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SHORT COMMUNICATION

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Y-STR haplotypes in populations from the Eastern Mediterranean region of Turkey

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Abstract We present the frequency distributions of Y-haplotypes determined by ten Y-chromosomal STR polymorphisms (i.e., DXYS156-Y, DYS19, DYS385, DYS389 I and II, DYS390, DYS391, DYS392, DYS393) in unrelated males from the Eastern Mediterranean region of Turkey (104 Turkish and Arabian-speaking Eti Turks from Adana area, 111 Roma and 110 Turks, Kahramanmara° area). The haplotype diversity was 0.974 in the Eti Turks, 0.979 in the Roma, and 0.989 in the Turks. Two variant alleles were characterized by sequencing, i.e., allele 9.2 at DXYS156 and 12.2 at DYS385. Some of the haplotypes are particular to one of the three populations; some are shared by all three populations. A search against the Y-Haplotype Reference Database revealed several matches to samples not only from Turkey and neighboring regions (e.g., Syria, Iraq) but also from all over Europe.

Keywords Y-STRs · Turkey · Haplotypes · Multiplex PCR

Introduction

The forensic application of Y-STRs requires the generation of population databases taking into consideration the existence of subpopulations. Recently, several Y-STR studies were reported for Turkey [1] and other Near East populations [e.g., 2]. In this paper, we present frequency distributions of Y-STR haplotypes in the Eastern Mediterranean region of Turkey.

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Materials and methods

Blood samples from 325 unrelated males from the Kahramanmara° and Adana (Eti Turks) area (Fig. S1) were extracted using the standard Chelex/ProteinaseK method. Amplification of the Y-STRs was carried out using two commercial kits, i.e., the *genRES* DYSplex-1 kit (DYS390, DYS391, DYS389 I/II, DYS385 and Amelogenin) and the *genRES* DYSplex-2 kit (including the DYS392, DYS393, DYS389 I/II, DYS19 loci) according to the instructions of the manufacturer (Serac, Bad Homburg, Germany [3]). DXYS156 was amplified as monoplex according to [4] and analyzed using a sequenced allelic ladder. Typing was carried out by capillary gel electrophoresis on an ABI PRISM 310 Genetic Analyzer and use of Genotyper 2.5.2 software (Applied Biosystems, Darmstadt, Germany). Variant alleles were sequenced on both strands according to [5]. Briefly stated, the samples were amplified using unlabelled primers [4, 6] and, after eluting the alleles of interest from polyacrylamide gels, the sequence was determined using the BigDye Terminator kit v2.0 and an ABI PRISM 310 Genetic Analyzer.

Results and discussion

All men included in this study carried allele 11.1 or 12.1 at DXYS156-Y, which is due to an adenine insertion in the fourth repeat motif from the 5′ end [7].

Sequencing of the variant alleles in two Turkish samples revealed the following sequence structures of the repetitive regions (EMBL AJ971428 and AJ971296, respectively; for comparison, allele 10.1 was submitted as AJ971429):

T96: 9.2 at DXYS156-X : $(TAAAA)_7$ **TA** $(TAAAA)_2$
T38: 12.2 at DYS385 : $(GAAA)_{12}$ **GA** GAG $(A)_5$

Table 1 Locus diversities d in the three populations from the Eastern Mediterranean region of Turkey

Locus diversity	Eti Turks	Roma	Turks
DXYS156-Y	0.221	0.164	0.195
DYS390	0.659	0.741	0.677
DYS385	0.989	0.942	0.942
DYS389 I	0.646	0.386	0.808
DYS389 II	0.7	0.705	0.77
DYS391	0.64	0.447	0.525
DYS393	0.686	0.637	0.603
DYS19	0.516	0.672	0.683
DYS392	0.517	0.404	0.583

Calculated according to $d = 1 - \sum_{i=1}^{h} (x_i/N_x)^2$, where x_i is the absolute frequency of the i-th haplotype and h is the total number of different haplotypes in the N_x samples [9]

Both variants can be explained as dinucleotide insertions within or at the very end of the repetitive region.

In the Eti Turks, Roma, and Turks, we have observed 93, 106, and 103 different haplotypes, respectively, of which 84, 103, and 98 were unique, respectively (Table S1). The other haplotypes were shared by two to 12 men; some of the haplotypes are present in at least two populations and one is present in all three populations (e.g., A27, G24, and T109).

The locus diversities range from 0.164 (DXYS156-Y, Roma) to 0.989 (DYS385, Eti Turks; Table 1), while the haplotype diversity was 0.974 in the Eti Turks, 0.979 in the Roma, and 0.989 in the Turks.

The haplotypes were searched against the minimal haplotypes in the Y-Haplotype Reference Database (YHRD, release 17 from 10/24/2005; http://www.yhrd.org) and 38 different Eti, 46 different Roma, and 47 different Turkish haplotypes matched to at least one YHRD sample. The haplotypes of the Eti Turk samples A3 and A11, which differ by a single repeat unit at DYS389 I and are shared by 17 males, match with nearly 200 YHRD samples, with approximately 70% of the haplotypes being sampled in Europe. The other haplotypes from this study also match predominantly with samples from Europe (e.g., T26 matching to 118 YHRD samples, 113 from Europe including two 'Bulgarian Turks' and two other Turkish samples), which may be partially explained by a sampling bias, i.e., the YHRD contains by far more samples from Europe than from the Middle East. To investigate this issue in more detail, we are currently typing Y-SNPs [8] to check if the haplogroup distribution within the three population groups and in comparison to neighboring populations (e.g., Syria and Iraq) is similar.

In conclusion, the ten Y-STR polymorphisms provide a powerful means for male identification in forensic crime cases and parentage testing in the Eastern Mediterranean region of Turkey.

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