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SHORT COMMUNICATION

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The STR loci HumTPO and HumLPL: population genetic data in eight populations

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Abstract The two STR systems HumTPO and HumLPL were investigated in eight human populations (Moroccans, Ovambos, Papuans, Australian aborigines, Germans, Turks, Japanese and Chinese). After electrophoresis, seven and eight alleles were identified in the HumTPO and HumLPL systems, respectively. In each population, no deviations from Hardy-Weinberg equilibrium were observed, but considerable differences in phenotype frequencies of each system were found between major ethnic groups.

Key words Short tandem repeats (STRs) · HumTPO · HumLPL · Population comparisons

Introduction

For population genetic comparisons and forensic applications, STR analysis has become one of the most powerful methods in DNA typing (Meyer et al. 1995; Brinkmann et al. 1996). The STR system HumLPL was first reported by Zuliani and Hobbs (1990) and shows a variation in the number of (TTTA)n repeats in intron 6 of the lipoprotein lipase gene at chromosome 8p22. HumTPO is a (AATG)n repeats system inside intron 10 of the thyroid peroxidase gene at 2p23-2pter (Anker et al. 1992).

In this communication, we present the allele frequency distributions of these STR systems in eight different populations which show significant differences between major ethnic groups.

Materials and methods

Population samples

The following Caucasian population samples were included: Germans living in the Münster area (Northwestern Germany), Turks in the Adana area (Southern Turkey) and a Moroccan subpopulation in Brussels, Belgium. Asian (mongoloid) representives were one Chinese from the Shen Yong area and Japanese from the Shiga area. Ovambos (Bantus) from Namibia were chosen as a Black African population sample. The New Guinean and Australian population samples were Papuans living in the eastern highlands and Aborigines from the Adelaide area, respectively. For DNA extraction all samples were obtained from healthy and unrelated donors. The number of donors analysed for each STR system are shown in Table 1.

DNA extraction

DNA from EDTA blood (Germans) was extracted as described previously (Brinkmann et al. 1991). Air dried blood samples (Turks, Moroccans, Ovambos, Papuans), dried saliva on cotton fabric (Japanese) and hair roots (Chinese) were extracted using Chelex 100 and Proteinase K (Wiegand et al. 1993).

DNA amplification and electrophoresis

PCR, separation of PCR products using high-resolution polyacrylamide gel electrophoresis and visualization of bands by silver staining were performed according to the previously described methods (Gusmao et al. 1995; Pestoni et al. 1995). Allele nomenclatures for each STR system were according to the number of repeats (Anker et al. 1992; Zuliani and Hobbs 1990). Genotyping was performed by side-to-side comparison using samples previously typed by sequencing.

Statistical evaluation

The Hardy-Weinberg analysis was performed with standard χ^2-analysis and the logarithmic likelihood ratio (G) test using the exact test by randomly shuffling the observed alleles 5000 times (HWE analysis, Version 3.0, C. Puers, Münster, Germany). The population comparisons were performed using a test for genetic heterogeneity (2-way R × C contingency table; χ^2 and G statistic; Carmody, Ottawa, Canada).

Results and discussion

In this survey of allele frequency distributions, seven and eight alleles were found for HumhTPO and HumLPL, respectively. We have observed allele 7 for HumTPO and

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Table 1 Allele frequency data of the short tandem repeats HumTPO and HumLPL in eight different populations. P-values are from the exact test

TPO	Moroccans (*n* = 130)	Turks (*n* = 97)	Germans (*n* = 488)	Japanese (*n* = 113)	Ovambos (*n* = 101	Chinese (*n* = 86)	Papuans (*n* = 104)	Aborigines (*n* = 67)
Allele								
6	0.017		0.001		0.084			
7	0.023		0.001		0.020			
8	0.430	0.516	0.544	0.443	0.371	0.506	0.178	0.149
9	0.134	0.103	0.107	0.124	0.129	0.151	0.466	0.552
10	0.081	0.098	0.062	0.040	0.055	0.012	0.019	0.060
11	0.297	0.284	0.250	0.336	0.302	0.302	0.308	0.239
12	0.017		0.036	0.058	0.040	0.029	0.029	
P-value	0.90	0.53	0.21	0.67	0.73	0.78	0.14	0.89
LPL	(*n* = 130)	(*n* = 147)	(*n* = 102)	(*n* = 119)	(*n* = 138)	(*n* = 79)	(*n* = 88)	(*n* = 74)
Allele								
1								0.006
2	0.004				0.007	0.006		
3	0.062	0.054	0.034		0.101	0.006		0.006
4	0.315	0.330	0.451	0.702	0.351	0.620	0.489	0.412
5	0.327	0.344	0.275	0.076	0.130	0.158	0.057	0.270
6	0.231	0.225	0.206	0.219	0.351	0.196	0.063	0.223
7	0.062	0.044	0.034	0.004	0.058	0.013	0.392	0.068
8		0.003						0.014
P-value	0.45	0.26	0.79	0.92	0.67	0.56	0.10	0.23

Table 2 Comparison of HumTPO (above diagonal) and HumLPL (below diagonal) between eight populations using the R × C contingency test by χ^2-values

	Moroccans	Turks	Germans	Japanese	Ovambos	Chinese	Papuans	Aborigines
Moroccans		0.025 ± 0.005	0.000 ± 0.000	0.003 ± 0.002	0.054 ± 0.007	0.002 ± 0.001	0.000 ± 0.000	0.000 ± 0.000
Turks	0.865 ± 0.011		0.096 ± 0.009	0.001 ± 0.001	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000
Germans	0.044 ± 0.007	0.094 ± 0.009		0.020 ± 0.004	0.000 ± 0.000	0.074 ± 0.008	0.000 ± 0.000	0.000 ± 0.000
Japanese	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000		0.000 ± 0.000	0.217 ± 0.013	0.000 ± 0.000	0.000 ± 0.000
Ovambos	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000		0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000
Chinese	0.000 ± 0.000	0.000 ± 0.000	0.001 ± 0.001	0.024 ± 0.005	0.000 ± 0.000		0.000 ± 0.000	0.000 ± 0.000
Papuans	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000		0.028 ± 0.005
Aborigines	0.016 ± 0.004	0.008 ± 0.003	0.110 ± 0.010	0.000 ± 0.000	0.000 ± 0.000	0.001 ± 0.001	0.000 ± 0.000	

allele 8 for HumLPL that have not been detected in other population studies (Anker et al. 1992; Huang et al. 1995; Luis and Caeiro 1995; Gusmao et al. 1995; Ahn et al. 1992; Wall et al. 1993; Pestoni et al. 1995; Takagi et al. 1996). Table 1 shows the observed allele frequency distributions of each STR system in the eight ethnic groups studied. No deviations from Hardy-Weinberg equilibrium were found in all eight populations for each STR systems (Exact-test $P > 0.05$). R × C contingency test revealed significant differences between almost all populations tested (Table 2), the exceptions are underlined. The data presented here can be useful in paternity or stain cases, if a member of one of the eight populations is involved.

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