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POPULATION ANALYSIS OF THE LOCAL ENDANGERED PŘEŠTICE BLACK-PIED PIG BREED

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Original scientific paper

SUMMARY

The pedigree analysis of the local endangered Přeštice Black-Pied pig breed (n=19 289) was performed. Animals born within the period 2012-2014 were assumed as the reference population (n=1 374). The pedigree completeness index reached 100% for four generations back. The 100 % of the genetic pool was explained by 66 ancestors. Although all animals of the reference population were inbred, 57% of them had inbreeding less than five percent. Average inbreeding, co-ancestry coefficient and rate of inbreeding reached 4.93%, 13.48% and 1.29% in reference population, respectively. The effective population size calculated by four different methods varied from 32 to 91 animals in 2014. Average generation interval, average family size for sire and dam parents was 2.5, 17.46 and 6.5 animals, respectively. Total number of founders, effective number of founders, effective number of founders' genomes and effective number of non-founders genomes reached values 299, 98.05, 21.92 and 28.23 founders, respectively. The average genetic diversity (GD) loss was 13.71% in reference population. The GD loss has increased within the last three year period mainly due to the random genetic drift (77.6%) and by unequal contribution of founders (22.4%). The Přeštice Black-Pied breed is highly endangered with GD loss. Mating of closely related animals has to be prevented in breeding and mating program of this breed.

Key-words: pig, endangered, pedigree analysis, inbreeding, genetic diversity

INTRODUCTION

The Přeštice Black-Pied breed (PBP) is a local Czech breed, whose origin comes to the end of the 19th century (Fiedler et al., 2004). The PBP breed is registered by the UN FAO as threatened with extinction and it is classified as Animal Genetic Resource – AnGR since 1992 (Vaclavková et al., 2012). The breed is kept in situ as AnGR in closed population from 1996. It is typical with the good reproduction and high adaptation to the environmental conditions. The mature weight of boars is 260-280 kg; whereas sow's mature weight varies from 215 to 235 kg. The objective of the presented study was to analyze the trend of genetic diversity using the parameters of probability of identity by descent and by gene origins in the pedigree datasets.

MATERIAL AND METHODS

The Czech Pig Breeders association provided the historical data. Pedigree information of the Přeštice Black

Pied breed (PBP) contains 19 289 animals. Animals born between 1990 and 2014 with known sex were used in the study only. The animals born within years 2012-2014 were assumed as the reference population. Quality of the pedigree was calculated by pedigree completeness index (PCI) with algorithm explained by MacCluer et al. (1983) and by maximum number of generations traced back. The average generation interval was assumed as average age of parents at their offspring birth expressed in years. Different methods were used to compute the effective population size (N_e). Based on the above mentioned, the N_e was calculated as $N_e = \frac{1}{2 \times \Delta F}$, where ΔF is rate of inbreeding. The first method was based on the average inbreeding of offspring and their direct parents ($N_e - \Delta F_p$). The average inbreeding of offspring and average inbreeding of average parent's generation was the next method

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($N_e - \Delta Fg$). Both methods were described by Falconer and MacKay (1996). Pérez-Ensico (1995) algorithm, based on logarithmic regression of $\ln(1-F)$ on the year of birth ($N_e - \ln$), was used as the further method. The last method ($N_e - Ecg$) was based on rate of individual inbreeding coefficient calculated as $1 - \sqrt{1 - F}$, where parameter t is computed as the sum of overall known ancestors of the term $(1/2)^n$ and was defined by Gutierrez et al. (2009).

Number of ancestors with unknown parents was assumed as total number of founders (f_t). Effective number of ancestors (f_a) was calculated as the minimum number of ancestors necessary to explain the total genetic diversity of the studied population by algorithm of Boichard et al. (1997). Effective number of founders f_e (Lacy, 1989), was defined as the number of equally contributing founders that would be expected to generate a similar amount of genetic diversity as in the population under the study. Effective number of founder genomes (f_{ge}) was defined as the number of equally contributing founders with no random loss of founder alleles that would give the same amount of genetic diversity as is presented in the population under the study and was calculated using the algorithm of Caballero and Toro (2000). Effective number of non-founders genomes (f_{ne}) was derived from difference of inverted values of f_{ge} and f_e . The genetic diversity loss was derived from f_e , f_{ge} and

f_{ne} . Total genetic diversity (GD) of the reference population was calculated according to Lacy (1995). The loss of the genetic diversity due to unequal number of founders (GDLf) was expressed as $1 - GD^*$, where GD^* was calculated by Caballero and Toro (2000) as $1 - \frac{1}{f_e}$. The

loss of GD due to the random genetic drift (GDLd) was calculated as the inverse of $2f_{ne}$ (Caballero and Toro, 2000). Detailed description of the presented methods can be found in Krupa et al. (2015). The POPREP package (Groeneveld and Lichtenberg, 2010), the CFC software package (Sargolzaei et al., 2006) and the PEDIG software (Boichard, 2002) were used for the analysis.

RESULTS AND DISCUSSION

The accuracy of the computed inbreeding and of consequently derived parameters depends mainly on the quality of analyzed datasets. The calculated pedigree completeness index (Figure 1) obtained maximum values (100%) up to four generations deep within the last five years. The PCI declined when four generations and more were considered. As mentioned by Gutierrez et al. (2003), a pedigree completeness level has sizable effect on the estimation of inbreeding coefficient, because the change of finding of common ancestors increases together with level of pedigree completeness.

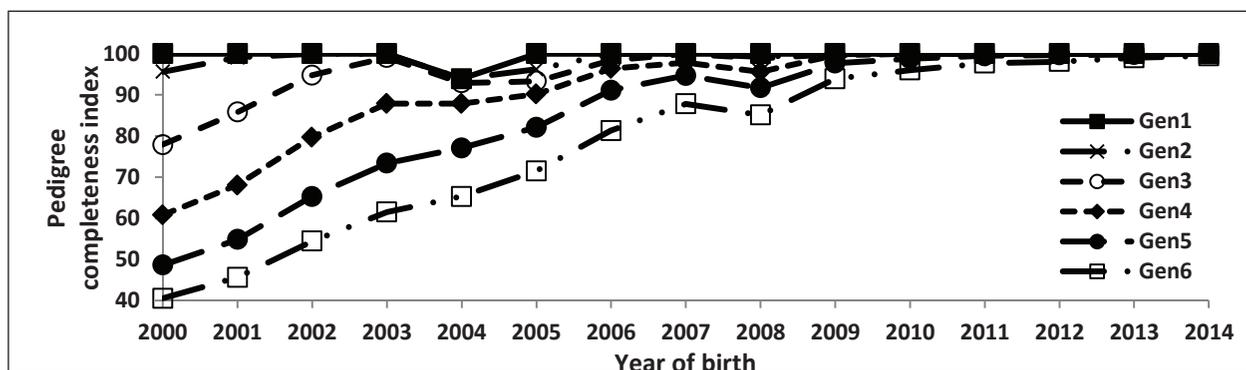


Figure 1. Pedigree completeness index

The basic characteristics of the reference population along with calculated inbreeding and co-ancestry coefficients are summarized in Table 1. The number of active animals (reference population) increased in the last years. The number of inbred animals, sires and dams was equal to hundred percent in reference population. Similarly, in our previous study (Krupa et al., 2015) high proportion of inbred individuals in reference population of five pig breeds was found, and exceeded 50% from all of the evaluated animals and 70% of sires. The average rate of inbreeding reached relative high value (1.29%) and exceeded the limits recommended by FAO (2000). The fact that PBP breed is kept as closed population could be a main factor of the prevalence of inbred animals in reference population. It is also important to mention that in reference population 57% of inbred animals had inbreeding coefficient up to five percent. The average inbreeding coefficient in reference popu-

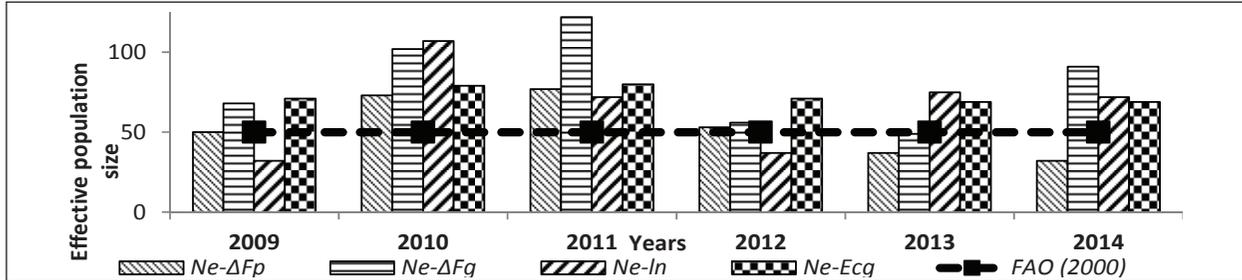
lation was 4.9% ($\pm 2.4\%$) and varied from 1.1% (minimum) to 17.3% (maximum). The average co-ancestry coefficient was 13.5% whereas the average rate of inbreeding in reference population was 1.3%.

Table 1. Base characteristics and inbreeding of the reference population

Trait	Value
Number of animals in pedigree	19289
Number of animals in reference population	1374
Maximum number of generations traced back	13
Proportion of inbred animals / Sires / Dams (%)	100/100/100
Average inbreeding (%)	4.93
Average co-ancestry (%)	13.48
Average increase of inbreeding - ΔF (%)	1.29

The effective population size (N_e) is one of the main parameters pointed to genetic variability of the population. The results of N_e computed by four different methods are shown in Figure 2. As Groeneveld and Lichtenberg (2010) mentioned, the choice of the best method depends on various conditions like used time window, PCI and also on changes in N_e from year to year. The decision tree in detail can be found in the population structure report as a result of the POPREP

software (Groeneveld and Lichtenberg, 2010). Generally, the N_e values obtained in our study were relatively low and varied from 32 to 91 animals in 2014. As the most appropriate method seems to be N_e -ln and N_e -Ecg. The N_e -Ecg method was the most stable, with minimal changes between the years. The N_e -ln method used the shortest time window, which allowed quickly responding to changes in population size and structure. It should be used as the default method.



* see Material and methods session for more details

Figure 2. Trends in the effective population size computed by different methods*

Parameters derived from analysis of gene origin of reference population are summarized in Table 2. The total number of founders and effective number of founders was 299 and 98, respectively suggesting the excessive use of certain animals in the reference population. Moreover, the ratio between the above mentioned parameters points to disequilibrium among founders in the analyzed population. On the other side, this ratio is not such high as the one observed for other Czech pig breeds (Krupa et al., 2015). It is probably caused by the fact that PBP breed is not under so high intensive selection compared to commercial pig's populations. Whilst the f_e / f_t ratio explained the GD loss caused by unequal contribution of founders, the f_{ge} / f_e ratio can be used to quantify GD loss due to random genetic drift. In generally, the lower values refer to the higher prevalence of GD loss. In our study, impact of random genetic drift on GD loss was higher compared to unequal contribution of founders when value for this ratio was lower than for f_e / f_t ratio (Table 2). The most influential ancestor explained 10.54% of genetic diversity. The trend in GD loss together with the average inbreeding coefficient is shown in Figure 3. The GD loss increases continuously within the last three

year period with the average value of 13.71% in the reference population. The loss of GD was caused mainly by random genetic drift (77.6%) and unequal contribution of founders (22.4) in the reference population. Furthermore, the value of GD loss due to random genetic drift over the years increased whereas the value of the GD loss due to unequal founder contribution diminished.

Table 2. Parameters of gene origin for the reference population

Parameter	Value
Total number of founders (f_t)	299
Effective number of founders (f_e)	98.05
Effective number of founders genomes (f_{ge})	21.92
Effective number of non-founders genomes (f_{ne})	28.23
f_e / f_t and f_{ge} / f_e ratio	0.33/0.22
Number of ancestor explaining 50/75/100 % of genetic variability	7/13/66
Average generation interval (years)	2.5
Average family size for male / female parents	17.46/6.5

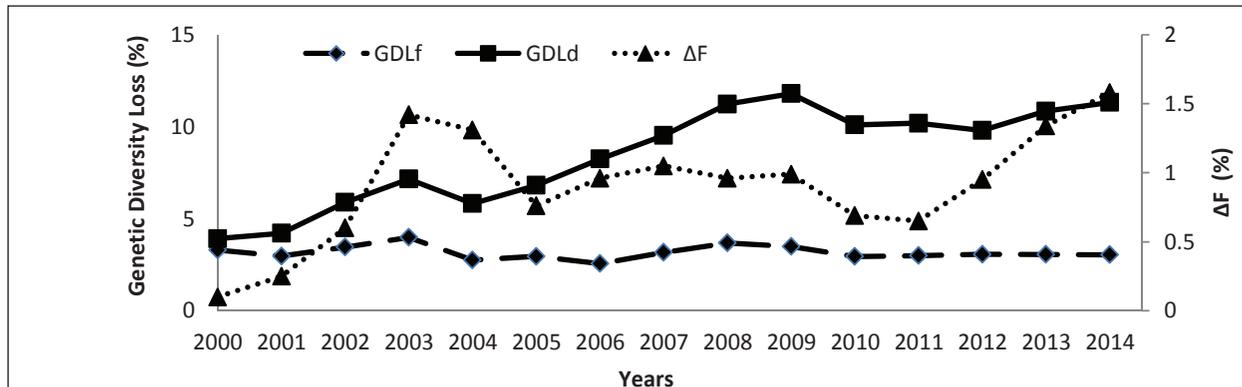


Figure 3. Genetic diversity loss due to unequal founder contribution (GDLf) and random genetic drift (GDLd) and average rate of inbreeding (ΔF)

CONCLUSION

The comprehensive pedigree analysis of the reference population of Přeštice Black-Pied pig breed was performed. The breed has been characterized by adequate quality of pedigree. Values of the average inbreeding and co-ancestry coefficients are high and increase from one generation to other. Parameters derived from the gene origin analysis are pointing to the continuous genetic diversity loss, caused mainly by random genetic drift. It is very important to avoid next genetic diversity loss. The breeding must be focused on mating the animals with lowest relationship with the each other in order to prevent increasing the inbreeding in next generations.

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