

DIVERSITY OF CATTLE BREEDS IN SLOVAKIA

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ABSTRACT

The aim of the study was to assess the diversity based on the pedigree information in three cattle breeds. The pedigree information was available from The Breeding Services of the Slovak Republic, s. e. The pedigree analyzed populations consisted of (reference populations in brackets) 274,756 (94,357) Holstein, 109,686 (36,949) Slovak Spotted and 9,756 (2,501) Slovak Pinzgau cattle. Indices of pedigrees completeness differed by breeds but in the 5th generations their values were 18.4 % in Slovak Pinzgau, 56 % in Slovak Spotted breed and 63.8 % in Holstein. Generation interval of Slovak Pinzgau was 7.2 years, tending to be shorter as the size of breed population was bigger. There were 30 % inbred Slovak Pinzgau, 42.8 % in Slovak Spotted and 83 % in Holstein cows and sires in the reference populations. The average inbreeding coefficient ranged from 0.36 % for the Slovak Spotted to 1.32 % for the Holstein. The highest average individual increase of inbreeding $\Delta F_i = 0.29$ % was found for the Holstein and the average individual relatedness coefficient $AR = 0.8$ % in Slovak Spotted cattle. Inbreeding trends in the reference populations as well as purebred animals were positive with increasing average values by animal birth years since 1990.

Key words: cattle; diversity; pedigree analysis; relatedness; inbreeding

INTRODUCTION

Breeding of Slovak Pinzgau and Slovak Spotted dual purpose breeds has a long tradition in Slovakia. The first imports of Pinzgau and Simmental purebred animals were organized long time ago before 1894 when system of cattle recording has started on territory of Slovakia. The size of both breeds was improving and in 1958 they were officially accepted as Slovak Pinzgau (P) and Slovak Spotted (S) breeds. Further breed development was positive from the point of population size and production. Purebred Slovak Spotted breed reach a maximum population size in 1975, Slovak Pinzgau in 1978. After 1990 size of both breeds has decreased significantly due to transformation processes in agriculture and exploitation of Holstein sires for crossbreeding. Today, Slovak Pinzgau is endangered breed. Imports of Holstein to Slovakia started about 1970 and since 1992 breed is managed under Slovak Holstein Association. All three breeds passed through

many changes that modified sizes of their populations, structure and breeding strategies over the last 25 years. Therefore, these populations are not under steady-state conditions and the possible consequences were not yet observed. One possibility to describe diversity and its evolution across generations is analysis of pedigree information. Genetic variability of populations and similarity of subpopulations in Austrian cattle breeds determined by analysis of pedigrees was described by Soelkner *et al.* (1998). Roughsedge *et al.* (1999) quantified genetic contributions to a dairy cattle population using pedigree analysis. Gutiérrez *et al.* (2003) analyzed herdbooks in order to know gene flow, population structure and potential danger for genetic diversity loss of eight Spanish local beef cattle breeds. Pedigree information for analysis of diversity in cattle populations was used also by Bartolomé *et al.* (2010) and Kadlečík and Pavlík (2012).

The objective of this study was to assess diversity of three cattle breeds basing on pedigree information.

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Diversity was analyzed in terms of the parameters of the probability of identity by descent.

MATERIAL AND METHODS

Three breeds were involved in the analysis: Holstein (H), Slovak Spotted (S) and Slovak Pinzgau (P). Both breeds, Slovak Spotted and Pinzgau are dual purpose types. Pedigree data registered by The Breeding Services of the Slovak Republic, s. e. were assumed to be representative of the whole (pedigree) population under milk recording system. The results of the reference population (RP) were independently analyzed and compared with purebred animals (H₀, S₀, P₀). The pedigree populations consisted of 274756 Holstein, 109686 Slovak Spotted and 9756 Slovak Pinzgau cattle. Reference population created cows living in 2009 and sires in insemination with frozen genetic material deposited in AI centres in Slovakia. The number of animals by breeds in reference and purebred groups is presented in Table 1. Parameters of diversity in three breeds were estimated using Endog v. 4.8 (Gutiérrez and Goyache, 2009).

Quality of pedigree information was estimated according to the index of pedigree completeness (PEC) (MacCluer *et al.*, 1983), calculated as follows:

$2 C_{sire} C_{dam} / C_{sire} + C_{dam}$, where C_{sire} and C_{dam} are contributions from the paternal and maternal lines.

$C = \frac{1}{d} \sum_{i=1}^d g_i$, where g_i is the proportion of known ancestors in generation i ; and d is the number of generations that are taken into account (Gutiérrez *et al.*, 2009). Generation intervals were defined as average age of parents at the birth of their offspring (either used for reproduction or not).

Diversity of breeds was evaluated by the parameters based on probability of identity by descent. The individual coefficient of inbreeding (F_i) reflects the probability that two individuals received two identical

alleles by descent (Gutiérrez *et al.*, 2009). Inbreeding coefficient value was computed according to algorithm of Meuwissen and Luo (1992). The average relatedness (AR) reflects the probability that an allele randomly chosen from the whole population in pedigree belongs to a given animal (Gutiérrez *et al.*, 2009). The individual increase in inbreeding (ΔF_i) was calculated by means of the classical formula $\Delta F_i = 1 - t^{-1} \sqrt{1 - F_i}$ where F_i is individual coefficient of inbreeding and t is the equivalent complete generation (Gutiérrez *et al.*, 2009). Effective population size (N_e) was defined as the number of breeding animals that would lead to actual increase in inbreeding if they contributed equally to the next generation (Gutiérrez *et al.*, 2009).

RESULTS AND DISCUSSION

Unbalanced development of three analyzed cattle breeds led to changes in population size and structure. Massive exploitation of Holstein sires for crossbreeding with Slovak Spotted but mainly Slovak Pinzgau cows led to decreasing of both breed population sizes. It was the reason that sizes of analyzed reference populations were different as well as number of purebred animals within each breed. Number of animals in reference and purebred populations within the breeds is presented in Table 1.

An independent analysis of pedigree completeness level of the breeds is important since all results in terms of parameters based on identity by descent and probability of gene origin are dependent on it. The percentages of parents and the other generations of ancestors including founders known are shown in Figure 1. The breed with the highest pedigree completeness was Holstein followed by Slovak Spotted and Slovak Pinzgau. Quality of pedigrees was higher in breed with large population size. This evaluation was based on index of pedigree completeness, namely the

Table 1: Description of analyzed breeds

Breed		n	% of inbred animals
Holstein	RP	94357	82.58
	H ₀	37657	95.52
Slovak Spotted	RP	36949	42.77
	S ₀	17355	66.76
Slovak Pinzgau	RP	2501	29.99
	P ₀	1184	48.40

description of the completeness of each ancestor in the pedigree to the 5th parental generation (MacCluer *et al.*, 2012). Completeness of pedigrees was higher mainly in Holstein and Slovak Spotted compared with results of Baumung and Sölkner (2002) in Pinzgau, Tux-Zillertal and Carinthian Blond breeds and Maignel *et al.* (1996) in

French dairy breeds. Nevertheless, pedigrees of breeds under study should be considered as incomplete because in the 5th generations indices values were only 18.4 % for Slovak Pinzgau, 56 % for Slovak spotted breed and 63.8 % for Holstein.

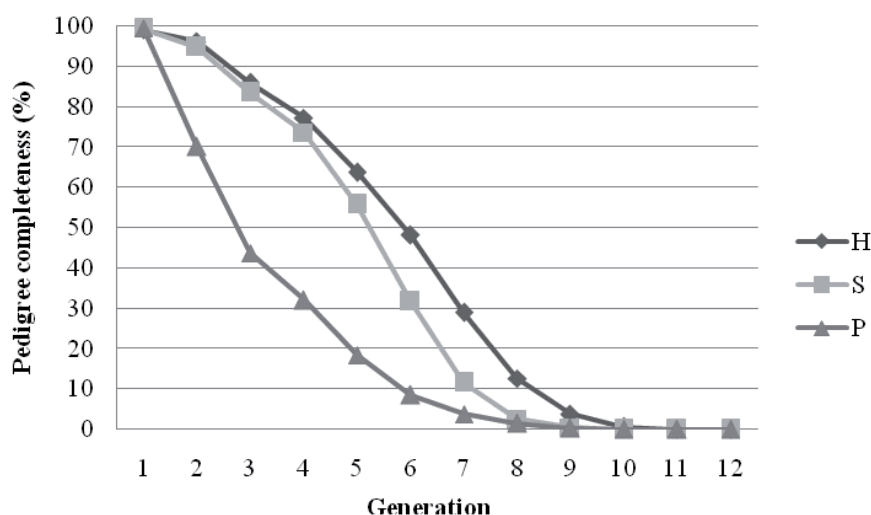


Fig. 1: Pedigree completeness in reference populations

Table 2 reports the average length of generation intervals for the three breeds and purebred animals calculated for all offspring. Generation intervals ranged from 5.7 to 7.2 years in reference populations, tending to be shorter as the population size was larger. Generation intervals of purebred animals were shorter in all analyzed breeds than in reference populations. Generation intervals were longer, as reported by Bozzi *et al.* (2006) in three Italian beef cattle breeds as well as Maignel *et al.* (1996) in French dairy breeds.

The long-term survival of population depends on the maintenance of sufficient genetic variation for individual fitness and population adaptability. Characteristics of diversity derived on probability of identity by descent are presented in Table 3.

The average inbreeding coefficient of a population is often used as a parameter of its homozygosity level. The average coefficient of inbreeding was found to be variable among the evaluated breeds. In Slovak Spotted and Slovak Pinzgau breeds level of inbreeding

Table 2: Generation intervals by breeds

Parameter		H	H ₀	S	S ₀	P	P ₀
Generation interval	n	19356	9051	8401	4811	419	260
	\bar{x}	5.70	5.59	6.90	6.76	7.22	7.01
	s	3.02	2.86	3.26	3.19	3.77	4.08

Table 3: Parameters based on probability of identity-by-descent

Parameter	Holstein		Slovak Spotted		Slovak Pinzgau	
	RP	H ₀	RP	S ₀	RP	P ₀
F in %	1.32	1.79	0.36	0.57	0.38	0.54
AR in %	1.41	1.59	0.80	0.90	0.61	0.74
ΔF_i in %	0.30	0.39	0.09	0.14	0.21	0.29
Realised N_e via ΔF_i	166.00	124.90	526.90	341.70	220.60	168.60

in reference populations was low with inbreeding coefficients under 0.4 % and 3.7-fold lower than level of inbreeding in reference population of Holstein. Inbreeding in purebred animals of all three breeds had higher values of coefficients than in the reference populations of H, S and P breeds. In S and P breeds the other parameters like increase in inbreeding and average kinship were more promising than in Holstein population. Better results in Slovak Spotted and Slovak Pinzgau reference populations were obtained in spite that these breeds have smaller populations, even the percentage of inbred animals in the reference population was smaller (S = 42.77 %, P = 29.99 %). If these results

are related to lower quality of pedigrees, system of genetic management of populations should be studied in the future. Results of Slovak Spotted and Slovak Pinzgau breeds are better than obtained by Baumung and Sölkner (2002) in Pinzgau, Tux-Zillertal and Carinthian Blond breeds and are comparable with some of Spanish beef cattle breeds in values of intensity of inbreeding and Italian beef cattle breeds (Bozzi *et al.*, 2006). In Holstein, Slovak Spotted and Slovak Pinzgau breeds the results of effective population size were better than in mentioned publications. Results of inbreeding in inbred reference and purebred populations are presented in Table 4.

Table 4: Parameters based on probability of identity-by-descent in inbred animals

Parameter	Holstein		Slovak Spotted		Slovak Pinzgau	
	RP	H ₀	RP	S ₀	RP	P ₀
F in %	1.60	1.87	0.85	0.86	1.26	1.12
AR in %	1.53	1.65	0.95	0.97	0.76	0.79
ΔF_i in %	0.36	0.41	0.21	0.21	0.69	0.60

Evolution of inbreeding intensity over year of birth in Holstein, Slovak Spotted, and Slovak Pinzgau breeds in reference and purebred populations is presented in Figures 2 and 3. All three breeds showed an increase in inbreeding by years of animal birth, but only in Holstein reference population (also in purebred animals) increasing of inbreeding over 1 % was recorded (in 2003).

The results of Holstein are the most problematic in comparison with the other two breeds due to very high ratio of inbred animals in reference population (82.58 %, but 95.52 % purebred animals), gain and trend in inbreeding as well as high level of kinship

in the both reference and purebred populations. This breed has large population size but results did not reflect it. Obtained results indicate that Holstein could be considered as genetically small breed. Very similar results were obtained by Maignel *et al.* (1996), who argued results of analyzed French dairy breeds by selection of a very few bull sires and wide spreading of elite germplasm concentrate gene origin on a few families.

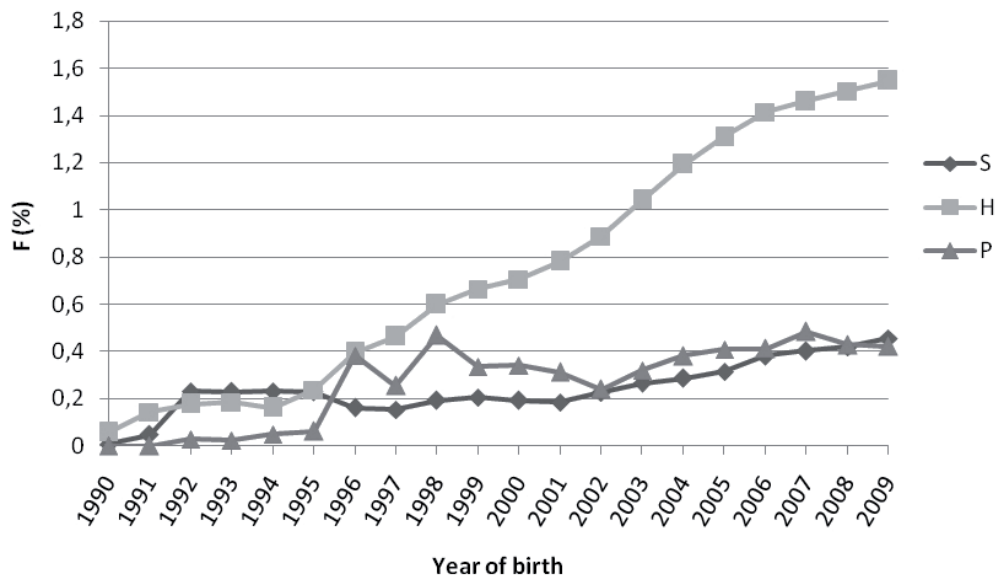


Fig. 2: Trends in inbreeding by reference populations of breeds

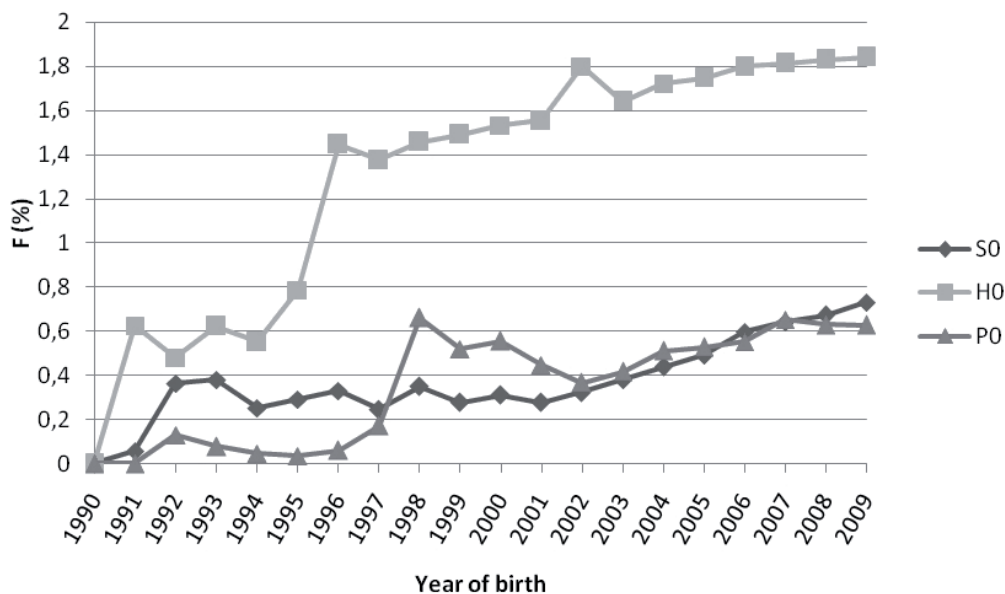


Fig. 3: Trends in inbreeding by purebred populations of breeds

CONCLUSION

Pedigree analysis of Holstein, Slovak Spotted and Slovak Pinzgau breeds based on parameters of identity by descent demonstrates that the genetic status regarding genetic variability differs among breeds. The results of

Holstein are the most unexpected in comparison with the other two evaluated breeds due to very high ratio of inbred animals in reference population (82.58 %, 95.52 % purebred animals), gain and trend in inbreeding as well as high level of kinship in the both reference and purebred populations. This breed has large population

size but results did not reflect it. Obtained results indicate that Holstein could be considered as genetically small breed. Pinzgau breed is endangered due to small size and negative development in population during the last two decades, mainly. The most promising results are noted in Slovak Spotted breed. The causes of these differences can be related to breeding policy of the breeds.

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