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Population genetics data of 23 autosomal STR loci for three Populations in United Arab Emirates

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ABSTRACT

In the present study, forensic parameters were estimated for three populations residing in the United Arab Emirates (UAE) including UAE Arabs, Pakistanis and Indians based on the population data of 23 autosomal short tandem repeats (STRs). The UAE Arabs is a vital population to study due to high rates of consanguineous marriages. Therefore, it is essential to estimate the allele distribution and frequencies within this population. In addition, it is crucial to study the largest communities living in the UAE such as Indians and Pakistanis. A total of 1272 blood samples were collected on FTA® cards, comprising of 571 UAE Arabs, 352 Indians and 349 Pakistanis. All of these samples were amplified directly using Verifiler® Express PCR Amplification Kit that focuses on 23 autosomal STR loci, namely D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, D10S1248, D1S1656, D12S391, D2S1338, D6S1043, Penta D and Penta E loci. The PCR products were electrophoresed on ABI 3500 Genetic Analyzer and analyzed using GeneMapper ID-X v1.4 software. Arlequin v3.5 and PowerStats software were utilized to determine the forensic parameters and population structure using AMOVA. Gene diversity, ranged from 0.67406 (TPOX) to 0.9226 (Penta E) in the UAE Arabs, 0.69955 (TPOX) to 0.9214 (Penta E) in Indian and 0.69853 (TPOX) to 0.921 (Penta E) in Pakistani population. The most discriminating autosomal STR loci observed was Penta E (PD = 0.985), (PD = 0.986), (PD = 0.986) in the UAE Arabs, Indian and Pakistani population, respectively. The obtained results showed the 23 STR loci had a relatively high genetic variation, confirming the suitability for forensic identification and kinship analysis, in the relevant populations. The significance of this study is to build an allelic frequency database for one of the most powerful commercially available STR amplification kits by using the current forensic workflow.

1. Introduction

UAE, is an Arab country located in the southeast region of the Arabian Peninsula. It's considered as home to over 200 nationalities [1]. The population of UAE is approximately 9.4 million out of which Emirati nationals constitute 1.1 million according to the Federal Competitiveness and Statistical Authority. The Indian community is considered as the largest community in the UAE, followed by the Pakistanis, Bangladeshis and other Asians [2]. This study aims to evaluate the allelic frequencies of the two largest communities; Indian and Pakistani alongside the UAE Arabs by utilizing one of the most powerful commercially available STR amplification kits (VeriFiler™ Express PCR Amplification Kit) and consequently to build an allelic frequency database.

2. Materials and methods

2.1. Samples collection

Consented blood samples were randomly collected from a total of 1272 unrelated individuals. This consisted of three populations residing in UAE; UAE Arabs (n =n571), Indian (n = 352), Pakistani (n = 349). Ethical approval was granted from Dubai scientific research ethics committee in (DHA)

2.2. DNA extraction

An FTA® card (Whatman, UK) was punched using the micro-puncher (Harries®) measuring (0.5 mm diameter). The disc was placed in 0.2ml PCR tubes. Quarter the volume of reagents suggested in the

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Table 1
Forensic efficiency parameters, genetic diversity and heterozygosity for 23 AUTOSOMAL -STR markers from UAE Arabs Population.

UAE	D3S1358 FGA	vWA D22S1045	D16S539 D5S818	CSF1PO D13S317	TPOX D7S820	D8S1179 D6S1043	D21S11 D10S1248	D18S51 D1S1656	Penta E D12S391	D2S441 D2S1338	D19S433 Penta D	TH01
PD	0.900	0.928	0.910	0.862	0.850	0.953	0.954	0.972	0.985	0.904	0.958	0.918
	0.969	0.883	0.894	0.922	0.930	0.947	0.914	0.973	0.974	0.973	0.960	
PE	0.571	0.543	0.543	0.460	0.410	0.666	0.629	0.746	0.803	0.555	0.676	0.524
	0.701	0.418	0.402	0.568	0.558	0.606	0.471	0.718	0.746	0.757	0.653	
GD	0.763	0.795	0.771	0.714	0.674	0.840	0.842	0.882	0.915	0.761	0.843	0.782
	0.870	0.717	0.740	0.784	0.799	0.822	0.772	0.881	0.885	0.883	0.850	
He	0.785	0.769	0.769	0.720	0.688	0.835	0.816	0.876	0.904	0.776	0.841	0.758
	0.853	0.694	0.683	0.783	0.778	0.804	0.727	0.862	0.876	0.881	0.828	

Table 2
Forensic efficiency parameters, genetic diversity and heterozygosity for 23 AUTOSOMAL -STR markers from Indian Population.

Indian	D3S1358 FGA	vWA D22S1045	D16S539 D5S818	CSF1PO D13S317	TPOX D7S820	D8S1179 D6S1043	D21S11 D10S1248	D18S51 D1S1656	Penta E D12S391	D2S441 D2S1338	D19S433 Penta D	TH01
PD	0.887	0.930	0.930	0.859	0.856	0.959	0.961	0.964	0.986	0.863	0.948	0.924
	0.967	0.888	0.889	0.937	0.934	0.952	0.917	0.974	0.963	0.971	0.942	
PE	0.529	0.580	0.5	0.444	0.422	0.677	0.666	0.722	0.82	0.458	0.633	0.534
	0.716	0.401	0.495	0.580	0.544	0.677	0.565	0.733	0.797	0.722	0.606	
GD	0.746	0.805	0.795	0.711	0.700	0.852	0.858	0.858	0.921	0.712	0.826	0.790
	0.870	0.732	0.744	0.813	0.808	0.836	0.784	0.888	0.865	0.880	0.824	
He	0.761	0.790	0.744	0.710	0.696	0.841	0.835	0.864	0.912	0.719	0.818	0.764
	0.861	0.682	0.741	0.790	0.770	0.841	0.781	0.869	0.901	0.864	0.804	

manufacturer's protocol was utilized.

2.3. DNA amplification and detection

The extracted DNA samples were amplified with the Verifiler® Express PCR Amplification Kit, based on 23 autosomal STRs: D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, D10S1248, D1S1656, D12S391, D2S1338, D6S1043, Penta D and Penta E loci. Amplification was performed on Veriti™ PCR Thermocycler using 25 cycles as per the conditions stated in the manufacturer's protocol (ThermoFisher Scientific). 1 µl of amplified product was added to 9.5µl Hi-Di Formamide and electrophoresed on an ABI3500 Genetic Analyzer (ThermoFisher Scientific). GeneMapper *ID-X* software V1.4 was used for analyzing and interpreting the data achieved.

2.4. Forensic and statistical analysis

PowerStats v1.2 software (Promega Corporation, Madison, WI, USA) was used to calculate allele frequencies, Random Match Probability (PM), Power of Discrimination (PD), Power of Exclusion (PE), observed homozygosity and observed heterozygosity. Arlequin v3.5 was used to test Hardy Weinberg equilibrium, calculate expected heterozygosity, perform AMOVA to investigate genetic diversity between the three geographical regions as well as to undertake population differentiation tests for UAE and other countries.

3. Results

Penta E locus represented the highest number of different alleles in UAE Arabs and Indian population (25 and 21 alleles, respectively). Whereas, FGA locus showed the topmost number of different alleles in the Pakistani population (24 alleles). The TH01 locus exhibited the least number of different alleles (6 alleles) in UAE Arabs, while TPOX locus showed the lowest number of different alleles (5 and 7 alleles) in the Indian and Pakistani population, respectively. Thereupon, the following results revealed that Penta E and FGA are the most polymorphic loci and TH01 and TPOX are the least polymorphic loci among the three studied populations. The highest genetic diversity was achieved in Penta E loci (0.915, 0.921 and 0.921) in UAE Arabs, Indian and Pakistani population, respectively as displayed in Tables 1 and 2; whereas the lowest genetic diversity in all the populations was shown for TPOX loci. The combined match probability attained was 2.9×10^{-29} for UAE Arabs, 5.4×10^{-29} for Indian and 2.9×10^{-29} for the Pakistani population.

4. Conclusion

The primary objective of this study was to determine the genetic structure of three populations residing in United Arab Emirates, including; UAE Arabs, Pakistani and Indian population as well as to evaluate the usefulness of these loci for forensic genetic purposes. The combined analysis of the 23 STR loci in VeriFiler™ Express PCR Amplification Kit showed high power of discrimination and genetic diversity. Consequently, the results obtained can be utilized for the establishment of a database and contribute to other studies in the region, pertaining to the genetic diversities of populations.

Declaration of Competing Interest

The authors declared no conflicts of interest

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.fsigss.2019.09.073.

References

[1] A.M. Al-Khouri, Population growth and government modernisation efforts, Population 2 (1) (2012).
[2] N. Vora, Unofficial citizens: indian entrepreneurs and the state-effect in Dubai, United Arab Emirates, Int. Labor Work. Hist. 79 (1) (2011) 122–139.