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DNA sequencing and genotyping profile of the microsatellites of Y-STRs of the Beer-Alsabaa bedouins of Jordan as part of the Arabian genome project since 1995

Abstract

An account has been given to determine the DNA sequencing and genotyping profile of the microsatellites of Y-STRs of the Beer-Alsabaa Bedouins of Jordan as part of the continuous project of Arabian genome since 1995. The Alleles frequencies range from (3.3–100%), whilst the genetic diversity ranges from (0-0.93). The Model of heliotype for the Beer-Alsabaa Bedouins of Jordan was constructed and thus their exclusive DNA markers were the loci DYS437 and DYS 438 for allele's values of 14 and 15 respectively, both reaching frequency of 100%. The DNA haplogroup of the Beer-Alsabaa Bedouins is (J1) which confirms that their belongings to the Qahtanite-lineage for their Y-chromosome genealogical landscape and thus match the tribal genealogical memory. The Phylogenetic-tree of Beer-Alsabaa Bedouin shows that they have very close divergence to both Palestinians and Yamani as they appeared in the same cluster. Moreover, the Fst between Beer-Alsabaa Bedouin and other Arabian populations ranged between (0.0242–0.0376) and thus shows the low genetic diversity and thus the high profile of genealogical relatedness. The results have been registered and deposited in the International DNA Gene Bank of Y-Chromosome Haplotype Reference Database (YHRD) under the Accession Numbers YA003522 and YA003523.

Keywords: arabian genealogy, arab qahtanite and adnanite, genetic distance

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Introduction

In humans, the Y chromosome spans 58 million base pairs and represents approximately 0.38% of the total DNA in a human cell. The human Y chromosome contains 86 genes,[1] many of the genes on Y-chromosome are involved in male sexual determination and development.[2] The bulk of the Y chromosome which does not recombine is called the non-recombining region of the Y chromosome (NRY), which is composed of the DNA segments known as Short Tandem Repeats (STRs). The STRs polymorphism are categorized by length of the repeated units such as Di nucleotide (CA), Trinucleotide (TAT), Tetra nucleotide (TTTA), Pentanucleotide (TAAAA), Hexa nucleotide (AGAGAT),[3,4] (Figure 1). As Y-chromosome is paternally inherited as haploid Y-DNA segment and passed down from father to son unchanged from generation to another except by the gradual accumulation of mutations, the STRs of the Y chromosome have proved to be a very powerful tool in tracing movements of males in human population history.[5] The applications of Y-STRs are becoming increasingly important because of their male specificity and the informativeness of the haplotypes they define and also provide useful discriminating power in individual identification and the geographical differentiation of Y haplotypes of the male genetic map.[6]

Recently, there has been a worldwide growing interest on the genotyping profile of Y-STRs among different nations, populations and some ethnic groups around the world.[7–10] In comparison with other parts of the world, there is a lack of information on the Arabian genealogy as well as their tribal migration and dispersal around the world.[11–13] Currently, many attempts are being made by the National Geographic Society and the private companies Family Tree DNA (https://www.familytreedna.com) to resolve the genealogical genotyping of Arabian tribes and lineages. Among other Bedouins of Jordan (Southern, Middle and Northern), the Beer-Alsabaa Bedouins of Jordan are recognized by the Jordanian constitution and Laws of Bedouins and that they are composed of four major clans (Alazazma, Al-Tayaha, Al-Tarabin, and Aljbarat) living mainly among the Middle Bedouins. Beer-Alsabaa Bedouins represent one of most conservative populations in the Arabian region, and has an exceptional genetic importance due to their genealogical culture and lifestyle driving force for the consanguineous marriage as favored and respected in all their communities reaching up to 60% as they lives in the isolated and rural communities. The aim of the present research, therefore, is to determine the DNA genotyping profile of the microsatellites of Y-STRs of the Beer-Alsabaa Bedouins of Jordan as part of the Arabian genome project.

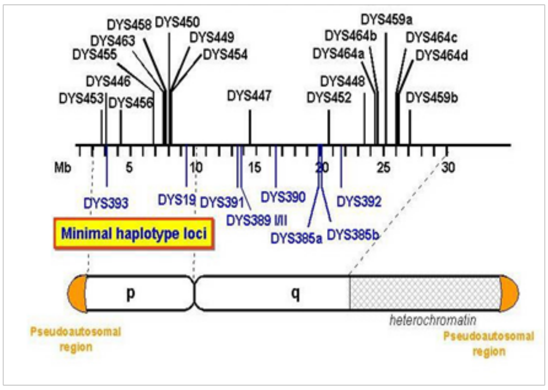


Figure 1 Y-STR positions along Y chromosome.[4]

Materials and methods

Sequencing and genotyping of the DNA Y-STRs

DNA isolation, amplification and allies sequencing and sizing was conducted according the manufacture protocols; using the wizard genomic DNA isolation-kit® (Promega, USA), Amp FlSTR® Yfiler™ PCR Amplification Kit on the Gene-Amp-PCR System 9700 Thermo Cycler (Applied Bio system) and the ABI Prism®310 Genetic Analyzer (Applied Bio systems) as equipped with the Gene Scan-500 Internal Lane Size Standard (LIZ-500), Data Collection Software Version 3.1 and Gene Mapper ID Software Version 4 from Applied Bio systems to determine the allelic repeats by applying Y Filer Allelic Ladder. The genealogical Haplogroup of each haplotype was determined using the Athey's Haplogroups Predictor version 3.16.

Statistical analysis

Allelic frequencies were estimated by direct counting and the gene diversity was calculated using in-house-built program. Using the public demine of the YHRD (www.yhrd.org), AMOVA test was used to determine the Pair wise values of Φst, an analogue of Fst, MDS plot as compared to the (6) Arabian populations. A dendrogram of clusters analysis was calculated using Dendroscope software, version 3.5.7).[14] Phylogeny analysis was created by online Trex statistical tool: http://www.trex.uqam.ca

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).

Results and discussion

The Alleles frequencies ranges from (3.3–100%), whilst the genetic diversity ranges from (0-0.93) (Table 1). The Model of haplotype for the Beer-Alsabaa Bedouins of Jordan was constructed and thus their exclusive DNA markers were the loci DYS437 and DYS 438 for allele's values of 14 and 15 respectively, both reaching frequency of 100% (Table 1). The Fst of AMOVA test between Beer-Alsabaa Bedouin from other Arabian populations were with Palestinians (0.0242), Yemeni (0.0262), Moroccan (0.0268), Libyan (0.0272), Tunisians (0.0376) respectively, with significant P-values ($P<0.05$) with all subjects: 0.00, 0.0007, 0.0008, 0.0008 and 0.0022 respectively (Table 2), which shows the low level of diversity and thus the high close relatedness with the DNA of the Palestinians and Yamani. The Phylogenetic divergence of Beer-Alsabaa Bedouins with other Arabian populations revealed that their closes lineages are Palestinians and Yamani as they appeared in the same cluster whilst the North African Arabs showed the second cluster (Figure 2). The DNA haplogroup of the Beer-Alsabaa Bedouins was (J1) which confirms that they do belong to the Qahtani-lineage for their Y-chromosome genealogical landscape and thus match the tribal genealogical memory. In contrast with the 2nd. Cluster for North African Arabs, they are have a different sub-divergence of genealogy as they belongs mainly to the E1b1 (African) haplogroup and also the Adnanite (J2) haplogroup of the migrated (from Arabian peninsula towards North Africa) tribes during the 7th century Banu Helal, Banu Maaqel and Banu Sulaym.

Table 1 Alleles Frequency and Diversity for 17-YSTRs Markers of Beer-Alsabaa Bedouin Population

Alleles sequence value	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	DYS H4	DYS 437	DYS 438	DYS 448
9							13.3										
10										56.6							
11										40	60		33.3	96.6		100	
12		6.6							43.3		33.3		3.3	3.3			
13		83				3.3	50		65.6								
14	40	10				86.6	3.3						50		100		
15	60																
16																	
17					3.3			10									
18					6.6			30									
19					53.3			6.6									16.6
20					6.6												83.3
21												100					
22			3.3														
23			53.3														
24			33														
25			3.3														

Citation: Almahasneh IA, Abumsimir B, Ennaji MM. DNA sequencing and genotyping profile of the microsatellites of Y-STRs of the Beer-Alsabaa bedouins of Jordan as part of the Arabian genome project since 1995. *Int J Mol Biol Open Access.* 2018;3(3):149–152. DOI: 10.15406/ijmboa.2018.03.00067

Table Continued

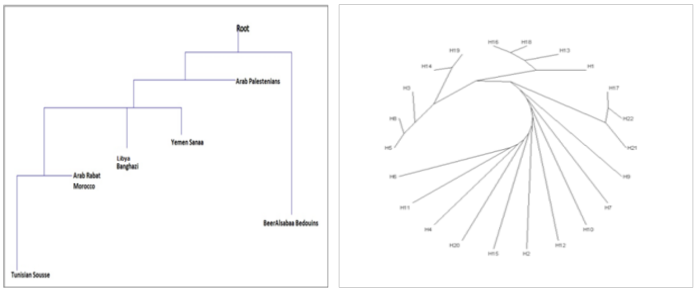
Alleles sequence value	**DYS 456**	**DYS 389i**	**DYS 390**	**DYS 389ii**	**DYS 458**	**DYS 19**	**DYS 385a**	**DYS 385b**	**DYS 393**	**DYS 391**	**DYS 439**	**DYS 635**	**DYS 392**	**DYS H4**	**DYS 437**	**DYS 438**	**DYS 448**
26																	
27																	
28				3.3													
29				6.6													
30				53.3													
31				6.6													
G.D.		0.31	0.63	0.73	0.63	0.26	0.76	0.93	0.51	0.54	0.55	0	0.66	0.68	0	0	0.29
Model ht.	15	13	23	30	18	14	13	18	13	10	11	21	14	11	14	10	20

GD, Genetic Diversity

Table 2 Pair wise Fst and P-values and Divergent signal Bloomberg K test parameters between Beer-Alsabaa Bedouins population and five neighboring populations

Population	**BB**	**AP**	**BL**	**AR**	**ST**	**SY**
BB	-	0	0.0007	0.0008	0.0022	0.0008
AP	0.0242	-	0	0	0	0
BL	0.0272	0.004	-	0	0	0
AR	0.0268	0.0039	0.0061	-	0.0002	0
ST	0.0376	0.0131	0.0162	0.0067	-	0
SY	0.0262	0.003	0.0061	0.0055	0.015	-
	Divergent signal blomberg K test parameters					
SD	0.02223927	0.0104466	0.00310227	0.00218096	0.000405831	0
PV	0.798806210	0.1762587	0.01554389	0.007682379	0.000266005	0
CP	0.79880621	0.9750649	0.99060876	0.998291138	1	1

BB, beer-alsabaa bedouins; AP, arab palestinians; BL, benghazi libyan; AR, arab rabat; SY. Sana'a yemeni; SD, standard deviation; PV, proportion of variance; CP, cumulative proportion



(A) **(B)**

Figure 2 **(A)** Phylogenetic Interfere tree for the compared Arabian populations with Beer-Alsabaa Bedouin population (Trex statistical online tool: http://www.trex.uqam.ca). **(B)** Circular Dendrogram for hierarchical cluster analysis of 30 samples (22 haplotype) of Beer-Alsabaa Bedouin population (Dendroscope software, V 3.5.7).

Conclusion

For the first time, we present a conclusive evidence on the Y-STRs DNA Model of haplotype for the Beer-Alsabaa Bedouins of Jordan and specified their exclusive Y-STRs DNA markers where the loci DYS437 and DYS 438 for alleles values of 14 and 15 respectively, both reaching frequency of 100%. The DNA haplogroup of the Beer-Alsabaa Bedouins is (J1) which confirms that their belongings to the Qahtanite-lineage for their Y-chromosome genealogical landscape and thus match the tribal genealogical memory. Moreover, the Fst between Beer-Alsabaa Bedouin and other Arabian populations ranged between (0.0242–0.0376) and thus shows the low genetic diversity and thus the high profile of genealogical relatedness. Our results are highly important in providing us with a better understanding of the genealogical genotyping profile to be correlated with the most common familial and genealogical-genetic diseases and the epidemiology among Arabian populations for better management towards establishment of gene therapy platform in the region.

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Conflict of interest

The author declares there is no conflict of interest.

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