

COMPARISON OF TURKISH SUBPOPULATIONS USING TWO STR's

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Abstract

The short tandem repeat (STR) systems HumTH01 and Hum VWA were used for PCR typing of two Caucasian subpopulations, one living in the Black sea area (northern Turkey), the other being a subpopulation from eastern Anatolia (eastern Turkey). The allele frequency data were compared with a turkish subpopulation from Adana area (southern Turkey) and a group of Turks living in Brussels (Belgium). The HumTH01 data showed a significant difference in the Black Sea region compared to the 3 other groups while the subpopulation from the eastern Anatolia showed significant differences in Hum VWA system.

Introduction

STR polymorphisms represent a widely used method for linkage studies and human identification (Edwards et al. 1991), even on highly degraded DNA (Brinkmann 1992). This study was carried out with the systems HumTH01 and HumVWA (Kimpton et al. 1992) on two turkish subpopulations living in the Black Sea and Eastern Anatolia. The population genetic data were compared with a turkish subpopulation living in Brussels, (Belgium) since 1960 and another population living in southern Turkey (Adana area) (Alper et al., in press).

Materials and Methods

The blood samples were collected from unrelated individuals living in two provinces the Artvin province in the eastern Black Sea and the Elazığ province situated in eastern Anatolia. DNA was extracted from 200 µl blood, air dried on sterile cotton fabric. The extraction procedure was carried out using 150 µl Chelex 100 (Biorad, Germany) with the addition of 50 ml proteinase K (2 mg/ml) as previously described (Wiegand et al. 1993 a). The reaction assay, the amplification and electrophoresis conditions for both systems were carried out as previously described (HumTH01: primers according to Gill et al. 1992, amplification conditions and electrophoresis according to Wiegand et al. 1993 b, HumVWA: primers according to Kimpton et al. 1992, amplification and electrophoresis according to Möller et al. 1994).

The statistical analysis was performed with standard Chi square method the logarithmic likelihood ratio (G) test, and the exact -test by random shuffling the observed alleles 5000 times (HWE analysis, version 3.0, C. Puers, Münster Germany). The mean paternity exclusion probability was calculated according to Brenner and Morris (1989); the polymorphic information content according to Botstein et al. (1980); the probability of match and the discrimination power according to Jones (1972). The frequency profile comparison between the populations was performed using a test for genetic heterogeneity (RXC contingency table; G. Carmody, Ottawa, Canada).

Results and Discussion

A total of 7 alleles in the Black Sea and 6 alleles in eastern Anatolian populations for HumTH01 system, and 8 and 7 alleles respectively for HumVWA system have been observed (Fig. 1a,b).

Due to allele number and distribution both systems showed relatively high forensic efficiency values (Table 1).

HumTH01 typing results for the Black Sea area showed significant differences in comparison to the other 3 subpopulations ($p > 0.05$) while the eastern Anatolia population show no significant difference in their allele frequencies from the Adana and Brussels Turks. For HumVWA a contrary situation was found. The Black Sea population did not differ significantly from Adana and Brussel subpopulations while significant differences were found in eastern Anatolia. No significant deviation from Hardy Weinberg equilibrium could be detected ($p > 0.05$).

Both subpopulations, each in its geographical position is considerably isolated. The differences found may be expected because these two subpopulations must have genetic diversity once they have geographical, ecological linguistic and cultural separation (Andrews 1989). The sample size for eastern Anatolia was too small for a reliable statistical evaluation. This part of the study is still under investigation.

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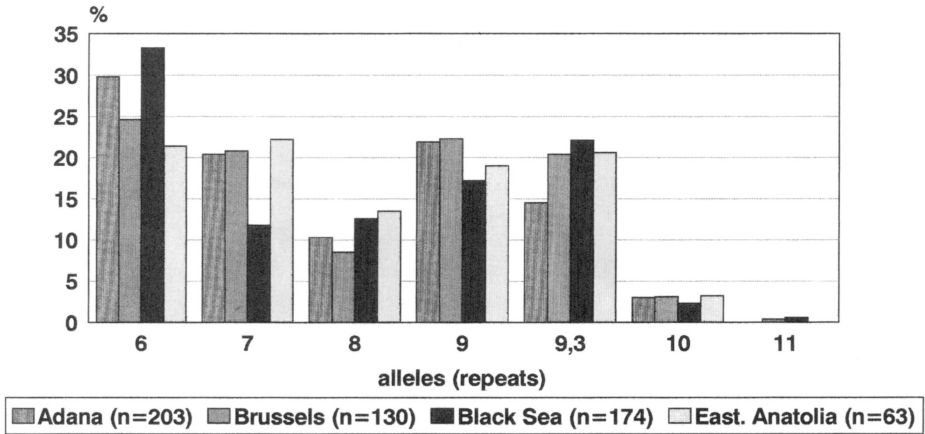
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Table1. Forensic efficiency values for HumTH01 and HumVWA.

Group I - Black Sea region		
	TH01	VWA
	<i>n = 174</i>	<i>n = 228</i>
MEC	0.57	0.62
MEP	0.56	0.61
PIC	0.75	0.78
pM	0.09	0.07
D		
Group II - Eastern Anatolia region		
	<i>n = 63</i>	<i>n = 76</i>
MEC	0.61	0.54
MEP	0.62	0.51
PIC	0.78	0.71
pM	0.09	0.11
D	0.91	0.89

MEC = mean exclusion chance
 MEP = mean exclusion probability
 PIC = polymorphic information content
 PM = match probability
 D = discrimination power

THO1



VWA

