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Key differences between high and low performing Australian Sheep flocks participating in genetic evaluation

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Summary

Rates of genetic gain, as measured by trends in the index, are not as high in the Australian sheep industry as needed. The Sheep CRC project "Ramping up Genetic Gain" aims to address this by providing users with better information about the performance of their breeding programs. The variables that impact rates of gain in Sheep Genetics flocks are the amount and quality of pedigree (proportion of full pedigree known), the quality of the data (index accuracy and effective progeny), and the use of this information (selection efficiency and generation interval). There are considerable differences in the averages of these parameters for the flocks that are in the top versus bottom twenty percent on average index trend. Through reporting and benchmarking individual flocks for the variables that influence genetic gain, more tailored and accurate actions can be made on-farm. With these actions implemented genetic gain should be achieved for the flock and the Australian sheep industry

Keywords: LAMBPLAN, MERINOSELECT, ASBVs, data quality, index trend, selection efficiency, breeding program

Introduction

The Australian sheep industry across flock genetic evaluation service is delivered by Sheep Genetics and focuses on three major analyses: a Maternal, Merino, and Terminal analysis for the respective breeds (Brown *et* al., 2007). Breeders are provided with Australian Sheep Breeding Values (ASBVs) for individual traits and selection indexes derived using Sheep Object that match the breeding objectives of their industries (Swan *et* al., 2007)

Work by Swan *et* al. (2017) demonstrated that the average rates of genetic gain achieved by participants in the three evaluations are sub-optimum: Terminal achieved 94% of "potential" gain, Maternal between 49 and 84%, depending on breed, and Merinos 47%. This reinforces earlier work that demonstrated both Maternal and Merino breeders were not achieving anywhere near the optimum gains (Swan *et al., 2009)*.

Brown *et al.* (2000) demonstrated that the accuracy of genetic evaluation was impacted by pedigree and data quality. More specifically, the areas that played a significant impact were the type of pedigree (animals with full pedigree, progeny with sire pedigree only, progeny where the sire is a syndicate of sires only, and progeny with no pedigree known) as well as the depth of pedigree used.

As part of the Australian sheep CRC project "RAMping up genetic gain", new measures calculated from the diagnostics of the respective analyses are available to help users identify potential areas for improvement within a flocks breeding program. This new data allows an in depth analysis of the flocks that are making genetic progress at a faster rate than those that are currently not. This paper looks at the key variables that affect the rate of genetic gain and the average index of member flocks of Sheep Genetics. The paper also quantifies the differences between flocks in regards to genetic gain.

Material and methods

Diagnostics of the three main Sheep Genetics evaluations were accessed to create the datasets on 15/08/2017 (LAMPLAN) and 21/08/2017 (MERINOSELECT). Only flocks with more than three years of recorded data were included with research flocks excluded, and three main indexes retrieved: LAMB2020 for Terminals, Maternal $ for Maternals, and Dual Purpose Plus for merinos (Table 1.). Those indexes were utilised for the analysis of trend, accuracy and selection efficiency.

The diagnostics averaged individual flock information for over 3 to maximum 5 year period depending on the flocks participation history in the evaluation. Diagnostic traits included; overall flock performance through index trend (**indextrend**), quality of information recorded included through effective progeny as stated by Brown *et al (2000)* (**eff**), full pedigree (**fullped**), and average pedigree known (**avpedknown**) and use of the information for male selection efficiency (**selM**) and female selection efficiency (**selF)**. Selection efficiency is defined as the percentage of selection differential achieved in the index by the selected candidates relative to what could have been achieved by selecting the best possible indexed candidates.

Rate of genetic gain of individual flocks (**indextrend**) were compared against the remaining variables identified above to ascertain significant factors that impact progress in the three datasets. These were fitted as linear regression models with **indextrend** being the dependent variable and the various diagnostic factors being the independent variables in a series of independent analyses.

Results and Discussion

Table 1 Summary of the data used in the three main SHEEP GENETICS analyses.

		Diagnostic Traits							
		cnt[1]	Index trend	Index accuracy	Eff[2]	Self[3]	selM[3]	Full ped[4]	av ped known[5]
	Mean	718	2.0	27.0	60.5	3.2	18.8	41.3	25.6
	Max	3163	10.2	47.6	90.8	31.1	63.6	99.7	92.9
Merino	Min	35	-4.2	10.2	4.1	-33.6	-35.9	0.0	0.6
n[6]=220	SD	615	2.1	7.1	17.6	8.7	15.4	37.0	21.9
	Mean	493	1.2	42.2	67.1	11.2	20.1	92.1	80.0
	Max	4702	3.1	54.6	90.8	41.1	52.2	100.0	99.9
Maternal	Min	23	-0.8	22.8	4.1	-9.7	-6.5	0.0	6.2
n[6]=136	SD	564	0.8	6.1	17.6	9.0	13.3	15.7	20.8
	Mean	311	3.4	59.7	60.1	8.2	24.6	93.3	82.5
	Max	1731	14.9	67.2	90.2	51.0	72.5	100.0	100.0
Terminal	Min	22	-5.9	20.2	0.4	-45.8	-21.5	0.0	3.7
n[6]=387	SD	254	2.1	5.7	19.5	13.5	18.7	13.1	18.7

[1] **cnt:** the average count of animals per flock, [2] **Eff:** effective progeny, [3] **SelM** and **SelF:** Male and Female selection efficiency, [4] **Full ped:** proportion of the flock with full pedigree known, [5] **av ped known:** Average back pedigree known, [6] **n:** number of flocks within analysis

Table 2. Regression coefficients and standard errors (s.e.) of index trend on diagnostic traits

Average Index, full pedigree ***fullped****, average pedigree known* ***av ped known****, male and female selection efficiency* ***SelM & SelF****, index accuracy* ***indexacc*** *and effective progeny* ***eff*** *for the three main SHEEP GENETICS analyses.*

	Merinos		Terminals		Maternals	
	Regression coefficients (s.e)	Adj R^2	Regression coefficients (s.e)	Adj R^2	Regression coefficients (s.e)	Adj R^2
Av Index	0.01 (0.01)	0	0.06 (0.01) ***	0.18	0.04 (0.01) ***	0.08
fullped	0.03 (0.00) ***	0.23	0.03 (0.01) ***	0.03	0.01 (0.00) .	0.01
av ped known	0.04 (0.01)***	0.22	0.03 (0.01) ***	0.07	0.01 (0.00) *	0.03
selM	0.03 (0.01) ***	0.06	0.03 (0.01)***	0.08	0.02 (0.00) **	0.06
selF	0.06 (0.02) ***	0.06	0.04 (0.01)***	0.05	0.02 (0.01) *	0.04
indexacc	0.12 (0.02) ***	0.16	0.12 (0.02)***	0.12	0.06 (0.01) ***	0.20
eff	0.02 (0.01)**	0.05	0.02 (0.01) ***	0.04	0.00 (0.00)	0.00

***$P<0.001$, **$P<0.01$, * $P<0.05$. $P<0.1$ ‘ ’$P< 1$

Across all three breed types full pedigree, average pedigree known, selM, selF and index accuracy had an effect significantly different from zero on index trend (Table 2.). There was no relationship between the average genetic merit of the flock in Merinos and their index trend; this means that the flocks that are making genetic gain are not necessarily flocks that have high genetic merit. Another potential reason for this may be differing breeding objectives within the Merino breed. Individual flock breeding objectives are not known, the method of using a uniform index to compare all flocks could hide a potential relationship

The effect of the use of genetic information (**selM** and **SelF**) was significant across all three analyses. This demonstrates that breeders that are using the genetic information to make selection decisions, as opposed to using it for the purposes of ram sales or marketing only, are making considerable gain. This was also highlighted by Swan et al (2017) on the ineffectiveness of selection in achieving optimal gains.

The accuracy of the data and index is a major leverage to improve rates of genetic gain. Recording more traits in the objective and increasing known relatives of selection candidates by better pedigree recording will increase the accuracy of ASBV’s and indexes.

Table 3 compares the averages for all diagnostic traits for the flocks that are in the top and bottom 20% of index trend and demonstrates that there are considerable differences for most of the parameters discussed. Standard errors are also shown and significance tests for each trait.

Table 3. Average of variables and standard errors (s.e) for the top and bottom 20% of flocks for index trend.

		Index trend	Full pedigree	Avped known	eff	Index acc	selF	giM	selM
Merino	Top 20%	5.1 (0.2)	70.9 (4.5)	43.7 (3.1)	64.7 (3.4)	32.9 (1.1)	6.3 (1.4)	3.0 (0.1)	22.5 (2.4)
	Bot 20%	-0.5 (0.2)	18.7 (4.3)	13.1 (3.0)	51. 4 (3.3)	24.4 (1.1)	-0.1 (1.3)	3.4 0.1)	9.3 (2.3)
	Signif.	Y	Y	Y	Y	Y	Y	N	Y
Maternal	Top 20%	2.4 (0.1)	92.5 (3.9)	82.6 (4.2)	66.5 (3.8)	45.9 (1.0)	13.9 (1.7)	2.5 (0.1)	24.3 (2.5)
	Bot 20%	0.2 (0.1)	86.5 (3.8)	70.7 (4.2)	62.7 (3.8)	38.7 (1.0)	7.1 (1.7)	2.7 (0.1)	13.7 (2.4)
	Signif.	Y	N	N	N	Y	Y	N	Y
Terminal	Top 20%	6.1 (1.7)	94.6 (1.7)	83.7 (2.2)	63.1 (2.2)	61.0 (0.7)	11.2 (1.6)	2.7 (0.1)	28.4 (1.9)
	Bot 20%	0.5 (1.7)	88.0 (1.6)	68.5 (2.2)	49.8 (2.2)	55.3 (0.7)	1.8 (1.6)	2.9 (0.1)	13.8 (1.9)
	Signif.	Y	Y	Y	Y	Y	Y	Y	Y

Comparing both **fullped** and **av ped known** across the different analyses in table 3 shows that merino flocks that have issues recording pedigree also experience sub optimal genetic gain. It is envisaged that advancements in maternal pedigree recording, such as new technologies and lower costs, will allow a larger proportion of the industry to increase the proportion of the flock with full pedigree identified. This supports Brown *et al* (2000), illustrating that lack of pedigree is still a considerable issue 17 years on.

Sheep Genetics and service providers now have the information and processes to do in-depth analysis of individual sheep flocks and identify areas of improvement. Benchmarking flocks for genetic gain instead of index value and narrowing this further into the diagnostic traits above, allows individual flocks to make the right actions on farm to increase rates of gain.

This information allows the identification of how to get the best return on their investment within their own breeding program. This project helps producers quantify the significant areas and make informed decisions. The tools presented in this study help the industry to achieve the potential gain required for a sustainable sheep industry.

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