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Evaluation of Genetic Variability of the Breed Norik of Muran according to Pedigree Information

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ABSTRACT

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The Norik of Muran, a unique draught horse bred in Slovakia, belongs to country's biodiversity treasures. The genetic diversity of this horse type was evaluated on the basis of indicators derived from the common ancestry and the probability of gene origin. The pedigree file of the analyzed horses involved 115 individuals (15 stallions and 100 mares). The number of complete generations was 4.49 on average. The maximum number of ancestor generations at the examined population of living horses was 5.38 and the equivalent number in the generation of ancestors was 5.14. The highest average length of the generation interval was 10.97 years in the father–son direction compared to father–daughter (9.74), mother–son (10.87), and mother–daughter (8.99 years – the lowest average length). The generation interval overall average length was 10.14 years. The total coefficient of relatedness was 1.72% on average. The efficient number of core ancestors evenly used in breeding in comparison with the core ancestors mildly decreased to 198. Therefore the Austrian Norik incorporation in the breeding program is the opportunity how to maintain genetic diversity.

Keywords: draught horse; interbreeding; local breed; gene origin

Genetic diversity orientation targeted at the international level is one of the cardinal aspects of biodiversity preservation of traditional breeds (Georgescu and Costache 2012). The Norik of Muran ranks among the traditional horse breeds in Slovakia thanks to its excellent qualities, high cultural and historical value. The Norik of Muran is a unique coldblood horse bred from original cold-blooded mares of different genetic background that were bred by Norik stud horses. The specific physiognomy making this breed unique is associated with demanding natural conditions moulding this breed. The pedigree book of this breed is closed, which means that in the Norik of Muran breeding only Norik horses may be used. And thus, the use of the Norik of Austria in the pedigree program enables to sustain genetic diversity.

In the breeding process of any breed, of small population size in particular, the genetic variability evaluation serves as a key indicator. To achieve the complex evaluation and minimize the inbreeding depression, the pedigree examination of individuals is crucial.

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From the viewpoint of genetic diversity preservation within the endangered populations the pedigree analyses are essential. They facilitate the breeding development and minimize inbreeding. The genetic analysis provides valuable insight into the genetic conditions of the contemporary population and it can also be beneficial for the comparative analysis with other breeds (Thomson et al. 2010). In general, a population's genetic diversity decrease could result in the loss of breed's adaptability and survival. High average values of inbreeding intensity, the accrual of generations approaching the value of 1%, and also high relatedness and small relative effective population size indicate the necessity to monitor the population from the direct proceeding mating of the animal in the breeding core (Kadlecik et al. 2012). More detailed genetic diversity studies in horse breeds are mostly based on the analysis of microsatellite markers (Petersen et al. 2013).

The aim of the work was to evaluate the genetic diversity of the Norik of Muran horses breeding core based on the indicators deduced from the common ancestors and based on the probability of gene origin.

MATERIAL AND METHODS

The genetic variability evaluation of the Norik of Muran breed draught horses was based on the pedigree information on the animals enrolled in breeding on the stud farm Dobšiná from 1955 to 2015. The pedigree group was formed by 115 animals (15 stallions and 100 mares). All the individuals complied with the criteria of the stud book. Each horse was characterized by the unique equine life number, mare's number and father's number, the date of birth, sex and generation. The completeness of pedigrees was expressed by the indicators calculated for each animal in the following way: (1) the number of complete generations of ancestors; (2) the maximal number of detected generations of ancestors; we used two types of indicators to evaluate genetic variability of the population based on the indicators deduced from the common ancestor (1–4) and the indicators of the gene origin probability (5–6); (3) the coefficient of inbreeding (F_i) defined as the probability that an individual has two identical alleles from one common ancestor (Wright 1931), calculated according to the algorithm of Mewissen and Luo (1992); (4) the individual increase of inbreeding for each animal (ΔFi) calculated according to Gutierrez et al. (2008); (5) the realized effective number of population calculated from the coancestry increase (Cervantez et al. 2011); (6) the average relatedness coefficient (AR) (Gutierrez et al. 2003); (7) the effective number of founders (f_e) defined as the number of equally contributing founders, which will produce the same genetic diversity as in the evaluated population (Lacy 1989); (8) the effective number of ancestors (f_a) defined as the minimal number of ancestors necessary for the explanation of the whole genetic diversity of the evaluated population (Boichard et al. 1997); (9) the generation interval (L) involving four real ways of gene transfer: from father to son (L_{mm}), from father to daughter (L_{mf}), from mother to son (L_{fm}), and from mother to daughter (L_{ff}) (Nomura et al. 2001).

All indicators were calculated by the program Endog 4.8 (Gutierrez and Goyache 2005) for monitoring the genetic variability in a population by using the pedigree information.

RESULTS AND DISCUSSION

Based on the total number of the detected generations of ancestors we analysed the completeness of pedigrees of the monitored Norik of Muran population. We evaluated the number of complete generations of ancestors and equivalent number of generations of ancestors (Table 1).

The results of analysis prove that the number of complete generations varied in the range from 3 to 6 generations, where the average value of the monitored indicator was at the level of 4.49 generations. The Norik of Muran breeding is at a low level according to the analysis of the maximal number of the detected generations of ancestors. The maximal number of generations of ancestors in the monitored population of living individuals was at the level of 5.38 and the equivalent number of generations of ancestors was 5.14. Zechner et al. (2002) determined the maximal number of detected generations of ancestors in Lippizan horses in Europe (32) and the equivalent number of generations of ancestors (15.2), which demonstrates a long-time breeding tradition. This tradition is missing in the Norik of Muran breeding. Vostra-Vydrova et al. (2016) analysed the genetic diver-

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Table 1. Completeness of the Norik of Muran pedigrees

Basic variance – statistical values	Indicators		
	maximal number of detected generations of ancestors	number of complete generations of ancestors	equivalent number of generations of ancestors
$\bar{x}$	5.38	4.49	5.14
SD	1.01	0.67	0.76
$\bar{x}_{min}$	3	3	4.05
$\bar{x}_{max}$	7	6	6.78

$\bar{x}$ = average, SD = standard deviation, $\bar{x}_{min}$ = average minimum, $\bar{x}_{max}$ = average maximum

sity in three draught horse breeds and based on the pedigree information they found out that the numbers of generations were 22 for the Silesian Noriker (SN), 32 for the Noriker (N), and 32 for the Czech-Moravian Belgian (CMB) breeds, with average equivalent known generations of 9.81, 8.45, and 8.91, respectively. The genetic variability of five horse breeds in France was analysed by Moureaux et al. (1996). They found out the complete pedigrees to the level of the fifth generation and detected less than 80% of ancestors from the sixth generation. In the seventh generation it was less than 50% of ancestors, apart from the Arab full blood.

In the breeding process of the Norik of Muran, the Austrian Noriker has been used in recent decades. For the Austrian Noriker population Druml et al. (2009) stated the maximum of 31 detected generations of ancestors and the equivalent of complete generations of ancestors 12.3. Therefore the use of the Norik of Muran is very effective, however, it must be genetically controlled.

The variability of the evaluated population from the genetic aspect is expressed by the generation interval. The parents transfer their genes in four ways. The length of the generation interval in the Norik of Muran population monitored is given in Table 2.

The average length of generation interval in the direction father–son was the highest and its value was 10.97 years. The length of generation interval father–daughter achieved 9.74 years. A little bit higher value was for the generation interval mother–son (10.87 years). The lowest average value 8.99 years was determined in the generation interval mother–daughter. The total average length of generation interval in the Norik of Muran horse population was 10.14 years. Similar values were also stated by Halo et al. (2011) who monitored the gene reserve of horses, in particular of the Nonius breed, and the generation interval in the monitored population was 12 years on average.

In the monitored population of horses the average values of generation interval between parents and descendants were detected by Capkova et al. (2010) – 8.53 years for SN, 8.88 for N, and 8.56 for CMB horse. Similar values were also stated by Druml et al. (2009) for the Austrian Norik (L = 7.9) and by Poncet et al. (2006) for the Franches-Montagnes breed (L = 8.4). Higher values were determined by Valera et al. (2005) in the breeding of Carthusian horses. Horses achieve a longer generation interval in comparison with other farm animals.

In small populations of horses, targeted at the breed preservation, long generation intervals are advantageous in order to minimize the increase of inbreeding. On the other hand, the increase of the generation interval should lead to a better examination of low number of stallions and mares

Table 2. Length of the generation interval (GI) (in years) in the Norik of Muran population

Basic variance – statistical values	Indicators				
	GI father–son	GI father–daughter	GI mother–son	GI mother–daughter	total GI
$\bar{x}$	10.97	9.74	10.87	8.99	10.14
SD	4.56	4.74	5.87	5.11	5.16
SEM	1.87	1.58	1.96	1.71	0.48
n	8	50	7	50	115

$\bar{x}$ = average, SD = standard deviation, SEM = standard error of the means, n = number of individuals

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Table 3. Indicators deduced from a common ancestor

Basic variance – statistical values	Indicators			
	coefficient of inbreeding (F, %)	average relatedness coefficient (AR, %)	average individual increase of inbreeding (%)	realized effective number of population (N_e)
$\bar{x}$	1.12	1.72	0.21	199.23
SD	1.81	0.55	0.45	22.54
$\bar{x}_{min}$	0	0.48	0	–
$\bar{x}_{max}$	7.92	2.82	2.04	–

$\bar{x}$ = average, SD = standard deviation, $\bar{x}_{min}$ = average minimum, $\bar{x}_{max}$ = average maximum

(Hamann and Distl 2008). Capkova et al. (2010) claim that lengthening of CMB horse generation interval would not be enough for the examination of the low number of individuals of this breed. However, significantly higher values were recorded for the Thoroughbred (L = 11.2 for stallions and L = 9.7 for mares) (Thiruvenkadan et al. 2009).

Coldblood horses have usually a shorter generation interval because they do not have to undergo as long dressage training as warmblood horses. A higher value of the generation interval for warmblood horses is related to the aspect of later integration of horses into the reproductive process and also longer use in the sport testing. Hamann and Distl (2008) evaluated the generation interval for the Hannoverian horses and they found out that for father–son it was 11.1, father–daughter 8.9, mother–son 10.7, and mother–daughter 9.3 years. The average generation interval in these ways of gene transfer was 10 years. For Arab horses the generation interval was at the level of 10.1–12 years (Cervantes et al. 2009), for Trakehn horses 10.2 years (Teegen et al. 2009), and for the French Saddle horses 9.7–11.8 years (Moureaux et al. 1996).

We consider the value of the generation interval in the population Norik of Muran to be standard as the generation interval for horses fluctuates between 8–12 years.

In the horse breeding the method of inbreeding is most frequently used compared to other farm animals. Especially in small populations inbreeding is more intensively used.

In the population of the draught horses Norik of Muran the values of relatedness coefficient varied from 0.86 to 2.59%, with the average of 1.72% (Table 3).

In two monitored endangered horse breeds in Slovakia Pjontek et al. (2012) reported higher average values of inbreeding (2.67% for Slovak Sport Pony, 6.26% for Hucul Horse). Contrarily, in the whole reference population (133 individuals) of the Thoroughbred in Slovakia the average inbreeding coefficient levelled just 0.86% (Pavlik et al. 2014). Next, we calculated the inbreeding coefficient which expresses the level of homozygosity in individuals in comparison with the parental generation. The average value of this indicator was 1.12% and it varied from 0 to 7.13%. The average individual acquisition of inbreeding achieved the level of 0.21%.

Higher values of the inbreeding coefficient for the reference horse population of the breed Black Forest were determined by Muller-Unterberg et al. (2013) – at the level of 9.12%. Zechner et al. (2002) reported the coefficient of inbreeding at Spanish breeds at the level of 11%. At Arab horses bred in Spain the coefficient was estimated at 7% (Cervantes et al. 2011). The high coefficient of inbreeding in populations of these horse breeds indicates the loss of genetic variability.

In our study, the stallions and mares from their reference populations had lower inbreeding coefficients (8.15–8.95%) and the average rate of inbreeding in the reference population was 2.18%. We found out that the effective number of population achieved 199.23 individuals.

Table 4. Probability of gene origins in the Norik of Muran population

Indicators	
Number of individuals (*n*)	115
Number of founders (f)	238
Effective number of founders (f_e)	198
Number of founders contributing to population	51
Effective number of ancestors (f_a)	32
Number of founders explaining 50% of genetic diversity	19

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The indicators of probability of gene origin showing that the evaluated population of 115 living individuals originated from 238 core founders are given in Table 4.

According to our study the effective number of ancestors (f_a) in the evaluated population of the Norik of Muran was at the level of 32. Similarly, Muller-Unterberg et al. (2013) evaluating the genetic population of the horse breed Black Forest specified the effective number of ancestors (f_a) at the level of 33.6. The rate between the number of effective founders and the number of effective ancestors was 2.9 for the reference population, 3.0 for the population of stallions, and 2.8 for mares. The ratio of genes of Black Forest breed in the reference population was 60% and the ratio of genes of Norik in the reference population Black Forest was 4%.

Generally, the decrease of population genetic diversity could result in the loss of breed adaptability and survival. Therefore, it is important to preserve the genetic diversity in the horse population in order to create more appropriate programs for maintaining of breeds (Cothran et al. 2005).

From the aspect of genetic diversity the effective number of core founders currently equally used in breeding is 198 individuals. Pjontek et al. (2012) identified the highest number of founders in the Shagya Arabian and Lipizzan populations (499 and 428 individuals, respectively). The populations of the Huzzul and the 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 value of this indicator is lower than the number of the core founders showing that in the process of development of this breed a slight decrease of genetic diversity was recorded.

The evaluation of gene origin probability showed that the effective number of founders out of 100% of the genetic diversity of the evaluated population is 32 founders, and out of 50% of the genetic diversity in the population Norik of Muran in Slovakia it is 19 individuals.

CONCLUSION

Sustainability of biodiversity requires deep knowledge of basic genetic parameters and overall structure of population. Particularly, in breeds of small population size, sustainability of genetic diversity is very demanding. From the pedigree analysis of the draught horse Norik of Muran we can state that the population of this young breed, in spite of different ancestors, is steady and the level of genetic diversity is not threatened at the moment. The use of Austrian Norik is a genetic contribution regarding their common ancestry but it should be controlled so as not to reduce the typical qualities of the Norik of Muran given by the environment of its origin.

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