

IMPACT OF KEY MESSAGES ON ACCURACY OF SHEEP BREEDING PROGRAMS

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SUMMARY

Sheep Genetics has been providing genetic evaluation services to the Australian Sheep Industry for Terminal, Maternal and Merino breeders since 2005. This paper looks at the average performance of flocks for genetic gain and other data quality metrics over two five year periods for the flocks that are represented in both time periods. These averages were compared using a t-test for significance. All three analyses have made significant improvements in the amount of pedigree being contributed to the analyses. Merino and maternal analyses have had significance differences in index gain. The terminal analyses were the only analysis that showed a significant improvement in the proportion of effective progeny, while no analyses improved the index accuracy over the study.

INTRODUCTION

Sheep Genetics is the national genetic evaluation for the Australian Sheep Industry, offering across flock services for the Maternal, Merino and Terminal breeds since 2005 (Brown *et al.* 2007). The two major pieces of information that they provide are Australian Sheep Breeding Values (ASBVs) for individual traits, and selection indexes that represent the standard breeding objectives. Sheep Genetics activities to increase adoption and use of genetic tools at the member level include:

- Individual breeder consultation on farm
- Regional forums for groups of geographically close clients
- Leading Breeding forums for breeders wishing to take their business further, and
- Service provider training aiming to upskill the people dealing with the client base (Collison *et al.* 2018).

Two key aims of these activities are: 1) to assist producers and service providers to increase their understanding in how to use genetic technologies in their breeding programs and 2) to improve the quality of information submitted to Sheep Genetics by the breeder. It has been noted that the variation of data quality within the analysis is high (Collison *et al.* 2018).

But have the messages been received? Banks (1990) noted that the lamb industry was slow to adopt recommendations and methods based on animal breeding theory. Swan *et al.* (2009) demonstrated that the rates of genetic gain being achieved across the sheep industry is sub optimum across the Merino and Maternal segments. Stephen *et al.* (2018) identified significant differences in key performance recording factors between the flocks that are in the top 20% of genetic gain and those in the bottom 20%.

This study will determine if the collective education activities undertaken provided by Sheep Genetics and the sheep industry has been able to not only significantly lift the rates of gain of the industry, but also the quality of the information that is contributing to the ASBVs provided to industry over its first ten years.

* A joint venture of NSW Department of Primary Industries and the University of New England

MATERIALS AND METHODS

Rolling five year averages were taken for the first two time periods since Sheep Genetics was launched (2006-2010) and (2011-2015) for each flock. The LAMBPLAN maternal and terminal analyses along with the MERINOSELECT analysis were used for flocks that had a minimum of 3 years data in both time periods. Data from research flocks and Central Test Sire Evaluation have been excluded as their primary objectives are not genetic gain.

The diagnostic traits included in this study were the overall flock performance through index trend (indextrend, average annual change in a the Sheep Genetics index), the quality of information recorded included through effective progeny as stated by Brown *et al.* (2000) (eff, averaged across years and key traits) and average pedigree known (avpedknown, completeness of pedigree know from last 3 generations). The amount of data recorded was reflected by the accuracy of the index that best represents the analyses (indexacc). The indexes used were the Merino Production plus for Merinos, Maternal Carcase Production plus for Maternal’s, and Lamb2020 for Terminals. For all data the mean, maximum and minimum flock performance and standard deviation was calculated. A summary of the data is shown in Table 1

Table 1. Number of flocks and average flock size of flocks included in analysis

		2005-2010	2011-2015
Merino	No of flocks	120	120
	Average flock size	614	779
Maternal	No of flocks	116	116
	Average flock size	530	586
Terminal	No of flocks	331	331
	Average flock size	313	347

The means were compared using a two-sided T-test to test for significance differences across the time periods $P < 0.05$. Values that are significant have been bolded in Table 2 below.

RESULTS AND DISCUSSION

Examination of the differences in index trend between the two time periods it is of note that the reductions in standard deviations for the maternal and terminal index trends indicates that the flocks participating in these analyses are tightening around the average index trend. It is of concern that the flocks that are at the minimum on rates of gain are falling further behind the industry with a decrease in the rate of gain.

There are at least 2 potential reasons why flocks are further behind;

1. The breeding objective of the flock does not match the index that has been used in this study
2. The flock in question is currently not using ASBVs in their own selection decisions and only relying on the ASBVs for their clients to use on ram sale day.

In examining the reasons it is thought that the second point is more common in the industry. While not every flocks breeding objective will be a direct match to the index, the key profit drivers are generally similar to those in the indexes used in this study. This generally sees a high correlation between their objective and the index that is most common to the analyses. However there is a sub-section of breeders who believe that the function of ASBVs and indexes is a marketing tool for use by the commercial ram buying sector and not in their breeding program selections.

Table 2. Summary of data from two time periods from the Sheep Genetics analysis¹

		Aypedknown		Index trend		Index acc		Eff	
		2005- 2010	2011- 2015	2005- 2010	2011- 2015	2005- 2010	2011- 2015	2005- 2010	2011- 2015
Merino	Mean	22.2	31.2	0.7	1.7	32.2	34.1	61.2	64.1
	Max	91.8	93	3.4	5.9	52.3	53.2	90.9	89.7
	Min	0.0	0.0	-4.8	-4.5	7.7	8.9	0.0	0.0
	SD	18.4	22.7	1.4	1.7	8.3	8.4	22.1	20.2
Maternal	Mean	74.3	82.2	1.7	1.3	42	42	67.8	70.6
	Max	99.4	99.8	5.2	4.3	52.6	52.4	92.7	91
	Min	10.8	23.3	-0.4	-0.8	25.4	28.2	0.0	3.0
	SD	21.2	15.8	1.2	1	5.5	5.6	17.7	14.9
Terminal	Mean	77.2	84.1	0.4	0.5	47.3	47.5	58.6	62.4
	Max	99.9	99.9	1.3	1.2	66.3	66.7	90.2	90.1
	Min	3.2	0.0	-0.2	-0.5	24	25.6	0.0	0.0
	SD	21.5	16.8	0.3	0.3	5.5	5.7	19.5	18.3

¹P<0.05 significant differences are bolded

When examining Table 2, it is noted that there has been an increase in the average pedigree known across all three analyses. This could be due to a range of factors including the increase in pedigree recording technologies that are now available. These technologies include DNA parentage testing and pedigree association tags. The latest drop from the Merino analysis that was not included in this study had 44% of data being from animals with full pedigree (Collison *et al* 2018). It is worth noting that this percentage is significantly higher than the work done by Casey and Hygate (1992), whose survey work showed only 6% of Merino flocks had full pedigree recorded. As a result of extensive awareness programs there has also been an increase in the perceived value that pedigree contribute to the analysis. This is encouraging as Stephen *et al.* (2018) showed that the Merino flocks that were making the most genetic gain had higher percentages of full pedigree recorded and pedigree known.

Table 2 shows there are significant differences in index trends across the Merino and Maternal analyses. The declining rate of gain in the maternal analysis could be due to the differing breeding objectives of breeds within the maternal analysis not aligning with the standard industry index. A contributing factor also being that prior to 2012 the flocks participating in maternal analysis were analysed within breed only. This result is consistent with the work of Swan (2017) in showing that the maternal breeds had a decrease in rates of gain.

In looking at the index trend for the Terminal genetic evaluation traits not included in the index would be contributing. Genomically predicted ASBVs for lean meat yield (LMY) and intramuscular fat (IMF) were first available for breeders to use for the 2012 drop of animals. Breeders have been able to use these breeding values in selection decisions however these were outside of the standard index selection. This results in a lower selection efficiency achieved against the index as animals that are highest on index may not be selected if the eating quality ASBVs are not acceptable to the breeders objectives. Swan (2017) has since developed indexes for the Terminal analysis that now include LMY and EQ ASBVs, these were deployed to industry in May 2017.

The Merino rates of gain more than doubled during this period which is significant and important for industry given the merino's large contribution to the Australian sheep flock. This is encouraging

as Brown *et al.* (2001) highlighted the lack of use of genetic technologies by Merino breeders, while Swan (2009) highlighted the sub optimum gains achieved in the industry. This increase in the rate of gain has coincided with a significant increase in the number of flocks participating in MERINOSELECT since 2010.

The Terminal analysis was the only analysis that has had a significant change in effective progeny although both the Maternal and Merino analyses have seen small non-significant increases. Table 1 illustrates that Terminal breeding programs are genuinely lower in numbers compared to Maternal and Merinos analyses. In addition to flock size being smaller the measurements in a terminal breeding program are taken earlier in life.

In examining index accuracy there hasn't been a significant increase across any of the three analyses. The Merino analysis has seen a slight increase in average index accuracy across the two time periods that could be attributed to the increase in pedigree. The data recorded for these indexes have generally remained the same number of key traits that breeders will record prior to ram sales, with little future trait recording on ewes. But with more recent innovations around recording dam pedigree and mating data included in commercial software packages there is no reason why more of the traits in the objectives cannot be measured in Merino and Maternal breeds.

CONCLUSIONS

This study shows that there are certain aspects of the key messages around improving rates of gain that have been adopted by breeders in their breeding programs. Across all three analyses there has been a concerted effort to increase the average pedigree known in their flocks across the time periods. Rates of gain for the Merino industry have managed to increase significantly which is also encouraging for the Australian sheep industry given the Merinos large contribution to the Australian sheep flock. However there is still more opportunities for breeders in improving the accuracy of the information through either recording more traits in the index or adding more historical pedigree. The future of genetic evaluation will be aided by technologies to improve pedigree and performance recording which will help improve the accuracy of the information. While the tools are now available in industry to identify flocks who are sub optimum for either genetic gain or data quality and provide targeted assistance to improve these metrics. It is envisaged with these tools breeders can be more proactive in increasing the accuracy of the information they are recording. This in turn with using the ASBVs and indexes to select the genetically superior animals will lead to an increase in genetic gain for the flocks and the Australian Sheep Industry.

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