

The analysis of breeding structure in the modern context

Charl Hunlun[#]

SA Stud Book and Animal Improvement Association, PO Box 270, Bloemfontein, 9300, South Africa

Abstract

The analysis of the breeding structure of a livestock breed is generally considered as “old” technology and was, generally, cumbersome to achieve. The advent of modern computerised animal recording databases and faster and more powerful computers have made this kind of analysis viable again and the information emanating from a breeding structure analysis can assist researchers, advisors and breeders in making the correct decisions in their efforts to improve the breeds they are working with. Animal breeders, like any other entrepreneur, 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 and ownership, researchers, breeders’ organisations and breeders can improve the quality of the decisions they have to make.

Keywords: animal recording, pedigree analysis, breed structure, Bonsmara

[#] Corresponding author: charl@studbook.co.za

Introduction

Information about the relative importance and the genetic contributions of individual herds in a breed is very important during the planning of any breed improvement programme and also has significant relevance for any individual herd in that breed. The breeding structure of a breed determines to a large extent the possibility and the efficiency of genetic improvement in the breed.

The seminal work in terms of the genetic analysis of whole breeds was done by Wright (1922; 1923) with the development of methods to calculate inbreeding- and relationship coefficients and the description of sampling methods for the calculation of these parameters for whole breeds (Wright & McPhee, 1925). The basic concept of a hierarchical breeding structure for livestock breeds was suggested by Lush (1946) and the concept was practically demonstrated for the first time by Robertson & Asker (1951) with British Friesian cattle. Robertson (1953) formally defined and described the basic procedures of the analysis of breeding structure, and these procedures were later further refined and developed by, amongst others, Wiener (1953) and Barker (1957).

A number of South African breeds were subjected to breeding structure analysis over the years. The first was probably the work of Allen (1958) with Jersey cattle in, which was followed by the work of Cilliers (1964) with Friesian cattle and Engelbrecht (1965) with Ayrshires. These initial analyses were later followed by a number of analyses of small stock breeds by Schoeman – Karakul (1972), Kotzé – SA Mutton Merino (1976), Erasmus – Merino (1977), and Delpont – Angora goats (1982). Breeding structure analyses were also done on three South African beef cattle breeds – Bonsmara (Van Zyl, 1982), Drakensberger (Dreyer, 1982) and Brahman (Kluyts, 1993).

Very few, if any, modern, empirical analyses of breeding structures of livestock breeds have since been done. This situation can probably be ascribed to the fact that the calculations involved in breeding structure analyses were very time-consuming and laborious before the advent of computerised herd books, even in the cases where only random samples from a breed’s herd book were analysed, as was mostly the case with the earlier analyses. Developments in the field of information technology over the past few decades and the consequent computerisation of the herd books of pure breeds makes it possible today to do these analyses quickly and efficiently and, most importantly, to use all the available data of a breed. A number of revolutionary innovations in livestock breeding that have been adopted since the concept of breeding structures were initially popularised, like the improvements in reproduction technology, may have a marked influence on traditional breeding structures. The livestock industry has also become irrevocably part of the

global village, and the ease with which animal genetics is traded globally has had a major impact on the genetic improvement of livestock populations. The periodic analysis of the breeding structure of a breed can play a vitally important role in quantifying these effects.

The breeding structure of a breed can be illustrated by a pyramid with a number of layers and sub-layers (Figure 1). The layers represent different strata of herds in the breed and the arrows indicate the flow of genes within and between the layers. The recipients of genetic material outside the pyramid represent the commercial or unregistered population, which only receives genes from the breed but makes no real contribution to the genetic composition or improvement of the breed, except in those cases where upgrading is allowed in the breed.

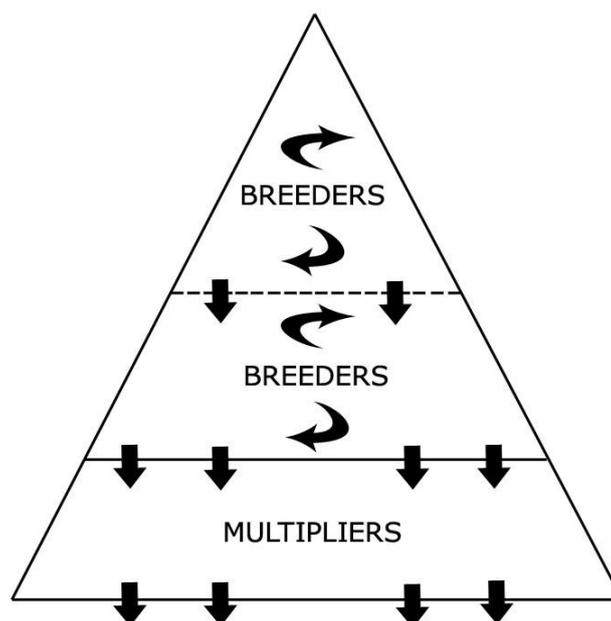


Figure 1 The pyramidal form of a breeding structure

A breeding structure analysis attempts to functionally stratify the herds in a breed according to the demand for and the use of animals emanating from a herd. A breeding structure analysis is primarily an indication of the perceptions of breeders of where in the breed the most effective genetic improvement takes place and is situated, but it also gives an indication of the flow of genes in the population.

With the possible exception of Angora goats in South Africa (Delpont, 1982) all the local breeds that were analysed exhibited the same classical breeding structure that was described in earlier international analyses, and can be characterised by the relatively large influence of a few elite herds. The breeding policy, -direction and the improvement of a breed are largely driven by this top layer of elite herds. Improved genetic material in time filters down through the intermediary layers in the breeding structure to the multiplier herds and the commercial segment of the industry. Several researchers (Erasmus, 1977; Delpont, 1982) have questioned this so-called one-way flow of genetics in the traditional purebred environment and postulated that a two-way flow of genetic material could contribute to more efficient genetic improvement in a breed.

The breeding structure of a breed is also inherently dynamic, and the position and role of an individual herd in a breed can change over time as the patterns of use of breeding material and preferences of breeders change. The quantification of this dynamics forms the basis for very important decision-making by the breeders of a breed.

Material and methods

The analysis of breeding structures is generally regarded as out-dated technology, and with the development of new technologies such as BLUP breeding values, allegedly has little bearing on modern breeding improvement programmes for livestock.

This view could only hold true if all selection criteria used for the selection of breeding stock could be quantified by BLUP breeding values and other newer technologies. The prices achieved for superior breeding stock and the trends in sales and on auctions, as well as the current patterns of use of breeding material and the recording practices of stud breeders is sufficient proof that this is not the case – the animals of some breeders are inherently more in demand than those of other breeders, irrespective of their genetic merit; and an analysis of the breeding structure of a breed is the only way in which these differences between herds can be quantified.

A set of data-processing routines was developed to extract the data from the routine animal recording database, Intergis, and to analyse the breeding structure of a breed from this data. The data-processing routines are mainly based on the methods as described by Robertson (1953) and Barker (1957), with the important adaptation that the information of all animals born in a specified period is used for the analysis instead of random samples, and that the male ancestors of both the sires and the dams of these animals are used in the calculations instead of only the male ancestors of the sires. Another important deviation from the procedures described in literature is that the genetic contributions of both the sires and the dams of the animals are used to determine the genetic contributions of the herds in a breed.

Due to these adaptations the breeding structures of breeds do not follow the 'classic' pattern of breeding structures as described in the literature, but they still show the typical pyramidal structure. Results obtained thus far with beef breeds suggest that in almost all cases the number and percentage of elite herds have increased; the number and percentage of second-tier herds have been dramatically reduced; and that it was difficult to identify the net suppliers of genetics in a breed with the existing traditional methods. This situation was mainly brought about by the effect of the role of dams in the genetic make-up of a progeny group. However other factors, such as the rapid advancement in and the wide application of improved reproduction technologies like artificial insemination and embryo transfer; radical developments in the fields of media- and information technology; and the fact that transport infrastructure has dramatically improved over the past few decades; all played a role. This enlarged top stratum of a breed is the source of genetic change in a breed and these herds are classified as elite because there is very effective interchange of genetic material amongst all these herds. There is evidence that the two-way flow of genetic material, as envisaged by Erasmus (1977) and Delpont (1982), is in fact achieved to some extent as the top strata in most breeds are enlarged to include more breeders – mostly because top stratum breeders are acquiring breeding material from more breeders that could have been ranked in the lower strata, reclassifying these herds to also rank in the top stratum.

In order to describe the role of herds in terms of the supply of genetics to the breed better it was necessary to define and calculate two additional parameters:

- The *partial contribution* of a herd to the genetic composition of a breed is that contribution which can be ascribed to the numbers of active breeding animals in the herd and in the breed – the larger a herd, the larger its partial contribution to the genetic composition of the breed.
- The *marginal contribution* of a herd is the relationship between the *relative contribution* of the herd (as defined and used by Barker (1957), Davey & Barker (1963), Schoeman (1972) and Kotzé (1976)) and the *partial contribution* of a herd, as defined above – the contribution of a herd in relation to the number of active breeding animals in the herd and the breed.

By using the parameter for the marginal contributions of herds, the net providers of genetics to the breed – the real elite herds – can be identified and quantified. It is interesting to note that the number of net providers in a breed has a rather high correlation ($r = 0.84$ in several South African beef cattle breeds analysed recently) with the H_s -parameter as defined by Robertson (1953).

Methodology

The basic methodology used for the analysis of a breeding structure comprises firstly the identification of all the herds¹ in the breed that recorded births² in a specified period. The number of male and female births during the period is summarised per herd. For each recorded birth the herd from which the sire and the dam came is also identified, as well as the herds from which the paternal and maternal grand- and great-grand-sires came. The section of the herd book in which the birth is recorded is also recorded against each birth, and all this data is summarised per herd.

Herds are then stratified according to which herds they received breeding material from and to which herds they supplied breeding material. The herds in a breed are then classified in two basic groups on the basis of this stratification (Barker, 1957):

- Breeder Herds (BH) – herds that supply genetic material to other purebred herds; and
 - Multiplier Herds (MH) – herds that don't supply any genetic material to other purebred herds.
- These two groups can be stratified further:
- Breeder Herds (BH) are stratified further according to the importance of the herds to which they supply breeding material:
 - Herds that supply breeding material only to Multiplier Herds (MH) but do not supply any breeding material to other Breeder Herds (BH) are classified as BH4;
 - Herds that supply breeding material to MH and BH4 are classified as BH3;
 - Herds that supply breeding material to MH, BH4 and BH3 are classified as BH2;
 - Herds that supply breeding material to MH, BH4, BH3 and BH2 are classified as BH1.
 - BH1 herds that supply breeding material only to themselves and MH, BH4, BH3 and BH2 herds are classified as BH1b;
 - BH1 herds that supply breeding material to themselves and MH, BH4, BH3, BH2 and other BH1 herds are classified as BH1a.
 - Multiplier Herds (MH) are stratified further into two groups, MHh and MHn, on the basis of the patterns of use of breeding material in those herds:
 - MHh herds use (amongst others) homebred sires; and
 - MHn herds only use breeding material emanating from Breeder Herds (BH).

The following population statistics are then calculated per herd (Robertson, 1953):

- The herd's relative genetic contribution to the generation (group of specified animals) being analysed
- The herd's relative genetic contribution to the parental and grandparental generations (the parents and grandparents of the group of specified animals)
- The herd's partial genetic contribution to the genetic composition of the generation being analysed
- The herd's marginal genetic contribution to the genetic composition of the generation being analysed
- The 'chance of herd identity'³ in the parental generation – C_s
- The 'chance of herd identity' in the grandparental generation – C_{ss}
- The 'chance of herd identity' in the great-grandparental generation – C_{sss}
- The effective number of herds⁴ in the parental generation – $H_s = 1/C_s$
- The effective number of herds in the grandparental generation – $H_{ss} = 1/C_{ss}$
- The effective number of herds in the great-grandparental generation – $H_{sss} = 1/C_{sss}$

¹Herds are identified by their herd designation marks, which form part of the unique identification of an animal.

²Only the births of animals eligible for registration are considered.

³The probability that the parents of two randomly-chosen animals come from the same herd.

⁴The effective number of herds supplying parents to the parental generation / sires to older generations.

The herds in the breed are then stratified in a pyramidal structure according to their importance as suppliers of genetic material to other herds. The relative size of each of the sub-divisions of the pyramid is determined by the percentages of herds and animals occurring in each of the sub-divisions.

The most important net providers of genetic material in the breed can be identified by their marginal genetic contributions.

The breeding structure can be graphically presented in the form of a triangle or pyramid (of which the sides needn't be straight) where –

- the horizontal axis (the base of the pyramid/sub-pyramid) represents the cumulative percentage of herds in each category; and
- the vertical axis (the height of the pyramid/sub-pyramid) represents the cumulative percentage of animals in each category.

Output

The data processing routines produce the following output:

- Summary diagram (breeding structure pyramid) depicting the basic structure of the breed with a few statistics which elucidate the breeding structure;
- Detailed table listing all herds (including non-active ancestral herds) that have an influence on the breeding structure of the breed, with relevant herd statistics and herd designation marks of the herds receiving breeding material from it, as well as the classification and the various genetic contributions of the herd to the breed;
- $C_s - C_{SSS}$ and $H_s - H_{SSS}$ parameters are listed at the end of the detailed table (Herd data);
- Table summarising the different categories in the breeding structure with the relevant statistics on animals and herds.

Results and Discussion

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.

1976 - 1978		
	% Herds	% Calves
Breeders	35.2	52.7
Multipliers	64.8	47.3
	Herds	Calves
	176	4064
	H_s	H_{SS}
	17.45	19.38

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

1976 - 1978	%
Herd supplying most	9.26
Herd supplying 2 nd -most	7.61
Ave. of 11 other herds	2.22
Contribution of 13 top herds	41.3

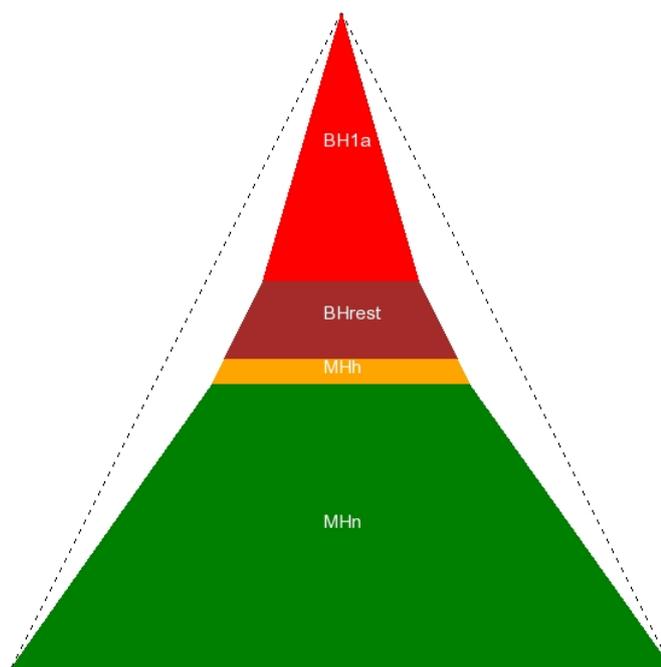


Figure 2 Breeding structure for the Bonsmara breed from 1976-1978 (Hunlun, 2009)

In the period 1976-1978 the Bonsmara breed displayed a typical breeding structure (Figure 2) 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). 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), which is 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 Herd Book. 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 3) the births of 24 844 Bonsmara calves were recorded by 250 active herds.

2006 - 2008	
	% Calves
Breeders	64.9
Multipliers	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
Contribution of 16 top herds	30.4

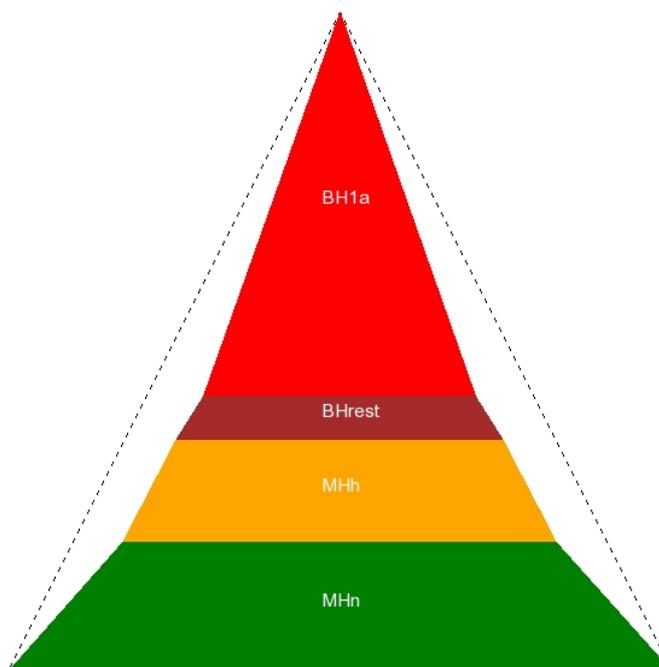


Figure 3 Breeding structure for the Bonsmara breed from 2006-2008 (Hunlun, 2009)

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 Herd Book 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.

Conclusion

Each breed of livestock differs in terms of developmental history, state of genetic variability in the breed and levels of genetic gain achieved and desired in the breed. Many of these parameters also vary over time within the same 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 breeding structure, pedigrees and some demographic parameters of the breed.

The breeding structure of the Bonsmara breed, although somewhat different to the breeding structures described in literature in the past in that it has a larger proportion of Breeder Herds, remained fairly constant over the 30 year period that was analysed, with Breeder Herds rising from about 35% to almost 50% and Multiplier herds declining from about 65% to about 50%. The altered shapes of the breeding structures was probably brought about by factors such as the slightly adapted methods of calculation employed, an improvement in the organisational structure and the role of breeders' societies, radical developments in the fields of media- and information technology, the fact that transport infrastructure has dramatically improved over the past few decades and also, in the later stages of the developmental history of breeds, the rapid advancement in and the wide application of improved reproduction technologies like artificial insemination (AI) and embryo transfer (ET). The possibility exists that the use and application of selection criteria derived from performance records also played a role in the changes in the breeding structures from the accepted 'classical' norm but this possibility could not be clarified by these analyses as the Bonsmara breed has been using selection criteria based on measured performance since its founding.

The shape and form of the basic breeding structure of the Bonsmara makes provision for effective dissemination of improved genetics in the breed and the fact that there are a relatively large number or proportion of Breeder Herds in the breed reduces the dependency of the breed on a small part of the breed for genetic progress. The relatively larger size of the Breeder Herds also ensures that enough suitable bull calves are available for use in all strata of the breed.

The effective number of herds supplying sires to the breed (H_s) shows a positive growth over the period that was investigated and with regards to this parameter the Bonsmara breed is currently in the best position since its formative years – the H_s -value per 1 000 calves born is the highest it has been for more than 25 years.

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 researchers and breeders' organisations in a good position to explore the underlying characteristics of a breed and 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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