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## Y-STR HAPLOTYPES AND PREDICTED HAPLOGROUPS IN THE SLOVAK HABAN POPULATION

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# Y-STR Haplotypes and Predicted Haplogroups in the Slovak Haban Population

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## Abstract

The Habans are a group of Hutterites, who converted to Catholicism and retained a separate ethnic identity in Western Slovakia. In the present day we can find several Haban communities who have maintained their cultural identity as descendents of the Hutterite population. Twelve Y-chromosome short tandem repeat (STR) polymorphisms included in the Powerplex® Y multiplex kit were analyzed in 39 unrelated males. The prediction of Y-haplogroups from Y-STR data was performed by the Athey Haplogroup Predictor program. The most frequent haplogroups were E1b1b (43.57%) and R1b (30.77%). Results indicate that the gene pool of descendents of Habans was different from the gene pool of the Slovak majority population, and that Habans have remained isolated from the surrounding populations.

## Introduction

The forerunners of the Hutterites were Anabaptist refugees from Switzerland, Tyrol (Northern Italy and Southern Austria), Bavaria, Hesse and Württemberg, who settled in Moravia in Central Europe (today in the Czech Republic). Moravia was to become the country of Hutterite origin. They were named after Jacob Hutter, who was a Tyrolean and Moravian Anabaptist leader (Hostetler, 1997). A basic tenet of Hutterian society has always been absolute pacifism, forbidding its members from taking part in military activities, taking orders, wearing a formal uniform (such as a soldier's or a police officer's) or contributing war taxes. This has led to expulsion or persecution of the Anabaptists in the several lands, such as Moravia, in which they have lived.

At the beginning of the 16<sup>th</sup> century some Hutterites migrated to Slovakia (then in the Kingdom of Hungary) for the first time (Kalesný, 1981), where they were welcomed by Hungarian lords in defiance of the emperor in Vienna (Hostetler, 1997). The western Slovakia had stayed unoccupied by Turks and enjoyed a relative freedom (Kalesný, 1981). Their first village was Sobotište, where they established their first settlement. Between the years 1546 and 1620, the Hutterites built twenty-three farming communities (Hofs) where they practiced their own religion with political and economic

autonomy. It is believed that their total population reached 25,000, who created more than sixty Hofs in Slovakia and Moravia. The number of inhabitants was about five hundred in each Hof.

In the late 1800's, during the subsequent re-Catholicization of the Slovak population, many Hutterites moved to Transylvania (Romania), Ukraine, Russia, and to the Molotschna district north of the Black Sea (Kalesný, 1981). Migrations of the Hutterites in Europe are shown in Figure 1. The majority of Hutterian Brethren migrated to North America in 1873, where in the United States they chose the prairie land of South Dakota for settlement, while others chose Canada (Hostetler, 1997).

According to the Hutterite Chronicles the exact number of Hutterites was 757 who stayed in Slovakia in four regions (Sobotište, Veľké Leváre, Moravský Svätý Ján, Trenčín). They converted to Catholicism, but retained a separate ethnic identity as Habans until the 19<sup>th</sup> century (Weisensee and Siváková, 2003). Today in western Slovakia there are several small communities that still identify themselves as the descendents of the Hutterite population. The exact number of Slovak Habans has not been officially counted; for comparison, the number of American Hutterites is about 45,000. They live scattered throughout the North American prairies in approximately 460 colonies (Hutterites, 2009).

In this study we estimated the frequency of the major Y-chromosome haplogroups from Y-STR data by use of the web-accessible program, Whit Athey's Haplogroup Predictor. By analysis of the genetic structure of the

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Figure 1. Hutterite migration in Europe in the 16<sup>th</sup> and 17<sup>th</sup> centuries.

Y-chromosome, the paternal ancestry of the Haban population and its genetic history can be revealed.

## Materials and Methods

Blood samples were collected from healthy and unrelated Slovak Haban males from three villages in northwestern Slovakia: Sobotište (19 samples), Veľké Leváre (11 samples) and Moravský Svätý Ján (9 samples). Written informed consent was obtained from all participants. Genomic DNA was extracted from blood by using the Jet Quick DNA tissue kit (Genomed GmbH, Germany) according to the manufacturer's instructions. Male samples were chosen from individuals of Haban ancestry according to chronicles which are recognized sources describing the structure of the Haban community.

The amplification was performed on the Biometra1 T-Personal 48 thermal cycles using the Powerplex Y System Kit (Promega). Amplified products were detected in a process of capillary electrophoresis using the MegaBACE1 1000 genetic analyzer (GE Healthcare). Alleles were named according to the recommendations of the DNA Commission of the International Society for Forensic Genetics (Bär et al., 1997).

Pairwise distance based on  $\Phi_{st}$  values and the statistical significance (10,000 permutations) was calculated using Arlequin version 3.1 software (Excoffier et al., 2006). The distances were visualized in two-dimensional space

using the multi-dimensional scaling (MDS) analysis included in the SPSS 15.0 software. Prediction of Y-chromosome haplogroups from Y-STR values was performed using Whit Athey's Haplogroup Predictor, version 5 (see Web Resources). The predictor determines the probability that a Y-STR haplotype belongs to a given haplogroup (Athey, 2006). We chose a version of the program capable of predicting 21 Y-haplogroups (E1b1a, E1b1b, G2a, G2c, H, I1, I2a\*, I2a1, I2b\*, I2b1, J1, J2a1b, J2a1h, J2a1(xJ2a1b,J2a1h), J2b, L, N, Q, R1a, R1b, T).

## Results and Discussion

Our analysis of twelve Y-chromosome STRs of 39 samples showed 18 different Y-STR haplotypes in the Slovak Haban descendants. Eleven haplotypes were observed only once. The most frequent haplotype, 13-16/17-13-30-24-10-11-13-14-10-12 (DYS19, DYS385a/b, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439) was present in eight cases.

The Hutterite Y-STR data were compared with data previously published for Switzerland (Haas et al., 2006), Tyrol (Austria) (Berger et al., 2005), Slovak population (Rebala et al., 2007), Southern Moravia (Czech Republic), Hungary, Transylvania (Romania), Moldavia, and Ukraine (YHRD, 2009) for nine Y-STRs (DYS391, DYS389I, DYS389II, DYS19, DYS392, DYS393,

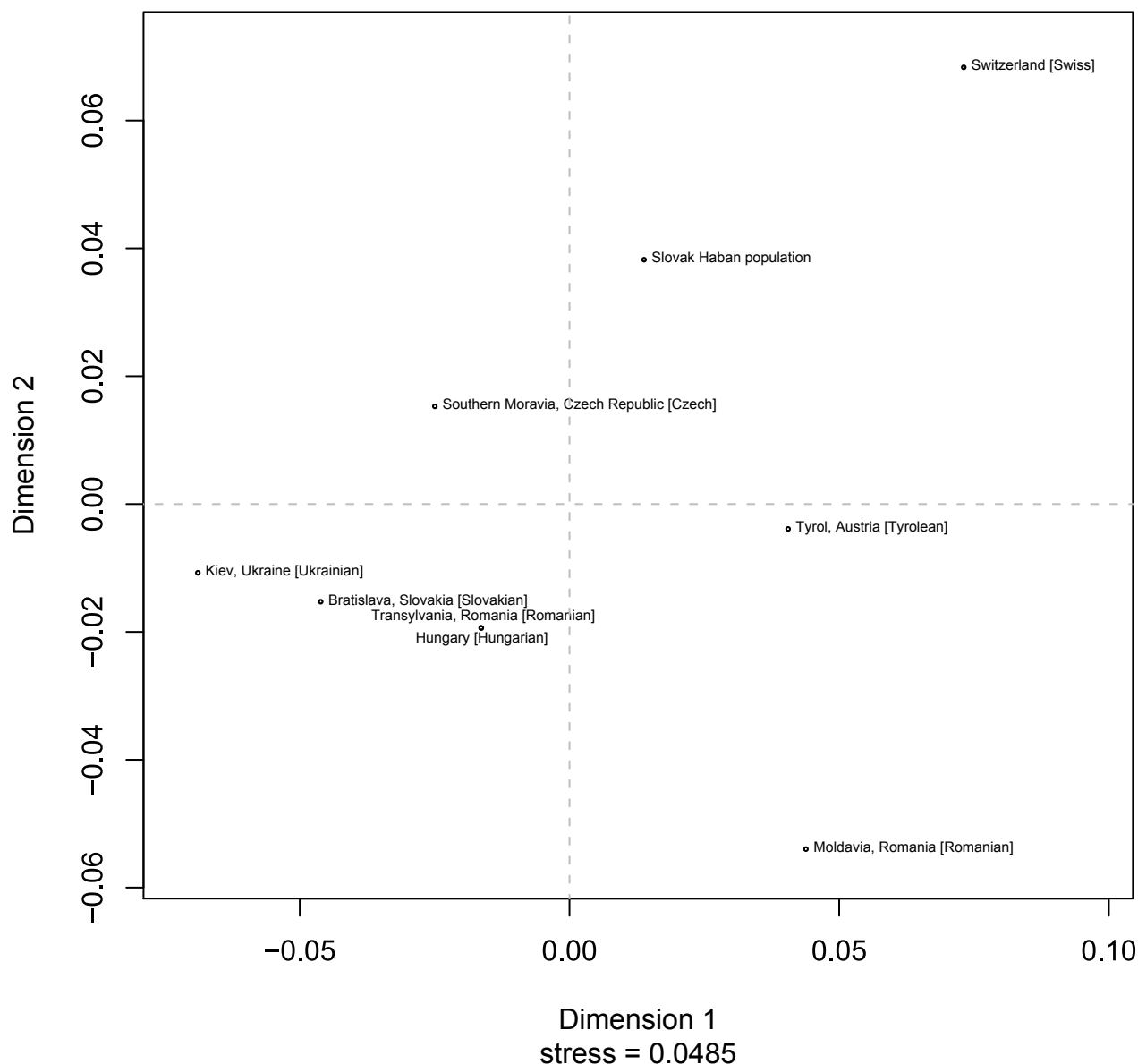


Figure 2. MDS plot based on  $\Phi_{st}$  values depicting the relationships among the nine populations.

DYS390, DYS385). We chose the populations from areas through which the Haban population migrated. The pairwise analysis based on  $\Phi_{st}$  values is shown in Table 1. The smallest genetic distances  $\Phi_{st}$  between the Haban population and the other populations were found with South Moravia (Czech Republic) ( $\Phi_{st} = 0.0134$ ). The largest pairwise difference for the Slovak Haban population was seen with the population sample from Ukraine ( $\Phi_{st} = 0.0832$ ) and that from Moldavia (0.0797), followed by the Slovak population (0.0634). The MDS plot of these differences is depicted in Figure 2.

The most frequent haplotypes were found in all three regions that were sampled. This means that although Haban communities were isolated from the surrounding majority population, the genetic structure is not different between the Haban groups. Table 2 shows the Y-STR haplotypes which were observed in the Haban population in three Slovak regions.

We predicted Y-chromosome haplogroups from our Y-STR data by the use of the Y-Haplogroup Predictor Program (Athey, 2006). The Bayesian probability was greater than 90% in all of the samples. Table 3 lists each

**Table 1**  
**Pairwise Distance Based on  $\Phi_{st}$  Values Between the Slovak Haban Population and Eight Populations from Countries Through Which they Migrated**

	$\Phi_{st}$	p
Switzerland (Swiss)	0.044	0.049
Tyrol, Austria (Tyrolean)	0.020	0.146
Southern Moravia, Czech Republic (Czech)	0.0134	0.201
Bratislava, Slovakia (Slovakian)	0.0634	0.023
Hungary (Hungarian)	0.0446	0.039
Transylvania, Romania (Romanian)	0.0282	0.201
Moldavia, Romania (Romanian)	0.0797	0.034
Kiev, Ukraine (Ukrainian)	0.0832	0.005

haplotype for the Haban samples and the corresponding predicted Y-haplogroup.

We found only five Y-haplogroups from the core 21 Y-haplogroups in the studied population. Haplogroup E1b1b (formerly E3b) was found in 17 individuals and represented 43.6% of the all samples. Previous genetic studies of the Slovak population showed that Haplogroup E1b1b was also found as the second most frequent haplogroup (21%) in the Slovak Romani population (Petrejčiková et al., 2009a), but in the Slovak population as a whole, its frequency was only 7.2% (Petrejčiková et al., 2009b). On the European continent it has the highest concentration in Romania (21.4%), Bulgaria (20.7%) (Cruciani et al., 2004), Albania (45.6%) (Pericic et al., 2005) and Greece (22.7%) (DiGiacomo et al., 2003).

Haplogroup R1b was present in the Slovak Haban population at a level of 30.8% (12 individuals). According to Wiik (2007), in Central Europe Haplogroup R1b forms a west-to-east gradient, with the highest percentages in westernmost Germany. Haplogroup R1b was the second most prevalent haplogroup in the Czech population (28%) (Luca et al., 2007) and was found as the third most frequent in the Slovak population as a whole (13.2%) (Petrejčiková et al., 2009b). A high frequency of Haplogroup R1b was also found in the Swiss (50%) and Tyrol population (59.4%) (Wiik, 2007).

The remaining haplogroups, I2a, R1a, and J1 were observed in smaller numbers of participants (I2a-12.8%; R1a-10.2% and J1- 2.6%). In the Slovak population as a whole, Haplogroups R1a and I2a were the most common Y-haplogroups with a frequency of 38% and 18.4% (Petrejčiková et al., 2009b).

According to the obtained results of Y-chromosome variation, the genetic structure of Haban population was influenced by the populations from areas through which they migrated, and shows a high degree of genetic relatedness with the population living in South Moravia, where the Hutterian Brethren were first established. On the other hand, results demonstrate genetic differentiation between the Haban population and the Slovak majority population. The Haban population lives as a collection of genetically isolated founder populations. This theory was confirmed by Weisensee and Siváková (2003). According to this study the Habans have remained isolated from the surrounding populations, and genetic drift has played an important part in the history of this population. Recently presented data from population structural studies and surname analysis in the three Haban villages also showed that all structural changes occurred over time within the Hutterite population (Siváková et al., 2000).

The data we have obtained may be useful for future population studies and for the comparison of the Slovak Haban population with Hutterite ethnic groups living in the USA and Canada.

## Quality Control

The laboratory has previously participated in the Y-STR haplotype reference database (see **Web Resources**) quality assurance exercise in 2008, where five quality control samples were typed correctly with the Power-Plex Y System.

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## Web Resources

Haplogroup Predictor Program

<http://www.hprg.com/hapest5/>

The Hutterian Brethren web site

<http://www.hutterites.org>

YHRD Y-STR haplotype reference database

<http://www.yhrd.org>

Arlequin Software for Population Genetics

<http://cmpg.unibe.ch/software/arlequin3/>

Table 2  
Y-STR Haplotypes and Predicted Y-Haplogroups in the Slovak Haban Population

Haplo-type	DYS 19	DYS 385 a/b	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	Region	n	Predicted Y-Haplogroup	Probability (%)
H1	13	10/14	14	31	24	10	11	13	14	10	13	Sobotište	1	E1b1b	96.1
H2	13	11/14	12	29	24	10	11	13	14	10	13	Sobotište	1	E1b1b	99.6
H3	13	16/17	13	30	24	10	11	13	14	10	12	Sobotište	2	E1b1b	100
												Veľké Leváre	3		
												Moravský Ján	3		
H4	13	16/17	14	32	24	10	11	13	14	10	12	Sobotište	2	E1b1b	100
												Moravský Ján	1		
H5	13	16/21	14	32	24	10	11	13	14	10	13	Sobotište	2	E1b1b	100
												Veľké Leváre	1		
												Moravský Ján	1		
H6	14	11/13	13	30	24	11	13	12	14	12	13	Moravský Ján	1	R1b	100
H7	14	11/13	14	31	24	10	11	12	14	10	12	Sobotište	1	J1	97.1
H8	14	11/14	13	29	23	11	13	13	15	12	13	Sobotište	1	R1b	100
H9	14	11/14	13	30	24	11	13	12	15	12	12	Veľké Leváre	1	R1b	100
H10	14	11/14	14	30	23	12	13	13	15	12	12	Sobotište	1	R1b	100
H11	14	11/15	13	29	24	10	13	13	15	12	11	Sobotište	1	R1b	100
H12	14	11/15	13	29	24	10	13	13	15	12	12	Sobotište	2	R1b	100
												Veľké Leváre	1		
												Moravský Ján	1		
H13	14	11/15	13	30	25	10	13	13	15	12	12	Veľké Leváre	1	R1b	100
H14	14	11/15	13	30	25	11	13	13	15	12	12	Veľké Leváre	2	R1b	100
H15	16	11/14	13	29	25	10	11	13	14	11	11	Veľké Leváre	1	R1a	100
												Moravský Ján	1		
H16	16	11/15	13	30	24	10	11	13	14	11	12	Sobotište	1	R1a	90.3
H17	16	11/15	13	30	24	11	11	13	14	11	10	Sobotište	1	R1a	99.9
H18	16	12/13	13	30	24	10	11	14	15	10	12	Sobotište	3	I2a	91.5
												Veľké Leváre	1		
												Moravský Ján	1		

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**Table 3**  
Distribution of Y-haplogroups in the Slovak Haban Population (n=39)

Y-Haplogroup	Number	Percent
E1b1b	17	43.59
I2a	5	12.82
J1	1	2.56
R1a	4	10.25
R1b	12	30.77
Total	39	100

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