

Y-chromosome variation in northeastern Poland

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Abstract. Podlasie—a frontier region in northeastern Poland—differs from the rest of the country due to its scanty population (1.2 million) and ethnical and cultural diversification. Biostatistical parameters were obtained for autochthonous Poles as well as for minorities of Belarussians, Lithuanians, Polish Tatars and Old Believers residing in region, based on the SWGDAM-recommended Y-STR minimal haplotype. DNA was amplified using commercial kits: PowerPlex Y System (Promega) or genRES DYSplex-1 and genRES DYSplex-2 (Serac). Electrophoresis and typing were performed in the ABI 310 Genetic Analyzer (Applied Biosystems). The pairwise population comparisons between autochthonous Poles and the studied minorities revealed a certain degree of genetic differentiation. We suggest that the differences in some haplotype frequencies should be taken into consideration in certain trace–donor match analyses within the population of northeastern Poland. © 2005 Published by Elsevier B.V.

Keywords: Y-chromosome STR; Northeastern Poland; Forensic genetics; Population genetics

1. Introduction

Ethnically, Poland has a largely homogeneous population, its percentage of national or ethnic minorities being one of the lowest in Europe, officially estimated at between 3% and 4% of the inhabitants, which is equivalent to about 1.5 million people. Podlasie in northeastern part of Poland is a frontier region where the influences of various countries and cultures have been clashing for centuries. The region differs from the others due to its scanty population (1.2 million) and ethnical and cultural diversification. It is estimated that northeastern corner of Poland is inhabited by 200,000–300,000 Belarussians, 20,000–

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Table 1
Haplotype statistics on minimal haplotype loci in northeastern Poland

	Poles	Old Believers	Belarussian minority	Polish Tatars	Lithuanian minority	Combined
Sample size	186	127	156	125	124	718
No. of haplotypes	168	100	134	101	110	613
GD	0.9836	0.9638	0.9754	0.9638	0.9750	0.9723
DC	0.9032	0.7874	0.8590	0.8080	0.8871	0.8489
Mean no. of pairwise differences	3.59	3.28	3.81	3.89	3.83	3.62

Table 2
Population pairwise F_{ST} (below diagonal) and P values of differentiation test (above diagonal)

	Poles	Old Believers	Belarussian minority	Polish Tatars	Lithuanian minority
Poles	–	0.00000	0.00000	0.01802	0.01802
Old Believers	0.06978	–	0.00000	0.00000	0.00000
Belarussian minority	0.01803	0.11498	–	0.00901	0.00000
Polish Tatars	0.01272	0.04855	0.02066	–	0.81982
Lithuanian minority	0.01622	0.02663	0.02760	0.00000	–

30,000 Lithuanians and also 2500 Polish Tatars and 600 Old Believers. Y-chromosomal microsatellite haplotypes are commonly used to differentiate male lineages within regional populations.

2. Material and methods

DNA was extracted using the Chelex 100 and proteinase K protocol [1]. DNA was amplified in PCR System 9700 (Applied Biosystems) using commercial kits: PowerPlex Y System (Promega) or genRES DYSplex-1 and genRES DYSplex-2 (Serac). The SWGDAM minimal haplotype was considered. Electrophoresis and typing were performed in the ABI 310 Genetic Analyzer (Applied Biosystems). The nomenclature according to the Y-STR Haplotype Reference Database (<http://www.yhrd.org>) was used. Allele frequencies for each locus were calculated by simple gene counting method. Gene diversity (GD) and discrimination capacity (DC) values were calculated [2,3]. AMOVA was performed using the Monte-Carlo test included in the Arlequin software v.2.000 [4,5]. The bilocal system DYS385a/b was not considered and the number of repeats in DYS389I was subtracted from DYS389II. Genetic distance matrices between populations were obtained by using pairwise difference

Table 3
AMOVA results with all the five populations (pairwise difference)

Source of variation	df	Sum of squares	Variance components	% of variation
Among populations	4	114.642	0.18952 Va	3.54
Within populations	718	3173.242	5.15974 Vb	96.46
Total	722	3287.884	5.34927	

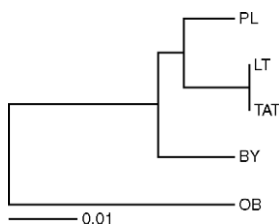


Fig. 1. UPGMA tree based on F_{ST} matrix values from Y-STR minimal haplotypes of five populations residing in NE Poland. PL: autochthonous Poles; LT: Lithuanian minority; TAT: Polish Tatars; BY: Belarussian minority; OB: Old Believers.

genetic distance. UPGMA tree was built from pairwise F_{ST} values matrix using NEIGHBOR program included in the Phylip v.3.63 package and visualized by the TreeView v.0.5.0 program.

3. Results and discussion

Biostatistical parameters for the population of northeastern Poland are presented in Table 1. The pairwise population comparisons between autochthonous Poles [6] and the studied minorities reveals statistically significant differences in F_{ST} values and relatively small values of interpopulation variation, that indicated a certain degree of genetic differentiation (Tables 2 and 3). The resulting data are consistent with the idea of a genetic proximity of Belarussians and Lithuanians to the Polish population due to the common Slavic origin and historical–political contacts and support the concept of a Polish admixture in Y-chromosomal lineages of Polish Tatars. Phylogenetic analyses and UPGMA tree show a close association between Lithuanian minority and Polish Tatars (Fig. 1). Old Believers appeared to be more distant from autochthonous Poles which may reflect their different history, religious affiliation and long-established principles of living. We suggest that the differences in some haplotype frequencies should be taken into consideration in certain trace–donor match analyses within the population of northeastern Poland.

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