



Genetic variability of Huzul horse breed families

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Introduction

The Huzul is a small-sized mountain horse originated in the Carpathian basin. The Huzul breed was used primarily in the forestry, but nowadays are used for children riding, hippotherapy and other fields also. Maintaining heterozygosity and precise identification of mare families are crucial for the management of small populations.

The aims of the study were to analyze genetic diversity and microsatellite variability among six Huzul horse breed families ("1 Panca", "12 Sarata", "4 Kitca", "5 Plosca", "Árvácska" and "Aspiráns").

Materials and methods

Blood samples were collected from 63 mares. Additionally, pedigree information of these horses was collected from the studbook and was analyzed. Microsatellite data (twelve markers) were analyzed using Molkin and pedigree analysis was done using EnDog. Furthermore, ten of these mares (from five families) were compared based on mitochondrial DNA data. Microsatellite markers were compared based on their PIC value. Distances among the mare families were measured with Nei's genetic distance and Reynold's genetic distance based on the microsatellite information. Distances were measured based on the pedigree information was characterized using Nei's genetic distance also.

Results and Discussion

The more informative marker was "ASB2" marker with 0.868 PIC value, the less informative was "HTG7" marker with 0.357 PIC value (Table 1.). Heterozygosity was also the highest for "ASB2" and was the lowest for "HTG7", respectively. Number of alleles was the highest for "ASB2", whereas the lowest were for "HMS6" and "HTG7".

Genetic distance based on molecular information was highest between "5 Plosca" and "4 Kitca" (Nei's minimum distance=0.361; Reynold's distance=0.4) families, and was the lowest between "Árvácska" and "Aspiráns" (Nei's minimum distance=0.0248; Reynold's distance=0.019) families (Table 2.,3.). The genetic distance based on pedigree information showed the following values: Nei's genetic distance and average distance were the highest (0.351 and 0.503) between "5 Plosca" and "4 Kitca". Nei's genetic distance was the lowest (0.0404) between "Árvácska" and "Aspiráns" families, average distance was the lowest (0.421) between "1 Panca" and "5 Plosca" families, respectively (Table 4.).

The DNA results sorted the ten mares into four separate groups which do not followed the family data (Figure 1.). The mare from "1 Panca" family was joined to horses from "Árvácska" family.

Table 2.
Nei's genetic distance based on microsatellite information

	1 Panca	12 Sarata	4 Kitca	5 Plosca	Árvácska
12 Sarata	0.108				
4 Kitca	0.186	0.123			
5 Plosca	0.221	0.266	0.361		
Árvácska	0.077	0.087	0.151	0.206	
Aspiráns	0.086	0.099	0.147	0.193	0.025

Table 3.
Reynold's genetic distance based on microsatellite information

	1 Panca	12 Sarata	4 Kitca	5 Plosca	Árvácska
12 Sarata	0.093				
4 Kitca	0.118	0.080			
5 Plosca	0.152	0.180	0.400		
Árvácska	0.040	0.050	0.036	0.050	
Aspiráns	0.042	0.054	0.032	0.043	0.019

Table 4.
Nei's genetic distance based on pedigree information

	1 Panca	12 Sarata	4 Kitca	5 Plosca	Árvácska
12 Sarata	0.161				
4 Kitca	0.241	0.208			
5 Plosca	0.216	0.234	0.352		
Árvácska	0.110	0.108	0.199	0.180	
Aspiráns	0.107	0.106	0.202	0.176	0.040



Huzul mare in children sport competition

Table 1.
The description of allele frequencies of the microsatellite analysis

Name	Alleles	Heterozygosity	PIC
AHT4	7	0.68	0.653
AHT5	6	0.72	0.674
ASB2	10	0.88	0.868
HMS2	6	0.69	0.632
HMS3	7	0.77	0.730
HMS6	4	0.61	0.544
HMS7	6	0.69	0.634
HTG10	8	0.68	0.645
HTG4	5	0.64	0.570
HTG6	6	0.62	0.585
HTG7	4	0.38	0.357
VHL20	7	0.84	0.825



Polo Polan, Huzul stallion

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Conclusions

Results of the microsatellite analysis suggest that Huzul horse population is maintained with reasonable levels of genetic diversity.

The results of the preliminary mitochondrial DNA analysis showed mistakes in the administration of the mare families. This suggests that identification of the present brood-mare stock is necessary, the precise administration of the mare families will be possible in this way.

Figure 1. Result of the mitochondrial DNA analysis (Mare's name – Family name)

