

Genetic markers (HP, TF, GC and PI) in two Polish population samples
Preliminary report

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INTRODUCTION

Our knowledge on the variability of genetic serum protein markers (HP,TF,GC, PI) in Central and East European populations is so far rather limited. We therefore started several research projects in CSFR (especially in Slovakia), in East Germany (especially in Thuringia: Jena, Erfurt, Suhl) and in Poland. The results of our studies in two population samples from this country - Poles from Central Poland and Kashubes from Northern Poland - are presented here. They are compared with those obtained in some populations samples from Hungary and Slovakia in order to estimate the extent of variation of these genetic markers among Central and East European populations.

MATERIALS AND METHODS

Serum samples of 198 unrelated male and female Poles from Ostrów Wielkopolski (Central Poland) and 228 Kashubes from Kościerzyna (Northern Poland) have been collected by us in 1990 at the blood transfusion centers of these two places. The serum samples were transported deep-frozen to Bremen, where the HP typing, and the TF, GC and PI sub-typings were done.

RESULTS AND DISCUSSION

Observed and expected phenotype frequencies do not differ significantly so that genetic equilibrium can be assumed for all the four polymorphic systems under study. The allele frequencies runs as follows:

n	Poles 196	Kashubes 225
HP*1	0.3699	0.4289
HP*2	<u>0.6301</u>	<u>0.5711</u>
	1.0000	1.0000

n	198	227
TF*C1	0.7677	0.8128
TF*C2	0.1641	0.1233
TF*C3	0.0631	0.0551
TF*B	<u>0.0051</u>	<u>0.0088</u>
	1.0000	1.0000
n	194	224
GC*1F	0.0876	0.1674
GC*1S	0.5722	0.5000
GC*2	<u>0.3402</u>	<u>0.3326</u>
	1.0000	1.0000
n	195	228
PI*M1	0.6897	0.6711
PI*M2	0.1359	0.1930
PI*M3	0.1359	0.0899
PI*S	0.0103	0.0219
PI*Z	0.0128	0.0153
PI*Var	<u>0.0154</u>	<u>0.0088</u>
	1.0000	1.0000

Considering corresponding data for Slovaks (Sivákóva et al. 1990) and Hungarians, Matyos and Gypsies (Goedde et al. 1987) we computed standard genetic distances according to Nei (1972). The results of a UPGMA clustering of these distances are shown in Fig. 1. Hungarians and Matyos as well as Poles and Slovaks are found in two subclusters, which are linked up to one cluster. Gypsies and especially Kashubes exhibit a distinct position from this cluster, which can be explained considering the ethnohistory of these two populations. This genetic distance pattern will be analyzed and discussed in more detail elsewhere.

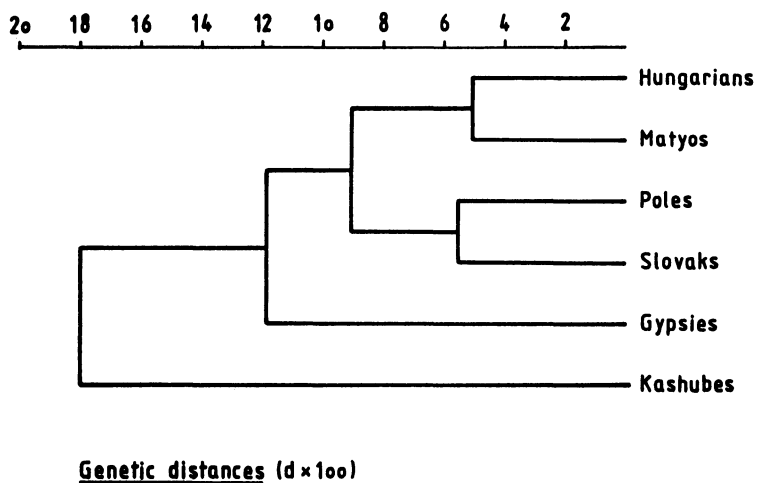


Fig. 1 Genetic distances based on four loci (HP, TF, GC, PI) among six Central and East European population groups

Summing up we can point out that within the populations of Central and East Europe one has to consider a marked genetic heterogeneity concerning HP, TF, GC and PI polymorphisms. This is not only of considerable interest to population genetics, but also with regard to the application of Essen-Møller values in cases of disputed paternity, when Central and East Europeans are involved.

REFERENCES

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