



Adding value to data emanating from routine animal recording processes

C. Hunlun

SA Stud Book and Animal Improvement Association, Bloemfontein, South Africa

Abstract

Animal breeders, like any other entrepreneurs, operate in a dynamic and competitive industry. Reliable and applicable information forms the core of good management and strategic decisions. By utilising existing records of origin, parentage, ownership and other features of recorded animals, breeders and breeders' organisations can improve the quality of the decisions they have to make. Breeders' organisations are generally in a good position to provide a value-adding service to their breeders and in the process make basic animal recording more cost-effective.

Some examples of value-adding to basic animal recording data and processes are given and discussed.

Keywords: animal recording, value adding, demography, pedigree analysis, breeding structure, Bonsmara

1. Introduction

The global community, in all its spheres, finds itself in the midst of an information revolution. Applicable and reliable information forms the basis of almost all processes and is at the core of any good management or strategic decision. It is almost inconceivable that any project or business can succeed without good management decisions. It is the business of animal breeders and breeders' organisations to constantly improve their animals genetically in order to meet the demands of their markets. To achieve this, information generated from basic routine animal recording processes can play a vital role, whether it is origin-, ownership- or pedigree information.

Generally, significant amounts of time, effort and money are spent on the collection, processing and storage of data that is used for the primary purposes of animal- and herd identification, parentage recording and herdbook registration. By utilising the same data to generate additional information, breeders and breeders' organisations can improve the quality of the decisions they have to make and in the process improve their competitive edge in the industry. The processes that drive genetic change in animal populations depend largely on the analytical use of pedigree and ownership information as recorded by breeders, breeders' organisations and recording authorities. Breeders' organisations and recording authorities are generally in a good position to provide a value-adding service to their customers and in the process make basic animal recording more cost-effective.

Demographic parameters and genetic analyses using pedigree information have been used extensively to assess the genetic structure of livestock populations. Some examples of such analyses may be found for horses (Moureaux *et al.*, 1996), dairy cattle (Maignel *et al.*, 1996; Sölkner *et al.*, 1998), beef cattle (Gutiérrez *et al.*, 2003) and sheep (Huby *et al.*, 2003). De Rochambeau *et al.* (2000) give an overview of some of the applicable methodology. The information that emanates from these kinds of analyses does not only have academic value but could also play a major role in the animal improvement efforts of breeders and breeders' organisations. The use of some of these parameters may give significant insight into the status of herds or breeds regarding the size of breeding populations, breeding practices, genetic variability and effective population sizes.

2. Demography

In the context of livestock populations, demographic analysis uses administrative records to develop an estimate of the relevant population(s), whether it is on a herd or breed level, in terms of the size, composition and spatial distribution of the populations and how these features change over time. Data is

generally obtained from a census of the population (herd / breed count) that is derived from registry records of events like births, deaths, cancellations and migrations (transfers of ownership).

Elements of demography are used to assist breeders to predict the demand for their animals and to analyse the demands on a breeder or a breeders' organisation's capacity in terms of products and services. It can also be used as an interpretive and analytic tool for the comparison of different markets and trends within a herd or breed. Breeders' organisations have an interest in the number and characteristics of their breeders and the animals in their possession so they can optimize their service to their breeders and focus the promotion of the breed and the sale of animals on behalf of the breeders. Demographic analysis is also used to reveal some of the consequences of the genetic management of herds and breeds and to contribute to the interpretation and understanding of genetic results.

A demographic analysis was done for the Bonsmara, a South African beef cattle breed (Hunlun *et al.*, 2009), and some of the results from that study will be used to illustrate the possible uses of these statistics.

2.1 Population Change

Livestock populations are inherently dynamic and continue to change. Changes in numbers of animals and herds have a wide application and can, amongst others, be used to describe the developmental history of a population and to make certain predictions about the future development of a population. The evolution of the number of herds and animals in the Bonsmara breed since its foundation is depicted in Figure 1.

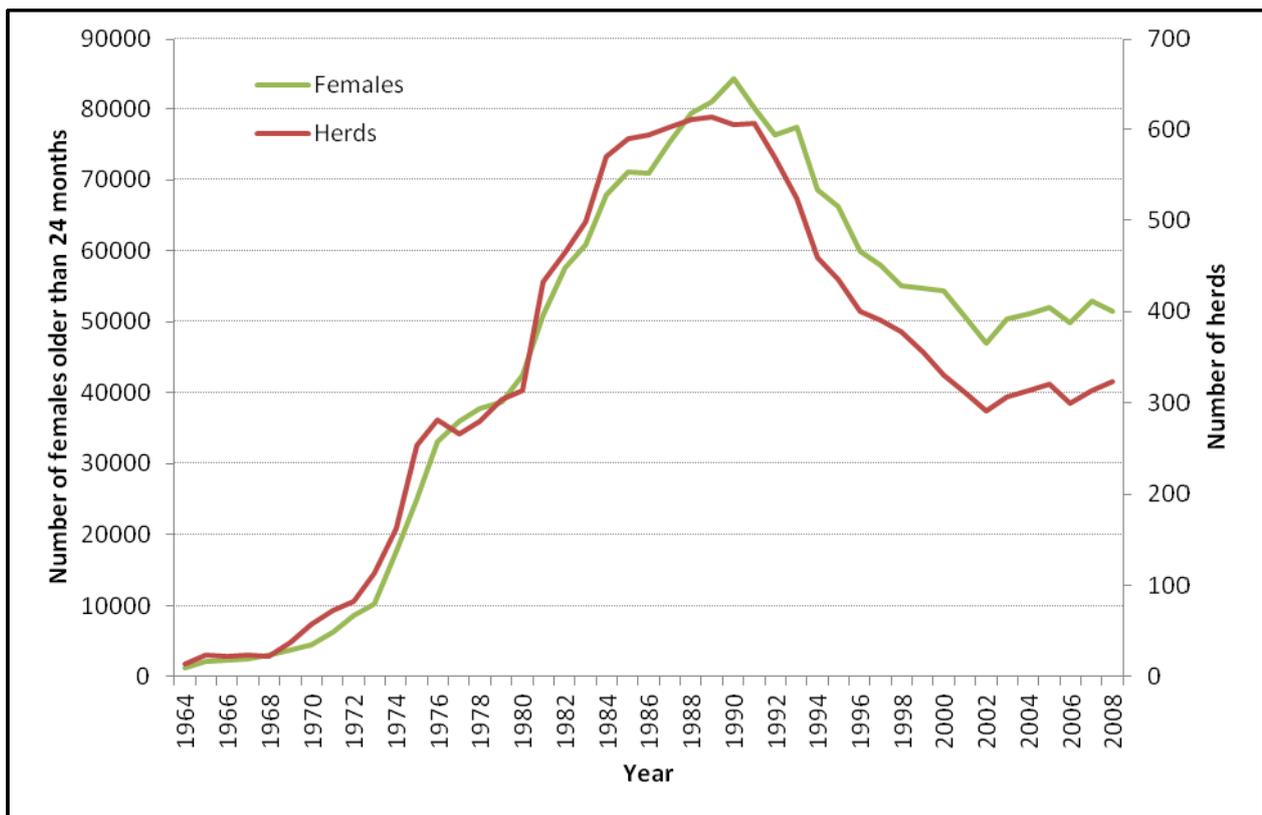


Figure 1. Number of herds and female animals older than 24 months in the Bonsmara breed (Hunlun *et al.*, 2009).

From Figure 1 several phases can be identified in the history of the breed, each phase having its own causes and consequences. Some interesting and important information can be learned about the evolution of average herd size over time and the effect of important events in the history of the breed on the average herd size, like the secession of the Namibian Bonsmara breeders to form their own breeders' society in 1993/94 and two periods of rather widespread drought in the summers of 1991/92 and 1994/95.

2.2 Population Composition

Population composition is the description of a population in terms of characteristics such as age, breed / line, gender or recording / registration status. These descriptions are sometimes necessary for understanding the dynamics of a breed from a historical perspective, for comparative research and to provide perspective on the capacity of the breed for future growth and, to some extent, genetic change. The characteristics of a herd or breed in terms of age and gender is often presented and compared by using a population pyramid (Figure 2).

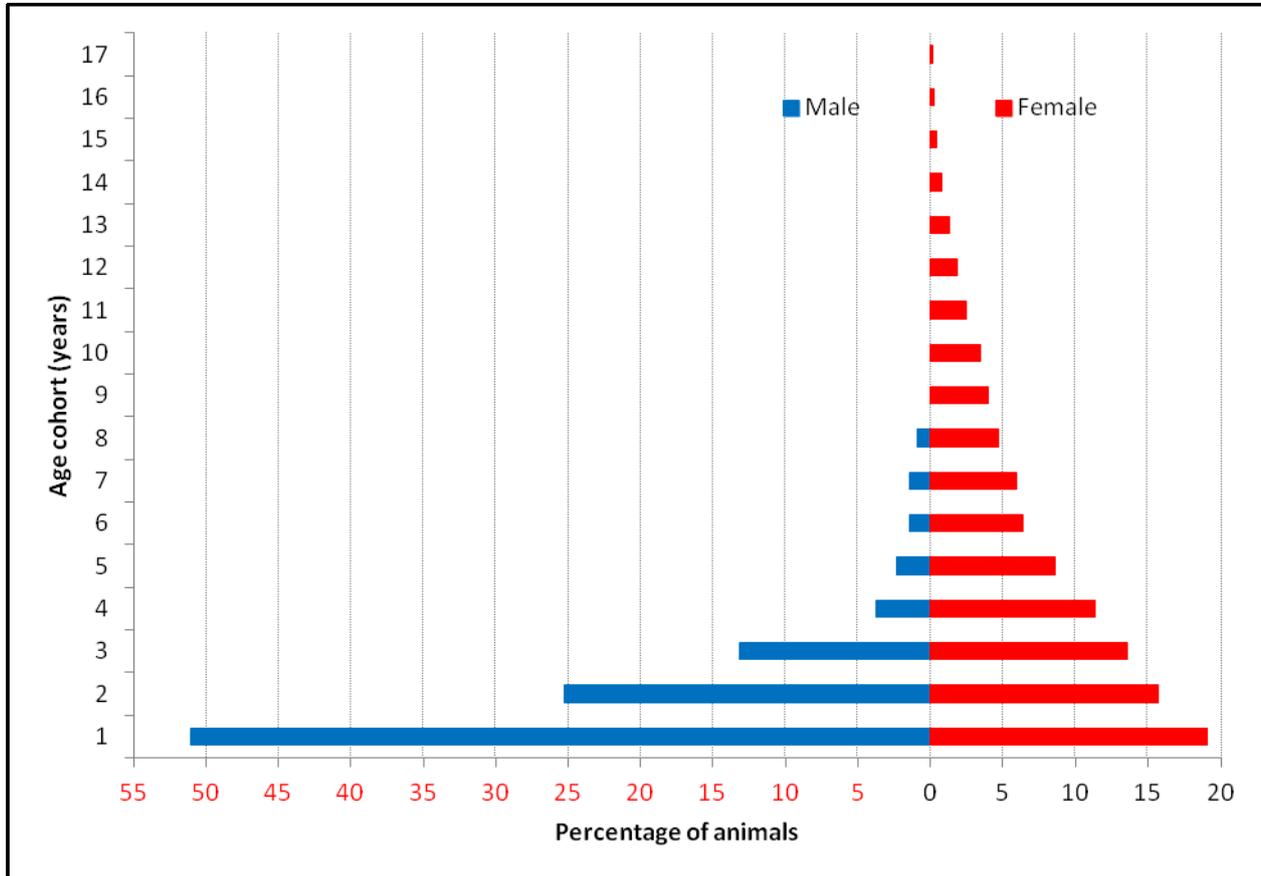


Figure 2. Age and gender distribution in the Bonsmara breed, as in July 2008 (Hunlun et al., 2009).

In July 2008 the Bonsmara breed consisted of 26% male animals and 74% female animals of all ages. The age distribution of these animals is very typical and shows a healthy age structure in the population with a noticeable degree of momentum for future growth appearing in the younger female age categories – the higher proportions of females in the categories 2-3 years and 3-4 years old (new entrants into the breeding population) bodes well for future growth in the breed.

The age distribution (Figure 2) follows a typical negative growth function which has very high predictive properties. In the case of Bonsmara females in 2008 –

$$y = 20.047 - 7.14 \ln(x) \quad (R^2 = 0.9706)$$

where y – the percentage of female animals in an age cohort

a – intercept with the horizontal (y -) axis, the percentage females in the first age cohort

b – logarithmic regression coefficient

x – age cohort

From this equation the annual erosion rates can be calculated between different age cohorts – in 2008 the erosion rate for Bonsmara heifers was *ca.* 25% between the groups 0-1 to 1-2 years of age and *ca.* 20% between the groups 1-2 to 2-3 years of age. The erosion rate for cows starts at *ca.* 17% for first calvers and decreases to *ca.* 15% between the cohorts 5-6 to 6-7 years of age but then increases steadily to *ca.* 30% between the age groups 12-13 to 13-14 years of age. The regression coefficients and

intercepts show a very high repeatability within breeds over years and are generally statistically significant.

The distribution of recording status in the breed, across the two genders is reflected in Table 1.

Table 1. Distribution of recording status of Bonsmara animals as in July 2008 (Hunlun *et al.*, 2009).

	Male	Female
Number of animals	27 319	77 320
Registration Pending (%)	14.12	3.50
Foundation (%)	-	4.90
Appendix A (%)	-	14.38
Appendix B (%)	11.61	12.11
Studbook Proper (%)	74.24	65.11

The majority of active animals in the breed are fully registered animals (SP). The high proportion of male SP animals is to be expected because only SP bulls can be used to beget registrable progeny. The proportion of Appendix A females is higher than that of the Appendix B females, which is an indication that there is a renewed interest in the upgrading programme of the breed and that the breed is bound to display positive growth in the future.

2.3 Generation interval

Generation interval is defined as the average age of parents when their 'useful' progeny are born – an offspring is considered to be useful if it, in turn, left at least one further offspring (Gutiérrez *et al.*, 2003). The evolution of the realised average generation interval (L) of the Bonsmara is shown in Table 2 and to some extent reflects the developmental history of the breed – a shorter generation interval during the formative years, gradually increasing as the breed established itself, with a slight decrease during the period when the breed experienced its highest census. The latest realised average generation interval for the breed (2007/2008) is 5.61 years, which is comparable to that of other beef breeds in South Africa. The average dam component (5.79 years) of the latest generation interval was slightly higher than the corresponding sire component (5.42 years).

2.4 Effective population size

Demographic parameters can also be used to infer the evolution of genetic variability in a breed by estimating the effective population size, N_e , from the numbers of parents in the breed (Gandini *et al.*, 2004). Although the use of Wright's well known equation for the effective population size (Wright, 1931),

$$N_e = 4MF/(M+F)$$

where M and F are numbers of reproducing males and females respectively, yields a gross overestimate of the true effective population size, it serves as a convenient descriptive measure. When used over time in the same population, it gives a fair indication of the relative changes in the genetic variability and genetic drift that may have occurred in the population.

The number of calves born per year, the number of sires and dams with progeny born in a particular year and the effective population size for the Bonsmara breed is also presented in Table 2.

Table 2. Number of Bonsmara herds, calves born per year, number of parents, effective population size (N_e) and average generation interval (L) (Hunlun *et al.*, 2009).

Year	Herds	Calves born	Male calves	Female calves	Dams	Sires	N_e	L
1972/73	42	551	152	399	281	92	277	4.34
1977/78	213	4881	794	4087	3662	572	1979	5.01
1982/83	405	17608	3604	14004	17244	1313	4880	5.67
1987/88	514	30332	9109	21223	30024	1848	6963	5.65
1992/93	462	35288	13476	21812	34892	1958	7416	5.57
1997/98	353	32149	13792	18357	31411	1742	6602	5.67
2002/03	296	28476	13119	15357	27861	1577	5970	5.61
2007/08	282	25138	12156	12982	24859	1433	5420	-

The realised effective population size can be estimated from the rate of inbreeding in a population (ΔF), which can be calculated from the existing parentage records in breed's registry (see § 3.3).

2.5 Proportion Retained

On average 43.63% of the female Bonsmara calves born eventually became mothers of Bonsmara calves and 5.65% of the male calves born eventually sired a Bonsmara calf (Hunlun *et al.*, 2009). These figures, also referred to as the 'Proportion Retained' (PR), can be readily calculated from registry records and give an indication of the selection intensity in the breed. The PR differs somewhat between calf crops and also reflects the dynamics of the breed in terms of the length of the productive life of animals and selection intensity. The PR tends to be somewhat higher during times when the breed is growing positively.

3. Pedigree analysis

It has long been established that selection changes the relationships between reproducing animals (Lush, 1946; Robertson, 1961) and that the inbreeding in the progeny of selected parents is higher than under pure genetic drift. Some simple demographic parameters have a large impact on the evolution of the genetic variability within a population and the effects of these depend largely on the management of the population in terms of the number of male and female parents, (dis)equilibrium of progeny size and length of reproductive life.

The genetic variability in a population can be studied through the analysis of the pedigree data of a breed and focuses mainly on the evolution of a population's gene pool. The fact that almost all the South African beef cattle breeds have initiated breed improvement programmes utilizing BLUP methodology necessitates periodic investigations of this kind. Verrier *et al.* (1991) have argued that the use of BLUP-derived selection parameters in populations of limited effective size leads to profound changes in the structure of the populations and that these measures could probably not be considered to be the optimum selection criterion in terms of the cumulated genetic progress or the maintenance of genetic variability.

The genetic structure of the Bonsmara breed was analysed recently (Hunlun, 2009; Van der Westhuizen, 2009) and some of the results of those studies will be used to demonstrate the possible use of information emanating from pedigree analyses to support the decision making processes of breeders and breeders' organisations.

3.1 Important ancestors

In most practical animal breeding situations it is important to know which ancestors are the most influential in a given population or sub-population. Several methods exist by which the contributions of ancestors to the genetic make-up of individual animals, herds or even whole breeds can be calculated. These methods vary in sophistication from mere summaries of numbers of progenies born per ancestor to the calculation of the relative contributions of ancestors to a specific cohort or generation of progeny, taking the numbers of effective progeny and the numbers of generations separating ancestors and progeny into account. Methods using the theory of gene origin to estimate the effective number of founders and ancestors in a population (Boichard *et al.*, 1997) can also yield information about the relative contribution of ancestors. Even more important is the fact that the parameters emanating from this analysis are considered to be very good indicators of genetic variation in the population analysed and it is less sensitive to the completeness of the pedigree data in the population. Parameters derived from probabilities of gene origin are especially useful in small populations and in populations where the genetic management is divided amongst several smaller units (herds).

Information about the relative importance of ancestors can be used with coefficients of additive genetic relationships (§ 3.2) to establish and manage breeding lines and to limit the effects of inbreeding in future generations.

3.2 Pedigree completeness

An in-depth analysis of the pedigree completeness level of a population is important since all results in terms of inbreeding and relationships are dependent upon it. Van der Westhuizen (2009) demonstrated the evolution of the average completeness of 2-, 3- and 5-generation pedigrees of the Bonsmara breed over a period of 45 years (Figure 3) and reported an average completeness of 85% for the 3-generation pedigrees of Bonsmara animals born between 2000 and 2007.

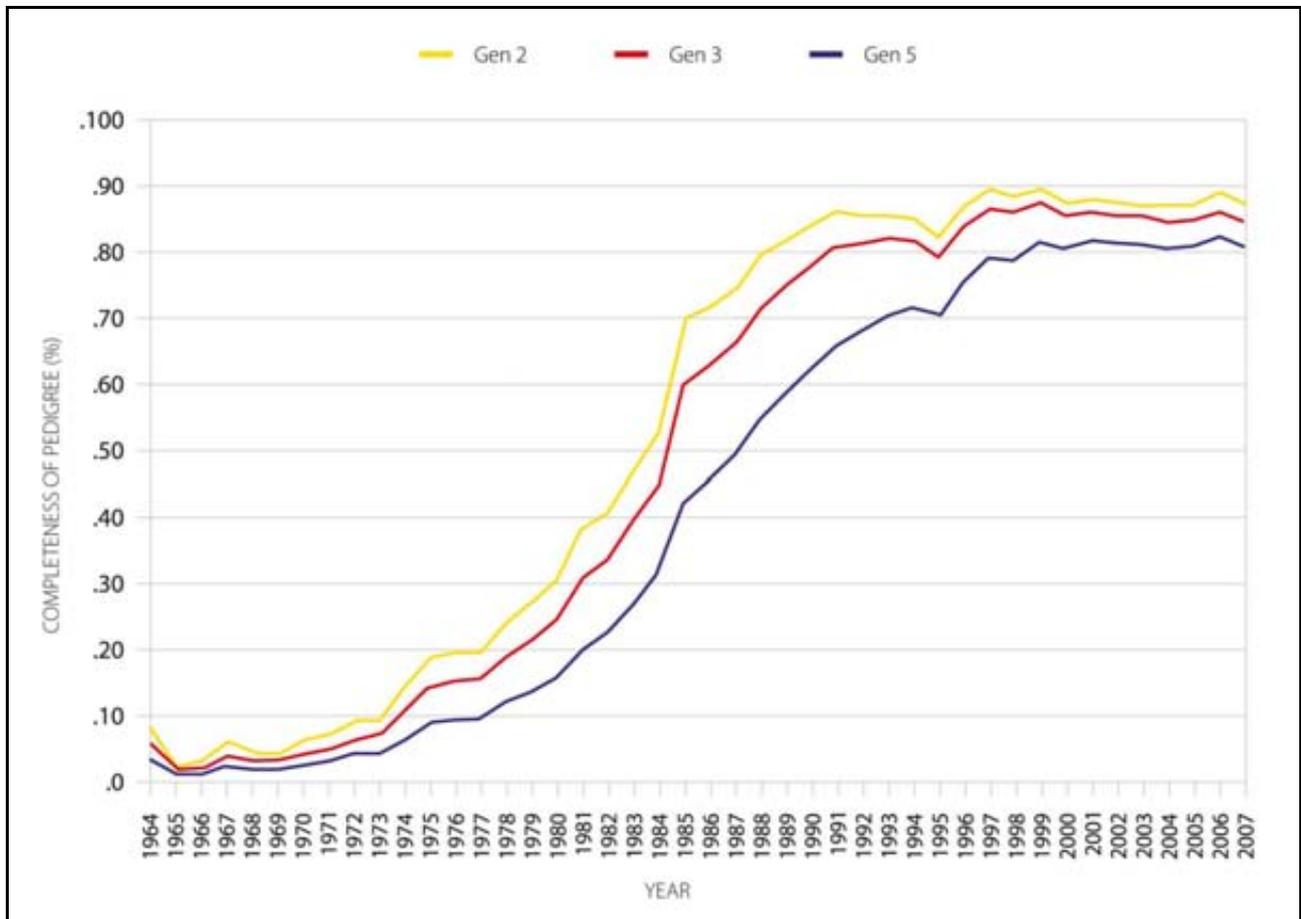


Figure 3. Percentage of pedigree completeness for a two, three and five generation deep pedigree in Bonsmara cattle (Van der Westhuizen, 2009).

Hunlun (2009) reported that 98.2% of the parents of Bonsmara animals born in the period July 2006 to June 2008 were known and recorded.

3.3 Inbreeding and relationships

The trend in inbreeding in a population is the method most frequently used to quantify the rate of change in genetic variability and is calculated from the pedigree records of a population. Several software packages exist to perform the necessary analyses (eg Minbreed (Gandini *et al.*, 1998), Pedig (Boichard, 2002) and ENDOG (Gutiérrez *et al.*, 2005)) and the inbreeding coefficients of animals in a population is also available as a by-product of a BLUP-analysis of the population.

Van der Westhuizen (2009) described the evolution of the average inbreeding coefficients, the additive genetic relationships and the percentage of inbred Bonsmara animals for the period 1964 to 2007 (Figure 4) and estimated a rate of inbreeding of 0.29% per generation.

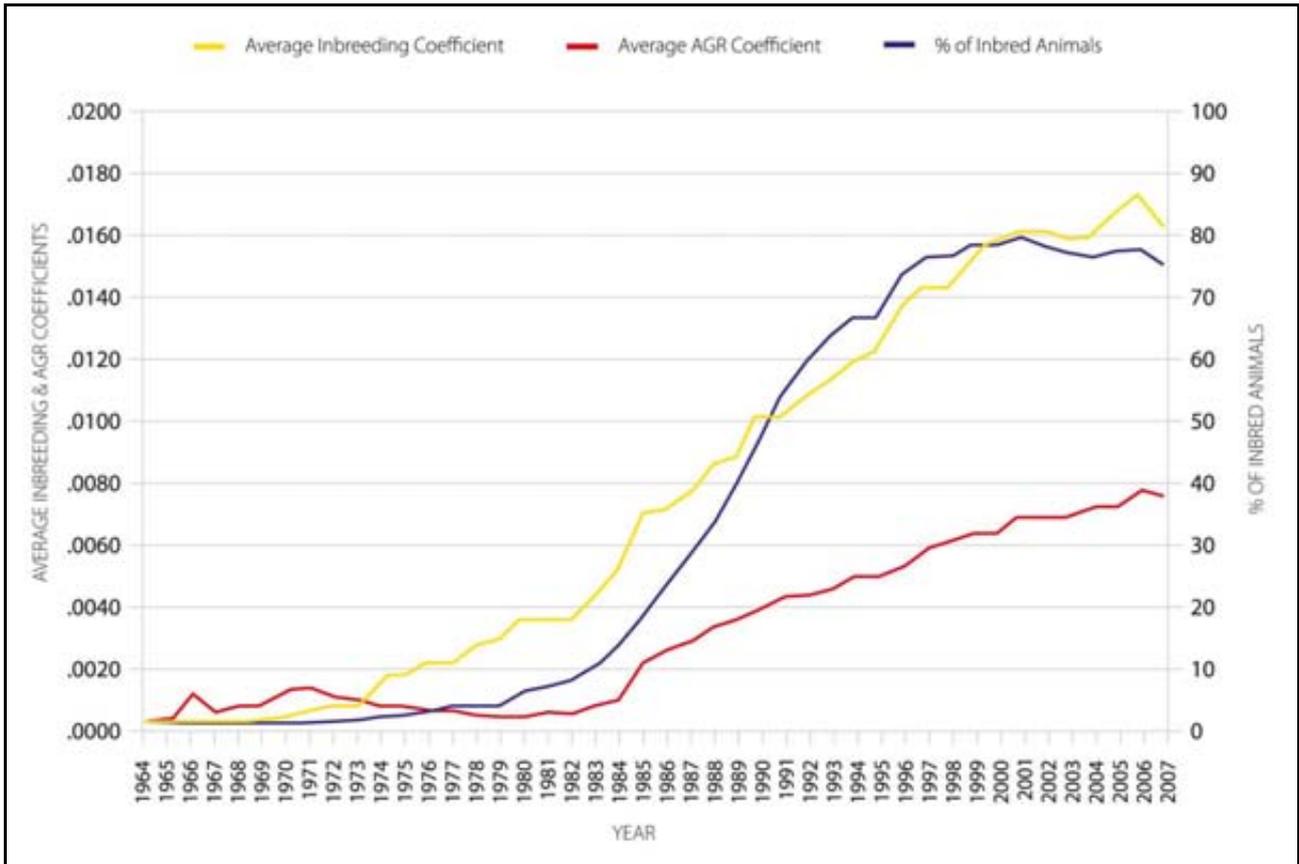


Figure 4. Average inbreeding coefficients, additive genetic relationships and the percentage of inbred Bonsmara calves born per year (Van der Westhuizen, 2009).

In many instances the inbreeding and relationships in sub-populations (herds) are more useful than the average inbreeding in whole populations as it is much easier to identify possible problem areas and to devise proper strategies to address these problems. The additive genetic relationships between animals can become available from the analysis of inbreeding, depending on the routine or calculation method used. These can be used to help a breeder plan future matings in order to avoid inbreeding in the herd.

3.4 Effective population size

The effective size of a population (N_e) is defined as the size of an idealized population which would give rise to the same rate of inbreeding (ΔF) as that experienced in the population. The rate of inbreeding per generation can be calculated from the inbreeding analysis (§ 3.2) and the generation interval (§ 2.3), and the effective population size can be derived as described by De Rochambeau *et al.* (2000) –

$$N_e = 1/(2 \Delta F)$$

The rate of inbreeding for the Bonsmara relates to a realised effective population size of 172.

3.5 Analysis of breeding structure

The analysis of the breeding structure of a breed (Robertson, 1953) provides vital information about where in the breed genetic change is being derived from and what the perceptions of the breeders are about where the most eligible genetics in the breed are to be found. Periodic analysis of the breeding structure of a breed also provides useful information about the development and evolution of a breed and about important herds that played a significant role in the genetic history of the breed. All this information is vital in the formulation of effective mating systems.

The breeding structure of the Bonsmara breed was analysed (Hunlun, 2009) in seven two-year periods, each five years apart, between 1976/77 and 2007/08.

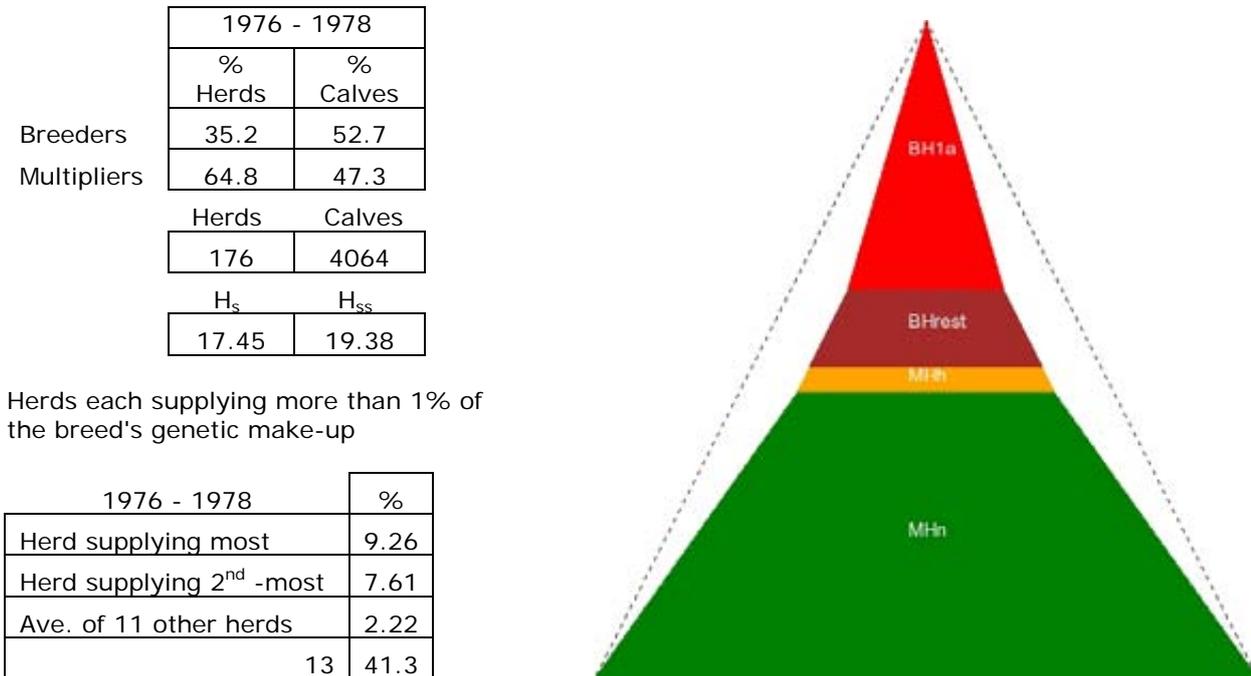


Figure 5: Breeding structure for the Bonsmara breed – 1976-1978 (Hunlun, 2009).

In the period 1976-1978 the Bonsmara breed displayed a typical breeding structure (Figure 5) with 35% of the 176 Bonsmara herds that recorded births being classified as ‘Breeder Herds’ (BH1a and BHrest)) and almost 65% of the herds being classified as ‘Multiplier Herds’ (MHh and MHn). Breeder Herds usually comprise an ‘elite’ minority with the majority of the herds in a breed being Multipliers. The distribution of cows amongst the two groups was somewhat skewed with 52.7% of the calves born in the Breeder Herds and 47.3% born in the Multiplier Herds – BH-herds on average having twice as many births per herd than MH-herds.

During this period, 13 herds (7.4% of the active herds) each supplied more than 1% of the breed’s genetic make-up and together these 13 herds contributed more than 41% to the genetic composition of the breed. The effective number of herds supplying sires (H_s) and grandsires (H_{ss}) to the breed (Robertson, 1953; Gutiérrez *et al.*, 2003), an indication of the levels of within-breed genetic diversity, were 17.45 and 19.38 respectively. The herd with the highest genetic contribution supplied 9.26% of the breed’s sires and dams. The next most important herd contributed 7.61% to the breed’s genetic make-up.

On average, 40% of the calves born annually during this period were fully registered calves and 161 of the 176 (91.5%) herds recorded calves in the appendixes to the Herdbook. A high percentage of both BH and MH made use of the appendixes although the MH (especially MHn) had higher percentages of appendix calves. The genetic origins of 77% of the two calf crops could be accounted for.

Only 17% of the calves recorded in the two years were male calves and 82.7% of the recorded male calves were born in Breeder Herds. In general, breeding herds were small (average size *ca.* 23 cows – foundation females excluded) but the average size for BH was almost twice that of MH.

During the period 2006-2008 (Figure 6) the births of 24 844 Bonsmara calves were recorded by 250 active herds.

Almost 50% of the herds were classified as BH and these herds recorded almost 65% of the births. The overall average number of births recorded per herd per year was 99 with the averages for BH 131 births per year and for MH 68 births per year.

Sixteen herds (6.4% of all herds) each supplied more than 1% of the genetic make-up of the breed and the combined genetic contribution of these herds was 30.4%. The two herds supplying the most breeding animals to the breed had contributions of 5.37% and 3.07% respectively.

The effective numbers of herds supplying sires (H_s) and grandsires (H_{ss}) to the breed rose to 52.63 and 22.37 respectively. The proportion of herds recording animals in the appendixes to the Herdbook was 86% but the proportion of animals born in the appendix sections was only 22% of all recorded animals. The overall proportion of male calves being recorded rose to 48% with more than 67% of the recorded bull calves emanating from Breeder Herds.

		2006 - 2008	
		%	%
		Herds	Calves
Breeders		49.2	64.9
Multipliers		50.8	35.1
		Herds	Calves
		250	24844
		H_s	H_{ss}
		52.63	22.37

Herds each supplying more than 1% of the breed's genetic make-up

2006 - 2008		%
Herd supplying most		5.37
Herd supplying 2 nd -most		3.07
Ave. of 14 other herds		1.57
16		30.4

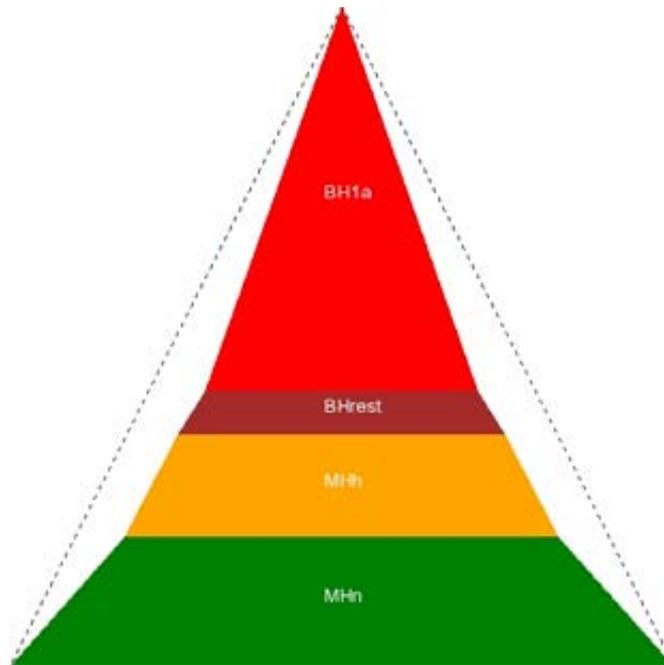


Figure 6: Breeding structure for the Bonsmara breed – 2006-2008 (Hunlun, 2009).

4. Conclusive remarks

Genetic improvement depends largely on the availability of genetic variability in the population under selection. The genetic variability in a population can be assessed from demographic and pedigree analyses, yielding various complementary criteria. In a population that undergoes selection, the roles of the breeders' organisation and the collective decisions taken by the breeders are crucial for creating and disseminating genetic gain. Too intense selection will reduce within-population genetic variability and hamper genetic gain. Breeders' organisations need to constantly monitor the use of animals as donors of embryos and semen through appropriate methodologies and parameters, as the over-use of animals may have detrimental effects on the genetic variability of the breed.

Each breed differs in terms of developmental history, state of genetic variability in the breed and levels of genetic gain achieved and desired in the breed. Consequently, every breed needs a different strategy to achieve its goals. These strategies can only be formulated accurately after an in depth analysis of the pedigrees and some demographic parameters of the breed. The improvement in the capacity and computing power of computers and the availability of computerised databases with the pedigree and ownership information of the animals in the breed puts recording authorities and breeders' organisations in a good position to render a service in this regard to their customers. In the process, they improve their ability to make better decision in terms of improving their herds and breeds.

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