

From Theory To Praxis: A Decision Tree For An Adequate Management Of Genetic Resources In Dairy Cattle Populations

F. Köhn*, C. Edel*, R. Emmerling* and K.-U. Götz*

Introduction

In the year 2004, an EU-wide council regulation on the conservation of genetic resources in agriculture (No.1590/2004) was enacted. As a consequence, livestock breeds should be monitored regularly and special programmes for the conservation of animal genetic resources should be established if necessary. Several software and web-based tools exist that facilitate the monitoring of genetic resources. All of them give estimates for different population parameters like the inbreeding and coancestry coefficients, the pedigree completeness, and the effective population size (N_e) that, thoroughly interpreted, can be used to categorize populations with respect to the risk of extinction.

The main challenge for breeding organisations, breeders and politicians is to draw the right conclusions from the monitoring results and to react if those are alarming. The most important reaction is the establishment or adaptation of a breeding or conservation programme in which tools for the management of genetic variability are incorporated. There is a huge amount of studies dealing with the development of different types of breeding programmes controlling the increase of inbreeding and the amount of drift. However, most of these studies deal with simulated data. The biggest difficulty for decision makers is to choose an optimal approach for the breed under real life conditions, additionally considering aspects of management and economical restrictions.

Therefore, the aim of this study was to develop a decision tree that might help in finding the most adequate strategy based on the results of a genetic monitoring in dairy cattle populations.

Current status in dairy cattle breeding

There are several characteristics in dairy cattle breeding that might promote a decrease in genetic diversity. Usually, the family structure is a harem structure with few males and many females resulting in large half-sib families. The extensive use of only a few top sires can result in a high variation of family size. Further, there are reproductive limitations in females.

The mating strategy in managed dairy cattle populations is hierarchical with overlapping generations. Additionally, most populations are selected using BLUP-EBVs resulting in a higher probability of selecting related animals (Dempfle (1990)). Managed breeding populations usually have complete pedigree information available whereas in small and unmanaged populations pedigrees are often incomplete or even not existent. An important aspect when incorporating tools for diversity management in breeding programmes is that the main focus is on

*Bavarian State Research Centre for Agriculture, Institute of Animal Breeding, 85586 Poing-Grub, Germany

genetic progress especially in highly competitive breeds.

Additional factors that have to be considered are management issues (e.g. bull testing capacity), economical considerations (e.g. financial support for breeders) and most important, acceptance of the breeders for the necessary actions.

Tools for the management of genetic resources

The design of the breeding programme is most important for the management of genetic resources because it directly influences the increase of inbreeding (ΔF) and the amount of genetic drift in a population. A simple and efficient way to slow down ΔF is to balance the sex ratio ($N_m \approx N_f$) because N_e is maximal and equal to N when $N_m = N_f$ (Caballero (1994)). This strategy is often overlooked because testing capacities are limited and there are concerns about losing selection intensity. However, even a small increase in N_m might have a large effect on N_e and negative side effects are negligible. Additionally, equalizing sire contributions (balancing sire family sizes, **BSC**) is also a simple and powerful concept. It is a well-known fact of population genetics theory, that by completely balancing family sizes a N_e of $2N$ can be achieved. Thus, strategies aiming at reducing family size variation are well worth to be considered. Selection within families can help and again the assumed negative impact on selection intensities is generally overrated (Dempfle (1990)). For populations with regular pedigree recording and a strong impact on genetic progress, optimum contribution selection (**OC**) (Meuwissen (1997)) can be the method of choice. However, implementing OC in an existing breeding programme requires a minimum amount of specialised knowledge.

Further, controlling the mating design like factorial or hierarchical mating (Sorensen et al. (2005)), matings that focus on optimizing a criterion, e.g. the average coancestry given optimized contributions (Sonesson and Meuwissen (2000, 2002)), or matings focusing on long-term genetic contributions (Woolliams and Bijma (2000)) can be considered. However, these methods presume a level of control that is hardly given in practical breeding. This is also true for advanced strategies that use DNA information to control selection and mating decisions aiming at a high degree of diversity in the next generation (Fernandez et al. (2004)). Controlled crossbreeding with similar breeds reduces the increase in ΔF but not the loss of breed specific alleles. A final strategy to avoid the irreversible loss of genes of populations close to extinction is merging them to a phenotypically similar population and creating a conservation plan for the meta-population (Bennewitz et al. (2008)). Additionally, cryo-conservation can be considered for creating a genetic back-up of a population.

A necessary tool to avoid a further decrease in population size in small populations are subsidies for breeders paid for each breeding animal he kept.

Taking the right path

We developed a decision tree (figure 1) for choosing adequate breeding and management tools for minimizing genetic drift in cattle populations. The root of the tree is the breeding population consisting of all breeding males and females. The first decision criterion is the true size of the breeding population. Following the FAO categories, a population can be categorized "not at risk" if it counts at least 1000 breeding females and at least 20 breeding males (Scherf (2000)). From this node on, the tree splits into a left part for populations not at risk and into

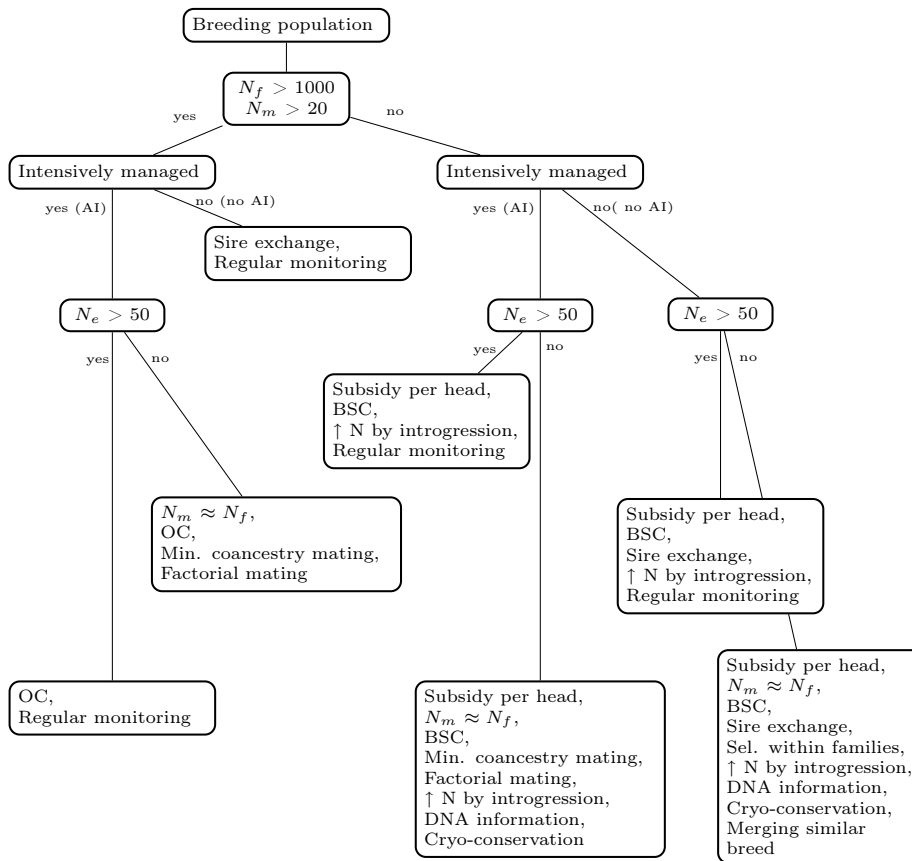


Figure 1: Decision tree for choosing adequate breeding and management tools for the conservation of genetic resources in dairy cattle populations

a right part for populations at risk. The next decision criterion is the intensity of management of the population. Intensively managed populations in our definition use an outlined breeding programme (artificial insemination, strong selection on the bull paths) to achieve a defined breeding goal. Breeding animals are registered in a herd book and there is a high impact on genetic progress. The case that a dairy cattle population has a high number of breeding animals but is not intensively managed might be rare in developed countries, but might occur in developing countries. An important parameter for the categorization of populations into risk classes is the N_e that is incorporated in the tree as last decision criterion. An N_e of 50 expresses an increase in ΔF of 1 % per generation. All conserved populations should achieve this minimum N_e (FAO (1998)). We assumed that the N_e of non-managed populations with a high population size is unlikely to drop below the critical level of 50.

As an example, monitoring results of two German dairy cattle breeds, Gelbvieh and Murnau-

Werdenfelser, are used to demonstrate the power of the tree. Gelbvieh has a population size of about 11,000 animals with 2,730 herd book cows distributed on 130 herd book farms (ASR (2009)), indicating the breed to be not at risk, whereas the population size is decreasing. There is a high AI proportion of 95 %. Gelbvieh has an N_e of around 80. As a dual purpose breed, Gelbvieh still has competitiveness with respect to milk production, thus genetic progress is mandatory. Using the OC method might be an adequate strategy and a regular monitoring of genetic variability should be conducted.

The Murnau–Werdenfelser breed is a very small and extensively managed breed counting 1,150 animals with 460 of them being herd book cows distributed over 9 herd book farms. In recent years, the population size was stable due to a considerable introduction of Tarentaise cattle in the population. The N_e is around 20. Regarding the true population size, this critical N_e is assumed to result from an inappropriate management of the population. Following always the right branch on every decision node, solutions for this breed are the payment of subsidies, a balanced sex ratio, fixed contributions of selected animals to avoid loss of genes, controlled sire exchange between herds without AI, selection within families, controlled cross-breeding, use of DNA material and cryo-conserves, and as a last resort the merge with a similar threatened breed to one meta-population.

Acknowledgements

This project was financed by the Ministry of Food, Agriculture and Consumer Protection (BMELV) and managed by the Federal Office for Agriculture and Food (BLE).

References

- ASR (2009). Technical report, Arbeitsgemeinschaft Sueddeutscher Rinderzucht- und Besamungsorganisationen e.V.
- Bennewitz, J., Simianer, H., and Meuwissen, T. H. E. (2008). *J. Dairy Sci.*, 91(6):2512–2519.
- Caballero, A. (1994). *Heredity*, 73:657–679.
- Dempfle, L. (1990). *J. Dairy Sci.*, 73(9):2593–2600.
- FAO (1998). Technical report, FAO.
- Fernandez, J., Toro, M. A., and Caballero, A. (2004). *Conservation Biology*, 18(5):1358–1367.
- Meuwissen, T. H. E. (1997). *J. Anim. Sci.*, 75:934–940.
- Scherf, B. D. (2000). FAO, Rome, 3rd edition.
- Sonesson, A. and Meuwissen, T. (2000). *Genetics Selection Evolution*, 32(3):231 – 248.
- Sonesson, A. and Meuwissen, T. (2002). *Genetics Selection Evolution*, 34(1):23 – 39.
- Sorensen, A., Berg, P., and Woolliams, J. (2005). *Genetics Selection Evolution*, 37(1):57 – 81.
- Woolliams, J. A. and Bijma, P. (2000). *Genetics*, 154:1851–1864.