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Population Genetic Data for 15 Autosomal Short Tandem Repeat (STR) loci of Mandaeans (Al-Sabean) population in Baghdad Governorate in Iraq

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Abstract

The analysis of allele frequencies for 15 autosomal short tandem repeat (STR)loci (D3S1358 TPOX, VWA, D16S539D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, CSF1PO, FGA, D19S433, D2S1338,) and Amelogenin for gender identification using the AmpFISTR® Identifiler Kit panel from Applied Bio systems was performed for 51 unrelated individuals from Mandaeans (Al-Sabean) population in Baghdad in Iraq. The data of 15 STR loci in Mandaeans (Al-Sabean) population showed high gene diversity, where 15 alleles were observed. These finding suggest that these allele frequency databases are suitable for the purpose of identification in paternity and forensic investigations.

Keywords: Short tandem repeat; Mandaeans; Iraqi population; Allele frequencies statistical parameters

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Introduction

Short tandem repeats loci (STR) are repeated sequenced and non-functional series with a certain base index with a length of 2-7 base pair in human genome [1]. The main characteristic feature of these STRs loci is having a high level of heterozygosity. On other words, STR loci show variability among individuals in population. Thus, the variability of these loci make them a useful markers in chromosome mapping, population genetics, paternity testing, missing persons investigations, and forensic studies [2-5]. At the end of 1990s the STR profile has emerged as a powerful tool in the investigation of crimes and has become the standard tool for every forensic laboratory in the world [6,7].

Iraq has a variety of populations; they may differ from each other either linguistically or religiously. The Mandaeans is one of the Iraqi religious populations.In fact, Mandaens represents one of the oldest linguistic and religious populations in Iraq, where they have been on Mesopotamia for more than 20 centuries [8]. In view of the current security situation in Iraq, the examining of allelic distributions in different populations and estimate their forensic parameters have an impact effect on enhancing personal identification. Hence, there is a clear need to generate proper DNA database for forensic genetics in purpose to identify the unknown person of victims' criminals. The establishing of standard DNA database may have accomplished through setting the probability of a specific genotype. Hence, a proper sample size and proper estimating of the frequency of each possible allele and genotype are what the generation of population data is required [9,10]. Therefore, this study has examined allelic distributions in Mandaeans population in Baghdad in Iraq for the purpose of establishing a database of this population. For this purpose, we have used 15 STRs (D3S1358, VWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO, D19S433, D2S1338, and D16S539) and Amelogenin for gender identification.

Materials and Methods

Buccal swabs (Sterile Omni Swab or Sterile Foam Tipped Swabs, Whatman International Ltd., Maidstone, UK) were collected from 51 unrelated individuals from Mandaeans (Al-Sabean) populations in Baghdad in Iraq. Each of these individuals were self-identified and randomly chosen (and, therefore likely to be unrelated) from the Iraqi Mandaeans (Al-Sabean) populations of Baghdad. Samples were extracted using a PrepFiler Forensic DNA Extraction Kit (Applied Biosystems, Foster City, CA) and their DNA content was quantified with NanoDrop (Thomson, Wilmington, DE). Fifteen autosomal

STR markers (the 13 CODIS core loci and D19S433 and D2S1338) were genotyped along with the amelogenin locus on the X and Y chromosomes using the Applied Biosystems AmpFlSTR® Identifiler™ kit. Approximately 1 ng of template DNA was amplified for each sample following the protocols described in the Identifiler™ User's Manual (Applied Biosystems). The samples were amplified with an Applied Biosystems Veriti® PCR System (Applied Biosystems). Amplification products were diluted 1:15 in Hi- Di™ formamide and GS500-LIZ internal size standard (Applied Biosystems) and analyzed on a 16-capillary ABI Prism® 3100 Genetic Analyzer. POP™-4 (Applied Biosystems) was utilized for higher resolution separations on a 36 cm array. Data collection was performed with Data Collection v. 2.0 software (Applied Biosystems) and samples were analyzed with GeneMapper v. 3.2 software (Applied Biosystems).

Statistical Data Analysis

Powerstats Version 1.2 program was used to calculate the allele frequencies and forensic efficiency, which are Matching Probability (MP), Power of Discrimination (PM), Polymorphism Information Content (PIC), Power of Exclusion (PE), Paternity Index (PI), Observed Homozygosity (Ho) and Observed Heterozygosity (He).

Results and Discussion

The rapid growing in STRs analysis technology has encouraged and facilitated forensic studies. Currently, STRs are representing as markers of choice in most forensic, paternity testing and individual identification studies. The fact that level of allele frequency for each STR marker is basically population dependent, has encouraged the generation of database on different populations in different countries[11].

Iraq populations are composing of various linguistic and ethnic groups of different tribes. Religious structure has an influence on genetic structure of Iraqi populations [12]. This study has performed on Iraqi Mandaeans-Sabean population and has investigated for the first time the sixteen loci (fifteen STR loci and Amelogenin), including D18S51, D21S11, TH01, D3S1358, FGA, TPOX, D8S1179, vWA, Amelogenin, Penta D, Penta E, CSF1PO, D16S539, D7S820, D13S317 and D5S818, which have been frequently used for forensic and paternity testing in different populations [3,4,13,14]. In this population study, allele frequencies and statistical analysis evaluation of these 15 autosomal STR loci from 50 unrelated individuals have reported in Table 1. The results showed that all loci showed a high level of genetic morphism and the data suggested that these genetic markers forming the DNA profile of Mandaeans- Sabean population are found at different frequencies. Furthermore, the data was statistically tested for the other forensic parameters including: Matching Probability, Power of Discrimination, Polymorphism Information Content, Power of Exclusion, Paternity Index, Heterozygosity Observed and Heterozygosity Expected. Data reported in Table 2 showed high degree of Matching Probability ranged from 0.052 (D19S433) to 0.173 (CSF1PO). Power of Discrimination ranged from 0.827 (CSF1PO) to 0.953 (FGA). Polymorphism Information Content ranged from 0.18 (D8S1179) to 0.85 (D19S433). Power of Exclusion ranged from 0.300 (TPOX) to 0.799 (D18S51). Paternity Index ranged from 1.28 (TPOX) to 5.10 (D18S51). Heterozygosity Observed ranged from 0.098 (D18S51) to 0.392 (TPOX). Heterozygosity expected ranged from 0.608 (TPOX) to 0.902 (D18S51).

Conclusion

In total, these parameters indicated the usefulness of these STR loci panel to evaluate individual forensic identification and paternity in Iraqi Mandaeans- Sabean population. There by further studies on analyzing populations based on geographic and religious is required to confirm their efficacy for forensic studies. In conclusion our data indicated that these well-known 15 Autosomal Short Tandem Repeat (STR) loci can be used as forensic tool and applied for personal identification in Iraqi populations in future. This study encourages further studies on the locus wise allele frequencies to be compare with the other published Iraqi populations.

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References

1. Butler JM (2006) Genetics and genomics of core short tandem repeat loci used in human identity testing. J Forensic Sci 51:253-265.
2. Zuniga J, Ilzarbe M, Acunha-Alonzo V, Rosetti F, Herbert Z, et al. (2006) Allele frequencies for 15 autosomal STR loci and admixture estimates in Puerto Rican Americans. Forensic Sci Int 164:266-270.
3. Barni F, Berti A, Pianese A, Boccellino A, Miller MP, et al. (2007) Allele frequencies of 15 autosomal STR loci in the Iraq population with comparisons to other populations from the middle-eastern region. Forensic Sci Int 167:87-92.
4. Gurkan C, Demirdov DK, Yamaci RF, Sevay H (2015) Population genetic data for 15 autosomal STR markers in Turkish Cypriots from Cyprus. Forensic Sci Int Genet 14:e1-e3.
5. Tokdemir M, Tunçez FT, Vicdanli NH (2016) Population genetic data for 15 autosomal STR markers in eastern Turkey. Gene 586:36-40.
6. Jeffreys AJ, Brookfield JF, Semeonoff R (1985) Positive identification of an immigration test-case using human DNA fingerprints. Nature 317:818-819.
7. Edwards AL, Hammond HA, Jin L, Caskey CT, Chakraborty R (1992) Genetic variation at five trimeric and tetrameric tandem repeat loci in four human population groups. Genomics12:241-53.
8. van Zoonen D, Wirya K (2017) The Sabean-Mandaeans: Perceptions of reconciliation and conflict, Middle East Research Institute, Iraq.
9. Thomson JA, Pilotti V, Stevens P, Ayres KL, Debenham PG (1999) Validation of short tandem repeat analysis for the investigation of cases of disputed paternity. Forensic Sci Int 100: 1-6.
10. Alonso A, Anđelinović Š, Martín P, Sutlović D, Erceg I, et al. (2001) DNA typing from skeletal remains: evaluation of multiplex and megaplex STR systems on DNA isolated from bone and teeth samples. Croat Med J 42:260-266.
11. Martínez G, Vázquez E, Schaller C, Quevedo N (2003) Genetic data on 11 STRs (CSF1PO, TPOX, TH01, F13A01, FESFPS, vWA, D16S539, D7S820, D13S317, F13B, LPL) in an Argentine northeast population. Forensic SciInt133:254-255.
12. Jaber MM, Almusawi IH, Mahmood TT (2018) Autosomal Short Tandem Repeat (STR) variation of 15 loci in Muthanaa–Iraqi population revealed of New Alleles. RJPT11:4090-4095.
13. ElOssmani H, Talbi J, Bouchrif B, Chafik A (2009) Allele frequencies of 15 autosomal STR loci in the southern Morocco population with phylogenetic structure among worldwide populations. Legal Medicine 11:155-158.
14. Budowle B, Ge J, Chakraborty R, Eisenberg AJ, Green R, et al. (2011) Population genetic analyses of the NGM STR loci. IntJLegal Med 125:101-109.