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Original Paper

Comparison of genetic diversity in dual-purpose and beef Pinzgau populations

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The aim of the study was to evaluate the genetic diversity in Slovak dual-purpose (dairy) and beef Pinzgau cattle. The reference population consisted of 3425 living cows (2501 dairy and 924 suckler cows) involved in animal recording. The average number of fully traced generations was 0.99 and 1.17 in dairy and suckler cows, respectively and the average complete generation equivalent was 2.78 in dairy population and 3.19 in beef population. Inbreeding coefficient was computed from three, five, seven and ten traced generations. The results of inbreeding analysis show an increasing trend of inbreeding coefficient with increasing number of traced generations taken into account. The average inbreeding coefficient F_5 was 0.3599% and 0.1112% in dairy and beef reference populations, respectively. The difference between inbreeding coefficient F_3 and F_{10} was 0.0778% in dairy cows and 0.0537% in suckler cows. The difference between F_7 and F_{10} values was minimal. Overall, the inbreeding level in dairy population was higher than in beef population. The average increase in inbreeding was 0.2070% in dairy and 0.0402% in beef population. The effective number of founders, effective number of ancestors and effective number of founder genomes were 210; 82 and 63.49 in dairy population, respectively and 293; 95 and 60.62 in beef population, respectively. These results point out bottleneck effect occurrence in given populations. Further population reduction can lead to serious inbreeding problems. Regular monitoring of genetic diversity including inbreeding trends is necessary, as this information should be used in population management.

Keywords: genetic diversity, gene origin, inbreeding, pedigree analysis, Pinzgau cattle

1. Introduction

Slovak Pinzgau cattle are divided into two separate populations. The first is represented by dual-purpose type (dairy) and the second by beef suckler cows (beef). In recent years, a significant decrease of dairy cows can be observed while an increase of beef cows can be seen. Pinzgau cattle are considered an endangered breed. The total Pinzgau population in Slovakia does not exceed 3500 Herd Book cows. Genetic variation is vital for the populations to adapt to varying environments and to respond to artificial selection; therefore, any conservation and development scheme should start from assessing the state of variation in the population (Toro et al., 2011). Hiemstra et al. (2007) defined inbreeding as the formation and accumulation of loci that are IBD (Identity-by-Descent), arising from the mating of parents with a common ancestor, which is inevitable over long periods of time. It is measured by a probability that a locus is IBD. Inbreeding is a very important factor affecting genetic variability within populations. Breeding strategies should be oriented to minimize the inbreeding level and its increase. Uncontrolled inbreeding can lead to inbreeding depression which is accompanied by deterioration of performance including fitness traits. Therefore, the control of inbreeding level is an important tool in population management as well as a precondition to maintain genetic diversity. Pedigree analysis is a useful tool for animal relatedness evaluation as presented by Rybanská and Bujko (2001). Many authors presented negative effects of inbreeding depression (González-Recio et al. (2007) in Spanish Holstein, Kasarda and Kadlečík (2007) in Slovak Pinzgau, Fuerst-Waltl and Fuerst (2012) in Austrian Braunvieh, Maximini et al. (2011) in Austrian Simmental bulls, and McParland et al. (2007) in Irish dairy and beef breeds. There are many other measures assessing the variations within population (measures based on the probability of gene origin).

The aim of the study was to evaluate genetic diversity in Slovak dairy and beef Pinzgau cattle.

2. Material and methods

Pedigree data was provided by The Breeding Services of Slovak Republic, s. e. This organization is responsible for providing animal recording, genetic evaluation and keeps register of breeding information. The reference population consisted of 3425 living cows (2501 dairy and 924 suckler cows) involved in animal recording. Dairy and suckler cows set up two separate subpopulations. Living animals and their ancestors set up pedigree populations (9756 individuals in dairy and 2751 animals in suckler cows' population). The

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gene proportion of Pinzgau breed was over 50% for each animal in the reference population.

Basic statistical procedures and modification of databases were performed by the SAS software (THE SAS SYSTEM V 9.2). Computation of inbreeding and measures based on the probability of gene origin was provided by the ENDOG v.4.8 (Gutiérrez and Goyache, 2005).

Pedigree completeness was evaluated before inbreeding computation. Following measures were used for pedigree completeness assessment:

- The number of fully traced generations (GenCom), defined as the number of generations separating the offspring of the furthest known generation where the 2^g ancestors of individual are known (Maignel et al., 1996).
- The maximum number of traced generations (GenMax), defined as the number of generations separating the individual from its furthest ancestors (Maignel et al., 1996).
- The equivalent complete generations (GenEqu), described 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 to each known ancestor (Maignel et al., 1996).

Inbreeding coefficient (F) was defined as the probability that an individual has two identical alleles by descent (Gutiérrez et al., 2009). It was computed according to the algorithm of Meuwissen and Luo (1992) for each individual in the population (individual inbreeding coefficient – F_i). We used an approach where three, five, seven, ten and all traced generations were taken into account. Therefore, we computed inbreeding coefficients F_3 (three generations traced), F_5 (five generations traced), F_7 (seven generations traced), and F_{10} (ten generations traced). Individual increase in inbreeding (ΔF_i) was the next calculated parameter. It can be defined as the difference between the average inbreeding coefficient of the offspring compared with the average inbreeding coefficient of the parents (Kaerney et al., 2004). The ΔF_i coefficient was calculated as $\Delta F_i = 1 - \sqrt[t-1]{1 - F_i}$, where F_i is the individual coefficient of inbreeding and t is the equivalent complete generation (Maignel et al., 1996; Gutiérrez et al., 2009).

Measures based on the probability of gene origin were defined as:

- Number of founders (*f*) – founder is an animal with no known genetic relationship to any other animal in the pedigree except for its own descendants (Lacy, 1989).
- Effective number of founders (f_e) represents the number of founders that would produce a population with the same diversity of founder alleles as in the reference population if all founders had contributed equally to each descendant generation.

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

where:

q_k – the probability of gene origin of the *k* ancestor (Lacy, 1989)

- Effective number of ancestors (f_a) defined as the number of equally contributing ancestors that will produce the same genetic diversity as assessed in the population:

$$f_a = 1 \Big/ \sum_{j=1}^{a} q_k^2$$

where:

q_j – the marginal contribution of ancestor *j* (Boichard et al., 1997)

- Effective number of founder genomes (N_g) describes the probability that a gene from the founder population has been maintained in the reference population for a given locus and how balanced their frequencies are:

$$N_g = 1 \Big/ 2\sum_{k=1}^{2f} c_k^2$$

where:

c_k – the frequency of founder allele k found by dividing the number of copies of this allele present in the reference population by the total number of alleles in this population (Sölkner et al., 1998)

Table 1 Pedigree completeness in Pinzgau dairy and beef populations

Population	*n*	Measure	Mean	Std Dev	Minimum	Maximum
Dairy	2501	GenMax	7.8916	1.6129	0	12
		GenCom	0.9928	0.0845	0	1
		GenEqu	2.7830	0.4394	0	3.9653
Beef	924	GenMax	6.7565	1.6544	1	11
		GenCom	1.1688	0.4338	0	3
		GenEqu	3.1863	0.6731	0.50	5.4921

3. Results and discussion

Pedigree quality is a very important factor affecting the reliability of diversity measures computation. The results of pedigree completeness are presented in Table 1. The average maximum number of traced generations was 7.89 in dairy population and 6.76 in suckler cows' population. The average number of fully traced generations was 0.99 and 1.17 in dairy and suckler cows, respectively. The average complete generation equivalent was 2.78 in dairy population and 3.19 in beef population. The beef population has been created from dairy population. The presented results of pedigree completeness point out a lower level of pedigree depth, which can overestimate the final results of diversity evaluation. Higher pedigree completeness was presented by Kadlečík et al. (2011) in purebred Slovak Pinzgau cattle, Baumung and Sölkner (2002) in Austrian endangered Pinzgau, Tux-Zillertal and Carinthian Blond populations and McParland et al. (2007) in Irish dairy and beef breeds.

Inbreeding significantly affects the genetic diversity, especially in small populations. Slovak Pinzgau is a small population; therefore it is necessary to know its inbreeding level. Most methodologies used for inbreeding computation take all traced generations into account. We used an approach where the inbreeding coefficient was computed from three, five, seven and ten traced generations. The results of such computation are presented in Table 2 and Figure 1.

The results of inbreeding analysis show an increasing trend of inbreeding coefficient with an increasing number of traced generations taken into account. The average inbreeding coefficient F_5 was 0.3599% and 0.1112% in dairy and beef reference populations, respectively. The F_{10} value was 0.3789% in dairy population and 0.1167% in suckler cows population. The F_{10} value represents all traced generations practically because the maximum traced generation was 12. The difference between the inbreeding coefficients F_3 and F_{10} was 0.0778% in dairy cows and 0.0537% in suckler cows. The difference between F_7 and F_{10} values was minimal. Overall, the inbreeding level was higher in dairy population than in beef population. This difference is significant, but the beef population was smaller (924 animals) than the dairy population (2501 animals). The reason of the lower inbreeding in beef population can be the use of natural service with more sires compared to the use of limited number of AI sires in dairy herds. The presented inbreeding analysis in Slovak Pinzgau cattle shows satisfying inbreeding values in the investigated population. Higher inbreeding coefficients were presented by Kadlečík et al. (2011) in Slovak Pinzgau population (GenEqu = 3.16) with 2399 animals (F = 0.57%) and Baumung and Sölkner (2002) in Austrian original Pinzgau population (GenEqu = 5.33) with 9706 animals (F = 2.09%). The higher inbreeding coefficient in the Austrian population could be caused by a higher pedigree completeness in the given population.

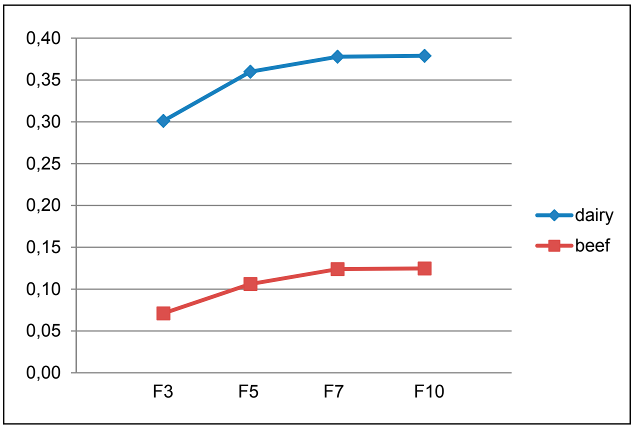

Figure 1 The inbreeding level in dairy and beef reference populationes

The average increase in inbreeding (ΔF_i) was 0.2070% in dairy and 0.0402% in beef population. The increase in inbreeding was significant especially in the dairy population. Lower ΔF_i in beef population comes with lower absolute inbreeding coefficient in the given population. Maignel et al. (1996) presented a very similar increase in inbreeding in French Simmental (0.24%) while in French Tarentaise, it was 1.83% which was a critical value. The absolute population size was 121239 in Simmental and 48320 in Tarentaise with the complete generation equivalent of 3.47 and 3.78, respectively. Bujko (2011) and Bujko and Pjontek (2009) found higher values of increase in inbreeding in a population (n = 133,786) of Slovak Simmental cattle (ΔF = 0,326%) and in selected herds (n = 8,971) of the same breed (0.867–1.987%). Incomparably higher inbreeding level and ΔF_i were computed by Panetto et al. (2011) in Brazil Guzerat Zebu cattle (n = 9,915) with a high level of pedigree completeness (GenEqu = 6.99). The average inbreeding coefficient was 13.88% and the increase in inbreeding was 2.54%. Kasarda and Kadlečík (2007) presented a very significant impact of inbreeding on milk production traits of Slovak Pinzgau breed as well as estimated breeding values.

Table 2 Inbreeding coefficients in three, five, seven and ten traced generations

Population		**F_3 in %**	**F_5 in %**	**F_7 in %**	**F_{10} in %**
Reference population	dairy	0.3011	0.3599	0.3778	0.3789
	beef	0.0710	0.1061	0.1240	0.1247
Pedigree population	dairy	0.0935	0.1112	0.1164	0.1167
	beef	0.0329	0.0554	0.0636	0.0639

Table 3 Measures based on the probability of gene origin

Population		***f***	***f***$_e$	***f***$_a$	***N***$_g$
Reference population	dairy	4110	210	82	63.49
	beef	1141	293	95	60.62
Pedigree population	dairy	4306	425	179	-
	beef	1371	327	129	-

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 3. There were 4110 and 1141 founders in the dairy and beef populations, respectively. 2160 founders were contributing to the dairy reference population and 789 to the beef reference population. The effective number of founders was 210 and 293 in the dairy and beef populations, respectively. The effective number of ancestors ranged from 82 in the dairy population to 95 in the beef population. The difference between fe and fa values points out the bottleneck effect occurrence caused mainly by the significant decline of Pinzgau population in recent years. Another reason for differences in fe and fa values can be the relatively shallow pedigrees of Pinzgau cattle. Presented results show the difference between the total number of founders and their effective number. This fact reflects the unbalanced use of founders and the loss of some founder gene contributions. The Ng values point out the loss of founder alleles in investigated populations.

Similar results for parameters characterizing gene origin were presented by Kadlečík et al. (2011) in the non-divided Slovak Pinzgau population (n = 2,399). Baumung and Sölkner (2002) presented significantly lower values of f_e = 65.4, f_a = 32.1 and N_g = 19.5 in purebred Austrian Pinzgau (n = 9,706). These results could be influenced by higher pedigree completeness of Austrian animals. Maignel et al. (1996) found lower fe and fa values in French Abondance (n = 106,520), Simmental (n = 121,239), Brown Swiss (n = 91,579), Tarentaise (n = 48,320), Montbeliarde (n = 1,664,506), Normande (n = 2,338,305) and Holstein cattle (n = 11,180,346) with higher level of pedigree completeness than in our populations. Higher f_e and f_a values were presented by Bouquet et al. (2011) in European Charolais (over 3 millions) and Limousin populations (over 2 millions) with very high level of pedigree completeness (GenEqu over 6).

4. Conclusion

Pinzgau is a unique breed adapted in Slovak mountain areas. In spite of the significant decline of the population, the value of inbreeding is not alarming. The population faces the bottleneck effect and the loss of diversity due to unequal use of founders. Further population size reduction can lead to serious problems. Therefore, it is necessary to preserve the given population in both types (dairy and beef). Regular monitoring of genetic diversity including inbreeding trends is necessary as this information is needed in population management. A new mating strategy could be very useful to control inbreeding and its increase.

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