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Norwegian population data for 15 autosomal STR loci

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Abstract. Autosomal STR polymorphisms at 15 loci (D3S1358, THO1, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta E, vWA, D8S1179, TPOX and FGA) are presented. Samples from current paternity analysis ($n=1380$) were analysed. The observed heterozygosities ranged from 0.610 (TPOX) to 0.896 (Penta E). Two significant deviations from Hardy–Weinberg equilibrium were observed at D3S1352 and Penta D. The number of observed alleles ranged from 7 (THO1 and TPOX) to 19 (D21S11 and FGA). The shortest tandem repeat observed was 2.2 at Penta D and the largest 44.2 at FGA. The power of discrimination and exclusion ranged from 0.787 (TPOX) to 0.967 (FGA) and from 0.303 (TPOX) to 0.788 (Penta E) respectively. A complete frequency databases and other relevant forensic genetic parameters are presented.

Keywords: PowerPLex16®; STR; Norwegian; Database; Forensic genetics

1. Introduction

Autosomal STR polymorphisms at 15 loci (Promega PowerPLex16®: D3S1358, THO1, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta E, vWA, D8S1179, TPOX and FGA) are presented. The database is used primarily in paternity casework.

2. Materials and methods

Samples of unrelated individuals from current paternity analysis ($n=1381$) were analysed. DNA was extracted from venous blood [1]. PCR amplification was performed

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Table 1
Database results and forensic statistical parameters for all loci included in PowerPLex16®

Locus	No. of alleles	Range (repeat units)	H obs.	H exp.	*p*-value	PD	PE
D3S1358	10	11–21	0.796	0.798	0.046	0.928	0.591
THO1	7	5–10	0.767	0.766	0.686	0.908	0.521
D21S11	19	24.2–35	0.825	0.834	0.289	0.952	0.647
D18S51	17	9–27	0.896	0.879	0.907	0.972	0.787
Penta E	18	5–21.2	0.896	0.897	0.807	0.980	0.788
D5S818	9	7–15	0.686	0.692	0.463	0.851	0.406
D13S317	8	8–15	0.789	0.801	0.557	0.933	0.579
D7S820	13	6.3–14	0.810	0.811	0.876	0.936	0.618
D16S539	8	8–15	0.775	0.770	0.321	0.911	0.554
CSF1PO	10	7–16	0.707	0.724	0.461	0.878	0.438
Penta D	16	2.2–18	0.812	0.826	<0.004	0.946	0.622
vWA	12	12–24	0.800	0.802	0.223	0.934	0.599
D8S1179	11	8–18	0.783	0.791	0.671	0.929	0.568
TPOX	7	6–12	0.610	0.603	0.721	0.787	0.303
FGA	18	17–28	0.878	0.868	0.437	0.967	0.750

PD: power of discrimination, PE: power of exclusion.

according to the manufacturer's protocol (PowerPLex16®). Fragment length analysis was done by capillary electrophoresis (ABI PRISM®3100, AB, Foster City, US). Evaluation of Hardy–Weinberg 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.htm).

3. Result and discussion

Allele distribution and forensic statistical parameters are given in Table 1. For details, see Table 1 online at http://folk.uio.no/msteners/index.html.htm. The observed heterozygosities ranged from 0.610 (TPOX) to 0.896 (Penta E). Two significant deviations from Hardy–Weinberg equilibrium were observed at D3S1358 and Penta D. The number of observed alleles ranged from 7 (THO1 and TPOX) to 19 (D21S11 and FGA). The number of tandem repeats ranged from 2.2 (Penta D) to 44.2 (FGA). The 15 loci possess a combined power of exclusion of 0.999999148.

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.