industry report

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Genetic improvement of Australian meat goats – PhD

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Executive summary

1. Based on KIDPLAN data, the kid survival trait for Australian Boer goats evaluated had a mean of 0.72, phenotypic variance of 0.14 and a heritability of 0.09.

2. Heritabilities and genetic correlations for production traits in KIDPLAN have been updated.

3. There was some evidence that genetically, survival of singles, twins and multiples should be treated as separate traits but this is difficult to implement.

4. Industry surveys showed that there was strong agreement between the seedstock breeders, commercial producers, and rangeland harvester groups. The key priorities were for increasing growth and weaning rates, and decreasing internal parasites.

5. Economic values were calculated using production and market values from industry, which showed weaning weight and reproductive traits to be the most important traits economically.

6. A new balanced selection index, “Kid Plus” was developed. It uses updated parameter estimates, industry requirements and economic values. It is a balanced index placing emphasis on growth, reproduction and health, while maintaining leanness.

7. To ensure ongoing genetic progress there needs to be an increase in the number of producers using KIDPLAN, an increase in the producers submitting data on carcase and health traits, and better recording practices of reproductive and pedigree information.

Contents

List of abbreviations

BWT – Birth weight (kg)

EMD – Eye muscle depth (mm)

LSB – Litter size at birth (Number)

FAT – Fat depth at the C-site (mm)

KSV – Kid survival to weaning as a trait of the kid (Alive or dead)

PEMD – Post-weaning eye muscle depth (mm)

PFAT – Post-weaning fat depth at the C-site (mm)

PhD – Doctor of Philosophy

PWEC – Post-weaning worm egg count (% or number/g on a log scale)

PWT – Post-weaning weight (kg)

RT/BT – Kid survival as a trait of the dam (Rearing type / Birth type)

WEC – Worm egg count (% or number/g on a log scale)

WWT – Weaning weight (kg)

YEMD – Yearling eye muscle depth (mm)

YFAT – Yearling fat depth (mm)

YWEC – Yearling worm egg count (% or number/g on a log scale)

YWT – Yearling weaning weight (kg)

1. Background to PhD research

During the planning phase of the project a large emphasis was placed on ensuring the results would have a practical contribution to goat breeders and fill a gap in goat genetic literature.

1.1. *Industry*

A series of meetings took place with the PhD student Michael Aldridge and representatives from the Animal Genetics and Breeding Unit, Sheep Genetics, Meat and Livestock Australia, and a number of Boer goat breeders. The reason for these meetings was to determine what updates and new research was a priority for KIDPLAN based on these discussions. From a list of possible research topics three were selected and achievable within a PhD timeframe. They included: updating the parameter estimates for traits in KIDPLAN, creating a survival trait for kids between birth and weaning, and designing a selection index specifically for Australian meat goats.

1.2. *Literature*

The Australian meat goat industry is the largest exporter of goat meat in the world, with the majority of production achieved from rangeland harvesting. However, the challenge is that the best potential for genetic improvement is with Boer goat breeders. The literature review focused on finding gaps in meat goat literature and what traits are most likely to improve lean meat production, by making a comparison to the sheep literature. Three areas of production were investigated for the potential improvement of lean meant yield which included; reproductive, growth, and carcase traits.

A sensitivity analysis of production traits identified the reproductive traits; fertility, fecundity, and survival would have the largest increase to lean meat production with an increase of one genetic standard deviation (28%, 35% and 30% increase to lean meat production respectively). The traits; weaning weight (13%) and lean meat production (4%), had a lower increase to total lean meat production and dressing percentage had a decrease (-7%). The greatest amount of genetic gain and the best opportunity to contribute to literature, was with kid survival.

1.3. PhD Objectives

All of the objectives and questions that the thesis addressed came back to the genetic improvement of Australian meat goats, with a focus on kid survival. It was hypothesised that kid survival is an economically important trait, that KIDPLAN can be used to calculate such a trait, and that it is worth focusing on the component of kid survival rather than number of kids weaned.

There were two key objectives: 1) to create a kid survival trait and 2) to include it in a selection index designed specifically for goat meat production. From these objectives came a series of questions that were investigated:

1) For goats, what research and what traits can be analysed to have the greatest potential increase in lean meat production?
2) What is a suitable processing and cleaning method to remove inaccurate records from the KIDPLAN database?
3) Can the KIDPLAN database be used to estimate parameter estimates for kid survival?
4) Using the KIDPLAN database, what are the genetic parameter estimates for traits in the growth, carcass, reproduction and health complexes?
5) What are the genetic relationships between kid survival and production traits?
6) What are the genetic relationships between the carcase traits and production traits?
7) Is kid survival a single trait, or should survival of different birth types be treated as separate traits?
8) What are the breeding goals for goat producers in Australia?
9) What are the economic values for the traits in those breeding goals?
10) Using the results from the above questions, what emphasis will a selection index place on growth, reproductive, carcase, and health traits?

1.4. Support for PhD research.

The research was supported financially by the Australian Government with an Australian Postgraduate Award and Meat and Livestock Australia with an industry top-up scholarship. Julie Petty and Terry Longhurst of Meat and Livestock Australia also provided a large amount of support to the project. Use of the KIDPLAN database was provided by Sheep Genetics. The Animal Genetics and Breeding Unit, and The University of Adelaide provided invaluable knowledge and resources for the research. The research was supervised by Prof. Wayne Pitchford (Adelaide) and Assoc. Prof. Daniel Brown (AGBU).

2. Key PhD research findings

2.1. Summary of Data and filtering methods

In total, records on 19,711 individuals were provided. The years 1987 to 1989 had no performance records and were filtered by any of the filter methods leaving 19,317 records from 773 known sires and 4,450 dams. The number of progeny per sire ranged between 1 to 492, with a mean and median of 27 and 10 respectively. The number of progeny per dam ranged between 1 and 31, with a mean of 3 and median of 2. A summary of the raw data is provided in Table 1.

Table 1: Summary of the raw data for each of the analysed traits.

Trait	Total No. of records	Minimum	Maximum	Mean ± SD	CV
BWT (kg)	11,705	0.3	7.7	3.6 ± 0.7	19.4
WWT (kg)	10,202	5.2	47.5	20.4 ± 5.5	27.0
PWT (kg)	9,332	10	85.5	28.3 ± 9.2	32.5
YWT (kg)	5,068	16	95.1	43.7 ± 11.9	27.2
PEMD (mm)	2,122	10	34	19.3 ± 4.4	22.8
YEMD (mm)	2,662	11	37	24.1 ± 3.6	14.9
EMD (mm)	4,782	10	37	22.0 ± 4.6	20.9
PFAT (mm)	2,159	0.6	4.1	1.8 ± 0.5	27.8
YFAT (mm)	2,662	0.5	5.1	2.0 ± 0.4	20.0
FAT (mm)	4,819	0.5	5.1	1.9 ± 0.5	26.3
PWEC (%)	289	0.1	16.3	7.1 ± 2.8	40.0
YWEC (%)	438	0.1	20.6	10.8 ± 2.8	26.4
LSB	8,228	0	5	1.64 ± 0.84	51.2
RT/BT	7,733	0	1	0.89 ± 0.28	31.5
KSV	19,711	0	1	0.87 ± 0.33	37.9

As in all datasets there were errors that needed to be addressed. The areas of concern were variation between breeders in recording birth and rearing type, and incorrectly identified dams. The data was filtered in two ways to address these concerns and each filter type also had two variations.

During data cleaning, some sites and small contemporary groups were identified that did not submit or record the expected variation in birth type or rearing type. The first filter (Site Filter 1), was designed, where if in that year, the site did not record any deaths, any records from that site was removed for that particular year. The second site filter (Site Filter 2), was used to determine if a site recorded variation in rearing type, for each year, if a site did not have a range of rearing types between zero and two records, records from that site were removed for that year. Site Filter 1 and Site Filter 2 both removed the same 9,837 records which means that sites that recorded deaths also recorded variation in birth type.

Some dams had records for more kids in a year than biologically possible (>5). This was likely due to an incorrectly identified dam or a data entry error. The first dam filter (Dam Filter 1), treated the trait record to be unknown if the recorded dam has more than five progeny recorded in one year. For the second dam filter (Dam Filter 2), the trait record was treated as unknown, if the number of progeny entered for a dam in one year was greater than the birth type recorded.

2.2. Parameter estimates for KIDPLAN traits

The first objective of the study was to address concerns about the accuracy of recording of birth and rearing type, and incorrectly identified dams. Dam filter 2, where the number of progeny was greater than the recorded birth type, was the best filter to achieve this objective. Each trait fitted birth type and / or rearing type as a fixed effect, and the reproductive traits (kid survival and litter size at birth) are calculated from them. That was why the site filters that ensure sites record variation in birth and rearing type was essential. Following this logic, the number of records removed and changes to parameter estimates were the reason for recommending data cleaning with both filters; Site and Dam filter 2. The second objective of the study was to determine if the KIDPLAN database can be used to calculate genetic parameter estimates for production traits including a new kid survival trait. The following results presented in Table 2, were parameter estimates for raw KIDPLAN data, and filtered with Site and Dam filter 2.

Table 2. Genetic parameters of Boer goats without data filtering and with data filtering by Site filter and Dam filter 2 (^{a}), phenotypic variance (σ_p^2), heritability (h^2), maternal heritability (m^2), and maternal permanent environmental variance (MPE). Standard errors are in parentheses ().

Trait	Records	Mean	σ_p^2	h^2	m^2	MPE
			Growth traits			
BWT	11,711	3.50	0.36 (0.01)	0.30 (0.03)	0.08 (0.02)	0.11 (0.02)
BWT^a	3,963	3.48	0.39 (0.01)	0.38 (0.07)	0.07 (0.05)	0.14 (0.04)
WWT	10,202	20.0	9.56 (0.17)	0.15 (0.03)	0.04 (0.02)	0.09 (0.02)
WWT^a	3,850	20.0	10.72 (0.28)	0.05 (0.03)	0.09 (0.04)	0.07 (0.04)
PWT	9,332	30.0	17.76 (0.32)	0.18 (0.03)	0.02 (0.02)	0.10 (0.02)
PWT^a	4,146	30.0	20.00 (0.51)	0.12 (0.04)	0.06 (0.04)	0.06 (0.04)
YWT	5,068	45.0	25.77 (0.66)	0.38 (0.05)	0.04 (0.02)	-
YWT^a	2,162	45.2	29.31 (1.12)	0.34 (0.09)	0.03 (0.04)	-
HWT	871	50.0	29.53 (1.92)	0.11 (0.14)	-	-
HWT^a	591	50.0	30.33 (2.34)	0.05 (0.17)	-	-
AWT	236	65.0	60.34 (14.06)	0.45 (0.94)	*	0.03 (0.48)
AWT^a	128	64.7	43.68 (15.34)	0.48 (0.65)	-	-
			Scanned carcase traits			
PEMD	2,122	19.4	2.79 (0.10)	0.08 (0.04)	-	-
PEMD^a	504	18.9	2.86 (0.22)	0.08 (0.12)	-	0.08 (0.10)
YEMD	2,662	24.1	2.25 (0.07)	0.17 (0.06)	0.01 (0.03)	0.04 (0.04)
YEMD^a	931	23.3	2.23 (0.12)	0.10 (0.08)	-	0.08 (0.06)
EMD	4,782	22.0	2.52 (0.06)	0.14 (0.03)	-	0.01 (0.02)
EMD^a	1,435	21.8	2.43 (0.10)	0.08 (0.05)	-	0.05 (0.04)
PFAT	2,159	1.8	0.19 (0.01)	0.05 (0.03)	-	-
PFAT^a	509	1.8	0.15 (0.01)	0.15 (0.11)	-	-
YFAT	2,662	2.0	0.15 (0.01)	0.15 (0.05)	-	0.03 (0.03)
YFAT^a	931	2.0	0.17 (0.01)	0.13 (0.10)	0.05 (0.06)	-
FAT	4,819	1.9	0.17 (0.01)	0.10 (0.03)	-	0.01 (0.01)
FAT^a	1,440	1.9	0.17 (0.01)	0.08 (0.05)	0.01 (0.04)	0.04 (0.06)
			Health traits			
PWEC	289	7.1	6.77 (0.68)	0.15 (0.16)	-	-
PWEC^a	268	7.1	6.87 (0.71)	0.16 (0.17)	-	-
YWEC	438	10.9	6.59 (0.50)	-	-	-
YWEC^a	416	10.8	6.74 (0.52)	-	-	-
			Reproductive traits			
KSV	19,711	0.87	0.07 (0.01)	0.13 (0.02)	0.01 (0.01)	0.05 (0.01)
KSV^a	7,713	0.72	0.14 (0.01)	0.09 (0.02)	-	0.04 (0.01)
RT/BT^b	7,733	0.89	0.05 (0.01)	0.03 (0.01)	*	0.04 (0.03)
RT/BT^{ab}	3,262	0.74	0.12 (0.01)	0.02 (0.02)	*	0.04 (0.02)
LSB^b	8,228	1.65	0.64 (0.01)	0.04 (0.01)	*	*
LSB^{ab}	4,095	1.63	0.82 (0.03)	0.03 (0.01)	*	*

^{a} Genetic parameters of Boer goats with data filtering by Site filter and Dam filter 2

RT/BT^b defined as a trait of the dam with a service sire variance (0.01 ± 0.01)

RT/BT^{ab} defined as a trait of the dam with a service sire variance (0.03 ± 0.01)

LSB^b defined as a trait of the dam with a service sire variance (0.06 ± 0.10)

LSB^{ab} defined as a trait of the dam with a service sire variance (0.12 ± 0.10)

* Not fitted, - Estimate went to the boundary

The mean birth weight was 3.5 kg, the same mean as Schoeman *et al.* (1997), and the phenotypic variance of 0.39 ± 0.01 was within the previous estimate range of 0.29 to 0.57 (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2008). The heritability of birth weight for Boer goats in literature ranged between 0.19-0.39 (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2008; Zhang *et al.* 2009b). The heritability for birth weight with Site and Dam filter 2 was within this range at 0.38 ± 0.03. The only difference was a lower estimate of 0.07 ± 0.05 for maternal heritability compared to between 0.14-0.26 (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2009b).

The mean WWT of 20.0 kg (raw mean 20.4kg) was within the range of other Boer goat publications (15.0 kg and 26.8 kg) (Schoeman *et al.* 1997; Zhang *et al.* 2009b). The heritability, however, was very low at 0.05 ± 0.03 compared to 0.18-0.32 for other Boer goat publications (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2009b). This was a serious concern for structure of the data for WWT and provided a low confidence, especially when the uncleaned data was much closer to previous estimates at 0.15 ± 0.03. Other breeds of goats have also been reported below this range (Mugambi *et al.* 2007; Boujenane and Hazzab 2008). Both previous estimates for maternal heritability of WWT in Boer goats was 0.16, higher than the KIDPLAN estimate of 0.09 ± 0.02 (Schoeman *et al.* 1997; Zhang *et al.* 2009b).

Previous estimates for PWT, and using the same KIDPLAN data source, Ball *et al.* (2001) had a heritability of 0.37 using 4,083 records. In comparison, the result from this study using the same KIDPLAN database but with filters Site and Dam filter 2, had a heritability estimate of 0.12 ± 0.04 which is significantly lower and used 4,146 records when 9,332 records were available. Merino sheep also had a higher estimate of 0.54 (Huisman *et al.* 2008). There was a clear pattern of low heritability estimates compared to previous literature of Boer goats, and reinforced the issues associated with inaccurate data records.

Yearling weight which had a heritability of 0.34 ± 0.09 was lower than the previous KIDPLAN estimate of 0.45 (Ball *et al.* 2001). A lower heritability estimate of 0.10 for Boer goats at 300 days was published by Zhang *et al.* (2009b). The phenotypic variance of 25.24 was similar to a corresponding Table 2 of Ball *et al.* (2001) at 24.27. Neither Ball *et al.* (2001) nor Zhang *et al.* (2009b) had an estimate for the maternal genetic component, which could be a function of the number of records (3,026 and 487 respectively). This was compared to 2,162 records using the same dataset as Ball *et al.* (2001), with Site and Dam filter 2, the ability to include a maternal genetic component could be because of errors in the data which were subsequently removed.

Hogget and adult weight only had 591 and 128 records remaining after filtering. This was not due to the data filtering but the lack of data submission for these traits. These numbers of records were likely not enough for accurate genetic parameter estimates, indicated by large standard errors and inability to estimate maternal genetic or maternal permanent environmental components. Due to the small number of records, it was suggested that further analysis of these traits be postponed until more records are submitted to KIDPLAN.

Parameter estimates for PEMD and YEMD were limited to those published by Ball *et al.* (2001), whom estimated the heritability of PEMD and YEMD to be 0.10 ± 0.06 and 0.05 ± 0.05 respectively. In comparison, estimates with Site and Dam filter 2 were 0.08 ± 0.12 for PEMD and 0.10 ± 0.08 for YEMD. Other goat literature focused on eye muscle area and did not provide genetic estimates. In comparison Australian Merino sheep have higher estimates for EMD of between 0.21 - 0.27 (Fogarty *et al.* 2003; Huisman *et al.* 2008; Fogarty *et al.* 2009). The limited literature, the small amount of variation in both PEMD and YEMD, the assumption that PEMD and YEMD were highly correlated were the main reasons for creating the combined trait EMD. The heritability of EMD was not significantly different to PEMD or YEMD but further investigation of the genetic correlation between these traits was required.

As with eye muscle depth there was very little literature on goat C-site fat depth. There are phenotypic parameters by Dhanda *et al.* (2003) on Boer crosses, but Ball *et al.* (2001) was the only reference to publish genetic parameters. The heritabilities estimated with Site and Dam filter 2 of 0.15 and 0.13 for PFAT and YFAT were not significantly different to those of 0.11 and 0.13 published by Ball *et al.* (2001). Goats are very lean with little variation in fat, which likely contributes to the difficulty in analysing the trait. This was the main reason for creating the combined trait FAT, which had a heritability of 0.08 ± 0.05. Further validation that PFAT and YFAT are highly genetically correlated is needed to confirm that combining them is appropriate. Most important is the need for more recording of C-site fat depths.

There were few breeders submitting data for worm egg counts to KIDPLAN with only 268 and 416 records remaining after filtering for post-weaning and yearling respectively. As there were very few records submitted the ability to estimate genetic components was greatly limited. There was no literature available on Boer goats and the only other breeds with estimates are Creole goats. An estimate of heritability for PWEC at 0.16 ± 0.17 was within the range for previous literature (0.14 to 0.37) (Mandonnet *et al.* 2001; Gunia *et al.* 2011; Gunia *et al.* 2013). More worm egg count records are needed for further analysis due to the high standard error.

When kid survival was treated as a trait of the doe (RT/BT) the heritability was low and not different to zero (0.02 ± 0.02). It was also lower than the mean heritability reported of between 0.06 - 0.10 as a trait of the dam for Black Bengal, Jamunapari, and Beetal goats (Singh *et al*. (1990). In comparison, lamb survival as a trait of the ewe was also lowly heritable ranging between 0.00 and 0.12 (Fogarty *et al*. 1994; Rosati *et al*. 2002; Afolayan *et al*. 2008; Bunter and Brown 2013; Newton *et al*. 2014). The estimate of heritability for KSV (0.09 ± 0.02) was within the range of the heritability for lamb survival treated as a trait of the lamb, indicating it was not an overestimate. The EBVs of sires for KSV and RT/BT were compared with a correlation of 0.90. This means there would be no difference in bucks selected for each kid survival trait but the differences in heritability indicated more progress can be made by focusing on survival as a trait of the kid not the doe. Although this study was conducted using

Australian goats they are descendants of South African importations, which means these results for kid survival as trait of the kid rather than the doe, could have broader implications globally.

The only other Boer goat, genetic parameters estimates found for LSB was by Zhang *et al.* (2009a) in Table 3, with a reported heritability of 0.12 ± 0.01. This was higher than the 0.03 ± 0.01 reported here, however both estimates are low. There was a possibility that there is a higher additive genetic component indicated by the service sire variance. This should be investigated further.

The most important result was the high direct heritability of kid survival (0.09) relative to the maternal heritability (0.01) and the heritability of kid survival as a trait of the dam (0.02). This supports the trait being analysed as a trait of the kid rather than the dam. That is to say, the genetics of the kid was much more important than the genetics of the dam. Further evidence to support this, which was surprising, came from analysing litter size where the dam heritability (0.03) was much lower than the service sire variance (0.12). Finally the correlation of EBVs for the kid trait and dam trait was very high (0.90) indicating they are a similar trait and the same bucks would be selected.

2.3. Genetic and phenotypic correlations between KIDPLAN traits

For a trait to be included in a genetic evaluation for KIDPLAN the genetic relationship between each production trait is required. Kid survival as a trait of the kid has variation and is heritable but the genetic relationship with other production traits was unknown. The genetic relationships between KIDPLAN traits have not been updated since 2001 and the relationship between carcase traits and growth traits were not reported. The purpose of this work was to determine the genetic relationship between the production traits in KIDPLAN and kid survival, the results for which are presented in Table 3. To achieve this a series of bivariate analyses were used to determine the genetic covariance between traits. Kid survival was found to have a positive genetic correlation with birth weight (0.19 ± 0.19) and was not different to zero with the other production traits. The amount of data and structure of the carcase traits did not provide the confidence required to use the estimated genetic correlations. Indirect selection of kid survival could be possible by selecting for birth weight but importantly it is not antagonistic with other traits, while more data is required for carcase traits.

Table 3: Bivariate parameter estimates of Boer goat production traits. Including; mean phenotypic variance (σ_{p}^2), mean additive genetic variance (σ_{A}^2), mean residual variance (σ_e^2), mean maternal permanent environmental variance (MPE), heritability on the diagonal (mean), genetic correlation below the diagonal, and phenotypic[A] correlation above the diagonal.

Traits	BWT	WWT	PWT	YWT	EMD	FAT	KSV
σ_{p}^2	0.40 ± 0.01	11.01 ± 0.29	20.43 ± 0.54	29.70 ± 1.14	2.35 ± 0.11	0.17 ± 0.01	0.153 ± 0.003
σ_{A}^2	0.21 ± 0.03	1.17 ± 0.44	2.45 ± 0.87	10.54 ± 2.47	0.25 ± 0.15	0.01 ± 0.01	0.013 ± 0.004
σ_{e}^2	0.12 ± 0.02	8.28 ± 0.36	15.56 ± 0.72	18.06 ± 1.70	2.01 ± 0.15	0.15 ± 0.01	0.133 ± 0.003
MPE	0.07 ± 0.01	1.56 ± 026	2.42 ± 0.49	1.09 ± 1.05	0.09 ± 0.11	0.01 ± 0.01	0.01 ± 0.01
BWT	**0.53 ± 0.07**	0.35 ± 0.02	0.32 ± 0.02	0.34 ± 0.03	0.01 ± 0.04	-0.02 ± 0.04	0.01 ± 0.03
WWT	0.53 ± 0.15	**0.11 ± 0.03**	0.81 ± 0.01	0.62 ± 0.02	0.03 ± 0.04	-0.06 ± 0.04	
PWT	0.50 ± 0.16	0.88 ± 0.07	**0.12 ± 0.03**	0.64 ± 0.02	0.06 ± 0.04	-0.04 ± 0.04	
YWT	0.48 ± 0.13	0.81 ± 0.11	0.84 ± 0.10	**0.35 ± 0.06**	-0.21 ± 0.04	0.06 ± 0.05	
EMD	0.12 ± 0.29	-0.75 ± 0.39	-0.60 ± 0.39	-0.84 ± 0.22	**0.11 ± 0.05**	0.27 ± 0.03	
FAT	0.10 ± 0.37	0.11 ± 0.52	-0.16 ± 0.53	0.30 ± 0.43	-0.04 ± 0.61	**0.06 ± 0.05**	
KSV	0.19 ± 0.19	0.04 ± 0.02	0.03 ± 0.02	-0.06 ± 0.03	0.05 ± 0.03	0.05 ± 0.03	**0.08 ± 0.02**

Residual covariances cannot be estimated for traits with survival because, by definition, all that were measured had survived so there was no variation in survival. It is still possible to estimate the genetic covariance.

The most important finding was the genetic correlation of survival is positive with birth weight and not different to zero for the other production traits. This limits the ability to exploit correlated traits already in KIDPLAN but the benefit is there are no obvious antagonistic traits for kid survival. Birth weight had the highest correlation of 0.19 (± 0.19), the high standard error was of some concern, however the positive correlation indicates there is a relationship. Rosati *et al.* (2002) also reported a positive genetic correlation in sheep (0.34), however this was with lamb survival as a trait of the dam. Selecting for higher birth weights could be a possible method of increasing survival rates.

Due to the different survival rates for different birth types; singles (0.71), twins (0.83), and multiples (0.72) (Figure 1), increasing birth weight is likely to increase the survival of multiples which have lower birth weights (3.2 kg) (Figure 1) but increasing birth weight of singles (4.1 kg) could lead to higher rates of dystocia which is not currently an issue for goats (2-3% prevalence) (Braun 2007; Zahraddeen *et al.* 2011; Sofi *et al.* 2012). Dystocia and difficult births in goats are not common and the cause was normally due to large litter sizes with more than one kid entering the birth canal at a time, rather than feto-pelvic disproportion such as in sheep (Braun 2007; Zahraddeen *et al.* 2011; Sofi *et al.* 2012). Investigating the relationship between birth weight, birth type and kid survival is warranted. The positive genetic correlation between kid survival, WWT and PWT was low but positive and for kid survival and yearling weight slightly negative. It indicates that selecting for kid survival will have a slightly positive effect on early growth rates but not on later growth rates. Selecting for kid survival will not affect muscularity and fat deposition.

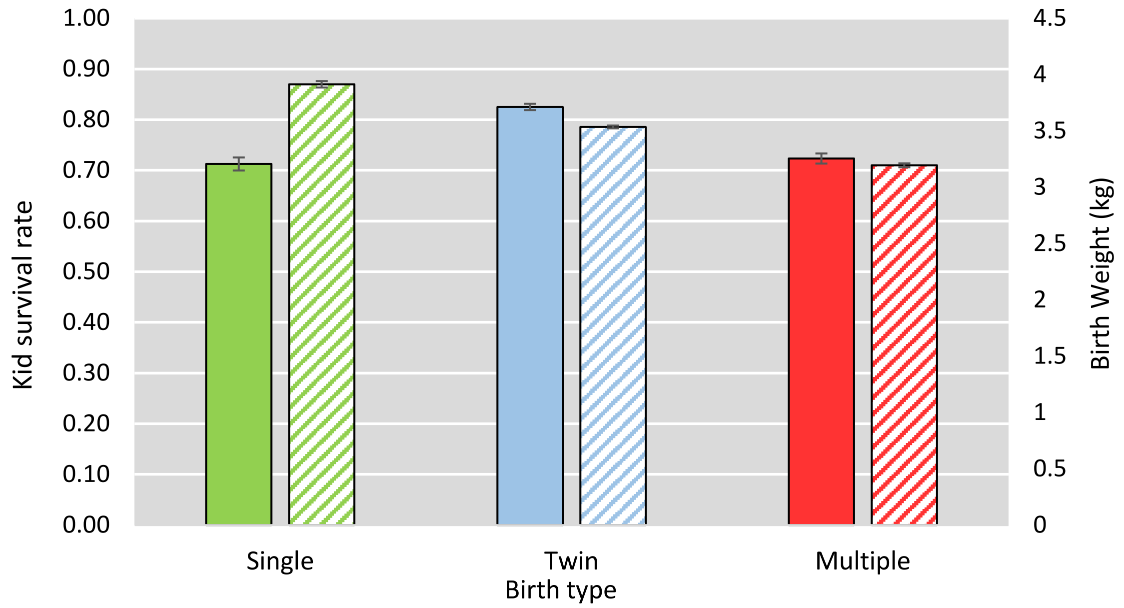

Figure 1: Effect of birth type on kid survival (solid) and birth weight (diagonal line).

As expected, BWT had a moderate positive genetic correlation with the other growth traits WWT, PWT, and YWT of between 0.48 and 0.53. These correlations were slightly lower than the previous estimates of Ball *et al.* (2001) which were between 0.60 and 0.69. The genetic correlation between the three growth traits WWT, PWT, and YWT was high (0.81 - 0.88) and higher than Table 2 of Ball *et al.* (2001) of between 0.59 and 0.83. These results were also similar to sheep of between 0.75 and 0.93 (Table 5, Safari *et al.* 2005).

There was no genetic correlation between EMD and FAT at -0.04 ± 0.61. All of the other genetic correlations with the scanned traits had high standard errors due to there being few records, across a limited number of sites across years, and the small amount of variation in the traits caused by the fact that goats tend to be lean and smaller compared to sheep. There was no genetic correlation between BWT and EMD but negative between the other growth traits, this was partially because the EMD model accounted for weight at recording. In comparison to sheep, the review by Safari *et al.* (2005) reported a 95% confidence interval for the genetic correlation between EMD and live weight between -0.25 and 0.68, and for FAT and live weight between -0.44 and 0.84. Recently Brown and Swan (2016) reported in Table 3 across breeds the genetic correlation of PFAT was negative for BWT (-0.27 ± 0.02), WWT (-0.24 ± 0.03), PWT (-0.19 ± 0.02), and YWT (-0.27 ± 0.08). It is possible that the stronger negative genetic correlation difference between the bivariate analyses and those of previous literature were due to the lower heritability and could be real, but it is possible that it was caused by inaccurate recording practices which have been highlighted by the data filters (Section 2.2.).

2.4. Kid survival can be considered a different trait based on birth type

The biological processes for the survival of kids born as singles, twins or multiples have different levels of importance. To advance this further, survival as a trait of the kid was redefined as three separate traits depending on birth type as a genotype x environment interaction. The genetic parameters and relationships for these traits were investigated to determine if they could be incorporated into a breeding program for a faster rate of genetic gain in kid survival and the main results are presented in Table 4. The three kid survival traits were heritable; 0.08 ± 0.05 for singles, 0.12 ± 0.03 for twins, and 0.13 ± 0.04 for multiples. Using an animal tri-variate model, the kid survival traits defined by birth type were positively genetically correlated with each other between 0.46 and 0.72. The genetic correlations indicate that they could be treated as separate traits however selection would be difficult to implement. The correlations between the kid survival traits and other production traits were not accurate with large standard errors and are biologically questionable. Further analysis with accurate reproductive data is required before the three separate survival traits can be seriously considered for implementation.

Table 4: Tri-variate analysis for separate birth type traits of birth weight and kid survival with a sire and animal model. The heritability is on the diagonal and genetic correlation below the diagonal.

		BWT			Survival		
		Single	Twin	Multiple	Single	Twin	Multiple
Sire model	Single	**0.34 ± 0.18**			**0.10 ± 0.18**		
	Twin	0.86 ± 0.14	**0.29 ± 0.10**		0.77 ± 0.31	**0.15 ± 0.11**	
	Multiple	0.35 ± 0.27	0.74 ± 0.17	**0.25 ± 0.15**	0.83 ± 0.27	0.84 ± 0.27	**0.19 ± 0.15**
Animal model	Single	**0.49 ± 0.08**			**0.08 ± 0.05**		
	Twin	0.91 ± 0.08	**0.41 ± 0.04**		0.46 ± 0.34	**0.12 ± 0.03**	
	Multiple	0.63 ± 0.15	0.87 ± 0.09	**0.32 ± 0.05**	0.72 ± 0.45	0.53 ± 0.29	**0.13 ± 0.04**

The tri-variate analysis was the best demonstration that it was possible to separate kid survival into three separate traits by birth type and that the genetic expression for kid survival was different depending on the birth type environment. It was possible, but there were issues in doing so. The standard errors were very high for both the heritabilities and correlations which are not different to zero. The sire model genetic correlations were higher than first expected (genetic correlations between 0.77 and 0.84 and low heritabilities of 0.10 to 0.19) and were higher than those of the animal model (0.46 and 0.72 for the genetic correlations and 0.08 to 0.13 for the heritabilities). This was evidence for kid survival being a different trait based on a birth type environment (Robertson 1959). The parameter estimates for the original KSV trait (Section 2.2.) compared to the tri-variate analysis were not significantly different however the standard errors were much higher with the tri-variate analysis. The χ^2 test of significance showed the univariate was a better fit and treating kid survival as one trait is currently the most appropriate method. However, the test may not be appropriate as birth type was included as a fixed effect in the original KSV trait but not implicitly in the tri-variate analysis and the assumption in the χ^2 test for random effects is that the same fixed effects model is fitted. That said, in the tri-variate analysis the means of each birth type were included as so this may not be an issue. These results were similar to previous sheep estimates for heritability of between 0.01 and 0.15 but different for genetic correlations between -0.08 and 0.60 (Kelly *et al.* 2016; Kelly *et al.* 2017). While the parameters could be estimated, the accuracy and the high genetic correlations make incorporating the three traits into an index impractical until more data is available.

The results from the tri-variate birth weight model supports the results of the kid survival traits. Birth weight had the largest amount of data of the production traits but there were very few sires with adequate numbers of progeny with records of single, twin, and multiple birth weight traits (27 sires with more than five progeny for each trait). High standard errors of the heritabilities and genetic correlations for the birth weight traits again showed the difficulty of separating the traits with available data in KIDPLAN.

To determine the relationship between the three kid survival traits and the other production traits, a series of bivariate analyses of the three kid survival traits and the original production traits were performed. There was no significant difference between the genetic correlations of the three kid survival traits and a single birth weight trait compared to three birth weight traits separated by birth type (Table 5). All of the genetic correlations had large standard errors associated with them. For KSV_S there were no genetic correlations that were different to zero but the production traits (excluding WWT) tended to be positively correlated. The genetic correlations for KSV_T with production traits were higher and significantly different from zero compared to KSV_S and KSV_M. There were convergence issues for several of the KSV_M bivariate models. Both weaning weight and post-weaning weight were positively correlated with KSV_M.

Table 5: Genetic correlations with animal model between kid survival birth type traits and individual production traits.

	Kid survival			
	Single	Twin	Multiple	[b]KSV
BWT	0.23 ± 0.40	-0.04 ± 0.23	-0.24 ± 0.25	0.19 ± 0.19
WWT	-0.01 ± 0.41	0.61 ± 0.21	0.11 ± 0.31	0.04 ± 0.02
PWT	0.23 ± 0.41	0.61 ± 0.21	0.39 ± 0.31	0.03 ± 0.02
YWT	0.19 ± 0.38	-0.16 ± 0.19	*	-0.06 ± 0.03
EMD	*	[a]0.48 ± 0.18	*	0.05 ± 0.03
FAT	0.45 ± 0.60	0.67 ± 0.32	[a]0.45 ± 0.60	0.05 ± 0.03

[a] - Log likelihood converged but parameters not converged

[b] - Values from Table 5-2

* - Did not converge.

The bivariate analysis between birth weight of singles and kid survival of singles was -0.26 for the sire model, and 0.17 for the animal model. The standard errors were high and so the correlations were not different to zero but it is concerning that the sire model was negative and the animal model positive. Biologically, single born kids are more likely to suffer dystocia due to fetal-pelvic disproportion as they are larger so it would be logical for a negative correlation not positive (Brounts *et al.* 2004; Brien *et al.* 2010; Hinch and Brien 2014). The genetic correlation between the multiple birth weight and kid survival traits were -0.46 and -0.43 for the sire and animal model respectively. It was predicted that this would be a positive correlation as multiples are smaller and have less of an ability to thermoregulate their body temperature (Plush *et al.* 2016). High birth weights for multiples would also increase the amount of brown adipose tissue available at birth (Plush *et al.* 2016).

The limited data especially for EMD and FAT was the main cause for the inaccurate estimates for the genetic correlations between production traits and the three kid survival traits. The estimates for the genetic correlations is a large limitation to the incorporation of three separate kid survival traits in a breeding program. Previously the genetic correlations between a single kid survival trait as a trait of the kid had low positive genetic correlations between the production traits and is not consistent with the higher estimates of three separate traits.

The issues with separating kid survival into three separate birth type traits, suggest there is no current need to, until more data is available. The most difficult issue, is the correlations between the three kid survival traits and birth weight, did not support the hypothesis, and the majority of these estimates had large standard errors. While the moderate correlations between the kid survival traits supports treating them as separate traits, they could be too high for this purpose when selecting for the individual KSV trait would be logistically easier. The correlations between EBV's from the univariate analysis appeared to be too low but moderate to high for the bivariate and tri-variate analysis. Finally the issues with convergence of the multivariate analysis between the three kid survival traits and with the other production traits increases the assumptions that need to be made for a selection index.

2.5. Key messages from industry surveys

The development of breeding objectives for an Australian meat goat production system needs to include input from rangeland harvesters, commercial producers, and seedstock breeders as they are all stakeholders in the genetic improvement of meat goats. The two aims for this study were to 1) determine the breeding goals for each of these production systems and 2) calculate economic values for traits in the breeding objective. To achieve this, surveys were distributed online to the producer groups and a total of 44 responses were returned. The most consistent message from producers, was that increasing meat production is the main objective. Internal parasites were also identified as an issue for the commercial producers and seedstock breeders. The largest problem identified, was the inconsistency between what producers said they recorded and what is submitted for genetic evaluation. Processors were also surveyed but had a limited response rate.

2.6. Economic values for Australian meat goats

The results from the survey on herd structure, reproduction, management, and marketing were used to calculate economic values. Weight at sale age had a large economic value with an increase of $2.53 per kg increase. Relative economic values were calculated as dollar gain per genetic standard deviation. Kid survival ($9.79) had the largest economic value per genetic standard deviation, followed by fertility ($5.94), body weight ($3.94), number of kids weaned ($3.00), mature weight ($0.70), and litter size ($0.33). The economic values for the reproductive traits were strongly supportive of their inclusion in the breeding objective. With clear breeding objectives from the surveys and the calculated economic values, an index for Australian meat goats was developed. The economic values are summarised in Table 6.

Table 6: Summary of meat goat economic values from SheepObject2.

Component	Economic value / Unit	Economic value / $\boldsymbol{\sigma_G}$
Fertility	$0.66 / %	$5.94
Litter size	$0.11 / %	$0.33
Number of kids weaned	$0.30 / %	$3.00
Kid survival	$0.87 / %	$9.79
Body weight	$2.53 / kg	$3.94
Mature weight	$0.46 / kg	$0.70
Dressing percentage	$1.78 / %	$1.78

2.7. An index designed specifically for meat goats in Australia

Previously meat goat breeders in Australia have used the Carcase Plus (CPLUS) index to make genetic selections. An index focused on lean meat production which used sheep parameter estimates and economic values. It is recommended that the old CPLUS index be replaced with

“Kid Plus” (K+), a dual purpose index specifically designed for increasing lean meat production and reproductive rate of goats. The K+ index uses parameter estimates and economic values calculated for goats. The new K+ index also places an economic value on reproductive traits, including kid survival as a trait of the kid. Two other indexes were created; “Lean Meat Goat” (LMG) and “Maternal Meat Goat” (MMG) for systems where the breeding objective is not as fully described as it is for K+. The dollar value for each doe joined using these indexes increased from CPLUS ($9.53), LMG ($9.24), MMG ($10.22) and K+ ($16.56). If producers improve their recording practices for eye muscle depth, C-site fat depth and worm egg counts then, further evaluation and development will be needed to better define them in the breeding objective. Comparisons to other indexes including a internal parasite (LP2020) and maternal index (SRC) were also made. The economic values used for all of the indexes are presented in Table 7.

Table 7: Summary of economic values used for each index (values in $AUD per trait unit).

Trait	Units	CPLUS	LP2020	SRC	LMG	MMG	K+
BWT	Kg	0.00	-0.21	-0.21	0.00	0.00	0.00
WWT	Kg	2.33	0.32	0.40	2.53	2.53	2.53
PWT	Kg	3.50	0.47	1.48	2.53	2.53	2.53
MWWT	Kg	0.00	0.00	1.88	0.00	0.00	0.00
EMD	Mm	11.40	1.54	2.40	11.40	11.40	11.40
FAT	Mm	-4.07	-0.55	0.00	-4.07	-4.07	-4.07
WEC	%	0.00	-1.71	-1.71	-1.71	-1.71	-1.71
NKB	Number	0.00	0.00	0.00	0.00	11.00	11.00
NKW	Number	0.00	0.00	75.00	0.00	30.00	30.00
KSV	Number	0.00	0.00	0.00	0.00	0.00	87.00

For each index there were six trait recording scenarios (Results for three presented). The first scenario was for Growth which assumed the only traits recorded were BWT, WWT, and PWT. The second scenario presented was Reproduction which included growth traits (BWT, WWT, and PWT) and reproductive traits (NLB, NLW, and KSV). The third scenario presented was Gold standard recording with full recording of all traits.

There were large differences comparing Growth, Reproductive, and Gold standard recording scenarios with differences in selection emphasis and trait changes (Table 8). It was predicted that the Growth scenario would place the majority of selection on the growth traits which was true. Once reproductive traits were recorded, the new KIDPLAN indexes greatly reduced the amount of pressure on growth traits and increased the selection on NKB, NKW, and KSV. With the current recording practices, a new KIDPLAN index will continue to increase growth and reproductive traits, but have a negative impact on EMD and FAT. Unlike CPLUS, the new KIDPLAN indexes reduced WEC which is beneficial. Importantly, under the Gold standard recording scenario there were no significant differences to the selection emphasis or trait changes for the three KIDPLAN indexes. This means that LMG, MMG, and K+ should each be considered to replace CPLUS.

Table 8: Summary of the relative emphasis placed on traits for each index under Growth, Reproductive and Gold standard recording practices.

Trait	CPLUS	LP2020	SRC	LMG	MMG	K+
			Growth recording scenario			
Body weight	69%	39%	26%	63%	53%	35%
MWWT	0%	0%	20%	0%	0%	0%
EMD	29%	12%	6%	30%	25%	20%
FAT	2%	1%	0%	2%	2%	2%
WEC	0%	48%	7%	4%	4%	2%
NKB	0%	0%	0%	0%	2%	2%
NKW	0%	0%	42%	0%	13%	7%
KSV	0%	0%	0%	0%	0%	33%
			Reproduction recording scenario			
Body weight	70%	39%	16%	64%	47%	17%
MWWT	0%	0%	10%	0%	0%	0%
EMD	28%	12%	3%	30%	19%	7%
FAT	2%	1%	0%	2%	1%	1%
WEC	0%	48%	4%	4%	3%	1%
NKB	0%	0%	0%	0%	6%	4%
NKW	0%	0%	68%	0%	24%	14%
KSV	0%	0%	0%	0%	0%	58%
			Gold standard recording scenario			
Body weight	49%	14%	15%	36%	32%	15%
MWWT	0%	0%	13%	0%	0%	0%
EMD	46%	7%	1%	53%	40%	13%
FAT	5%	0%	0%	5%	3%	1%
WEC	0%	79%	9%	7%	6%	1%
NKB	0%	0%	0%	0%	4%	4%
NKW	0%	0%	62%	0%	15%	12%
KSV	0%	0%	0%	0%	0%	54%

For each index and recording scenario, the change in each trait was calculated for a ten year response (Table 9). Under the Growth recording scenario, where the only data submitted to KIDPLAN are records for BWT, WWT, and PWT, all of the indexes had a positive trait change for body weight and maternal weaning weight. The trait change was lowest for LP2020 at 1.05 kg for body weight (50% emphasis of WWT and PWT), and for maternal weaning weight 0.33 kg. The body weight and maternal weaning weight changes were higher for the three new indexes, between 1.36 kg and 1.38 kg for body weight and between 0.59 kg and 0.70 kg for maternal weaning weight. This was similar to the sheep maternal index SRC with a body weight change of 1.31 kg and 0.56 kg for maternal weaning weight. The CPLUS index had the largest trait change for body weight (1.41 kg) and maternal weaning weight (0.66 kg). For the other recording practices, the trait changes for body weight and maternal weaning weight followed these same patterns.

With the Carcase recording scenario, EMD had an increase of 0.26 mm and 0.11 mm for CPLUS and LP2020 respectively. The LMG index had the greatest change to EMD at 0.31 mm when compared with the MMG (0.27 mm) and K+ (0.20 mm) indexes. Under the Carcase recording scenario, there was a decrease in fat of -0.07 mm and -0.02 mm for CPLUS and LP2020, while the new KIDPLAN indexes all had a decrease of 0.07 mm. With the other recording scenarios where carcase traits are recorded, there was a trend for all the indexes to have positive changes to EMD, and decreases for FAT. If carcase traits were not recorded, EMD had an undesirable negative change, and for FAT the desired negative change was lower at a constant carcase weight.

The only recording scenario that included WEC was Gold standard. LP2020 had a negative economic value (-$1.71) for WEC which was also used for the new KIDPLAN indexes. With WEC recorded, LP2020 resulted in a decrease of -0.95 % and the new KIDPLAN indexes were between -0.11 and -0.26 %. With the other recording practices, LP2020, the KIDPLAN indexes, and the maternal index SRC, all resulted in negative or no changes to WEC.

All the reproductive traits (NLB, NLW, and KSV) had a positive change for each recording scenario. For the Reproductive recording scenario K+ had the largest increases, of 5% to kids born, 6% kids weaned, and 9% kids surviving. The MMG index had similar results with an increase of 4% kids born, 5% kids weaned, and 6% kids surviving. The results were similar to the sheep maternal index SRC which had increases of 5% kids born, 6% kids weaned, and 7% kids surviving. The other indexes (CPLUS, LP2020, and LMG) had smaller increases of 1% to 2% for NKB, between 3% and 4% for NKW, and for KSV an increase of between 2% and 4%.

Table 9: Summary of each trait change with different indexes and under different recording scenarios.

Index	Body weight (WWT & PWT)	MWWT	EMD	FAT	WEC	NKB	NKW	KSV
Growth recording scenario								
CPLUS	1.41	0.66	-0.16	-0.04	-0.09	0.01	0.02	0.03
LP2020	1.05	0.33	-0.09	-0.01	-0.31	0.01	0.03	0.01
SRC	1.31	0.56	-0.14	-0.03	-0.20	0.01	0.03	0.02
LMG	1.38	0.62	-0.15	-0.03	-0.13	0.01	0.03	0.02
MMG	1.36	0.59	-0.14	-0.03	-0.16	0.01	0.03	0.02
K+	1.37	0.70	-0.17	-0.04	-0.09	0.02	0.02	0.04
Reproduction recording scenario								
CPLUS	1.41	0.64	-0.15	-0.04	-0.09	0.02	0.03	0.04
LP2020	1.05	0.32	-0.09	-0.01	-0.31	0.01	0.04	0.02
SRC	1.04	0.38	-0.08	-0.02	-0.15	0.05	0.06	0.07
LMG	1.38	0.60	-0.14	-0.03	-0.13	0.02	0.03	0.04
MMG	1.25	0.50	-0.11	-0.02	-0.14	0.04	0.05	0.06
K+	0.94	0.38	-0.08	-0.02	-0.05	0.05	0.06	0.09
Gold standard recording scenario								
CPLUS	1.03	0.89	0.26	-0.08	-0.07	0.01	0.02	0.03
LP2020	0.69	0.40	0.09	-0.02	-0.95	0.00	0.02	0.01
SRC	1.06	0.45	-0.06	-0.02	-0.15	0.04	0.06	0.06
LMG	0.92	0.84	0.30	-0.07	-0.26	0.01	0.02	0.03
MMG	0.96	0.77	0.26	-0.06	-0.25	0.03	0.04	0.05
K+	0.84	0.61	0.16	-0.04	-0.11	0.05	0.06	0.09

3. Publication plan

From the completed PhD thesis there are two full papers planned for publication. The papers are divided into parameter estimates, and selection index. Additional papers have also been considered for a literature review, and to describe the differences between kid survival based on birth type.

4. Future research recommendations

1. Kid survival research

The greatest limitation in the analysis of kid survival was data available both in quantity and quality. The results from the bivariate analysis of the production traits and the multivariate analysis of kid survival demonstrated a need for re-analysis when more data becomes available. If a greater volume of more accurate data becomes available further analysis of the kid survival trait that includes the maternal genetic effect or a kid survival trait of the doe should be investigated further.

1. Future research on kid survival should continue to treat kid survival as trait of the kid rather than the doe.

2. This project focused on kid survival but there are still potential correlated traits such as birth coat score, time to bleating after handling, lamb vigour when handled, rectal temperature, lambing ease, and maternal behaviour score that could be useful but do not have sufficient records for analysis.

3. Other traits (including litter size, number of kids weaned, and fertility rate) and other factors (such as dam age) could be investigated.

4. Another option would be to combine two of the three kid survival traits. The response to selection for three traits compared to the original kid survival trait was 19% greater, and when twin and multiples were assumed to be the same trait the response compared to the original trait was 31% greater.

5. Is it possible to select for more twin litters without increasing the incidence of multiples? Out of interest a brief univariate analysis was done, using a sire model with doe age as a fixed effect, with doe as a maternal permanent environmental effect and a service sire effect using 3,757 records with a mean of 0.44 ± 0.50 (SD). The phenotypic variance was 0.24 ± 0.01, the heritability was 0.03 ± 0.02, maternal permanent environmental variance was 0.01 ± 0.02, and service sire variance of 0.04 ± 0.01.

6. With the new kid survival trait, the welfare issue of increasing the number of kids born but not their survival is addressed, which means fertility and fecundity should be further investigated if breeders report dry does.

2. *Production trait research*

1. From a production aspect breeders should first focus on improving recording practices of dam identification, birth and rearing type information first.

2. Breeders should also begin collecting data on carcase weight where possible, as a key production trait. If more data becomes available for the scanned carcase traits then they should be re-analysed to update the genetic parameters in KIDPLAN.

3. The largest issues that need to be addressed for the carcase quality traits is lack of data, the current inability to justify the value of eating quality due to zero price premiums and the fact that the current scanned carcase traits are not consistently recorded.

4. There is currently adequate data for parameter estimates and EBVs of weights traits from birth to yearling. More data is needed for later age growth traits.

3. *Australian meat goat index research*

The top research priority should be on-farm testing of the KIDPLAN indexes from Chapter 8. This can be used as case studies similar to those available for LAMBPLAN and MERINOSELECT (Sheep Genetics 2017a). It is strongly recommended that breeding programs be further developed with breeders using KIDPLAN. A long term project (5+ years of progress) to demonstrate differences in reproduction between current selection practices (Carcase Plus, random control, or visual selection) and the K+ index would be beneficial for the promotion of KIDPLAN. Results can be used to both assess the theoretical gains and be used as promotion for KIDPLAN. If the index proves to be successful then there should be a long term goal to evaluate the crossing of these KIDPLAN animals with rangeland goats. This is recommended as rangeland goats are and continue to be the largest contributor to meat goat production in Australia.

5. Industry recommendations

1. *Engage with seedstock breeders*

1. Consultation with breeders using KIDPLAN about the results from this project should be a priority. This will help demonstrate to breeders that there is active work on improving KIDPLAN.

2. Updating of the parameters used in the KIDPLAN analysis and the indexes developed should be adopted.

3. KIDPLAN should utilize the new kid survival trait which increases the response to selection compared to only selecting for NKW (Including KSV in the index increased the 10 year trait change for NKW from 0.04 to 0.06 and an increase for KSV of 0.05 to 0.09, Table 8-4).

4. Providing current KIDPLAN users and future users with more education about how to use KIDPLAN, and how to record and submit accurate phenotypes is of very high importance.

    - Increase the number of active users
    - improve the accuracy of the data submitted

5. If one of the KIDPLAN indexes is adopted there needs to be a campaign that brings that to the attention of current and potential breeders. It is also important to highlight it as a development for investors and commercial producers that are beginning to reach a point where genetic improvement is becoming an option with improved fencing.

2. Engage with rangeland producers

The majority of production (90%) is achieved by harvesting from rangeland populations (MLA 2013), but the focus of the thesis has been on Boer goats. This focus was well justified as it is the predominant meat breed in Australia with the ability to make genetic gains using KIDPLAN. The goat industry continues to develop; producers are increasing their goat fencing, laws and regulations are being adapted, and the value of goat meat is increasing. It is a matter of time before genetic improvement of commercially farmed rangeland goats becomes an opportunity. The thesis results could have a significant impact on this opportunity. If KIDPLAN adopts an industry relevant index such as Kid Plus then breeders using KIDPLAN will be best suited to meet the new demand.

- Ideally changing the index will lead to seedstock breeders selling genetically superior bucks to commercial producers and rangeland harvesters based on EBVs and indexes provided by KIDPLAN.
- As management systems change with controlled mating and animal identification within commercial production systems, then phenotypic and pedigree information could be captured and returned to KIDPLAN and seedstock breeders.
- Finally if rangeland producers become engaged with genetic improvement there needs to be feedback and communication to commercial and seedstock breeders to ensure genetic progress continues in the desired direction and addresses future industry issues.
- This project is a large step to addressing the lower survival rates of seedstock kids but the question remains how should the superior genetics for higher production be

introduced to the rangeland? This requires the control or culling of rangeland bucks and the introduction of superior Boer bucks.

3. *What steps I believe the industry should prioritise*

From my experience during working on my PhD I have produced a list of things that I believe the industry can improve, should be relatively easy to implement, and should be given priority.

1. There are far too many does misidentified and animals with incorrect birth types. If a dam is unknown it should be recorded as such, this should also be better communicated to producers.

2. If point 1 is implemented then KIDPLAN needs to use a maternal self-replacing index not a terminal sire index. In hindsight it should have been the original choice however due to limited accurate recording of reproductive data it would probably have had a negligible improvement.

3. KIDPLAN should adopt one of the indexes developed as part of this project, ideally that would be Kid Plus.

4. Following those improvements, selection of animals based on the EBVs and indexes from KIDPLAN should be made using the updated parameter estimates.

5. Finally this work is another step to improving the productivity of Australian rangeland goats. This last step requires an improvement in the engagement and uptake of KIDPLAN by seedstock breeders and commercial producers.

Thank you

I hope this work has made a valuable contribution to meat goat production and wish breeders all the best as they work together to maximise rates of genetic improvement in their exciting industry.

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