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Kurdish (Iraq) and Somalian population data for 15 autosomal and 9 Y-chromosomal STR loci

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Abstract. Autosomal STR polymorphisms at 15 loci and Y-chromosomal STR polymorphisms at 9 loci are presented. Samples from current immigration casework including individuals from Somalia ($n \sim 100$) and northern Iraq (Kurds) ($n \sim 100$) were analysed. For the autosomal polymorphisms, the observed heterozygosities ranged from 0.602 (TPOX) to 0.918 (PentaD) in the Iraqi sample and from 0.614 (D13S317) to 0.958 (PentaE) in the Somali sample. One significant deviation from Hardy–Weinberg equilibrium was observed in the Somali sample at D13S317, the expected heterozygosity rate is 0.761 and the observed is 0.614. For the Y-chromosome polymorphisms, 61 and 99 different haplotypes were observed in the samples from Somalia and Iraq, respectively. Combined gene diversity was 0.97 (Somalia) and 0.99 (Iraq). Locus diversity ranged from 0.24 (DYS391) to 0.82 (DYS385) in the population sample from Somalia and from 0.45 (DYS392) to 0.96 (DYS385) in the population sample from Iraq. None of the haplotypes in the two populations were identical. Locus diversity, allele distributions and other relevant forensic genetic parameters will be presented.

Keywords: Forensic population database; PowerPlex 16; Y-STR; Iraqi Kurds; Somali

1. Introduction

In order to establish a database for immigration and paternity casework, two population samples of different ethnic origin were analysed at the fifteen autosomal STR polymorphisms D3S1358, THO1, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta E, vWA, D8S1179, TPOX and FGA, included in the PowerPLex16® multiplex (Promega, Madison, US). Furthermore, nine Y-chromosomal STR polymorphisms were analysed (DYS19, DYS385, DYS388, DYS389I, DYS389II, DYS390, DYS391, DYS392 and DYS393).

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2. Materials and methods

Samples were obtained from current immigration casework—98 unrelated individuals from northern Iraq (Kurds) and 96 unrelated individuals from Somalia. DNA was extracted from venous blood by the method of Ref. [1]. PCR amplification was performed according to the manufacturer's manual (PowerPlex16) and Ref. [3] (Y-chromosome loci). Fragment analysis was done by capillary electrophoresis (ABI PRISM® 3100, AB, Foster City, US). Evaluation of Hardy–Weinberg equilibrium was performed by a modified version of the Markov-chain random walk algorithm (10 000 shuffles) provided by the Arlequin Software (http://anthro.unige.ch/arlequin). Other forensic statistical parameters were obtained by the PowerStats, Promega (http://www.promega.com/geneticidtools/powerstats/Default.htm).

3. Results and discussion

In both population samples, alleles not present in the allelic ladder were observed at several loci. (For details, allele distributions and forensic statistical parameters—see Tables 1 and 2 at http://folk.uio.no/msteners/index.html.htm.) A significant deviation from Hardy–Weinberg equilibrium was observed at the D13S317 locus in the Somalian population (the expected heterozygosity rate was 0.761 and the observed was 0.614, $p = 0.002$). To investigate the possibility of ''0-alleles'' at this locus, families of homozygous individuals (two to six children and the other parent) were analysed. No evidence of 0-alleles was observed. Further experiments, to uncover a possible primer binding site polymorphism, is necessary. No significant deviation from Hardy–Weinberg equilibrium was observed in the Iraqi population sample. The 15 loci possess a combined power of exclusion of 0.9999995 for each population group.

For the Y-chromosome polymorphisms, 61 and 99 different haplotypes were observed in the samples from Somalia and Iraq, respectively. Combined gene diversity (Table 1) was 0.97 (Somalia) and 0.99 (Iraq). Locus diversity [3] ranged from 0.24 (DYS391) to 0.82 (DYS385) in the population sample from Somalia and from 0.45 (DYS392) to 0.96 (DYS385) in the population sample from Iraq. None of the haplotypes in the two populations were identical. The Y-haplotype distributions are presented in Figs. 1 and 2 at http://folk.uio.no/msteners/index.html.htm.

Table 1
Y-chromosome locus diversity and haplotype (HT) diversity

Locus	Somalia	Iraq
DYS19	0.3897	0.6579
DYS389I	0.3172	0.5599
DYS389II	0.6783	0.7247
DYS390	0.3990	0.7168
DYS391	0.2377	0.4996
DYS392	0.3743	0.4521
DYS393	0.3045	0.5918
DYS385[a]	0.8213	0.9586
DYS388	0.3833	0.7240
HT diversity	0.9703	0.9984

[a] Calculated on the basis of recommended nomenclature [2], which may differ from the genomic haplotype.

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