

AN UPDATE ON GENETIC PROGRESS IN THE AUSTRALIAN SHEEP INDUSTRY

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SUMMARY

Substantial genetic progress has been made by the Australian sheep industry in the era of across-flock genetic evaluation which began in the early 1990s. Rates of gain in standard indexes increased throughout the 2000's for maternal breeds and terminal sires, but have plateaued or slightly decreased since 2010. For Merinos, the rate of gain has remained relatively constant over the same period. Average rates of gain for each breed group are currently as high as 94% of "potential" gain for terminal sires, 84% for Coopworth and maternal composite flocks, 49% for Border Leicesters, and up to 47% for Merinos. However, the top 20% of breeders are exceeding potential gain for all breed groups except Border Leicester, and it is the poor performance of the bottom 20% of breeders which leads to lower performance on average for a breed group, particularly for Merinos.

INTRODUCTION

The Australian sheep industry has made substantial and measurable genetic progress since the advent of across-flock genetic evaluation systems in the early 1990's, underpinned by pedigree and performance recording in ram breeding flocks and extensive use of artificial insemination. The effectiveness of selection has varied across different breed groups, with Swan *et al.* (2009) finding that terminal sire breeds were achieving 110% of "potential" gain, maternal breeds up to 79%, and Merinos 33%. In this study we present an updated analysis of genetic progress for the major Australian sheep breed groups.

MATERIALS AND METHODS

The main across-flock genetic evaluations for Australian sheep are currently conducted within three breed groups, maternal breeds, Merinos, and terminal sire breeds (Brown *et al.* 2007). Genetic trends were estimated from analyses published in January 2017, averaging estimated breeding values (ASBVs) and index values by year of birth, starting at 1989, the first year where significant numbers of animals were available, and ending at 2015, the most complete recent cohort. For terminal sires, the breeds selected were Poll Dorset, Dorset, Texel, and White Suffolk, while for Merinos, flocks of Australian Merino or Australian Poll Merino origin were selected, excluding central test sire evaluation flocks. For maternal breeds, Border Leicester (BL) was considered separately to Coopworth and maternal composite flocks (CM), because the former are used in a production system based on crossbred ewes, while the latter are used in self-replacing production systems.

Trends were calculated for six standard indexes, the Maternal Dollar index (MATDOL) for both BL and CM; Dual Purpose Plus (DPP), Merino Production Plus (MPP), and Fibre Production Plus (FPP) for Merinos; and Carcass Plus (CPLUS) and Lamb 2020 (LP2020) for terminal sires. Because these indexes are presented to breeders expressed on different scales, the results were scaled by the standard deviation of each breeding objective.

Rates of gain in indexes were calculated in sliding 10 year windows, by regressing average index value on year of birth. So for example, the rate of gain for the year 2000 was the estimated slope of the regression for years 1991 to 2000.

Rates of gain in indexes were compared to potential rates of gain based on deterministic selection index predictions. The assumptions used in these calculations were full pedigree recording, with the traits typically recorded by breeders in each breed group, including birth weight (BWT), weaning

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weight (WWT), post-weaning weight (PWT), yearling weight (YWT), adult weight (AWT), eye muscle (EMD), fat (FAT), worm egg count (WEC), fleece weight (CFW), fibre diameter (FD), staple strength (SS), and number of lambs weaned (NLW). A summary of the traits included for each index is shown in Table 1, along with index accuracy based on the traits measured, and potential gain per year. The latter was calculated as the index accuracy multiplied by i/L , where i is the selection intensity and L the generation interval, both calculated from recent data in the evaluation databases for each breed group.

Table 1: index accuracy, potential gain per year (per standard deviation of objective), and traits measured to calculate index accuracy.

Index	Accuracy	Potential gain	Traits measured to calculate index accuracy
MATDOL	0.45	0.199	BWT, WWT, PWT, EMD, WEC, CFW, NLW
DPP	0.30	0.078	YWT, AWT, EMD, CFW, FD, SS
MPP	0.36	0.094	YWT, AWT, CFW, FD, SS
FPP	0.44	0.116	YWT, AWT, CFW, FD, SS, WEC
CPLUS	0.61	0.230	WWT, PWT, EMD, FAT
LP2020	0.60	0.228	BWT, WWT, PWT, EMD, FAT, WEC

Trends were also calculated for individual flocks currently in the evaluation, restricted to those with more than 50 progeny per year with ASBVs, and 7 or more cohorts present out of the most recent 10. There were 38 BL flocks and 20 CM flocks in the maternal analysis, 138 flocks in the Merino analysis, and 274 flocks in the terminal sire analysis. The rate of gain for each flock was calculated between 2006 and 2015, and compared to the potential gain. These results were summarised within the top 20% of flocks and bottom 20% of flocks.

Finally, the contribution of individual traits to index gain over time was calculated by estimating the rate of gain for each trait within the sliding 10 year windows described above, multiplying by the relative economic value, and expressing as a percentage of the total index gain.

RESULTS AND DISCUSSION

Index trends in Figure 1 show that substantial genetic progress has been achieved since 1989. Most is observed for the CPLUS index in terminal sires (approximately 5 Standard Deviations), followed by LP2020. For the MATDOL index, CM have increased by over 3 SD, and BL by 1.5 SD. Merinos have made the least gain, between 0.5 and 1 SD.

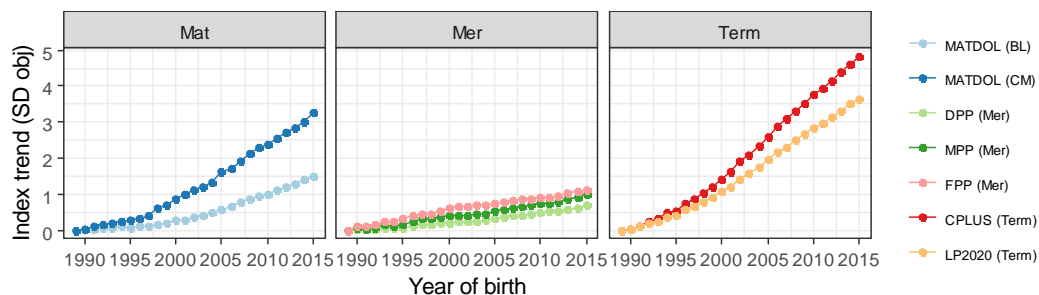


Figure 1: Trends in index performance for maternal breeds (Mat), Merinos (Mer), and terminal sires (Term).

As shown in Table 1, Merino indexes have the lowest index accuracies and potential genetic gain, and this is accounted for in Figure 2. In addition, Figure 2 shows that the rate of gain in terminal

sires and the maternal breeds increased substantially through to approximately 2010, but has since plateaued, or perhaps declined slightly in the case of terminal sires. For Merinos, the rate of gain has been slowly increasing for the DPP and MPP indexes from a low point in 2005, while the rate of gain has been declining for the FPP index, which reflects a reduction in emphasis throughout the industry on fibre diameter, the dominant trait in this index.

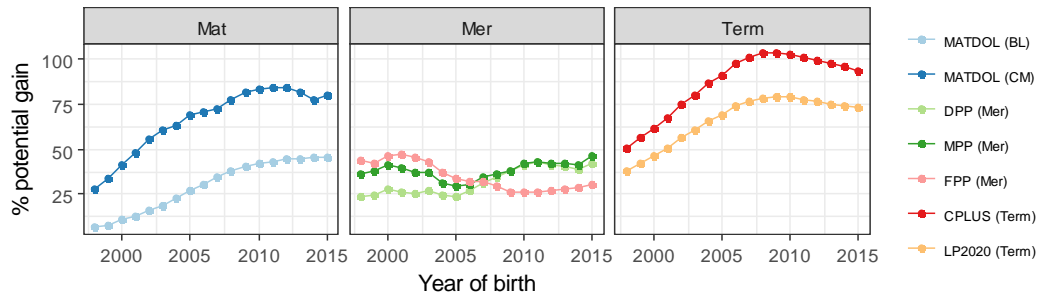


Figure 2: Percentage of potential rate of index gain for maternal breeds (Mat), Merinos (Mer), and terminal sires (Term).

While a plateauing of the rate of gain may not necessarily be an issue, it needs to be noted that the potential rates of gain we have used here have been deliberately set at a conservative level in order to match the recording programs and population structures within the current databases. Exceeding these potential gains is possible, by increasing selection accuracy with better recording programs, optimising breeding programs, and/or utilisation of across-flock and across-breed differences in performance. As shown in Table 2, the top 20% of breeders exceed the potential gain in most cases. In addition, for all cases with the exception of CPLUS in terminal sires (94% of potential gain) and MATDOL in CM (84%), the realised gain is substantially lower than the potential: 49% for MATDOL in BL, and 43, 47, and 37% for DPP, MPP, and FPP in Merinos.

Table 2: Percentage of potential genetic gain for top 20% of flocks, bottom 20% of flocks and mean across flocks.

Percentile	MATDOL (BL)	MATDOL (CM)	DPP (Mer)	MPP (Mer)	FPP (Mer)	CPLUS (Term)	LP2020 (Term)
Top 20%	82	125	102	111	91	134	107
Bottom 20%	19	39	-4	-6	-3	45	35
Mean	49	84	43	47	37	94	73

Possible reasons for not achieving potential rates of gain include firstly the lack of measurement of key traits in the index. This is the case for the LP2020 index in terminal sires, where the measurement of WEC is not common in ram breeding flocks. Secondly, selection may be taking place on traits outside the index, for example, in Merinos there has been a move from horned to poll Merinos over the last decade, and possible selection on breech and other visual traits. In terminal sires, ASBVs for eating quality traits have been available since 2011, and these are negatively correlated to some traits in the CPLUS and LP2020 indexes. An additional factor in maternal breeds is that maternal composites and Coopworths have had greater ability to capitalise on across-breed effects than Border Leicesters. However, taking these points into account, it seems that the biggest issue is simply that selection is ineffective in some flocks. On average, selection in Merinos and BL is much less effective than in CM and terminal sires, but the top 20% of flocks are approaching and

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exceeding the potential gain in all breeds (Table 2). It is poor performance in the bottom 20% of flocks which is reducing average gain, particularly for Merinos. This means that one strategy to increase industry gain would be to focus on improving poor performing flocks, which could be achieved by better application of relatively simple technology. Sheep Genetics is introducing a program working with individual breeders through the “RAMping Up Genetic Gain” project in collaboration with NSW DPI, AGBU, and the Sheep CRC. Through this program, breeders can assess the quality and quantity of information in their breeding program, determine how effectively it can be used in the evaluation analysis, and consider how well it is then used to make selection decisions. It should also be noted that while the differences between the top and bottom flocks are shown to be large, we have not assessed how the industry impact of different flocks may vary.

The changing contribution of individual traits is shown for the main indexes (those which are achieving the most gain for their respective breeds) in Figure 3. In the early phases of across-flock evaluation, body weight (WWT and PWT) made the biggest contribution to gain for maternal breeds and terminal sires. Since 2005, the contribution of eye muscle depth (EMD) has increased for both breed groups, as well as reproduction (NLW) for the maternal breeds. This is partly due to measurement of these traits becoming more common, and has contributed to increases in the overall rates of gain seen in Figure 2. In the CPLUS index, fat depth (FAT) has a negative relative economic value, because the breeding goal has essentially been to improve lean meat yield. The influence of fat on the index has been declining, partly because of periodic updates to CPLUS to reduce the relative economic value, and because of a positive genetic correlation between FAT and EMD.

In the early phases of evaluation for Merinos, fibre diameter was the dominant trait, but from 2005 the influence of body weight (YWT) began to increase. Note that adult body weight in Merinos (AWT) is making a negative contribution to index gain because although the genetic trend is positive, the relative economic value is negative due to the impact of the trait on ewe flock feed costs. In terms of overall response, higher adult weight is favourably associated with early growth and reproduction. In a third phase from 2010, emphasis on fleece weight (CFW) has substantially increased, and this is related to a small negative contribution to the index from fibre diameter (FD) caused by a small positive trend in the trait.

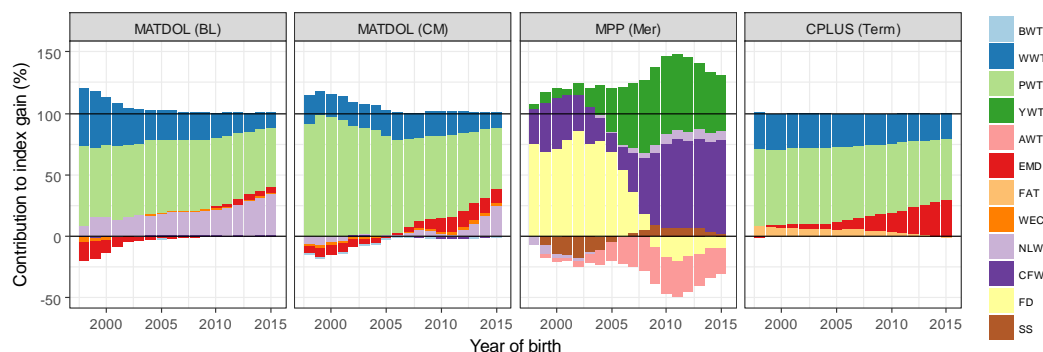


Figure 3: Changes in the contribution of individual traits to gain in selected indexes (Maternal Dollar index (MATDOL) for Border Leicester (BL) and maternal composite flocks (CM), Merino Production Plus (MPP), and Carcass Plus (CPLUS) for terminal sires over time.

REFERENCES

- Brown, D.J., Huisman, A.E., Swan, A.A., Graser, H-U., Woolaston, R.R., Ball, A.J., Atkins, K.D., and Banks, R.G. (2007) *Proc. Conf. Assoc. Anim. Breed. Genet.* **17**: 187.
 Swan, A.A., Brown, D.J., and Banks, R.G. (2009) *Proc. Conf. Assoc. Anim. Breed Genet.* **18**: 326.