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Letter to the Editor

Population genetic analyses of 15 STR loci from seven forensically-relevant populations residing in the state of Kuwait

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ABSTRACT

Allele frequencies and population statistics of 15 forensically-important STR loci were estimated for seven populations residing in the State of Kuwait. The populations were: Saudi Arabian, Iraqi, Egyptian, Iranian, Sri Lankan, Bangladeshi, and Indian. All loci were highly polymorphic. After correction, only one locus in one population sample (Saudi Arabian) showed departure from Hardy–Weinberg equilibrium. The populations cluster (MDS Plot) generally with geographic distance and substructure effects for even these seven diverse populations is Fst < 0.01.

Dear Editor,

Short tandem repeat (STR) typing is the standard analysis for human identification. To provide significance in cases where there is a failure to exclude an individual(s) as the source of DNA evidence population data are needed. The AmpFℓSTR® Identifiler® Direct PCR Amplification Kit (Life Technologies, Warrington WA1 4SR, UK) enables a multiplex assay that amplifies the sex determination locus Amelogenin and the 15 autosomal short tandem repeat (STR) loci: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA. To date there has been only one study reported on populations residing in the State of Kuwait and that was solely descriptive of Kuwaitis [1]. However, residents of Kuwait derive from many populations, primarily from the Middle East and neighboring areas. To determine the population dynamics in Kuwait for forensic applications a study was performed on seven different foreign national populations residing within the country. The Kuwait population is 3,065,850 according to 2011 census [2]. The Kuwaiti peoples represent 35.55% and the other nationalities represent 64.35%. The Indian nationality represents 22.2%, Egyptians 15.3%, Iraqis 6%, Bangladeshi 6%, Iranians 1.4%, Sri Lankans 3.5%, Saudis 2.8% and the remainder is other nationalities not included in this study.

As part of routine work in the Identification Department, blood samples were collected on FTA® cards (Whatman, UK) from the suspects in criminal cases from different nationalities. Informed consent was obtained from all suspects. Samples were collected from unrelated Saudis ($N = 250$), Iraqis ($N = 146$), Egyptians ($N = 421$), Iranians ($N = 287$), Sri Lankans ($N = 300$), Bangladeshi ($N = 410$), and Indians ($N = 415$) which they self-declared as representative of the population of their countries.

Genomic DNA was extracted from blood stains collected on FTA® card (Whatman, UK). One 1.2 mm disk per sample was amplified using the AmpFℓSTR® Identifiler® Direct PCR Amplification Kit (Life Technologies, WarringtonWA1 4SR, UK) in the GeneAmp 9700 PCR system (Life Technologies) according to the manufacturer's recommendations. The electrophoretic separation of the amplified PCR products was performed on the ABI 3130xl Genetic Analyzer (Life Technologies). GeneScan-500 LIZ was used as the internal lane standard. The data analysis and allele identification were performed using GeneMapper® ID (version 3.2) and GeneMapper® ID-X (version 3.2) analysis software (Life Technologies).

Allele frequencies, observed heterozygosity (Ho), expected heterozygosity (He), Power of discrimination (PD) of each locus were calculated using a software program developed by Ge [3]. Departures from Hardy–Weinberg Equilibrium (HWE) expectations and Linkage Disequilibrium (LD) between each pair of loci were derived using Arlequin [4]. Fst values were determined using Arlequin [4].

Allele frequencies and applicable forensic statistics for the STR loci in each population are displayed in supplemental Table 1. All loci are polymorphic in all populations. After Bonferroni correction [5] (p-value = 0.05/15 = 0.0033 for HWE test and 0.05/105 = 0.000476 for LD test), D21S11 in the Saudi population and D2S1338 in the Indian population departed from HWE; one pair of loci (D2S1338 and D19S433) in the Saudi population departed from LD.

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The data from the seven populations are consistent with other population data from the region [6,7]. An MDS plot, based on Fst distances, of the seven populations and several others (i.e., Iranian, Omani, Saudi, Yemen, and Tamil) [6,7] are generally consistent with geographical distances (Fig. 1). The average Fst value for the seven populations in Kuwait was 0.00659, which is less than the recommended value for casework statistics of Fst < 0.01 [8].

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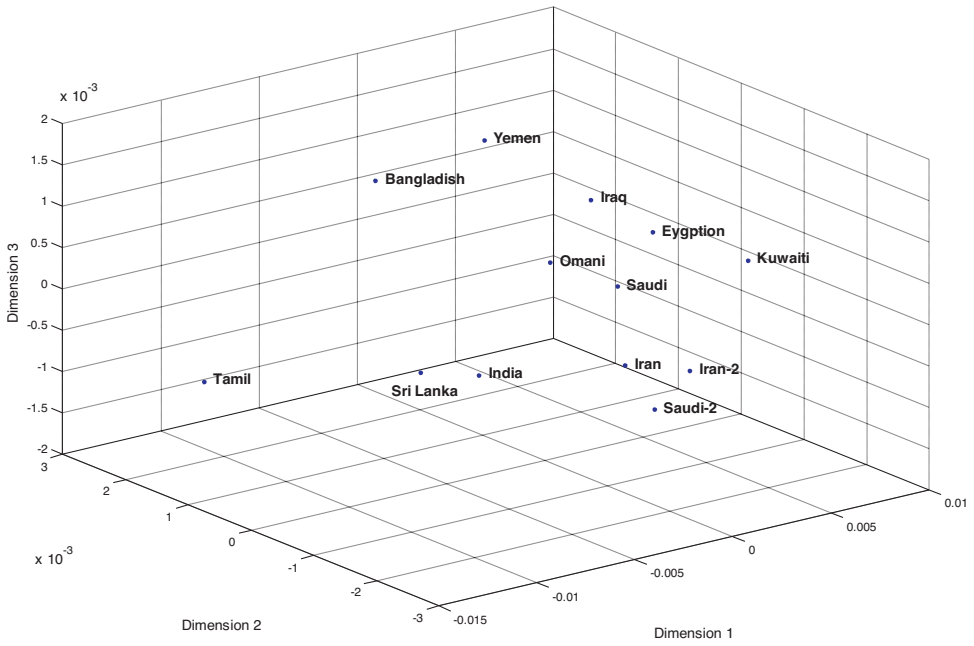

Fig. 1. MDS plot based on Fst distances. "Saudi-2" and "Iran-2" are population data from [6,7], which are different sampling from current sampling in this study.

This study supports that the 15 STR loci have high discrimination power in populations residing in Kuwait. In addition, the allele frequencies are similar for geographically close population groups. These data can be used for estimating the rarity of STR profiles derived from DNA evidence for human identification applications.

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