



## Letter to the Editor

### A genetic overview of 23Y-STR markers in UAE population



Dear Editor,

The United Arab Emirates (UAE) is comprised of seven Emirates that were united in December 2, 1971. They are Abu Dhabi, Dubai, Sharjah, Ajman, Umm Al Qaiwain, Ras Al Khaimah and Fujairah. Geographically, the UAE is situated along the coast of the southern Arabian Gulf Sea, sharing borders with Oman and Saudi Arabia. The indigenous inhabitants are called Emirati and constitute only 20% of the total population. The rest of the population is migrants and include South Asians (Indians, Pakistanis and Bangladeshis), Afghans, Iranians, and people from other Arab countries such as Palestine, Yemen and Oman ([www.vesitabudhabi.ae](http://www.vesitabudhabi.ae)).

This study assessed Y-STR population variation in the UAE that could provide relevant forensic information for the Emirates as well as other countries around the world. Whole blood samples from 278 unrelated, male individuals from UAE populations were collected with informed consent and placed on FTA<sup>®</sup> cards (Whatman, UK) following the lab's standard operating protocol. Disks (1.2-mm diameter) were punched out of a blood-stained FTA-card and placed directly into a Microtiter plate (Eppendorf, Hamburg, Germany) using a BSD600-duet puncher (BSD Robotics, Brendale, QLD, Australia). Amplification was carried out on a GeneAmp<sup>®</sup> PCR System 9700 thermal cycler (Life Technologies, South San Francisco, CA) using the reagents in the PowerPlex<sup>®</sup> Y23 System (Promega Corporation, Madison, WI) and following the manufacturer's recommended protocol. The PCR products were prepared and run on Applied Biosystems 3500xL Genetic Analyzer using POP-41 polymer and a 36-cm 3500xL 24-capillary array according to the manufacturer's recommended protocol. Data were analyzed with GeneMapper<sup>®</sup> ID-X Software v1.4 software (Life Technologies).

Population based analyses were performed using the open source R statistical computing program (<http://www.r-project.org/>) and standard built-in functions. Genotypes of twenty-one Y-chromosome markers from five populations were included in the study. The DYS385a/b locus was not considered, and the number of repeats in DYS389I was subtracted from those of DYS389II, so that its diversity was not considered twice. Chromosomes with duplicated alleles at a locus were removed from the analyses. Four populations belong to the Middle East and they are UAE, Kuwait, Iraq, and Lebanon. An East Asian population from the Philippines was used as an out-group (Table 1). The populations were combined to form a population denoted as "All". This population was created to give an overview of the markers' summary statistics and to provide a reference by which any population can be compared.

Since data in the form of haplotypes are the most relevant, only those data are described. Number of alleles per marker per population and allele frequencies can be derived from the haplotype data. A principal component analysis was performed using the variation in the genotypes. The data were compared with the haplotype data from unrelated population samples of UAE, Iraq, Lebanon and Philippines, as these population data were the most complete and accessible. The  $F_{ST}$  distances of these populations were calculated with Arlequin [1]. A PCA plot was drawn (Fig. 1) based on the  $F_{ST}$  distances among populations, using PAST software ([folk.uio.no/ohammer/past/](http://folk.uio.no/ohammer/past/)).

Twenty-three Y chromosome STR markers were included in the study (Supplementary Table 1). These data were submitted to YHRD (<http://www.yhrd.org/>) receiving an accession number (YA004093).

The number of different haplotypes in each population is high which supports a relatively high discrimination power for forensic identity testing. The UAE population has 228 distinct haplotypes in the sampled 278 individuals, which is similar to that of the other populations. A small number of haplotypes are represented by two or more individuals. The UAE population tends to show a higher degree of haplotype sharing among its individuals compared to other populations. For example, the number of haplotypes represented by two individuals in the UAE population sample is 21 haplotypes whereas only 12 haplotypes are represented by two individuals in the Philippines population despite the difference in the sample size (i.e.,  $n=278$  vs  $n=626$ , respectively). Haplotype sharing between populations was absent except for four haplotypes shared between the UAE and Kuwaiti population samples.

Five populations were included in the current analysis [3]. While the focus is on the UAE population, four other populations were used for comparison purposes. Individuals from three Middle-Eastern populations (Kuwait, Iraq, and Lebanon) within the UAE geographic region were included for comparison. The Philippines sample population was included to provide an out-group. The UAE samples ( $n=278$ ) represent ~16% of the total number of samples ( $n=1773$ ) (Table 1).

The results generally are consistent with geographical distances (Fig. 1 and Table 2). The significant correlation between geographic and genetic diversity was confirmed by the Mantel test ( $r=0.916$ ;  $p=0.003$ ), performed in XLSTAT. The haplotype  $F_{ST}$  for the five populations of UAE, Iraq, Kuwait, Lebanon and Philippines is 0.082676 ( $p<0.001$ ). Considering the parameter for population correction without Philippines, the value is 0.020081 ( $p<0.001$ ).

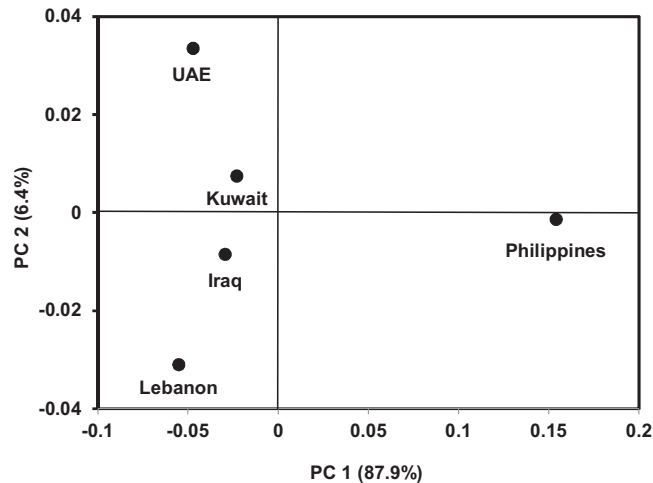
Studies using Y specific STR genetic markers have been carried out specifically on an UAE population sample, and the data were compared with samples of three other Middle-Eastern populations with the objective to understand, or to strengthen, the knowledge of human diversity. The data support that there is high diversity in the UAE population, and the data are consistent with the

**Table 1**

Population statistics summary of 21 Y chromosome markers and resulting haplotypes in five populations.

Population	Sample size (n)	Avg. allele No./marker	No. Haplotypes	Haplotype representation <sup>a</sup>					
				1	2	3	4	5	6
UAE	278	8.36	228	195	21	8	3	1	0
Kuwait	244	9	227	213	11	3	0	0	0
Iraq	122	7.90	121	120	1	0	0	0	0
Lebanon	503	10	488	474	13	1	0	0	0
Philippines	626	10.18	609	595	12	1	1	0	0
All	1773	13.09	1669	1595	56	11	3	3	1

<sup>a</sup> 1 indicates a haplotype represented by 1 individual and 2–6 are haplotypes represented by 2–6 individuals.



**Fig. 1.** Principal Component Analysis of five populations was produced using the computed genetic distances ( $F_{ST}$ ) [2]. The amount of variance extracted of each component is shown in parentheses.

**Table 2**

Genetic Diversity, measured as  $F_{ST}$  distance (all values are significant,  $p < 0.05$ ), among five populations is shown below the diagonal and geographic distances (Km, approximately) are above the diagonal.

Kuwait	*	835	535	1244	7649
UAE	0.0141	*	1420	2145	6981
Iraq	0.0237	0.0439	*	824	7903
Lebanon	0.0169	0.0321	0.0047	*	8710
Philippines	0.1341	0.1449	0.0977	0.0984	*

geographic distance among the populations. This information is useful for human identification. This paper follows the recommendations of the ISFG on the use of Y-STRs in forensic analysis and the guidelines for publication of population data requested by the journal [4].

### Acknowledgments

We gratefully acknowledge Advance Technology Company ATC, the local distributor of Promega Corporation, Madison WI, in the State of Kuwait, for supplying the kits and the General Department of Criminal Evidence, Ministry of Interior, Kuwait for providing the place for carrying out this study. Also we acknowledge the College of Biotechnology, University of Modern Sciences, Dubai, UAE for samples collection.

### Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.fsigen.2016.04.009>.

### References

- [1] L. Excoffier, H.E.L. Lischer, Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows, *Mol. Ecol. Res.* 10 (2010) 564–565.
- [2] Z. Taqi, M. Alenizi, H. Alenizi, S. Ismael, A. Bin Dukhyil, M. Nazir, S. Sanqoor, E. Al Harbi, J. Al-Jaber, J. Theyab, R. Moura-Neto, B. Budowle, Population genetics of 23 Y-STR markers in Kuwaiti population, *Forensic Sci. Int. Genet.* 16 (2015) 203–204.

- [3] J. Purps, S. Siegert, S. Willuweit, et al., A global analysis of Y-chromosomal haplotype diversity for 23 STR loci, *Forensic Sci. Int. Genet.* 12 (2014) 12–23.
- [4] J.M. Carracedo, A. Gusmão, W. Linacre, L. Roewer, et al., Update of the guidelines for the publication of genetic population data, *Forensic Sci. Int. Genet.* 10 (2014) A1–A2.

Muhammad Nazir

*College of Biotechnology, University of Modern Sciences, Dubai,  
United Arab Emirates*

Hasan Alhaddad

*College of Science, Department of Biological Sciences, Kuwait  
University, Kuwait*

Mohammad Alenizi\*

Homod Alenizi

*Ministry of Interior, General Department of Criminal Evidences,  
Identification Department, Kuwait*

Zainab Taqi

*College of Science, Department of Biological Sciences, Kuwait  
University, Kuwait*

Sheikha Sanqoor

Amna Alrazouqi

*Biology and DNA Section, Gen. Dep. of Forensic Science and  
Criminology—Biology and DNA Section, Dubai Police General H.Q.,  
Dubai, United Arab Emirates*

Ahmed Hassan

Roudha Alfalasi

Suruchika Gaur

*College of Biotechnology, University of Modern Sciences, Dubai,  
United Arab Emirates*

Jaber Al Jaber

*Department of Pharmacology and Toxicology, Faculty of Medicine,  
University of Kuwait, Kuwait*

Jassem Ziab

*Department of Sociology and Social Work, Kuwait University, Kuwait*

Enas Al-Harbi

*Princess Al-Jawhara Center for Molecular Medicine, Genetics and  
Inherited Disorders, Arabian Gulf University, Bahrain*

Rodrigo S. Moura-Neto

*Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de  
Janeiro, Brazil*

Bruce Budowle<sup>a,b</sup>

<sup>a</sup>*Institute of Applied Genetics, Department of Medical and Molecular  
Genetics, University of North Texas Health Science Center, Fort Worth,  
TX, USA*

<sup>b</sup>*Center of Excellence in Genomic Medicine Research (CEGMR), King  
Abdulaziz University, Jeddah, Saudi Arabia*

\* Corresponding author.

E-mail addresses: [mohammad.a.e\\_gdce@moi.gov.kw](mailto:mohammad.a.e_gdce@moi.gov.kw),  
[mohd\\_80@hotmail.com](mailto:mohd_80@hotmail.com) (M. Alenizi).

Received 1 March 2016

Received in revised form 11 April 2016

Accepted 16 April 2016

Available online 19 April 2016