

Short communication

Genetic variation of 15 STR loci (D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317, D7S820, D16S539, D2S1338, D8S1179, D21S11, D18S51, and D19S433) in populations of north and central Poland

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Abstract

Allele frequencies for 15 short tandem repeats (STRs) included in AmpFISTR Profiler and AmpFISTR SGM Plus kits were obtained from populations of Pomorze Gdańskie, Wielkopolska, Kujawy, Pomorze Zachodnie, Mazury and Mazowsze regions of Poland.

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Population: 412 healthy unrelated individuals from the Pomorze Gdańskie (64), Wielkopolska (69), Kujawy (100), Pomorze Zachodnie (29), Mazury (88) and Mazowsze (62) regions of Poland.

Extraction: Organic extraction.

PCR: One nanogram DNA template using AmpFISTR Profiler PCR amplification Kit and AmpFISTR SGM Plus PCR amplification Kit (PE Applied Biosystems) according to manufacturers' instructions.

Typing: ABI 377 and reference sequenced ladders (PE Applied Biosystems).

Results: See Table 1.

Quality control: Proficiency tests organised by GED-NAP and Collaborative Testing Services Inc.

Analysis of data: Genetic data analysis [1], PowerStats Excel spreadsheet [2], G-statistic [3].

Access to the data: <http://www.zms-bydgoszcz.w.pl>.

Other remarks: All loci, except for TPOX locus in Mazury population, CSF1PO locus in Mazowsze population, D13S317 locus in Pomorze Gdańskie population and D2S1338 locus in Wielkopolska population showed no significant deviation from Hardy–Weinberg equilibrium (exact $P < 0.05$). No correlation between and across loci was found. F_{st} value for analysed populations was 0.001011. No differences in allele frequency distributions between populations studied were observed. The combined PD value for all populations studied was 0.999 999 999 999 992 560 (0.999 999 999 653 270 for AmpFISTR Profiler and 0.999 999 999 999 611 for AmpFISTR SGM Plus). The combined PE value for all analysed populations was 0.999 999 272 464 (0.999 495 241 465 for AmpFISTR Profiler and 0.999 976 059 036 for AmpFISTR SGM Plus). The alleles frequency comparisons between population studied and population from central Poland (10 loci) [4,5], population from Lodz region of Poland (10 loci) [6], population of Podlasie region of Poland (15 loci) [7], population from

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Table 1
Allele frequencies for 15 STR loci in populations of North and central Poland ($N = 824$)^a

Allele	D3S1358	vWA	FGA	TH01	TPOX	CSF1PO	D5S818	D13S317	D7S820	D16S539	D2S1338	D8S1179	D21S11	D18S51	D19S433
5	–	–	–	0.001	–	–	–	–	–	–	–	–	–	–	–
6	–	–	–	0.228	0.001	–	–	–	–	–	–	–	–	–	–
7	–	–	–	0.119	–	–	–	–	0.017	–	–	–	–	–	–
8	–	–	–	0.096	0.580	0.002	0.001	0.147	0.165	0.005	–	0.018	–	–	–
8.3	–	–	–	0.002	–	–	–	–	–	–	–	–	–	–	–
9	–	–	–	0.195	0.076	0.035	0.053	0.069	0.130	0.086	–	0.015	–	–	–
9.3	–	–	–	0.349	–	–	–	–	–	–	–	–	–	–	–
10	–	–	–	0.010	0.063	0.268	0.076	0.035	0.295	0.036	–	0.070	–	0.006	–
11	0.002	–	–	–	0.250	0.262	0.335	0.356	0.220	0.301	–	0.059	–	0.013	0.002
12	–	0.001	–	–	0.030	0.345	0.354	0.246	0.143	0.348	–	0.152	–	0.091	0.096
13	0.002	0.001	–	–	–	0.070	0.167	0.101	0.022	0.198	–	0.347	–	0.103	0.198
13.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.013
14	0.117	0.095	–	–	–	0.017	0.012	0.045	0.008	0.025	–	0.200	–	0.129	0.374
14.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.022
15	0.249	0.108	–	–	–	0.001	0.002	0.001	–	0.001	0.001	0.107	–	0.180	0.170
15.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.032
16	0.223	0.166	–	–	–	–	–	–	–	–	0.044	0.024	–	0.193	0.053
16.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.024
17	0.239	0.280	–	–	–	–	–	–	–	–	0.190	0.008	–	0.113	0.002
17.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.007
18	0.155	0.225	0.012	–	–	–	–	–	–	–	0.102	–	–	0.084	0.001
18.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.006
19	0.012	0.108	0.078	–	–	–	–	–	–	–	0.106	–	–	0.042	–
20	0.001	0.015	0.148	–	–	–	–	–	–	–	0.142	–	–	0.029	–
21	–	0.001	0.200	–	–	–	–	–	–	–	0.047	–	–	0.013	–
21.2	–	–	0.002	–	–	–	–	–	–	–	–	–	–	–	–
22	–	–	0.210	–	–	–	–	–	–	–	0.017	–	–	0.002	–
22.2	–	–	0.015	–	–	–	–	–	–	–	–	–	–	–	–
23	–	–	0.109	–	–	–	–	–	–	–	0.092	–	–	0.001	–
23.3	–	–	0.010	–	–	–	–	–	–	–	–	–	–	–	–
24	–	–	0.117	–	–	–	–	–	–	–	0.095	–	–	0.001	–
24.2	–	–	0.001	–	–	–	–	–	–	–	–	–	–	–	–
25	–	–	0.075	–	–	–	–	–	–	–	0.137	–	–	–	–
26	–	–	0.021	–	–	–	–	–	–	–	0.023	–	0.002	–	–
27	–	–	0.002	–	–	–	–	–	–	–	0.004	–	0.029	–	–
28	–	–	–	–	–	–	–	–	–	–	–	–	0.175	–	–
29	–	–	–	–	–	–	–	–	–	–	–	–	0.184	–	–
29.2	–	–	–	–	–	–	–	–	–	–	–	–	0.002	–	–
30	–	–	–	–	–	–	–	–	–	–	–	–	0.238	–	–
30.2	–	–	–	–	–	–	–	–	–	–	–	–	0.062	–	–
31	–	–	–	–	–	–	–	–	–	–	–	–	0.070	–	–

31.2	–	–	–	–	–	–	–	–	–	–	–	–	–	0.095	–	–
32	–	–	–	–	–	–	–	–	–	–	–	–	–	0.010	–	–
32.2	–	–	–	–	–	–	–	–	–	–	–	–	–	0.075	–	–
33	–	–	–	–	–	–	–	–	–	–	–	–	–	0.001	–	–
33.1	–	–	–	–	–	–	–	–	–	–	–	–	–	0.001	–	–
33.2	–	–	–	–	–	–	–	–	–	–	–	–	–	0.050	–	–
34.2	–	–	–	–	–	–	–	–	–	–	–	–	–	0.005	–	–
35	–	–	–	–	–	–	–	–	–	–	–	–	–	0.001	–	–
PD	0.924	0.936	0.962	0.902	0.776	0.880	0.882	0.915	0.929	0.883	0.971	0.932	0.960	0.969	0.925	
MEC	0.601	0.619	0.699	0.637	0.308	0.497	0.469	0.552	0.633	0.527	0.787	0.619	0.694	0.723	0.557	
MPI	2.51	2.64	3.38	2.78	1.30	1.94	1.82	2.22	2.75	2.08	4.79	2.64	3.32	3.68	2.24	
PIC	0.76	0.78	0.84	0.73	0.54	0.69	0.68	0.74	0.77	0.70	0.87	0.77	0.84	0.86	0.75	
He	0.795	0.812	0.857	0.766	0.592	0.736	0.728	0.774	0.800	0.741	0.882	0.797	0.854	0.874	0.780	
Ho	0.801	0.811	0.852	0.820	0.614	0.743	0.726	0.774	0.818	0.760	0.896	0.811	0.850	0.864	0.777	
p	0.979	0.160	0.106	0.661	0.056	0.979	0.853	0.222	0.385	0.815	0.056	0.099	0.264	0.603	0.913	

^a PD: power of discrimination, MEC: mean exclusion chance, MPI: mean paternity index, PIC: polymorphic information content, H_e : expected heterozygosity, H_o : observed heterozygosity, P: probability values of Exact test for Hardy–Weinberg.

south Poland (10 loci) [8] and population from south-east Poland (13 loci) [9] showed no significant differences ($P > 0.05$). This paper follows the guidelines for publication of population data in *Forensic Science International* [10].

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