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Allele frequencies and population data for 11 Y-chromosome STRs in samples from Eastern Slovakia

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ABSTRACT

Haplotype data of 11 Y-STR loci (DYS391, DYS389I, DYS439, DYS389II, DYS438, DYS437, DYS19, DYS392, DYS393, DYS390 and DYS385) was obtained from 629 Slovak Caucasian men living in Eastern Slovakia. A total of 474 haplotypes were identified, of which 395 were unique. The haplotype diversity value was 0.9982. Pairwise haplotype distances showed that the Eastern Slovak Caucasian population is not significantly different from the Slavs populations and is separated from the Balkan nations and the German speaking populations.

1. Population

The buccal swabs of 629 unrelated Slovak Caucasian males from a general resident population were collected from several regions of Eastern Slovakia (see Fig. 1). Historic, geographic and linguistic records indicate that the Slovak population belongs to the Slavic population, who settled the Danube River region in the 6th and 7th centuries [1,2]. The written informed consent was obtained from all participants.

2. DNA extraction

Genomic DNA was extracted by using Jet Quick DNA tissue kit (Genomed GmbH, Germany) according to the manufacturer's instructions.

3. PCR and typing

DNA amplifications were performed by using the commercially available Promega Powerplex® Y System (Promega Corporation Madison, USA) that includes 11 Y-STRs (DYS391, DYS389I, DYS439, DYS389II, DYS438, DYS437, DYS19, DYS392, DYS393, DYS390 and DYS385) following the manufacturer's recommendations. Capillary electrophoresis of the amplified products was performed on a MegaBACE® 1000 Genetic Analyzer (Molecular Dynamics, Sunnyvale, USA).

4. Data analysis

Arlequin software Version 3.1 [3] was used to calculate allele and haplotype frequencies, gene diversities, haplotype diversity, an analysis of molecular variance (Φ_{ST} value) and statistical significance (10 000 permutations). Our population data were compared with the previously published for Austria (Vienna) [4], Bulgaria [5], Czech republic (Prague) [6], Croatia (Zagreb) [4], Germany (Berlin) [7], Hungary (Budapest) [8], Poland (Warsaw) [9], Russian Federation (Moscow) [10], Ukraine (Kiev) [6] and Slovenia (Ljubljana) [11] for the set of 8 Y-STRs (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385). The phylogenetic tree was constructed from genetic distances with Neighbor-Joining method included in the program MEGA (version 4.1) [12].

5. Quality control

The laboratory has previously participated in the Y-STR haplotype reference database (http://www.yhrd.org) quality assurance exercise in 2008, where five quality control samples

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Fig. 1. Regions of Eastern Slovakia, where samples were collected.

were typed correctly with the Powerplex® Y System (QC certificate: 20.3.2008).

6. Results

The allele frequency distribution and gene diversity values which were found for each locus are listed in Table 1. The haplotypes detected in the Eastern Slovak Caucasian population are summarized in Table 2. The AMOVA analysis based on Φ_{ST} value between Eastern Slovak Caucasians and the other European neighboring populations are shown in Table 3. Variations among the Eastern Slovak Caucasian population and 10 European populations can be seen in the phylogenetic tree in Fig. 2.

7. Other remarks

In the 629 East-Slovak males analyzed in the study, a total of 474 different Y-STR haplotypes were observed, 395 haplotypes

Table 1
Allele frequencies and gene diversities (GD) for 11 Y-STRs in the Eastern Slovak population ($n = 629$).

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS437	DYS439	Allele class	DYS385	Allele class	DYS385
9					0.017			0.069	0.004		7,14	0.001		
10					0.608	0.014		0.403	0.268		9,14	0.001		
11		0.004			0.367	0.761	0.001	0.386	0.305		10,10	0.003		
12		0.133			0.006	0.034	0.135	0.131	0.282		10,12	0.001		
13	0.069	0.678				0.143	0.737	0.007	0.124	0.015	10,13	0.003		
14	0.260	0.179				0.036	0.117		0.014	0.570	10,14	0.119	13,18	0.003
15	0.192	0.003				0.007	0.007			0.273	10,15	0.015	13,19	0.003
16	0.324					0.001				0.135	11,11	0.011	13,20	0.001
17	0.147									0.004	11,12	0.004	14,14	0.050
18	0.003										11,13	0.034	14,15	0.130
19	0.001										11,14	0.278	14,16	0.017
21				0.004							11,15	0.039	14,17	0.004
22				0.133							11,16	0.003	14,18	0.001
23				0.131							11,18	0.001	15,15	0.019
24				0.338							12,13	0.015	15,16	0.025
25				0.354							12,14	0.017	15,17	0.025
26				0.034							12,15	0.006	15,18	0.004
27			0.004	0.001							12,16	0.001	16,16	0.004
28			0.985								12,17	0.001	16,17	0.003
29			0.220								12,18	0.003	16,18	0.025
30			0.387								12,19	0.001	16,19	0.003
31			0.217								13,13	0.011	16,21	0.001
32			0.063								13,14	0.030	17,17	0.007
33			0.006								13,15	0.022	17,18	0.011
											13,16	0.009	17,19	0.003
											13,17	0.009	19,20	0.001
GD	0.764	0.489	0.740	0.724	0.494	0.397	0.424	0.666	0.740	0.581				0.881