

## TO THE RESEARCH OF THE GENETIC DIFFERENTIATION OF THE SLOVAK HABANS

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**Abstract:** *Genetic data (antigenes, plasmaproteins, enzymes) and dermatoglyphic traits have been used to assess population structure and affinities of the Slovak Habans (Hutterites) and the Non-Habans from three villages in West Slovakia. The coefficient of inbreeding (F), its random (Fr) and nonrandom (Fn) components indicate the relative structural changes that occurred over time in these populations, however, these seem to have had any appreciable effect on local differentiation. The obtained results suggest balanced gene flow between the studied populations. The serogenetic and dermatoglyphic structure of the Habans' fail to give congruence. The Habans' villages do not group against the Non-Habans (control population), in the same way.*

**Keywords:** *Habans; Genetic differentiation; Inbreeding; Genetic markers; Dermatoglyphics.*

### Introduction

A multidisciplinary research project that has been set up on the ethnogenesis, demography and genetics of the Slovak Habans (in German Habaner, in Hungarian habánerek, habánok, habánusok, in Russian chabani, in French les habans), was motivated on the one hand, by their quite well documented history as well as their most gorgeous handicraft production – faience ceramics, by which the Habans have entered the cultural history of Middle Europe. On the other hand, by a complete absence of data on the population genetic structure of this unique population group.

The Slovak Habans, known as “Hutterite Brethren” whose origin can be traced back to the Swiss and German anabaptists, immigrated into Slovakia in the early 16th century and settled down in several small villages, mainly in West Slovakia. The most significant Haban courts have been established in the villages Sobotište, Moravský Ján and Veľké Leváre (Kalesný 1981), near Bratislava (Figure 1). Descendants of the founders still live in the region, where they represent the last stock of the Hutterites in Middle Europe.

The aim of the study is:

— on the basis of different data sets to address the hypothesis as to whether the Habans form a specific genetic unit due to their ethnohistory (considering the preserved common genetic heritage).

— to ascertain whether they exhibit genetic differentiation as it is reasonable to assume that the sociocultural isolation derived from historical factors and genetic drift have influenced the gene pool of these populations.

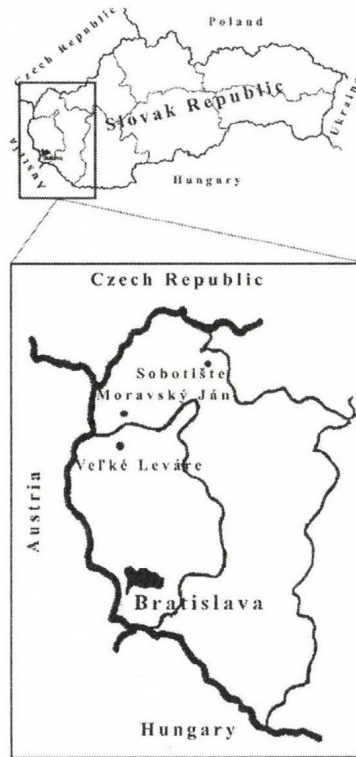


Fig. 1: Geographical location of the villages Sobotište, Moravský Ján and Veľké Leváre in West Slovakia.

### Material and methods

In our earlier paper of the genetic structure of the Habans the detailed population structural measures and the surname analysis were reported in the villages Sobotište, Moravský Ján and Veľké Leváre, respectively (Siváková and Sádovská 1999). The survey of the variability of different genetic markers in the studied populations and in the Non-Haban Slovaks as a control group was published in some detail by Siváková, Scheffrahn and Nechvátalová (2000). For details on dermatoglyphic traits I refer to Siváková and Pospíšil (2000). The same data form the base for the current paper, though it attempts to illustrate the biological affinities between the Habans and the Non-Habans in the two sets of data (genetic and dermatoglyphic). For the sake of convenience, the population sample sizes for different sets of data are furnished in Table 1.

The Crow and Mange (1965) approach was used for estimation of the total coefficient of inbreeding from isonymy and its random and nonrandom components. Biostatistical analysis of the blood group data has been achieved by applying the computer program of Nabulsi (1993) and Swofford and Selander (1989). The dermatoglyphic relations between particular groups were tested by application of the Hiernaux (1965) distance coefficient

on the basis of selected characters (as indicated in the table 1). The cluster analysis was performed using complete linkage method of the nclas program (Podani 1993).

Table 1. Sample sizes of different data sets for the three Habans and the Non – Habans Slovak populations.

Population	Parish records	Total population <sup>a</sup>	Genetic markers <sup>b</sup>	Dermatoglyphic markers <sup>c</sup>
Sobotište	1844–1910	1693 (83)	54	54
Moravský Ján	1830–1950	1958 (35)	17	15
Veľké Leváre	1850–1950	3193 (43)	28	22
Non-Habans*			103	162

a: Last census (1991) including number of the Habans' inhabitants. Figures in the brackets (number of the Habans) were recorded by the leaders of the Habans' community in particular villages.

b: Genetic markers include A1A2B0, MN, Ss, RH, Kell, ALB, TF-subtypes, C3, BF, HP, CP, Gc-subtypes, ACP, ESD, ADA, AK, 6PGD, PGM1-subtypes.

c: Dermatoglyphic variables used are frequency of arches, whorls and loops on fingers, frequency of pattern in thenar/1. interdigital area, 4. interdigital area, pattern intensity index, total finger ridge count.

\*: Control population - the sample was created from inhabitants of the same villages.

### Results and discussion

The implications of mating structure for the maintenance of genetic variability are great in small populations and in those ones substructured as a consequence of involved cultural, social and economic preferences in choice of mate.

Table 2 presents distribution of the inbreeding coefficients and isonymy over entire time spans in the three villages. The isonymy ranged between 1.97–4.87 % in particular villages and consequently the coefficient of inbreeding (F), with the highest value in Sobotište and the lowest one in Moravský Ján.

Table 2. Inbreeding coefficients versus isonymy for the populations of Sobotište, Veľké Leváre and Moravský Ján.

Population	N	Ni	I	F	Fr	Fn
Sobotište (1844–1910)	308	15	0.0487	0.0122	0.0036	0.0086
Veľké Leváre (1850–1950)	1911	39	0.0204	0.0051	0.0016	0.0035
Moravský Ján (1830–1950)	2232	46	0.0197	0.0049	0.0034	0.0016

N: total number of marriages, Ni: number of isonymous marriages, I: isonymy, F: coefficient of inbreeding, Fr: random component of F, Fn: nonrandom component of F



Looking at the table we can see, that the contribution of the coefficients – the random ( $F_r$ ) and nonrandom ( $F_n$ ), on the total inbreeding ( $F$ ) is different in particular villages. While in Sobotište and Veľké Leváre the nonrandom inbreeding is prevailing, suggesting that marital isonymy was a major factor of  $F$  in these populations. In Moravský Ján the random component of inbreeding ( $F_r$ ) proves to be as a dominant indicating that the total inbreeding in this sample is rather result of restricted effective size of the population. These results indicate the relative structural changes that occurred over time in the overall population (including Habans as well as non-Habans), of particular villages.

Table 3 shows the average heterozygosity value for all the population groups investigated, based on 19 polymorphic loci. The tendency of exhibiting lower average heterozygosity values in the Habans' groups is apparent although Veľké Leváre comes very close to the Non-Habans. The genetic resemblance of Veľké Leváre to the control group may indicate a higher degree of admixture in this village as a result of migration over the last generations. This is presumably due to the closeness to Bratislava, as the capital, and breakdown of social barriers especially since 1945 (these facts are related to the general pattern of the breakdown of isolates which characterized rural Slovakia after the World War II).

Table 3. Mean heterozygosity in the four populations.

Population	Mean heterozygosity HW expected **
Sobotište	0.260±0.056
Veľké Leváre	0.270±0.062
Moravský Ján	0.243±0.056
Non-Habans	0.279±0.062

\*\* Unbiased estimate (see Nei 1978)

Paired estimates of genetic distance (Wright 1978), are set out in Table 4. An inspection of this table reveals that the minimum genetic distance (0.084) occurred between the populations of Sobotište and Veľké Leváre. These two populations show quite similar distances from the Non-Habans what is in accordance with the already mentioned values of the mean heterozygosity and what reflects the recent gene flow between these groups. The population of Moravský Ján shows consistently high genetic distance (range 0.121–0.136) with each of the remaining populations. This fact can be attributed to the result of genetic drift which has led to a higher degree of genetic differentiation of this small population. The overall genetic distance between investigated populations (based on 19 proteins), is graphically demonstrated in dendrogram (Fig. 2).

Table 4. Genetic distance (Wright 1978) between the four populations.

Population	1	2	3	4
1. Sobotište	*****			
2. Veľké Leváre	0.084	*****		
3. Moravský Ján	0.121	0.136	*****	
4. Non-Habans	0.106	0.109	0.129	*****

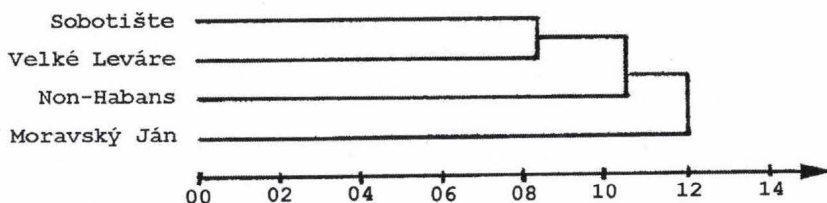


Fig.: Genetic distance for three Slovak Habans and Non-Habans groups (Wright 1978).

From the figures given in Table 5 it is seen that the population from Sobotište shows the most significant differences from the Non-Habans in the digito-palmar dermatoglyphs. They show also the highest number of triradii expressed by the index of pattern intensity (PII). However, this difference is not significant.

Table 5. Variability of digito-palmar dermatoglyphs and some indices in the three Habans and the Non-Habans population samples, West Slovakia.

	Sobotište	p	Moravský Ján	p	Velké Leváre	p	Non-Habans
A	1.67	*	4.25		9.66	*	3.34
L	45.17	***	61.79		63.45		61.68
W	53.16	***	33.96		26.9	*	34.98
HYP	40.74		46.51		48.28		40.74
TH/I	10.78		11.63		0	***	9.26
IIida	5.56		4.65		3.45		4.94
IIIida	43.52		53.49		37.93		45.99
IVida	61.11	*	44.18		65.52		50.31
t	60.19		53.49		65.52		58.02
t'	14.81		16.28		13.79		19.75
t''	4.63		4.65		0	***	4.32
T combinations	20.37		20.93		17.24		16.36
missing t	0	*	4.65		3.45		1.545
a - b	82.19		80.27		84.27		81.64
b - c	49.94		51.73		56.13		51.88
c - d	69.41	**	71.95		68.13		74.04
PII	15.15		12.97		11.72		13.16
TRC	159.69	***	141.82		124.13		139.06
P	26.48		28.15		25.65		26.92
MLI	8.06		8.99	*	7.62		8.21

\*:  $p < 0.05$     \*\*:  $p < 0.01$     \*\*\*:  $p < 0.001$

A = arch, L = loop, W = whorl, HYP = hypothenar, TH/I = thenar/ I ida, II, III, IV ida = 2, 3, 4 interdigital area, t, t', t'' = carpal triradii, a - b, b - c, c - d = interdigital ridge counts, PII = pattern intensity index, TRC = total ridge count, P = Valšík's papillary number, MLI = Cummins' main-line index

The Hiernaux distance matrix between the study samples (Table 6) has been calculated using the chosen dermatoglyphic characters (see table 1), with known worldwide span of variation (the list of variables considered was published by Olivier 1972 and Sanchez 1975). The table 6 and the dendrogram (Fig. 3) reveal that the smallest distance exists between the Non-Habans and the Habans from Vel'ké Leváre, while the greatest distance was between the Non-Habans and the Habans from Sobotište. Thus, the dermatoglyphic analysis fails to give congruence with respect to the serogenetic structure of the Habans' population. Here, in turn, the "bigger" Habans' village of Sobotište is more distinct from the neighbored (Non-Haban) population.

Table 6. Values of Hiernaux  $\Delta_g$  distance between the pairs of populations.

Population	1	2	3	4
1. Sobotište	*****			
2. Vel'ké Leváre	31293	*****		
3. Moravský Ján	63653	18891	*****	
4. Non-Habans	29577	1528	14962	*****

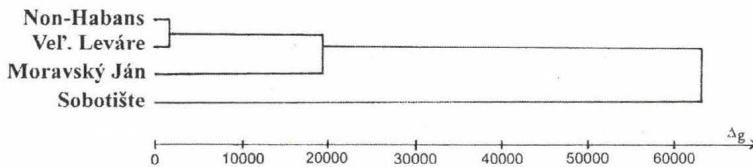


Fig. 3: Dendrogram for three Habans and Non-Habans groups from the Hiernaux  $\Delta_g$  distance matrix using the complete linkage clustering method.

This apparant contradiction is not easy to explain. The fact that blood genetic traits respond readily to microevolutionary processes could be one of the probable causes of such discordance, however rather speculative in the sample of this size. This conception is not new and has already been considered by other authors (Arrieta et al. 1990, Froehlich and Giles 1981, Newman 1960, Rothhammer et al. 1977) as the result of similar disparities between polygenic versus monogenic biological markers in population-genetic studies.

### Conclusions

1. The genetic data (proteins) and dermatoglyphics distinguish the Habans from the Non-Habans in the same villages. The differences are more marked in the dermatoglyphic traits.
2. Serogenetic and dermatoglyphic structure is noncompatible, i.e. the Habans' villages do not group against the Non-Habans in the same way.
3. No evidence from the present data indicate that isolation and inbreeding in the past had any appreciable effect on local differentiation. The values of the mean heterozygosity reflect the balance gene flow between the populations. Only the small village Moravský



Ján shows lower similarity to the others, likely as a result of genetic drift. However, the group size effect results in the divergence can not be excluded, too.

4. More proteins and molecular markers (DNA-STR, Y-chromosomal microsatellites) are necessary to verify the genetic position of particular Habans' villages.

5. Mitochondrial DNA studies have to be undertaken to link the Slovak Habans with genetically related populations of the Mennonites, Old Amish and Hutterites that migrated to the American continent.

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