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SHORT COMMUNICATION

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Frequencies of the 5 PCR-based genetic markers LDLR, GYPA, HBGG, D7S8, and GC in a North Bavarian population

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Abstract Genotype and allele frequencies for the 5 PCR-based genetic markers LDLR, GYPA, HBGG, D7S8 and GC were determined in a North Bavarian population (n = 150) using a new multiplex PCR-amplification and typing kit. Results did not diverge from Hardy-Weinberg expectations.

Key words DNA · Polymorphism · PCR · Genetic markers · LDLR, GYPA, HBGG, D7S8, GC · North Bavarian population database

Zusammenfassung Die Genotyp- und Allelfrequenzen der 5 PCR-Systeme LDLR, GYPA, HBGG, D7S8 und GC in einer nordbayerischen Bevölkerungsstichprobe wurden mit einem neuen Kit für die Multiplex-PCR-Amplifikation und Typisierung untersucht. Die Ergebnisse entsprachen dem Hardy-Weinberg-Gleichgewicht.

Schlüsselwörter DNA · Polymorphismus · PCR · Genetische Marker · LDLR, GYPA, HBGG, D7S8, GC · nordbayerische Bevölkerungsstichprobe

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Table 1 Characteristics of the genetic markers investigated (AmpliType)

Locus	Chromosome	PCR-Product (bp)	No. Alleles	Alleles
LDLR	19	214	2	A, B
GYPA	4	190	2	A, B
HBGG	11	172	3	A, B, C
D7S8	7	151	2	A, B
Gc	4	138	3	A, B, C

Table 2 Observed and expected PM genotypes in a North Bavarian population

System	genotype	observed	expected	allele frequencies
LDLR	AA	23	21.1	LDLR* A = 0.377
	AB	67	70.3	
	BB	60	58.6	LDLR* B = 0.623
$\chi^2 = 0.3566$; $0.5 < p < 0.7$; df = 1				
System	genotype	observed	expected	allele fequencies
GYPA	AA	53	51.3	GYPA* A = 0.587
	AB	70	72.9	
	BB	27	25.8	GYPA* B = 0.413
$\chi^2 = 0.2146$; $0.5 < p < 0.7$; df = 1				
System	genotype	observed	expected	allele frequencies
HBGG	AA	33	37.5	HBGG* A = 0.500
	AB	82	72.7	
	BB	30	35.2	HBGG* B = 0.483
	BC	2	2.3	
	CC	0	0.0	HBGG* C = 0.017
	AC	3	2.3	
$\chi^2 = 2.7279$; $0.05 < p < 0.1$; df = 1				
System	genotype	observed	expected	allele frequencies
D7S8	AA	49	54.0	D7S8* A = 0.600
	AB	82	72.0	
	BB	19	24.0	D7S8* B = 0.400
$\chi^2 = 2.8936$; $0.05 < p < 0.1$; df = 1				
System	genotype	observed	expected	allele frequencies
Gc	AA	12	13.0	Gc* A = 0.293
	AB	14	13.7	
	BB	2	3.6	Gc* B = 0.157
	BC	28	25.5	
	CC	45	45.4	Gc* C = 0.550
	AC	49	48.8	
$\chi^2 = 1.0276$; $0.5 < p < 0.7$; df = 2				

Table 3 Distribution of PM allele frequencies in 3 different populations

System	Allele	USA, Caucasians $n = 100$ (according to Perkin Elmer PM User Guide)	Swiss Population $n = 100$ (Hochmeister et al., [1])	North Bavarian Population, $n = 150$ (this study)
LDLR	A	0.43	0.435	0.377
	B	0.57	0.565	0.623
GYPA	A	0.48	0.525	0.587
	B	0.52	0.475	0.413
HBGG	A	0.53	0.475	0.500
	B	0.45	0.525	0.483
	C	0.02	0.000	0.017
D7S8	A	0.58	0.585	0.600
	B	0.42	0.415	0.400
Gc	A	0.33	0.280	0.293
	B	0.15	0.175	0.157
	C	0.52	0.545	0.550

Introduction

The polymarker kit (Amplitype PM PCR Amplification and Typing Kit, Perkin Elmer) is a new multiplex PCR amplification and typing system, based on the reverse dot blot technology and the use of sequence specific oligonucleotide probes. A simultaneous typing of the loci LDLR [5], GYPA [3], HBGG [4], D7S8 [2] and GC [6] is effected. In Table 1 the PM-Kit genetic marker characteristics are shown. This study presents the data of the genotype and allele frequencies in a North-Bavarian population sample.

Material and methods

Blood was obtained from 150 unrelated donors from routine forensic investigations.

DNA extraction, amplification and typing were carried out according to the recommended protocols. However the amplified samples were enhanced with 160 µg BSA/ml (BSA-Serva, Cat # 3961) not stated in the protocols.

Results and discussion

The distribution of genotypes and allele frequencies for the 5 genetic loci (Table 2) met the expectations of Hardy-Weinberg equilibrium. Table 3 shows the genotype frequencies of our North-Bavarian sample compared to other population studies. The frequencies obtained in our data enabled us to calculate the combined power of discrimination (Pd) value to be 0.994.

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