

Degree Of Endangerment Of Different German Pig Herdbook Populations

*E. Tholen**, *J. Staack†*, *P. Müller**, *J. Ingwersen^κ*

Introduction

Within 13 German pig herdbook associations several indigenous and imported breeds are organized. The breeds Piétrain (Pi), German Landrace (DL) and German Edelschwein (DE) are part of the most popular crossbreeding schemes (Pi×F1) used across all regions in Germany. In 2008, 18268 (DL), 4648 (Pi) and 2789 (DE) herdbook animals have been recorded (ZDS, 2009). In comparison to the year 2004, the numbers of registered animals within the breeds DL (-39,6%), Pi (-56,4%) and DE (-55,4%) decreased drastically up to 56%. The synthetic breed Leicoma (LC, N=1227) is used in the crossbred scheme of commercial sows, particularly in Baden-Württemberg and in eastern parts of Germany. Breeds like Angler/German Sattelschwein (AS, 222), Rote Husumer (RH), Schwäbisch Hällische (SH, 97) and Bunte Bentheimer (BB, 291) are of particular regional importance. Due to the low and/or decreasing number of registered animals, inbreeding in German herdbook pig populations is expected to increase with detrimental effects, such as inbreeding depression, genetic defects, and loss of usable genetic variability for genetic improvements. In view of these increased risks, the objective of this study was to analyze trends in inbreeding and effective population size (N_e) of purebred herdbook pigs in Germany. This project was financed by the German Federal Ministry of Food, Agriculture and Consumer Protection (BMELV) through the Federal Office for Agriculture and Food (BLE).

Material and methods

Classically, monitoring of genetic diversity has been carried out by assessing the evolution of inbreeding (F) and relationships (R) in the population of interest, often converted to N_e , which is regarded as a good indicator of the risk of genetic erosion. Many attempts have been made to deal with different real world scenarios. In our study we compared different methods to estimate N_e , which were suggested by Gutiérrez et al. (2008). Using genealogies, N_e can be estimated from the increase in inbreeding (ΔF) between two discrete generations t and t-1 using the formulas $N_e=1:(2\cdot\Delta F)$ and $\Delta F=(F_t-F_{t-1}):(1-F_{t-1})$. On condition of an ideal population, discrete generation can be defined according to the number of available complete pedigree generations of each animal. In pig populations, which we have studied, the depth of pedigree information is different and a considerable number of animals were immigrated from breeding organizations outside of our data acquisition. Because of these problems, animals could not be arranged into different generations accurately. Various approaches have been used to estimate ΔF via regression of F on different years of birth or generation. Besides difficulties in fitting individuals to discrete generations, in real data of

* Institute of Animal Science, University of Bonn, Endenicher Allee 115, 53115 Bonn, Germany

† German Society for Animal Production (DGfZ), Adenauerallee 174, 53113 Bonn, Germany

^κ Zentralverband der deutschen Schweineproduktion (ZDS), Bonn, Adenauerallee 174, 53113 Bonn, Germany

German herdbook populations the trend of inbreeding is flat or even negative. This could be explained by selection strategies which aim to avoid inbreeding or by immigration of animals. However under these circumstances regressive methods can hardly be used to estimate N_e . Hill (1979) suggested to estimate N_e from the number of male (m) and female (f), the average generation interval (L) and individuals variances (σ^2) and covariances (cov) of family sizes of males (m) and females (f) without the need of ranking the individuals to certain generations as:

$$\frac{1}{N_e} = \frac{1}{16mL} \left[2 + \sigma_{mm}^2 + 2 \left(\frac{m}{f} \right) cov_{mm, mf} + \left(\frac{m}{f} \right)^2 \sigma_{mf}^2 \right] + \frac{1}{16fL} \left[2 + \left(\frac{f}{m} \right)^2 \sigma_{fm}^2 + 2 \left(\frac{f}{m} \right) cov_{fm, ff} + \sigma_{ff}^2 \right]$$

This method is frequently used to classify the degree of endangerment of livestock populations. However, in scenarios of overlapping generations, computation of N_e based on family variances unrealistically ignores population subdivision, mating between relatives, migration, or different representations of founders.

Gutiérrez et al. (2008 and 2009) have introduced the concept of the individual increase in inbreeding (ΔF_i). Similar to the formula of Hill (1979), this method does not rely on the assignment of an animal to a specific discrete generation t . Under the assumption that for a hypothetical population with all individuals having the same pedigree structure ($F_t = F_i$), ΔF_i can be calculated by $\Delta F_i = 1 - \sqrt[ECG]{1 - F_i}$ for each animal i . The number of equivalent complete generations (ECG) describes the pedigree depth of each animal (Maignel et al., 1996). N_e is calculated by averaging ΔF_i of animals, which belong to a defined reference population. An approximative formula to estimate the standard error (SE) of N_e based on ΔF_i ($Ne\Delta F_i$) is given by Cervantes et al. (2008). Gutiérrez et al. (2008) have emphasized, that $Ne\Delta F_i$ is not dependent on the whole reference subpopulation mating policy but on the mating carried out throughout the pedigree of each individual.

Pedigree information was transferred from five herdbook computer centers to a central relational database (MS SQL-Server). Identification numbers (ID) of identical animals registered in different herdbook organizations are merged by complex SQL database routines while importing the data into the central database. Data inconsistencies like pedigree loops and inconsistent birth dates were solved by removing the pedigree information or birthday information of affected animals. All N_e calculations were performed by using the software ENDOG v4.6 (Gutiérrez et al., 2009) and Relax2 (Stranden & Vuori 2006).

Results and discussion

Curves of yearly inbreeding averages of recent years (Fig. 1) for the small breeds AS, SH and BB show mostly a flat slightly decreasing trend. This unexpected trend can be explained by migration and specific efforts to reduce inbreeding in these organizations. The low (<15) number of yearly registered animals are responsible for the high F values within the RH in the years 2001–2004. The interpretation of F is only useful, if a sufficient number of generations can be traced back. The number of ECG for most breeds during the years 2000–2008 was more than 3.5 (Fig. 2). This was not the case for the breeds BB and RH, where only in most recent years more than three ECG can be observed. The results of the breed Lc are not presented, because the number of ECG exceeds only in the years 2007/08 two generations. As expected, a relative small annual F (<1%) can be observed for the most

popular breeds DL, DE and Pi. With the exception of the Pi breed most slopes of the inbreeding trends for all breeds since 2003 are negative or close to zero. From this follows, that the calculations of N_e by regressing F on years of birth will lead to unrealistic estimators. For a Pi reference population comprising animals born after 2003, N_e was calculated by different regression methods between 522 and 532 animals. These estimators are much higher than those calculated by methods of Hill (1979) and Gutiérrez et al. (2009).

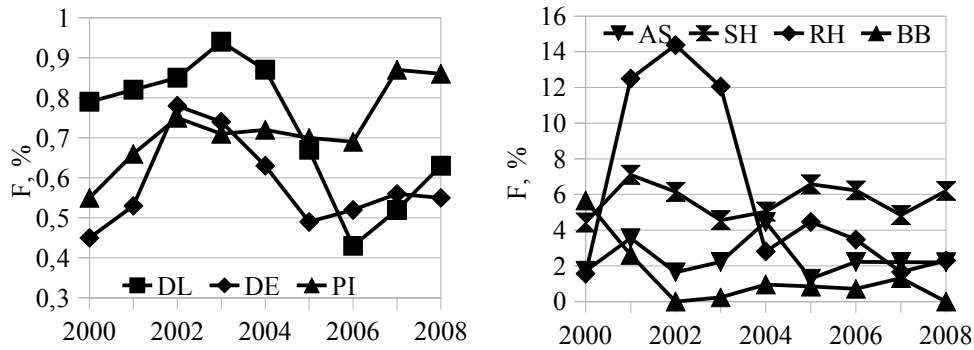


Fig. 1: Yearly average inbreeding coefficients (F)

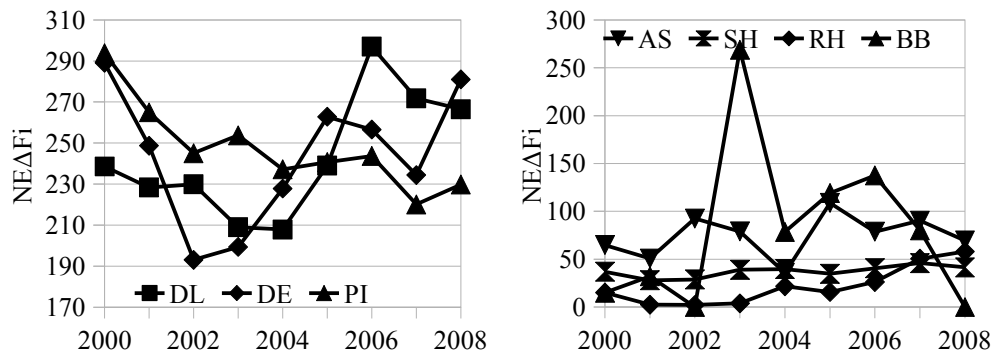


Fig. 2: Yearly effective population size, calculated by average individual increase of inbreeding ($N_e\Delta F_i$)

N_e calculated by the individual increase of inbreeding is presented in figure 2. With the exception of the BB breed, yearly fluctuation of $N_e\Delta F_i$ is generally small (<15%). The large differences in $N_e\Delta F_i$ between the successive years within the BB breed could be the result of the low number of ECGs. A distinct negative trend in $N_e\Delta F_i$ can be observed in the Pi breed. These values dropped continuously from 290 in the year 2000 to 230 in 2008.

In order to compare the effective population sizes, calculated by the formula from Hill (1979) and by the individual increase of inbreeding from Gutiérrez et al. (2008) of the current generation, only animals born before 2003 were considered as a reference population. In addition, $N_e\Delta F_i$ comprises only animals, which proves to have more than three ECGs. The corresponding results for the breeds DL, DE, SH and RH show only marginal differences between the two methods (Tab. 1). Regarding the breeds AS and BB,

$Ne\Delta F_i$, exceeds Ne_{Hill} considerably. With respect to the small population size and these unexpected small increase of inbreeding (Fig. 2), it can be assumed, that AS and BB breeders efficiently avoid inbreeding. In contrast to Ne_{Hill} , $Ne\Delta F_i$ considers individual inbreeding, so that this method seems to be more accurate in this situation. Moreover, Ne_{Hill} unrealistically ignores population subdivision (Guitierrez et al., 2008). This disadvantage could explain the large difference between the two methods within the Pi breed, which was bred in different, autonomous herdbook breeding organizations across Germany.

Tab 1: Effective population size (Ne), calculated by formulas from Hill (1979) (Ne_{Hill}) and Gutiérrez et al. (2009) ($Ne\Delta F_i$, including animals with ECG >2) for reference populations with animals born after 2003

Breed	Ne_{Hill}	$Ne\Delta F_i \pm SE$	Breed	Ne_{Hill}	$Ne\Delta F_i \pm SE$
Pi	604,1	281,0 ± 43,4	AS	37,3	73,4 ± 24,2
DL	363,1	291,2 ± 51,1	SH	39,1	43,0 ± 5,7
DE	297,3	304,2 ± 51,6	Lc	42,9	-
BB	48,4	109,1 ± 26,5	RH	23,1	31,3 ± 8,4

Conclusion

The method of Ne calculations based on individual increase in inbreeding (Gutiérrez et al., 2008) provides reliable and applicable estimators to classify the degree of endangerment of different German pig herdbook populations. Only in the situation of shallow pedigree information the application of methods based on variance of family sizes seems to be justified within these populations.

References

- Cervantes, I., Goyache, F., Molina, A., Valera, M, Gutiérrez, J.P. (2008). *J. Anim. Breed. Genet.*, 125:301-310.
- Gutiérrez, J.P, Molina, A., Valera M., Cervantes I., Goyache, F. (2008). *Genet. Sel. Evol.*, 40:359–378.
- Gutiérrez, J.P, Cervantes I., Goyache, F. (2009). *J. Anim. Breed. Genet.*, 126:327-332.
- Hill, W.G. (1979). *Genetics*, 92:317-322.
- Maignel, L., Boichard ,D., Verrier, E. (1996). *Interbull Bull.* 14:49-54.
- Stranden, I., Vuori, K. (2006). *Congress on Genetics Applied to Livestock Production, August 13-18, 2006, Belo Horizonte, MG, Brasil.* 4 p.
- ZDS (Zentralverband der deutschen Schweineproduktion) (2009): *Schweineproduktion, 2008 in Deutschland.*