

Population	iraq-Diyala	Algeria	Bahrain	Egypt	Iran	Iraq	Kuwait	Lebanon	Libya	Morocco	Saudi Arabia	Sudan	Tunisia	Turkey	UAE	Yemen
"iraq-Diyala"	_	0.0000	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
"Algeria"	0.2343	_	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0005	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
"Bahrain"	0.0451	0.1468	_	0.0000	0.0086	0.1463	0.0456	0.0000	0.0000	0.0006	0.0000	0.0000	0.0000	0.0007	0.0000	0.0006
"Egypt"	0.0651	0.1126	0.0362	_	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.2099	0.0000	0.0000	0.0000	0.0013	0.008
"Iran"	0.0722	0.1448	0.0085	0.0687	_	0.0152	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
"Iraq"	0.0785	0.1307	0.0112	0.0551	0.0021	_	0.0000	0.0002	0.0000	0.0000	0.0000	0.0000	0.0000	0.0128	0.0000	0.0000
"Kuwait"	0.0557	0.136	0.0028	0.0229	0.0182	0.0145	_	0.0062	0.0000	0.0000	0.0029	0.0000	0.0000	0.0000	0.0000	0.0004
"Lebanon"	0.0638	0.1401	0.0058	0.036	0.0119	0.0081	0.0059	_	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0004
"Libya"	0.0439	0.1185	0.0605	0.0578	0.0867	0.0857	0.0654	0.0655	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
"Morocco"	0.1648	0.0969	0.1146	0.0968	0.0183	0.084	0.1053	0.1055	0.074	_	0.0000	0.0000	0.0004	0.0000	0.0000	0.0000
"Saudi Arabia"	0.0627	0.132	0.0248	0.0016	0.0528	0.0414	0.0116	0.0225	0.0652	0.0964	_	0.0000	0.0000	0.0000	0.0334	0.0345
"Sudan"	0.286	0.2606	0.1625	0.1634	0.1634	0.1542	0.1668	0.1932	0.2828	0.2058	0.1617	_	0.0000	0.0000	0.0000	0.0000
"Tunisia"	0.2005	0.0524	0.1087	0.0907	0.1194	0.1093	0.1083	0.1047	0.0773	0.0157	0.0986	0.2872	_	0.0000	0.0000	0.0000
"Turkey"	0.0963	0.133	0.0141	0.0742	0.0038	0.0024	0.0226	0.0158	0.1013	0.1058	0.057	0.1486	0.1128	_	0.0000	0.0000
"United Arab Emirate	0.0658	0.1763	0.0375	0.0126	0.0585	0.0519	0.0195	0.0309	0.0595	0.1212	0.0058	0.2335	0.1294	0.0706	_	0.0002
"Yemen"	0.0497	0.1911	0.0394	0.0212	0.0674	0.059	0.0341	0.0339	0.0732	0.132	0.0133	0.2573	0.1495	0.0758	0.0347	_

Fst = fixation index.

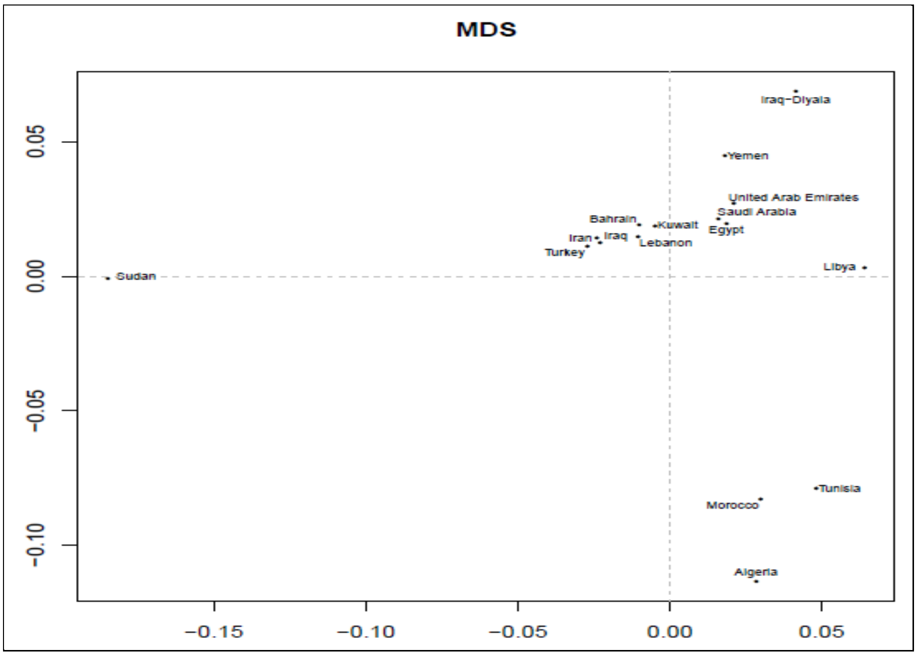

Figure (1): Multidimensional scaling (MDS) plot based on pairwise Fst genetic distance among Diyala Arab of Iraq male population and other Arab populations.

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