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Announcement of Population Data

Allele frequencies of 15 autosomal STR loci in the Iraq population with comparisons to other populations from the middle-eastern region

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Abstract

Allele frequencies for the 15 autosomal STR loci included in the AmpFlSTR® IdentifilerTM PCR Amplification Kit panel from Applied Biosystems (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO, D19S433, D2S1338, D16S539) and several statistical parameters were estimated from a sample of 103 unrelated individuals, mostly Shia and Sunni Arabs, living in most of central and southern Iraq provinces. We compared the allele frequency spectrum detected in the Iraqi population to allele frequencies from 11 other data sets from published studies of individuals from Turkey, Iraqi-Kurdistan, Saudi Arabia, Arab Emarates, Oman, Iran, Syria, and Jordan. Significant global differences in allele frequencies were detected in 9 of the 11 comparisons following sequential Bonferroni corrections. Comparisons with the two independent panels from Saudi Arabia were not significant after applying Bonferroni corrections, however, low *P*-values ($P < 0.05$) associated with these two contrasts nonetheless suggested that at least slight genetic differences between populations may exist.

Keywords: Iraq population; Shia and Sunni Arabs; STR DNA typing; Population data; Allele frequencies

Population: Buccal cells were collected by oral brushes (Sterile Omni Swab or Sterile Foam Tipped Swabs, Whatman International Ltd., Maidstone, UK) from 103 healthy, randomly chosen individuals deriving from most of Iraq central and southern provinces (Fig. 1). The number and ethnicity of individuals were chosen in order to obtain a population sample resembling the Iraq population structure and to achieve the highest possible representation of the major ethno-religious and tribal groups of the Country living in these central and southern areas. Our sample was mainly constituted by Shia Arabs and, secondly, by Sunni Arabs. Shia Arabs comprise about 65–70% of the entire Iraq population while Sunni Arabs represent about 25% of Iraq population (Fig. 2).

DNA extraction: DNA from these samples was extracted using QIAmp® DNA Mini Kit (QIAGEN, Hagen, Germany) according to manufacturer's instructions.

DNA quantification: The total amount of human genomic extracted DNA was determined by using Quantifiler™ Human DNA Quantification Kit (Applied Biosystems, Foster City, CA, USA) [1], which employs a TaqMan® MGB Probe-based technology (Applied Biosystems, Foster City, CA, USA) on ABI Prism® 7000 Sequence Detection System (Applied Biosystems, Foster City, CA, USA).

PCR: Simultaneous amplifications of 16 STR loci (multiplexed PCR) were performed by using the AmpF*l*STR® Identifiler™ PCR Amplification Kit according to the user's manual recommendations [2]. The 16 loci amplified in this study are D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO, D19S433, D2S1338, D16S539 and the gender determination marker, Amelogenin.

Typing: The separation and detection of amplified products were conducted with the ABI Prism® 3100 Genetic Analyzer 16-capillary array system (Applied Biosystems, Foster City, CA, USA) following manufacturer's protocols. Data collection was performed with Data Collection v. 2.0 software (Applied Biosystems, Foster City, CA, USA) and samples were analyzed

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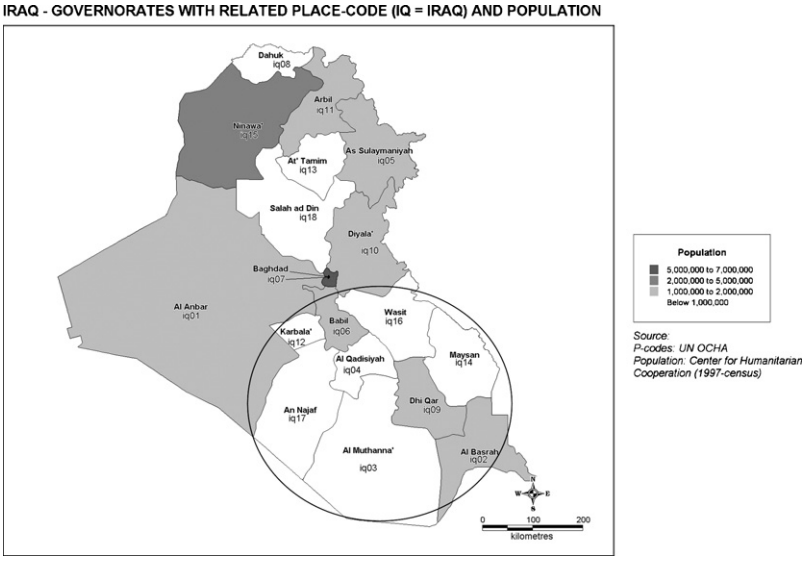

Fig. 1. Iraq administrative map showing the population density and the central and southern governorates where our samples came from (areas included in the black circle) (Source: UNOSAT, www.unosat.org, United Nations).

by GeneMapper® v. 3.2 software (Applied Biosystems, Foster City, CA, USA).

Quality control: Experimental procedures were performed according to the guidelines of the external blind proficiency test of the GEDNAP (http://www.gednap.org) [3,4].

Statistical analyses: Several forensic and population parameters such as the power of discrimination (PD), the a priori chance of exclusion (CE), the polymorphism information content (PIC), the paternity index (PI), the random match probability (RMP) and marker's observed and expected heterozygosity (Ho and He, respectively) of the 15 loci were estimated by using the statistical Microsoft Windows™-based software Popgene v. 1.31 [5] and Cervus v. 2.0 [6,7] while Hardy-Weinberg equilibrium analysis was performed for each locus by the Chi-square test (χ^2).

A set of interpopulation comparisons of allele frequencies from this study and 11 additional published population data sets were performed. Our analyses compared the Iraqi data to data from Turkey [8,9], Iraqi-Kurdistan (northern Iraq) [10], Saudi Arabia [11,12], Arabs Emirates [12], Oman [12], Iran [12,13], Syria [14], and Jordan [15] whenever the same loci studied were shared. In these cases, allele frequency data reported in these studies were converted to counts by multiplying allele frequencies from these publications by reported diploid ($2N$) sample sizes. Tests for homogeneity of allele frequencies between locus-specific data sets were performed using the computer program $R \times C$ (M.P. Miller, available at http://www.marksgeneticsoftware.net), which implements a Markov Chain Monte Carlo variation of Fisher's Exact test [16]. A global P-value over shared loci from comparisons with each panel was

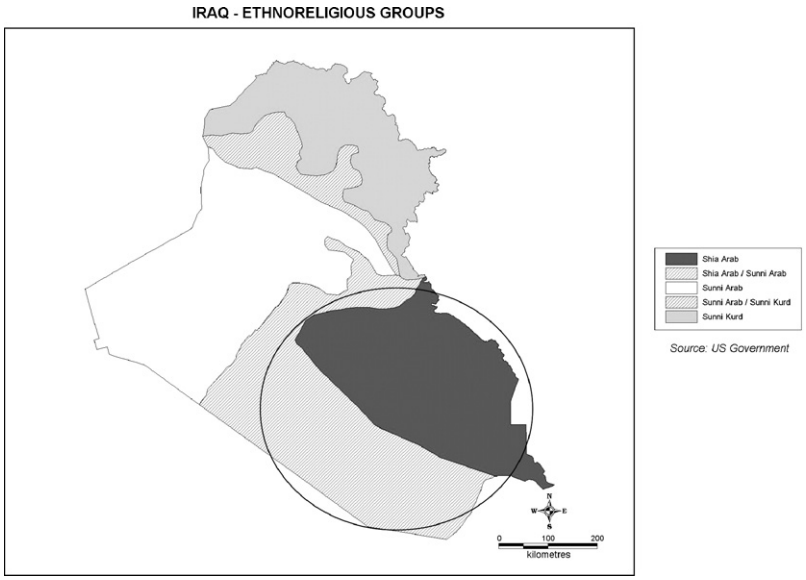

Fig. 2. Iraq ethno-religious map showing the ethnic and religious population composition and the central and southern governorates, mostly constituted by Shia Arabs and, secondly, by Sunni Arabs, where our samples came from (areas included in the black circle) (Source: UNOSAT, www.unosat.org, United Nations).