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Creators	Ali Alhmoudi, Osamah, Jones, Rebecca J, Tay, Guan K, Alsafar, Habiba and Hadi, Ss

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1 Forensic Population Genetics-Letter to Editor

2 Dear JM,

DNA samples were analysed from 519 healthy, unrelated and consenting individuals who 3 reside in the United Arab Emirates (UAE) and were randomly chosen for this study. The 4 UAE is one of the middle-eastern countries located on the Arabian Gulf. It shares a border 5 6 with Iran, Saudi Arabia and Oman. The UAE was founded in 1971, and consists of seven Emirates: Abu Dhabi, Dubai, Sharjah, Ajman, Ra's Al-Khaymah, Al-Fujairah and Umm Al-7 Quwain [1]. According to the National Bureau of Statistics, (2012), the total UAE 8 population was reported to be around 8.26 million in 2010 [2]. The statistics showed that 9 some 11.5% of the total population comprised of native Arabs, with majority of the 10 population being of Indian and Pakistani ethnicities. In the early part of the twentieth 11 century, the different Arabic tribes migrated in different directions in search of suitable 12 locations to colonize. Some moved into coastal regions, while others inhabited the desert. 13 Despite the modernization throughout the union, the basic family structure and pattern of 14 native UAE Arab population has remained unchanged. Culturally, the preference for 15 consanguineous marriages remains embedded in the society [3]. However, as the 16 awareness of the social and medical impact of consanguinity increases and with 17 diversification, non-consanguineous marriages appear to be on the increase, which has 18 possibly resulted in greater genetic diversity throughout the population [4, 5]. The 19 increase in genetic diversity in the population is of interest to assess whether STR 20 markers can be used for forensic and paternity purposes. This study expands on previous 21 publications with regards to the analysis of UAE populations with the amplification of 22 23 additional STR markers and a larger population sample size [6].

The DNA samples analysed in the current study were obtained from indigenous UAE nationals residing in Abu Dhabi, UAE in accordance with approval from the Ethics committee of the Ministry of Health of the United Arab Emirates (2011). Informed consent was received from every volunteer during this collection process and de-identified data is presented. This study was also approved by the Ethics committee of the University of Central Lancashire (2014) as it was carried out as part of Masters Project in DNA profiling. 30 The DNA samples provided for this study were collected and extracted using the

- 31 Genotek's Oragene-DNA kit (Genotek, Ottawa, Canada) in accordance with
- 32 manufacturer's guidelines. The quantities of extracted DNA samples were determined
- using a NanoDrop spectrophotometer (Thermo Scientific, Wilmington DE, USA).

³⁴ Using half volume (7.5 μl) reactions, samples were amplified using the GlobalFiler[®]

35 PCR amplification kit (Life Technologies, Foster City CA, USA) and alleles were called

- using the allelic ladder provided by the manufacturer. The PCR was performed in the
- 37 GeneAmp® PCR System 9700 (Life Technologies). The GlobalFiler® PCR amplification
- kit (Life Technologies) amplifies 21 autosomal STR loci, a Y-STR locus DYS 391, a Y-
- indel marker and Amelogenin. The 21 autosomal STR loci within this amplification kit
- 40 were of interest for the purposes of this study. The 21 autosomal loci amplified and
- 41 focused on within this study were D3S1358, vWA, D16S539, CSF1PO, TPOX,

42 D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818,

- 43 D13S317, D7S820, SE33, D10S1248, D1S1656, D12S391, D2S1338.
- 44 The PCR products were analysed using an 8 capillary ABI 3500 DNA Genetic

45 Analyser with POP-4[™] polymer (Life Technologies). GeneMapper® Software version

46 4.0 (Life Technologies) was then used for analysis. LIZ-600 was used as internal

- 47 Standard (Life Technologies).
- 48 The alleles from all loci reported here were designated using the allelic ladder supplied
- 49 by the manufacturer, according to the published nomenclatures and the guidelines of
- the International Society for Forensic Genetics (ISFG) for performing STR analyses [7].
- 51 The STR allele frequencies along with the parameters of population genetics: observed
- and expected heterozygosity (Ho and He, respectively), power of discrimination (PD),
- 53 probability of exclusion (PE), and polymorphic information content (PIC) were estimated
- using PowerStats version 1.2 (Promega, Madison, USA) (Supplementary Table 1).
- 55 Version 3.11 of the Arlequin software was used to perform an exact test to investigate
- any departures from the Hardy-Weinberg equilibrium (HWE) [8]. The theoretical profile
- 57 frequency range was estimated signifying the rarest and most common heterozygous
- 58 genotypes. Furthermore, the number of possible genotypes was also calculated
- 59 (Supplementary Table 2).

60 The data generated from this study was compared to 5 published population data sets

for available loci [9]. Exact test comparisons were made between this current study of

the UAE population in this study and data from Kuwaiti, India, Saudi Arabia, Egypt, and

63 Iran.

64 Data is available upon request from shadi@uclan.ac.uk

Through the analysis of allele frequency data, allele 8 of TPOX was found to exhibit the 65 highest allele frequency with 49.4% in the total samples analysed for the population. 66 During analysis, two off ladder allelic variants were observed at locus SE33. These 67 variants were allele 7.3 (within 3 samples) and allele 17.3 (within 1 sample). Both of these 68 variants have been previously reported on STRBase [9]. A tri-allelic pattern (allele 6, 8, 69 10) was observed for TPOX during analysis which has also been previously reported on 70 STRBase [10]. The SE33 locus showed the largest number of different alleles (50 alleles) 71 and D13S1358, D16S539 and CSF1PO loci showed the smallest number of different 72 alleles (8 alleles). The heterozygosity (Ho) of the 21 autosomal STR loci ranged from 65% 73 (TPOX) to 92% (SE33). The power of discrimination values (PD) for all tested loci was 74 above 85%; the highest observed at SE33 with 99.3% and the least at TPOX with 85%. 75 76 The combined probability of exclusion (CPE), power of discrimination (CPD) and 77 99.999x10⁻² and 6.2468x10⁻²⁷ respectively. When HWE was tested, there was no 78 statistical significance observed for 19 out of 21 autosomal STR loci. Bonferroni correction 79 80 was applied to the two loci (D8S1179 and D22S1045) that showed deviation from HWE 81 after which no significant departure was observed. The data for the most common STR profile from the UAE population (based on this dataset) showed that even using a very 82 conservative value of 0.05 for F_{ST} leads to a discrimination power in the order of 10^{15} . 83 which translates into a value which is much higher than 1 in a billion. These estimates 84 85 indicate that UAE might like to adopt a match probability estimates to be reported by the laboratories (in case of a full match) based on statistics generated using its own 86 population allele frequency data. Further work is indicated in this area in order to develop 87 guidelines for forensic DNA laboratories in UAE. 88

89 Some significant differences were identified between the obtained UAE population data 90 and the other published data. The populations from Iran and Saudi Arabia showed significant differences at fewer loci when compared with populations from Kuwait, Egypt and India (P > 0.05). This is also supported by low F_{ST} value for the Iranian and Saudi Arabian populations. These results support the development of population or location specific databases even when considering populations that are geographically close such as within the Middle East (Supplementary Table 3).

This current dataset establishes the characteristics of the 21 STR loci panel for the identification of individuals, in paternity testing and for crime scene analysis in the UAE.

- ⁹⁸ This manuscript of population data follows the journal guidelines for publication of data
- 99 described [11, 12 and 13].

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- 104
- 105 Appendix A. Supplementary data
- 106 Publication\Supplementary Table 1.xlsx
- 107 Publication\Supplementary Table 2.xlsx
- 108 Publication\Supplementary Table 3.xlsx

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