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Icelandic population data for the 10 autosomal STR loci in the AMP*Fl*STR®SGM Plus™ system and the 12 Y-STR loci in the PowerPlex® Y-system

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Abstract. The aim of this study was to determine allele frequencies and other statistical parameters of interest in STRs widely used as tools for forensic investigations in an Icelandic population sample. The individuals were analysed using the AMP*Fl*STR®SGM Plus™ system ($n=110$) and the PowerPlex® Y-system ($n=76$) as described by the manufacturer. For the ten autosomal STR loci the observed heterozygosities ranged from 0.764 (vWA) to 0.891 (FGA). No significant deviation from Hardy–Weinberg equilibrium was observed. For the Y-chromosome polymorphisms 64 different haplotypes were observed in the 76 male samples analysed. No haplotype was observed more than three times in the population sample. The haplotype diversity when combining all loci was 0.995.

Keywords: Iceland; Population; STR; Y-chromosome; Polymorphism

1. Introduction

This study presents data from typing of an Icelandic population sample in autosomal STR polymorphisms at ten loci (D3S1358, vWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA) and Y-STR polymorphisms at twelve loci (DYS391, DYS389I/II, DYS439, DYS393, DYS390, DYS385a/b, DYS438, DYS437, DYS19, DYS392).

2. Results

The allele frequencies ($n=110$) in the ten autosomal loci are presented in Table 1 at http://folk.uio.no/runean/table1.xls. Other statistical parameters are given in Table 1 in this

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Table 1
Statistical parameters for Amp*FI*STR SGM plus loci in an icelandic population sample of 110 individuals

	D3S1358	vWA	D16S539	D2S1338	D8S1179	D21S11	D18S51	D19S433	TH01	FGA
Obs. H[a]	0.791	0.764	0.855	0.881	0.855	0.873	0.809	0.818	0.818	0.891
Exp. H[b]	0.799	0.800	0.770	0.876	0.813	0.827	0.882	0.769	0.776	0.862
P[c]	0.911	0.247	0.052	0.271	0.690	0.217	0.055	0.890	0.512	0.246
PD[d]	0.923	0.925	0.889	0.962	0.926	0.934	0.965	0.906	0.904	0.953
PE[e]	0.582	0.533	0.704	0.758	0.704	0.740	0.616	0.633	0.633	0.777

[a] Observed heterozygosity.
[b] Expected heterozygosity.
[c] *P*-value Hardy–Weinberg equilibrium exact test (Markov chain 100 000 steps).
[d] Power of discrimination.
[e] Power of exclusion.

paper. The heterozygosity frequencies ranged from 0.764 (vWA) to 0.891 (FGA). No significant deviation from Hardy Weinberg equilibrium was observed. However, two loci showed *P*-values of 0.052 (D16S539) and 0.055 (D18S51). The observed Y-haplotypes from typing of the twelve Y-STR polymorphisms in 76 males are presented in Table 2 at http://folk.uio.no/runean/table2.xls. A total of 64 different Y-haplotypes were observed in the 76 males typed giving a discrimination capacity of 0.84.

No haplotypes were observed more than three times (4%) while fifty-six haplotypes were observed only once (unique).

Table 2

Allele	DYS 391	DYS 389 1	DYS 439	DYS 389 11	DYS 438	DYS 437	DYS 19	DYS 392	DYS 393	DYS 390	Haplotype	DYS 385a/b
9	0.013				0.026						9,12	0.013
10	0.553		0.250		0.303						11,13	0.079
11	0.408		0.342		0.303			0.500			11,14	0.421
12	0.013	0.329	0.342		0.386			0.105			11,15	0.079
13	0.013	0.474	0.040				0.065	0.342	0.895		11,16	0.013
14		0.171	0.026			0.382	0.592	0.052	0.065		12,14	0.013
15		0.026				0.355	0.276		0.040		13,14	0.053
16						0.263	0.026				13,17	0.053
17							0.040				14,14	0.105
22										0.092	14,15	0.118
23										0.395	14,16	0.013
24										0.237	14,17	0.013
25										0.263	15,15	0.013
26										0.013	15,16	0.013
27				0.026								
28				0.316								
29				0.329								
30				0.158								
31				0.092								
32				0.079								
GD[a]	0.534	0.646	0.711	0.762	0.689	0.668	0.574	0.628	0.196	0.719		0.792[b]

[a] Gene diversity.
[b] Haplotype diversity.

Table 2 (this paper) shows the haplotype frequency of loci DYS 385 a/b and the allele frequencies of the ten Y-STRs included in the PowerPlex® Y-system. Locus diversity ranged from 0.196 (DYS393) to 0.719 (DYS390) while loci DYS385 a/b showed a diversity of 0.792. The haplotype diversity when combining all Y-STR markers was 0.995.

3. Discussion

Testing for deviation from H/W equilibrium, two markers revealed low *P*-values (D16S539 and D18S51). In D18S51 there was a tendency towards more homozygotes than expected. All individuals typed as homozygeous in D18S51 revealed allele peak-heights well above the threshold. Thus, the low *P*-value for this marker is not likely to represent a typing error.

4. Material and methods

Samples from a population material of unrelated individuals from Iceland were analysed at ten autosomal STR-loci ($n=110$) and twelve Y-STR-loci ($n=76$). Autosomal STRs and Y-STRs were PCR amplified using the AMP*Fl*STR®SGM Plus™ system and the PowerPlex® Y-system as described by the manufacturer. PCR-products were separated by capillary electrophoresis using an ABI PRISM® 3100. Allele typing was performed using allele ladders provided with the multiplex kits. A threshold-value of 200 rfu was used for accepting homozygeous genotypes.

Evaluation of Hardy–Weinberg equilibrium was performed by a modified version of the Markov chain random walk algorithm (100 000 steps) provided by the Arlequin software (http://anthro.unique.ch/arlequin). Other statistical parameters in Table 1 were obtained by PowerStats (http://www.promega.com/genetictools/powerstats/Default.htm).