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SHORT COMMUNICATION

M. Iwasa · P. Wiegand · S. Rand · M. Schürenkamp
S. Atasoy · B. Brinkmann

Genetic variation at five STR loci in subpopulations living in Turkey

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Abstract Five short tandem repeat (STR) systems HumVWA, HumTH01, HumCD4, HumF13B and HumFES were investigated in 2 subpopulations living in Turkey (Laz Turks and Kurds). The population genetic data were compared to a Turkish population sample from the Adana area. A closer genetic relationship was found to the Laz Turks than to the Kurdish sample which was also confirmed by phylogenetic tree reconstruction with seven populations from three major ethnic groups (Caucasian, Asian and African). In contrast to the Laz and Adana populations the Kurdish sample showed relatively low heterozygosity values and deviations from Hardy-Weinberg equilibrium in four of the five systems.

Key words Short tandem repeats (STR) · Forensic validation · Population genetics

Introduction

Two subpopulations living in Turkey were investigated using the short tandem repeat (STR) systems HumVWA (Kimpton et al. 1992), HumTH01 (Edwards et al. 1991), HumCD4 (Edwards et al. 1992), HumF13B (Nishimura and Murray 1992) and HumFES (Polymeropoulos et al. 1991). The 2 subpopulations were Laz/Turks from the Black Sea coast located between Sinop and Samsun speaking the "Laz" language (Abaci-Kalfoglu and Atasoy 1993) and Kurds living in the boundary between Turkey, Irak and Iran. The population genetic data were compared with those from previous studies involving a Turkish subpopulation from the Adana area (Alper et al. 1995).

M. Iwasa
Department of Legal Medicine, Nagoya City University, Medical School, Kawasumi Mizuho-Ku, Nagoya 467, Japan

P. Wiegand
Institute of Legal Medicine, Martin-Luther-University, Franzosenweg 1, D-06112 Halle/Saale, Germany

S. Atasoy
Institute of Forensic Science, Laboratory of Haemogenetics, Istanbul University, 34303 Cerrahpasa, Istanbul, Turkey

S. Rand · M. Schürenkamp · B. Brinkmann (✉)
Institute of Legal Medicine, Westfälische Wilhelms-Universität, Von-Esmarch-Strasse 86, D-48149 Münster, Germany
FAX: +49 (251) 8355 158

Materials and methods

Typing protocol

DNA was extracted from blood stains with 150 µl Chelex (Walsh et al. 1991) containing 50 µl proteinase K (2 mg/ml) (Wiegand et al. 1993a). PCR was carried out in 25 µl reaction volumes, using 5 ng of template DNA, 1 U Taq DNA polymerase (Promega), 200 mM each deoxynucleotide, 1 mM each primer and 2 µl reaction buffer (500 mM KCl, 100 mM Tris-HCl pH 8.8, 1% Triton X-100, 0.1% gelatine). The PCR primers and reaction conditions for HumVWA (Kimpton et al. 1992; Möller et al. 1994a), HumTH01 (Edwards et al. 1992; Wiegand et al. 1993b), HumCD4 (Edwards et al. 1991), HumF13B (Nishimura and Murray 1992; Alper et al. 1995), and HumFES (Polymeropoulos et al. 1991; Möller et al. 1994b; Alper et al. 1995) have been described previously.

Electrophoretic separation of PCR products was performed by high resolution polyacrylamide gel electrophoresis according to Allen et al. (1989) as essentially described by Möller et al. (1994a, b). Silver staining of the gels was performed according to the method of Budowle et al. (1991) using the published conditions (Wiegand et al. 1993a; Möller et al. 1994a).

Statistical tests and evaluation

The statistical tests for Hardy-Weinberg equilibrium by the exact test (Guo and Thompson 1992), heterozygosity (Nei 1978), and discrimination power (Jones 1972) were carried out.

The population comparisons were carried out using a test for heterogeneity (2-way R × C contingency table calculating the χ^2 and G-statistic) with a program kindly provided by G. Carmody (Ottawa, Canada).

A phylogenetic tree reconstruction was carried out using all frequency data to evaluate genetic distances between population pairs. The standard distance (Nei 1972) was used as a distance matrix for the reconstruction of phylogenetic trees (UPGMA-average linkage analyses: Cavalli-Sforza et al. 1994).

Table 1 Allele frequencies for five STR systems in three Turkish subpopulations. The nomenclature of alleles is according to the number of repeats

HumVWA

Allele	ADA (n = 201)	LAZ (n = 228)	KUR (n = 167)
14	0.077	0.103	0.147
15	0.092	0.114	0.030
16	0.234	0.162	0.198
17	0.321	0.333	0.407
18	0.184	0.173	0.162
19	0.075	0.072	0.051
20	0.017	0.037	0.006
21	–	0.004	–

HumF13B

Allele	ADA (n = 199)	LAZ (n = 188)	KUR (n = 118)
6	0.075	0.096	0.038
7	0.030	0.005	0.004
8	0.317	0.388	0.284
9	0.244	0.181	0.220
10	0.332	0.330	0.453
11	0.003	–	–

HumTH01

Allele	ADA (n = 202)	LAZ (n = 174)	KUR (n = 114)
6	0.297	0.333	0.205
7	0.208	0.118	0.253
8	0.104	0.126	0.149
9	0.215	0.172	0.188
9.3	0.146	0.221	0.188
10	0.030	0.023	0.017
11	–	0.006	–

HumFES

Allele	ADA (n = 202)	LAZ (n = 211)	KUR (n = 100)
7	–	0.002	0.020
8	0.010	0.005	–
9	0.005	–	–
10A	0.214	0.166	0.260
10	0.037	0.026	0.105
11A	0.010	0.009	0.005
11	0.371	0.445	0.410
12A	0.002	0.002	0.005
12	0.299	0.291	0.155
13	0.045	0.050	0.040
14	0.007	0.002	–

HumCD4

Allele	ADA (n = 202)	LAZ (n = 188)	KUR (n = 137)
5	0.366	0.346	0.354
6	0.272	0.293	0.223
7	0.002	–	–
8	–	–	–
9	0.012	0.005	0.040
10	0.272	0.287	0.350
11	0.062	0.069	0.029
12	0.012	–	0.004

ADA: ADA-Turks; LAZ: LAZ-Turks; KUR: Kurds

Results and discussion

A comparison of the allele frequencies showed some slight differences between Adana and Laz Turks (e.g. VWA allele 16, TH01 allele 7) and clear differences between Laz Turks and Kurds (Table 1). Pairwise comparisons between the Adana and the Laz samples show no significant deviations for the STRs VWA, CD4 and FES, but significant deviations for TH01 and F13B. In contrast, the other pairwise comparisons (Laz Turks – Kurds and Adana Turks – Kurds) led to significant deviations in all systems (Table 2). The significant deviations could be explained by clear genetic boundaries between these subpopulations due to, for example differences in language and culture which reduce interpopulation genetic admixture (Cavalli-Sforza et al. 1994).

The reconstruction of phylogenetic trees showed similar results (Brinkmann 1996) with high bootstrap values supporting the validity of the branching pattern (Fig. 1).

Table 2 Population comparison test for pairwise comparisons. The P-values for a χ^2 test are given

Comparison	System	χ^2-test	P-value
ADA-LAZ	HumVWA	13.200	0.055
	HumTH01	20.994	$< 10^{-3}$
	HumCD4	7.494	0.285
	HumF13B	14.893	0.005
	HumFES	11.225	0.363
LAZ-KUR	HumVWA	35.507	$< 10^{-3}$
	HumTH01	29.206	$< 10^{-3}$
	HumCD4	20.811	$< 10^{-3}$
	HumF13B	18.141	$< 10^{-3}$
	HumFES	40.739	$< 10^{-3}$
KUR-ADA	HumVWA	28.101	0.001
	HumTH01	13.327	0.019
	HumCD4	15.943	0.008
	HumF13B	15.473	0.007
	HumFES	36.209	$< 10^{-3}$

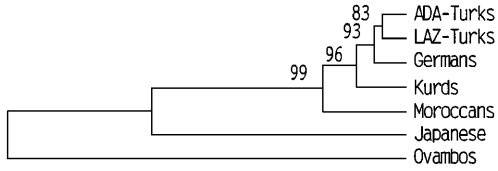

Fig. 1 Phylogenetic tree constructed using DA-UPGMA method. The numbers represent the bootstrap values obtained in 1000 replications

Table 3 Forensic efficiency values for five STR systems in Turkish subpopulations

Population	System	Heterozygosity rate	Mean exclusion chance	Discrimination power
ADA	HumVWA	0.75	0.59	0.93
	HumTH01	0.81	0.59	0.92
	HumCD4	0.70	0.46	0.86
	HumF13B	0.73	0.47	0.87
	HumFES	0.66	0.48	0.88
LAZ	HumVWA	0.79	0.62	0.93
	HumTH01	0.76	0.57	0.92
	HumCD4	0.68	0.44	0.86
	HumF13B	0.67	0.44	0.86
	HumFES	0.70	0.44	0.85
KUR	HumVWA	0.71	0.53	0.89
	HumTH01	0.78	0.60	0.91
	HumCD4	0.61	0.44	0.86
	HumF13B	0.61	0.39	0.83
	HumFES	0.72	0.50	0.87

The Adana, Laz, Kurdish and German populations formed the Caucasian branch to which the Moroccans are genetically related. The Asian (Japanese) and African (Ovambos) populations were clearly separated by showing long branches.

The comparison of forensic efficiency values (Table 3) shows that the heterozygosity rates for the Adana population are slightly higher while in the Kurdish sample deviations from Hardy-Weinberg equilibrium were found in four STRs (VWA, TH01, CD4 and F13B). The later could be a sampling effect (Deka et al. 1995) but could also be due to inbreeding effects in such genetically isolated subpopulations.

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