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 (Kadlečík 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 (Kadlečík et al., 2011; Danchin - Burge et al., 2012; Pavlík et al., 2012), loss of genetic diversity (Hazuchová et al., 2013; Kadlečík 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 $\Delta F_i$, 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).
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 \( 1 - F_{n-1} \) is increase of inbreeding in last generation. The individual increase in inbreeding is computed as:

\[
\Delta F_i = 1 - \sqrt[1-F_i]{t-1},
\]

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:

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

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 McParland 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 ($F_i = 0.57\%, \Delta F_i = 0.25\%, AR = 1.17\%$) or Slovak Holstein population ($F_i = 1.92\%, \Delta F_i = 0.48\%, AR = 2.38\%$) (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.

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) signalized 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