

Pedigree Analysis of Slovak Pinzgau Breed

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Summary

The aim of the study was to assess genetic variability in Slovak Pinzgau breed using pedigree analysis. The whole population consisted of 8311 individuals of that 2399 living animals (2373 cows and 26 sires) in the reference population. Pedigree completeness, parameters based on probability of identity by descent and gene origin was analysed. The mean inbreeding level in the reference population was low 0.57%, mean individual increase in inbreeding 0.25% and average relatedness 1.17%. A total 141 effective founders and 51 effective ancestors were found in the reference, resp. 257 effective founders and 103 effective ancestors in the whole population. The number of 21 effective ancestor explained 50% of diversity in the reference and 51 in the whole population. The results demonstrate need for better monitoring of population and can be implemented in preparation of the strategy for development of breed.

Key words

Pinzgau cattle, pedigree analysis, genetic diversity, inbreeding, relatedness, probability of gene origin

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Introduction

Pinzgau cattle are bred in Slovak Republic for more than 150 years. It was imported from region of the Austrian Alps and populations' breeding in Slovakia is from its constitution over connected (Pšenica, 1990). In 1970 re-building of purpose and breed type of cattle started. In this period several breeding bulls were imported, from which 24% were of Pinzgau origin (Pšenica and Tretinová, 1998). From 1970 to 1992 in pedigrees of Pinzgau cattle were introduced seven breeds, almost 50% Pinzgau bulls imported from Austria and 34% from Slovakia. After 1990 considerable decrease of Pinzgau population size was observed in Slovakia. In several papers need for management of genetic resources (Toro et al., 2011) and evaluation of genetic diversity of species and breeds was emphasized. Evaluation was based on pedigree information (Boichard et al., 1997; Sölkner et al., 1998; Baumung and Sölkner, 2002; Gutiérrez et al., 2003). The aim of the publication was to assess the genetic variability of Slovak Pinzgau cattle in terms of parameters of the probability of identity by descent and gene origin. A number of genealogical characteristics in the breed have been obtained.

Material and methods

Pedigree analysis was made in the whole dataset of 8311 individuals of those 2399 living animals (2373 cows and 26 sires) in the reference population. Animals of reference population were born from 1988 to 2008 years. Dataset of cows included purebred animals with less than 6.25% share of foreign breeds as well as Pinzgau crossbreds with more than 6.25% of different breeds. Breeding bulls, excluding one, were purebred. We tend to create dataset with maximum pedigree information, to reach good completeness of pedigrees. Whole dataset presented animals of reference population with all known ancestors and base animals. Pedigree information was obtained from animal recording database of Breeding Services of Slovak republic, Bratislava. For data management software SAS V9.2 was used. Individuals were sorted chronologically. For calculation of evaluation parameters was used software Endog V4.8 for monitoring of genetic variability in populations (Gutiérrez and Goyache, 2005).

Pedigree completeness was evaluated in relation to number of fully traced generations, maximum number of generations, equivalent number of generation (Maignel et al., 1996) and index of completeness by MacCluer et al. (1996).

Genetic diversity was evaluated in relation to two groups of parameters:

- 1) Parameters based on probability of identity by descent
 - The coefficient of inbreeding (F_i), defined as probability, that two individuals receive identical alleles by descent (Gutiérrez et al., 2009).
 - The individual increase in inbreeding of each individual (ΔF_i) calculated as difference of coefficient of inbreeding of individual i and its parents (Kaerney et al., 2004).
 - The coefficient of average relatedness of each individual (AR) as probability, that randomly selected allele from population belongs to particular animal (Gutiérrez et al., 2009).

- 2) Parameters based on probability of gene origin

- The number of founders (f) – founder is animal with unknown genetic connections to other animals in pedigree except its own progeny (Lacy, 1989).
- The effective number of founders, f_e is defined as the number of equally contributing founders that will produce the same genetic diversity as assessed in the population (Boichard et al., 1997).
- The effective number of ancestors is the minimum number of ancestors necessary to explain the genetic diversity in the reference population (Boichard et al., 1997)
- The number of ancestors explaining 50% of genetic diversity.

Results and discussion

Pedigree completeness was analysed in the whole dataset of 8311 individuals of those 7713 cows and 598 sires. The reference population consisted of 2399 individuals of those 2373 were cows and 26 were sires. Pedigree completeness expressed by different parameters has important influence on quality of inbreeding estimation and consequently evaluation of inbreeding depression. This was shown by Cassell et al. (2003), Weigel and Lin (2000). They emphasized need to use more than two ancestor generations on commercial farms in calculations, as well as influence of pedigree completeness of sires on quality of pedigree information.

Pedigree completeness in the reference population was expressed by average value of maximum number of generations traced (5.0), the number of fully traced generation (2.05) and equivalent number of complete generation (3.16). Pedigree completeness in the whole population was lower, maximum number of generations traced was 2.77, the number of fully traced generations was 1.12 and equivalent number of complete generations 1.73. Share of known ancestors in the whole and the reference populations was expressed by index of completeness described by MacCluer et al. (1983) and results are shown in Graph 1. Pedigree completeness was lower than presented by Baumung and Sölkner (2002) and Sölkner et al. (1998) in Austrian Pinzgau cattle. Average pedigree completeness in reference file was 39.47% and in pedigree file was 21.64%.

In Table 1 are presented results of estimated genetic variability parameters. Average coefficient of inbreeding in reference

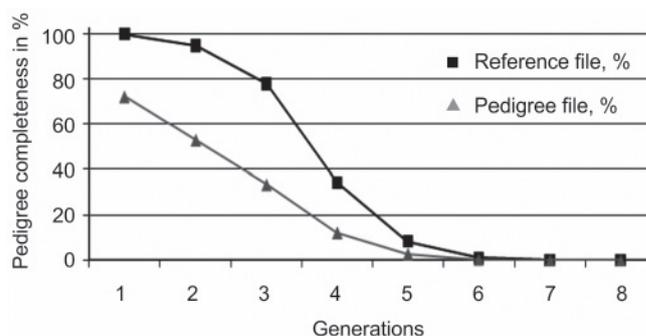


Figure 1. Pedigree completeness

Table 1. Characteristics based on probability of identity by descent

Parameter		Reference population		Whole pedigree population	
		Whole	Inbred animals	Whole	Inbred animals
Inbreeding coefficient	\bar{X}	0.57	5.02	0.22	5.70
(F_i v %)	s	0.27	6.54	1.78	7.09
Average relatedness	\bar{X}	1.17	1.38	0.61	1.36
(AR v %)	s	0.51	0.45	0.63	0.48
Individual increase in inbreeding	\bar{X}	0.25	2.21	0.11	2.81
(ΔF_i v %)	s	1.35	3.42	1.03	4.45

s=standard deviation

population was 0.57%, increase in inbreeding per generation 0.25%, which was more than estimates in pedigree file. Average values of coefficients of relatedness were in reference as well as in whole pedigree population higher than coefficients of inbreeding. These results showed that in the next generation could be expected, that number of inbred individuals will increase in spite effort of farmers to minimize mating of relative animals. In reference population were 11.37% of inbred individuals. Values of parameters of diversity were in group of inbred individuals significantly higher, expressing lower diversity. Increase in inbreeding per generation point on breeding strategy, in particular on selection of parental pairs, which results into higher resp. lower increase in inbreeding. Presented results point on effort of farmers to manage mating of animals to minimize mating of relatives. Lower values of parameters derived from common ancestor could be in relation with lower quality of pedigrees. Our results are comparable with values of relationship and inbreeding estimated in purebred and crossbred population by Sölkner et al. (1998). High values of increase in inbreeding presented Maignel et al. (1996) in France. The highest value was in Tarentaise (1.83%) breed, followed in Holstein (1.09%), Normande (1.07%) and Brown Swiss (0.90%).

Reference population was derived from 2496 founder animals (Table 2). Effective number of founders and effective size of ancestors were computed as described previously. Both parameters considered account for the chance of gene loss, which increases with the number of generations (Boichard et al., 1997). A total of 141 effective founders were found. A difference between number of founders and effective number of founders shows disbalance between founder contributions and excessive utilization of some animals as parents of the next generation. It also accounts for selection rate. The concept of the effective number of ancestors was accepted to account bottleneck. A bottleneck may be not only result of changes in size of population related to political, economical circumstances but can also occur due to a change in breeding goal (Druml et al., 2009). The effective number of ancestors 51 in reference and 103 in the whole populations compared with 25 in Abondance, 40 Normandale breeds (Boichard et al., 1997), 46.7 in Pinzgau (Sölkner et al., 1998) and 32.1 in Original Pinzgau, 14.2 in Tux-Zillertal, 29.0 in Carintian Blond (Baumung and Sölkner, 2002) gives higher values for Slovak Pinzgau breed. The calculation of f_a gives possibility for estimation the most important gene contributions of ancestors. Table 3 shows the marginal proportions of five the most contributing ancestors to the reference Slovak Pinzgau population. Sölkner

et al. (1998) estimated in four breeds of cattle 16 – 55 ancestors explaining 50% of diversity, Bozzi et al. (2006) in three populations 21-37 and in Slovak Pinzgau breed 21 ancestors in reference and 51 in the whole population. Effective number of founders/effective number of ancestors' ratio for the reference population of the Slovak Pinzgau was 2.4 resp. 2.1 for the whole pedigree population. Whereas f_e/f_a ratio was 2.19 in Limousine, 2.76 in Abondance and 3.3 in Normande (Boichard et al., 1997), in the whole Pinzgau population 1.41 (Sölkner et al., 1998) and Original Pinzgau 2.03 (Baumung and Sölkner, 2002). According to authors these results illustrate the narrower bottleneck in popula-

Table 2. Results of pedigree analysis

Parameter	Reference population	Whole population
Number of founders (f)	2496	2501
Effective number of founders (f_e)	141	257
Effective number of ancestors (f_a)	51	103
Number of ancestors explaining 50% diversity	21	51

Table 3. The most important ancestors contributing to the reference population from the whole pedigree population

Ancestor	Contributions (%)
First	3.69
Second	3.48
Third	3.41
Fourth	3.34
Fifth	3.20

tion due to fact that only limited number of sire was preferred for reproduction because of insemination used.

Conclusion

The analysis of Slovak Pinzgau population identifies the specific characteristics based on probability of identity by descent and gene origin. Level of inbreeding and its individual increase per generation are small in population but higher value of average relatedness indicates possible increasing of inbreeding

intensity in the next generation. A better monitoring system is needed to increase population size without reduction of genetic diversity. The analysis revealed the findings that can be implemented in preparation of the strategy for mating animals with optimal contributions.

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