

Estimate Of The Effective Population Size (N_e) For The Horse Breed Saxon-Thuringian Heavy Warmblood

C. Kehr*, M. Klunker*, R. Fischer†, E. Groeneveld‡ and U. Bergfeld†

Introduction

Maintaining genetic variability plays an increasingly socially relevant role, even in the field of livestock breeding. With the establishment of the "National Programme for Animal Genetic Resources" (TGR-NFTR (2003)) as well as the amendment to the German livestock breeding regulations of 2006, Germany has already taken the first steps towards this aim. Evaluation of the endangered status in the TGR-NFTR takes place on the basis of the effective population size (N_e). These parameters were calculated in a project sponsored by the Federal State of Saxony (Kehr et al. (2009)) for the livestock breeds living in Saxony. This article focuses primarily on the N_e -values for the horse breed Saxon-Thuringian Heavy Warmblood population (SW) because the main breeding region for this breed is located in the federal states of Saxony and Thuringia (Germany). Although the SW population has stabilised following a genetic bottleneck effect during the 1970s, the existence of the horse breed is still threatened in Germany, due to low animal numbers. In calculating the N_e , various pedigree-based methods pursuing different approaches will be put forward. This study will also examine to what extent the SWs' pedigree completeness index (PCI) affects the N_e .

Material and methods

Material. The SW has been bred in Saxony and Thuringia for over 100 years, although it originated in the breeding regions of Oldenburg and East Frisia. During the 1960s and 70s the breed nearly died out when breeding focused on horses for riding and sports. In 1973, the Ministry of Agriculture of the German Democratic Republic (GDR) decided to exclude all SW stallions from breeding programmes. In order to maintain the SW breed, despite this decree, the director of the state stud farm in Moritzburg, Ms. Dr. Steiner, set approximately some stallions in the driving school and, thus, prevented the rapid extinction of this breed. The basis for calculating the N_e of the SW in the present study are studbook data, taken from the Saxon-Thuringian Horse Breeding Association e.V.. The fact that breeding is supervised by an association and that a closed studbook has been used for the breed since 2003 ensures high data quality. The pedigree includes 12,355 records (registered horses) from the year 1907 through 2008. For the SW the generation interval (gi) for the selection path between parents to selected offspring was 9.6 years.

*University of Applied Science (HTW), 01326 Dresden, Germany

†LfULG Köllitsch, 04886 Köllitsch, Germany

‡Institute for Farm Animal Genetics (FLI), 31535 Neustadt/Mariensee, Germany

Methods. To estimate the N_e , boundary conditions for the pedigree in relation to the population need to be defined:

1. Method of N_e calculation
2. Time period for estimating the N_e (all years or current generation)
3. Starting year of pedigree for calculation F
4. Constraints on the pedigree completeness index (PCI)
5. Basis of generational depth in the pedigree

For this study, different aspects of the issues mentioned above will be examined. Calculation of the N_e were done with the POPREP software system (Groeneveld et al. (2009)) for the following census and pedigree based methods:

- 1) N_e : Census-based according to Falconer and Mackay (1996)
- 2) N_e : ΔF from path offspring – direct parents (p), according to Falconer and Mackay (1996)
- 3) N_e : ΔF from path offspring – animals born a generation interval before (g)
- 4) N_e : additive-genetic relationship, Δf from path offspring - animals born a generation interval before (g)
- 5) N_e : ΔF based on log regression of F (Perez-Enciso (1995)) with time interval of one generation (1999-2008) and pedigree completeness index (PCI) = 0 (a) or 70% (b).

Furthermore, the effect of the PCI on the estimate of N_e (method 5) is investigated.

Results and discussion

The number of breeding horses represented in each birth year are shown in Figure 1a, clearly depicting the bottle neck in the late seventies. Figure 1 b) shows the development of the PCI for pedigree depths of 1 to 6 generations per birth year.

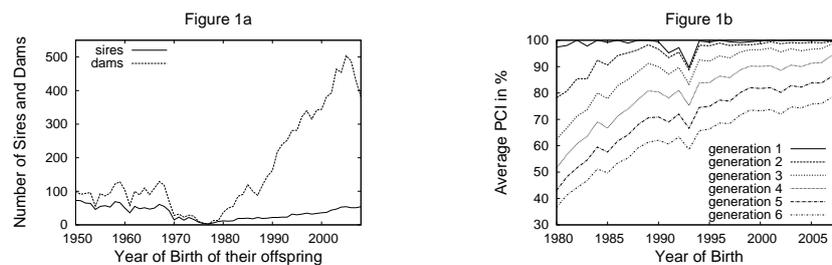


Figure 1: 1a) Number of sires and dams in the birth year of their offspring; 1b) Pedigree completeness index (PCI) of the offspring

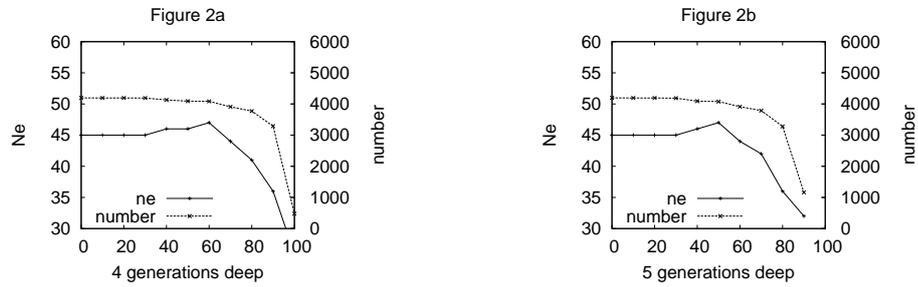


Figure 2: PCI and N_e (method 5) for 4 (2a) and 5 (2b) generational depth pedigrees calculated by log-regression for rate of inbreeding (animals born between 1999 and 2008)

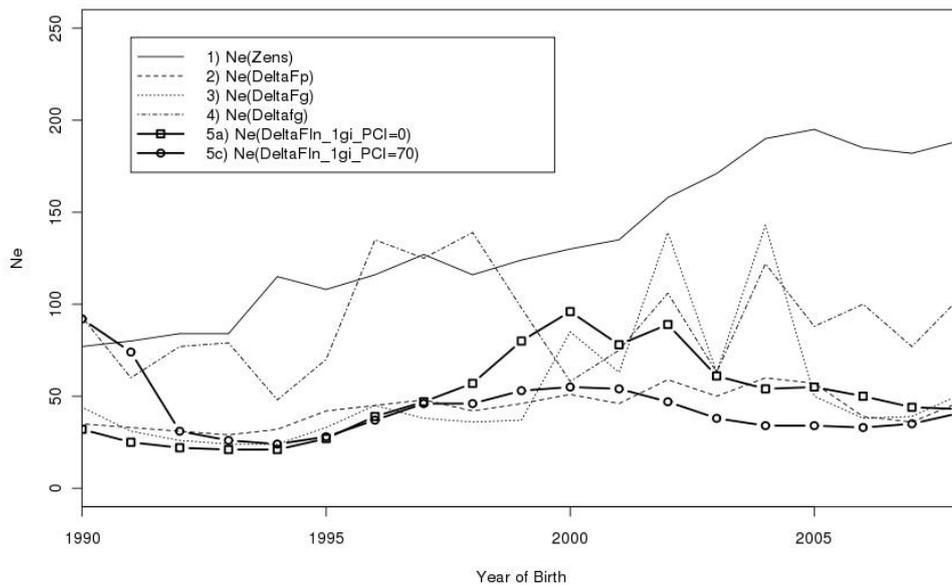


Figure 3) N_e in relation to the calculation method and the PCI

As the requirements for horses to be included in the analysis on the basis of the PCI increase from 0 to 100, so Figure 2 shows the relation of N_e plotted on the PCI required for the horses to be considered in the computation of N_e . This increase in stringency of the pedigree com-

pletteness obviously results in a decrease of number of animals involved. The relationship is shown for the two pedigree depths of 4 and 5 generations. Figure 2 shows for this population a decline of N_e for high levels of PCI.

Figure 3 depicts the N_e according to birth year and methodology. The calculated N_e -values for horses born during the year 2007 lie between 36 and 99 for methods 2, 3, 4, and 5a (all with a PCI constraint of 0). N_e for method 5b with a PCI of 70% for the 5 generation pedigree depth was 35, while the census based estimate was 182.

The latter estimate clearly has to be disregarded as the assumptions for method 1 are not met in our population.

Conclusion

For the current population (offspring from birth year 2005 and onwards), the N_e -values from methods 2, 3, 5 are between 35 and 50. The evaluation of the PCI gradient shows that the N_e will even be smaller if the PCI is based on a pedigree depth of 5 generations. Independent of the constraints in terms of PCI and number of generations, the SW breed would fall into the lowest category "phenotypically sustainable" as defined by the TGR-NFTR (2003), and therefore, appears to be critically endangered.

For the calculation of the N_e , further in-depth research needs to be done, to examine how incomplete pedigrees (which are abundant even in studbooks) affect the estimates and which methods can be used to account for gaps to obtain sensible results.

References

- Falconer, D. S. and Mackay, T. F. C. (1996). Longman, Essex, U.K., 4th ed. edition.
- Groeneveld, E., v.d. Westhuizen, B., Maiwashe, A., et al. (2009). *Genetics and Molecular Research (GMR)*, 8(3):1158–1178.
- Kehr, C., Klunker, M., and Fischer, R. (2009). *LfULG Schriftenreihe*, 37/2008.
- Perez-Enciso, M. (1995). *J.Anim.Breed.Genet.*, 112:327–332.
- TGR-NFTR (2003). URL:<http://tgrdeu.genres.de>.