Inbreeding and Genetic Diversity Loss in Slovak Pinzgau Breed

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Summary

The objective of the paper was to evaluate trends in inbreeding and genetic diversity loss of Slovak Pinzgau. Genealogic information had good informative value. Inbreeding trends were positive in pedigree as well as reference populations. Intensity of inbreeding and average relationship have not reach the level of 1 % at which inbreeding gains per generation was low in the reference population. Almost the same results were obtained in the population of cows. Sires influenced inbreeding and its gain in reference population less than cows, but higher sires average relationship may create not optimistic prognosis for future sire inbreeding development. Total loss of genetic diversity in sire group was 3.17 % at which this level was more influenced by genetic drift (2.69 %) than bottleneck.

Key words

cattle, genetic diversity loss, inbreeding, Slovak Pinzgau

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Introduction

Traditional breeding programmes lead to genetic gain and higher rates of inbreeding. It is why many attention has been given to evaluation of the inbreeding level in animal populations (Kearney et al., 2004; Stachowicz et al., 2011; Melka et al., 2013; Pavlík et al., 2013), genetic diversity loss (Melka et al., 2012; Hazuchová et al., 2013; Kadlecik et al., 2016) what relate with management of small and endangered populations (Mészáros et al., 2015). The objective of the paper was to evaluate trends in inbreeding and genetic diversity loss of Slovak Pinzgau.

Material and methods

The reference population of Slovak Pinzgau cattle analysis covered living animals, sires in insemination, frozen genetic material deposited in reproduction centres (26 animals) and 2749 Pinzgau cows, altogether 2775 animals. Pedigree population created animal of reference populations and animals in pedigrees of their parents.

Inbreeding trends and genetic diversity loss were estimated from genealogic information of animals using the data obtained from SBS, a.s. of the Slovak Republic. Pedigree completeness, the parameters of diversity based on probability of identity by descent and based on probability of gene origin were estimated by the software Endog v.4.8 (Gutiérrez and Goyache, 2005).

The pedigree completeness have influence on estimated genetic diversity parameters. Pedigree completeness index (PCI) described by MacCluer et al. (1983) was estimated as follows: PCI = $2\,C_{sire}\,C_{dam}\,/\,C_{sire} + C_{dam}$; where C_{sire} and C_{dam} are contributions from the paternal and maternals lines, and $C = \dfrac{1}{d}\sum\limits_{i=1}^{d} g_i$;

where g_i is the proportion of known ancestors in generation i; and d is the number of generations that are taken into account.

Genetic diversity was evaluated according to three parameters based on the probability of the identity by descent and seven measures based on probability of gene origin.

Inbreeding coefficient of an animal (F) was calculated 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 where F_i is individual coefficient of inbreeding and t is the complete equivalent generation (Gutiérrez et al., 2009). The trends of inbreeding, coancestry and inbreeding gain were estimated as F averages on birth years of animals. From parameters based on probability of gene origin was number of founders (f) defined as ancestors with unknown parents, or animals with unknown genetic connections to other animals in pedigrees except its own progenies (Lacy, 1989). The effective number of founders (f_e) was estimated as the number of equally contributing founders that will produce the same genetic diversity as assessed in the population (Boichard et al., 1997), calculated as:

$$f_e = \left[\sum_{k=1}^{f} q_k^2\right]^{-1}$$

q_k is the probability of gene origin of the k ancestor.

The effective number of ancestors (f_a) is the minimal number of ancestors necessary to explain the genetic diversity in the reference population (Boichard et al., 1997), was calculated by formula:

$$f_a = \left[\sum_{j=1}^{a} q_j^k\right]^{-1}$$

q_j is the marginal contribution of an ancestor j which is the genetic contribution made by ancestor that is not explained by other ancestors chosen before. The f_a account for recent bottleneck and thus partially account for the loss of allelic diversity in descendant population (Boichard et al., 1997).

Founder genome equivalents (f_g) expresses the number of founders that would be expected to give the same level of genetic diversity in the population under study if the founders were equally represented and no loss of alleles occurred (Lacy, 1989). The f_g was calculated by the Caballero and Toro (2000) algorithm, as follows:

$$f_g = \left[\sum_{j=1}^{N_f}\left(\frac{p_j^2}{r_j}\right)\right]^{-1}$$

N_f is the number of founders, p_j is the contribution of the founder j and r_j is retention of alleles. The f_g accounts for unequal contributions of founders, bottleneck, and random loss of alleles due to genetic drift (Lacy, 1995). Lower values of the ratio are connected with higher loss of genetic diversity due to genetic drift.

The loss of genetic diversity (GD) was derived from parameters f_e, f_g. Total GD of the reference population was estimated by formula of Lacy (1995):

$$GD = 1 - \frac{1}{2f_g}$$

The genetic diversity loss due to bottlenecks and genetic drift in the population was calculated as 1 – GD. The amount of genetic diversity in the reference population considered for the loss of diversity due to unequal founder contributions (GD*) was calculated as (Lacy, 1995):

$$GD^* = 1 - \frac{1}{2f_e}$$

Similarly, 1 - GD* represented the loss of genetic diversity due to unequal founder contributions. The difference GD* - GD measures the loss of diversity by genetic drift accumulated over nonfounder generations and was calculated by Caballero and Toro (2000).

Results and discussion

The pedigree completeness index is presented in Figure 1. The reference populations had hundred percent completed pedigrees in the 1st generation and had decreasing trend with increasing generations. Melka et al. (2013) evaluated genetic diversity of Guersey population on the average pedigree completeness level PCI = 74 – 97%, Kearny et al. (2004) estimated that 85 % of Holstein animals had in 4 or more generations complete genealogic information.
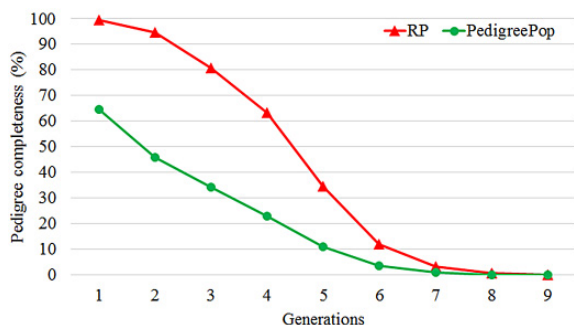
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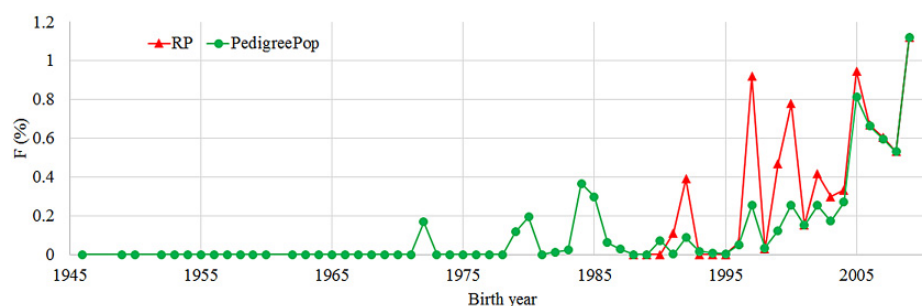**Figure 1.** Pedigree completeness index in reference and pedigree populations

Figure 2. Inbreeding trends

Table 1. Diversity parameters based on probability of identity by descent

Characteristics	RP	Cows	Sires
F	0.55	0.55	0.47
AR	0.85	0.84	0.97
ΔF	0.18	0.18	0.16
% inbred animals	35	35	35

Table 2. Diversity parameters based on gene origin

Characteristics	RP	Cows	Sires
f	4349	4331	177
f_e	341	198	104
f_a	152	72	25
f_g	47	47	16

Table 3. Level and the loss of genetic diversity

Characteristics	RP	Cows	Sires
GD	98.94	98.94	96.83
1-GD	1.06	1.06	3.17
GD*	99.86	99.75	99.52
1-GD*	0.14	0.25	0.48
GD*- GD	0.92	0.81	2.69

Inbreeding trends were positive in pedigree as well as reference populations. In the reference population was trend more intense since 1990 year than in pedigree population (Figure 2). The parameters of diversity based on probability of identity by descent are presented in Table 1. Values of intensity of inbreeding and average relationship have not reach the level of 1 % at which inbreeding gains per generation was low in the reference population, almost the same results were obtained in the population of cows. Sires influenced inbreeding and its gains in reference population less than cows, but higher sires average relationship may create not optimistic prognosis for future sire inbreeding development.

The preservation of founder alleles describing genetic diversity is expressed by the measures based on the probability of gene origin. The overview of these measures is presented in Table 2. Results in reference and cow populations were similar in two parameters. Also levels of genetic diversity were the same, in the cow population was found out slightly higher level of genetic diversity loss due to unequal contributions of founders. Total loss of GD in sire group was 3.17 % at which this level was more influenced by genetic drift (2.69 %) than bottleneck (Table 3). Similar level of genetic diversity loss described Kadlecik et al. (2016) in four beef breeds. The amount of genetic diversity in the reference population accounting for diversity loss due to genetic drift and unequal founder contributions was the highest in the Simental (6.2 %), following the Blonde d´Aquitaine, (3.5 %), Limousine (1.1 %) and Charolais (0.9 %). Genetic drift was identifying as dominant cause of genetic diversity loss in some more Canadian milk breeds of cattle (Melka et al., 2008).

Conclusion

Intensity of inbreeding and average relationship have not reach the level of 1 % in the reference population. Inbreeding trends were positive in pedigree as well as reference populations. Total loss of genetic diversity in sire group was 3.17 % at which this level was more influenced by genetic drift (2.69 %) than bottleneck.

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