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Genetic Profiling of the Short Tandem Repeats (STRs) of Y-Chromosome of Populations of South Jordan

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Abstract

The aim of this study is to explore the differentiation capacity of 17 Y-Chromosomal Short Tandem Repeat markers (Y-STRs) and to enrich the forensic Y-chromosome databases southern districts of Jordan data for a better knowledge of the frequency and distribution of Y-chromosome markers across these populations. 17 Y-Chromosome Short Tandem Repeats loci (DYS456, DYS389i, DYS390, DYS389ii, DYS458, DYS19, DYS385a, DYS385b, DYS393, DYS391, DYS439, DYS635, DYS392, TAGA H4, DYS437, DYS438, and DYS448) were analyzed in blood samples of 160 unrelated males which were collected freshly and randomly from the governmental hospitals from the Southern Districts of Jordan (Ma'an, Karak, Tafila, Aqaba). The frequency of the alleles among Southern Districts of Jordan ranged from 0.61 to 89.6. The genetic diversity values for each Y-chromosome STRs ranged from a minimum of 0.2 to a maximum of 0.8. The minimal haplotype (calculated manually ≥ 75%) is composed of four STRs which were observed in the Southern Districts samples equivalent to most commonly loci which would be appear at this order, DYS392, DYS437, DYS438 and DYS439, ranged from a minimum of 75.5 % for (DYS439), 82.4% for (DYS438), 87.5 % for (DYS437), 89.7% for (DYS392), with mean value equal 83.8%. The similarity of our result to other Districts of Jordan is in the following order: Ajloun (100%), Irbid (75%), Jarash (25%), Mafraq (75%), Amman (75%), Zarqa (50%), Madaba (50%), and Salt (50%). The similarity of our result to other regional countries is in the following order: (Saudi Arabia (75%), Iraq (75%), Qatar (100%), Kuwait (25%), and United Arab Emirates (50%) Bahrain (50%), Oman (100%) and Yemen (75%), Syria (50%), Lebanon (0%), Libya (75%), Egypt (75%), Mauritania (75%), Tunis (75%), Algeria (75%) Morocco (100 %), Sudan (100%), Somali (25%). Our data shows that all Y –STR's loci typed were a bimodal distribution in paternity testing and in individual identification cases. These analyses support use of the haplotype population data for estimating Y-STR profile frequencies for populations residing in South Jordan and provides an informative analysis of the Y-Chromosomal STR diversity in the Arab population and emphasizes the discrimination capacity of high-resolution Y-STR typing that can be achieved in the Arab population for the forensic DNAcasework.

Keywords: Human genealogy; Loci; Short tandem repeats; Haplotype; Allele; Y-STR; PCR; Mutation; Gel electrophoreses

Introduction

Recently, there has been a worldwide growing interest on the genealogical profile among different nations, populations and some ethnic groups around the world using of the short tandem repeats (STRs) of the Y-chromosome [1-4]. In comparison with other parts of the world and a part from the sporadic studies on some limited Arabian populations [5-7], there is a lack of data on the Arabian genealogical landscape as well as their tribal migration and dispersal around the world. The genealogical culture and lifestyle of Arabs (422 million) is the driving force for the consanguineous marriage as favored and respected in all their communities with a range of 20-60 % [8-10], which is higher than the isolated and rural communities particularly among the Bedouins. The prevailing rate of the congenital genetic diseases and disorder are being directed by the genealogical land escape all over the Arabs Countries. In fact, the vast majority of their internal marriages occur within the first-cousin relationship which highly increases the prevalence of the autosomal recessive disorders in particular. The Nucleotide repeat expansions (NRTEs) disorders (such as CAG, CCG,CGG, CAACAG) comprise a heterogeneous group of diseases that result from expansion of specific repetitive DNA microsatellite sequences as the pathogenic expansions can occur in coding or non-coding regions of genes which used to be known as junk-DNA, where the main cause for such diseases includes: transcriptional regulation, mRNA splicing and metabolism, RNA binding protein distribution, signal transduction and cellular homeostatic pathways [11]. The genetic complexity and pathogenesis of the repeats expansion mutations have unexpectedly cause at least 22 inherited neurological diseases include some of the most common inherited diseases, such as Huntington's disease (HD) and myotonic dystrophy, neuraxis, the X-linked disorders fragile X syndrome of mental retardation (FMR1), X-linked spinal & bulbar muscular atrophy (SBMA) as caused by expansion of the (CAG/polyglutamine tracts) [12,13]. Furthermore, the Microsatellites instability has been reported to cause the colorectal cancer [14] and that STRs represent hypermutable region in human genome that are linked to human disease such as chronic prostatitis/chronic pelvic pain syndrome [15]. Therefore, the aim of this study, is to determine the genealogical profiling of the YSTRs among Arabian populations in the south of Jordan as a northward extension of the genetic outflow from the Arabian Peninsula, in order to help establishment of gene therapy platform as a new therapeutic approach for better managements of the familial genetic disease associated with the STRs expansion and instability.

Method and Materials

For the Southern districts of Jordan population genetic analysis, three ml of fresh blood collected using Citrate-anticoagulant tubes from random, unrelated, and healthy males from the Military and Public hospitals of Southern Districts of Jordan (Ma'an, Karak, Tafila, Aqaba). We genotyped Y-STRs in 160 samples, using 17 loci: (DYS456, DYS389i, DYS390,

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DYS389ii, DYS458, DYS19, DYS385a, DYS385b, DYS393, DYS391, DYS439, DYS635, DYS392, TAGA H4, DYS437, DYS438, and DYS448). DNA was extracted by using Promega Kit procedure. The Electrophoreses was used the HORIZON 58 apparatus in process to detect for the DNA which is isolated before, as stated by manufactures. Camera (Polaroid Gel Cam), and UV light source (BDH, serial no. 994716), Electrophoreses Hood 0.85x), Polaroid 667 Black & White instant pack film, are required for photographing the Ethidium bromide stained gel. The stained gel was placed directly on the top of a 300 nm Tran illuminator and photographed for a few second exposures at maximum aperture. Using spectrophotometer (BIO-RAD Smart Spec Plus spectrophotometer serial no. 273BR04037) to determine the purity of DNA. For DNA amplified we used the silver (96-Well Gene Amp PCR System 9700 PE Applied Biosystems, Serial no. 805S0030916), we used the PCR Amplification Kit (AmpFlSTR® Yfiler™). Running the Samples on the (ABI PRISM310™) Genetic Analysis PE Applied Bio-system, Code no. 100000738. The Date was analyzed by using the Data Collection Software v 3.1 and gene mapper ID software v 4, (Gene Scan analysis software + Genotyper software). Allele frequencies were estimated by gene counting. Allele diversity values were calculated using the formula D (n/n-1)/ (1-Σpi2), where n= number of samples and pi allele frequency. Allele frequencies for 17Y-STR markers are calculated.For Statistic Analysis to the Data, this was calculated by Standard Division SD, Mean M, P value, ANOVA.

Results

Ma'an district

Single locus analysis: The allele frequencies of Ma'an scored, for the seventeen Y–chromosome STR's with exception of DYS393, DYS390, DYS437and DYS448, DYS392 and DYS389i (which were predominant), and Y –STR's loci typed showed a bimodal distribution. The Frequency of alleles found ranged from 1.3% for (DYS389i, DYS390, DYS19, DYS393, and DYS448) to 93% for (DYS392) (Table 1). The gene diversity values for each Y- chromosome STR (Tables 2 and 3), ranged from a minimum of 0.53 for (DYS389i) to a maximum of 0.90 for (DYS385b). The most diverse loci were 0.68 for (DYS437 and DYS438), 0.73 for (GATA H4 and DYS393) and 0.74 for (DYS19 and DYS385a) with allele Diversity equal 0.72 (Tables 2 and 3).

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H 4	DYS 437	DYS 438	DYS 448
HM-JMN-1-1	17	13	24	29	15	15	13	16	12	10	11	21	11	12	15	-	21
HM-JMN-1-2	15	13	22	30	17	15	13	18	12	10	12	20	11	11	14	10	20
HM-JMN-1-3	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-4	17	13	24	29	15	15	13	16	12	10	11	23	11	12	15	-	21
HM-JMN-1-5	14	13	23	30	19	14	12	19	12	11	12	21	11	11	14	10	20
HM-JMN-1-6	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-7	16	13	24	29	20	13	14	16	13	9	10	21	11	12	14	10	20
HM-JMN-1-8	17	13	24	29	15	15	14	16	12	10	11	22	11	12	15	-	21
HM-JMN-1-9	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	20
HM-JMN-1-10	15	13	23	29	15	14	16	17	12	10	12	22	14	11	14	11	19
HM-JMN-1-11	17	13	24	29	15	15	13	16	12	10	12	23	11	12	15	-	21
HM-JMN-1-12	15	13	23	30	18	14	13	18	12	10	11	21	11	11	14	10	21
HM-JMN-1-13	13	13	22	29	20	14	13	17	12	10	12	21	11	11	14	10	20
HM-JMN-1-14	15	13	24	31	16	14	15	17	13	10	12	20	11	12	14	10	20
HM-JMN-1-15	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	-
HM-JMN-1-16	16	14	23	30	18	15	14	18	13	10	11	22	13	11	14	-	19
HM-JMN-1-17	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20
HM-JMN-1-18	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	18
HM-JMN-1-19	17	14	25	30	16	15	11	14	12	11	10	23	11	12	14	11	20
HM-JMN-1-20	17	13	24	29	15	15	13	16	12	10	11	23	11	12	15	9	21
HM-JMN-1-21	17	13	24	29	15	15	12	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-22	17	13	24	29	15	15	13	16	12	10	11	23	11	12	15	9	21
HM-JMN-1-23	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-24	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	20
HM-JMN-1-25	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-26	17	14	25	30	16	15	11	14	12	11	10	23	11	12	14	11	20
HM-JMN-1-27	15	13	23	30	18	14	13	19	13	10	11	21	11	11	14	10	20
HM-JMN-1-28	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JMN-1-29	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	20
HM-JMN-1-30	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-31	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-32	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-33	14	13	21	30	18	15	11	12	13	10	11	20	11	12	14	10	22
HM-JMN-1-34	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-35	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-36	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20
HM-JMN-1-37	15	13	23	31	15	14	15	17	12	10	11	23	11	12	15	9	21
HM-JMN-1-38	15	13	25	30	16	14	-	-	13	10	11	22	-	12	14	10	20
HM-JMN-1-39	15	13	23	29	16	14	13	13	13	10	11	21	-	11	14	10	20
HM-JMN-1-40	15	13	23	29	18	14	13	20	13	10	11	20	11	11	14	10	20
HM-JMN-1-41	15	13	23	30	18	14	13	18	13	10	11	21	-	11	14	10	20
HM-JMN-1-42	15	13	23	30	18	14	-	-	13	10	11	21	11	11	14	10	20
HM-JMN-1-43	15	13	23	29	16	14	13	19	13	10	11	21	11	11	14	10	20

HM-JMN-1-44	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20
HM-JMN-1-45	15	13	24	30	16	13	-	-	13	10	11	21	-	13	14	10	20
HM-JMN-1-46	14	13	23	30	18	14	12	19	12	11	12	20	11	11	14	10	20
HM-JMN-1-47	15	13	22	30	18	14	13	20	13	10	11	21	11	11	14	10	20
HM-JMN-1-48	15	12	24	30	15	13	14	17	14	10	11	21	11	13	14	10	20
HM-JMN-1-49	15	13	24	30	16	14	16	17	14	10	11	22	11	12	14	10	20
HM-JMN-1-50	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JMN-1-51	16	14	24	30	17	13	13	15	13	9	10	21	11	12	14	10	20
HM-JMN-1-52	15	13	22	30	18	14	13	20	13	10	11	21	11	11	14	10	20
HM-JMN-1-53	17	14	25	30	16	15	11	14	12	11	10	23	11	12	14	11	20
HM-JMN-1-54	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-55	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-56	15	13	23	29	19	14	13	19	13	10	11	21	11	11	14	10	20
HM-JMN-1-57	15	13	24	30	16	14	16	17	14	10	11	22	11	12	14	10	20
HM-JMN-1-58	15	14	23	29	17	14	13	20	12	9	11	20	11	10	14	10	20
HM-JMN-1-59	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-60	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20
HM-JMN-1-61	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	20
HM-JMN-1-62	15	14	23	29	17	14	13	20	12	9	11	20	11	10	14	10	20
HM-JMN-1-63	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JMN-1-64	15	13	23	30	18	14	13	18	12	10	11	21	11	11	14	10	21
HM-JMN-1-65	15	13	23	30	18	14	11	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-66	17	13	24	30	15	15	13	16	12	10	11	22	11	12	-	9	21
HM-JMN-1-67	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-68	15	13	23	29	18	14	13	18	13	10	11	21	11	11	14	10	20
HM-JMN-1-69	13	13	22	29	20	14	14	17	12	10	11	21	11	11	14	10	20
HM-JMN-1-70	17	13	24	29	15	15	13	16	11	10	11	22	11	12	-	9	21
HM-JMN-1-71	15	13	23	29	20	14	13	18	12	10	12	20	11	11	14	11	20
HM-JMN-1-72	17	13	22	30	18	13	13	20	13	12	11	21	11	11	14	10	20
HM-JMN-1-73	15	13	23	29	15	14	16	17	12	10	12	22	-	11	14	11	19
HM-JMN-1-74	17	13	24	29	15	14	13	16	12	10	11	22	11	12	-	9	21
HM-JMN-1-75	15	13	24	31	17	16	14	14	13	11	12	22	11	11	-	10	19
HM-JMN-1-76	17	13	24	29	15	15	13	16	12	10	11	21	11	12	-	9	20
HM-JMN-1-77	13	13	22	29	20	13	13	17	12	12	11	21	11	11	14	10	20

Table 1: Y-chromosomal STRs Detected in Ma'an District.

ALLEL	DYS 456	DYS 389 i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
9										5.2						25	
10										82	6.5		4.2	2.6		75	
11							6.8		1.3	10	77		93	53			
12		1.3					8.1	1.4	55	2.6	17		1.4	42			
13	6.5	88				7.8	69	1.4	40				1.4	2.6			
14	3.9	10				57	8.1	5.4	3.9						75		
15	53				32	34	2.7	1.4							25		
16	3.9				13	1.3	5.4	30									
17	32				6.5			16									
18					27			23									1.3
19					2.6			8.1									5.3
20					9.1			14				10					64
21			1.3									47					28
22			12									32					1.3
23			44									10					
24			38														
25			5.2														
26																	
27																	
28																	
29				44													
30				40													
31				3.9													

Table 2: Allele Frequency % for Ma'an District.

Allele Diversity	DYS 456	DYS 389 i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
	0.77	0.53	0.8	0.79	0.88	0.74	0.74	0.9	0.73	0.6	0.64	0.8	0.55	0.73	0.68	0.68	0.72

Table 3: Allele Diversity for Ma'an District.

The most common haplotype: The most common haplotype refers to the least of the most common frequencies (≥ 75%) among the tested samples. The most common haplotype is composed of six Y-STR's which were observed in the Ma'an district samples equivalent to most commonly loci which would be appeared at this order DYS391, DYS392, DYS389i, DYS437, DYS438, DYS439 ranged from a minimum of 75 % for (DYS437 and DYS438), 77% for DYS439, 82% for (DYS 391), 88% for DYS389i, to a maximum of 93 % for (DYS392) with mean value equal 81.6%. These results suggest that these loci improve the regional haplotype, which could be used for the genealogical studies for this geographical area in particular. This MinHt reflect a marked contrast of a minimum genetic homogeneity of the population despite, the apparent genetic heterogeneity in other circumstances as revealed by the G.D. The Ma'ani model haplotype was shown in (Table 4a) (as calculated by Y-utility software at probability equal 50%) and can be considered here for discussion due to low value of confidence limits at such model, (Table 4b) shows the MinHt Calculated manually ≥ 75%.

Karak district

Single locus analysis: The allele frequencies of Karak samples scored, for the seventeen Y–chromosome STR's with exception of DYS438 and DYS448, DYS392, DYS389i, and TAGA H4 (which were predominant), all Y–STR's loci typed showed a bimodal distribution. The Frequency of alleles found ranged from 2.56 for (DYS458, DYS393, DYS391, and DYS635) to 94.9 for (DYS437), (Table 5). The gene diversity values for each Y- chromosome STR (Tables 6 and 7),

DYS 456	DYS 389 i	DYS 390	DYS 389 ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
-	14	16	11	15	11	11	29	13	13	18	-	20	32	10	-	21

Table 4a: A Model Calculated by Y-Utility software as probability=50%

Markers	DYS391	DYS392	DYS389i	DYS437	DYS438	DYS439
Alleles	10	11	13	14	10	11
Percentage %	82	93	88	75	75	77

Table 4b: Minimal Haplotype Calculated manually ≥75%; Total Similarity of Minimal Haplotype Model=81.6 %.

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
HM-JK-1-1	14	13	22	29	20	14	13	18	12	11	12	21	11	11	14	10	20
HM-JK-1-2	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JK-1-3	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20
HM-JK-1-4	15	13	23	31	19	14	12	20	12	10	11	20	11	11	14	10	20
HM-JK-1-5	15	13	24	30	16	13	17	17	13	10	11	21	-	11	14	10	20
HM-JK-1-6	17	13	24	29	16	14	11	14	12	11	12	23	13	12	15	12	19
HM-JK-1-7	13	13	22	29	20	14	13	16	12	11	11	21	11	11	14	10	20
HM-JK-1-8	15	13	24	29	17	13	-	-	13	10	12	23	-	12	14	12	19
HM-JK-1-9	15	13	23	31	20	15	13	19	12	11	11	21	11	11	14	10	20
HM-JK-1-10	15	13	24	30	16	13	18	18	13	10	11	21	11	13	14	10	20
HM-JK-1-11	15	13	24	29	17	13	12	15	13	11	12	23	13	12	14	12	19
HM-JK-1-12	15	13	23	30	18	15	17	18	13	10	12	20	11	13	14	10	20
HM-JK-1-13	15	13	23	30	17	15	17	18	13	10	12	20	11	13	14	10	20
HM-JK-1-14	14	12	23	29	20	14	13	19	12	11	11	21	11	11	14	10	20
HM-JK-1-15	15	13	23	29	18	14	13	19	13	10	11	20	11	11	14	10	20
HM-JK-1-16	15	13	24	30	16	14	16	17	14	10	11	22	11	12	14	10	20
HM-JK-1-17	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JK-1-18	16	13	24	30	19	15	-	-	13	11	11	21	9	12	14	-	21
HM-JK-1-19	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	21
HM-JK-1-20	15	13	23	30	19	15	13	18	12	12	11	21	11	11	14	10	20
HM-JK-1-21	13	13	22	29	20	14	13	17	12	11	11	20	11	11	14	10	20
HM-JK-1-22	13	14	22	31	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JK-1-23	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	19
HM-JK-1-24	15	13	23	31	17	13	15	17	13	10	11	24	11	11	14	10	20
HM-JK-1-25	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21
HM-JK-1-26	15	13	24	30	16	14	17	18	13	10	11	22	11	12	14	10	20
HM-JK-1-27	13	13	22	29	20	14	14	19	12	11	11	21	11	11	14	10	20
HM-JK-1-28	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JK-1-29	15	13	24	30	16	13	17	18	13	10	11	21	11	12	14	10	20
HM-JK-1-30	15	13	23	30	17	15	17	18	12	11	12	20	11	13	14	10	20
HM-JK-1-31	17	13	24	30	16	13	-	-	13	12	11	21	10	12	14	10	20
HM-JK-1-32	13	14	22	30	20	13	13	17	12	12	11	21	11	11	14	10	20
HM-JK-1-33	13	13	22	29	20	14	13	18	12	10	11	21	11	11	14	10	20
HM-JK-1-34	13	13	22	29	20	14	13	18	12	9	12	22	11	11	14	10	20
HM-JK-1-35	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	21
HM-JK-1-36	13	13	22	29	20	13	13	17	12	11	11	20	-	11	14	10	20
HM-JK-1-37	13	13	22	29	20	13	13	17	12	11	11	21	13	11	14	10	20
HM-JK-1-38	16	13	23	30	16	13	16	18	13	10	11	22	11	11	14	10	19
HM-JK-1-39	14	12	24	29	17	14	15	16	12	10	12	21	11	11	14	9	19

Table 5: Y-chromosomal STRs Detected In Karak District; (-) Not Detected.

ranged from a minimum of 0.25 for (DYS392) to a maximum of 0.82 for (DYS385b). The most diverse loci were 0.63 for (DYS19 and DYS385a) and 0.25 for (DYS392 and DYS438).

The most common haplotype: The most common haplotype refers to the least of the most common frequencies (≥ 75%) among the tested samples. The most common haplotype is composed of five Y-STR's which were observed in the Karak district samples equivalent to most commonly loci which, would be appeared at this order DYS392, DYS389i, DYS437, DYS438, DYS439 and DYS 448, ranged from a minimum of 75% for (DYS439 and DYS 448), 79.5 for (DYS 389i), 86% for (DYS 392), 87% (DYS 438), to a maximum of 94.9 % for (DYS437) with mean value equal 82.9%. These results suggest that these loci and may will be considered in order to improve the regional haplotype, which could be used for the genealogical studies for this geographical area in particular. This MinHt reflect a marked contrast of a minimum genetic homogeneity of the population despite, the apparent genetic heterogeneity in other circumstances as revealed by the G.D. The Karak district model haplotype shown in Table 8a (as calculated by Y-utility software at probability equal 50%), and can be considered here for discussion due to low value of confidence limits at such model, Table 8b shows the MinHt calculated manually ≥75%.

Tafila district

Single locus analysis: The allele frequencies of Tafila samples scored, for the seventeen Y–chromosome STRs with exception of DYS438, DYS448, DYS391, DYS389i, DYS389ii, DYS458 and DYS437 (which were predominant), all Y–STRs loci typed showed a bimodal distribution. The Frequency of alleles found ranged from 3.13 for (DYS456, DYS389ii, DYS458, DYS391, DYS439, DYS635, DYS437), to 96.8 for 437 (Table 9). The gene diversity values for each Y- chromosome STR (Tables 10 and 11), ranged from a minimum of 0.06 for (DYS437) to a maximum of 0.64 for (DYS385b and DYS392) with mean value equal 0.4. The most divers' loci were 0.43 for (DYS390, DYS635) and 0.33 for (DYS389i, and DYS19) and 0.64 for (DYS385b and DYS392).

The most common haplotype: The most common haplotype refers to the least for the most common frequencies (≥ 75%) among the tested samples. The most common haplotype is composed of twelve

ALLEL	DYS 456	DYS 389 i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
9										2.5			3			5	
10										43.6			3			87	
11							3			46.2	75		86	66.7			
12		5.13					6		59	7.7	25			23.1		8	
13	38.5	79.5				28.2	58		38.5				8	10.3			
14	7.69	15.4				53.8	3	3	2.56						94.9		
15	41				2.56	17.9	6	3							5.13		
16	5.13				20.5			8									
17	7.69				15.4		17	39									
18					7.69		3	31									
19					7.69			14									14.7
20					46.2			3				17.9					75
21												59					10.3
22			41									12.8					
23			28.2									7.69					
24			30.8									2.56					
25																	
26																	
27																	
28																	
29																	
30																	
31																	

Table 6: Allele Frequency % for Karak District.

	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385 a	DYS 385 b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
Allele Diversity	0.71	0.36	0.68	0.61	0.74	0.63	0.63	0.82	0.52	0.61	0.58	0.62	0.25	0.52	0.11	0.25	0.43

Table 7: Allele Diversity for Karak District.

DYS 456	DYS 389 i	DYS 390	DYS 389 ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
-	14	17	11	13	11	11	29	13	13	20	-	20	31	10	-	21

Table 8a: Model Calculated by Y-Utility software as probability=50%.

Markers	DYS392	DYS389i	DYS437	DYS438	DYS439	DYS448
Alleles	11	13	14	10	11	20
Percentage%	86	79.5	94.9	87	75	75

Table 8b: Minimal Haplotype Calculated manually ≥75%; Total Similarity of Minimal Haplotype Model =82.9%.

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
HM-JT-1-1	13	13	22	29	20	14	13	18	12	11	12	22	11	11	14	10	20
HM-JT-1-2	13	13	22	29	20	14	13	18	12	11	11	21	11	11	14	10	20
HM-JT-1-3	13	13	22	29	20	14	13	17	12	11	11	21	11	12	14	10	20
HM-JT-1-4	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-5	15	13	23	30	19	14	13	18	13	10	11	21	11	11	14	10	20
HM-JT-1-6	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-7	15	13	23	29	18	14	13	19	13	9	11	21	11	11	14	10	20
HM-JT-1-8	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20
HM-JT-1-9	15	13	22	29	15	14	-	-	12	10	12	22	-	11	14	9	-
HM-JT-1-10	15	13	24	29	16	14	17	-	12	10	12	22	-	11	15	9	20
HM-JT-1-11	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	20
HM-JT-1-12	13	13	22	29	20	14	13	18	12	11	11	21	11	11	14	10	20
HM-JT-1-13	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-14	15	13	23	29	18	14	13	13	13	10	11	21	11	11	14	10	20
HM-JT-1-15	13	14	22	30	20	14	13	17	12	10	11	21	11	11	14	10	20
HM-JT-1-16	17	14	24	31	16	13	11	-	13	11	10	23	-	12	14	11	20
HM-JT-1-17	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20
HM-JT-1-18	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-19	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-20	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	20
HM-JT-1-21	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	19
HM-JT-1-22	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20
HM-JT-1-23	13	13	22	30	20	14	13	17	12	11	11	20	11	11	14	10	20
HM-JT-1-24	13	13	22	29	20	14	13	17	12	10	11	21	11	11	14	10	20
HM-JT-1-25	16	13	25	30	15	15	11	14	13	10	11	23	11	13	14	11	20
HM-JT-1-26	16	13	25	30	15	15	11	14	13	10	11	23	11	13	14	11	20
HM-JT-1-27	13	13	22	29	20	14	13	17	12	10	11	21	11	11	14	10	20
HM-JT-1-28	13	13	22	29	20	13	13	17	12	12	11	21	11	11	14	10	20
HM-JT-1-29	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-30	13	13	22	29	20	13	13	17	12	11	11	21	11	11	14	10	20
HM-JT-1-31	13	13	22	29	20	13	13	18	12	10	11	21	11	11	14	10	20
HM-JT-1-32	13	13	22	29	20	14	13	18	12	11	11	21	11	11	14	10	20

Table 9: Y-chromosomal STRs Detected in Tafila District; (-) Not Detected.

ALLEL	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
9										3.13						6.25	
10										40.6	3.1		3.45			84.4	
11							9.68			53.1	75		96.6	88		9.38	
12							3.23		75	3.13	22			6.3			
13	65.6	93.8				12.5	83.9	3.5	25					6.3			
14		6.2				81.3		6.9							96.9		
15	25				9.38	6.25									3.13		
16	6.25				6.25												
17	3.13						3.23	55									
18					15.6			24									
19					3.13			10									3.23
20					65.6							3.1					96.8
21												75					
22			73.3									13					
23			20									9.4					
24			6.67														
25																	
26																	
27																	
28																	
29				81.3													
30				15.6													
31				3.13													

Table 10: Allele Frequency % for Tafila District.

Allele Diversity	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385 a	DYS 385 b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
	0.55	0.13	0.43	0.33	0.56	0.33	0.36	0.64	0.38	0.57	0.4	0.43	0.64	0.24	0.06	0.29	0.6

Table 11: Allele Diversity for Tafila District.

Y-STRs which were observed in the Tafila district samples equivalent to most commonly loci which, would be appeared at this order DYS389i, DYS389ii, DYS458, DYS19, DYS385a, DYS393, DYS439, DYS635, DYS392, TAGA H4, DYS437, DYS438, DYS448, ranged from a minimum of 75 % for (DYS393, DYS439, DYS635), 81.3 % for (DYS389ii, DYS19), 83.95% for (DYS385a), 84.4% for (DYS438), 87.5% for (TAGA H4), 93.8% for (DYS389I), 96.6% for (DYS392), 96.8% for (DYS448), to a maximum of 96.9% for (DYS437) with mean value equal 85.6% . These results suggest that these loci improve the regional haplotype, which could be used for the genealogical studies for this geographical area in particular. This MinHt reflect a marked contrast of a minimum genetic homogeneity of the population despite, the apparent genetic heterogeneity in other circumstances as revealed by the G.D. The Tafila model haplotype shown in Table 12a (as calculated by Y-utility software at probability equal 50%), can be considered for to discussion due to low value of confidence limits at such model, Table 12b shows the MinHt Calculated manually ≥ 75%.

Aqaba district

Single locus analysis: The allele frequencies of Syria scored, for the seventeen Y-chromosome STR's with exception of DYS437 and DYS448, DYS392, DYS391, and DYS456 (which were predominant), and all Y-STRs loci typed showed a bimodal distribution.

The Frequency of alleles found ranged from 8.33 for (DYS456, DYS391, DYS390, DYS389ii, DYS458, DYS19, DYS385a, DYS385b, DYS439, DYS635, TAGA H4, DYS437, and DYS448, to 100 for DYS391 (Table 13).

The gene diversity values for each Y-chromosome STR (Tables 14 and 15), ranged from a minimum of 0.00 for DYS391, to a maximum of 0.82 for (DYS390 and DYS 385a) with mean value equal 0.5. The most diverse loci were 0.61 for (DYS456, DYS389i, DYS439).

The most common haplotype: The most common haplotype refers to the least of the most common frequencies (≥ 75%) among the tested samples. The most common haplotype is composed of seven Y-STRs which were observed in the Aqaba district samples equivalent to most commonly loci which, would be appeared at this order DYS19, DYS391, DYS635, DYS392, DYS437, DYS438, DYS448. 75% for (DYS635, DYS439 and DYS448), 83.3% for (DYS392, DYS437 and DYS438), 91.7% for DYS19 and 100% for DYS391with mean equal 83.3%.

These results suggest that these loci improve the regional haplotype, which could be used for the genealogical studies for this geographical area in particular. This MinHt reflect a marked contrast of a minimum genetic homogeneity of the population despite, the apparent genetic heterogeneity in other circumstances as revealed by the G.D. The Aqaba district model haplotype shown in Table 16a (as calculated by Y-utility software at probability equal 50%), and can be considered here for discussion due to low value of confidence limits at such model, Table 16b shows the MinHt Calculated manually ≥ 75%.

STR Frequency and Similarity among populations of Southern Districts (Ma'an, Karak, Tafila and Aqaba)

Single locus analysis: A set of seventeen STR's loci was able effectively to separate populations into region clusters. The STR's may have different abilities to distinguish population within each class of markers, the number of alleles and the within population variance vary greatly from locus to locus. 165 males from Southern districts scored, for the seventeen Y –chromosome STR's and their Similarities are shown in Tables 17-20 with exception of DYS389i, DYS393, DYS392, TAGA H4, DYS438 and DYS448 (which were predominant), all Y –STR's loci typed showed a bimodal distribution. The Frequency of alleles found ranged from 0.61 for (DYS389i, DYS390, DYS389ii, DYS19, DYS393, DYS391, DYS439, and DYS437) to 89.6 for (DYS392), for the whole area of Jordan Southern districts. The genetic diversity values for each Y- chromosome STR (Tables 21 and 22), ranged from a minimum of 0.2 for (DYS392) to a maximum of 0.8 for (DYS385b). The most diverse loci were 0.69 for (DYS456 and DYS635), and 0.34 for (DYS389i & DYS437) with heterogeneity of allele equal 60.0 %, and Diversity of 0.54.

DYS 456	DYS 389 i	DYS 390	DYS 389 ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
-	14	17	11	13	11	11	29	13	13	20	-	20	21	10	-	21

Table12a: A Model Calculated by Y-Utility software as probability=50%.

Markers	DYS 19	DYS 392	DYS 393	DYS 385a	DYS 389i	DYS 389 ii	DYS 439	DYS 635	TAGA H4	DYS 437	DYS 438	DYS 448
Alleles	14	11	12	13	13	29	11	21	11	14	10	20
Percentage%	81.3	96.6	75	83.9	93.8	81.3	75	75	87.5	96.9	84.4	96.8

Table12b: Minimal Haplotype Calculated manual ≥75%; Total Similarity of Minimal Haplotype Model =85.6 %.

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
HM-JAQ-1-1	15	12	23	30	18	13	16	17	13	10	12	21	11	9	14	10	20
HM-JAQ-1-2	15	12	21	29	16	13	15	18	14	10	12	21	11	11	14	11	21
HM-JAQ-1-3	15	13	23	30	18	13	13	18	13	10	11	21	11	11	14	10	20
HM-JAQ-1-4	15	12	22	30	18	13	16	17	13	10	12	21	11	9	14	10	20
HM-JAQ-1-5	15	12	22	30	18	13	16	17	13	10	11	21	11	9	14	10	20
HM-JAQ-1-6	16	13	23	29	18	13	13	20	13	10	11	21	11	10	14	10	20
HM-JAQ-1-7	15	13	23	30	18	13	13	18	13	10	11	21	11	11	14	10	20
HM-JAQ-1-8	13	13	22	30	20	13	13	18	12	10	11	21	11	11	14	10	20
HM-JAQ-1-9	15	13	23	30	18	14	13	17	13	10	11	21	11	11	14	10	20
HM-JAQ-1-10	16	14	26	31	16	13	14	18	14	10	11	22	12	12	15	10	21
HM-JAQ-1-11	16	13	24	31	16	13	14	16	12	10	11	22	12	11	13	11	19
HM-JAQ-1-12	16	13	24	30	18	13	15	16	13	10	11	24	11	11	14	10	20

Table 13: Y-chromosomal STRs detected in Aqaba District.

ALLEL	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
9														25			
10										100				8.33		83	
11											75		83.3	58.3		17	
12		33.3							16.6		25		16.7	8.33			
13	8.33	58.3				91.7	41.7		66.6						8.33		
14		8.33				8.33	16.7		16.6						83.3		
15	58.3						8.33								8.33		
16	33.3				25		25	16.7									
17								33.3									
18					67			41.7									
19																	8.33
20					8.3			8.33									75
21			8.33									75					16.7
22			25									16.7					
23			41.7														
24			16.7									8.33					
25																	
26			8.33														
27																	
28																	
29				16.67													
30				66.67													
31				16.67													

Table14: Allele Frequency % for Aqaba District.

Allele Diversity	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385 a	DYS 385 b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
	0.61	0.61	0.82	0.55	0.54	0.18	0.82	0.78	0.56	0.00	0.61	0.52	0.31	0.64	0.32	0.31	0.44

Table 15: Allele Diversity for Aqaba District.

Table 16 a: A Model Calculated by Y-Utility software as probability=50%.

DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
-	14	16	11	9	11	11	11	10	13	18	-	20	31	10	-	21

Table 16b: Minimal Haplotype Calculated manual ≥75%; Total Similarity of Minimal Haplotype Model=83.3%.

Markers	DYS19	DYS391	DYS392	DYS635	DYS437	DYS438	DYS439	DYS448
Alleles	13	10	11	21	14	10	11	20
Percentage%	91.7	100	83.3	75	83.3	83.3	75	75

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448	Allele Similarity to the Model %	Similarity to the model/ District%	Similarity % To our MN model
Model	-	14	16	11	15	11	11	29	13	13	18	-	20	32	10	-	21	*	**	***
HM-JMN-1-1	17	13	24	29	15	15	13	16	12	10	11	21	11	12	15	-	21	12	7%	81.60%
HM-JMN-1-2	15	13	22	30	17	15	13	18	12	10	12	20	11	11	14	10	20	0		
HM-JMN-1-3	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-4	17	13	24	29	15	15	13	16	12	10	11	23	11	12	15	-	21	12		
HM-JMN-1-5	14	13	23	30	19	14	12	19	12	11	12	21	11	11	14	10	20	0		
HM-JMN-1-6	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-7	16	13	24	29	20	13	14	16	13	9	10	21	11	12	14	10	20	6		
HM-JMN-1-8	17	13	24	29	15	15	14	16	12	10	11	22	11	12	15	-	21	12		
HM-JMN-1-9	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-10	15	13	23	29	15	14	16	17	12	10	12	22	14	11	16	11	19	6		
HM-JMN-1-11	17	13	24	29	15	15	13	16	12	10	12	23	11	12	15	-	21	12		
HM-JMN-1-12	15	13	23	30	18	14	13	18	12	10	11	21	11	11	14	10	21	6		
HM-JMN-1-13	13	13	22	29	20	14	13	17	12	10	12	21	11	11	14	10	20	0		
HM-JMN-1-14	15	13	24	31	16	14	15	17	13	10	12	20	11	12	14	10	20	6		
HM-JMN-1-15	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	-	6		
HM-JMN-1-16	16	14	23	30	18	15	14	18	13	10	11	22	13	11	14	-	19	12		
HM-JMN-1-17	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20	6		

HM-JMN-1-18	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	18	6		
HM-JMN-1-19	17	14	25	30	16	15	11	14	12	11	10	23	11	12	14	11	20	12		
HM-JMN-1-20	17	13	24	29	15	15	13	16	12	10	11	23	11	12	15	9	21	12		
HM-JMN-1-21	17	13	24	29	15	15	12	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-22	17	13	24	29	15	15	13	16	12	10	11	23	11	12	15	9	21	12		
HM-JMN-1-23	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-24	15	13	23	29	18	14	13	20	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-25	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-26	17	14	25	30	16	15	11	14	12	11	10	23	11	12	14	11	20	12		
HM-JMN-1-27	15	13	23	30	18	14	13	19	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-28	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JMN-1-29	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	20	6		
HM-JMN-1-30	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-31	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-32	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-33	14	13	21	30	18	15	11	12	13	10	11	20	11	12	16	10	22	12		
HM-JMN-1-34	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-35	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-36	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20	0		
HM-JMN-1-37	15	13	23	31	15	14	15	17	12	10	13	23	11	12	15	9	21	12		
HM-JMN-1-38	15	13	25	30	16	14	-	--	13	10	11	22	-	12	14	10	20	6		
HM-JMN-1-39	15	13	23	29	16	14	13	13	13	10	11	21	-	11	14	10	20	6		
HM-JMN-1-40	15	13	23	29	18	14	13	20	13	10	11	20	11	11	14	10	20	6		
HM-JMN-1-41	15	13	23	30	18	14	13	18	13	10	11	21	-	11	14	10	20	6		
HM-JMN-1-42	15	13	23	30	18	14	-	-	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-43	15	13	23	29	16	14	13	19	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-44	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20	0		
HM-JMN-1-45	15	13	24	30	16	13	-	-	13	10	13	21	-	13	14	10	20	6		
HM-JMN-1-46	14	13	23	30	18	14	12	19	12	11	12	20	11	11	14	10	20	0		
HM-JMN-1-47	15	13	22	30	18	14	13	20	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-48	15	12	24	30	15	13	14	17	14	10	13	21	11	13	14	10	20	6		
HM-JMN-1-49	15	13	24	30	16	14	16	17	14	10	11	22	11	12	14	10	20	0		
HM-JMN-1-50	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20	6		
HM-JMN-1-51	16	14	24	30	17	13	13	15	13	9	10	21	11	12	14	10	20	12		
HM-JMN-1-52	15	13	22	30	18	14	13	20	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-53	17	14	25	30	16	15	11	14	12	11	10	23	11	12	14	11	20	12		
HM-JMN-1-54	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-55	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-56	15	13	23	29	19	14	13	19	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-57	15	13	24	30	16	14	16	17	14	10	11	22	11	12	14	10	20	0		
HM-JMN-1-58	15	14	23	29	17	14	13	20	12	9	11	20	11	10	14	10	20	6		
HM-JMN-1-59	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-60	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20	0		
HM-JMN-1-61	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	20	6		
HM-JMN-1-62	15	14	23	29	17	14	13	20	12	9	11	20	11	10	14	10	20	6		
HM-JMN-1-63	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	12		
HM-JMN-1-64	15	13	23	30	18	14	13	18	12	10	11	21	11	11	14	10	21	6		
HM-JMN-1-65	15	13	23	30	18	14	11	18	13	10	11	21	11	11	14	10	20	12		
HM-JMN-1-66	17	13	24	30	15	15	13	16	12	10	11	22	11	12	-	9	21	12		
HM-JMN-1-67	15	13	23	30	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-68	15	13	23	29	18	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JMN-1-69	13	13	22	29	20	14	14	17	12	10	11	21	11	11	14	10	20	0		
HM-JMN-1-70	17	13	24	29	15	15	13	16	11	10	11	22	11	12	-	9	21	12		
HM-JMN-1-71	15	13	23	29	20	14	13	18	12	10	12	20	11	11	14	11	20	0		
HM-JMN-1-72	17	13	22	30	18	13	13	20	13	12	11	21	11	11	14	10	20	6		
HM-JMN-1-73	15	13	23	29	15	14	16	17	12	10	12	22	-	11	16	11	19	6		
HM-JMN-1-74	17	13	24	29	15	14	13	16	12	10	11	22	11	12	-	9	21	12		
HM-JMN-1-75	15	13	24	31	17	16	14	14	13	11	12	22	11	11	-	10	19	6		
HM-JMN-1-76	17	13	24	29	15	15	13	16	12	10	11	21	11	12	-	9	20	6		
HM-JMN-1-77	13	13	22	29	20	13	13	17	12	12	11	21	11	11	14	10	20	0		

Table17: Similarity of Ma'an District STRs Samples with the model proposed by Y-utility research; (-) Not Detected, (*) Allele Similarity to the model %, (**)Allele Similarity to the model/District %, (***)Allele Similarity to our Minimal Haplotype model %.

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448	Allele Similarity to the Model %	Similarity to the model/ District%	Similarity % To our MN model
Model	-	14	17	11	13	11	11	29	13	13	20	-	20	31	10	-	21	*	**	***
HM-JK-1-1	14	13	22	29	20	14	13	18	12	11	12	21	11	11	14	10	20	0	4%	82.90%
HM-JK-1-2	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20	6		
HM-JK-1-3	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20	6		
HM-JK-1-4	15	13	23	31	19	14	12	20	12	10	11	20	11	11	14	10	20	0		
HM-JK-1-5	15	13	24	30	16	13	17	17	13	10	11	21	-	11	14	10	20	6		
HM-JK-1-6	17	13	24	29	16	14	11	14	12	11	12	23	13	12	15	12	19	6		
HM-JK-1-7	13	13	22	29	20	14	13	16	12	11	11	21	11	11	14	10	20	0		
HM-JK-1-8	15	13	24	29	17	13	-	-	13	10	12	23	-	12	14	12	19	6		
HM-JK-1-9	15	13	23	31	20	15	13	19	12	11	11	21	11	11	14	10	20	0		
HM-JK-1-10	15	13	24	30	16	13	18	18	13	10	11	21	11	13	14	10	20	6		
HM-JK-1-11	15	13	24	29	17	13	12	15	13	11	12	23	13	12	14	12	19	6		
HM-JK-1-12	15	13	23	30	18	15	17	18	13	10	12	20	11	13	14	10	20	6		
HM-JK-1-13	15	13	23	30	17	15	17	18	13	10	12	20	11	13	14	10	20	6		
HM-JK-1-14	14	12	23	29	20	14	13	19	12	11	11	21	11	11	14	10	20	0		
HM-JK-1-15	15	13	23	29	18	14	13	19	13	10	11	20	11	11	14	10	20	6		
HM-JK-1-16	15	13	24	30	16	14	16	17	14	10	11	22	11	12	14	10	20	0		
HM-JK-1-17	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20	6		
HM-JK-1-18	16	13	24	30	19	15	-	-	13	11	11	21	9	12	14	-	21	12		
HM-JK-1-19	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	21	12		
HM-JK-1-20	15	13	23	30	19	15	13	18	12	12	11	21	11	11	14	10	20	0		
HM-JK-1-21	13	13	22	29	20	14	13	17	12	11	11	20	11	11	14	10	20	0		
HM-JK-1-22	13	14	22	31	20	14	13	17	12	11	11	21	11	11	14	10	20	6		
HM-JK-1-23	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	19	0		
HM-JK-1-24	15	13	23	31	17	13	15	17	13	10	11	24	11	11	14	10	20	6		
HM-JK-1-25	17	13	24	29	15	15	13	16	12	10	11	22	11	12	15	9	21	6		
HM-JK-1-26	15	13	24	30	16	14	17	18	13	10	11	22	11	12	14	10	20	6		
HM-JK-1-27	13	13	22	29	20	14	14	19	12	11	11	21	11	11	14	10	20	0		
HM-JK-1-28	13	14	22	30	20	14	13	17	12	11	11	21	11	11	14	10	20	6		
HM-JK-1-29	15	13	24	30	16	13	17	18	13	10	13	21	11	12	14	10	20	6		
HM-JK-1-30	15	13	23	30	17	15	17	18	1	31	12	20	11	13	14	10	20	0		
HM-JK-1-31	17	13	24	30	16	13	-	-	13	12	13	21	10	12	14	10	20	6		
HM-JK-1-32	13	14	22	30	20	13	13	17	12	12	11	21	11	11	14	10	20	6		
HM-JK-1-33	13	13	22	29	20	14	13	18	12	10	11	21	11	11	14	10	20	0		
HM-JK-1-34	13	13	22	29	20	14	13	18	12	9	12	22	11	11	14	10	20	0		
HM-JK-1-35	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	21	6		
HM-JK-1-36	13	13	22	29	20	13	13	17	12	11	11	20	-	11	14	10	20	0		
HM-JK-1-37	13	13	22	29	20	13	13	17	12	11	11	21	13	11	14	10	20	0		
HM-JK-1-38	16	13	23	30	16	13	16	18	13	10	11	22	11	11	14	10	19	6		
HM-JK-1-39	14	12	24	29	17	14	15	16	12	10	12	21	11	11	14	9	19	0		

Table18: Similarity of Karak District STRs Samples with the model proposed by Y-utility research; (-) Not Detected, (*) Allele Similarity to the model %, (**)Allele Similarity to the model/District %, (***)Allele Similarity to our Minimal Haplotype model %.

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448	Allele Similarity to the Model %	Similarity to the model/ District%	Similarity % To our MN model
Model	-	14	17	11	13	11	11	29	13	13	20	-	20	21	10	-	21	*	**	**
HM-JT-1-1	13	13	22	29	20	14	13	18	12	11	12	22	11	11	14	10	20	0	2%	85.6%
HM-JT-1-2	13	13	22	29	20	14	13	18	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-3	13	13	22	29	20	14	13	17	12	11	11	21	11	12	14	10	20	0		
HM-JT-1-4	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-5	15	13	23	30	19	14	13	18	13	10	11	21	11	11	14	10	20	6		
HM-JT-1-6	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-7	15	13	23	29	18	14	13	19	13	9	11	21	11	11	14	10	20	6		
HM-JT-1-8	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20	6		

Citation: Mahasneh IA, Zuriegat QH (2019) Genetic Profiling of the Short Tandem Repeats (STRs) of Y-Chromosome of Populations of South Jordan. J Forensic Med 4: 127.

HM-JT-1-9	15	13	22	29	15	14	-	-	12	10	12	22	-	11	14	9	-	0		
HM-JT-1-10	15	13	24	29	16	14	17	-	12	10	12	22	-	11	15	9	20	0		
HM-JT-1-11	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	20	0		
HM-JT-1-12	13	13	22	29	20	14	13	18	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-13	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-14	15	13	23	29	18	14	13	13	13	10	11	21	11	11	14	10	20	6		
HM-JT-1-15	13	14	22	30	20	14	13	17	12	10	11	21	11	11	14	10	20	6		
HM-JT-1-16	17	14	24	31	16	13	11	-	13	11	10	23	-	12	14	11	20	12		
HM-JT-1-17	15	13	23	29	18	14	13	19	13	10	11	21	11	11	14	10	20	6		
HM-JT-1-18	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-19	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-20	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	20	0		
HM-JT-1-21	13	13	22	29	20	14	13	17	12	11	12	21	11	11	14	10	19	0		
HM-JT-1-22	15	13	23	29	18	14	12	18	12	10	12	22	10	11	14	10	20	0		
HM-JT-1-23	13	13	22	30	20	14	13	17	12	11	11	20	11	11	14	10	20	0		
HM-JT-1-24	13	13	22	29	20	14	13	17	12	10	11	21	11	11	14	10	20	0		
HM-JT-1-25	16	13	25	30	15	15	11	14	13	10	11	23	11	13	14	11	20	12		
HM-JT-1-26	16	13	25	30	15	15	11	14	13	10	11	23	11	13	14	11	20	12		
HM-JT-1-27	13	13	22	29	20	14	13	17	12	10	11	21	11	11	14	10	20	0		
HM-JT-1-28	13	13	22	29	20	13	13	17	12	12	11	21	11	11	14	10	20	0		
HM-JT-1-29	13	13	22	29	20	14	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-30	13	13	22	29	20	13	13	17	12	11	11	21	11	11	14	10	20	0		
HM-JT-1-31	13	13	22	29	20	13	13	18	12	10	11	21	11	11	14	10	20	0		
HM-JT-1-32	13	13	22	29	20	14	13	18	12	11	11	21	11	11	14	10	20	0		

Table19: Similarity of Tafila District STRs Samples with the model proposed by Y-utility research; (-) Not Detected, (*) Allele Similarity to the model %, (**)Allele Similarity to the model/District %, (***)Allele Similarity to our Minimal Haplotype model %.

ID	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448	Allele Similarity to the Model %	Similarity to the model/ District%	Similarity % To our MN model
Model	-	14	16	11	9	11	11	11	10	13	18	-	20	31	10	-	21	*	**	***
HM-JAQ-1-1	15	12	23	30	18	13	16	17	13	10	12	21	11	9	14	10	20	0	1.5%	83.3%
HM-JAQ-1-2	15	12	21	29	16	13	15	18	14	10	12	21	11	11	14	11	21	6		
HM-JAQ-1-3	15	13	23	30	18	13	13	18	13	10	11	21	11	11	14	10	20	0		
HM-JAQ-1-4	15	12	22	30	18	13	16	17	13	10	12	21	11	9	14	10	20	0		
HM-JAQ-1-5	15	12	22	30	18	13	16	17	13	10	12	21	11	9	14	10	20	0		
HM-JAQ-1-6	16	13	23	29	18	13	13	20	13	10	11	21	11	10	14	10	20	0		
HM-JAQ-1-7	15	13	23	30	18	13	13	18	13	10	11	21	11	11	14	10	20	0		
HM-JAQ-1-8	13	13	22	30	20	13	13	18	12	10	11	21	11	11	14	10	20	0		
HM-JAQ-1-9	15	13	23	30	18	14	13	17	13	10	11	21	11	11	14	10	20	0		
HM-JAQ-1-10	16	14	26	31	16	13	14	18	14	10	14	22	12	12	15	10	21	12		
HM-JAQ-1-11	16	13	24	31	16	13	14	16	12	10	11	22	12	11	13	11	19	0		
HM-JAQ-1-12	16	13	24	30	18	13	15	16	13	10	11	24	11	11	14	10	20	0		

Table 20: Similarity of Aqaba District STRs Samples with the model proposed by Y-utility research; (*) Allele Similarity to the model %, (**)Allele Similarity to the model/ District %, (***)Allele Similarity to our Minimal Haplotype model %.

ALLEL	DYS 456	DYS 389 i	DYS 390	DYS 389 ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
9										2.71			0.75	6.25		9.06	
10										66.6	2.41		2.66	2.73		82.4	
11							4.87		0.33	27.3	75.5		89.7	66.4		6.52	
12		33.4					4.33	0.35	51.4	3.36	22.2		4.53	19.9		2	
13	29.7	58				35.1	66.2	1.21	42.5				2.35	4.79	2.08		29.7
14	2.9	8.43				50.1	6.95	3.83	5.78						87.5		2.9
15	44.3				13.4	14.5	4.26	1.1							10.4		44.3
16	12.1				16.2	0.33	7.6	13.7									12.1
17	10.7				5.48		5.06	35.9									10.7
18					29.2		0.75	30									

19					3.36			8.1									
20					32.3			6.33				7.76					
21			2.41									64					
22			37.8									18.5					
23			33.5									6.77					
24			23									2.72					
25			1.3														
26			2.08														
27																	
28																	
29				50													
30				41.5													
31				8.5													

Table 21: Allele Frequency % for Southern Districts Samples.

Allele Diversity	DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGAH4	DYS 437	DYS 438	DYS 448
	0.69	0.34	0.7	0.56	0.79	0.59	0.63	0.8	0.54	0.51	0.5	069	0.2	0.6	0.34	0.44	0.4

Table 22: Allele Diversity for all Southern districts.

Markers	DYS392	DYS437	DYS438	DYS439
alleles	11	14	10	11
Percentage %	89.7	87.5	82.4	75.5

Table 23: Minimal Haplotype Calculated manual ≥75%; Total Similarity of Minimal Haplotype model for all Southern Districts= 83.8%.

DYS 456	DYS 389i	DYS 390	DYS 389ii	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	TAGA H4	DYS 437	DYS 438	DYS 448
-	14	17	11	15	11	11	29	13	13	20	-	20	31	10	-	21

Table 24: All Model Calculated by Y-Utility software as probability=50%.

The most common haplotype: The most common haplotype refers to the least of the most common frequencies (≥ 75%) among the tested samples. The most common haplotype is composed of four STR's which were observed in the Southern district samples equivalent to most commonly loci, which would be appeared at this order DYS392, DYS437, DYS438 and DYS439, ranged from a minimum of 75.5 % for (DYS439), 82.4 for (DYS438), 87.5 % for (DYS437), to a maximum of 89.7% for (DYS392), with mean value equal 83.8%. These results suggest that these loci and may will be considered in order to improve the regional haplotype, which could be used for the genealogical studies for this geographical area in particular. This MinHt reflect a marked contrast of a minimum genetic homogeneity of the population despite, the apparent genetic heterogeneity in other circumstances as revealed by the G.D. Table 23 shows the Minimal Haplotype Calculated manually ≥ 75%.

Statistical analyses

The means and Standard Deviations (S.D) were calculated and Mean for seventeen Y-STR's among all Southern District of Jordan as provided in Table 24. The SD ranged from a minimum of 0.000 for DYS391 in Aqaba, to maximum of 3.334 for DYS391 in Karak. The mean value ranged from a minimum of 09.84 for DYS 438 in Ma'an, to a maximum of 30.0 for DYS389ii in Aqaba. From these results we found converging between Southern of Jordan Population that means have similarity in genetic profile. A comparison of the P - Value for the mean values results for these seventeen Y-STR's systems of a study of Ma'an males with the results obtained from other districts (Southern of Jordan) (Table 25), showed no statistically significant difference between seventeen Y-STR's Except DYS456, DYS458, DYS385a (0.00), DYS390 (0.045), DYS19 (0.005), DYS393 (0.097), DYS391(0.003), DYS439 (0.08), DYS437 (0.001) and DYS448 (0.025) for Karak District. DYS456, DYS458, DYS437 (0.000) and DYS390 (0.007), DYS389i (0.009), DYS19 (0.001), DYS438 (0.014) for Tafila.GATAH4, DYS19 (0.000), DYS385a (0.004) for Aqaba. A comparison of the P - Value for the mean values results for these seventeen Y-STR's system of a study of Karak males with the results obtained from other districts (Southern of Jordan) (Table 26), showed no statistically significant difference between seventeen Y-STR's Except DYS456, DYS458, DYS385a (0.000), DYS390 (0.045), DYS19 (0.005), DYS393 (0.097), DYS391(0.003),DYS439 (0.08), DYS437 (0.001) and DYS448 (0.025) for Ma'an District. DYS389ii (0.002) for Tafila, DYS19, GATAH4 (0.000), DYS393 (0.015) for Aqaba District. A comparison of the P-Value for the mean values results for these seventeen Y-STRs system of a study of Tafila males with the results obtained from other districts (Southern of Jordan), Table 27 showed no statistically significant difference between seventeen Y-STR's Except DYS456, DYS458, DYS437 (0.00), DYS390 (0.007), DYS19 (0.011), DYS389ii (0.009), DYS635 (0.029), DYS438 (0.014), DYS448 (0.056) for Ma'an District, DYS 458(0.056),DYS389ii(0.002), DYS385a (0.005) for Karak District,

Country	No. markers	Comparison of predominant markers of Southern districts with Middle Districts.		Similarity %
Amman	17	3	DYS392, DYS437, DYS438 11 14 10	75
Zarqa	17	2	DYS392, DYS437 11 14	50
Madaba	17	2	DYS392, DYS437 11 14	50
Salt	17	2	DYS392, DYS437 11 14	50

Table 25: Comparison of predominant markers of Southern districts with Middle Districts. (Amman, Zarqa, Madaba, and Salt).

Country	No. markers	comparison of predominant markers of Southern districts with African countries		Similarity %
Libya	17	3	DYS392, DYS437, DYS438 11 14 10	75
Egypt	17	3	DYS392, DYS437, DYS438 11 14 10	75
Mauritania	17	3	DYS437, DYS438, DYS439 14 10 11	75
Tunis	17	3	DYS392, DYS437, DYS438 11 14 10	75
Algeria	17	3	DYS392, DYS437, DYS438 11 14 10	75
Morocco	17	4	DYS392,DYS437,DYS438, DYS439 11 14 10 11	100
Sudan	17	4	DYS392,DYS437, DYS438,DYS439 11 14 10 11	100
Somali	17	1	DYS437 14	25

Table 26: Comparison of predominant markers of Southern districts with African countries Libya, Egypt, Mauritania, Tunis, Algeria, Morocco, Sudan and Somali. Milad thesis.

Country	No. markers	Comparison of predominant markers of Southern districts with Arabian Gulf countries, Syria and Lebanon		Similarity %
Saudi Arabia	17	3	DYS392, DYS437,DYS438 11 14 10	75
Yemen	17	3	DYS392, DYS437,DYS438 11 14 10	75
Oman	17	4	DYS392,DYS437,DYS438,DYS439 11 14 10 11	100
United Arab Emirates	17	2	DYS437,DYS438 11 14 10	50
Bahrain	17	2	DYS392,DYS439 11 11	50
Kuwait	17	1	DYS438 10	25
Qatar	17	4	DYS392, DYS437,DYS438,DYS439 11 14 10 11	100
Iraq	17	3	DYS392, DYS437, DYS438 11 14 10	75
Syria	17	2	DYS392, DYS437 11 14	50
Lebanon	17	0	-	0

Table 27: Comparison of predominant markers of Southern districts with Arabian Gulf countries, Syria and Lebanon.

DYS19(0.000)DYS456, DYS389ii, GATAH4 (0.001), DYS389i (0.029), DYS385a(0.010) for Aqaba District. A comparison of the P - Value for the mean values results for these seventeen Y-STR's system of a study of Aqaba males with the results obtained from other districts (Southern of Jordan), Table 28 showed no statistically significant difference between seventeen Y-STRs Except DYS19,GATAH4 (0.00), DYS389ii (0.058), DYS385a(0.004), DYS437(0.016) for Ma'an District,DYS19, GATAH4(0.000) DYS456 (0.041),DYS393 (0.015), DYS391 (0.044) for Karak District, DYS19(0.000), DYS456, DYS389ii,GATAH4 (0.001), DYS389i(0.029), DYS458(0.064), DYS393(0.032) for Aqaba District. An ANOVA analysis of the Southern Districts of Jordan (Ma'an, Karak, Tafila, Aqaba), seventeen Y-STRs system which observed in this study. Table 29 F_{st} ranged from a minimum of 0.552 for DYS392 with P 0.648 (no significant differences) to a maximum of 18.725 for DYS456 with P 0.000 (significant differences).

Populations Markers	Ma'an		Karak		Tafila		Aqaba	
	M	SD	M	SD	M	SD	M	SD
DYS 456	15.5	1.189	14.36	1.267	13.81	1.203	15.17	0.835
DYS 389i	13.1	0.372	13.1	0.447	13.34	1.599	12.75	0.622
DYS 390	23.3	0.885	22.9	0.852	22.72	1.442	23	1.279
DYS389ii	29.45	0.591	29.64	0.668	28.94	1.703	30	0.603
DYS 458	16.94	1.673	18.36	1.755	18.75	1.918	17.76	1.155
DYS19	14.23	0.654	13.9	0.68	13.91	0.466	13.08	0.289
DYS 385a	13.03	1.044	14	1.836	13.06	1.34	14.25	1.288
DYS 385b	17.06	1.847	17.44	1.182	16.9	1.655	17.5	1.087
DYS 393	12.48	0.652	12.13	1.908	12.22	0.491	13	0.603
DYS 391	10.13	0.515	11.13	3.334	10.56	0.619	10	0
DYS 439	11.22	0.629	11.56	0.754	11.5	1.796	11.58	0.9
DYS 635	21.5	0.85	21.18	0.914	20.97	1.942	21.42	0.9
DYS 392	11.1	0.598	11.08	0.692	10.97	0.186	11.17	0.389
DYS H4	11.45	0.632	11.44	0.68	11.28	0.729	10.5	1
DYS 437	14.41	0.857	14.05	0.223	13.91	0.734	14	0.426
DYS 438	9.84	0.661	10.11	0.606	10.34	1.807	10.17	0.389
DYS 448	20.2	0.679	19.95	0.51	19.97	0.18	20.08	0.515
No. of sample	77		39		32		12	

Table 28: Standard Deviation and Mean analysis of the 17 of the Y-STR markers.

Quality assurance

We have participated in the Quality Assurance Test as stipulated by the YHRD and therefore our results have been registered and deposited in the International Y-Chromosome Haplotype Reference Database (YHRD), under the Accession Numbers YA003522 and YA003523 (www.yhrd.org). Furthermore, the data were then stored in our local Mahasneh Arabian Y-linage Database (MAYD).

Discussion

For population genetics studies and forensic purposes, Y-STRs discrimination power and marked genetic variation enabled to compose highly informative Y chromosome STR haplotypes [16,17]. Y-STRs are very powerful in the detection of genetic differences between populations, due to the greater sensitivity of nonrecombining Y-chromosomal markers to founder effects and genetic drift, especially among the Arabian populations [17,18]. The use of Y-STR provides evidence for population genetic profile with the elaboration of large number of databases. Since the whole haplotype must be typed for each sample the suitability of Y-STR databases for practical use will be greatly increased with the typing of each individual at as many loci as possible, as opposed to typing a great number of Y-STR [19]. This inter population variability of Y-profile makes the definition of local databases crucial for the practical of Y-specific markers. The Y-STR haplotype reference databases is important not only for estimating the haplotype frequency and for calculating the subsequent match probability, but it also for comparative population analysis [20]. Y-STRs are used to investigate the mutation frequencies in these STRs among various nations. Therefore, this problem is to define the genetic diversity in Southern Districts of Jordan. The analysis of Y-STRs has become increasingly important for population genetics. Yet, in contrast with other populations of the world, the genetic diversity of the Arabian populations has not been studied. The southern part of Jordan is an integral part of the Arabian genetic makeup which needs to be explored and thus its genetic information needs to be correlated with that of the other Jordanian districts and other parts of the world. The similarity of the Y-chromosomal STR gene pool among Arab populations could be a

Markers	DYS 456	DYS 389I	DYS 390	DYS 389II	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	GATA H4	DYS 437	DYS 438	DYS 448
Districts	Ma'an																
Karak	.000	.974	.045	.295	.000	.005	.000	.249	.097	.003	.080	.157	.855	.910	.001	.168	.025
Tafila	.000	.140	.007	.009	.000	.011	.891	.637	.251	.224	.182	.029	.256	.241	.000	.014	.056
Aqaba	.366	.160	.343	.058	.171	.000	.004	.390	.115	.797	.243	.816	.717	.000	.016	.280	.514

Table 29: P-Value for the mean values of the17 Y-STR between Ma'an and others Southern Districts.

result of the geographical proximity, linguistic coherence and common history of the populations. Also, a close genetic relation between Arab populations and cultures have been tied together for long time ago. Overall, genetic differences and similarities between populations revealed in the Y-STR analysis may depend on the geographical, linguistic and/or historical influences, which could come through population bottlenecks, founder effects, genetic drift, gene flow and/or non-random mating. These forces of population evolution should be considered before drawing any decisive conclusions about the genomic origin of the Arab population and its genetic relationships with neighboring populations.

Conclusions

Based on molecular variation and phylogenetic analysis by estimating the closely and distantly related populations, the interpopulation genetic links according to forensic Y-STR markers Among southern districts of Jordan and their neighboring districts and other Arabian countries have been studied. Our result shows a close genetic relation to Northern and middle districts of Jordan populations with a clear genetic similarity (Tables 30 and 31). Therefore, in our Y-STR analysis the Sothern districts population is more phylogenetically and have genetic similarity among Southern Districts of Jordan (Figure 1) and to Arabian Gulf populations (Table 32). This genetic relationship became apparent due to genetic contribution of the genetic similarity with Saudi Arabian population, which represent male founder population movements from north Gulf region to Sothern and Northern Districts of Jordan(Table 33). Due a close geographical vicinity, our results indicate no significant population differentiation between Arab population countries (Table 34), that is explicable by a nonlinguistic barrier and suggests a distinct history of these Arab male populations. Our results indicate, a high-resolution Y-chromosomal DNA profile can be achieved

Markers	DYS 456	DYS 389I	DYS 390	DYS 389II	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	GATA H4	DYS 437	DYS 438	DYS 448
Districts	Karak																
Ma'an	.000	.974	.045	.295	.000	.005	.000	.249	.097	.003	.080	.157	.855	.910	.001	.168	.025
Tafila	.056	.206	.471	.002	.340	.952	.005	.180	.723	.161	.789	.447	.398	.351	.270	.310	.889
Aqaba	.041	.182	.765	.244	.223	.000	.576	.919	.015	.044	.954	.536	.654	.000	.778	.850	.471

Table 30: P–Value for the mean values of the17 Y-STR between Karak and others Southern Districts

Markers	DYS 456	DYS 389I	DYS 390	DYS 389II	DYS 458	DYS 19	DYS 385a	DYS 385b	DYS 393	DYS 391	DYS 439	DYS 635	DYS 392	GATA H4	DYS 437	DYS 438	DYS 448
Districts	Tafila																
Ma'an	.000	.140	.007	.009	.000	.011	.891	.637	.251	.224	.182	.029	.256	.241	.000	.014	.056
Karak	.056	.206	.471	.002	.340	.952	.005	.180	.723	.161	.789	.447	.398	.351	.270	.310	.889
Aqaba	.001	.029	.425	.001	.064	.000	.010	.283	.032	.325	.807	.255	.295	.001	.615	.593	.548

Table 31: P-Value for the mean values of the17 Y-STR between Tafila and others Southern Districts.

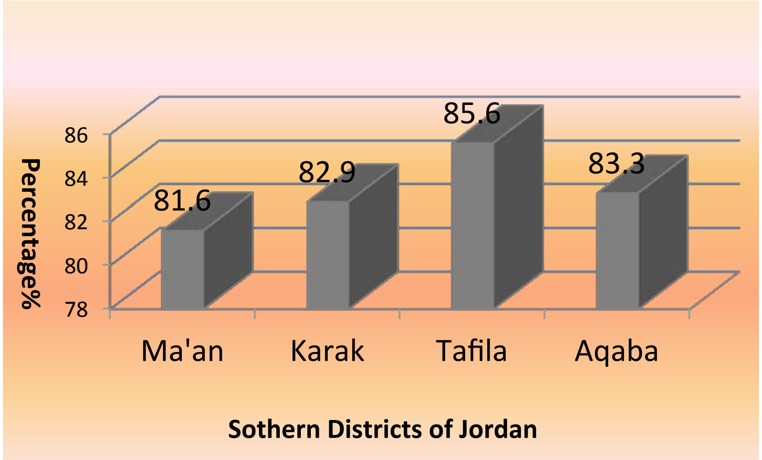

Figure 1: The similarity among southern districts of Jordan %.

Markers **Districts**	**DYS456**	**DYS389I**	**DYS390**	**DYS389II**	**DYS458**	**DYS19**	**DYS385a**	**DYS385b**	**DYS393**	**DYS391**	**DYS439**	**DYS635**	**DYS392**	**GATA H4**	**DYS437**	**DYS438**	**DYS448**
	Aqaba																
Ma'an	.366	.160	.343	.058	.171	.000	.004	.390	.115	.797	.243	.816	.717	.000	.016	.280	.514
Karak	.041	.182	.765	.244	.223	.000	.576	.919	.015	.044	.954	.536	.654	.000	.778	.850	.471
Tafila	.001	.029	.425	.001	.064	.000	.010	.283	.032	.325	.807	.255	.295	.001	.615	.593	.548

Table 32: P-Value for the mean values of the17 Y-STR between Aqaba and others Southern Districts.

Northern districts	**No. markers**	**Comparison of predominant markers of Southern districts with Northern District**		**Similarity %**
Ajloun	17	4	DYS392,DYS437,DYS438,DYS439 11 14 10 11	100
Irbid	17	3	DYS437, DYS438, DYS439 14 10 11	75
Jarash	17	1	DYS392 11	25
Mafraq	17	3	DYS392, DYS437,DYS438 11 14 10	75

Table 33: Comparison of predominant markers of Southern districts with Northern Districts (Ajloun, Irbid, Jarash and Mafraq). Wafa'a thesis

Loci	**F_{st}**	**P- value**	**Variation among population %**	**Variation within population %**
DYS 456	18.725	.000	79.560	228.016
DYS 389i	1.730	.163	3.298	102.278
DYS 390	2.999	.032	9.691	173.437
DYS 389ii	5.179	.002	13.428	139.154
DYS 458	11.321	.000	99.640	472.336
DYS 19	13.610	.000	15.171	59.823
DYS 385a	6.636	.000	35.663	274.070
DYS 385b	.881	.452	7.026	401.258
DYS 393	2.524	.060	8.667	184.279
DYS 391	3.408	.019	28.945	455.758
DYS 439	1.449	.230	4.390	162.555
DYS 635	1.858	.139	7.483	216.129
DYS 392	.552	.648	.514	46.551
TAGA H4	6.899	.000	9.946	77.363
DYS 437	8.718	.000	7.881	48.519
DYS 438	2.284	.081	6.524	151.378
DYS 448	2.278	.082	2.176	50.621

Table 34: Fst and ANOVA analysis of the seventeen of the Y-STR markers among Southern Districts of Jordan (Ma'an, Karak, Tafila, and Aqaba).

in the Arabian population. However, the Y-STR haplotype sharing with the Arabian populations of the close geographical neighborhoods that could be influenced by recurrent mutations and/or common ancestry is observed. These analyses support use of the haplotype population data for estimating Y-STR profile frequencies for populations residing in Sothern districts of Jordan. Our data indicates that Y-STRs alleles and haplotypes differentiate effectively inside Jordan population, and between Jordan population and its geographical neighbors. This suggests that Arab population including Southern district population of Jordan are closely related not only by geography and language but also by the Y chromosome gene pool represented by forensic Y-STR markers. Consequently, more forensic Y-STR markers should be included in the Y-STR haplotype in order to achieve a resolution between the Y chromosomes of Southern districts of Jordan males.

Declarations

Author's contributions: Qussai Hussein Qasem Zuriegat: Performed the research, result analysis and manuscript writing.

Ihsan Ali Al-mahasneh: The idea, design and supervision of the research.

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