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GENETIC DIVERSITY IN SLOVAK SPOTTED BREED

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ABSTRACT

The objective of the study was to evaluate inbreeding and genetic diversity in Slovak Spotted cattle. Reference population contained genealogic information on 36949 animals (129 sires and 36820 cows) that were used in the analyses. Pedigree completeness indexes in the first three generations were on the level of 100 %, in the 5th generation it was 60 %. Since 1970, inbreeding trend was positive with significant increasing in 1990. Average relationship was 0.8 %, inbreeding rate 0.36 % and $F = 0.094$ %. In the reference population 43 % animals was inbred, 68 % of sires and 33 % cows, with also 67 % purebred cows, as well. Total genetic diversity loss in the reference population and population of cows was the same, closely under 1%, in purebred cows 1.19 % and sires even due to higher inbreeding level 1.78 %. Genetic diversity loss was more influenced by the genetic drift 0.80% in the reference population, 1.47% in sire group, than by effective number of founder unequal contributions. F statistic showed fines superiority of heterozygosity by sire lines subpopulations, in the whole sire group ($F_{IS} = -0.12$) and their minimal differentiation ($F_{ST} = 0,098$). Obtained results showed that inbreedization process started in this population. Monitoring and better genetic management are important from the point of its further sustainable development.

Keywords: *diversity, inbreeding, pedigree analysis, Slovak spotted, sustainable agriculture.*

INTRODUCTION

The Slovak Spotted cattle is an important dual-purpose breed has a long tradition in Slovakia mainly due to its excellent dairy as well as beef production. This autochthonous breed belongs to the Simmental cattle group. The Simmental cattle is one of the oldest and most widespread breed in the world. It is characterized by fast growth development, excellent milk production and the ability to easy adapt to climatic conditions. Mainly for these reason it is necessary to assess its current state of genetic diversity, propose measures that will prevent losses of variability and ensure the sustainable diversity of this breed for future generation. The Slovak Spotted breed were officially accepted as autochthonous breed in 1958. Purebred

Slovak Spotted breed reach a maximum population size in 1975. After 1990 size of breed has decreased significantly due to transformation processes in agriculture and exploitation of Holstein sires for crossbreeding (Kadleík et al., 2013).

Genetic variation is vital for the populations to adapt to varying environments and to respond to artificial selection. Any conservation and development strategy should start from assessing the state of variation in the population (Toro et al., 2011). 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 (Pavlík et al., 2013). Pedigree analysis is very effective method in evaluation of inbreeding level (Kadleík et al., 2011; Danchin - Burge et al., 2012; Pavlík et al., 2012), loss of genetic diversity (Hazuchová et al., 2013; Kadleík et al., 2016), and genetic management of small endangered populations (Mészáros et al., 2015). The aim of the study was to evaluate level of inbreeding and genetic diversity in Slovak Spotted cattle.

MATERIALS AND METHODS

The genetic diversity analysis of Slovak Spotted cattle was performed using genealogical data obtained from SBS, a. s. of the Slovak Republic. The pedigree file (RodS) consisted of 109,686 individuals (105,229 dams and 4,457 sires). The reference population (RP) of Slovak Spotted cattle covered living animals, sires in insemination (129) and dams included in performance testing (36,949). The database of individuals was prepared by SAS v9.3 software and recoded in CFC software (Sargolzaei et al., 2006). The current state of diversity and trends of inbreeding were estimated by using Endog v4.8 software (Gutiérrez and Goyache, 2005).

The pedigree completeness was evaluated based on the equivalent complete generations of ancestors and pedigree completeness index described by MacCluer et al. (1983). The equivalent complete generations is computed as the sum over all known ancestors of the terms computed as sum of $(1/2)^n$ where n is the number of generations separating the individual to each known ancestor (Maignel et al., 1996). The pedigree completeness index was estimated as follows:

$$PCI = \frac{2C_{sire}C_{dam}}{C_{sire} + C_{dam}},$$

where C_{sire} and C_{dam} are contributions from the paternal and maternal lines, and $C = \frac{1}{d} \sum_{i=1}^d g_i$; where g_i is the proportion of known ancestors in generation i ; and d is the number of generations that are taken into account.

The loss of diversity was expressed through parameters based on the probability of identity by descent (inbreeding coefficient of an animal F , individual increase in inbreeding F_i , average relatedness AR), and Wright's F-statistic. A measure of inbreeding of an individual (F) is defined as the probability that both alleles in one locus are derived from the same ancestor or are identical by descent (IBD). The

increase in inbreeding (F) is calculated according to Gutiérrez et al. (2009) as follow:

$$\Delta F = \frac{(F_t - F_{t-1})}{(1 - F_{t-1})},$$

where F_t and F_{t-1} are the average inbreeding at the t^{th} generation and $1 - F_{t-1}$ is increase of inbreeding in last generation. The individual increase in inbreeding is computed 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 generations (Maignel et al., 1996). The average relatedness coefficient (AR) of each individual is defined as the probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal. AR can be interpreted as the representation of the animal in the whole pedigree regardless of the knowledge of its own pedigree. AR is an alternative or complement to F and can be used to predict the long-term inbreeding of a population because it takes into account the percentage of the complete pedigree originating from a founder at population level Gutiérrez et al. (2009).

The genealogical information of Slovak Spotted population was also used to infer its genetic structure based on F-statistic according to Wright (1978). Caballero and Toro (2002) formalized the pedigree tools necessary for the analysis of genetic differentiation in subdivided populations starting with the average pairwise coancestry coefficient (f_{ij}) between individuals of two populations, i and j , of a given metapopulation including all $N_i \times N_j$ pairs. For a given subpopulation i , the average coancestry, the average selfcoancestry of the N_i individuals and the average coefficient of inbreeding would be, f_{ii} , s_i , $F_i = 2s_i - 1$ respectively. From these parameters and the corresponding mean value for the entire metapopulation Caballero and Toro (2002) obtained Wright's (1978) F-statistic as:

$$F_{IS} = \frac{\bar{F} - \bar{f}}{1 - \bar{f}}, F_{ST} = \frac{\bar{f} - \bar{f}}{1 - \bar{f}} = \frac{\bar{D}}{1 - \bar{f}}, \text{ and } F_{IT} = \frac{\bar{F} - \bar{f}}{1 - \bar{f}},$$

where \bar{f} and \bar{F} are the mean coancestry and the inbreeding coefficient for the entire population respectively, and \bar{f} the average coancestry for the subpopulation so that $(1 - F_{ST}) = (1 - F_{IS})(1 - F_{IT})$. In our study the subpopulations were defined according to sire lines. The line of sire was considered as separate subpopulation only if it contained minimally 5 bulls, regardless number of their offspring. Based on this, overall 32 subpopulations were found in pedigree file.

RESULTS AND DISCUSSION

In the reference population of Slovak Spotted cattle the equivalent complete generations of ancestors reached average value 4.53 that indicated good level of pedigree completeness comparable also with previous studies (Mc Parland et al., 2007; Sölkner et al., 1998). The average MacCluer's index of pedigree completeness was higher than 80% in the first five generation, hence presented results have good reliability. The reference population had hundred percent

completed pedigrees in the 1st generation and had decreasing tendency with increasing generations (Fig. 1).

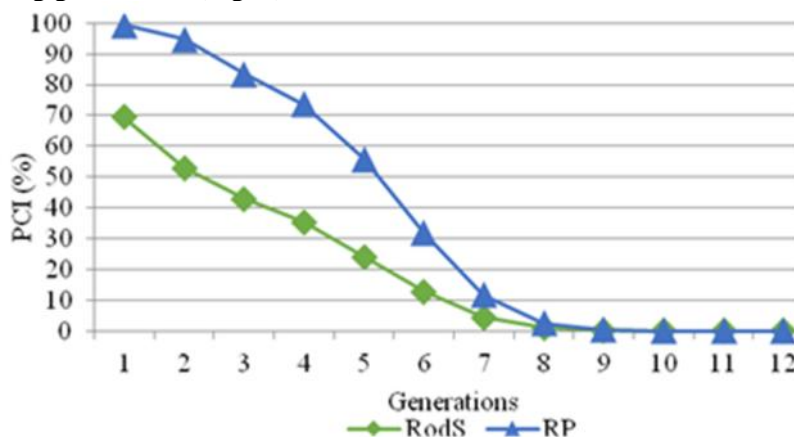


Figure 1. Pedigree completeness index by generations

Generally, the average relationship was 0.8 %, inbreeding rate 0.36 % and $F = 0.094$ %. The average value of inbreeding coefficient was 0.14% in pedigree file and 0.76% in group of sires. The average F_i among generations was highest in the group of sires (0.19%), whereas the average relatedness was relative balanced regardless gender of animals. In the future, it is therefore possible to expect the increase of inbreeding with the same intensity in population of sires as well as in dams. Compared to our results, in Irish population of Simmental cattle was found much higher level of inbreeding (around 1.35%). This value presented by Mc Parland et al. (2007) is probably overestimated due to low completeness of available pedigree information. Similarly, higher value of average F was reported for French population of Simmental cattle (Danchin - Burge et al., 2012). Baumung and Sölkner (2003) indicated that if the value of equivalent complete generations of ancestors is close to 5 or higher the effect of the pedigree data on the resulting value of inbreeding coefficient is only non-significant. The obtained values of all parameters derived from the probability of identity by descent indicated higher level of diversity within Slovak Spotted cattle compared to Slovak Pinzgau cattle ($F_i = 0.57\%$, $F_i = 0.25\%$, $AR = 1.17\%$) or Slovak Holstein population ($F_i = 1.92\%$, $F_i = 0.48\%$, $AR = 2.38\%$) (Kadlečík et al., 2011; Pavlík et al., 2012). The proportion of inbred animals in reference population of Slovak Spotted cattle (42.77%) was comparable with Irish Simmental cattle (50%), while the average inbreeding coefficient of inbred animals was lower (0.85% vs. 2.21%) (Mc Parland et al., 2007). If we taking into account pedigree file of Slovak Spotted cattle than the proportion of inbred animals was 15.95% with $F_i = 0.88$ %. Within inbred animals the highest level of inbreeding was found in sires (1.11%). Observed average value of inbreeding coefficient should correspond to its real value. The level of inbreeding was generally low (1 %). The trend of inbreeding increase in reference population and pedigree file by birth year (± 2 years) is shown on Figure

2. The average value of inbreeding coefficient in inbred animals decreased, whereas the proportion of inbred animals and level of inbreeding in metapopulation had increasing tendency probably due to common ancestors in more distant generations in pedigree. In last decade, the higher increase of inbreeding was found in population of sires compared to dams. The average value of inbreeding coefficient in group of sires increased by 0.3% compared to the previous period (1991-2000). One of the reason can be mainly the utilization of older ancestors that can be found in a large part of the pedigree file in insemination process.

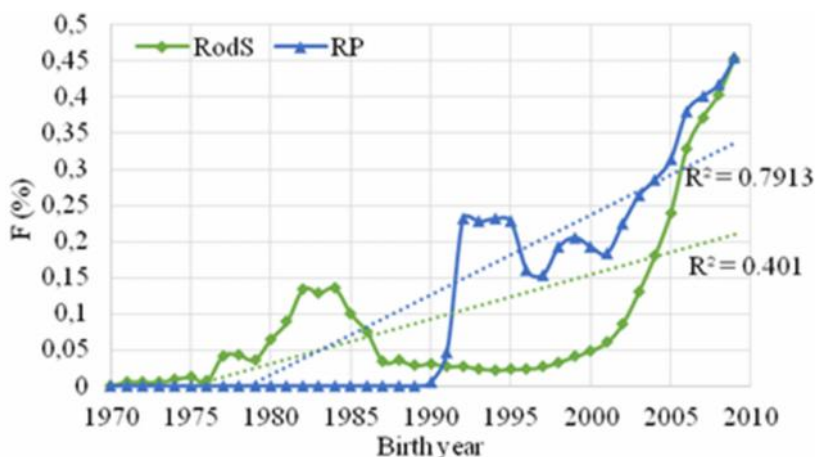


Figure 2. Trend of inbreeding in reference birth population and pedigree file by year of birth.

As we can see on the Figure 3 the highest increase of average relatedness in both pedigree and reference populations was found in period 2001 - 2010. The cows and heifers revealed higher average relatedness (0.65%) compared to bulls (0.57%). Total genetic diversity loss in the reference population and population of cows was the same, closely under 1%, in purebred cows 1.19 % and sires even due to higher inbreeding level 1.78 %. Genetic diversity loss was more influenced by the genetic drift 0.80% in the reference population, 1.47% in sire group, than by effective number of founder unequal contributions.

Genetic differences among subpopulations derived from sire lines was tested by using Wright's F-statistic. The average coefficient of coancestry in metapopulation defined based on the sire lines was 0.0125. The observed negative value of Wright's F_{IS} index (-0.118) signaled sufficient proportion of heterozygote animals within each subpopulation. The F_{ST} index reflects amount of differences in allele frequencies among subpopulations. Its value close to zero ($F_{ST}=0.098$) indicated only slight level of genetic differentiation within them. All subpopulations of each defined metapopulation have almost the same allele frequency (the differences between the subpopulations are small) as the whole population, although each subpopulation has a significant amount of heterozygotes. Based on F_{ST} values we were able to detect three main genetic clusters reflecting the genetic distances

among subpopulations defined by sire lines or in other words the genetic background of most frequently used ancestors (Fig. 4).

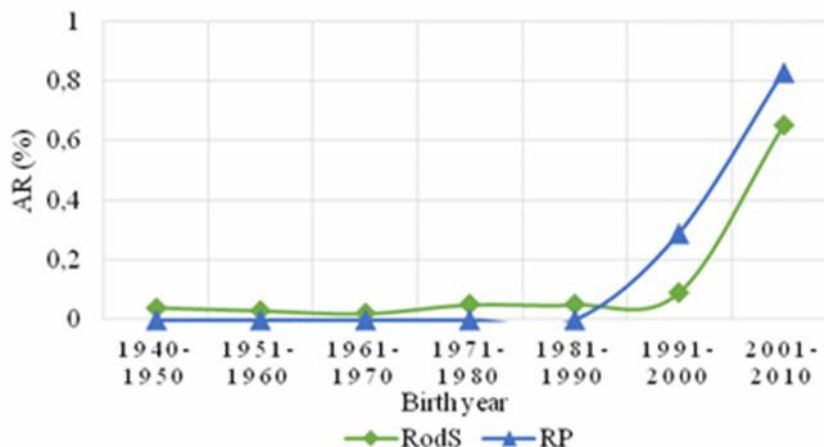


Figure 3. Average relatedness in pedigree and reference populations by birth year.

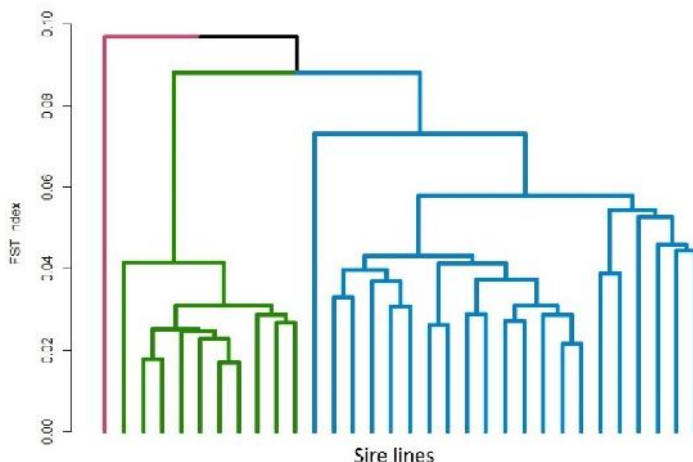


Figure 4. Genetic structure of Slovak Spotted population based on F-statistic.

CONCLUSIONS

The low obtained values of parameters derived from the probability of identity by descent point up to the fact that the breeder's effort was aimed to prepare the breeding strategy to minimize mating of inbred individuals. Compared to other breeds, these results suggest a wider genetic basis of the Slovak Spotted cattle. However, the average value of relatedness coefficient in reference as well as in the whole pedigree file was higher than inbreeding coefficient. Therefore it could be assumed that the number of inbred individuals will increase in the next generation, while continuing to practice the system of selection techniques. Mating programs are widely used already, and these can be easily modified to consider inbreeding avoidance in the next generation. Therefore long-term maintenance of genetic

diversity will depend on methods minimizing mating of inbred parents. Our results may be used in genetic management of breeding practices of Slovak Spotted cattle.

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REFERENCES

- Baumung, R., Sölkner, J. (2003). Pedigree and marker information requirements to monitor genetic variability. *Genetics Selection Evolution*, 35, 369 - 383.
- Caballero, A., Toro, M.A. (2002). Analysis of genetic diversity for the management of conserved subdivided populations. *Conservation genetics*, 3, 289 - 299.
- Danchin - Burge, C., Leroy, G., Brochard, M., Moureaux, S., Verrier, E. (2012). Evolution of the genetic variability of eight French dairy cattle breeds assessed by pedigree analysis. *Journal of Animal Breeding and Genetics*, 129, 206 - 217.
- Gutiérrez, J. P., Goyache, F. 2005. A note on ENDOG: a computer program for Analysis pedigree information. *Journal of Animal Breeding and genetics*, 122, 172 - 176.
- Gutiérrez, J. P., Goyarche, F., Cervantes, I. (2009). User's Guide-ENDOG v 4.6 a Computer Program for Monitoring Genetic Variability of Populations Using Pedigree Information.
- Hazuchová, E., Kadle ík, O., Pavlík, I., Kasarda, R. (2013). Assessment of genetic diversity using characteristics based on the probability of gene origin in the Slovak Spotted breed. *Acta fytotechnica et zootechnica*, 16, 45 – 48.
- Kadle ík, O., Hazuchová, E., Pavlík, I., Kasarda, R. (2013). Diversity of cattle breeds in Slovakia. *Slovak Journal of Animal Science*, 46, 145 - 150.
- Kadle ík, O., Kasarda, R., Pavlík, I., Hazuchová, E. (2011). Pedigree Analysis of Slovak Pinzgau Breed. *Agriculturae Conspectus Scientificus*, 76, 165 - 168.
- Kadle ík, O., Pavlík, I., Morav íková, N., Kasarda, R. (2016). Inbreeding and genetic diversity loss of four cattle beef breeds in Slovakia. *Acta fytotechnica et zootechnica*, 19, 59 – 63.
- MacCluer, J.W., Boyce, A.J., Dyke, B., Weitkamp, L.R., Pfenning, D.W., Parsons, C.J. (1983). Inbreeding and pedigree structure in Standardbred horses. *Journal of Heredity*, 74, 394 - 399.
- Maignel, L., Boichard, D., Verrier, E. (1996). Genetic variability of French dairy breeds estimated from pedigree information. *Interbull Bulltein*, 14, 49 - 54.
- Mc Parland, S., Kearney, J.F., Rath, M., Berry, D.P. (2007). Inbreeding trends and pedigree analysis of Irish dairy and beef cattle population. *Journal of Animal Science*, 85, 322 - 331.
- Mészáros, G., A. Boison, S.A., Pérez O'Brien, A.M., Feren akovic, M., Curik, I., Barbosa Da Silva, M.V., Utsunomiya, Y.T., Garcia, J.F. Sölkner, J. (2015). Genomic analysis for managing small and endangered populations: A case study in Tyrol Grey cattle. *Frontiers Genetics*, 6, 1 – 12.

- Pavlík I., Kadlečík O., Kasarda R., Šidlová V., Žitný J. (2013). Comparison of genetic diversity in dual-purpose and beef Pinzgau populations. *Acta fytotechnica et zootechnica*, 16, 69 - 73.
- Pavlík, I., Hazuchová, E., Kadlečík, O., Kasarda, R. (2012). Pedigree analysis of Slovak Holstein cattle. *Book of Abstracts of the 63rd Annual Meeting of the European Federation of Animal Science*, 18, 246.
- Sargolzaei, M., Iwaisaki, H., Colleau, J. J. (2006). CFC (Contribution, Inbreeding, Coancestry). A software package for pedigree analysis and monitoring genetic diversity.
- Sölkner, J., Filipčić, L., Hampshire, N. (1998). Genetic variability of populations and similarity of subpopulations in Austrian cattle breeds determined by analysis of pedigrees. *Journal of Animal Science*, 67, 249 - 256.
- Toro, M.A., Meuwissen, T.H., Fernández, J., Shaat, I., Mäki-Tanila, A. (2011). Assessing the genetic diversity in small farm animal populations. *Animal*, 5, 1669 - 1683.
- Wright, S. (1978). *Evolution and the genetics of populations. Vol. 4, Variability Within and among Natural populations.* University of Chicago Press, Chicago, USA.