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Norwegian population data for 2 autosomal STR loci; D12S392 and D17S906

M. Stenersen *, D. Perchla, B.M. Dupuy

Institute of Forensic Medicine, University of Oslo, Norway

Abstract. Autosomal STR polymorphisms at 2 loci (D12S392 and D17S906) are presented. Samples from current paternity analysis ($n=909$) were analysed. The observed heterozygosities were 0.878 (D12S392) and 0.915 (D17S906). No significant deviation from Hardy–Weinberg equilibrium was observed. 17 different alleles were observed at D12S392 whereas a total of 57 different alleles were observed at D17S906. The repeat numbers ranged from 15 to 27 at D12S392. For D17S906 the allele sizes ranged from 331 to 441 bases. Sequence variation at both loci is presented as well as frequency databases and other relevant forensic genetic parameters. © 2006 Published by Elsevier B.V.

Keywords: D12S392; D17S906; STR; Norwegian; Database; Forensic genetic

1. Introduction

Autosomal STR polymorphisms at 2 loci (D12S392 and D17S906) are presented. These loci are used in addition to PowerPLex16® in paternity casework and in other questioned genetic relationships between family members.

2. Materials and methods

Samples from current paternity analysis ($n=909$) were analysed. DNA was extracted from venous blood [1]. PCR amplification was performed according to the manufacturer's protocol of PowerPLex16®. Fragment length analysis was done by capillary electrophoresis (ABI PRISM®3100. AB. Foster City. US). Evaluation of Hardy–Weinberg

* Corresponding author. Tel.: +47 23071317; fax: +47 23071318.
E-mail address: margurethe.stenersen@medisin.uio.no (M. Stenersen).

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Table 1
Forensic statistical parameters for D12S392 and D17S906

Parameter	D12S392	D17S906
Heterozygosity observed	0.87789	0.91529
Heterozygosity expected	0.89137	0.93552
p-value	0.974	0.063
Power of discrimination	0.978	0.991
Power of exclusion	0.751	0.823

equilibrium was performed by a modified version of the Markov-chain random walk algorithm (10 000 shuffles) provided by the Arlequin Software (http://anthro.unige.ch/arlequin). Other forensic statistical parameters were obtained by the PowerStats, Promega (http://www.promega.com/geneticidtools/powerstats/Default). A total of 24 different alleles were sequenced for D17S906. Of these were six pairs (a and b) and one triplet (a, b and c) of alleles of equal fragment length. For D12S392, a total of six alleles of different fragment lengths were sequenced.

3. Result and discussion

The observed heterozygosities were 0.878 (D12S392) and 0.915 (D17S906), Table 1. No significant deviation from Hardy–Weinberg equilibrium was observed. 17 different alleles were observed at D12S392 whereas a total of 57 different alleles were observed at D17S906 (Tables 2 and 3). The repeat numbers ranged from 15 to 27 at D12S392. For D17S906 the allele sizes ranged from 331 to 441 basepairs. DNA sequencing of D17S906 alleles revealed as much as 15 variable repeat units at this locus as well as several other sequence differences between alleles (Fig. 1, online). Two pairs and one triplet of alleles of equal length had identical sequences (alleles: 335, 358 and 361). Four pairs of alleles had different sequences (alleles: 365, 369, 373 and 405). The alleles seem to fall into two groups according to both fragment length and sequence differences. Alleles with fragment

Table 2
D12S392 frequencies in a Norwegian database of 909 individuals

Allele (repeat)	Allele (bp)	Frequency
15	209	0.0446
16	213	0.0242
17	217	0.1304
17.3	220	0.0149
18	221	0.1716
18.3	224	0.0121
19	225	0.1095
19.3	228	0.0050
20	229	0.1139
20.3	232	0.0006
21	233	0.1084
22	237	0.1155
23	241	0.0880
24	245	0.0413
25	249	0.0143
26	253	0.0055
27	257	0.0006

Table 3
D17S906 frequencies in a Norwegian database of 909 individuals

Allele	Frequency	Allele	Frequency	Allele	Frequency
331	0.0011	357	0.0787	401	0.0237
334	0.0022	358	0.0710	403	0.0050
335	0.0792	359	0.0072	405	0.0270
337	0.0006	361	0.0963	407	0.0121
338	0.0105	362	0.0259	409	0.0116
339	0.0028	363	0.0044	410	0.0011
342	0.0281	365	0.1425	411	0.0176
344	0.0011	366	0.0099	412	0.0011
345	0.0028	367	0.0022	413	0.0055
346	0.0253	369	0.0715	415	0.0160
347	0.0006	370	0.0017	417	0.0061
349	0.0154	371	0.0033	419	0.0039
350	0.0396	373	0.0072	421	0.0028
351	0.0017	374	0.0006	423	0.0011
352	0.0006	375	0.0006	426	0.0006
353	0.0407	377	0.0006	429	0.0022
354	0.0671	393	0.0006	433	0.0017
355	0.0033	397	0.0105	437	0.0011
356	0.0006	399	0.0022	441	0.0011

lengths larger than 365 basepairs had, with one exception, two additional repeat units $(AG)_{4–17}$ and $(AAAG)_{6–14}$ (Fig. 1, red box). It might be that the additional repeat units trigger mutational events at the longer alleles. Sequencing of D12S392 alleles demonstrated repeat length differences at two repeat units $(AGAT)_{7–18}$ and $(AGAC)_{6–9}$ (Fig. 2, online). No further sequence differences were observed at this locus. All sequences are presented in Figs. 1 and 2 at http://folk.uio.no/msteners/index.html.htm.

Reference

[1] S.A. Miller, D.D. Dykes, H.F. Polesky, A simple salting out procedure for extracting DNA from human nucleated cells, Nucleic Acids Res. 16 (3) (1988) 1215.