

GENETIC DIVERSITY IN AUSTRALIAN ANGUS BEEF CATTLE

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SUMMARY

This study examined trends in the genetic diversity in the Australian Angus cattle population through the calculation of inbreeding, effective population size, effective number of ancestors and effective number of founders over time. The effective population size ranged from 68 to 122 depending on the assumed generation interval. For animals born in 2018, 10 key ancestors explained ~42% of the genetic diversity within the population. Knowledge of overall genetic diversity will help manage the population to maintain long-term rates of genetic gain.

INTRODUCTION

The practice of selection in livestock breeding programs has been shown to lead to increases in inbreeding over time. This has become particularly evident in populations where there is widespread use of artificial breeding technologies (Bijma 2000). Inbreeding is essentially an increase in the number of homozygous individuals within a population. With this increase in homozygosity (or the subsequent reduction in heterozygosity) genetic variation is reduced, which can cause a depression in fitness (inbreeding depression) and a decrease in future selection response (Falconer and Mackay 1996). Selection based on estimated breeding values (EBVs) that incorporate family information (genomic or pedigree based) can lead to increased rates of inbreeding due to the high correlation between EBVs within family, especially when animals are selected at a young age and EBVs are based on ancestral information.

A number of measures have been used to describe genetic diversity in a selected population, including the rate of inbreeding, the effective number of founder individuals, ancestral contributions and effective population size (Boichard *et al.* 1997). Such measures can give a useful insight into whether potential reductions in future response to selection may be expected. Knowledge about the ancestral make up of a population can also have important application in genomic selection where key ancestors are ideal candidates for genotyping at higher marker densities or whole genome sequencing.

The Australian Angus cattle population has achieved substantial genetic progress in the last several decades (Parnell 2015). This genetic progress may have impacted the amount of genetic diversity within the population. The aim of this study was to examine the past and current genetic diversity present in the Angus Australia population.

MATERIALS AND METHODS

This study used data provided by the Angus Society of Australia. The analysis focused on pedigree information on animals born between 1990 to 2018. In total, the pedigree data consisted of 1,551,078 animals, including 42,476 unique sires and 447,000 unique dams.

Measures of diversity. Inbreeding. Inbreeding was estimated using the algorithm suggested by Meuwissen and Luo (1992) for the entire pedigree. The rate of inbreeding per year was estimated as the regression of year on inbreeding. As stated in Falconer and Mackay (1997) the effective population size (N_e) is a function of the rate of inbreeding (ΔF) observed per generation. Therefore, the rate of inbreeding per year was estimated for assumed generation intervals ranging from 5 years to 9 years. Effective population size can be described as:

$$Ne = \frac{1}{2\Delta F}$$

Effective number of ancestors. The effective number of ancestors (f_a) accounts for bottlenecks since the population formation, adjusting for losses of allelic diversity since the founder generation. It is estimated by:

$$f_a = \left[\sum_{i=1}^{N_t} p_i^2 \right]^{-1}$$

where p_i is the marginal genetic contribution of ancestor i as defined by Boichard *et al.*, (1997). The marginal contribution was generated for a given number of ancestors such that the upper and lower limits to the effective number of ancestors were zero ($N_t=1000$).

Effective number of founders. The effective number of founders (f_e) is an alternative measure to estimating the total number of ancestors in the population, accounting for the fact that some ancestors contributed more descendants than others. It is calculated as the number of equally contributing founders it would take to achieve a similar amount of genetic diversity observed in the current population, i.e.

$$f_e = \left[\sum_{i=1}^{N_t} q_i^2 \right]^{-1}$$

where q is the genetic contribution of founder i as defined by Lacey (1989)).

As noted by Sorensen *et al.* (2005), the effective number of founders is a useful historical observation of changes in population structure. It can be used in conjunction with the effective number of ancestors such that if the ratio between the two measures is less than 1 then some bottlenecks have occurred since the foundation generation in the population.

RESULTS AND DISCUSSION

Inbreeding. The rate of inbreeding since 1990, shown in Figure 1, was estimated as 0.0082 per year. The total inbreeding level was on average of 0.03 in 2018. Inbreeding was steadily accumulating until 2011, after which it has remained steady or slightly reduced. The reduction in inbreeding is most likely a reaction from breeders to greater efforts to utilise “outcross” genetics, partially in response to avoidance of sires known to be carriers of recessive genetic disorders identified in the Angus population (Beever 2009).

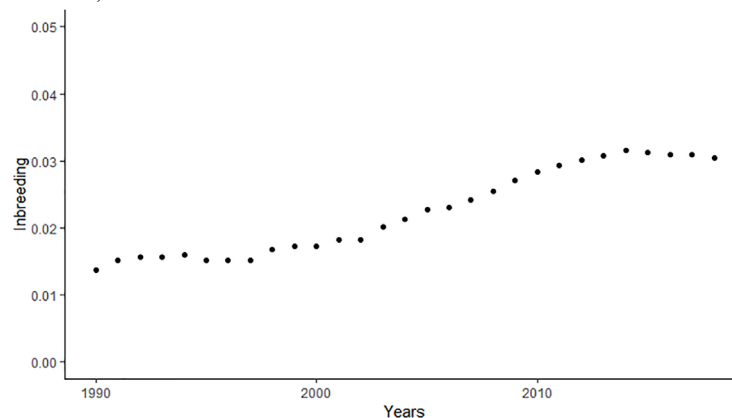


Figure 1. Average inbreeding since 1990 in the Angus Australia population

Table 1 shows the rate of inbreeding per generation and the corresponding effective population size for different assumed generation intervals. The effective population size is higher than those estimated in dairy populations, where values of below 50 are regularly observed (Sorensen *et al.*, 2005). It is often recommended in animal breeding that it is important to maintain an effective population size of at least 50 to 100 (Bijma 2000). Such values have been derived from theoretical expectations, where natural selection counteracts inbreeding depression. Although this is usually not the case in livestock breeding it gives a useful guide for the management of diversity. The maintenance of the current level of diversity will ensure that long-term response to selection can be maintained.

It is likely that the estimates of N_e presented are an overestimate of true genetic diversity, given that the pedigree of the population is relative to a given base. Although, recent estimates of N_e from genomic data ($N_e=93$) (results not shown) agree with the current estimates from pedigree data.

Table 1. The rate of inbreeding and effective population for alternative generation intervals

	Assumed Generation Interval				
	5	6	7	8	9
ΔF	0.0041	0.0049	0.0057	0.0067	0.0074
N_e	122	102	87	76	68

The effective number of founders (f_c) and ancestors (f_a) rapidly declined until 2008, where both measures plateau (Figure 2). In 2018, the ratio between f_c and f_a was 0.32 indicating that a genetic bottleneck has occurred since the founder generation as a result of selection applied in the population.

Individual marginal contributions of founders to the population were required for the estimation of the effective number of ancestors. This gave the opportunity to observe the importance of key ancestors to the population. Table 2 shows the top 10 ancestors based on their marginal contribution to the population. The top sire explained ~12% of the genetic contributions to the population. The top 10 ancestors collectively accounted for 42% of the total genetic diversity, with the top 50 ancestors explaining 70% (results not shown).

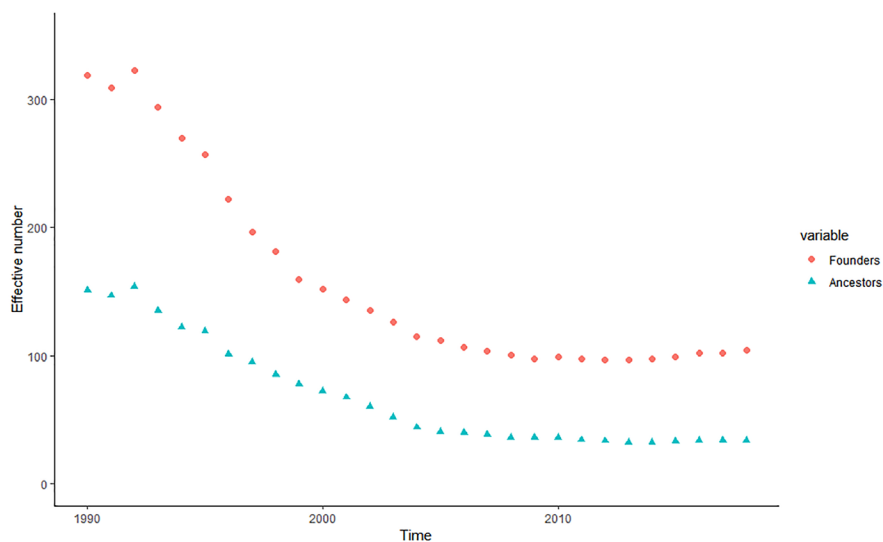


Figure 2. Effective number of founders and ancestors since 1990

Table 2. Summary of marginal contributions for the top 10 individuals

Sire	Birth Year	Total	Marginal	Cumulative	Offspring
1	1990	0.117	0.117	0.117	7772
2	1995	0.0619	0.0619	0.1789	9862
3	1982	0.0609	0.0609	0.2398	2969
4	1978	0.0548	0.051	0.2908	1272
5	1986	0.0322	0.0322	0.323	1265
6	2006	0.0459	0.027	0.35	5356
7	1988	0.0803	0.0204	0.3704	3708
8	1980	0.0242	0.0196	0.39	117
9	1990	0.0169	0.0169	0.4069	3774
10	1992	0.0205	0.0153	0.4222	703

CONCLUSIONS

This study shows that while the diversity of the Angus cattle population in Australia reduced until 2008, the amount of diversity has been maintained since this time. The Angus population has been founded by a relatively small number of ancestors, with the top 10 ancestors explaining 42% of the genetic diversity. Current levels of diversity need to be maintained to ensure losses in response due to inbreeding are not observed.

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