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SHORT COMMUNICATION

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Short tandem repeat polymorphism at the HUMCD4 and HUMF13B loci in a Croatian population

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Abstract Population studies were carried out on unrelated individuals of Croatian ancestry. Genomic DNA was amplified by the polymerase chain reaction (PCR) at the polymorphic microsatellite loci HUMCD4 (n = 105 individuals) and HUMF13B (n = 108 individuals). After horizontal polyacrylamide gel electrophoresis followed by silver staining 6 alleles and 12 genotypes were observed for HUMCD4 and 6 alleles and 13 genotypes could be identified for HUMF13B. Data obtained were in concordance with the prediction of Hardy-Weinberg equilibrium. The allele frequency data were compared with Austrian and Italian population samples and no significant deviations between these populations were observed.

Key words Short tandem repeats · HUMCD4 · HUMF13B · Population studies · Croatia

Introduction

Short tandem repeat polymorphisms (STRs) represent a rich source of highly polymorphic markers for personal identification. The STR loci are associated with high heterozygosities in the human population with notable differences in allele frequencies and heterozygosities between population groups (Wall et al. 1993). Since HUMCD4 and HUMF13B loci are widely used in paternity testing and forensic casework, we present here allele distribution data for these two loci in a Croatian population sample.

Materials and methods

Genomic DNA was isolated from peripheral blood leukocytes using a standard extraction method by salting out with saturated NaCl solution followed by ethanol precipitation. Standard PCR amplification was carried out in a total volume of 25 µl containing 5 ng template DNA, 10 pmol each primer, 100 µM each dNTP, 1.5 mM $MgCl_2$, 0.3 units of Goldstar DNA Polymerase (Eurogentech) and reaction buffer. Primer sequences and PCR conditions were as published (Edwards et al. 1991; Nishimura and Murray 1992). The amplification products were separated by horizontal polyacrylamide electrophoresis and visualization was performed by silver staining. Alleles were determined relative to a locus-specific allelic ladder.

Tests for Hardy-Weinberg equilibrium and determination of mean exclusion chance (MEC), mean exclusion probability (MEP), polymorphism information content (PIC), probability of match (pM) and discrimination power (D) were performed using the software HWE-Analysis, Version 3.2 (C. Puers, Institute for Legal Medicine, University of Münster). The frequency profile comparisons were performed using a χ^2-test.

Table 1 Allele frequencies for HUMCD4 and HUMF13B

Allele	Allele frequencies		
	Croats	Italians	Austrians
HUMCD4[a]			
5	0.310	0.351	0.337
6	0.424	0.284	0.331
7	0.005	–	0.003
8	–	–	0.003
9	–	0.041	0.010
10	0.181	0.272	0.278
11	0.062	0.037	0.025
12	0.019	0.015	0.013
HUMF13B[b]			
6	0.074	0.038	0.090
7	0.023	0.008	0.016
8	0.269	0.231	0.245
9	0.208	0.223	0.225
10	0.412	0.500	0.419
11	0.005	–	0.005

[a] Number of individuals: 105 Croats, 134 Italians, 198 Austrians
[b] Number of individuals: 108 Croats, 119 Italians, 216 Austrians

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Table 2 Statistical data for HUMCD4 and HUMF13B

	HUMCD4 (n = 105)	HUMF13B (n = 108)
Observed heterozygosity	0.7143	0.6759
Expected heterozygosity	0.6909	0.7042
MEC	0.4319	0.4517
MEP	0.4143	0.4348
PIC	0.6326	0.6502
pM	0.1597	0.1423
D	0.8403	0.8577

(MEC mean exclusion chance, MEP mean exclusion probability, PIC polymorphism information content, pM probability of match, D discrimination power)

Results and discussion

A total of 6 alleles and 12 genotypes were detected for HUMCD4 and 6 alleles and 13 genotypes for HUM F13B (Table 1). Data obtained for HUMCD4 (χ^2-test: χ^2 = 10.08, p = 0.842; G-test: G-value = 11.07; p = 0.844) as well as for HUMF13B (χ^2-test: χ^2 = 10.44, p = 0.767; G-test: G-value = 12.37; p = 0.685) are in concordance with the prediction of Hardy-Weinberg equilibrium. Statistical data for these loci are listed in Table 2. The allele frequency data were compared with an Austrian and Italian population sample (Neuhuber et al. 1996; Piccinini et al. 1996) and no significant deviations between these populations for both loci were observed ($p > 0.05$ in χ^2-test).

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