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SHORT COMMUNICATION

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Hungarian population data for six STR loci

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Abstract Population genetic studies were carried out on a South Hungarian population (n = 111 individuals). The short tandem repeat (STR) systems HumVWA, HumTH01, HumF13B, HumCD4, HumFES and HumFIBRA (FGA) were investigated by PCR amplification. All loci met Hardy-Weinberg expectations.

Key words Short tandem repeats · Population studies · Hungary

Introduction

Population studies were carried out on individuals from southern Hungary for six short tandem repeat (STR) loci using the polymerase chain reaction (PCR). This study presents the allele and genotype frequency data for the STR loci HumVWA (Kimpton et al. 1992), HumTH01 (Edwards et al. 1991 a), HumF13B (Nishimura and Murray 1992), HumCD4 (Edwards et al. 1991 b; Hammond et al. 1994), HumFES (Polymeropoulos et al. 1991) and HumFIBRA (Barber et al. 1996).

Material and methods

Blood samples were taken from 111 unrelated individuals from southern Hungary. DNA extraction, amplification, electrophoretic separation and typing of PCR products were performed as previously described (Allen et al. 1989; Wiegand et al. 1993; Hammond et al. 1994; Martin et al. 1995). The PCR reaction conditions for HumCD4 were as follows: 5 ng template DNA, 1 µ*M* of each primer (5′-primer: GCATTGTACTTCATCTGTAGC; 3′-primer: Hammond et al. 1994), 0.25 units of Taq polymerase, 1 × reaction buffer, 200 µ*M* of each dNTP and 1.5 m*M* $MgCl_2$ in a final volume of 25 µl. Cycle parameters were 94° C/60 s, 62° C/60 s, 72° C/120 s for 30 cycles. Statistical analysis was carried out using the exact test to check for Hardy-Weinberg equilibrium (Guo and Thompson 1992). The population genetic comparisons were carried out using a test for heterogeneity (R × C contingency table; G. Carmody, Ottawa, Canada). Population data for Turks and Germans were derived from other studies (Alper et al. 1995 a; Meyer et al. 1995).

Results and discussion

No deviations from Hardy-Weinberg equilibrium were found for all six loci examined (Table 1). Pairwise testing for population homogeneity between South Hungarians and Germans using the χ^2-test according to Carmody revealed no significant differences for the STR loci VWA, TH01, F13B, FGA and FES ($P > 0.05$).

The results for VWA and FES showed no differences between the population from South Hungary and a Turkish population (Alper et al. 1995 b) whereas significant differences could be demonstrated for TH01, F13B, CD4 and FGA (Table 1). Interpopulation differences were also found between Turks and Germans in the STR Systems TH01 (Alper et al. 1995 b) and F13B (Alper et al. 1995 a). The significant differences for the STR system CD4 in both comparisons (Hungarians-Germans, Hungarians-Turks) demonstrate the high efficiency of this system to discriminate even between subpopulations (Wall et al. 1993; Brinkmann 1996).

Our typing results showed no significant differences in the systems VWA, TH01 and FES in comparison with the corresponding data observed in another Hungarian population from Central Hungary (Füredi et al. 1996).

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Table 1 Allele frequencies for six STR loci in a South Hungarian population with statistical evaluation and pairwise testing for population comparisons

Allele	VWA *n* = 110	TH01 *n* = 111	F13B *n* = 111	CD4 *n* = 110	FGA *n* = 111	FES *n* = 109
5		0.010		0.323		
6		0.270	0.095	0.432		
7		0.150				0.005
8		0.070	0.261			0.009
9		0.200	0.194	0.009		0.005
9.3		0.290				
10		0.020	0.446	0.214		0.073
10A						0.197
11			0.005	0.014		0.459
11A						0.009
12				0.005		0.211
13	0.005			0.005		0.032
14	0.123					
15	0.105					
16	0.182					
17	0.305					
18	0.186				0.018	
19	0.077				0.082	
20	0.018				0.198	
21					0.176	
21.2					0.005	
22					0.203	
22.2					0.009	
23					0.117	
23.2					0.005	
24					0.095	
25					0.068	
26					0.027	
observed heterozygosity	0.8091	0.8198	0.7117	0.7091	0.9009	0.7248
exact test probability	0.8072	0.4570	0.5998	0.6510	0.1554	0.5172
χ^2-test probability	0.8562	0.4864	0.6522	0.6022	0.1318	0.6830
G-test probability	0.8336	0.4138	0.6746	0.5670	0.1656	0.5526
South Hungarians/Germans						
P-value (χ^2-test)	0.665	0.264	0.591	0.008	0.326	0.189
SE	± 0.0149	± 0.0139	± 0.0155	± 0.0028	± 0.0148	± 0.0124
South Hungarians/Turks						
P-value (χ^2-test)	0.430	0.002	0.008	0	0	0.157
SE	± 0.0157	± 0.0014	± 0.0028			± 0.0115

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