Monitoring of livestock breeds at risk in Portugal

Luís Telo da Gama, Nuno Carolino and António Vicente
Unidade de Investigação de Recursos Genéticos, Reprodução e Melhoramento Animal – INRB
Fonte Boa, 2000-763 Vale de Santarém, PORTUGAL
genetica.ezn@mail.telepac.pt

The heterogeneity of climate, soil, social, etc., conditions prevailing in different regions of the country have resulted in the development of a large number of native breeds of livestock in Portugal (15 breeds of cattle, 15 of sheep, 5 of goats, 3 of pigs and 3 of horses). The majority of these breeds is considered to be at risk of extinction and/or abandonment, mostly as a result of uncontrolled and unplanned crossbreeding with exotic breeds. In the last few years, several measures have been taken to reverse the declining trend of native breeds, including the establishment of herdbooks managed by breed associations, development of selection programs, recognition of protected designations of origin, and inclusion in the group of breeds at risk and eligible for financial support in the framework of European programs for conservation of genetic resources. However, the bottlenecks that these breeds have experienced in the recent past may have resulted in irreversible losses in genetic diversity, even though preventing extinction is currently the major, if not the only, concern.

Management of genetic diversity of a breed is essential for its sustainable use in the future, because a limited number of breeders will inevitably lead to increased inbreeding, and thus to a reduction in additive genetic variance and possibly to inbreeding depression. As a consequence, controlling inbreeding is usually one of the major targets in conservation and selection programs. Classically, monitoring of genetic diversity has been carried out by assessing the evolution of inbreeding and relationships in the population of interest, often converted to effective population size, which is regarded as a good indicator of the risk of genetic erosion. Nevertheless, inbreeding-related parameters are dependent on the completeness of pedigree information, and changes in inbreeding due to different breeding practices (e.g., genetic bottlenecks) are not immediately perceivable. Therefore, parameters based on the probability of genetic origin from different herds, founders, and ancestors have been proposed as complementary indicators, as they provide more insight into changes occurring in the population over a short period of time (Boichard et al., 1997).

In order to take appropriate measures aimed at maintaining genetic variability for the future, it is therefore important to:

- assess the risk of extinction of a given breed, and monitor the factors contributing to it
- evaluate the occurrence of genetic erosion in a breed, by surveying the breeding practices that may affect within-breed genetic variability.

These two approaches have been followed in investigating the most critical issues affecting genetic variability in livestock breeds in Portugal, and the resulting indicators were used to develop guidelines and recommendations for “in situ” conservation programs. The baseline information deriving from demographic analyses has provided interesting clues on how different approaches may be required to address conservation of genetic resources, depending on the scenario considered.

As an example of the need for different approaches, Table 1 summarizes key demographic indicators computed for the Alentejana cattle breed, and the Malhado de Alcobaça pig breed. The Alentejana is the major native breed of cattle in Portugal, and it has gone through a period of strong census decline in the 1970's, but has now recovered to about 12000 cows registered in the herdbook. On the other hand, Malhado de Alcobaça is a pig breed which was thought to be extinct, and has recovered from a very narrow base to less than 200 registered sows in only one herd. Pedigree information on these breeds was analyzed, to assess demographic trends and adopt appropriate conservation strategies, as might be needed for their specific situation.

Even though the two breeds have a rather distinct population size and development history, their loss of genetic variability is surprisingly similar, i.e., the rate of inbreeding per generation is very much alike. Indeed, in both cases effective population size is nearly half that recommended as the minimum number to maintain genetic diversity, both in conservation (Meuwissen and Woolliams, 1994; FAO, 1998) and in selection programs (Goddard and Smith, 1990), and represents a warning to reassess the management of these breeds in the future.

The major point, however, is that what seemed to be the same pattern of genetic erosion resulted from two very distinct situations; while the high rate of inbreeding in Malhado de Alcobaça results from a very small breeding population, in Alentejana the increase in inbreeding was mainly due to the extensive use of a few prominent sires and sire families (less than 3 effective Y-chromosomes), with limited exchange of breeding animals across herds.

Table 1. Demographic parameters in Alentejana cattle[1] and Malhado de Alcobaça pigs[2]

	Alentejana cattle	Malhado de Alcobaça pigs
Number of breeding females in the herdbook	12,000	160
Reference population for calculations (n)	28,631[3]	236[4]
Number of generations known	4.1	4.2
Average inbreeding coefficient (%)	8.35	9.03
Animals with inbreeding coefficient ≠ 0 (%)	79	98
ΔF/year (%)	0.33	0.76
ΔF/generation (%)	2.15	1.99
Effective population size	23.3	25.1
Number of founders	6,842	72
Effective numbers		
Founders	121.6	13.1
Ancestors	55.0	12.7
Contribution to 50% of the genetic pool		
Founders	46	5
Ancestors	33	5
Contribution of 2 most influential ancestors (%)	15.1	28.1

[1] Carolino and Gama (2008).

[2] Vicente (2006).

[3] Calves born between 2000 and 2003

[4] Pigs born between 2003 and 2004

The importance of different factors contributing to genetic erosion in the two populations could only be clarified by assessing the genetic contributions of founders and ancestors in each breed. These results indicate that the very narrow base from which Malhado de Alcobaça was established would inevitably result in losses of genetic variability, and this pattern is expected to continue in the future. On the other hand, the situation in Alentejana suggests that strategies aimed at minimizing inbreeding must be adopted urgently, to avoid further losses of genetic diversity, for example by enhancing the exchange of genetic material across herds, and by placing restrictions on family size.

The objective of maintaining long term genetic diversity in “in situ” conservation programs requires a detailed analysis of the major factors contributing to genetic erosion in a given population, to develop the appropriate strategies aimed at minimizing genetic erosion. Factors such as the rate of inbreeding and effective population size are clearly insufficient as indicators of the path to be followed.

Literature cited

Boichard, D., L. Maignel, and E. Verrier. 1997. The value of using probabilities of gene origin to measure genetic variability in a population. Genet. Sel. Evol. 29:5–23.

Carolino, N. and L.T. Gama. 2008. Indicators of genetic erosion in an endangered population: the Alentejana cattle breed in Portugal. Journal of Animal Science 86:47.

FAO. 1998. Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans: Management of Small Populations at Risk. FAO, Rome, Italy.

Goddard, M. G., and C. Smith. 1990. Optimum number of bull sires in dairy cattle breeding. J. Dairy Sci. 73:1113–1122.

Meuwissen, T. H. E., and J. A. Woolliams. 1994. Effective sizes of livestock populations to prevent a decline in fitness. Theor. Appl. Genet. 89:1019–1026.

Vicente, A. 2006. Characterization of the “Malhado de Alcobaça” swine population. M.S. Thesis. Faculty of Veterinary Medicine. Technical University of Lisbon. 174 pp.