Pedigree analysis in four Slovak endangered horse breeds

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ABSTRACT: The aim of this study was to perform an analysis of genetic diversity in four endangered horse populations bred in Slovakia, describing parameters on the probability of identity by descent and gene origin. The analysed populations consisted of (reference populations in brackets) 656 (158) Hucul horses, 2052 (162) Lipizzan horses, 1951 (171) Shagya Arabian horses, and 220 (42) Slovak Sport Ponies. The equivalent complete generations ranged from 4.93 for the Slovak Sport Pony to 10.25 for the Lipizzan horses. The average value of inbreeding ranged from 2.67% for the Slovak Sport Pony to 6.26% for the Hucul. The mean average relationship coefficients varied from 3.08% for the Shagya Arabian to 9.34% for the Hucul. Individual increases in inbreeding ranged from 0.43% for the Lipizzan to 1.06% for the Hucul, while the realized effective sizes were from 117.14 to 47.67 animals. The evaluated populations were derived from 80 to 499 founders. The effective number of founders ranged from 26 to 160, while the effective number of ancestors from 7 to 32.

Keywords: coefficient of inbreeding; effective population size; effective number of founders; effective number of ancestors; pedigree analysis

Animal breeding resolves problems of genetic evaluation (Vostrý et al., 2009), structure and assessment of genetic variability (Álvárez et al., 2010). Domestication of livestock species and a long history of migrations, selection, and adaptation have created an enormous variety of breeds of these animals (Groeneveld et al., 2010). Biodiversity is the variety of ecosystems, species, populations within species, and genetic diversity within species. Genetic variability has been defined as the variety of alleles and genotypes present in a population (Frankham et al., 2002). Variability of a gene pool over time reflects the change of genotype frequencies, which is closely connected with evolution. In animal breeding, genealogical information is important for genetic evaluation as well as for the evaluation of genetic variability (de Rochambeau et al., 2000). Results of the pedigree analysis provide an expected value of the increase in homozygosity and decrease in heterozygosity for the whole genome and can be considered as an appropriate strategy for monitoring populations for mating programs and for the management of genetic variability (Folch and Jordana, 1998; Valera et al., 2005; Mäki-Tanila et al., 2010). The pedigree analyses allow to assess inbreeding levels and population structuring (Gutiérrez et al., 2005). Results of such analyses can indicate the breeders of relatively small closed populations the size of genetic losses that could potentially appear.

The aim of this study was to estimate genetic diversity in four Slovak horse breeds using parameters on probability of identity by descent and gene

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origin. The results will be used for implementation of conservation strategies of the evaluated breeds.

MATERIAL AND METHODS

The pedigree information on the Hucul, Shagya Arabian, and Lipizzan horses was available from the Central Register of Breeding Horses in Slovakia and the National Stud Farm Topoľčianky. The National Stud Farm founded in 1921 plays an important role in horse breeding, management of closed herd books by breeds, etc. The data on the Slovak Sport Pony were obtained from the open stud book of the Slovak Sport Pony Association. A total of 4879 animals (3177 out of them females) were registered. The analysed reference populations consisted of 533 animals registered in the stud books of the individual breeds within the years 2002–2007. The analysis covered living mares and stallions as well as frozen genetic materials of stallions deposited in the Reproduction Centre of the National Stud Farm at Topoľčianky. Population sizes differentiated by sex, reference populations and totals for the four assessed breeds are given in Table 1. Populations of the Lipizzan and Shagya Arabian were the largest. The animals were bred in the Topoľčianky stud as well as in other small private studs in Slovakia. An organized exchange of genetic materials among all the studs was assured. The genealogical information was completed to maximise the number of the ancestral generations used in the analysis. The pedigree information was used to calculate the parameters associated with the completeness of the pedigrees and genetic variability.

The quality level of the pedigree information was characterized by computing:

(1) The number of fully traced generations was defined as the number separating the offspring from the furthest generation in which the ancestors of an individual are known. Ancestors with unknown parents are considered as founders (generation 0).

(2) The maximum number of generations traced is the number of generations separating an individual from its furthest ancestors.

(3) The equivalent complete generations are computed as the sum over all known ancestors of the terms computed as the sum of $(1/2)^n$, where n is the number of generations separating the individual from each known ancestor (Maignel et al., 1996). This is calculated using the equation:

$$\mathrm{t} = \frac{1}{N}\sum_{j=1}^{N}\sum_{i=1}^{n_j}\frac{1}{2^{g_{ij}}} \qquad (1)$$

where:

n_j = number of ancestors of individual j in the evaluated population

g_{ij} = number of generations between the individuals and ancestor i

N = number of animals in the reference population

(4) The index of completeness describes the completeness of each ancestor in the pedigree of the parental generation (MacCluer et al., 1983) and is calculated separately for paternal and maternal lines according to the equation:

$$id_{par} = 1/d\sum_{j=1}^{a} a_i \qquad (2)$$

where:

a_i = proportion of known ancestors in generation i

d = number of generations found

Table 1. Description of the Slovak horse breeds analysed

Sex		HK		LK		SAK		SSP	
	n	158		162		171		42	
RP	sex	M	F	M	F	M	F	M	F
	n	20	138	19	143	28	143	6	36
	n	656		2052		1951		220	
WP	sex	M	F	M	F	M	F	M	F
	n	195	461	733	1319	689	1262	85	135

HK = Hucul horse, LK = Lipizzan horse, SAK = Shagya Arabian horse, SSP = Slovak Sport Pony, RP = reference population, WP = whole population, M = male, F = female

The pedigree completeness index for each individual is calculated as the harmonic mean of paternal and maternal lines according to the equation:

$$Id = 4Id_{par} + d_{mat} / Id_{par} + Id_{mat} \tag{3}$$

Generation interval

The generation interval was defined as the average age of the parents at the birth of the offspring used to replace them.

Genetic variability

To characterize the genetic variability of the population, two types of parameters were analysed based on the probability of the identity by descent (1–4) and gene origin (5–6), estimated as follows:

(1) The individual inbreeding coefficient (F_i) is defined as the probability that an individual has two identical genes by descent (Wright, 1922), calculated according to equation based on the algorithm described by Meuwissen and Luo (1992):

$$F_X = \sum 0.5^{n_1 + n_2 + 1}(1 + F_A) \tag{4}$$

(2) The increase of inbreeding for each individual (ΔF_i) was computed as follows:

$$\Delta F_i = 1 - \sqrt[t-1]{1 - F_i} \tag{5}$$

where:

F_i = individual inbreeding coefficient of individual i

t = equivalent complete generations of ancestors for a given individual (Gutiérrez et al., 2009)

(3) The effective population size, referred to as the realized effective size by Cervantes et al. (2008a, 2011), was calculated in real populations of pedigrees as the individual increase of inbreeding based on the method of Gutiérrez et al. (2009) according to the equation:

$$\bar{N}_e = 1/2\ \bar{\Delta}\bar{F}_i \tag{6}$$

(4) The average relatedness coefficient for each individual (AR coefficient) is defined as the probability that a random allele selected from the whole pedigree of the population belongs to each individual (Dunner et al., 1998) and was calculated according to the equation:

$$c' = (1/n)\ 1' A \tag{7}$$

where:

c' = row vector where c_i is the average of the coefficients in the row of individual i in the numerator relationship matrix, A, of the dimension $_n$

A = relationship matrix of size $n \times n$

(5) The effective number of founders, f_e (Lacy, 1989; Boichard et al., 1997), is defined as the number of equally contributing founders that would be expected to produce the same genetic diversity as in the population under study and was calculated according to the equation:

$$f_e = 1 \Big/ \sum_{k=1}^{f} q_k^2 \tag{8}$$

where:

q_k = expected contribution of the founders to the gene pool of the present population, i.e., the probability that a randomly selected gene in this population comes from founder k. All of the founders contribute to the completeness of the assessed popuation without surplus, and the sum of all founders equals to 1

(6) The effective number of ancestors (Boichard et al., 1997) is the minimum number of ancestors explaining the genetic diversity in a population. This is calculated according to the equation:

$$f_a = 1 \Big/ \sum_{k=1}^{f} p_k^2 \tag{9}$$

where:

p_k^2 = marginal contribution, which is derived on the basis of expected contributions, with redundant contributions being eliminated

Boichard et al. (1997) identified two types of surplus contributions. In the first case, $n - 1$ selected ancestors may be the ancestors of individual k. Therefore, the marginal contribution is adjusted for the expected genetic contributions (a_i) of the $n - 1$ selected ancestors to individual k. This is calculated according to the equation:

$$p_k^2 = q_k \left(1 - \sum_{i=1}^{n-1} \mathrm{a}_\mathrm{i}\right) \tag{10}$$

In the second case of surplus contributions, $n - 1$ selected ancestors may move away from individual k. When their contributions were included, they should not be imputed to individual k. Therefore, all important ancestors in its pedigree are deleted and become pseudo-founders.

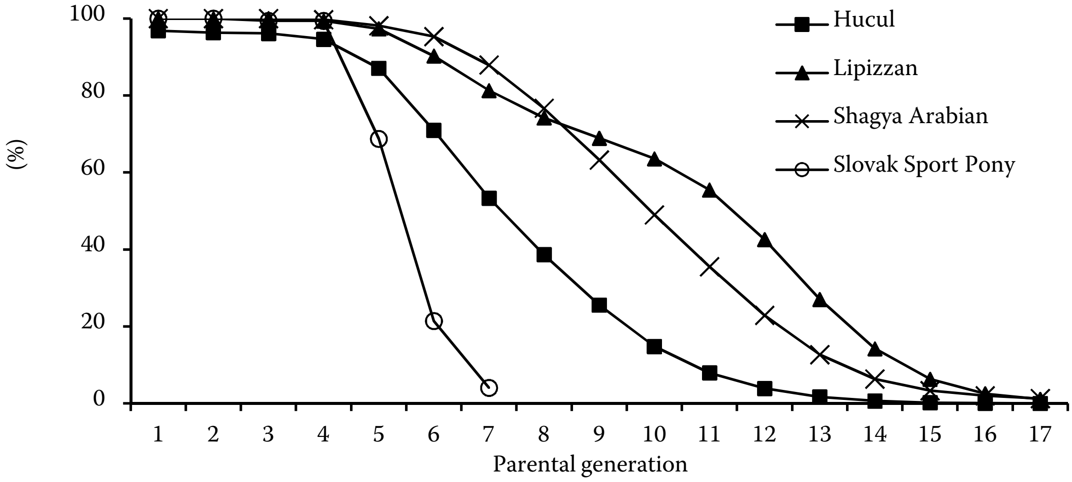

Figure 1. Ratio of known ancestors per parental generation

The above parameters were calculated using the program Endog v.4.8 (Gutiérrez and Goyache, 2005).

RESULTS

Demographic analysis

Figure 1 and Table 2 show the pedigree completeness. Except for the Hucul and the Slovak Sport Pony, the first 4 generations of pedigrees are virtually complete in the Lipizzan and Shagya Arabian and from then differences among the breeds increase. Proportion of the known ancestors dropped to less than 50% after 11 generations in the Lipizzan, 10 in the Shagya Arabian and 7 in the Hucul. The Slovak Sport Pony is a young breed which originated in the year 1982. It is perhaps the reason for the existing gap in the pedigree recording after the 4 generations and the shortening of the pedigrees to the maximum of 7 generations. The most complete pedigrees were found in the Lipizzan and Shagya Arabian. The pedigree data were used to calculate the other pedigree completeness parameters. The average values of the maximum number of genera-

Table 2. Average values of parameters of the pedigree completeness

Parameters		Breed			
		HK (n = 158)	LK (n = 162)	SAK (n = 171)	SSP (n = 42)
Maximum number of traced generations	$\bar{x}$	17.54	24.56	34.82	5.76
	s	1.42	1.17	6.46	0.85
	$x_{\min}$	13.00	22.00	13.00	4.00
	$x_{\max}$	20.00	27.00	42.00	7.00
Number of fully traced generations	$\bar{x}$	4.29	5.90	5.58	4.31
	s	0.85	1.12	0.86	0.60
	$x_{\min}$	1.00	3.00	3.00	2.00
	$\mathrm{x}_{\max}$	6.00	8.00	7.00	5.00
Equivalent complete generations	$\bar{x}$	7.10	10.25	9.56	4.93
	s	0.80	1.68	1.13	0.63
	$x_{\min}$	4.30	5.05	6.07	3.84
	$x_{\max}$	8.93	12.52	11.40	6.28

Table 3. Generation intervals in the studied populations of horses

Parameter		Breed			
		HK	LK	SAK	SSP
Generation interval	$\bar{x}$	11.14	11.61	12.27	9.96
	s	5.18	5.24	5.53	4.43

tions traced ranged from 5.76 for the Slovak Sport Pony to 34.82 for the Shagya Arabian, the number of fully traced generations was from 4.29 to 5.9 and the equivalent complete generations of ancestors ranged from 4.93 for the Slovak Sport Pony to 10.25 for the Lipizzan. The pedigree information was used to calculate parameters related to genetic variability.

Generation intervals in horses are long. The average age of parents at the birth of offspring kept for reproduction made from 9.96 years for the Slovak Sport Pony to 12.27 years for the Shagya Arabian. The average generation interval for the Hucul was 11.14 years and for the Lipizzan it was 11.61 years. More information on the generation intervals is given in Table 3.

Inbreeding and effective size of population

The average value of inbreeding was calculated and it ranged from 2.67% for the Slovak Sport Pony to 6.26% for the Hucul. For the Lipizzan and Shagya Arabian it was 4.02% and 3.95%, respectively. The lowest average individual increase in inbreeding was recorded for the assessed population of the Lipizzan, having a value of ΔF_i = 0.43%, the highest average value of ΔF_i = 1.06% was calculated in the population of the Hucul. Values ΔF_i were used to estimate effective size of the population. The coefficient of average relatedness had the highest values in the populations of the Hucul (9.34%) and the Slovak Sport Pony (7.19%). In these two breeds, the average AR values were higher than F_i and in the next generation inbreeding increase can be

Table 4. Parameters related to the probability of identity by descent of gene origin

Parameters		Breed			
		HK	LK	SAK	SSP
Individual inbreeding coefficient (F_i)	$\bar{x}$	6.26	4.02	3.95	2.67
	s	3.56	2.54	2.78	4.03
	$x_{\min}$	0.00	0.12	0.01	0.00
	$x_{\max}$	27.67	16.19	11.66	14.93
Average relatedness coefficient (AR)	$\bar{x}$	9.34	3.73	3.08	7.19
	s	1.47	1.10	0.79	0.95
	$x_{\min}$	4.22	0.74	1.00	5.08
	$x_{\max}$	12.31	5.07	4.13	8.85

Table 5. Individual increase of inbreeding and realized population size

Parameters		Breed			
		HK	LK	SAK	SSP
Individual increase of inbreeding (ΔF_i)	$\bar{x}$	1.06	0.43	0.46	0.62
	s	0.62	0.26	0.31	0.93
	$x_{\min}$	0,00	0.02	0.00	0.00
	$x_{\max}$	5,79	1.82	1.38	3.33
Realized population size (N_e)	$\bar{x}$	47.67	117.14	109.80	81.18
	s	4.09	6.46	7.03	13.63

Table 6. Parameters of gene origin

Parameters	Breed			
	HK	LK	SAK	SSP
Number of animals (n)	158	162	171	42
Number of founders (f)	134	428	499	80
Effective number of founders (f_e)	26	94	160	47
Number of ancestors contributing to population	46	82	74	17
Number of ancestors explaining 50% of genetic variability	6	11	7	3
Effective number of ancestors (f_a)	16	32	20	7

expected. More results for these parameters are published in Table 4 and Table 5.

Parameters of gene origin

A summary of genetic variability results based on the parameters related to probability of a gene origin is shown in Table 6. A founder was defined as an animal with no genetic relationship to another individual in the whole pedigree file with the exception of his own offspring, i.e. an animal with unknown parents (Lacy, 1989). The highest number of founders was identified in the Shagya Arabian and Lipizzan populations, in total 499 and 428 individuals, respectively. The populations of the Hucul and Slovak Sport Pony were derived from 134 and 80 founders, respectively. The effective number of founders indicates the loss of genetic diversity caused by unbalanced contributions of the founders. If the founders were used equally in animal breeding, the effective number of founders would equal the actual number of founders.

The genetic variability of the Hucul, Lipizzan, Shagya Arabian and Slovak Sport Pony indicate the unbalanced contributions of 26, 94, 160 and 47 ancestors, respectively, representing the effective number of ancestors. With respect to the loss of genetic variability of the populations caused by unbalanced contributions of ancestors in relative terms, the lowest value of 41.25% was found for the population of the Slovak Sport Pony, while the highest value of 80.6% was found for the Hucul. In the populations of the Lipizzan and Shagya Arabian, the values for the loss of founders were 78.04 and 67.94%, respectively. Another parameter related to the probability of the gene origin is the effective number of ancestors. This parameter evaluates the loss of genetic diversity of an assessed population caused by a bottleneck in a pedigree,

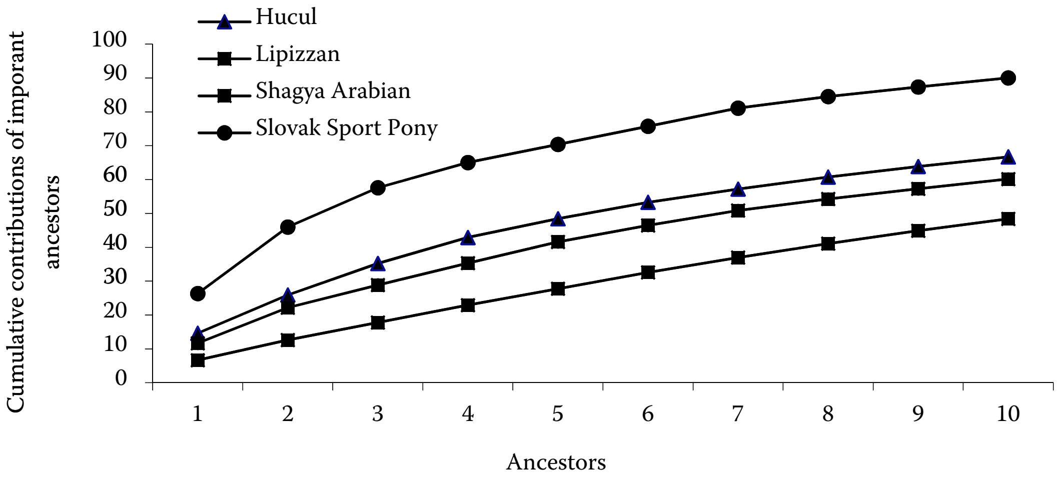

Figure 2. Cumulative contributions (%) to the gene pool of the reference populations

and according to Boichard et al. (1997) this is the minimum number of ancestors to allow a full explanation of the genetic diversity of the population. These ancestors did not have to be founders. The number of ancestors required to explain 100% of the observed genetic diversity of the populations varied from 17 ancestors in the Slovak Sport Pony to 82 ancestors in the Lipizzan. In the Hucul and Shagya Arabian populations, the values for this parameter were 46 and 74 ancestors, respectively. As a result of the bottleneck, the effective number of ancestors was lower than the number of ancestors contributing to the population. From the data presented in Table 6, the number of ancestors explaining 50% of genetic diversity ranged from 3 to 11 ancestors. Figure 2 shows cumulative contributions of the most important ancestors explaining genetic variability in the studied populations. The first ten most important ancestors for the Hucul were born during the years 1895–1979, and these animals came from Slovakia (4), Austria (2), Poland (2), Romania (1) and the Czech Republic (1). The ten most important ancestors explained 66.71% of the genetic variability in the studied population of the Hucul. Other ancestors explained 33.29% of the genetic variability. Figure 2 shows that the marginal contributions of the individuals were unbalanced and that the first three ancestors explained over 35% of the genetic variability of the Hucul population. The Lipizzan population exhibited marginally more balanced ancestral contributions, which was also reflected in the higher number of ancestors, explaining the genetic variability. A less unfavourable situation was observed in the evaluated population of the Shagya Arabian. A different breeding policy characterizing the Slovak Sport Pony is presented in Figure 2, where 50% and 90% of the gene pool was explained by only three and ten ancestors, respectively. The Slovak Sport Pony originates from different breeds that participated in its formation.

DISCUSSION

The level of pedigree information quality affects the average coefficient of inbreeding. The length of pedigrees has an impact on the parameter indicating the effective number of ancestors (Boichard et al., 1997). In the previous study on the populations of eight European Lipizzan breeds, more than 32 generations of ancestors were indicated (Zechner et al., 2002). In the population of the Andalusian breed, Valera et al. (2005) found more than 20 generations of ancestors. Druml et al. (2009) reported a maximum pedigree length (31 generations of ancestors) in the Austrian Norik population. They evaluated 2808 individuals, and the size of pedigree information was 13 035 individuals based on the book of the Austrian Norik but only 4649 individuals had to be supplemented from the original pedigree, which could be the factor causing our results to be lower. In the population of the Hanoverian warm-blooded horses, Hamann and Distl (2008) found more than 23 generations of ancestors. Our results for the Slovak Sport Pony do not correspond with the findings of these authors as within preparing the pedigree file for the fifth generation of ancestors, our work had to be suspended due to the short history of the breed.

The best criterion for assessing the quality of pedigree information is the equivalent number of generations (Maignel et al., 1996). This was used in the calculation of the individual increase of inbreeding and, subsequently, in the estimation of the realized population size. In the Spanish Arabian population born within the years 1995 to 2004 Cervantes et al. (2008b) found 7.9 equivalent generations of ancestors. In 8 studs of the Lipizzan horses, including individuals from the National Stud Farm Topoľčianky (42 individuals), Zechner et al. (2002) indicated 15.2 equivalent generations of ancestors, which is by up to five equivalent generations of ancestors more than was found in our study. They found that the quality of the pedigree information varied according to the study. They proposed to evaluate the pedigree information for more studs to create a dataset of pedigrees more complete and interdependent, which could have a major influence on the higher average value of this parameter. Curik et al. (2003) indicated 15.07 equivalent generations of ancestors for 360 mares of the Lipizzan horses. Álvarez et al. (2010) investigated the population of the Mallorquí horses born within the years 2005–2007 and found 2.4 equivalent generations of ancestors. Cervantes et al. (2008b) found that up to 6 generations were known for over 90% of ancestors in the population of the Spanish Arabian horses born within the years 1995–2004. This was consistent with our results, as we found that 90.56% of ancestors were known up to 6 generations. Zechner et al. (2002) reported that in 10 generations of the Lipizzan population, 90% of the ancestors were known. For the Lipizzan population in Slovakia, 90% of ancestors were known in the sixth generation and 50% in the twelfth generation. In the Andalusian horse population, Valera et al. (2005) found 90% of known ancestors in the fifth generation. From the seventh to the tenth generations, the value of this parameter significantly decreased from 80% to 33% of the known ancestors. After the eleventh generation of ancestors, less than 10% were known. A similar trend was also found in our study in the Hucul, Lipizzan and Shagya Arabian horses.

Generation intervals are also important factors of population management measures. In the population of the Arabian horses in France, Moureaux et al. (1996) found an average generation interval of 10.6 years. In the Andalusian horse population Valera et al. (2005) reported an average generation interval of 11.01 years, while for the Carthusian strain it was 12.43 years. Vostrý et al. (2011) found a value of 8.53 years for the Silesian Norik breed, 8.88 years for the Norik horses and 8.56 years for the Czech-Moravian Belgian horses; these findings correspond to the results of our study.

The average value of inbreeding characterizes a population in terms of changing its genetic structure in favour of homozygotes, thus resulting in a loss of genetic diversity, which may affect the fitness of the population. High levels of the coefficient of inbreeding, the average relatedness coefficient, individual increase of inbreeding and low effective population size values indicate the loss of genetic variability and possible phenotypic expression of genetic defects. Our results for the Shagya Arabian were similar to those found in the French population (Moureaux et al., 1996) and the Polish population of the Arabian horse (Głażewska and Jezierski, 2004), which is related to the similar quality of pedigree information employed. However, Zechner et al. (2002), Curik et al. (2003), Valera et al. (2005), and Cervantes et al. (2008b) recorded lower values in the populations they evaluated, which could be due to a lower level of pedigree completeness. This finding was also confirmed in a study by Curik et al. (2003), who found an average value of inbreeding of 10.13%, with 15.07 known equivalent generations of ancestors in Lipizzan mares. As only 10.57 of equivalent generations of ancestors were found, the average value of inbreeding was only 5.78%. These investigators found a highly significant correlation between high inbreeding, as calculated from all available pedigree information, and five generations of pedigrees. In our study, the equivalent number of generations of ancestors in the Lipizzan population was 10.25. The average value of the coefficient of inbreeding was 4.02% based on the pedigree information. The lower value of the average coefficient of inbreeding may be due to the fact that for the most important ancestors explaining the genetic diversity, their marginal contributions are not homogeneous. In the next generation, the average value of inbreeding is expected to grow mainly in the Hucul and Slovak Sport Pony due to higher values of average coancestry coefficient. Parland et al. (2007) explained the lower average value of inbreeding found in populations of Irish dairy and meat cattle by the import of genetic material into Ireland. Migration can be a significant factor lowering the level of inbreeding coefficient, especially in the populations of the Shagya Arabian and the Lipizzan. A different situation was found in Mallorquí horses, where the average value of inbreeding was found to be 4.7%, and in the equivalent generations it was 2.4%. In Czech populations of the cold-blooded Norik, Silesian Norik and Czech-Moravian Belgian horses, Vostrý et al. (2011) found average values of inbreeding of 1.51, 3.23 and 3.53%, respectively.

The parameter of the effective population size is one of the most sensitive parameters, depending on the quality of pedigree information (Boichard et al., 1997; Zechner et al., 2002; Goyache et al., 2003). The Slovak Sport Pony presented a larger realized size than the actual population size. According to the definition of effective population size, it is evident that this size can never exceed the real size because it represents the conversion of a number of unrelated individuals in a randomly mating population, which it is in reality. The calculation of the realized effective size is limited by the number of complete generations. Gutiérrez et al. (2009) recommend a minimum of two full generations before giving the individuals the opportunity to be inbred. There are three main factors that may be obtained by calculating the effective population size and that may have caused unexpected results in the present study. The first factor is a small number of generations of ancestors that was available for calculating the intensity of inbreeding. A missing parent was considered a founder. Additionally, foreign imported individuals may have been present in the population, therefore interdependency would arise only after many generations. The effective population size calculated through the increase of inbreeding is dependent on the individual inbreeding coefficient. For the Austrian Norik horses, Druml et al. (2009) indicated an effective population size of 157.4. The actual population size was 2808 individuals. The average value of inbreeding was 5%. However, when the effective population size was computed by studs, it made from 137 to 194.5 individuals. The average value of inbreeding ranged from 4.5% to 5%. For example, the effective population size of 130.4 individuals was calculated in Vorarlberg studs. Negative values of the effective population size were discussed by Boichard et al. (1997), Zechner et al. (2002), and Cervantes et al. (2008b). Vostrý et al. (2011) indicated the effective population size of 86.3 for the Silesian Norik, 162.3 for the Norik and 104.4 for the Czech-Moravian Belgian horses; the average inbreeding increase was 1.22, 0.35 and 1.01%, respectively. Cervantes et al. (2010) presented a method for estimating the effective population size through the increase of coancestry. The method employed the calculation of the equivalent number of generations of parents and their ancestry, as well as the calculation of all possible mating combinations of individuals in the reference population. Parameters related to the probability of a gene origin detected recent significant changes in breeding strategies before the sequence of increasing inbreeding can be uncovered. Only a small number of ancestors were needed to explain half of the genetic variability in the studied populations. Thus, it is likely that these groups will produce half sibs, which will mate, and subsequent generations of descendants will increase the average value of inbreeding. The use of these parameters is important when the breeding strategy encourages the population gene pool (genetic program management) and where a small population exists when reviewing the selection of animals. The decrease of genetic variability assessed through parameters related to the probability of the gene origin is reflected in lower values as concerns effective number of founders and effective number of ancestors. An offspring population with unequal representation of the fundamental founders will exhibit less genetic variation due to the reduction of heterozygosity and allelic variation than a population with the same founders in which the founders made equal contributions to future generations. Moureaux et al. (1996) evaluated 860 Arabian thoroughbreds born in 1992 in France, and their results indicated 962 founders and the effective number of founders of 135. The loss of genetic diversity due to unequal contributions of founders was 86% in relative terms. Głażewska and Jezierski (2004) reported that the thoroughbred Arabian population of horses in Poland born within the years 1993 to 1997 was derived from 203 founders. Kwiecińska and Purzyc (2009) indicated that the population of the Hucul in Poland with individuals born in the years 1999–2003 originated from 112 founders, which is similar to the results of our stock assessment, indicating the origin from 134 founders. For 6240 individuals, Cervantes et al. (2008b) listed 860 founders and the effective number of founders of 39.5, explaining the present total genetic diversity based on 13 effective ancestors. Zechner et al. (2002) reported from 39.3 to 55.2 founders in the eight Lipizzan studs. For the population of the Lipizzan horses, our results indicated 428 founders. Compared with the results of Zechner et al. (2002), our values were much higher, which may be due to the lower level of pedigree information available for creating the pedigree file. This is also reflected in lower values of inbreeding and a larger realized effective size. In accord with Zechner et al. (2002), reduction in genetic diversity was caused by an unbalanced contribution of founders. To explain all the genetic diversity of the eight Lipizzan populations, the effective number of ancestors of 26.2 was required. In the population of the Lipizzan bred in Slovakia, 32 effective ancestors explained 100% of the genetic variability. The Norik population in Austria was derived from 1991 founders. Unequal contributions of founders to the population study indicated an effective number of founders of 157.4. For explanation of 100% of the genetic diversity, the effective number of ancestors of 29.3 was required (Druml et al., 2009).

CONCLUSION

The pedigree information on the endangered Hucul, Lipizzan, Shagya Arabian and Slovak Sport Pony breeds was analysed to estimate genetic diversity using parameters on probability of identity by descent and gene origin. Higher concentration of gene origin was found in the Lipizzan and Shagya Arabian populations. Higher values of relatedness coefficients in the Hucul and Small Sport Pony will reflect improvement of inbreeding coefficient in the next generation. In spite of breeders' efforts to manage breeds to minimize inbreeding, improvement of the monitoring system would be useful. To maintain the genetic diversity, use of stallions with optimal contributions for mating will be proposed for the genetic management of breeds.

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