GENETIC TRENDS IN AUSTRALIAN BEEF CATTLE – MAKING REAL PROGRESS

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SUMMARY

Significant genetic change has occurred in many domestic livestock species and is evident in most Australian beef breeds across a range of economically important traits and selection indexes. Large variation in rates of gain is apparent across breeds, and even larger differences between herds within breeds. Reasons for these differences are examined and results show the selection differential of sires was the key factor explaining the across herd differences in genetic progress for all breeds. Validating genetic trends is important to ensure change is reported accurately. Evidence is presented that show the estimated genetic trends are real and key assumptions used in genetic evaluations are examined, in particular the accuracy of the assumed genetic parameters. The paper identifies opportunities which exist to increase rates of gain across the beef industry, including improvements to the genetic evaluation system, increased levels of performance recording, clearer breeding objectives, and adoption of new technologies.

INTRODUCTION

The development of mixed model procedures and best linear unbiased prediction (BLUP) methodology, coupled with advances in computing technology and variance component estimation techniques saw the emergence of genetic evaluation systems in the 1970s and 80s across a range of livestock species. An important feature of BLUP estimated breeding values (EBVs) is that they can be used to estimate genetic trends for a population by averaging the EBVs of groups of animals (e.g. generation or year of birth) over time (Henderson 1973). This is particularly useful in field populations with large unbalanced fixed effect structures relating to management units, in which the mixed model approach can be used to partition phenotypic trends into genetic and environmental components provided certain assumptions are met. These include the following: that the heritability is known, that the model is correctly described, including assumptions regarding the infinitesimal model of genes, that natural selection has not overcome artificial selection (Sorensen and Kennedy 1986) and that adequate linkage exists across herds and years. Importantly, heritabilities should be estimated from the same model that is subsequently used for prediction of breeding values. This requirement also extends to estimation of parameters from multiple trait models when correlated traits are involved (Sorensen and Johansson 1992).

In Australia, the Simmental breed produced the first set of BLUP EBVs in 1982 and this led to the introduction of the BREEDPLAN beef genetic evaluation system in 1984. Over the ensuing two decades all major beef breeds commenced regular across herd genetic evaluations. Today many beef breeds in Australia have a 15-20 year history of computing EBVs. In addition, many of the herds involved had been performance and pedigree recording for at least another decade prior to that, with the National Beef Recording Scheme coming into existence in 1972. Genetic trends are routinely estimated for all beef breeds and show, almost universally, that change has been occurring in the

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average genetic merit of breeds across a range of economically important traits, and also in selection indexes ($Indexes). The aims of this paper are to demonstrate that genetic gain has occurred in Australian beef breeds, provide evidence to validate these trends, investigate the key drivers of genetic trend, and discuss how rates of genetic progress might be increased in the future.

BREED AND HERD GENETIC TRENDS

Breed genetic trends. Genetic gain across the Australian beef industry has increased substantially for the periods 1980-85, 1985-92, 1992-98, 1998-03, 2002-03 with values of 0.03, 0.48, 1.08, 1.71, 2.13 $/cow/year respectively (Barwick and Henzell 2005). Rates of gain for the 1998 to 2003 period ranged from less than 0.02 to almost 0.16 genetic standard deviations per year across the 8 breeds and 23 market production system combinations considered. Results for the Angus breed showed significant genetic trends occurred in all key traits, with some traits approaching 0.15 genetic standard deviations of change per year e.g. 400d wt, calving ease. All trends were computed using BREEDPLAN multi-trait EBVs (Graser *et al.* 2005) by averaging the EBV of all animals born by year of birth.

Herd genetic trends. Herd genetic trends are routinely computed for each individual herd in a breed by averaging the EBVs of all animals born each year. Figure 1 shows evidence of significant genetic trend within a herd for increasing carcase intramuscular fat (IMF%) and Figure 2 in another herd for 400d weight.

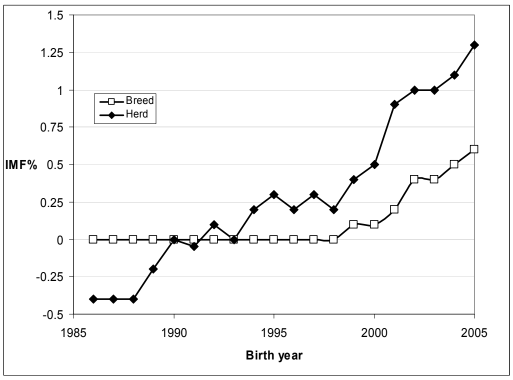

Figure 1. Genetic trend for an individual herd and breed average IMF

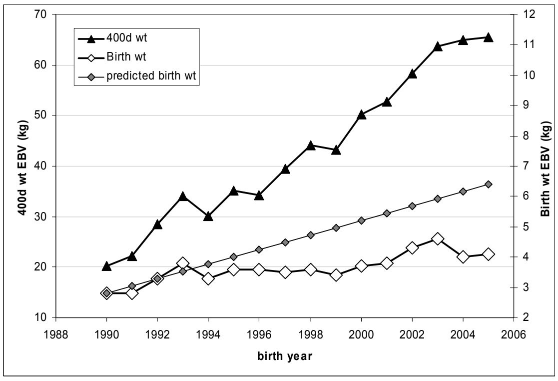

Figure 2. Herd genetic trends for birth weight and 400d wt

Trends in correlated traits. Genetic trends can also be examined to determine the response to selection in correlated traits, provided EBVs are from multiple trait evaluations (Sorensen and Johansson 1992). All BREEDPLAN EBVs are computed in multiple trait analyses (with the exception of calving ease) using breed specific genetic parameters (i.e. estimated heritabilities and genetic correlations). However, it is possible to simultaneously change genetically correlated traits through the recording and subsequent selection of both traits. Figure 2 presents the genetic trend for 400d weight and birth weight for a large herd over a 16 year period. Also plotted is a theoretical predicted birth weight trend based on the underlying genetic correlation and single trait selection on the 400d wt EBV. The graph provides strong evidence that differential trends in the two traits have been achieved despite a genetic correlation of 0.55. The breeder has therefore been able to successfully act on an objective of improving 400d weight while maintaining birth weight relatively constant.

VALIDATING GENETIC TRENDS

Genetic change has been demonstrated in selection line experiments in beef cattle (e.g. Parnell 1997). Divergent selection is commonly practiced over several decades and the response to selection can be accurately estimated using either least squares or mixed model estimates. However, this methodology cannot be used to validate industry based EBV estimated genetic trends due to overlapping generations and confounding environmental effects. Therefore, as suggested by Sorensen and Kennedy (1986), a key factor determining the validity of EBV estimated trends is the accuracy of the assumed heritability used for each trait, where over or under estimation of the heritability will lead to biased genetic trend estimates in a population.

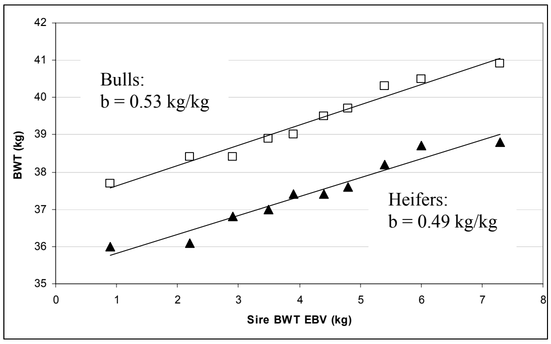

Figure 3. Relationship between progeny birth weight (BWT) and sire BWT EBV (Note: regressions computed using all data, and illustrated here by categorizing sire BWT EBV)

In BREEDPLAN evaluations, the majority of breeds use variance components that have been estimated from their own data. Periodically these are re-estimated with the aim of ensuring that the correct population estimates are used, particularly as the number of records on traits increases over time. The accuracy of an assumed heritability can be assessed by measuring phenotypic differences in progeny of sires that are divergent in EBV for a given trait (see review of Thrift and Thrift 2006). Another validation method using existing performance data is to exclude phenotypes on certain groups of animals from the computation of EBVs. The excluded phenotypes are then regressed on the EBV of their sire, or mid-parent, and the estimated regression coefficient is assessed against its expectation. In Figure 3, birth weights of 2000 and 2001 born Hereford bull (N=20361) and heifer (N=20660) calves are plotted against their sire's EBV computed using all birth weight data recorded before 2000. The regression coefficients were 0.53±0.02 and 0.49±0.02 kg phenotype/kg EBV for bull and heifer calves respectively. These were not significantly from the expectation of 0.50 kg/kg providing strong evidence that the assumed heritability must be very close to the true value for this population.

A more direct approach to show that EBV estimated genetic trends are accurate is challenging because the true genetic trend is overlaid with a constantly fluctuating environmental influence, which includes yearly seasonal fluctuations, management and supplementation changes. However, there are isolated cases historically where well evaluated sires are re-used decades later, and provided sufficient numbers of progeny are generated which are not confounded with fixed or dam genetic effects, these data can provide a good comparison of the actual versus predicted differences in mean genetic performance of animals over time. Sires that have been repeatedly used over a long period of time can also be used for this purpose. The progeny of these reference sires are unique in that, on average, their sire's contribution to their breeding values does not change over time, allowing two key observations to be made. Firstly, any genetic trend observed in the progeny represents genetic trend in the dams. Secondly, if we assume the reference sires are on average joined to genetically similar dams as non-reference sires in a given year, then the phenotypic difference between the two progeny groups, when averaged over all contemporary groups will be an estimate of the average genetic difference between reference and non-reference sires at that time. This can then be compared to the difference in average EBV between the two groups. Under the assumptions made, we would expect that the genetic trend in the progeny of non-reference sires to be approximately twice the trend in the progeny of reference sires, and that with time, the superiority of reference sires will be reduced.

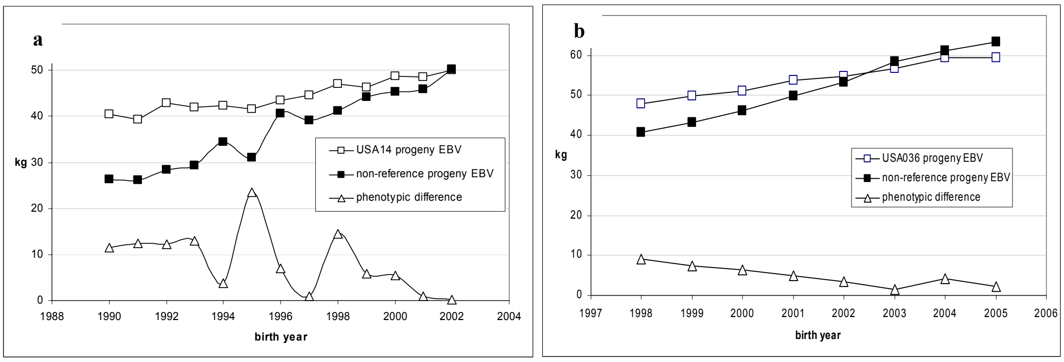

Figure 4. 400d weight genetic trends and observed phenotypic differences for USA14 (a) and USA036 (b) progeny compared to progeny of contemporaries from non-reference sires.

Evidence of this was obtained by identifying widely used sires in the Australian Angus database. A number of North American AI sires were imported to Australia from the late 1980s onwards, with some generating large numbers of progeny over the subsequent years. USA14 (Scotch Cap) produced 2361 performance recorded calves over a 13 year period (1990-2002) and USA036 (B/R New Design 036) generated 6301 calves over an 8 year period (1998-2005). Figure 4a shows the average progeny 400d wt EBV for USA14 compared to the average EBV of all other animals (N=9678) in common contemporary groups. Also plotted is the difference (USA14-others) in the adjusted 400d weight records of the two groups of progeny averaged over all contemporary groups in a given year (weighted by minimum number of the two progeny groups). The results show a 0.84±0.04 kg/yr (i.e. 10 kg EBV change) genetic trend occurred in USA14 progeny compared to 2.11±0.03 kg/yr (i.e. 25 kg change) in the other progeny and represents the genetic trend in the cows that USA14 was joined to over those years. Whilst large yearly fluctuations were observed, the average difference over time in the phenotypes of the two groups declined at -0.91±0.24 kg/yr, representing an 11 kg decline in the average difference over the 13 years. This estimated difference was slightly lower than the expected decline computed from the EBV difference (-1.27±0.03 kg/yr). For USA036 (figure 4b), the expected phenotypic difference (compared to 21582 other progeny) was also slightly less than expected.

DRIVERS OF GENETIC CHANGE

Breed trends. Large differences across breeds were reported by Barwick and Henzell (2005) for gain in $Indexes and also in new results presented in Table 1. Whilst no formal analyses were undertaken for this paper it is possible to surmise likely reasons for the differences based on selection theory. Genetic change is a function of the standard deviation of the $Index (SDI), selection intensity, and generation interval. The SDI is determined by the availability of information, especially in relation to which traits are most important to the breeding objective. The SDI can be further described as a function of accuracy of selection and standard deviation of the breeding objective. Intensity of selection will differ across breeds primarily due to the diversity of breeding goals within breeds, but also due to the levels of AI and ET within each breed. Accuracy of selection is also expected to differ across breeds, depending on the number of traits in the breeding objective and the level of performance recording which is observed to vary widely between breeds. For most breeds, the average generation interval is likely to be similar, with the exceptions being breeds that calve first as three year olds, and those where progeny testing of sires occurs (e.g. for abattoir carcase traits).

Barwick and Henzell (2005) observed that differences in trends between breeds can also be associated with differences in the recording history of a given trait, and subsequent availability of an EBV. Other changes also often coincided with major enhancements in the evaluation systems. Since 1985, the BREEDPLAN system has been constantly improved and new versions of the analytical software have been regularly released to industry. Major enhancements have included: across herd evaluations, addition of new traits into the multiple trait analysis, improved modelling of fixed and random effects, inclusion of overseas EBVs, modelling of sire by herd interaction effects, adjustment for heterogeneous variances, improved genetic grouping strategies, and modelling of crossbred data (see Graser *et al.* 2005). An example of the impact of BREEDPLAN enhancements is shown in Figure 1 where prior to the introduction of ultrasound scanning for intramuscular fat, and the subsequent development of an EBV for the trait in the late 1990s, the breed genetic trend was negligible. However after the release of BREEDPLAN version 4.1 in 1998, a significant genetic trend has occurred as breeders more effectively selected for this trait.

Herd trends within breeds (Progress over 2001-2005). Differences exist between herds for the rate of gain in individual traits (e.g. Figure 1) and Table 1 presents the mean and variability in individual herd progress for each breed with published breed standard $Indexes. For ease of reporting, only the main $Index was chosen for each breed.

The results show that a large variation exists between herds within a breed, and even for those breeds making lower average progress, the top herds are making considerable gains (i.e. up to 0.15 genetic standard deviations). To examine the possible factors explaining the observed variation in progress between herds for each $Indexes the TakeStock® software (Johnston and Moore 2003) was used. For each eligible herd within a breed (based on a set of minimum size and structure statistics) a set of variables were computed (see Johnston and Moore 2003) using animals born in the specified period (2001-05) and included the genetic progress for each herd. A series of stepwise regression analyses were used to identify significant variables explaining across herd progress for each breed $Index. Results are listed in Table 2 and significant variables are classified into three groups based on their partial R^2. This dataset represented nine breeds and over 1100 BREEDPLAN evaluated herds producing more than 113,000 seedstock animals per year between 2001 and 2005.

Table 1. Mean herd genetic progress per year (genetic standard deviations) for breed standard $Indexes for 2001-05 drop animals

Breed	Breed $Index	N herds*	Mean trend*	sd	min.	max.
Angus	Jap B3	290	0.11	0.06	-0.07	0.36
Shorthorn	Export B3	77	0.03	0.03	-0.03	0.08
Brahman	Jap Ox	55	0.02	0.02	-0.04	0.09
Santa	Export	56	0.02	0.02	-0.02	0.10
Hereford	Supermarket	296	0.03	0.04	-0.07	0.18
Charolais	Export	67	0.04	0.04	-0.04	0.15
Murray Grey	Long Fed Export	136	0.05	0.04	-0.07	0.15
Limousin	Terminal domestic	104	0.03	0.05	-0.11	0.16
Simmental	Supermarket	100	0.02	0.03	-0.07	0.15

* note: statistics only for herds qualified for TakeStock® evaluation (i.e. not entire breed)

Results in Table 2 show that significant variables ($P<0.05$) accounted for 26 to 63% of the variation in genetic progress across herds for 2001 to 2005 born animals. Lower total R^2 were generally associated with $Indexes for breeds with low between herd variability. Of all the explanatory variables (KPI) selection differential of sires (SDS) was the most important for the majority of $Indexes considered, and in all cases the sign on the partial regression coefficient was positive, clearly showing the impact of selection intensity on genetic gain. Secondary KPI included selection differential of dams (SDD), and the correlation between sire and mate EBV (MC). Several minor KPI also existed but were generally different across the breeds and likely reflect differences in the structure and evaluation history of the various breeds.

FASTER FUTURE GAINS

Given that the highest rates of genetic gain are around 0.15 genetic standard deviation/year and theoretical gains in beef cattle could approach 0.3 then there is a large opportunity to increase future genetic gains in all breeds. There are several initiatives underway that will assist beef producers to capture some of the potential gains. The TakeStock® software gives beef herds the ability to benchmark their progress in a $Index and their performance in KPI compared to other herds. This allows herds to identify strategies to improve their future progress. Recent developments in ensuring data quality, including computation of record effectiveness for every herd, will also lead to improvements in accuracy of recording and greater genetic progress.

Advances in genetic evaluation procedures will also be important for future progress, including improved modeling of non-additive genetic effects within and across breeds, and genotype by environment interactions. However a current constraint to greater industry wide progress is the segmented nature of the beef industry and the large number of relatively small breeding operations. Increased rates of progress with the potential to have widespread impact on the commercial production sector are more likely if larger breeding operations develop in the future. These may arise through cooperation between innovative seedstock breeders with similar breeding goals, or more likely through investment by agricultural corporations, taking advantage of vertical integration and control over patented gene products, such as gene marker tests for economically important traits.

Table 2. KPI group[#] of variables[*] explaining across herd variation in $Index genetic progress

			KPI group		
Breed	$Index	Total R^2	Major	Secondary	Minor
Charolais	Export	**63**	SDS	SDD, ISD	
Murray Grey	Long Fed Export	**61**		SDS, SDD, MC	ISD
Angus	JAP B3	**60**	SDS	MC, SDD	SD2, SA
Simmental	Supermarket	**49**		SDS, SD2, MC	ET%
Santa	Export	**45**	SDS, SDD		
Limousin	Terminal super	**38**	SDS	EM, EW	
Hereford	Supermarket	**38**		SDS, MC	SDD, SDET
Brahman	JapOx	**37**	SDS	SDD, P1	
Shorthorn	B3	**26**	SDS	SDD	

[#] Significant variables ($P<0.05$) grouped on their partial R^2: Major (≥20%); Secondary (5-19%) and Minor (<5%)

[*] SDS=selection differential of sires; MC=correlation of sire and mate EBV; SDD=selection differential of dams; SD2=selection differential of sires joined to 2yr old cows; ISD= standard deviation of the index; EW=error birth day of week; EM=error birth day of month; ET%=percent embryo transfer; SDET=selection differential in ET donor cows; P1=average $EBV in previous 5yr period; SA=sire age

The results in Table 2 showed that herds using genetically superior sires (based on $Index) made more genetic progress in their 2001 to 2005 born animals. Higher sire selection differentials could be achieved in individual herds by ensuring there is a clear breeding focus and selection is based on a specific $Index. However due to industry segmentation and limited vertical integration, a more conservative approach is often taken, and the impact on breeding decisions of fads such as “US perceived superiority” in some breeds cannot be ignored. High SDS can be achieved relatively easily for genetically inferior herds by sourcing high EBV bulls (or AI sires) provided across herd evaluations are available. However, for the best performing herds, increasing SDS will likely rely on importing superior genetics from overseas, which is difficult in the absence of global beef evaluations, or by selecting genetically superior home bred sires by increasing numbers of performance recorded animals in their herd and/or the level of performance recording. Top herds may also need to increase SDD through use of ET to make additional progress, although constraints on levels of inbreeding will need to be imposed in this situation.

Increased levels of complete recording, increased size of the recorded population, and greater accuracy of young bulls and their wide dissemination will likely have the greatest impact on future genetic progress. This was illustrated in Barwick and Henzell (2005) where cow weaning rate for a model Angus production system was calculated to be the objective trait with the second highest relative importance, yet the corresponding EBV of days to calving showed the lowest improvement across all the trait EBVs. This model example reflects a current industry wide difficulty in recording of certain groups of traits (e.g. female fertility). Structured steer progeny tests may increase data collection for feed intake and abattoir carcase traits in the future but these programs have often proved difficult to conduct, although, successful examples exist of on-farm (e.g. Te Mania Angus) and independently run central test programs (e.g. Shorthorn Durham R&D project, Angus young sire scheme). For the female fertility traits, efforts are underway to enhance data capture of joining details, including AI information to improve the days to calving EBV. In northern Australia, research results will be available within the next five years on new genetic measures of female reproductive performance and longevity for tropical genotypes.

DNA based tests will have an increasing role in generating faster future rates of genetic gain. DNA fingerprinting allows increased accuracy of parentage assignment and larger numbers of animals will be tested in the future as testing becomes cheaper. This will be of particular benefit to breeders using multiple sire mating systems in the more extensive systems of northern Australia. In addition, the rapidly expanding technology of whole genome scans and the completed bovine sequence map are greatly enhancing our ability to identify panels of single nucleotide polymorphisms (SNPs) which explain significant amounts of additive variance, which will be of particular benefit for difficult to record traits. Future widespread genotyping of seedstock animals for panels of SNPs will increase the accuracy of selection and reduce generation interval, therefore significantly increasing the potential to improve rates of gain. Nevertheless, there will be an ongoing need to collect a significant numbers of phenotypes to calibrate the predictive power of the SNP tests over generations and across different breeds.

Finally, while EBVs are the primary tool for selection it is important to regularly validate heritabilities and genetic correlations, particularly for new breeds and traits. Validation of $Index trends is a greater challenge. Currently the only evidence that $Indexes are effective is that desirable trends have been observed across the range of contributing EBVs. However, more comprehensive validation will require the collection of commercial data from designed studies.

CONCLUSIONS

Significant genetic progress is occurring in Australian beef cattle across a range of traits but large variation exists and there is potential to capture greater gain. This will require improving existing genetic evaluation systems, increased levels of performance recording, having clear industry wide breeding directions, and adopting new genetic technologies appropriately.

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