

Genetic data on 10 STRs in a population sample of Old Believers living in the northeastern Poland

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Abstract. This study provides a 10-STR database for a population sample of Old Believers ($n = 116$) living in the northeastern Poland. For the FGA and TH01 loci, a departure from HWE was observed. The combined values of the Matching Probability and of the Power of Exclusion are 3.48×10^{-12} and 0.9949, respectively. Significant differences were found for FGA and D21S11 between the Old Believers and the autochthonous Polish population by using $R \times C$ test. © 2003 Elsevier B.V. All rights reserved.

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1. Introduction

Old Believers are a fraction of the Russian Orthodox Church who split in opposition to the Russian Church Reform, adopting the liturgy and practices of the Greek Church. The Reform was opposed by a group of Muscovite priests who were persecuted and whose leaders were executed. The harassed people sought shelter in many countries, including Lithuania and Poland. Presently, no more than 600 Old Believers inhabit mostly two villages in Suwalki Landscape Park [1,2]. The objective of this study was to provide a 10-STR database for a population sample of Old Believers living in NE Poland and to discuss its relationship with the reference population of autochthonous Polish Caucasians.

2. Materials and methods

DNA was extracted with the use of Chelex-100 and proteinase K method [3] from the buccal swabs of 116 unrelated Old Believers. AmpFISTR SGM Plus and ABI 310 (Applied Biosystems, USA) were used for typing.

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Table 1
Observed allele frequencies and forensic efficiency parameters for the 10-STR loci in the population of Old Believers (NE Poland), $n = 116$

Allele	D3S1358	VWA	FGA ^a	TH01 ^a	D16S539	D2S1338	D21S11	D18S51	D8S1179	D19S433
6	–	–	–	0.271	–	–	–	–	–	–
7	–	–	–	0.079	–	–	–	–	–	–
8	–	–	–	0.079	0.007	–	–	–	–	–
9	–	–	–	0.229	0.107	–	–	–	0.007	–
9.3	–	–	–	0.336	–	–	–	–	–	–
10	–	–	–	0.007	0.007	0.007	–	0.037	0.057	–
11	–	–	–	–	0.279	–	–	0.015	0.064	–
12	–	–	–	–	0.386	–	–	0.074	0.150	0.100
12.2	–	–	–	–	–	–	–	–	–	–
13	–	–	–	–	0.186	–	–	0.118	0.364	0.200
13.2	–	–	–	–	–	–	–	–	–	0.029
14	0.143	0.121	–	–	0.014	–	–	0.154	0.271	0.421
14.2	–	–	–	–	–	–	–	–	–	0.029
15	0.229	0.093	–	–	–	–	–	0.132	0.064	0.136
15.2	–	–	–	–	–	–	–	–	–	0.043
16	0.293	0.179	0.004	–	0.007	0.088	–	0.140	0.021	0.021
16.2	–	–	–	–	0.007	–	–	–	–	0.007
17	0.214	0.321	0.004	–	–	0.213	–	0.169	–	0.007
18	0.107	0.221	0.004	–	–	0.051	–	0.044	–	–
18.2	–	–	–	–	–	–	–	–	–	0.007
19	0.014	0.050	0.095	–	–	0.096	–	0.088	–	–
20	–	0.014	0.153	–	–	0.184	–	0.007	–	–
20.2	–	–	0.004	–	–	–	–	–	–	–
21	–	–	0.207	–	–	0.059	–	0.022	–	–
21.2	–	–	–	–	–	–	–	–	–	–
22	–	–	0.182	–	–	0.037	–	–	–	–
22.2	–	–	0.004	–	–	–	–	–	–	–
23	–	–	0.083	–	–	0.081	–	–	–	–
23.2	–	–	0.004	–	–	–	–	–	–	–
24	–	–	0.140	–	–	0.096	–	–	–	–
25	–	–	0.066	–	–	0.081	–	–	–	–
25.2	–	–	0.004	–	–	–	–	–	–	–
26	–	–	0.045	–	–	0.007	0.020	–	–	–
27	–	–	–	–	–	–	0.004	–	–	–
28	–	–	–	–	–	–	0.168	–	–	–
29	–	–	–	–	–	–	0.172	–	–	–
30	–	–	–	–	–	–	0.320	–	–	–
30.2	–	–	–	–	–	–	0.074	–	–	–
31	–	–	–	–	–	–	0.070	–	–	–
31.2	–	–	–	–	–	–	0.078	–	–	–
32	–	–	–	–	–	–	–	–	–	–
32.2	–	–	–	–	–	–	0.066	–	–	–
33.2	–	–	–	–	–	–	0.025	–	–	–
34.2	–	–	–	–	–	–	0.004	–	–	–
Ho	0.829	0.829	0.829	0.671	0.743	0.800	0.843	0.771	0.708	0.829
He	0.790	0.795	0.861	0.753	0.727	0.875	0.816	0.760	0.888	0.756
P	0.430	0.667	0.017	0.028	0.687	0.062	0.462	0.816	0.792	0.981
PIC	0.75	0.76	0.84	0.71	0.68	0.86	0.80	0.87	0.72	0.72
DP	0.902	0.919	0.958	0.892	0.869	0.960	0.943	0.967	0.904	0.898
MP	0.098	0.081	0.042	0.108	0.131	0.040	0.057	0.033	0.096	0.102
TPI	2.92	2.92	3.56	1.52	1.94	4.43	2.65	3.09	2.19	2.92
PE	0.653	0.653	0.714	0.385	0.498	0.588	0.621	0.672	0.547	0.653

Ho: heterozygosity observed, He: heterozygosity expected, P: fisher exact test probability, PIC: polymorphism information content, DP: discrimination power, MP: matching probability, TPI: typical paternity index, PE: power of exclusion.

^a Departure from HWE.

HWE was tested by the exact test [4] using the GDA software [5]. Comparison of allele frequency distributions was performed by means of $R \times C$ test. For the calculations of the forensic efficiency parameters, PowerStats software was used [6].

Table 2

A pairwise comparison (R × C) between the population of Old Believers and the autochthonous Poles

Locus	χ^2	<i>P</i>	<i>G</i>	<i>P</i>
D3S1358	4.2415	0.50100 ± 0.0158	4.5066	0.5220 ± 0.0158
VWA	2.8028	0.9170 ± 0.0087	3.5446	0.8860 ± 0.0101
FGA ^a	45.8666	0.0000 ± 0.0000	26.6576	0.0130 ± 0.0036
TH01	3.7633	0.5740 ± 0.0156	4.0713	0.5790 ± 0.0156
D16S539	7.9641	0.3180 ± 0.0147	8.5249	0.3030 ± 0.0145
D2S1338	10.8335	0.3710 ± 0.0153	10.3364	0.4680 ± 0.0158
D21S11 ^a	29.8799	0.0050 ± 0.0022	23.7198	0.0180 ± 0.0042
D18S51	22.0503	0.0980 ± 0.0094	20.5669	0.1170 ± 0.0102
D8S1179	5.0646	0.6340 ± 0.0152	5.4914	0.6220 ± 0.0153
D19S433	21.2792	0.0540 ± 0.0071	18.3280	0.0730 ± 0.0082

 χ^2 : Chi-square test, *G*: *G* statistics, *P*: probability.^a Difference is statistically significant.

3. Results and discussion

FGA and TH01 loci showed a significant departure from HWE in the examined population sample ($p < 0.05$) (Table 1). An average observed value of heterozygosity was 0.799, which is slightly lower than the average calculated for Polish Caucasians (0.826) [7]. The combined forensic efficiency values calculated for the population of Old Believers ($MP = 3.48 \times 10^{-12}$, $PE = 0.9949$) were somewhat different from those reported for the population of the northeastern Poland ($MP = 4.18 \times 10^{-13}$, $PE = 0.9914$) [7]. A pairwise testing for heterogeneity revealed statistically significant differences between the Old Believers and autochthonous Poles for FGA and D21S11 ($p < 0.05$) (Table 2).

4. Conclusion

A population database for the ethnic group of the Old Believers has been established for 10-STR systems included in AmpFISTR SGM Plus kit.

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