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SHORT COMMUNICATION

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Population genetics of ten STR loci (AmpFℓSTR SGM plus) in Austria

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Abstract A population study on the ten short tandem repeat (STR) loci D3S1358, VWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA was performed on 204 unrelated Austrian Caucasians. The DNA was amplified by multiplex PCR using the AmpFℓSTR SGM plus kit. All loci met Hardy-Weinberg expectations. The combined power of exclusion for the ten STR loci was 0.999976. The results show that these loci are very useful for forensic purposes.

Keywords DNA · Short tandem repeats · Population study · Forensic science · Austria

Introduction

A population study was carried out on unrelated Austrian Caucasian individuals to determine allele and genotype frequencies for forensic purposes. In the current study, population data were obtained for the ten STR loci included in the AmpFℓSTR SGM Plus kit (Perkin Elmer, Foster City, Calif.). These loci are the PCR-based markers currently used for the Austrian National DNA intelligence database.

Material and methods

Buccal swabs were taken from 204 unrelated Austrian Caucasians and DNA was extracted by chelex extraction [1]. Amplification was carried out using 10 ng of template DNA applying the AmpFℓSTR SGM plus systems kit (Perkin Elmer) in a Perkin Elmer 9600 thermal cycler, according to the manufacturer's recommendations and products were loaded on the CE310 Genetic Analyser (ABI), using Genescan-500 ROX (Perkin Elmer) as internal lane standard. GeneScan analysis was performed on the raw data, and alleles were

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Table 1 Distribution of allele frequencies and counts for the 10 STR loci in 204 unrelated Austrians

D21S11			TH01		
Allele	*n*	Frequency	Allele	*n*	Frequency
26	2	0.005	5	3	0.007
27	7	0.017	6	95	0.233
28	71	0.174	7	55	0.135
29	85	0.208	8	43	0.105
29.2	1	0.002	8.3	1	0.002
30	85	0.208	9	80	0.196
30.2	23	0.056	9.3	126	0.309
31	42	0.103	10	5	0.012
31.2	34	0.083			
32	6	0.015			
32.2	28	0.069			
33.2	22	0.054			
34.2	1	0.002			
35.2	1	0.002			
D18S51			D8S1179		
Allele	*n*	Frequency	Allele	*n*	Frequency
10	4	0.010	8	5	0.012
11	7	0.017	9	6	0.015
12	63	0.154	10	39	0.096
13	52	0.127	11	21	0.051
14	53	0.130	12	64	0.157
15	64	0.157	13	126	0.309
15.1	1	0.002	14	104	0.255
16	60	0.147	15	32	0.078
17	44	0.108	16	11	0.027
18	30	0.074			
19	17	0.042			
20	7	0.017			
21	3	0.007			
22	2	0.005			
23	1	0.002			

Table 1 (continued)

VWA			FGA		
Allele	*n*	Frequency	Allele	*n*	Frequency
13	1	0.002	15	1	0.002
14	41	0.100	17	1	0.002
15	42	0.103	18	8	0.020
16	92	0.225	19	24	0.059
17	91	0.223	20	48	0.118
18	91	0.223	20.2	1	0.002
19	44	0.108	21	67	0.164
20	5	0.012	21.2	1	0.002
21	1	0.002	22	70	0.172
			22.2	3	0.007
			23	65	0.159
			23.2	4	0.010
			24	69	0.169
			25	29	0.071
			26	11	0.027
			27	5	0.012
			28	1	0.002
D3S1358			D16S539		
Allele	*n*	Frequency	Allele	*n*	Frequency
13	2	0.005	8	6	0.015
14	48	0.118	9	39	0.096
15	103	0.252	10	16	0.039
16	90	0.221	11	128	0.314
17	87	0.213	12	129	0.316
18	76	0.186	13	79	0.194
19	2	0.005	14	8	0.020
			14	8	0.020
			15	3	0.007

Table 1 (continued)

D2S1338			D19S433		
Allele	*n*	Frequency	Allele	*n*	Frequency
16	11	0.027	9	1	0.002
17	97	0.238	11	1	0.002
18	45	0.110	12	35	0.086
19	53	0.130	12.2	1	0.002
20	46	0.113	13	88	0.216
21	13	0.032	13.2	8	0.020
22	11	0.027	14	147	0.360
23	32	0.078	14.2	13	0.032
24	45	0.110	15	63	0.154
25	44	0.108	15.2	14	0.034
26	11	0.027	16	25	0.061
			16.2	8	0.020
			17	2	0.005
			17.2	1	0.002
			18.2	1	0.002

labelled according to the international nomenclature [2] using the Genotyper Software package (Perkin Elmer).

Allele frequencies were calculated from the numbers of each genotype obtained in the sample set. Unbiased estimates of expected heterozygosity were computed as described by Edwards et al. [3]. Possible divergence from Hardy-Weinberg expectations was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies [4], the likelihood ratio test [3, 4, 5] and the exact test [6]. An interclass criterion was used for detecting disequilibrium between loci [7]. The power of exclusion was calculated according to Garber and Morris [8] and the power of discrimination was calculated according to Fisher [9]. Analyses were facilitated using a computer program kindly provided by Bruce Budowle (FBI Academy, Quantico, Va.) and DNAVIEW software designed by Charles Brenner (Berkeley, Calif.).

Results and discussion

Allele frequencies of the ten STR loci investigated are shown in Table 1.

All ten loci showed no significant deviation from Hardy-Weinberg expectations (Table 2). Pair-wise interclass correlation tests were performed for all possible two-locus combinations, and no deviations were detected in 45 pairwise comparisons. The PD and PE for this Austrian Caucasian population sample are listed in Table 3.

The Austrian population allele frequencies were similar to those found in other Caucasian populations for the same loci (data not shown) [10, 11, 12, 13, 14, 15].

In conclusion, the use of the AmpFℓSTR SGM plus PCR system offers a highly polymorphic tool for paternity testing and DNA intelligence databases.

Table 2 Summary of statistical analysis for the STR loci in AmpFℓSTR SGM plus ([a]these values are probability values)

Statistical parameters	Locus									
	D21S11	TH01	D18S51	D8S1179	VWA	FGA	D3S1358	D16S539	D2S1338	D19S433
Observed homozygosity	15.7%	20.1%	9.8%	20.6%	16.7%	9.8%	20.1%	27.9%	13.2%	23.0%
Expected homozygosity (unbiased)	14.4%	21.6%	12.1%	20.2%	18.1%	13.2%	20.4%	24.5%	12.9%	21.2%
Homozygosity test[a]	0.597	0.612	0.323	0.891	0.599	0.151	0.901	0.258	0.896	0.529
Likelihood test[a]	0.120	0.621	0.621	0.463	0.161	0.516	0.888	0.101	0.211	0.573
Exact test[a]	0.123	0.690	0.743	0.746	0.144	0.597	0.934	0.059	0.183	0.418

Table 3 Power of discrimination (*PD*) and probability of exclusion (*PE*) for the STR loci in AmpFℓSTR SGM plus

Locus	PD[a]	PD[b]	PE
D21S11	0.9582	0.9623	0.7093
TH01	0.9158	0.9193	0.5747
D18S51	0.9687	0.9722	0.7510
D8S1179	0.9323	0.9308	0.6078
VWA	0.9336	0.9410	0.6354
FGA	0.9628	0.9673	0.7295
D3S1358	0.9223	0.9247	0.5871
D16S539	0.8945	0.8989	0.5294
D2S1338	0.9648	0.9696	0.7383
D19S433	0.9250	0.9278	0.5999

[a] PD calculated using observed data
[b] PD calculated using expected data

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