

# Genetic improvement of Australian meat goats

By

Michael Nicholas Aldridge

B. Ag. Sc. Hons (Ani. Sc.)

This thesis is presented for the degree of Doctor of Philosophy at The  
University of Adelaide, School of Animal and Veterinary Sciences

September 2017



# Declaration

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in my name, in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree. I give consent to this copy of my thesis, when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968. I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library Search and also through web search engines, unless permission has been granted by the University to restrict access for a period of time. I acknowledge the support I have received for my research through the provision of an Australian Government Research Training Program Scholarship.

Michael Aldridge

Date: 10/02/2018

# Dedication

For my loving grandmother

**Rita Threlfall**

who always believed in me.

# Abstract

The Australian meat goat industry is rapidly changing. This change is predominantly due to the value of goat meat increasing and production moving from rangeland harvesting to fenced commercial systems. The aim of the project was to determine how goat meat production can be increased through genetic improvement. A meta-analysis and sensitivity analysis in the literature review identified selection for kid survival could increase lean meat production by 12.3 kg per genetic standard deviation and became the main trait of interest for the project.

The national performance recording scheme (KIDPLAN) is a database that was made available by Sheep Genetics. This producer recorded data contained pedigree and phenotypic information on 19,711 Boer goats. The KIDPLAN system provides estimated breeding values for Australian goat breeders and is the best opportunity for genetic improvement of meat goats.

A new kid survival trait was created from the birth and rearing type information. The mean kid survival rate was 0.72, with a phenotypic variance of 0.14 and a heritability of 0.09. As the kid survival trait showed variation and was heritable, bivariate analyses with the growth and carcass traits was done to determine its suitability to be included in a selection index. Birth type had a significant effect on kid survival. Kid survival was positively genetically correlated or not different to zero with all of the production traits. The survival trait was separated into three traits based on birth type for singles, twins and multiples. A multivariate analysis showed they were different traits with genetic

correlations of between 0.46 and 0.72. More work and accurate data is needed for them to be included in an index as separate traits and so kid survival should currently be treated as a single trait with birth type fitted as a fixed effect.

The current KIDPLAN index is based on modified sheep parameter estimates and economic values. Surveys were conducted nationally and were used to calculate economic values for the goat production traits. The results from the parameter estimates and surveys showed that goat genetic parameters are different to sheep and the current index is not representative of the industry. Three breeding objectives were created and simulated with six different recording practices. The key finding and recommendation for industry was to adopt a new index based on goat parameter estimates and economic values, also to include reproductive traits such as kid survival as it would lead to a faster rate of gain in reproductive rate than just focusing on number of kids weaned. It was estimated that this would lead to a \$6.75 improvement per doe joined per year compared to the current index.

# Acknowledgments

It is hard to believe that after three years I am finally writing this section. To any PhD, masters or honours student reading this please know that there were many failures and times I wanted to quit but with hard work and the support of others you will write this section too. To all those who supported me I am truly thankful for your help.

I would like to start with the two people I owe the greatest thanks. My supervisors Prof. Wayne Pitchford and Assoc. Prof. Daniel Brown. You have both been an inspiration, you have helped me professionally and personally. I know, I would not be the person I am today without your influence.

To Assoc. Prof Forbes Brien, Dr. Michelle Hebart and Octavia Kelly. All of your lunch time chats, comments, forwarding of papers and ideas have made a significant contribution to my work. Thank you both so much for your input.

I would also like to thank Meat and Livestock Australia for the financial support throughout the project. The networking opportunities and the professional development you offered are also greatly appreciated. Julie Petty and Terry Longhurst I would also like to thank you personally for looking after me during my PhD.

Without the support of Sheep Genetics this work would never have been accomplished. I don't know what I would have done if I hadn't been allowed to use the KIDPLAN data.

The knowledge and networking of people such as Hamish Chandler, Tom Hooke, Will Chaffey and Caris Jones was invaluable.

The Animal Genetics and Breeding Unit and the University of New England have been amazing. The resources, training, support and assistance they provided ensured I had everything I needed. A special thank you to Dr. Andrew Swan, Dr. Rob Banks and Dr. Sam Walkom.

To all the other students I have shared an office, a beer or a cry with, thank you. There are so many of you, I know I will forget some. The Wolf Pack; James, Adam and Thomas. McCulloch Boys; James, Callum, Patrick and Oliver. The Davies Crew; Cathy, Emily, Farrah and Veronica. My genetics buddy; Sarita. And all the others at Davies, Roseworthy, Waite, Postgrad especially Caitlin, Armidale and Fort Kemp.

A special thank you to Colin Ramsey and Nick van den Berg for always wanting to hear what I was doing and for your ideas. Your passion for the goat industry always gives me motivation to work harder. To every goat producer in Australia thank you for making this a great industry to work for, it has been a pleasure.

Finally, to my supporting friends and family I love you all. Especially my Rainbow, Baukje Hollema and my mother Lee Aldridge.

# Table of contents

Declaration .....	ii
Dedication .....	iii
Abstract .....	iv
Acknowledgments .....	vi
Table of contents .....	viii
List of abbreviations .....	xi
List of Figures .....	xii
List of Tables.....	xiii
1 General introduction: Genetic improvement of Australian meat goats .....	1
1.1 Thesis motivation .....	2
1.2 Thesis context within literature and industry .....	3
1.3 Thesis objectives and questions.....	5
1.4 Thesis structure.....	6
2 Review of literature on parameter estimates for meat goat production traits in comparison to sheep.....	7
2.1 Abstract.....	8
2.2 Introduction .....	8
2.3 Growth traits .....	10
2.4 Meat yield and quality traits .....	14
2.5 Reproductive traits.....	18
2.6 Health traits.....	28
2.7 Sensitivity analysis .....	29
2.8 Conclusion .....	34
3 Thesis methodology.....	37
3.1 Trait definitions .....	38
3.2 Data cleaning filters.....	40
3.3 Records available.....	41
3.4 Checking traits are normally distributed .....	42
3.5 Contemporary group components .....	46
3.6 Summary of fixed effects for kid survival.....	47
3.7 Genetic model definitions.....	53



3.8	Conclusion.....	53
4	Producer recorded data on Australian Boer goats needs cleaning for genetic parameter estimates using univariate analyses. ....	55
4.1	Abstract .....	56
4.2	Introduction .....	56
4.3	Materials and Method .....	59
4.4	Results .....	63
4.5	Discussion .....	73
4.6	Conclusion.....	79
5	Genetic and phenotypic relationships between production traits in Australian Boer goats. ....	81
5.1	Abstract .....	82
5.2	Introduction .....	82
5.3	Materials and Methods .....	83
5.4	Results .....	85
5.5	Discussion .....	88
5.6	Conclusion.....	92
6	Kid survival should not be treated as a separate trait for different birth types. ....	93
6.1	Abstract .....	94
6.2	Introduction .....	94
6.3	Materials and Method .....	96
6.4	Results .....	98
6.5	Discussion .....	107
6.6	Conclusion.....	111
7	Australian goat producers say they want to sell more meat. ....	113
7.1	Abstract .....	114
7.2	Introduction .....	115
7.3	Materials and Method .....	116
7.4	Industry Surveys.....	120
7.5	Economic Values .....	131
7.6	Conclusion.....	136
8	An Australian meat goat selection index to increase growth and reproductive rates.....	139
8.1	Abstract .....	140
8.2	Introduction .....	140
8.3	Materials and Method .....	142

*Genetic improvement of Australian Meat goats*

8.4	Results .....	147
8.5	Discussion.....	161
8.6	Conclusion.....	166
9	General discussion: Genetic improvement of Australian meat goats .....	167
9.1	Introduction .....	168
9.2	Key findings .....	168
9.3	Future genetic research for Australian meat goats .....	170
9.4	Extension of genetic evaluation in the meat goat industry .....	178
9.5	Conclusion.....	183
	Appendices.....	185
	Appendix 7.1 Rangeland survey.....	185
	Appendix 7.2 Commercial survey.....	188
	Appendix 7.3 Seedstock survey.....	192
	Appendix 7.4 Processor survey .....	197
	Reference List .....	200

# List of abbreviations

AGBU	Animal genetics and breeding unit	LWT	Live weight (kg)
AI	Artificial insemination	MLA	Meat and Livestock Australia
AWT	Adult weight (kg)	MMG	Maternal Meat Goat index (\$)
Boer	Boer goat breed	MWWT	Maternal weaning weight (kg)
BT	Birth type (Single, twin, multiple)	NDK/DJ	Doe fertility (Number of does kidding per doe joined)
BWT	Birth weight (kg)	NKB	Number of kids born per doe joined
CPLUS	Carcase Plus index (\$)	NLB	Number of lambs born per ewe joined
CFA	Cast for age doe	NKW	Number of kids weaned per doe joined
CWT	Hot carcass weight (kg)	NKW/NKB	Literature kid survival estimate
DJ	Number of does joined	NLW	Number of lambs weaned per ewe joined
DP	Dressing percentage (%) (CWT / LWT x 100)	NS	Not significant ( $p \geq 0.05$ )
EBV	Estimated breeding value	P	Post-weaning (7 to 10 months of age)
EMA	Eye muscle area (cm <sup>2</sup> )	PEMD	Post-weaning eye muscle depth (mm)
EMD	Eye muscle depth (mm)	PFAT	Post-weaning C-site fat depth (mm)
ET	Embryo transfer	PWEC	Post-weaning worm egg count (#/gram)
FAT	C-site fat depth (mm)	PWT	Post-weaning weight (kg)
G x E	Genotype by environment	RT	Rearing type (Single, twin, multiple)
HWT	Hogget weight (kg)	RT/BT	Calculated KSV as a trait of the dam
K+	Kid Plus index (\$)	SE	Standard Error
KSV	Kid survival (RT / BT)	SRC	Self-replacing Carcass index (\$)
LM	Lean meat (kg)	WEC	Worm egg count (No. / gram)
LMP	Lean meat production (kg) (LM/DJ)	WWT	Weaning weight (kg)
LMG	Lean Meat Goat index (\$)	Y	Yearling (10 to 13 months of age)
LMY	Lean meat yield (%) (LM/CWT)	YEMD	Yearling eye muscle depth (mm)
LP2020	Lamb 2020 index (\$)	YFAT	Yearling C-site fat depth (mm)
LSB	Litter size at birth (No. kids born per doe kidding)	YWEC	Yearling worm egg count (No. / gram)
		YWT	Yearling weight (kg)

# List of Figures

Figure 3-1: Distributions of the records for growth traits in the KIDPLAN dataset. ....	43
Figure 3-2: Distributions of the records for scanned carcass traits in the KIDPLAN dataset.....	44
Figure 3-3: Distributions of the records for health traits in the KIDPLAN dataset .....	45
Figure 3-4: Distributions of the records for reproductive traits in the KIDPLAN dataset .....	45
Figure 3-5: Differences in kid survival rate by year of birth. ....	46
Figure 3-6: Relationship between birth weight and kid survival. Data is filtered based on Dam Filter 2 and Site Filter 1.....	47
Figure 3-7: Effect of birth type on kid survival (solid) and birth weight (diagonal line). .....	49
Figure 3-8: Relationship between birth weight (kg) and kid survival rate for different birth types; singles (green), twins (blue), multiples (red).....	50
Figure 3-9: Relationship between doe age and kid survival rate. ....	51
Figure 3-10: Relationship between doe age and litter size.....	51
Figure 3-11: Relationship between doe age and birth weight. ....	52
Figure 3-12: Relationship between sex, kid survival rate (white) and birth weight (black diagonal line).....	52
Figure 4-1: Correlation of EBVs for kid survival as a trait of the kid (KSV) and kid survival as a trait of the dam (RT/BT). ....	72
Figure 6-1: Correlation of EBVs for birth weight traits separated by birth type, with a sire model.....	99
Figure 6-2: Correlation of EBVs for birth weight traits separated by birth type, with an animal model.....	99
Figure 6-3: Correlation of EBVs for kid survival traits separated by birth type, with a sire model.....	101
Figure 6-4: Correlation of EBVs for kid survival traits separated by birth type, without and with logistic transformation, using animal models. ....	101
Figure 8-1: Summary of index values (\$ / doe joined / generation) for each index type and under Growth (white), Carcass (grey), Reproduction (black), Standard practice (green), Best practice (blue) and Gold standard (red) recording scenarios.....	148

# List of Tables

Table 2-1. Weighted mean parameter estimates for across goat breeds (a), Boer goats (b) and across sheep breeds (c), including; the trait mean, heritability ( $h^2$ ), maternal heritability ( $m^2$ ) and phenotypic variance ( $\sigma_p^2$ ), weighted mean standard error of the estimate (S.E.), and number of references used in parentheses ().	11
Table 2-2. Weighted mean parameter estimates for all goat breeds (a), Boer goats (b) and all sheep breeds (c), including; the trait mean, heritability ( $h^2$ ) and phenotypic variance ( $\sigma_p^2$ ) weighted mean standard error of the estimate (S.E.), and number of references used in parentheses ().	15
Table 2-3. Summary of the means for each trait used in the sensitivity analysis and the references used for the estimate.	30
Table 2-4. Summary of the phenotypic standard deviations for each trait used in the sensitivity analysis and the references used for the estimate.	31
Table 2-5. Summary of the heritabilities for each trait used in the sensitivity analysis and the references used for the calculation.	32
Table 2-6. Summary of the heritabilities (diagonal) and genetic correlations (below diagonal) for each trait used in the sensitivity.	33
Table 2-7. Sensitivity analysis of the key traits for goat lean meat production (LMP) per doe joined (DJ). Phenotypic standard deviation ( $\sigma_p$ ), heritability ( $h^2$ ), additive genetic standard deviation ( $\sigma_G$ ).	34
Table 3-1: Summary of the raw data for each of the analysed traits.	42
Table 4-1. Summary of the number of records for each production trait submitted to KIDPLAN before data cleaning.	60
Table 4-2. Filter combinations used to analyse KIDPLAN data, ticks represent filters used in each analysis.	62
Table 4-3: Birth weight genetic parameters of Boer goats, phenotypic variance ( $\sigma_p^2$ ), heritability ( $h^2$ ), maternal heritability ( $m^2$ ), and maternal permanent environmental variance (MPE), with various data cleaning filters. Standard errors are in parentheses ().	64
Table 4-4. Kid survival genetic parameters of Boer goats, phenotypic variance ( $\sigma_p^2$ ), heritability ( $h^2$ ), maternal heritability ( $m^2$ ), and maternal permanent environmental variance (MPE), with various cleaning filters. Standard errors are in parentheses ().	66
Table 4-5. Genetic parameters of Boer goats without data filtering and with data filtering by Site filter and Dam filter 2 ( <sup>a</sup> ), phenotypic variance ( $\sigma_p^2$ ), heritability ( $h^2$ ), maternal heritability ( $m^2$ ), and maternal permanent environmental variance (MPE). Standard errors are in parentheses ().	68
Table 5-1: Data summary for production traits. Total number of records for each trait (diagonal), number of progeny with both traits (above diagonal), the number of sires with both traits recorded (below the diagonal).	85
Table 5-2: Bivariate parameter estimates of Boer goat production traits. Including; mean phenotypic variance ( $\sigma_p^2$ ), mean additive genetic variance ( $\sigma_A^2$ ), mean residual variance ( $\sigma_e^2$ ), mean maternal permanent environmental variance (MPE), heritability on the diagonal (mean), genetic correlation below the diagonal, and phenotypic <sup>A</sup> correlation above the diagonal.	86

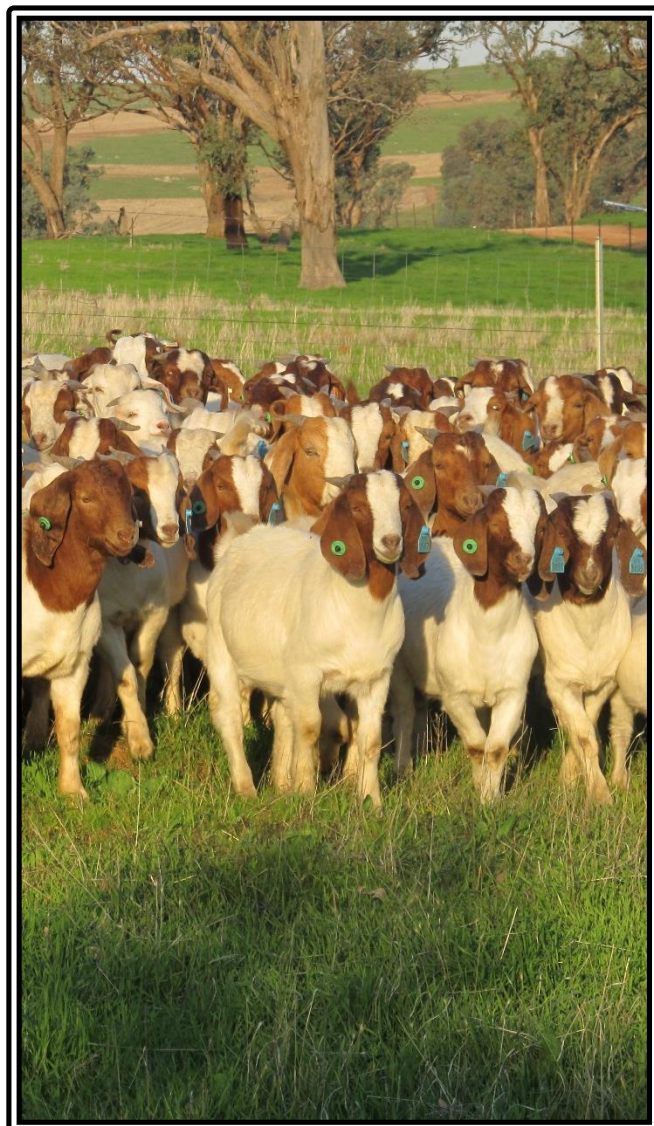
Table 6-1: Tri-variate analysis for separate birth type traits of birth weight and kid survival with a sire and animal model. The heritability is on the diagonal and genetic correlation below the diagonal. ....	103
Table 6-2: Tri-variate analysis for separate birth type traits of weaning weight (WWT) and post-weaning weight (PWT) with an animal model. The heritability is on the diagonal and genetic correlation below the diagonal. ....	105
Table 6-3: Genetic correlations between birth weight (BWT) and kid survival (KSV) birth type traits with a sire and animal model. ....	105
Table 6-4: Genetic correlations with animal model between kid survival birth type traits and individual production traits. ....	107
Table 7-1: Summary of the number of responses and annual herd size for each survey by production system and survey group. ....	118
Table 7-2: Summary of management questions asked and the results of tests of significant difference for those questions. ....	121
Table 7-3: Summary of categorical reproductive questions and the $\chi^2$ tests of significant difference production systems and groups. ....	125
Table 7-4: Summary of the proportion of producers for the age which does are first joined. ....	126
Table 7-5: Summary of the age (months) that does and bucks are first joined. ....	126
Table 7-6: Summary of marketing questions asked and the results of tests of significant difference for those questions. ....	129
Table 7-7: Summary of age and value of animals sold. ....	130
Table 7-8: Summary of breeding objective questions asked and the results of tests of significant difference for those questions. ....	131
Table 7-9: Summary of reproductive inputs, from survey responses and KIDPLAN data, for SheepObject2. ....	132
Table 7-10: Summary of survey responses for male and female progeny sold, as inputs used for SheepObject2. ....	133
Table 7-11: Summary of meat goat economic values from SheepObject2. ....	135
Table 8-1: Summary of parameter estimates. Genetic variance ( $\sigma_A^2$ ), residual variance ( $\sigma_e^2$ ) and maternal permanent environmental variance (MPE). The genetic correlations are below the diagonal the phenotypic correlations above. ....	143
Table 8-2: Summary of economic values used for each index (values in \$AUD per trait unit). ....	145
Table 8-3: Summary of own / half-sib traits recorded for each scenario. ....	146
Table 8-4: Summary of each trait change with different indexes and under different recording scenarios. ....	151
Table 8-5: Summary of the relative emphasis placed on traits for each index under Growth, Reproductive and Gold standard recording practices. ....	153
Table 8-6: Trait and index superiority of the top 10% of KIDPLAN sires selected on each index. ....	155
Table 8-7: Sensitivity analysis of economic values for number of kids born. ....	159
Table 8-8: Sensitivity analysis of economic values for number of kids weaned. ....	159
Table 8-9: Sensitivity analysis of economic values for kid survival. ....	160
Table 8-10: Sensitivity analysis of economic values for worm egg count. ....	160







# 1 General introduction: Genetic improvement of Australian meat goats



A single question was asked at the beginning of the project that became the main theme for the thesis. “What traits need to be genetically improved to have the greatest effect on increasing goat meat profitability?”

## 1.1 Thesis motivation

Several discussions in early 2014 had a large influence on the research strategy. The first meetings occurred with Tom Hooke who was the project officer for KIDPLAN and LAMBPLAN at Sheep Genetics. He had significant input during these discussions. It was during this meeting that a list of traits of interest was created, and the first time kid survival was mentioned. It was also decided during this meeting that the national performance recording scheme (KIDPLAN) database was the best resource for a goat genetic improvement project. By the conclusion of the meeting there was an outline for a potential thesis structure that included parameter estimation, genetic correlations between traits, and developing breeding programs for Australian meat goat producers.

Tom Hooke introduced me to Colin Ramsey, who is an innovative Boer goat breeder. At the time Colin was the leader of a producer demonstration site. On a visit to his property to help with artificial insemination there was an introduction to a leading goat reproductive specialist, Paul Hamilton. This meeting was one of the defining moments of the project. Both Colin and Paul had been involved with the goat industry since the importation of Boer goats in the early 1990’s. They provided firsthand knowledge of the breed development and the issues it faced until present.

Colin and Paul shared their knowledge of the import of Boer goats from South Africa to Australia. Colin has ties to the Terraweena Stud which was used for the original importations. In the mid 1990's Boer goats were released in the rangeland but Boer bucks could not compete with the rangeland goats and most progeny had low survival rates. They also experienced the exportation of Australian Boer goats to China in the early 2000's which saw a preference of animals with a white body and red head but not for production traits. Over this time KIDPLAN had a large number of producers adopt the system but after a number of years each would stop using it, preferring selection for the show ring or completely leaving the industry. Colin identified the progress that sheep and cattle breeders were making by moving to performance recording and made major changes to his system. Most importantly Colin and Paul provided anecdotal evidence that kid survival was a major issue and potentially the most important trait that producers need to improve.

## 1.2 Thesis context within literature and industry

The Australian meat goat industry is the largest exporter of goat meat in the world, predominantly due to production being based on rangeland harvesting and the low local consumption (MLA 2016). Since the importation of Boer goats in the 1990's there has been interest in the genetic improvement of the breed (MLA 2004a). Meat and Livestock Australia published the Research and Development Strategy in 2012 (MLA 2012). That report identified kid mortality as a serious issue for producers. It also identified the need to invest research into improving KIDPLAN.

With kid survival as a key trait of interest, a gap in the literature was identified. The majority of parameter estimates for reproductive traits in goats are on number of kids born or weaned as a trait of the doe (Mourad 1996; Odubote 1996; Walkden-Brown and Bocquier 2000; Marai *et al.* 2002; Hamed *et al.* 2009; Zhang *et al.* 2009a; Alade *et al.* 2010; Mellado *et al.* 2011). There is limited published literature on goat survival. Snyman (2010) reported on causes of death for Angora goats. Genetic parameter estimates on kid survival as a trait of the doe have been reported by Singh *et al.* (1990) on page 201, and did not include Boer goats. In comparison to sheep, there has been a large focus on lamb survival as a trait of the ewe (Fogarty *et al.* 1994; Rosati *et al.* 2002; Afolayan *et al.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014). There are three clear gaps in the literature: 1) kid survival of Boer goats; 2) treating survival as a trait of the kid rather than the dam; 3) the genetic correlation between kid survival with other production traits.

Currently goat breeders using KIDPLAN are using the index Carcase Plus (CPLUS) (BCS Agribusiness 2012; Sheep Genetics 2016). The issue with CPLUS is that the breeding objective used to create the index relied heavily on sheep parameter estimates and economic values. The majority of selection for CPLUS is on high growth rates (60%), followed by increasing eye muscle depth (20%), and decreasing fat depth (20%) (Sheep Genetics 2016). There are a limited number of producers using KIDPLAN that record carcase traits despite this being the focus of the current index. Creating a new index designed specifically for Australian meat goat producers requires updating the parameters, economic values, and including a new kid survival trait. This could help achieve the recommendations identified in the research and development strategy.

### 1.3 Thesis objectives and questions

All of the objectives and questions that this thesis address all 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 carcass 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 above what emphasis will a selection index place on growth, reproductive, carcass, and health traits?

## 1.4 Thesis structure

The literature review (Chapter 2) was used to determine what gaps were in the goat literature, and where the best opportunity was for genetic gain. This reaffirmed the initial focus on kid survival. As the thesis progressed more traits and cleaning methods were added. It became important to clearly define each before they appeared in the research chapters, this was done in Chapter 3 on methodology.

As the KIDPLAN database is industry recorded data there are a wide range of inconsistencies and human errors. Chapter 4 addressed errors in the database caused by inaccurate dams and inconsistent recording of birth type and rearing type at different sites. Chapter 4 included univariate analyses of kid survival and all the other production traits, and tests these cleaning methods. The univariate analyses provided the parameter estimates, starting values, and was the basis for Chapters 5 and 6. The bivariate analyses of Chapter 5 were used to determine the genetic relationships between kid survival and the other production traits. The results for kid survival and birth weight from Chapters 4 and 5 were motivation to treat kid survival as three different traits based on birth type (Chapter 6).

The results from Chapters 4, 5 and 6 fill gaps in the goat literature but did not provide an outcome that can be used for the genetic improvement of Australian meat goats. To do that breeding objectives and economic values for the traits analysed were needed. Chapter 7 reported on industry surveys to determine breeding objectives and to calculate economic values. Finally, Chapter 8 combined the results from Chapters 2 to 7 to create a meat goat index for Australian meat goat breeders.

## 2 Review of literature on parameter estimates for meat goat production traits in comparison to sheep.



## 2.1 Abstract

The Australian meat goat industry is the largest exporter of goat in the world with the majority of production achieved from rangeland harvesting but the best potential for genetic improvement is with Boer goat breeders. This 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 meat yield which included; reproductive, growth, and carcass traits. Health traits were also briefly examined but there was very limited available literature for meat goats.

The largest gaps in the goat genetic literature are for carcass, reproductive and health traits. Carcass weight, dressing percentage, eye muscle depth, and fat depth are all missing parameter estimates. For reproduction, kid survival between birth and weaning has the largest gap in the literature. 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% increase) 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 addition to literature through this research project was with kid survival.

## 2.2 Introduction

Australia is the world's largest exporter of live goats and goat meat products, with a value of \$241.8 million AUD in 2014 (MLA 2015). Over 90% of Australian goat meat



production has been achieved by harvesting from wild rangeland populations (MLA 2013). The remainder of farmed production was predominantly from the South African Boer breed (Ball *et al.* 2001; MLA 2004b). The Boer has been the focus of seedstock breeders and intensive producers in Australia, with the majority of phenotypic records submitted to the national performance recording scheme; KIDPLAN coming from these goats (Ball *et al.* 2001; BCS Agribusiness 2012).

While goat production (2-5 million head) will probably never compete with lamb production (approximately 75.5 million head), there is a lot that the goat industry can learn from lamb production, particularly in relation to genetics (MLA 2004b; Australian Bureau of Statistics 2013). This review focused on parameter estimates for goat production traits and compare it to sheep production traits. Where possible, Boer goats and Merino sheep were examined in more detail as the two major breeds in Australia. Studies that only report phenotypic components were limited to demonstrating the lack of genetic estimates. If a literature review that provides weighted means for a trait is available those results were presented. The parameter estimates presented are weighted means based on standard errors and number of progeny for across all breeds of goat, for Boer goats and for across all breeds of sheep, and were calculated as:

$$\text{Weighted heritability} = \left( \sum_{i=1}^n \frac{h_i^2}{SE_i} \right) \times \left( \frac{1}{\sum_{i=1}^n \frac{1}{SE_i}} \right)$$

$$\text{Weighted standard error} = \sqrt{\frac{1}{\sum_{i=1}^n \frac{1}{SE_i}}}$$

The largest drivers of profit are the efficiency of meat production and the total weight weaned, which has three components: the number of animals available for slaughter, growth rate, and lean meat production of the carcass (Turner 1972). Efficiency of meat production is more effectively increased by increasing the number of animals for slaughter than the amount of meat produced by each animal (Turner 1972). Increasing the number of animals is achieved by increasing the reproductive rate, which herein is defined as the number of kids weaned per doe joined. Following Turner (1969), reproductive rate can be partitioned to the three components of; fertility, fecundity, and kid survival.

### 2.3 Growth traits

The commonly recorded growth traits for goats were birth weight (BWT), weaning weight (WWT), and yearling weight (YWT) were summarised in Table 2-1. For sheep and goats the weighted mean heritabilities for these traits were moderate, between 0.18 and 0.33. Boer goats did not have significantly different heritabilities for growth traits compared to other breeds of goats and sheep. Boer goats did tend to have lower heritabilities for birth weight (0.18) and higher heritabilities for weaning (0.29) and yearling weight (0.29), but considering the standard errors they were not significantly different to other goat breeds or sheep.

**Table 2-1. Weighted mean parameter estimates for across goat breeds (a), Boer goats (b) and across sheep breeds (c), including; the trait mean, heritability ( $h^2$ ), maternal heritability ( $m^2$ ) and phenotypic variance ( $\sigma_p^2$ ), weighted mean standard error of the estimate (S.E.), and number of references used in parentheses ().**

Trait	Mean (kg)	$h^2 \pm$ S.E.	$m^2 \pm$ S.E.	$\sigma_p^2$
Birth weight (kg) <sup>a</sup>	3.51 (8)	$0.22 \pm 0.08$ (9)	$0.19 \pm 0.11$ (5)	0.36 (4)
Birth weight (kg) <sup>b</sup>	3.70 (3)	$0.18 \pm 0.11$ (4)	$0.18 \pm 0.15$ (3)	0.39 (2)
Birth weight (kg) <sup>c</sup>	4.18 (12)	$0.21 \pm 0.04$ (1)	$0.19 \pm 0.01$ (1)	0.48 (1)
Weaning weight (kg) <sup>a</sup>	12.0 (9)	$0.22 \pm 0.07$ (9)	$0.07 \pm 0.11$ (3)	7.8 (5)
Weaning weight (kg) <sup>b</sup>	20.9 (2)	$0.24 \pm 0.14$ (3)	$0.08 \pm 0.15$ (2)	12.9 (2)
Weaning weight (kg) <sup>c</sup>	27.8 (10)	$0.29 \pm 0.01$ (1)	$0.12 \pm 0.01$ (1)	11.7 (1)
Yearling weight (kg) <sup>a</sup>	19.3 (5)	$0.24 \pm 0.13$ (4)	-	17.5 (2)
Yearling weight (kg) <sup>b</sup>	23.8 (2)	$0.29 \pm 0.19$ (2)	-	24.3 (1)
Yearling weight (kg) <sup>c</sup>	45.0 (9)	$0.33 \pm 0.12$ (8)	$0.03 \pm 0.02$ (3)	31.2 (8)

Mean birth weights have been reported for several breeds of goats and ranged between 2.32 kg and 3.87 kg (Boujenane and Hazzab 2008; Zhang *et al.* 2008). It is important to note that the Boer breed has consistently higher birth weights of 3.50 kg, 3.70 kg, and 3.87 kg (Schoeman *et al.* 1997; Zhang *et al.* 2008; Zhang *et al.* 2009b). Of the three Boer papers that reported heritability of BWT; Schoeman *et al.* (1997) and Zhang *et al.* (2009b) reported a phenotypic variance of 0.29 and 0.57 respectively. The mean heritability for BWT without maternal genetic effects included in the model is 0.39 across all breeds, and with maternal genetic effects included in the model a mean heritability of 0.17. The maternal heritabilities for Boer kid BWT had a range between 0.17 and 0.26 and a weighted mean across breeds of 0.19.

As for most traits, the sheep literature had a much larger number of papers published with parameter estimates for BWT and for a wider range of breeds compared to goats. The mean BWT for sheep ranged between 2.80 kg and 4.68 kg, which was considerably higher than goats (Matika *et al.* 2003; Hanford *et al.* 2005; Safari *et al.* 2005). There was a large

range of heritabilities across the breeds of sheep between 0.07 and 0.40 (Maniatis and Pollott 2002; Ozcan *et al.* 2005; Safari *et al.* 2005; Safari *et al.* 2007).

As goats are often marketed at weaning, WWT is a key production trait. Weaning weights ranged between 8.2 kg and 26.8 kg with a mean of 12.0 kg. The mean WWT for goats not including Boers, was lower at 9.5 kg. The Boer breed had larger WWTs of 15.0 kg and 26.8 kg compared to the other breeds with a mean of 20.9 kg (Schoeman *et al.* 1997; Mandonnet *et al.* 2001; Zhang *et al.* 2009b). There was again a large range in the heritabilities across breeds for WWT, with estimates between 0.08 and 0.49 (Mourad and Anous 1998; Barazandeh *et al.* 2012). The heritability for Boer WWT ranged between 0.16 and 0.22 for the two published articles, which had a weighted mean maternal heritability of 0.16 (Schoeman *et al.* 1997; Zhang *et al.* 2009b).

Sheep are much larger than goats as reflected by the WWT for sheep which ranged between 17.8 kg and 36.9 kg across breeds (Tosh and Kemp 1994; Matika *et al.* 2003). The heritabilities across sheep breeds for WWT ranged between 0.09 and 0.29 (Mousa *et al.* 1999; Safari *et al.* 2007). It is also important to note that each of the sheep publications included also published the phenotypic variance, with a mean of 20.3. The maternal heritability has also been included in each of the publications, ranging from 0.04 to 0.19, with a weighted mean of 0.12 (Tosh and Kemp 1994; Mousa *et al.* 1999; Nesor *et al.* 2001; Matika *et al.* 2003; Hanford *et al.* 2005; Ozcan *et al.* 2005; Hanford *et al.* 2006; Safari *et al.* 2007; Mortimer *et al.* 2010).

There was a gap in the available parameter estimates across the goat literature for yearling weights. The weighted mean heritability for goat yearling weight was 0.24 (Mourad and Anous 1998; Ball *et al.* 2001; Mandonnet *et al.* 2001; Mugambi *et al.* 2007; Zhang *et al.* 2009b). There were many more published parameter estimates for sheep yearling weight compared to goats. The mean yearling weight across the sheep breeds included is 45.0 kg and ranged between 23.9 kg and 63 kg (Brash *et al.* 1992; Matika *et al.* 2003). The heritability for yearling weight was higher than for birth and weaning weight, with a weighted mean of 0.33, and comparable to the mean heritability for goat yearling weight (0.24). Unlike the goat literature, maternal heritability has been included for yearling weight in sheep but was very low, ranging between <0.01 and 0.07 (Matika *et al.* 2003; Ozcan *et al.* 2005; Safari *et al.* 2007). These low values suggested that maternal heritability is generally not needed in models for yearling traits.

Birth weight of goats had a positive genetic correlation with weaning weight, which is a key production trait. The published correlations ranged between 0.15 and 0.65, with a weighted mean of 0.54 (Mourad and Anous 1998; Ball *et al.* 2001; Al-Shorepy *et al.* 2002; Portolano *et al.* 2002; Mugambi *et al.* 2007; Boujenane and Hazzab 2008). Genetic correlations between BWT and PWT were positive, and reported by Mourad and Anous (1998) and Ball *et al.* (2001) at 0.30 and 0.60 respectively. Ball *et al.* (2001) also reported a positive genetic correlation for Boer goats between birth weight and yearling weight of 0.69. Positive genetic correlations between weaning weight and post-weaning weight were 0.69 reported by Mourad and Anous (1998) and 0.83 by Ball *et al.* (2001). Ball *et al.* (2001) also reported a genetic correlation for Boer goats between weaning weight and yearling weight at 0.59.

## 2.4 Meat yield and quality traits

There was a large amount of missing information on meat yield and quality traits for goats in comparison to sheep research. The differences in the following traits were discussed; hot carcass weight (CWT), dressing percentage (DP), eye muscle depth (EMD), and eye muscle area (EMA), fat depth at the C-Site (FAT), and meat pH (ultimate pH). The goal of selection for meat traits is to provide a consistent, high yield, and high quality product for consumers (MLA 2012, 2013).

No heritability estimates for goats were found for CWT or DP, but the weighted heritability means from sheep literature were  $0.29 \pm 0.15$  and  $0.33 \pm 0.12$  respectively. The estimates for EMD in goats had a weighted mean heritability of  $0.07 \pm 0.18$  which was much lower than sheep, with EMA and EMD heritabilities of  $0.27 \pm 0.10$  and  $0.27 \pm 0.12$  respectively. Fat depth showed a similar trend with the heritability for goats being  $0.12 \pm 0.19$  and sheep  $0.24 \pm 0.08$ . No estimates for the heritability of goat meat pH were available but for sheep it was  $0.18 \pm 0.09$ . A summary of each of the meat carcass traits are in Table 2-2.

**Table 2-2. Weighted mean parameter estimates for all goat breeds (a), Boer goats (b) and all sheep breeds (c), including; the trait mean, heritability ( $h^2$ ) and phenotypic variance ( $\sigma_p^2$ ), weighted mean standard error of the estimate (S.E.), and number of references used in parentheses ().**

Trait	Mean	$h^2 \pm$ S.E.	$\sigma_p^2$
Hot carcass weight (kg) <sup>a</sup>	11.1 (9)	-	0.7 (4)
Hot carcass weight (kg) <sup>b</sup>	11.7 (3)	-	-
Hot carcass weight (kg) <sup>c</sup>	21.1 (4)	0.29 $\pm$ 0.15 (3)	5.1 (3)
Dressing percentage (%) <sup>a</sup>	53.4 (9)	-	2.3 (4)
Dressing percentage (%) <sup>b</sup>	52.2 (3)	-	-
Dressing percentage (%) <sup>c</sup>	45.8 (5)	0.33 $\pm$ 0.12 (5)	7.4 (4)
Eye muscle area (cm <sup>2</sup> ) <sup>a</sup>	11.3 (7)	-	6.6 (3)
Eye muscle area (cm <sup>2</sup> ) <sup>b</sup>	-	-	-
Eye muscle area (cm <sup>2</sup> ) <sup>c</sup>	18.2 (5)	0.27 $\pm$ 0.10 (5)	3.6 (4)
Eye muscle depth (mm) <sup>a</sup>	-	0.07 $\pm$ 0.18 (2)	2.1 (2)
Eye muscle depth (mm) <sup>b</sup>	-	0.07 $\pm$ 0.18 (2)	2.1 (2)
Eye muscle depth (mm) <sup>c</sup>	27.1 (4)	0.27 $\pm$ 0.12 (4)	7.8 (3)
Fat depth (mm) <sup>a</sup>	1.9 (4)	0.12 $\pm$ 0.19 (2)	0.1 (2)
Fat depth (mm) <sup>b</sup>	-	0.12 $\pm$ 0.19 (2)	0.1 (2)
Fat depth (mm) <sup>c</sup>	3.7 (10)	0.24 $\pm$ 0.08 (10)	2.0 (4)
Meat pH <sup>a</sup>	5.7 (8)	-	0.1 (4)
Meat pH <sup>b</sup>	5.8 (3)	-	-
Meat pH <sup>c</sup>	5.8 (4)	0.18 $\pm$ 0.09 (5)	0.1 (3)

The carcass weights (CWT) of goats have been recorded for several breeds, but estimates of the heritabilities and phenotypic variance were absent. For comparison of parameter estimates across breeds, only papers that used animals under 12 months of age were included. The mean carcass weight was not calculated, as the age of measurement varied between days and classes used; capretto (young goats not weaned with carcass weights between 5-12 kg), and chevon (older goats with carcass weights between 12-22 kg) (Mahgoub and Lodge 1996; Dhanda *et al.* 2003; Marichal *et al.* 2003; Kadim *et al.* 2004; MLA 2004b). Only four of the six papers reported the phenotypic variance of the recorded trait, while no papers with heritability were found.

Only the papers that reported heritability for carcass weight in sheep were included to indicate the difference in research between the species. Fogarty *et al.* (2009) reported a

mean CWT of 25.4kg and did not report heritability for CWT but was included as a standard for the Merino which was used in each of the following meat traits. The mean carcass weight across breeds was not calculated due to large age variations within and between papers but the mean heritability for the trait was 0.29 (Matika *et al.* 2003; Ingham *et al.* 2007; Mortimer *et al.* 2010).

Similar to carcass weight, there are a large number of papers that have recorded dressing percentage across goat breeds. None of these papers reported heritability of the trait and a limited number published the phenotypic variance. The mean dressing percentage across goat breeds is 53.4% (Table 2, Dhanda *et al.* 2003). As with the sheep carcass weight there were several sheep papers that include the dressing percentage for sheep with the heritability and phenotypic variance included. The mean dressing percentage across sheep papers with heritability was 45.8% which is lower than the goat. The weighted mean heritability of dressing percentage in sheep was 0.33 and ranged between 0.24 and 0.53 (Moreno *et al.* 2001; Mortimer *et al.* 2010).

The most common indirect trait of carcass meat yield, was loin eye muscle area (EMA) or depth (EMD). Eye muscle area was not commonly recorded in goats, the following papers Dhanda *et al.* (2003) and Kadim *et al.* (2004) recorded the trait for several breeds. Neither of these papers published the heritability of the trait. The mean eye muscle area across the breeds was 11.3 cm<sup>2</sup>. Ball *et al.* (2001) in Table 3 reported a heritability of 0.10 for EMD post-weaning and a heritability of 0.05 for yearling EMD. The weighted mean heritability for EMA in sheep was 0.27 (Fogarty *et al.* 2003; Ingham *et al.* 2007; Huisman *et al.* 2008; Fogarty *et al.* 2009; Mortimer *et al.* 2010). The mean eye muscle depth for



sheep was 27.1 mm with a heritability of 0.27. EMA and EMD are highly genetically correlated (0.85) as reported by Fogarty *et al.* (2003) in Table 5.

More recently, lean meat production has been used to measure total meat yield, which is the proportion of red meat available after fat trimming. No genetic estimates have been reported for lean meat production in goats, but a phenotypic mean of 77% was reported by Webb *et al.* (2005). Heritabilities for lean meat production in sheep were reported as 0.35 and 0.34 by Safari *et al.* (2005) and Mortimer *et al.* (2010) respectively. Mortimer *et al.* (2010) also reported a phenotypic variance for sheep lean meat production as 6.26 %<sup>2</sup>.

Fat thickness in the C-site (12/13<sup>th</sup> Rib) is not extensively recorded in goats. Of the two papers included, both focused on crosses with Boer goats. Ball *et al.* (2001) reported the heritability (0.13) and phenotypic variance (0.15 mm<sup>2</sup>), but not the mean for fat thickness. The mean for fat thickness recorded by Dhanda *et al.* (2003) was 1.9 mm. Fat thickness in sheep at the C-Site was much more extensively reported. All of the papers included have the mean and heritability of the trait, as well as some that included the phenotypic variance. The mean fat thickness in sheep across breeds was 3.7 mm, much thicker than in goats and the heritability was also much higher at 0.24 (Atkins *et al.* 1991; Brash *et al.* 1992; Fogarty *et al.* 1994; Maniatis and Pollott 2002; Fogarty *et al.* 2003; Ingham *et al.* 2007; Mortimer *et al.* 2010).

Meat pH is another trait that has been recorded for various breeds of goat but the heritability was not included in any publications. The mean pH for the papers across

breeds of goat was 5.71 (Dhanda *et al.* 2003; Marichal *et al.* 2003; Kadim *et al.* 2004). For sheep the mean pH is slightly higher at 5.81 (Fogarty *et al.* 2003; Ingham *et al.* 2007; Fogarty *et al.* 2009; Mortimer *et al.* 2010). The weighted mean heritability for sheep was 0.18 and the phenotypic variance was very low for all of the included papers. The genetic correlation between meat pH and EMD was 0.19 and 0.13, by Fogarty *et al.* (2003) and Ingham *et al.* (2007) respectively. The same publications however reported the genetic correlation of meat pH and EMA as -0.02 and 0.28 respectively.

The disparity in the published literature between goats and sheep suggests that further research into goat genetic parameters for meat traits is needed and highly recommended. Very few of the published articles on the correlated traits to meat yield and quality included the heritability or phenotypic variance. Future research should address this gap in the literature.

## 2.5 Reproductive traits

### 2.5.1 Fertility

Fertility rate was defined as the number of does kidding per doe joined during the mating period. Fertility has been treated as trait of the doe or ewe. None of the papers found in the goat literature contain the heritability of fertility. Fertility of goats ranged between 78% for low fertile animals and 86% for high fertility (Walkden-Brown and Bocquier 2000), with high fertility rates the heritability for the trait is expected to be low.

The mean sheep fertility was 76%, which ranged between 59% and 91% (Fogarty *et al.* 1994; Rosati *et al.* 2002; Matika *et al.* 2003; Safari *et al.* 2007; Afolayan *et al.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014). However fertility was also greatly affected by age with yearling ewes having lower fertility than adult ewes (Bunter and Brown 2013; Newton *et al.* 2014). The weighted mean heritability of fertility in sheep was  $0.11 \pm 0.08$ , and ranged between 0.00 and 0.15, with younger animals having higher heritabilities than older sheep (Fogarty *et al.* 1994; Rosati *et al.* 2002; Matika *et al.* 2003; Safari *et al.* 2007; Afolayan *et al.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014). Fertility is therefore a lowly heritable trait but there is phenotypic variation with a mean variance of 0.14, which improves the prospect of genetic selection (Rosati *et al.* 2002; Safari *et al.* 2007; Afolayan *et al.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014).

### 2.5.2 Fecundity

Fecundity is a function of fertility, ovulation rate, and the survival of embryos to birth. The following section has focused on the two areas of measurable traits for fecundity. Traits recorded pre-partum including fetal number and embryo loss, recorded by ultrasound. The second are traits recorded post-partum as litter size or number of kids born per doe joined.

Unless producers fetal scan early, producers don't witness embryo losses but cause an identified decrease in potential production. There was no information published on embryo survival in goats but Zhang *et al.* (2009a) did suggest that the high litter size at birth of Boer goats is likely due to high ovulation rates (2.13), and embryo survival to birth (1.82-2.03) (Walkden-Brown and Bocquier 2000). The fetal number as recorded by

Afolayan *et al.* (2008a) in crossbred sheep would suggest that selection could be made with a heritability of 0.18, mean of 1.57, and phenotypic variance of 0.53. However, in that study litter size and number of lambs weaned was also more highly heritable than in other studies, the higher estimate could be more a function of the data-set specific rather than indicating fetal number as a clear trait to focus on.

The percentage of embryo losses in sheep has been reported to regularly be above 20% in a review by Meyer (2002). A study by Davis *et al.* (1998) used Romney, Coopworth, and Perendale sheep to calculate parameter estimates for ovulation rate and embryo survival. The mean ovulation rate was 2.32, and mean embryo survival rate was 84%, for a mean litter size of 1.92. The ovulation rate had a heritability of 0.14, and phenotypic variance of 0.57, the heritability is low but increasing ovulation rate could be achieved with the relatively high level of phenotypic variation. Embryo survival had a very low heritability of 0.02, and a low phenotypic variance of 0.23, which would make genetic progress slow.

Zhang *et al.* (2009a) calculated the mean litter size at birth (LSB) for Boer goats to be 1.76 kids with a heritability of 0.12. Across all breeds the mean LSB was 1.66 with a range between 1.34 and 2.90 (Mourad 1996; Odubote 1996; Marai *et al.* 2002; Hamed *et al.* 2009; Zhang *et al.* 2009a; Alade *et al.* 2010; Mellado *et al.* 2011). For those that reported heritability, the mean was 0.23, ranging between 0.08 and 0.39 (Odubote 1996; Hamed *et al.* 2009; Zhang *et al.* 2009a; Alade *et al.* 2010). In sheep, there are several papers that report the litter size of sheep to be very similar to goats, with a mean of 1.67 lambs and a mean heritability of 0.11 (Fogarty *et al.* 1994; Rao and Notter 2000; Safari

*et al.* 2007; Fogarty *et al.* 2009). The phenotypic variance was also reported in the sheep literature with a mean of 0.37 but not for goats. At this time, with the limited research on goats, sheep could be a useful model for reproductive traits. Similar to fertility rate, litter size was lower for yearling animals (1.40) compared to adults (1.74), with heritabilities of  $0.05 \pm 0.02$  and  $0.11 \pm 0.02$  respectively (Table 1 and 2, Bunter and Brown 2013). Across breeds with higher litter sizes; Targhee (1.69), Suffolk (1.95), and Polypay (2.09) also had low heritabilities; 0.11, 0.09, and 0.09 respectively (Rao and Notter 2000).

Number of kids born per doe joined (NKB for goats or NLB for sheep) combined both fertility rate and litter size at birth. Unfortunately there were no estimates published for the genetic component of NKB for goats. In contrast, sheep literature has covered NLB extensively. The mean NLB is 1.00 and ranged between 0.22 to 1.53 (Rosati *et al.* 2002; Afolayan *et al.* 2008a; Afolayan *et al.* 2008b; Newton *et al.* 2014; Brown and Swan 2016a). Yearling animals tended to have a lower NLB than older animals and should be treated as a separate trait (Newton *et al.* 2014). The heritability of NLB was low with a mean of 0.11, ranged between 0.00 to 0.27, however the phenotypic variance was considerable for selection at 0.42 (Rosati *et al.* 2002; Safari and Fogarty 2003; Safari *et al.* 2005; Afolayan *et al.* 2008a; Afolayan *et al.* 2008b; Bunter and Brown 2013; Newton *et al.* 2014).

### 2.5.3 Kid survival, birth to weaning with direct selection

There was a clear gap identified in the estimation of genetic parameters and breeding programs for kid survival. There has been a large amount of work on neonatal survival in sheep but to date has been limited to phenotypic parameters for kid survival. The causes

of death for Angora goats included predation (39.1%), premature birth/ small kid/ help needed for suckling (18.6%), insufficient milk production (6.8%), abandoned (6.8%), illness (6.0 %), accident (5.8%), rain or cold (5.3%), deformation at birth (4.5%), teat/udder deformity (3.5%), and doe death (2.5%) (Snyman 2010). The leading causes for kid deaths was non-genetic but it should be noted that that of the remaining causes a greater proportion can be considered a trait of the kid rather than the doe. This was different to observations in sheep where the leading cause of lamb losses were due to the ewe. Lamb losses were reported by Luff (1980) and more recently by Brown *et al.* (2014), were due to mismothering and exposure (58.2% and 30.5%), dystocia (17.8% and 47.4%), predation (7.8% and 6.7%), illness or infection was similar to goats (4.4% and 1.4%), and the remainder of deaths were by other causes (11.8% and 13.9%). The main difference between causes of death for goats and sheep were; the majority of kid deaths were due to the animal's ability to survive but the majority of lamb deaths were due to the ewe's ability to keep its lamb alive. With most non-environmental causes of death in goats being due to the kid and different to sheep, it was hypothesised that an individual's ability to survive would be important for goats.

The literature on goat survival tends to focus more on environmental causes than genetic. There were two traits of interest; the proportion of kids weaned to those born dead or alive, and the number of kids weaned per doe joined. The sheep literature has treated lamb survival as a trait of the ewe and as a trait of the lamb, both have been presented for sheep but the limited goat literature only reported survival as a trait of the doe. The causes of death reported by Snyman (2010) would suggest that treating survival as a trait of the kid could be more appropriate. Other correlated traits for indirect selection have also been discussed.

The pooled heritability for survival as a trait of the doe across breeds was reported by Singh *et al.* (1990) at  $0.07 \pm 0.04$  (0-15 days),  $0.05 \pm 0.05$  (16-30 days),  $0.09 \pm 0.06$  (31-60 days),  $0.06 \pm 0.03$  (61-90 days), and  $0.10 \pm 0.05$  (0-90 days). No other publications reported genetic parameter estimates for kid survival. Reports on heritability for lamb survival as a trait of ewe in sheep were also low. In comparison, lamb survival as a trait of the ewe was also lowly heritable with a weighted mean of 0.06, ranged between 0.00 and 0.12 with a mean phenotypic variance of 0.12 (Fogarty *et al.* 1994; Rosati *et al.* 2002; Afolayan *et al.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014).

No published literature for kid survival as a trait of the kid could be found. Brien *et al.* (2010) reported the direct heritability of lamb survival between birth to 3 days as 0.014 and survival to weaning as 0.01. The maternal variance was reported to be 0.01 and 0.02 but could not be separated into maternal genetic and maternal environmental effects. The review by Safari *et al.* (2005) reported a mean heritability for lamb survival of 0.03, similar to 0.03 used by Brien *et al.* (2014) which gave a relative response to selection of 14% per generation. For a lowly heritable trait, direct selection can have a positive effect on survival when combined with pedigree data (Brien *et al.* 2010).

The number of kids weaned per doe joined (NKW) is a function of fertility, fecundity, and survival and was reported as a trait of the doe. The heritability for NKW for Boer goats by Zhang *et al.* (2009a) was 0.10, and a mean for the phenotype of 1.62, similar to Zaraibi goats by Hamed *et al.* (2009) with a heritability of 0.05, and mean of 1.60. The mean for sheep NLW was lower at 1.01, with a mean heritability of 0.06, and mean

phenotypic variance of 0.47 (Fogarty *et al.* 1994; Rosati *et al.* 2002; Matika *et al.* 2003; Safari *et al.* 2007; Afolayan *et al.* 2008a). While NLW has a low heritability, the variation in the trait suggests selection could increase the number of animals weaned.

#### *2.5.4 Kid survival, birth to weaning with indirect selection*

Including indirect selection for survival using traits that can be recorded in the paddock could be used to increase accuracy or rate of genetic gain in kid survival. Some traits in the sheep literature suggest the following candidate traits of the lamb; birth coat score, time to bleating after handling, lamb vigour when handled, and rectal temperature (Brien *et al.* 2010; Plush *et al.* 2011; Brien *et al.* 2014; Brown *et al.* 2014; Young *et al.* 2014; Brien *et al.* 2015; Li and Brown 2016). Traits of the doe include lambing ease and ewe maternal behaviour (Brien *et al.* 2010). Birth weight, birth type, and dystocia were also considered as they have strong interactions together and with kid survival.

Time to bleating after handling as a trait of the kid is a relatively easy trait to record and could easily be adopted by goat breeders. For sheep it was a lowly heritable trait (0.11) however it was negatively genetically correlated to survival at -0.43 (Brien *et al.* 2014). A more recent estimate for the heritability of time to bleating in sheep was lower (0.04) but still with a moderate genetic correlation to survival of -0.25 (Brien *et al.* 2015).

Lamb vigour at birth as a trait of the kid is difficult for breeders to incorporate as it is a subjective measure. It also has a low heritability reported of 0.16 and 0.11 by Brien *et al.* (2014) and Brien *et al.* (2015) respectively. Lamb vigour was moderately correlated to lamb survival at -0.25 (Brien *et al.* 2015). Lamb vigour is a more difficult trait to measure



but could still be incorporated into goat breeding programs if it has similar parameter estimates to sheep.

Birth coat scores as a measure of how hairy or fine the coat is, has not been widely researched or been adopted for goats. Low genetic correlations have been reported between 0.09 and 0.32, with further analysis required to determine the usefulness of the trait in relation to survival in sheep (Brien *et al.* 2014).

Rectal temperature has not been widely researched in relation to survival. The possibility of welfare concerns and breeder willingness for adoption should be considered. Brien *et al.* (2010) reported rectal temperature of lambs to have a heritability of  $0.10 \pm 0.02$  and a genetic correlation to NLW as 0.56. Rectal temperature was lowly heritable but it is as a promising potential trait to be used for survival selection; with easy recording methods, a strong genetic correlation and variation in the trait (Brien *et al.* 2014).

Dystocia and hypoxia caused by difficult births have been identified as leading causes of death in sheep within the first 48 hours after birth and provides potential traits of the ewe to be selected (Brien *et al.* 2014; Hinch and Brien 2014). The main cause of dystocia and hypoxia in sheep was fetopelvic disproportion (Brounts *et al.* 2004; Brien *et al.* 2010; Hinch and Brien 2014). Dystocia and difficult births in goats are not common (2-3% prevalence), and the cause was normally due to large litter sizes with more than one kid entering the birth canal at a time rather than fetopelvic disproportion such as in sheep (Braun 2007; Zahraddeen *et al.* 2011; Sofi *et al.* 2012). Fetopelvic disproportion does occur in goats but is most commonly due to a kid born as a single which was also the case

in sheep (Sofi *et al.* 2012). Lambing ease had a negative correlation to number of lambs weaned of -0.26 and -0.14 reported by Brien *et al.* (2014) and Brien *et al.* (2015) respectively. Lambing ease also had a very low heritability of 0.03 (Brien *et al.* 2015),  $0.08 \pm 0.01$  (Brown *et al.* 2014) and 0.06 (Li and Brown 2016). Incorporating lambing ease which is difficult to measure, moderate genetic correlation to NKW and low heritability reduce its prospect of adoption in goats for survival selection.

Ewe maternal behaviour scores have been reported in a range of breeds and are a promising trait of the ewe to be incorporated into breeding programs. The most common was the distance a ewe travels from the lamb during handling but could also include birth site selection, staying at the birth site and maternal care. The heritability for maternal behaviour scores was higher but range between 0.09 and 0.35, and had lower genetic correlations to lamb survival of between -0.09 and -0.29 (Plush *et al.* 2011; Brien *et al.* 2014; Brown *et al.* 2016c). Brown *et al.* (2016c) also used temperament measures; flight time leaving a weighing crate, and agitation during isolation which had heritabilities of  $0.18 \pm 0.02$ , and  $0.26 \pm 0.02$  respectively. Differences in behaviour such as hiding kids or pressuring them to follow could be an additional effect that needs to be considered with such behavioural traits, which has been demonstrated in goats (Lickliter 1984; Carl and Robbins 1988).

There was a strong interaction between birth weights, litter size and dystocia which needs to be addressed when considering kid survival. Small kids at birth and large litter sizes have been identified to have an increased risk of mortality (Singh *et al.* 1990; Gebrelul *et al.* 1994; Husain *et al.* 1995; Snyman 2010). Significant effects and positive phenotypic

correlations between birth weight and survival have been reported by Singh *et al.* (1990). Both Husain *et al.* (1995) and Snyman (2010) reported increasing mortality rates from single born (14.1% and 10%) to twin born (15.9% and 13%), and then triplets (16.7% and 22%). There was however a difference reported by Singh *et al.* (1990) that the mortality rate of singles was 19.5%, twins 22.0%, and triplets being much lower at 13.4%, this difference was due to a disproportion in the number of birth types of 525 singles, 658 twins, and only 60 triplets. In comparison, Hanford *et al.* (2005) reported mortality rates for Rambouillet sheep of 9.9% (singles), 5.2% (twins), 11.2% (triplets), and 9.1% (quads).

By increasing the litter size of goats the chance of dystocia increased and the birth weight would also decrease, further reducing the chance of survival. It was for this reason that increasing the number of animals born would not be as effective as increasing the survival of animals that will be born. Brown *et al.* (2014) demonstrated that triplets had a higher incidents of dystocia and that there was an optimum birth weight for lambs of 4.8 kg. No genetic correlations between survival and birth weight has been estimated in goats, but there were strong curvilinear relationships, such as that reported by Snyman (2010) and Browning and Leite-Browning (2011). There was little to no genetic relationship between lamb survival and birth weight in sheep, with the literature ranging between 0.00 and 0.45, however there was a consistent curvilinear phenotypic relationship (Brien *et al.* 2014).

Genetic selection for goats and sheep were very different when selection is based on birth weight. Sheep are often selected for having a lower birth weight due to decreased risk of

dystocia but goats have a lower incidence than sheep with birthing difficulties due to larger birth weights with most cases in goats being due to more than one fetus entering the birth canal at one time (Braun 2007). Goats did have a higher mortality after birth likely due to exposure and predation, thus there is a potential opportunity to increase birth weight thereby decreasing the risk of mortality (Alade *et al.* 2010; Snyman 2010; MLA 2012).

## 2.6 Health Traits

The largest gap in published genetic parameter estimates for meat goats was on health traits. Health is an important factor for meat production and has complex interactions with growth, meat yield and quality, and survival. Estimates of heritability for worm egg count (WEC) in meat goats was limited to the Creole breed (Mandonnet *et al.*, 2001; Gunia *et al.*, 2011; Gunia *et al.*, 2013). The weighted heritability for WEC between weaning and 11 months was  $0.21 \pm 0.08$  (Mandonnet *et al.*, 2001; Gunia *et al.*, 2011; Gunia *et al.*, 2013). A similar paper by Pollott *et al.* (2004) for Merino sheep had a heritability of  $0.24 \pm 0.02$ .

Though there was very limited literature on the parameter estimates for health traits in goats there are genetic correlations to live weight as reported by Mandonnet *et al.* (2001). The genetic correlation between worm egg count and live weight were -0.01 (weaning), 0.19 (4 months), -0.03 (6 months), -0.14 (8 months) and -0.09 (10 months). Mandonnet *et al.* (2001) reported positive genetic correlations between packed cell volume and live weight of 0.47 (4 months), 0.28 (6 months), 0.07 (8 months) and 0.10 (10 months). From the sheep literature genetic correlations by Pollott *et al.* (2004) and Pollott and Greeff

(2004) for worm egg count and body weight were -0.32 and -0.09 respectively. Ingham et al. (2007) reported genetic correlations between worm egg counts and birth weight (0.21), weaning weight (-0.15) and post weaning weight (0.36). Pollott and Greeff (2004) also reported negative genetic correlations for worm egg counts and eye muscle depth (-0.19) and fat depth (-0.25).

Further research is highly recommended for calculating the parameter estimates in goat health traits. This would be in line with the suggestions made by MLA (2012) to reduce the parasite problems associated with grazing goats. The majority of literature on parasites in goats focused on the chemical resistance of parasites while efforts should now be made to improve the resistance of the goats against such parasites.

## 2.7 Sensitivity analysis

The following section described a sensitivity analysis for fertility, fecundity, kid survival, growth, and meat yield for total meat yield per doe joined. The aim of the analysis was to establish which trait will have the largest impact on meat production with an increase in one genetic standard deviation. The analysis used the weighted mean of the values presented throughout this review. Where possible the values used are those for Boer goats as they are most likely to represent genetic improvement of meat goats in Australia.

All of the means except for kid survival were calculated for Boer goats. Fertility defined by the number of does kidding per doe joined (NDK/DJ) used the mean fertility rate of 0.82 calculated from the low (0.78) and high (0.86) fertility rates, by Walkden-Brown and

Bocquier (2000). Fecundity as the litter size at birth (LSB) was calculated as the mean number from Odubote (1996), Zhang *et al.* (2009a) and Mellado *et al.* (2011) to be 1.67. As no goat papers reported kid survival as a trait of the kid, number of kids weaned per kids born (NKW/NKB) as a trait of the doe was used. Mean survival was calculated from Husain *et al.* (1995), Perez-Razo (1998), and Singh *et al.* (1990) for a survival rate of 0.82. The calculated mean weaning weight was 20.9 kg (Schoeman *et al.* 1997; Zhang *et al.* 2009b). Meat yield used a function of dressing percentage and lean meat production. The dressing percentage of 52% was calculated from the Boer crossbreds reported by Dhanda *et al.* (2003) and lean meat yield was 77%, as reported by Webb *et al.* (2005). A summary of the means used in the sensitivity analysis and their source is provided in Table 2-3.

**Table 2-3. Summary of the means for each trait used in the sensitivity analysis and the references used for the estimate.**

Component	Mean	References
Fertility (NDK/DJ)	0.82	(Walkden-Brown and Bocquier 2000)
Fecundity (LSB)	1.67	(Odubote 1996; Zhang <i>et al.</i> 2009a; Mellado <i>et al.</i> 2011)
Survival (NKW/NKB)	0.82	(Singh <i>et al.</i> 1990; Husain <i>et al.</i> 1995; Perez-Razo 1998)
Weaning Weight (WWT)	20.9	(Schoeman <i>et al.</i> 1997; Zhang <i>et al.</i> 2009b)
Dressing % (CWT/WWT)	52	(Dhanda <i>et al.</i> 2003)
Lean meat yield % (LM/CWT)	77	(Webb <i>et al.</i> 2005)

As no phenotypic standard deviation for goat fertility have been published to date, means from the sheep literature were used. The mean phenotypic standard deviation for fertility was 0.41 (Rosati *et al.* 2002; Safari *et al.* 2007; Afolayan *et al.* 2008a; Bunter and Brown 2013). Fecundity mean phenotypic standard deviation was calculated from Safari *et al.* (2007), Rosati *et al.* (2002), Hanford *et al.* (2005), and (Hanford *et al.* 2006) to be 0.59. Phenotypic standard deviation for kid survival was calculated by multiplying the variance

of living (0.82) by the variance of dead kids (0.18) and square rooting it for 0.38. The phenotypic standard deviation for weaning weight used values reported for Boer goats and was 0.24 (Schoeman *et al.* 1997; Ball *et al.* 2001). The mean phenotypic standard deviation for dressing percentage used was 0.02 and did not include values for Boer goats (Marichal *et al.* 2003; Kadim *et al.* 2004). No phenotypic variation has been reported for lean meat yield and so the values used were from sheep. The phenotypic standard deviation used was 0.03 (Safari *et al.* 2005; Mortimer *et al.* 2010). A summary of the phenotypic variances used in the sensitivity analysis are provided in Table 2-4.

**Table 2-4. Summary of the phenotypic standard deviations for each trait used in the sensitivity analysis and the references used for the estimate.**

Component	$\sigma_p$	References
Fertility (NDK/DJ)	0.41	(Rosati <i>et al.</i> 2002; Safari <i>et al.</i> 2007; Afolayan <i>et al.</i> 2008a)
Fecundity (LSB)	0.59	(Rosati <i>et al.</i> 2002; Hanford <i>et al.</i> 2005; Hanford <i>et al.</i> 2006; Safari <i>et al.</i> 2007)
Survival (NKW/NKB)	0.38	(Singh <i>et al.</i> 1990; Husain <i>et al.</i> 1995; Snyman 2010)
Weaning Weight (WWT)	3.58	(Schoeman <i>et al.</i> 1997; Ball <i>et al.</i> 2001)
Dressing % (CWT/WWT)	0.02	(Marichal <i>et al.</i> 2003; Kadim <i>et al.</i> 2004)
Lean meat yield (LM/CWT)	0.03	(Mortimer <i>et al.</i> 2010)

No heritability estimate for goat fertility rate has been reported so a mean from the sheep literature were used as 0.05 (Fogarty *et al.* 1994; Rosati *et al.* 2002; Matika *et al.* 2003; Safari *et al.* 2007; Afolayan *et al.* 2008a). The mean heritability of litter size at birth was 0.32 and included Boer goats (Odubote 1996; Zhang *et al.* 2009a; Mellado *et al.* 2011). The only heritability estimate for goat survival to weaning was 0.10 by Singh *et al.* (1990) but an average across the sheep literature as a trait of the ewe was included instead at 0.06. The heritability for weaning weight used values reported for Boer goats and was 0.24 (Schoeman *et al.* 1997; Ball *et al.* 2001). As the heritability for dressing percentage for goats has not been reported the mean was calculated using sheep heritabilities which was 0.39 (Moreno *et al.* 2001; Fogarty *et al.* 2003; Safari *et al.* 2005; Ingham *et al.* 2007;

Fogarty *et al.* 2009; Mortimer *et al.* 2010). No heritability was reported for lean meat production in goats so the values used were from those reported in sheep. The heritability for lean meat yield in sheep was 0.35 (Safari *et al.* 2005; Mortimer *et al.* 2010). A summary of the heritabilities and sources used in the sensitivity analysis are provided in Table 2-5.

**Table 2-5. Summary of the heritabilities for each trait used in the sensitivity analysis and the references used for the calculation.**

Component	h <sup>2</sup>	References
Fertility (NDK/DJ)	0.05	(Fogarty <i>et al.</i> 1994; Rosati <i>et al.</i> 2002; Matika <i>et al.</i> 2003; Safari <i>et al.</i> 2007; Afolayan <i>et al.</i> 2008a)
Fecundity (LSB)	0.22	(Odubote 1996; Zhang <i>et al.</i> 2009a)
Survival (NKW/NKB)	0.06	(Fogarty <i>et al.</i> 1994; Rosati <i>et al.</i> 2002; Afolayan <i>et al.</i> 2008a; Bunter and Brown 2013; Newton <i>et al.</i> 2014)
Weaning Weight (WWT)	0.24	(Schoeman <i>et al.</i> 1997; Ball <i>et al.</i> 2001)
Dressing % (CWT/WWT)	0.39	(Moreno <i>et al.</i> 2001; Fogarty <i>et al.</i> 2003; Ingham <i>et al.</i> 2007; Fogarty <i>et al.</i> 2009; Mortimer <i>et al.</i> 2010)
Lean meat yield (LM/CWT)	0.35	(Safari <i>et al.</i> 2005; Mortimer <i>et al.</i> 2010)

To determine the relative response when one trait is increased, the genetic correlation between traits was needed. The correlations between the reproductive traits for fertility, fecundity, and survival were all positively correlated between 0.44 and 0.79 (Safari *et al.* 2005). Weaning weight was negatively correlated with fertility rate (-0.28), and positively correlated with fecundity and kid survival (0.15 and 0.34 respectively) (Rosati *et al.* 2002; Safari *et al.* 2005). Dressing percentage was negatively correlated with fertility rate and fecundity, -0.28 and -0.43 respectively (Afolayan *et al.* 2008b), but positively correlated with weaning weight (0.03) (Mortimer *et al.* 2010). The only published genetic correlation between lean meat production and the other mentioned traits, was with weaning weight at 0.19 (Mortimer *et al.* 2010). Where there was no published estimate the genetic correlation was assumed to be not significantly different to zero, a summary of the correlations used in the sensitivity analysis are provided in Table 2-6.



**Table 2-6. Summary of the heritabilities (diagonal) and genetic correlations (below diagonal) for each trait used in the sensitivity.**

	Fertility rate	Fecundity	Kid survival	WWT	DP	LMP
Fertility rate	<b>0.05</b>					
Fecundity	0.79	<b>0.22</b>				
Kid survival	0.44	0.52	<b>0.06</b>			
WWT	-0.28	0.15	0.34	<b>0.24</b>		
Dressing % (DP)	-0.19	-0.43	0.00	0.03	<b>0.39</b>	
Lean meat yield (LMY)	0.00	0.00	0.00	0.19	0.00	<b>0.35</b>

By multiplying the mean components of fertility, fecundity, survival, weaning weight, dressing percentage, and meat production, the resulting lean meat production per doe joined (LMP/DJ) was 9.4 kg. Separately 100% of selection pressure was placed on each trait. The change in trait response and the change in each correlated trait response were calculated to determine the total change to LMP/DJ. The analysis could have been achieved with selection index theory but would have required covariances between lean meat production and all of the component traits which have not been reported.

Reproductive traits had the largest impact on production when one trait was increased by one genetic standard deviation. Fecundity and survival had the largest increase to 12.66 kg/DJ and 12.25 kg/DJ respectively. Fertility was third at 12.05 kg/DJ followed by weaning weight 10.58 kg/DJ. The smallest increase was achieved with the meat yield traits, dressing percentage caused a decrease to 8.72 kg/DJ due to the negative correlations with other traits and lean meat production increased production to 9.79 kg/DJ. The results for the sensitivity analysis are summarised in Table 2-7.

**Table 2-7. Sensitivity analysis of the key traits for goat lean meat production (LMP) per doe joined (DJ). Phenotypic standard deviation ( $\sigma_P$ ), heritability ( $h^2$ ), additive genetic standard deviation ( $\sigma_G$ ).**

Component	Mean	$h^2$	$\sigma_P$	$\sigma_G$	LMP/DJ with one $\sigma_G$ increase (kg/DJ)	LMP change with one $\sigma_G$ increase (%)
Fertility (NDK/DJ)	0.82	0.05	0.41	0.09	12.05	28
Fecundity (LSB)	1.67	0.22	0.59	0.26	12.66	35
Survival (NKW/NKB)	0.82	0.06	0.38	0.09	12.25	30
Weaning Weight (WWT)	20.9	0.24	3.58	1.75	10.58	13
Dressing % (CWT/WWT)	0.52	0.39	0.02	0.01	8.72	-7
Lean meat yield (LM/CWT)	0.77	0.35	0.03	0.02	9.79	4
Total lean meat production (LMP/DJ)	9.40					

Calculation for additive genetic standard deviation ( $\sigma_G = \sigma_P * h$ )

Greater improvements would be made if genetic selection was based on the fecundity and survival traits, than if it was placed on fertility. However placing the selection on fecundity could increase the mortality rate due to most dystocia cases in goats being caused by too many kids trying to enter the birth canal at once (Braun 2007). Increasing fecundity without increasing survival is also a welfare issue, as more kids would be born but also more kids would die. Therefore focusing on survival of the kids that are born could be most beneficial. Increasing weaning weight would increase production per animal and also reduce time to the market specification for capretto (5-12 kg) and chevon (12-22 kg) hot carcass weights.

## 2.8 Conclusion

Australia is the world largest exporter of live goats and goat meat with 90% of production being exported. Approximately 90% of this production was from goats harvested from the rangeland environment. This has made genetic improvement of the national herd limited to the small holders of South African Boer goats. The largest impact genetic selection can have is by increasing survival of the kids that are born alive. There are a

range of traits that can be selected for and a strong emphasis must be placed on traits recorded within the first 24 hours of birth as this was when the majority of losses occur. There has been no published literature on kid survival as a trait of the kid however selecting for direct survival as a trait of the doe with birth weight and birth type will likely have a significant impact. Selection for other novel and correlated traits such as; kid rectal temperature, kid vigour, doe maternal behaviour, and birth coat scores could increase the rate of genetic gain. Further work is also needed on carcase traits to fill gaps in the goat literature that are currently covered by sheep and to report the genetic covariances between indicator traits and lean meat production.



# 3 Thesis methodology.



Data for the analysis of this thesis was sourced from Sheep Genetics and the Animal Genetics and Breeding Unit, Armidale, New South Wales. The database was referred to as KIDPLAN and represents the performance of Australian bred South African Boer goats between the years 1987 and 2015. The data available was provided by industry from 150 sites across Australia.

### 3.1 Trait definitions

Reproduction, growth, and carcass composition records were recorded on farm. All records submitted required site, management group, date of birth, birth type (BT) and rearing type (RT) of the kid, dam age (calculated if not provided), sex, and conception method (natural, AI or ET). The following performance traits were defined for analysis and where necessary derived from the available records:

- 1) Birth weight (BWT, kg). The weight of the kid within 24 hours of birth.
- 2) Kid survival to weaning as a trait of the kid (KSV). Binary trait of the kid, 0 for dead and 1 for living at weaning. If the kid recorded had a RT greater than zero and had a trait recorded at or post-weaning it was assumed to be living at weaning.
- 3) Kid survival to weaning as a trait of the doe (RT/BT). Mean litter survival for the year of recording calculated from KSV. Only recorded for does that had a kid.
- 4) Fertility. Number of does pregnant per doe joined.
- 5) Fecundity. Number of kids born per doe joined.
- 6) Litter size at birth as a trait of the doe (LSB). Number of kids born that litter including alive and dead kids.
- 7) Weaning weight (WWT, kg). The weight of the kid when the average group age is between 1 to 4 months post birth.

- 8) Post-weaning weight (PWT, kg). The weight of the kid when the average group age is between 7 to 10 months.
- 9) Yearling weight (YWT, kg). Weight of the kid when the average group age is between 10 to 13 months.
- 10) Hogget weight (HWT, kg). Weight of the kid when the average group age is between 13 to 18 months.
- 11) Adult weight (AWT, kg). Weight of the kid when the average group age is over 18 months.
- 12) Post-weaning eye muscle depth (PEMD, mm). Depth of the eye muscle at the C-site recorded at mean group age between 7 to 10 months.
- 13) Yearling eye muscle depth (YEMD, mm). Depth of the eye muscle at the C-site recorded in millimetres. Recorded at mean group age between 10 to 13 months.
- 14) Combined eye muscle depth (EMD, mm). Both PEMD and YEMD records treated as the same trait. No animals had both a PEMD and YEMD record.
- 15) Post-weaning C-site fat depth (PFAT, mm). Depth of fat recorded at the C-site in millimetres. Recorded at mean group age between 7 and 10 months.
- 16) Yearling C-site fat depth (YFAT, mm). Depth of fat recorded at the C-site in millimetres. Recorded at mean group age between 10 and 13 months.
- 17) Combined C-site fat depth (FAT, mm). Both PFAT and YFAT records treated as the same trait. No animals had both a PFAT and YFAT record.
- 18) Post-weaning worm egg count (PWEC, number/g). Faecal worm egg counts with cube root transformation, when mean group age was between 7 and 10 months.
- 19) Yearling worm egg count (YWEC, number/g). Faecal worm egg counts with cube root transformation, when mean group age was between 10 and 13 months.

## 3.2 Data cleaning filters

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 to remove records for a site where if in that year that site did not record any deaths. 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.



### 3.3 Records available

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.

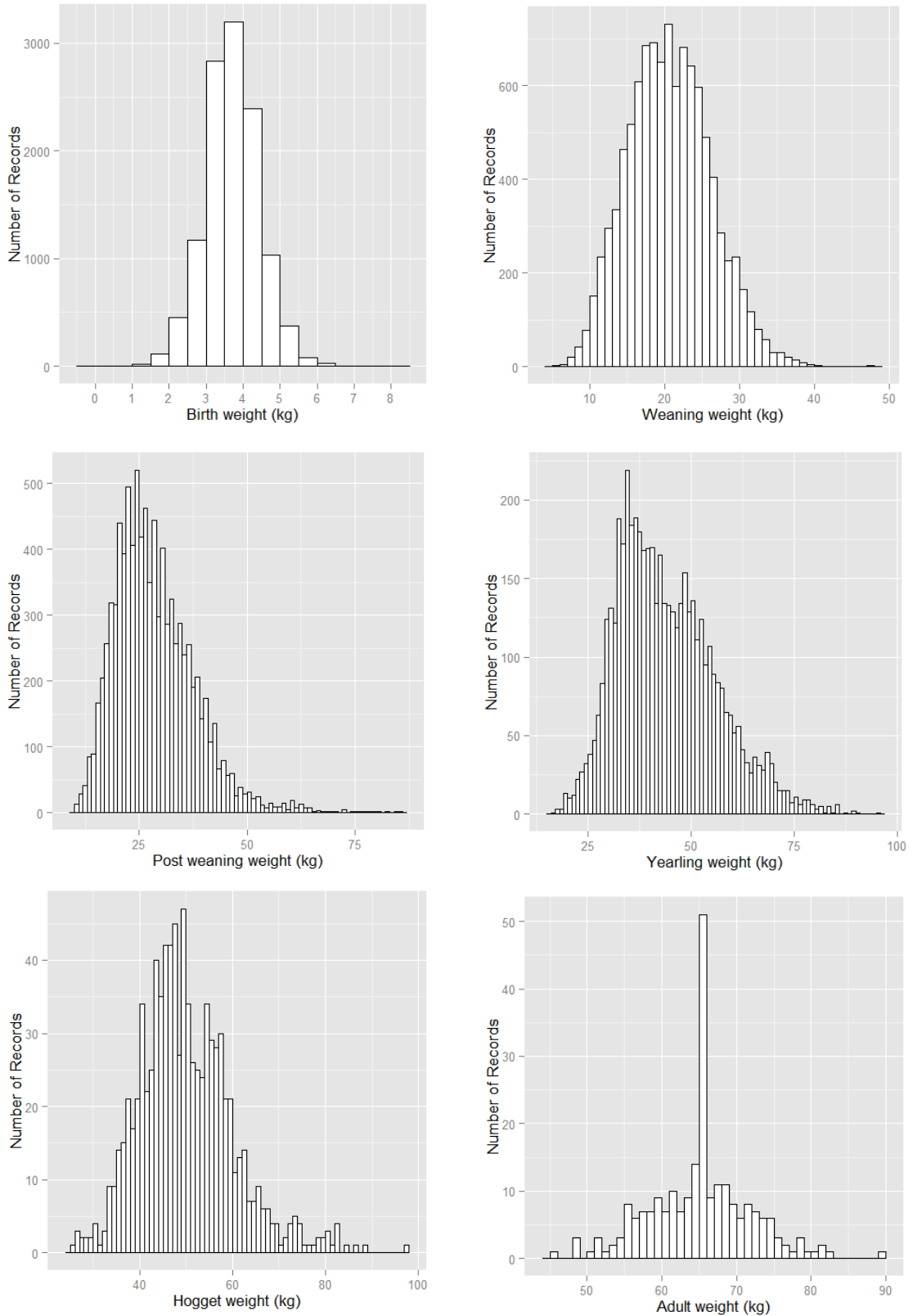
The first assumption was that the available data represented a large population. There were insufficient records for HWT (871), AWT (236), PWEC (289), and YWEC (438). There was also concern that there were not enough records for the post-weaning and yearling eye muscle depth, and C-site fat depth traits which was the reason for creating the two combined traits EMD and FAT (4,782 and 4,819 records respectively) age was then used to regress weight. There were no concerns about the number of records for the other traits. All of the means were within ranges of previous literature (Chapter 2). A summary of the number of records and means for each trait analysed are provided in Table 3-1.

**Table 3-1: Summary of the raw data for each of the analysed traits.**

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

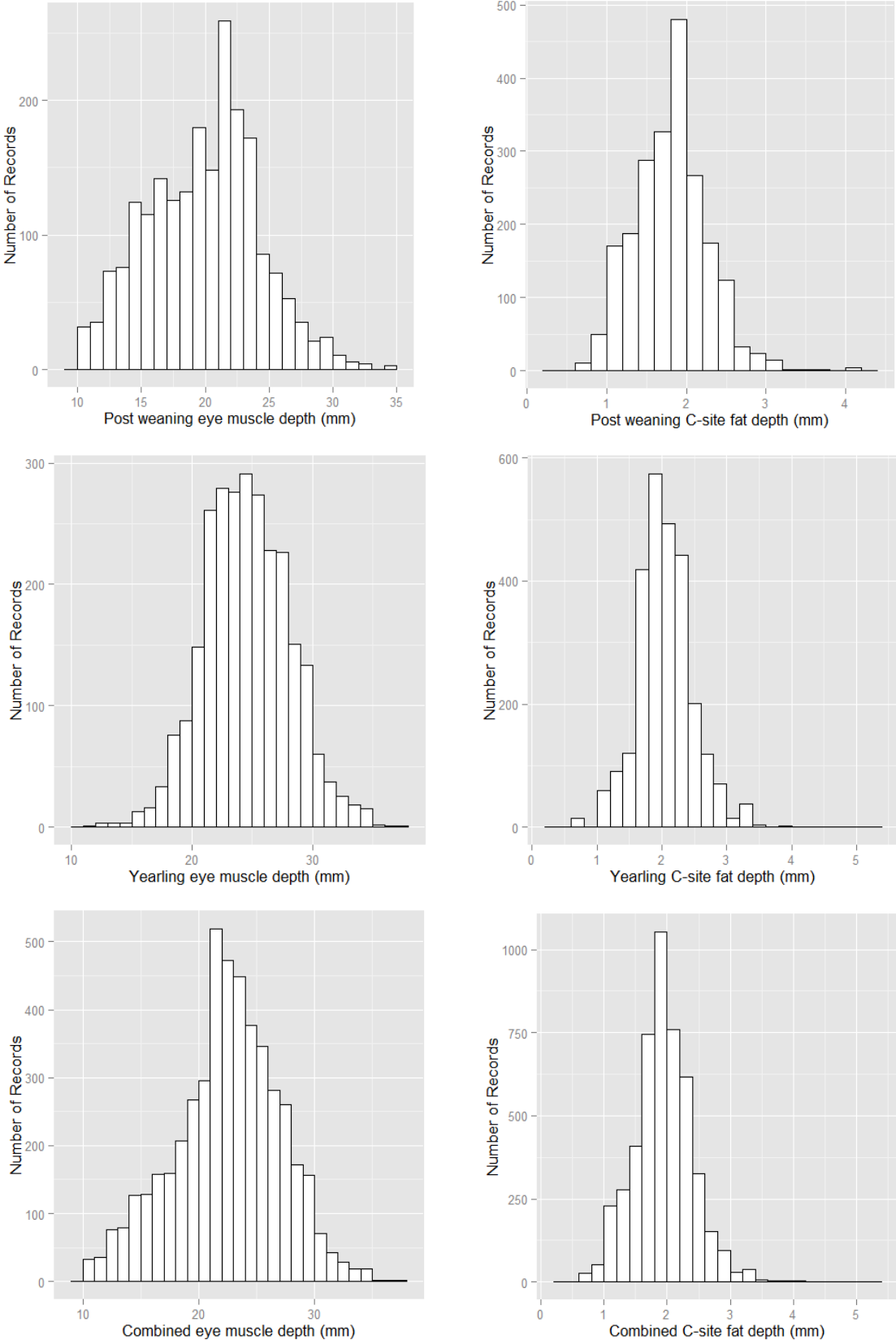
### 3.4 Checking traits are normally distributed

All of the growth and scanned carcass traits were normally distributed (Figure 3-1 and Figure 3-2). Post-weaning weight and yearling weight were slightly skewed. Both PWEC and YWEC were normally distributed (Figure 3-3). As all of the growth and scanned traits were normally distributed, it was decided they were suitable to be analysed as animal traits with a univariate model.

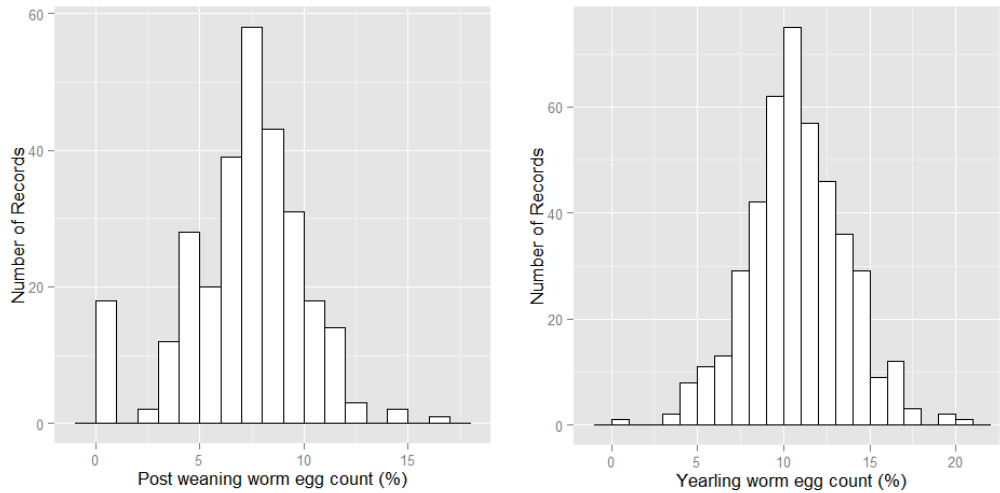


**Figure 3-1: Distributions of the records for growth traits in the KIDPLAN dataset.**

*Genetic improvement of Australian Meat goats*

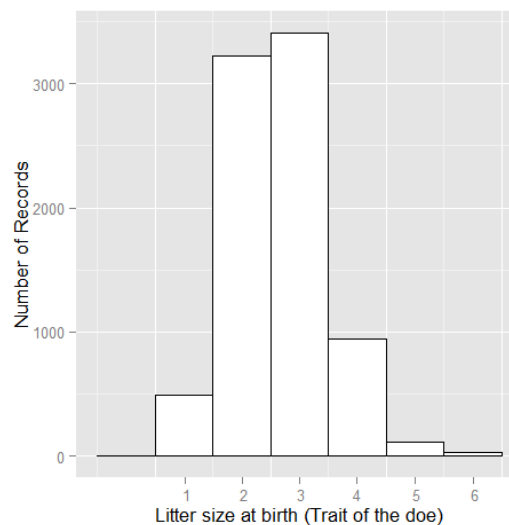


**Figure 3-2: Distributions of the records for scanned carcass traits in the KIDPLAN dataset.**



**Figure 3-3: Distributions of the records for health traits in the KIDPLAN dataset**

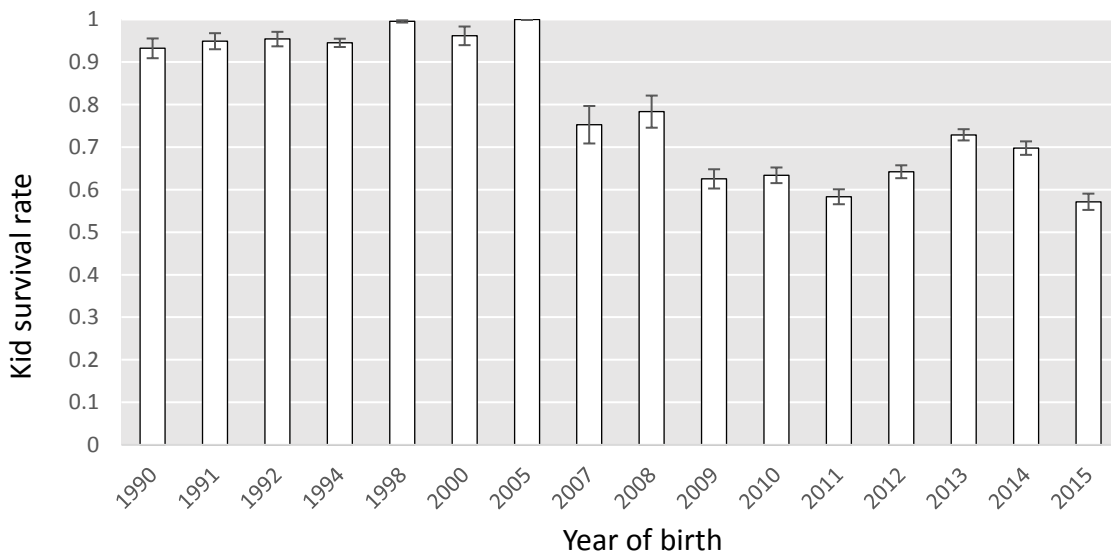
As survival as a trait of the kid is binary, it was analysed using a logistic transformation as well as assuming normality. It was later demonstrated that a logistic transformation was not necessary. Litter size at birth as a trait of the doe was normally distributed but as it was a repeated measure trait an animal model is not appropriate and was later limited to a sire model (Figure 3-4). Note that there were a small number of records with a litter size  $>5$  which demonstrates Dam filter 1 was not as effective as Dam Filter 2 which filtered based on differences between the recorded birth type and number of progeny submitted.



**Figure 3-4: Distributions of the records for reproductive traits in the KIDPLAN dataset**

### 3.5 Contemporary group components

The contemporary group was based on year of birth, sex, conception type, and site. For kid survival there were 76 contemporary groups with a mean of 72 records per group (range between 1 and 409 records). There were 15 contemporary groups that had less than 10 records which were filtered during analysis. Of the contemporary group components, males had a lower survival rate ( $0.68 \pm 0.01$ ) compared to females ( $0.78 \pm 0.01$ ). Kids conceived by artificial insemination also had a higher survival rate ( $0.73 \pm 0.01$ ) compared to natural mating ( $0.67 \pm 0.02$ ), there were too few records (12) for embryo transfer to make a conclusion on its relationship with kid survival and were removed from the analysis. Including site and dam filters only retained years with variation in kid survival, however the years 1990 to 2005 have kid survival rates over 0.90 (Figure 3-5). In comparison, years post 2005 had kid survival rates under 0.80, this was likely due to improvements in recording and submission practices with more sites accurately recording survival. After filtering there were just seven sites with a mean of 1,073 records each, the site with the fewest number of records had a total of 66. For site by year combinations the mean survival rate ranged between 0.44 and 1.00.

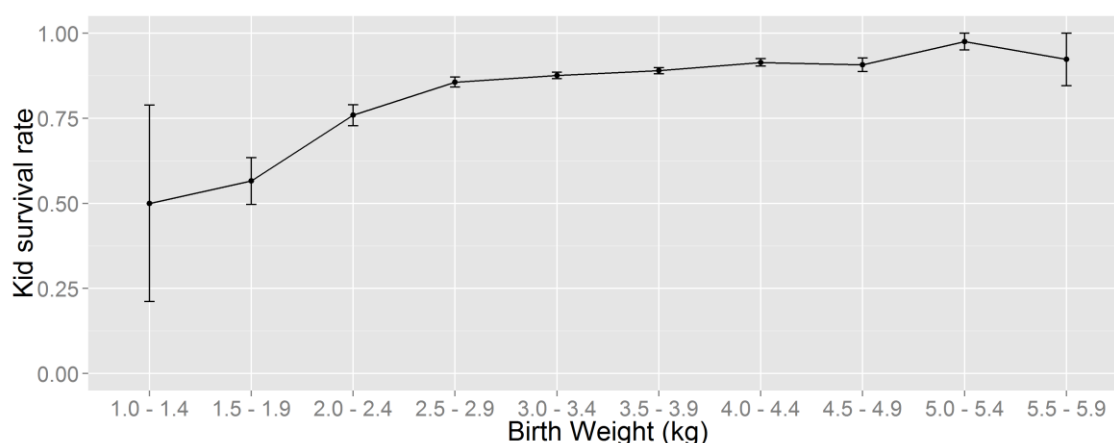


**Figure 3-5: Differences in kid survival rate by year of birth.**

### 3.6 Summary of fixed effects for kid survival

As the main focus of this thesis was on kid survival to weaning as a trait of the kid, it was important to understand the effect fixed factors has on survival. Unless specified otherwise, an animal model was used for the analysis of kid survival with the following fixed effects; BWT, BT (single, twin, and multiple) as a factor, doe age (2 to 7 years), doe age as a quadratic polynomial, and contemporary group as a factor. Presented below are the relationships between kid survival and the raw data for the mentioned effects.

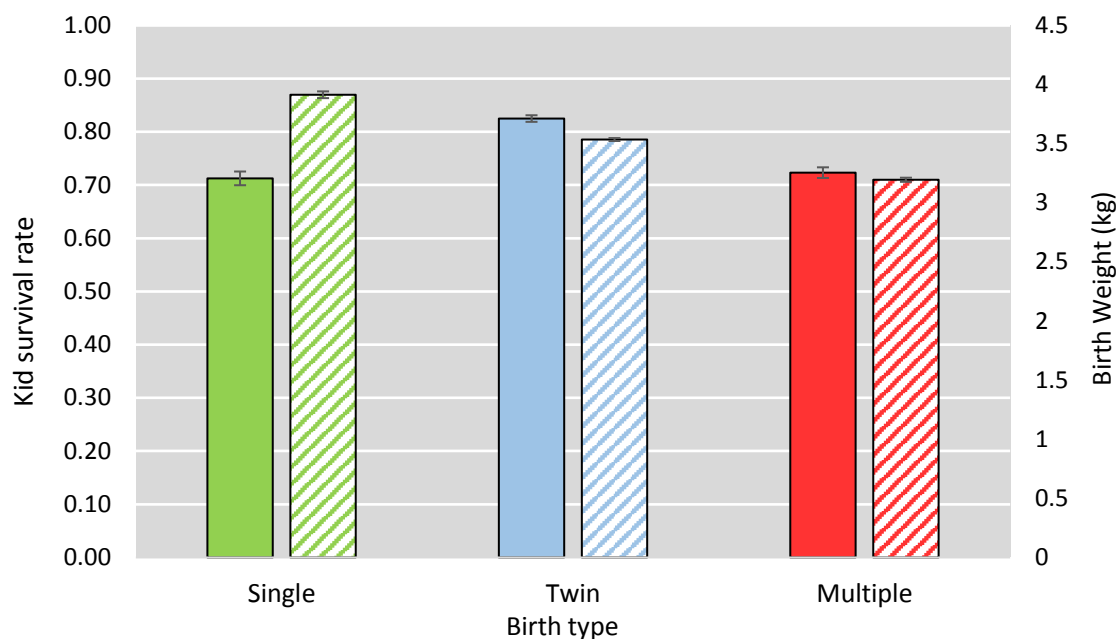
From sheep literature and results from Angora goats, a curvilinear relationship between birth weight and kid survival was expected, based on a quadratic polynomial (Snyman 2010; Brien *et al.* 2014). As birth weight increased from 1.0 kg to 3.0 kg, the survival rate increased from  $0.44 \pm 0.18$  to  $0.88 \pm 0.01$ , and then plateaued. A decline at high birth weights due to dystocia was expected but there was negligible evidence for this (Figure 3-6). The relationship between birth weight and kid survival was further investigated in the bivariate analysis of Chapter 5 to determine the genetic relationship.



**Figure 3-6: Relationship between birth weight and kid survival. Data is filtered based on Dam Filter 2 and Site Filter 1.**

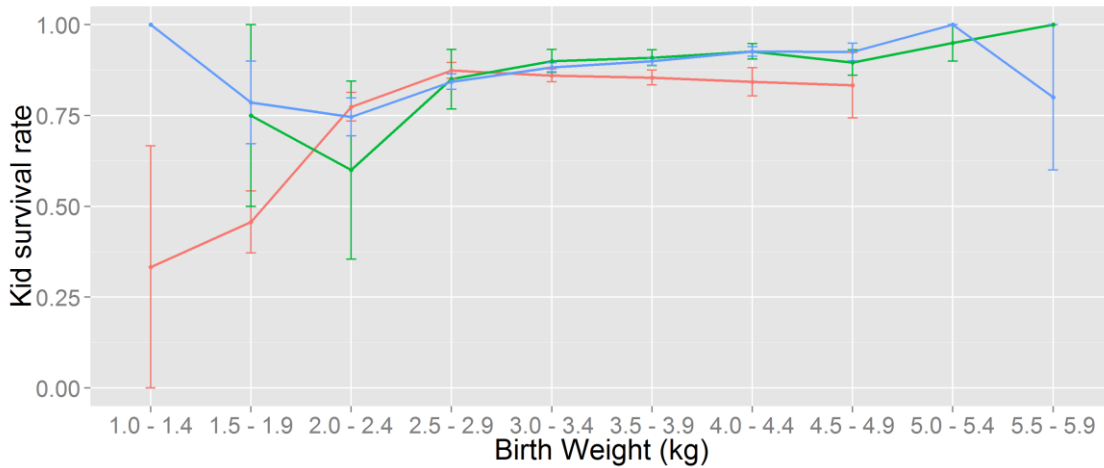
Birth type also had a relationship with kid survival rates with singles (18% of animals and 71% survival rate) and multiples (29% of animals and 72% survival rate) having lower survival rates than twins (53% of animals and 83% survival rate) (Figure 3-7). This was different to previous goat literature where both Husain *et al.* (1995) and Snyman (2010) report increasing mortality rates from single born (14.1% and 10%) to twin born (15.9% and 13%), and then triplets (16.7% and 22%). Differences in survival rates caused by birth type are common and often different such as those observed in Rambouillet sheep with survival rates for singles (81.1%), twins (94.8%), and triplets (88.8%) (Hanford *et al.* 2005). The multiple birth losses were likely due to too many kids trying to enter the birth canal at once, entangling and causing dystocia or kids were born too small and weak, unable to maintain their body temperature, feed or abandoned by their dam (Snyman 2010). Singles were less likely to have a lower birth weight than twins and multiples. Proportionately more singles born at a low birth weight die. The significant difference in survival caused by birth type was the main reason for the multivariate analysis of Chapter 6.)





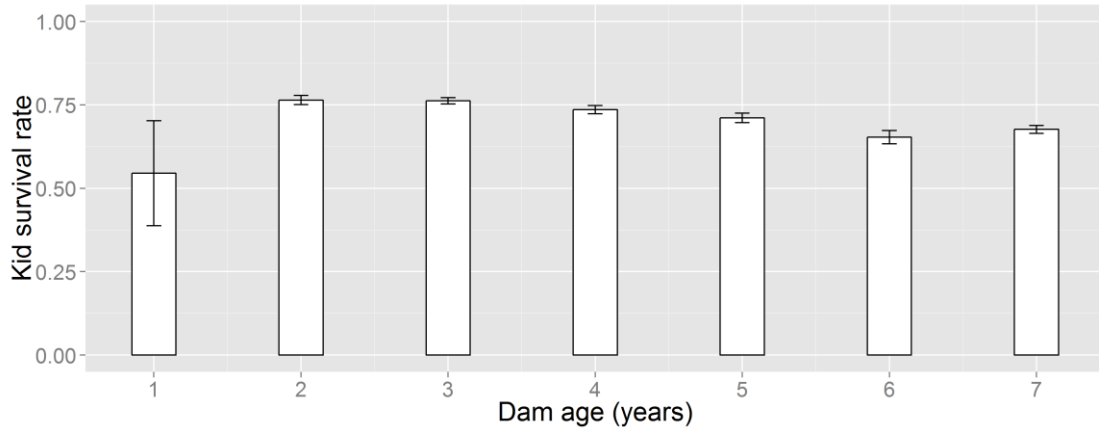
**Figure 3-7: Effect of birth type on kid survival (solid) and birth weight (diagonal line).**

To try and explain why the expected relationship between birth weight and survival was curvilinear, but not quadratic, and why more single born kids die compared to twins, the relationship between birth weight and kid survival was replotted, but separated by birth type. The new relationship is displayed in Figure 3-8 and shows some important differences compared to the total population. There were so few single born kids with birth weights less than 3.0 kg illustrated by the large standard errors but accounted for a large proportion of losses. There appeared to be more of a curvilinear relationship between birth weight and survival compared to the total population but was only a trend and requires further investigation, and more data of weights over 5.0 kg. This helped explain the differences in survival rate by birth type compared to the previous goat literature which was previously described for Figure 3-7.



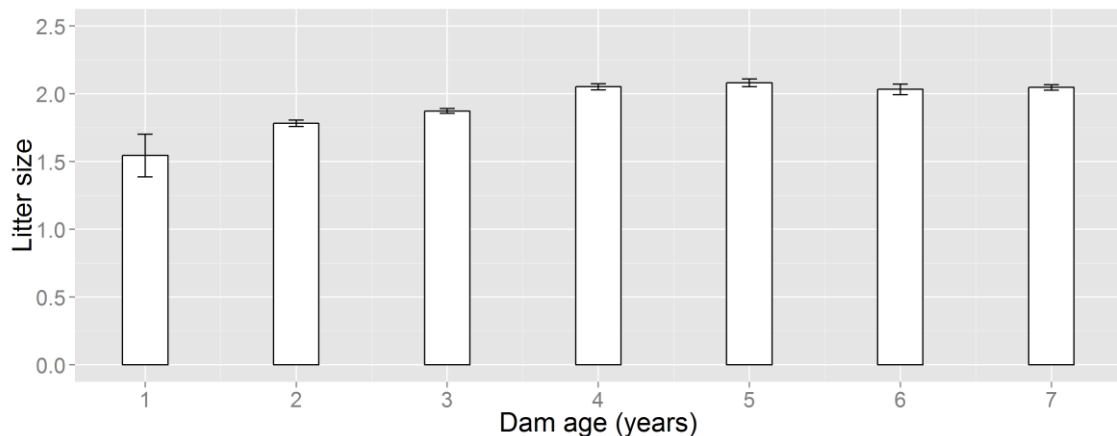
**Figure 3-8: Relationship between birth weight (kg) and kid survival rate for different birth types; singles (green), twins (blue), multiples (red).**

Doe age appeared to have a negative effect on survival. As a doe became older, its rearing ability decreased (Figure 3-9). Maiden does appeared to have the highest survival rate which was unexpected but could be due to higher monitoring management practices of these animals. Two, three, and four year old does have survival rates over 0.80 and older animals less than 0.80 (Figure 3-9). Previously Bunter and Brown (2013) have suggested that lamb survival should be treated as different traits for different ewe age groups (genetic correlations of 0.38 to 0.65 between ewe age groups). The analysis for doe age was not repeated for this project but did provide evidence that separating reproductive traits is possible. It also confirmed fitting doe age as a fixed effect it appropriate.



**Figure 3-9: Relationship between doe age and kid survival rate.**

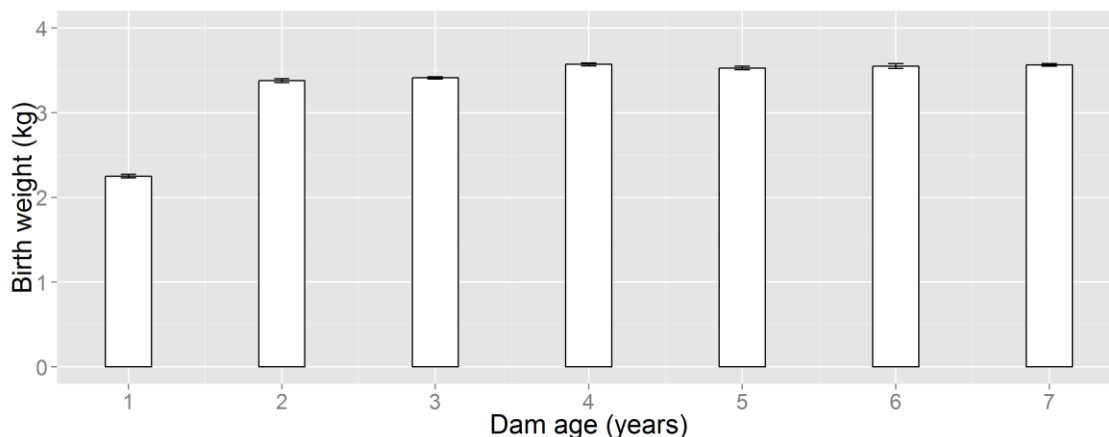
As birth type and dam age both affected kid survival, the relationship between dam age and birth type was investigated (Figure 3-10). Younger dams had lower litter sizes which increased until four years of age. After four years of age the mean litter size was above two and close to the optimum birth type for higher kid survival.



**Figure 3-10: Relationship between doe age and litter size.**

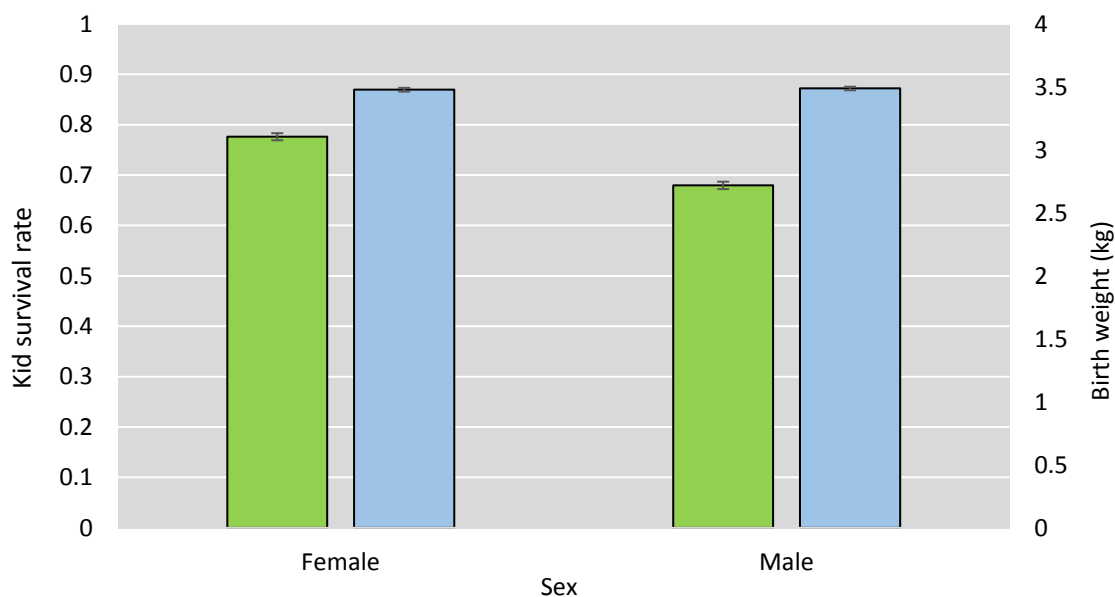
The relationship between dam age and average birth weight of the kid was examined (Figure 3-11). Dams under two years of age gave birth to kids with a lower birth weight. This put the progeny within the birth weight range under 2.5 kg where kid survival

decreases. After two years of age on average dams gave birth to kids above 3 kg where kid survival is less of an issue (Figure 3-6).



**Figure 3-11: Relationship between doe age and birth weight.**

Finally the relationship between sex and kid survival was investigated (Figure 3-12). As expected males had a lower survival rate compared to females. Males also tended to be heavier at  $3.74 \text{ kg} \pm 0.01$  ( $\pm \text{SE}$ ) compared to females  $3.41 \text{ kg} \pm 0.01$  but did not place either sex in the range of lower survival due to low or high birth weights.



**Figure 3-12: Relationship between sex, kid survival rate (white) and birth weight (black diagonal line).**

### 3.7 Genetic model definitions

In chapter 4 and 6 univariate sire and animal models were used. Primarily to estimate the phenotypic variance, heritability, maternal heritability and permanent environmental variance. The univariate models used are defined in equation 3.1 and 3.2 below. Chapters 5 and 6 use bivariate animal models defined as follows in equation 3.3 below.

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zs} + \mathbf{e} \text{ (Sire, Eq. 3.1)}$$

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Zmp} + \mathbf{e} \text{ (Animal, Eq. 3.2)}$$

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{A1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{A2} \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{M1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{M2} \end{bmatrix} \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} \text{ (Bivariate, Eq. 3.3)}$$

For the sire, animal and bivariate animal models, the vector of observations for each trait is denoted as  $\mathbf{y}$ , fixed effects were defined in vector  $\mathbf{b}$ , direct genetic effects were defined in vector  $\mathbf{a}$  for each animal in the pedigree, maternal permanent environmental effects were defined in vector  $\mathbf{p}$ , and  $\mathbf{e}$  was a vector of random residual effects. The indices matrices  $\mathbf{X}$ ,  $\mathbf{Z}$  and  $\mathbf{Zm}$  relate the respective effects of  $\mathbf{y}$ . The subscript 1 and 2 was the trait of interest.

### 3.8 Conclusion

For the remainder of the project it was determined that the trait definitions, KIDPLAN data, data filters, contemporary groups, and fixed effects would be used in each analysis unless otherwise specified. The trait definitions were appropriate as they were the same as those used by KIDPLAN for breeders and are similar to previous literature. Each of the traits in KIDPLAN appeared to have enough data (excluding; HWT, AWT, PWEC, and YWEC) and were distributed appropriately for univariate analysis. The data filters

were necessary due to errors in the data caused by not recording variation in birth or rearing type, and incorrectly identifying dams. Further validation of these filters was required with univariate analysis. The contemporary groups based on year of birth, sex, conception type, and site was standard practice for genetic evaluation. Each of the fixed effects (BWT, BT doe age, doe age as a quadratic polynomial, and contemporary group) were significant for kid survival. The fixed effects of birth weight and birth type were grounds for further bivariate and multivariate analysis of kid survival.

## 4 Producer recorded data on Australian Boer goats needs cleaning for genetic parameter estimates using univariate analyses.



## 4.1 Abstract

A new kid survival trait as a trait of the kid was created, this was a first for the goat literature. The national performance recording scheme database for goats (KIDPLAN) was used to create it. There were 19,711 animal records in the KIDPLAN database but due to errors in dam identification and other site inaccuracies it was not appropriate for parameter estimation. Several data filters in various combinations were used to clean the data of inaccurate records. Two filters were selected to be used for future analyses, one removes records where the dam has biologically too many progeny and the other removed records where sites record no variation in birth or rearing type. Univariate models were used to make parameter estimates for growth, carcass, health, and reproductive traits. Most importantly after data cleaning, kid survival as a trait of the kid had a phenotypic variance of 0.14 and a heritability of 0.09. This was significantly higher than the maternal heritability (0.01), and maternal permanent environmental variance (0.04). Further work determining the genetic relationship between the new kid survival traits and other production traits is needed.

## 4.2 Introduction

The export of Australian goat meat was valued at \$241.8m AUD in 2014 with continuing growing demands (MLA 2015). The genetic improvement of Australian meat goats is focused on the South African Boer breed. The national performance recording scheme; KIDPLAN was established in the 1990's for genetic selection based on estimated breeding values (MLA 2004a).



The last genetic estimates published for this dataset was in 2001 by Ball *et al.* (2001) which called for further work on growth and scanned traits. There was a reasonable expectation that the ability to estimate more accurate genetic parameters has improved. Since then the industry has had major structural changes with a reduction in the number of breeders and shifts in production areas, and with this there has been a recent increase in the number of records submitted for evaluation. The biggest concern accompanying this influx was the introduction of data errors to the KIDPLAN dataset due to varying producer recording and submission practices.

The majority of parameter estimates for Boer goats globally are from small experimental herds. With the majority of Boer goat publications coming from, South Africa, and China, with a small amount of work from Australia (Ball *et al.* 2001; Zhang *et al.* 2009b). While the Boer goats in Australia were originally sourced from South Africa there has been crossing with the local Australian rangeland goats. It is important to have accurate parameter estimates for the Australian Boer goats for genetic selection. The four trait groups of interest for the KIDPLAN dataset were; growth traits, scanned carcass traits, reproductive traits, and health traits.

The most recorded traits were the growth traits: birth weight (BWT) within 24 hours of birth, weaning weight (WWT) 6-17 weeks, and yearling weight (YWT) 10-13 months (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2009b). The main reason for this was they are the easiest traits to record. KIDPLAN data should have been appropriate to estimate these weight traits, as well as post-weaning weight (PWT) 4-10 months, hogget weight (HWT) 13-18 months, and adult weight (AWT) 18+ months.

Of the scanned carcass traits, eye muscle depth (EMD), and C-site fat depth (FAT) had some previous genetic parameter estimates for Boer goats (Ball *et al.* 2001; Dhanda *et al.* 2003). KIDPLAN estimates for these traits were available for post-weaning (P) and yearling (Y) reported by Ball *et al.* (2001). The heritabilities for these traits were low, but Ball *et al.* (2001) did suggest genetic improvements could be made and that further investigation is needed.

The largest gap in the literature for goat genetics was on reproductive traits. Heritability estimates of between 0.06-0.10 as a trait of the dam for Black Bengal, Jamunapari, and Beetal goats have been reported by Singh *et al.* (1990). It was hypothesised that an individual's ability to survive would be important for goats and there was an opportunity to have a broader contribution to animal breeding by focusing on the kid rather than the doe, thus accounting for genes inherited from both parents. There are reported genetic parameters for Boer goats on litter size at birth (NKB), number of kids weaned (NKW), and gestation length by Zhang *et al.* (2009a). Attempts to confirm Australian estimates for some of these reproductive traits needed to be attempted. The best candidate traits using KIDPLAN data for reproduction analysis were kid survival and litter size at birth (LSB). As there have been no estimates for any goat breeds with kid survival treated as a trait of the kid further investigation was warranted.

The recording and submission of health traits was very limited in KIDPLAN. The only health traits recorded are worm egg counts (WEC) at post-weaning and yearling age groups. Animals with lower WEC numbers have a resistance to internal parasites, and therefore improved health. The only genetic parameter estimates in goats for worm egg

counts was on Creole goats with heritability ranging between 0.14 and 0.37 (Mandonnet *et al.* 2001; Gunia *et al.* 2011).

Issues with KIDPLAN data were identified during data processing, primarily where birth and rearing records were not biologically possible. There were two objectives to this study. The first was to determine suitable cleaning methods that address concerns around the KIDPLAN dataset. The second objective of the study was to determine if the KIDPLAN dataset can be used to estimate genetic parameters for kid survival.

## 4.3 Materials and Method

### 4.3.1 KIDPLAN dataset

Australian Boer goat breeders submit performance and pedigree data to Sheep Genetics for genetic evaluation as part of the KIDPLAN service. Sheep Genetics maintain the KIDPLAN database. The analysis completed included records of 19,711 individual animals from 30 years and 150 sites across Australia. The progeny were represented by 774 sires and 4,451 dams. A summary of the number of records for each trait is in Table 4-1.

**Table 4-1. Summary of the number of records for each production trait submitted to KIDPLAN before data cleaning.**

Trait	Units	Number of					Raw Mean
		Animals	Sires	Dams	Progeny/Sire	Progeny/Dam	
BWT	kg	11,655	480	3,008	24.3	3.9	3.62
WWT	kg	10,042	451	2,814	22.3	3.6	20.5
PWT	kg	9,180	402	2,827	22.8	3.2	28.4
YWT	kg	5,068	342	2,163	14.8	2.3	43.7
HWT	kg	871	122	546	7.1	1.6	49.8
AWT	kg	236	69	173	3.4	1.4	65.0
PEMD	mm	2,121	149	814	14.2	2.6	19.4
YEMD	mm	2,662	185	1,191	14.4	2.2	24.1
PFAT	mm	2,156	149	819	14.5	2.6	1.8
YFAT	mm	2,662	185	2,662	14.4	1.0	2.0
PWEC	%	289	24	199	12.0	1.5	7.1
YWEC	%	417	20	262	20.9	1.6	10.8

Due to the small number of records for scanned traits and that only two animals had both a post-weaning and yearling record, two new traits were created by combining these records. The combined eye muscle depth (EMD) had 4,782 records. The combined C-site fat depth (FAT) had 4,819 records.

A survival trait of the kid from birth to weaning (KSV) was calculated from the extracted birth and rearing type data. All animals submitted to KIDPLAN required the birth type (number of kids born dead or alive) and rearing type (number of kids weaned) to be included. If a kid had a rearing type greater than zero it was treated as surviving to weaning. If a kid had a rearing type equal to zero it was treated as dead. Individuals were checked for a recorded trait post-weaning, to confirm that dead kids were not due to incorrect submission of rearing type. No individuals that had a rearing type zero had a trait recorded post-weaning.

For kid survival to weaning as a trait of the doe (RT/BT), a new trait was created for each dam in each year and using the same birth and rearing type records for kid survival. Only the first progeny for each litter had a calculated RT/BT record. The total number of kid survival as a trait of the dam records calculated was 7,733 with a mean of 3.6 records per dam across years.

For litter size, a new trait was created for each dam in each year and using the same birth type records used for kid survival. Litter size at birth (LSB) was a trait of the dam; only the first progeny for each litter has a calculated LSB record. The total number of dam litter size records calculated was 8,228 with a mean of 1.8 records per dam across years.

#### *4.3.2 Filters used for data cleaning*

As KIDPLAN is industry recorded data, there were errors in the submitted records that needed to be addressed. The areas of concern were recording variation in birth and rearing type, and incorrectly identified dams. To try to address these concerns two filter types were created.

Some sites were identified that were not submitting or recording the expected variation in birth type or rearing type. These records were included to test how they affect the genetic parameter estimates. A site filter (Site filter) was used that removes records of sites in years where no variation in birth or rearing type was observed.

It was noticed during data processing that some dams had more kids entered in a year than biologically possible. 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.

The univariate models were tested with a combination of filter types. No filters and all filters were tested; individual filters were tested separately and with both variations. In addition, a number of alternating combinations using one site and one dam filter were tested. A summary of the filter combinations with results presented are in Table 4-2.

**Table 4-2. Filter combinations used to analyse KIDPLAN data, ticks represent filters used in each analysis.**

Analysis	Site filter	Dam filter 1	Dam filter 2
1. No filters			
2. Site filter only	✓		
3. Dam filter 1		✓	
4. Dam filter 2			✓
5. Dam filters 1 and 2		✓	✓
6. Site filter and Dam filter 1	✓	✓	
7. Site filter and Dam filter 2	✓		✓
8. All filters	✓	✓	✓

#### 4.3.3 Statistical analysis

All of the traits were run with a univariate animal model, except for LSB and RT/BT, which were analysed with a sire model as it was repeated trait of the dam. The mean predictions, phenotypic variances, and heritabilities were estimated using ASREML (Gilmour *et al.* 2009). The random effects for all the models (excluding RT/BT and LSB) included a direct genetic effect, maternal permanent environmental, and maternal genetic component.

All traits included a fixed effect for the contemporary management group. The fixed effects for the growth traits; BWT, WWT, PWT, YWT, HWT, and AWT included birth type, rearing type (fitted separately), age at recording, and a quadratic polynomial of the doe age. The weight traits were centred using raw means to reduce recording errors across sites. The scanned traits; PEMD, YEMD, EMD, PFAT, YFAT, and FAT included the previous fixed effects for growth traits but also were adjusted for age at recording, and a quadratic polynomial of the weight at recording. The worm egg counts; PWEC and YWEC had the same fixed effects as the growth traits. The calculated survival trait (KSV) had the fixed effects of birth type, doe age, adjusted for both with and without birth weight, and a contemporary group based on date of birth, sex, conception method, and site. Litter size at birth only had the fixed effects for doe age and contemporary management group.

## 4.4 Results

### 4.4.1 *Effect of different filters on birth weight parameter estimates.*

#### 4.4.1.1 *Birth weight*

The number of BWT records used when no filters are applied was 11,711. The weights were centred at a mean of 3.5 kg from a raw mean of 3.6 kg to reduce effects across sites of recording errors. The Site filter removed 55% of the BWT records. The dam accuracy filters only removed 21% of records (Dam filter 1) and 17% of records (Dam filter 2). Combining the filters removed a large number of records, with the combination of all filters removing 67% of all BWT records, leaving 3,963 records for analysis.

Combinations that used site accuracy had a higher phenotypic variance with a small significant difference compared to filter combinations that did not use site accuracy. The phenotypic variance of BWT without filters was  $0.36 \pm 0.01 \text{ kg}^2$  which was not significantly different to Dam filter 1, nor Dam filter 2 both with phenotypic variances of  $0.35 \pm 0.01 \text{ kg}^2$ . In comparison, the combinations that included a site filter were higher at  $0.38\text{-}0.39 \text{ kg}^2$ .

There were some differences in the heritability between the filter combinations of birth weight. The heritability for combinations that only included dam filters ranged between  $0.30\text{-}0.32$  compared to no filters, which was  $0.31 \pm 0.03$ , and were not significantly different (Table 4-3). The heritability of BWT was  $0.40 \pm 0.05$  when only site filters were used. The standard errors increased when site variation filters were used. There was no significant difference in maternal heritability between filter combinations, ranging between  $0.07\text{-}0.11$ . There was also no significant difference in the maternal permanent environmental variance ranging between  $0.10\text{-}0.14$ .

**Table 4-3: Birth weight genetic parameters of Boer goats, phenotypic variance ( $\sigma_p^2$ ), heritability ( $h^2$ ), maternal heritability ( $m^2$ ), and maternal permanent environmental variance (MPE), with various data cleaning filters. Standard errors are in parentheses ().**

Analysis	Records	$\sigma_p^2$	$h^2$	$m^2$	MPE
1. No Filters	11,711	0.36 (0.01)	0.30 (0.03)	0.08 (0.02)	0.11 (0.02)
2. Site filter	5,240	0.39 (0.01)	0.40 (0.05)	0.08 (0.04)	0.10 (0.03)
3. Dam filter 1	9,263	0.36 (0.01)	0.31 (0.04)	0.09 (0.03)	0.12 (0.02)
4. Dam filter 2	9,725	0.35 (0.01)	0.30 (0.03)	0.09 (0.03)	0.13 (0.02)
5. Dam filter 1 and 2	8,815	0.35 (0.01)	0.32 (0.04)	0.09 (0.03)	0.13 (0.02)
6. Site and Dam filter 1	4,085	0.38 (0.01)	0.32 (0.07)	0.11 (0.05)	0.11 (0.04)
7. Site and Dam filter 2	3,963	0.39 (0.01)	0.40 (0.07)	0.08 (0.05)	0.14 (0.04)
8. All filters	3,816	0.38 (0.01)	0.35 (0.07)	0.09 (0.05)	0.13 (0.04)



#### 4.4.1.2 Kid survival

The number of kid survival records used when no filters were applied was 19,711 with a mean survival rate of 0.87. Using Dam filter 1, removed 29% of records and Dam filter 2 only removed 25% of records. Site filters removed a larger number of records with 50% of records removed. There was no significant difference in mean survival rate between no filters and dam filter combinations, when the site variation filters are included the mean survival rate was significantly lower at 0.72 compared to 0.85 and 0.86 with only dam accuracy filters.

The phenotypic variance of survival with no filters was 0.07. There was a small significant difference in phenotypic variance between dam accuracy filters at  $0.08 \pm 0.01$  and site variation filters of  $0.14 \pm 0.01$ . Without filters, the heritability of kid survival was  $0.13 \pm 0.02$ . The highest heritability was for the Site filter at  $0.17 \pm 0.03$  followed by any of the dam filters at  $0.12 \pm 0.02$ . When filter types were combined, the heritability dropped further to between 0.09 and 0.10. A summary of the parameter estimates for kid survival are included in Table 4-4. Estimating the maternal genetic component was limited to when no filters were applied or both dam filters were included. There was also no significant difference in the maternal permanent environmental variance ranging between 0.03-0.05. When KSV was adjusted for birth weight there was no significant difference to any of the results.

**Table 4-4. Kid survival genetic parameters of Boer goats, phenotypic variance ( $\sigma_p^2$ ), heritability ( $h^2$ ), maternal heritability ( $m^2$ ), and maternal permanent environmental variance (MPE), with various cleaning filters. Standard errors are in parentheses ().**

Analysis	Records	$\sigma_p^2$	$h^2$	$m^2$	MPE
1. No Filters	19,711	0.07 (0.01)	0.13 (0.02)	0.01 (0.01)	0.05 (0.01)
2. Site Filter	9,874	0.14 (0.01)	0.17 (0.03)	-	0.05 (0.01)
3. Dam Filter 1	14,014	0.08 (0.01)	0.12 (0.02)	-	0.04 (0.01)
4. Dam Filter 2	14,817	0.08 (0.01)	0.12 (0.02)	-	0.04 (0.01)
5. Dam Filters 1 and 2	13,381	0.08 (0.01)	0.12 (0.02)	0.01 (0.01)	0.03 (0.01)
6. Site and Dam filter 1	7,512	0.14 (0.01)	0.10 (0.02)	-	0.04 (0.01)
7. Site and Dam filter 2	7,713	0.14 (0.01)	0.09 (0.02)	-	0.04 (0.01)
8. All filters	7,162	0.14 (0.01)	0.09 (0.03)	0.01 (0.01)	0.04 (0.01)

- Fitted but not estimable.

#### 4.4.2 Number of records and phenotypic parameters

The weight traits had the largest number of records. The Site and Dam filter 2 combination removed 62% of the WWT records, 56% from PWT, 58% from YWT, only 32% from HWT, and 46% from AWT. When no data filtering was implemented WWT, PWT and YWT had means of 20 kg, 30 kg, and 45 kg centred from 20.5 kg, 28.4 kg, and 43.7 kg. The mean weights were not significantly different from the centred means of 20 kg for weaning weight, 30 kg for post-weaning weight, 45 kg for yearling weight, 50 kg for hogget weight, and 65 kg for adult weight.

Using PEMD and YEMD to create the combined trait EMD provided 4,782 records for analysis. The combined C-site fat depth which used PFAT and YFAT had 4,819 records. In comparison to PFAT and YFAT estimates, Post-weaning eye muscle depth lost 76% of records due to Site and Dam filter 2. The combined trait EMD lost 70% but there was no significant change to the mean from 22.0 mm to 21.8 mm. The C-site fat traits PFAT, YFAT, and FAT had 76%, 65%, and 60% of records removed respectively with Site and Dam filter 2.

After applying Site and Dam filter 2 the worm egg counts only included 268 and 416 records for post-weaning worm egg counts and yearling worm egg counts respectively. That was only a 5% to 10% reduction in records but is prohibitive to genetic evaluation.

Kid survival as a trait of the dam had 7,733 records with a mean survival rate of 0.89. When site and dam filter 2 were applied, 42% of the records were removed to 3,262 records. The removal of records significantly changed the mean from a survival rate of 0.89 to 0.74.

Litter size at birth as a trait of the dam (LSB) had 8,228 records with a mean of 1.65 kids per litter. When site and dam filter 2 were applied, 50% of the records were removed to 4,095 records. The removal of records did not significantly change the mean from 1.65 to 1.63 kids born per litter.

#### *4.4.3 Estimates of variance components*

The estimates for phenotypic variance, heritability, maternal heritability, and maternal permanent environmental variance with analysis 1 (No filters) and analysis 7 (Site filter and Dam filter 2) are presented in Table 4-5. The previous sections described the estimates for birth weight and kid survival, this section provided no further details on these traits.

**Table 4-5. Genetic parameters of Boer goats without data filtering and with data filtering by Site filter and Dam filter 2 <sup>(a)</sup>, phenotypic variance ( $\sigma_p^2$ ), heritability ( $h^2$ ), maternal heritability ( $m^2$ ), and maternal permanent environmental variance (MPE). Standard errors are in parentheses ( ).**

Trait	Records	Mean	$\sigma_p^2$	$h^2$	$m^2$	MPE
<i>Growth traits</i>						
BWT	11,711	3.50	0.36 (0.01)	0.30 (0.03)	0.08 (0.02)	0.11 (0.02)
BWT <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	128	64.7	43.68 (15.34)	0.48 (0.65)	-	-
<i>Scanned carcass traits</i>						
PEMD	2,122	19.4	2.79 (0.10)	0.08 (0.04)	-	-
PEMD <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	1,440	1.9	0.17 (0.01)	0.08 (0.05)	0.01 (0.04)	0.04 (0.06)
<i>Health traits</i>						
PWEC	289	7.1	6.77 (0.68)	0.15 (0.16)	-	-
PWEC <sup>a</sup>	268	7.1	6.87 (0.71)	0.16 (0.17)	-	-
YWEC	438	10.9	6.59 (0.50)	-	-	-
YWEC <sup>a</sup>	416	10.8	6.74 (0.52)	-	-	-
<i>Reproductive traits</i>						
KSV	19,711	0.87	0.07 (0.01)	0.13 (0.02)	0.01 (0.01)	0.05 (0.01)
KSV <sup>a</sup>	7,713	0.72	0.14 (0.01)	0.09 (0.02)	-	0.04 (0.01)
RT/BT <sup>b</sup>	7,733	0.89	0.05 (0.01)	0.03 (0.01)	*	0.04 (0.03)
RT/BT <sup>ab</sup>	3,262	0.74	0.12 (0.01)	0.02 (0.02)	*	0.04 (0.02)
LSB <sup>b</sup>	8,228	1.65	0.64 (0.01)	0.04 (0.01)	*	*
LSB <sup>ab</sup>	4,095	1.63	0.82 (0.03)	0.03 (0.01)	*	*

<sup>a</sup> Genetic parameters of Boer goats with data filtering by Site filter and Dam filter 2

RT/BT<sup>b</sup> defined as a trait of the dam with a service sire variance ( $0.01 \pm 0.01$ )

RT/BT<sup>ab</sup> defined as a trait of the dam with a service sire variance ( $0.03 \pm 0.01$ )

LSB<sup>b</sup> defined as a trait of the dam with a service sire variance ( $0.06 \pm 0.10$ )

LSB<sup>ab</sup> defined as a trait of the dam with a service sire variance ( $0.12 \pm 0.10$ )

\* Not fitted, - Estimate went to the boundary

#### 4.4.3.1 Growth traits

When no data filtering was implemented WWT, PWT, and YWT had phenotypic variances of  $9.56 \pm 0.17 \text{ kg}^2$ ,  $17.76 \pm 0.33 \text{ kg}^2$ , and  $25.77 \pm 0.65 \text{ kg}^2$ , respectively. WWT and PWT had similar heritabilities of  $0.15 \pm 0.03$  and  $0.18 \pm 0.03$  respectively. The heritability for YWT was higher at  $0.38 \pm 0.05$ . The maternal heritabilities were all very similar and low, between 0.03-0.04. The maternal permanent environmental variance was higher for WWT and PWT ( $0.09 \pm 0.02$  and  $0.10 \pm 0.02$  respectively) than YWT, which was not estimable. Hogget weight and AWT had very high standard errors for all components estimated or had no estimate. The phenotypic variances were  $29.53 \pm 1.92$  for HWT, and  $60.61 \pm 14.18$  for AWT. The heritability for HWT and AWT was  $0.11 \pm 0.14$  and  $0.07 \pm 0.89$  respectively. Maternal genetic and permanent environmental components fitted for hogget weight were not estimable. Adult weight had a maternal heritability of  $0.27 \pm 0.51$  and no estimate for the maternal permanent environmental component.

With Site filter and Dam filter 2 applied the phenotypic variances tended to be higher for WWT ( $10.72 \pm 0.28$ ), PWT ( $20.00 \pm 0.51$ ), YWT ( $29.31 \pm 1.12$ ), and HWT ( $30.33 \pm 2.34$ ). There were some significant changes to heritabilities and with larger standard errors when the filters were applied. Heritability for WWT decreased to  $0.05 \pm 0.03$ , PWT to  $0.12 \pm 0.04$ , YWT to  $0.34 \pm 0.09$ , and HWT to  $0.05 \pm 0.17$ . There was a small trend for maternal heritability to increase for WWT ( $0.09 \pm 0.04$ ) and PWT ( $0.06 \pm 0.04$ ), when using Site filter and Dam filter 2.

*4.4.3.2 Scanned carcass traits*

The phenotypic variance for PEMD was  $2.79 \pm 0.10$ , with a heritability of  $0.08 \pm 0.04$ . There was no estimation for the maternal genetic or maternal permanent environmental components; they were fitted but not estimable. The heritability for EMD was  $0.14 \pm 0.03$ . There was no maternal genetic estimate but the maternal permanent environmental had an estimate  $0.05 \pm 0.04$ , which was higher than PEMD and lower than YEMD but were not significantly different.

There was more success with estimating the components of YFAT than PFAT. Post-weaning C-site fat depth had a higher phenotypic variance of  $0.19 \pm 0.01$  compared to YFAT which was  $0.15 \pm <0.01$ . However, PFAT had a lower heritability of  $0.05 \pm 0.03$  compared to YFAT at  $0.15 \pm <0.01$ . Both PFAT and YFAT did not have a maternal genetic component estimated. Yearling C-site fat depth did have a maternal permanent environmental variance of  $0.03 \pm 0.03$ . All estimates for FAT were within the range of these two traits, which provides some confidence in its accuracy. It had a phenotypic variance of  $0.17 \pm <0.01$ . The heritability was  $0.10 \pm 0.03$ , and as with PFAT and YFAT there was no maternal heritability estimate but there was a lower maternal permanent environmental estimate for YFAT of  $0.01 \pm 0.01$ .

Phenotypic variances and heritabilities were not significantly changed. Before filters were applied PEMD had no estimate for maternal heritability or maternal permanent environment, with filters the maternal permanent environmental variance was estimated at  $0.08 \pm 0.10$ . The maternal heritability for EMD was not estimable, and the maternal permanent environmental variance was  $0.05 \pm 0.04$ .

Using Site and Dam filter 2 did not significantly affect the phenotypic variances, heritabilities or maternal permanent environmental variance for the fat depth traits. There were some differences between heritability estimates with filters applied with a tendency for larger standard errors  $0.15 \pm 0.11$  (PFAT),  $0.13 \pm 0.10$  (YFAT), and  $0.08 \pm 0.05$  (FAT) due to less animals. With the Site and Dam filter 2 applied estimates of maternal heritability for YFAT and FAT were  $0.05 \pm 0.06$  and  $0.01 \pm 0.04$  which were previously not estimable.

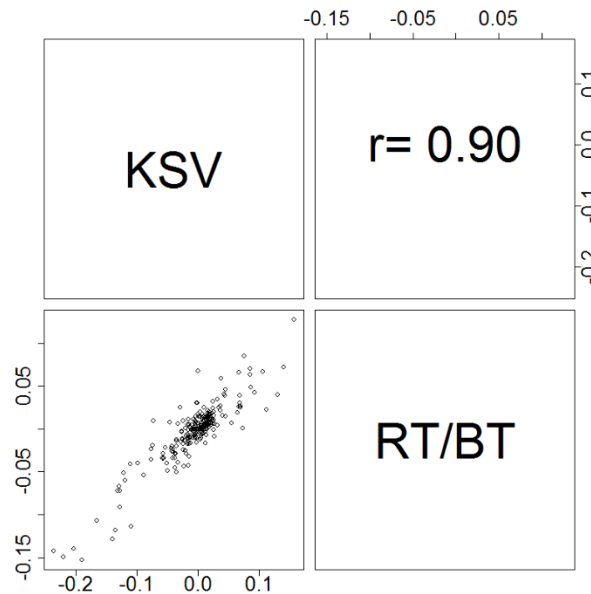
#### 4.4.3.3 Health traits

The parameters for worm egg counts were difficult to estimate. PWEC had similar phenotypic variation to YWEC with variances of  $6.77 \pm 0.68$  and  $6.59 \pm 0.50$  respectively. Post-weaning worm egg count had a heritability of  $0.15 \pm 0.16$  compared to YWEC which did not have an estimate for the additive genetic variance. Neither PWEC nor YWEC had a maternal genetic or maternal permanent environmental component estimated. When Site and Dam filter 2 were applied, the heritability for PWEC was  $0.16 \pm 0.17$  which was similar to no filtering at  $0.15 \pm 0.16$ . There were again no estimates for maternal heritability or maternal permanent environmental variance estimates with the Site and Dam filter 2 applied.

#### 4.4.3.4 Reproductive traits

A very important result was that survival to weaning as a trait of the dam was lowly heritable both without filtering ( $0.03 \pm 0.01$ ) and with filtering ( $0.02 \pm 0.02$ ) even when service sire was fitted in the model ( $0.01 \pm 0.01$  no filtering and  $0.03 \pm 0.01$  with filtering).

There was no significant difference in variation in survival as a trait of the dam ( $0.12 \pm 0.01$ ) compared to the kid ( $0.14 \pm 0.01$ ). Only a small amount of the phenotypic variation was accounted for by the service sire variance in the dam model ( $0.03 \pm 0.01$ ). The EBVs of sires were compared between the kid trait and the dam with a correlation of 0.90 (Figure 4-1).



**Figure 4-1: Correlation of EBVs for kid survival as a trait of the kid (KSV) and kid survival as a trait of the dam (RT/BT).**

It was important to remember that LSB was also treated as a trait of the doe not the kid. There was variation in the trait with a phenotypic variance of  $0.64 \pm 0.01$ . However, the heritability of it was low at  $0.04 \pm 0.01$  (Table 4-5). There was more variation accounted for by the service sire variance at  $0.06 \pm <0.01$ . There was no estimate for the maternal permanent environmental component. With the Site and Dam filter 2 applied, the phenotypic variance increased to  $0.82 \pm 0.03$ , and the service sire variance increased to  $0.12 \pm 0.10$ , but with a larger standard error. There was no significant change to the heritability with filters at ( $0.03 \pm 0.01$ ).



## 4.5 Discussion

### 4.5.1 *Removing records from sites with no variation in birth type and with incorrectly identified dams were suitable filters for KIDPLAN data*

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 main problem with using a Site filter was the number of records removed. For the traits BWT and kid survival; 50%-58% of the records are removed. The best reason for using a Site filter was it brings the mean survival rate from 0.87 to 0.75, which would be similar to the mean survival rate reported to the corresponding Table 2 by Singh *et al.* (1990) for Black Bengal, Jamunapari, and Beetal goats between 0.82 (days 0-15) and 0.70 (days 0-90). The reported survival rate was much lower than 0.92 for Boer goats in a research herd (MLA 2004b)

Dam filter 2 was selected over Dam filter 1 for four reasons. There was no difference in the parameter estimates, second it addressed concerns over recording variation in birth type, third it better addressed incorrectly identified dams, and fourth it retained more

accurate records. Dam filter 1 identified records where the number of progeny recorded was greater than five. It failed to account for animals that were embryo transferred across years and did not take into account the recorded birth type. Dam filter 2 accounted for embryo transfers and was able to identify when either the birth type was incorrect, or the dam was incorrect and creates a more specific filter. Dam filter 1 and 2 removed many of the same records but Dam filter 2 was more deliberate so that only 17% and 25% of records were removed from BWT and kid survival respectively, compared to 21%, 29% for Dam filter 1.

The various filter combinations for BWT or kid survival did not have a significant effect on the parameter estimates. Filters based on site compared to no filtering of the data had a tendency for higher genetic and maternal estimates while dam filters had a tendency to be lower. When considering the other production traits dam filter 2 still had a tendency for higher genetic and maternal estimates

Some key recommendations were made for the KIDPLAN data based on the results from applying different data filtering strategies. KIDPLAN data should be cleaned based on the number of progeny per dam and the recorded birth type to address issues with both recorded birth type and over estimation of the relationship of animals in the pedigree due to incorrectly identified dams. This applies to all traits which include either a birth or rearing type fixed effect but especially to the reproductive traits. An attempt to encourage new and existing breeders to submit more data needs to be made. Clearer instructions and practices for recording and submitting pedigree, birth and rearing type data is needed.

#### 4.5.2 Comparison of KIDPLAN parameter estimates to previous literature

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 results for all the production traits using Site and Dam filter 2 to those for other published estimates of Boer goats have been compared. Where there were no published estimates for Boer goats these have used other breeds of goats, and where no goat estimates were available Australian Merino sheep estimates were used.

Birth weight was centred at 3.5 kg, the same mean as Schoeman *et al.* (1997), and the phenotypic variance of  $0.39 \pm 0.01$  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  $0.38 \pm 0.03$ . The only difference was a lower estimate of  $0.07 \pm 0.05$  for maternal heritability compared to between 0.14-0.26 (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2009b).

The centred 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  $0.05 \pm 0.03$  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  $0.15 \pm 0.03$ . Other breeds of goats have also been reported below this range (Mugambi *et al.* 2007;

Boujenane and Hazzab 2008). Both previous estimates maternal heritability of WWT in Boer goats was 0.16, higher than the KIDPLAN estimate of  $0.09 \pm 0.02$  (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 Site and Dam filter 2 had a heritability estimate of  $0.12 \pm 0.04$  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  $0.34 \pm 0.09$  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), who estimated the heritability of PEMD and YEMD to be  $0.10 \pm 0.06$  and  $0.05 \pm 0.05$  respectively. In comparison, estimates with Site and Dam filter 2 were  $0.08 \pm 0.12$  for PEMD and  $0.10 \pm 0.08$  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 is needed.

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  $0.08 \pm 0.05$ . 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  $0.16 \pm 0.17$  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 ( $0.02 \pm 0.02$ ). 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.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014). The estimate of heritability for KSV ( $0.09 \pm 0.02$ ) 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

indicate 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  $0.12 \pm 0.01$ . This was higher than the  $0.03 \pm 0.01$  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 (Table 4-4). 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), (Table 4-5). 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.

## 4.6 Conclusion

A combination of filters that removes inaccurately recorded dams and sites that don't record variation in birth or rearing type, was a suitable data cleaning method for

KIDPLAN. The KIDPLAN database can be used to create a kid survival trait as a trait of the kid and make genetic parameter estimates. Survival as a trait of the kid has a much higher heritability than when treated as a trait of the dam and as the variances were similar it is recommended to be treated as a trait of the kid in future. The parameter estimates for the production traits were similar to Boer goats and other breeds, but the growth traits did have lower heritabilities than those previously published. Future work should focus on the genetic and phenotypic relationships between the KIDPLAN traits. More data is also needed for later age growth traits, scanned traits, and health traits to analyse the data with more confidence and accuracy.



# 5 Genetic and phenotypic relationships between production traits in Australian Boer goats.



## 5.1 Abstract

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 is 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 chapter is to determine the genetic relationship between the production traits in KIDPLAN and kid survival. 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 ( $0.19 \pm 0.19$ ) 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.

## 5.2 Introduction

Australia is the world's largest exporter and one of the few countries that exports a significant number of goats (MLA 2015). Increasing production of meat goats in Australia can be achieved with genetic selection (MLA 2012). The genetic improvement of Australian meat goats is based on the South African Boer breed. While much of the genetic selection has been based on conformation traits for the show ring, there is a need to base selection on production traits (MLA 2012). The genetic and phenotypic relationships between the production traits of Boer goats needs to be established so that they can be incorporated into a selection index.

The growth traits that are commonly recorded are birth weight (BWT), weaning weight (WWT), post-weaning weight (PWT), and yearling weight (YWT). The scanned carcass traits included eye muscle (EMD) and fat depth (FAT) measured at the C-site. The reproductive traits had the largest gap in the literature, mostly due to their difficulty in recording, and the ability to estimate them.

There were no published estimates for the genetic relationships between production traits and kid survival in any breed of goats. With the parameter estimates for kid survival in Chapter 4 it was determined that the gap in the literature could be filled using the KIDPLAN dataset. There were two main objectives to this study. The first is to establish the genetic relationships between kid survival and production traits including growth and body composition. The second was to determine the relationships between the scanned traits (EMD and FAT) and growth traits, which has not previously been reported in goat literature.

## 5.3 Materials and Methods

### 5.3.1 *KIDPLAN data set*

The national performance recording scheme KIDPLAN has 30 years of data recorded by industry Boer goat breeders. Producers submitted their data to Sheep Genetics for evaluation by the Animal Genetics and Breeding Unit, Armidale. The data set contained records from 19,711 individuals from 150 sites across Australia. Inaccuracies due to incorrectly recorded dams were identified during data processing. Records where the number of submitted progeny is greater than the recorded birth type were removed. Sites where there was no variation in birth type or rearing type were also removed from the

analysis. Every record was assigned a contemporary group based on year of birth, sex, conception method, and site. Attempting to further specify the contemporary group based on range of kidding date limited the number of contemporary groups with adequate animals in each group. Contemporary groups with no variation in kid survival or had fewer than ten records were removed from analysis. This data filtering left 6,863 records for analysis, from 7 sites, and 62 contemporary groups.

Kid survival to weaning (KSV) has been defined as a trait of the kid (not dam) for its own ability to survive. It was calculated as a binary trait, dead or alive, calculated from the birth and rearing type records, and confirmed by checking for any traits recorded after weaning. Post-weaning and yearling records, for eye muscle depth and C-site fat depth, were combined into single traits for eye muscle depth (EMD) and C-site fat depth (FAT). This was done as, no animals have both a post-weaning and yearling record, there are few records for either post-weaning and yearling eye muscle depth or C-site fat depth, they were recorded in a short period of time, and when they were not combined there were insufficient records to make parameter estimates with a univariate model or had convergence issues with bivariate models.

The growth traits; birth weight (BWT), weaning weight (WWT), post-weaning weight (PWT), and yearling weight (YWT) had between 2,063 and 3,343 records with earlier recorded traits having more records (Table 5-1). The scanned traits; EMD and FAT had the fewest records with 1,122 and 1,126 records respectively (originally 4,782 and 4,819 respectively but was significantly reduced by data cleaning). As all records submitted required birth and rearing types, all 6,863 records had a KSV record. Contemporary

groups with survival of 100% were removed. All traits had between 80 and 189 sires, and the number of animals with both traits recorded ranged between 921 and 3,655.

**Table 5-1: Data summary for production traits. Total number of records for each trait (diagonal), number of progeny with both traits (above diagonal), the number of sires with both traits recorded (below the diagonal).**

Trait	BWT	WWT	PWT	YWT	EMD	FAT	KSV
BWT	<b>3,343</b>	2,084	2,285	1,416	1,085	1,090	3,343
WWT	153	<b>3,655</b>	3,024	1,565	1,034	1,039	3,655
PWT	159	160	<b>3,638</b>	1,910	1,091	1,095	3,638
YWT	131	131	156	<b>2,063</b>	921	921	2,063
EMD	91	80	98	86	<b>1,122</b>	1,121	1,122
FAT	93	82	100	86	98	<b>1,126</b>	1,126
KSV	182	178	189	160	98	100	<b>6,863</b>

### 5.3.2 Statistical analysis

All traits were analysed using bivariate animal models with ASREML version 3 (Gilmour *et al.* 2009). All models fitted birth type, doe age (linear, and quadratic polynomial), contemporary group (62 groups), and age at recording as fixed effects. The scanned carcass traits were also adjusted for weight at recording as a covariate and as a quadratic polynomial. The random effects fitted included the direct genetic effect, and a maternal permanent environmental component. The dam genetic effect was not fitted due to models not converging with it included. Models that included KSV adjusted for birth weight did not converge and have been presented without birth weight fitted as a covariate.

## 5.4 Results

All models converged and were positive definite, the heritabilities were calculated as means across analyses. All traits were low to moderately heritable (Table 5-2). The heritability for BWT was 0.53 ( $\pm$  0.07), 0.11 ( $\pm$  0.03) for WWT, 0.12 ( $\pm$  0.03) for PWT,

and 0.35 ( $\pm$  0.06) for YWT. The two scanned traits were lowly heritable at 0.11 ( $\pm$  0.05) for EMD and 0.06 ( $\pm$  0.05) FAT. The heritability for KSV was also low at 0.08 ( $\pm$  0.02).

**Table 5-2: Bivariate parameter estimates of Boer goat production traits. Including; mean phenotypic variance ( $\sigma_p^2$ ), mean additive genetic variance ( $\sigma_A^2$ ), mean residual variance ( $\sigma_e^2$ ), mean maternal permanent environmental variance (MPE), heritability on the diagonal (mean), genetic correlation below the diagonal, and phenotypic<sup>A</sup> correlation above the diagonal.**

Traits	BWT	WWT	PWT	YWT	EMD	FAT	KSV
$\sigma_p^2$	0.40 $\pm$ 0.01	11.01 $\pm$ 0.29	20.43 $\pm$ 0.54	29.70 $\pm$ 1.14	2.35 $\pm$ 0.11	0.17 $\pm$ 0.01	0.153 $\pm$ 0.003
$\sigma_A^2$	0.21 $\pm$ 0.03	1.17 $\pm$ 0.44	2.45 $\pm$ 0.87	10.54 $\pm$ 2.47	0.25 $\pm$ 0.15	0.01 $\pm$ 0.01	0.013 $\pm$ 0.004
$\sigma_e^2$	0.12 $\pm$ 0.02	8.28 $\pm$ 0.36	15.56 $\pm$ 0.72	18.06 $\pm$ 1.70	2.01 $\pm$ 0.15	0.15 $\pm$ 0.01	0.133 $\pm$ 0.003
MPE	0.07 $\pm$ 0.01	1.56 $\pm$ 0.26	2.42 $\pm$ 0.49	1.09 $\pm$ 1.05	0.09 $\pm$ 0.11	0.01 $\pm$ 0.01	0.01 $\pm$ 0.01
BWT	<b>0.53 <math>\pm</math> 0.07</b>	0.35 $\pm$ 0.02	0.32 $\pm$ 0.02	0.34 $\pm$ 0.03	0.01 $\pm$ 0.04	-0.02 $\pm$ 0.04	0.01 $\pm$ 0.03
WWT	0.53 $\pm$ 0.15	<b>0.11 <math>\pm</math> 0.03</b>	0.81 $\pm$ 0.01	0.62 $\pm$ 0.02	0.03 $\pm$ 0.04	-0.06 $\pm$ 0.04	
PWT	0.50 $\pm$ 0.16	0.88 $\pm$ 0.07	<b>0.12 <math>\pm</math> 0.03</b>	0.64 $\pm$ 0.02	0.06 $\pm$ 0.04	-0.04 $\pm$ 0.04	
YWT	0.48 $\pm$ 0.13	0.81 $\pm$ 0.11	0.84 $\pm$ 0.10	<b>0.35 <math>\pm</math> 0.06</b>	-0.21 $\pm$ 0.04	0.06 $\pm$ 0.05	
EMD	0.12 $\pm$ 0.29	-0.75 $\pm$ 0.39	-0.60 $\pm$ 0.39	-0.84 $\pm$ 0.22	<b>0.11 <math>\pm</math> 0.05</b>	0.27 $\pm$ 0.03	
FAT	0.10 $\pm$ 0.37	0.11 $\pm$ 0.52	-0.16 $\pm$ 0.53	0.30 $\pm$ 0.43	-0.04 $\pm$ 0.61	<b>0.06 <math>\pm</math> 0.05</b>	
KSV	0.19 $\pm$ 0.19	0.04 $\pm$ 0.02	0.03 $\pm$ 0.02	-0.06 $\pm$ 0.03	0.05 $\pm$ 0.03	0.05 $\pm$ 0.03	<b>0.08 <math>\pm</math> 0.02</b>

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 genetic correlations between the growth traits were moderately to highly positively correlated, between 0.48 and 0.81. For BWT the genetic correlations were moderate with WWT, PWT, and YWT of between 0.48 and 0.53. The high genetic correlations were between WWT, PWT, and YWT of between 0.81 and 0.88. There was a zero genetic correlation ( $-0.04 \pm 0.61$ ) between the scanned traits EMD and FAT but there was a large standard error. The genetic correlations for EMD with the growth traits were 0.12 ( $\pm 0.29$ ) for BWT and negatively correlated at  $-0.75 (\pm 0.39)$  for WWT,  $-0.60 (\pm 0.39)$  for PWT, and  $-0.84 (\pm 0.22)$  for YWT. There was a positive genetic correlation between FAT with BWT, WWT, and YWT of between 0.10 and 0.30 but a negative correlation of  $-0.16$  for PWT. Kid survival was correlated with BWT (0.19) but not with other traits ( $-0.06$  to  $0.05$ ) and considering the standard errors none were significantly different to zero.

The phenotypic correlations between the growth traits were moderately to highly positively correlated, between 0.32 and 0.81. Birth weight had lower phenotypic correlations with WWT, PWT, and YWT of between 0.32 and 0.35 compared to the correlations between WWT, PWT, and YWT which were between 0.62 and 0.81. The phenotypic correlation between the two scanned traits ( $0.27 \pm 0.03$ ) was stronger than the genetic relationship. Phenotypic relationships between composition and weight traits were all low. As KSV was a trait of the kid until weaning and there were no records for dead kids after weaning, the only phenotypic correlation reported was for BWT and that was negligible ( $0.01 \pm 0.03$ ).

## 5.5 Discussion

### 5.5.1 Heritability

The heritability estimate of 0.08 ( $\pm 0.02$ ) for survival was not significantly different to the previous estimate of 0.09 ( $\pm 0.02$ ) with the univariate model including maternal genetic effects and similar data filtering (Chapter 4). There were no published estimates for the heritability of kid survival to weaning as a trait of the kid in goats. For sheep the estimates of heritability were lower between 0.01 and 0.03 (Safari *et al.* 2005; Brien *et al.* 2010; Brien *et al.* 2014) which was the same as the maternal heritability herein (Table 4-4). Literature about survival for goats and sheep focused on survival of the kid or lamb as a trait of the doe or ewe not as a trait of the kid as with this analysis. For Black Bengal and cross bred goats, Singh *et al.* (1990) reported heritability of kid survival as a trait of the dam to be between 0.05 to 0.10.

The heritability of birth weight 0.53 ( $\pm 0.07$ ) was higher than the previous estimate from the univariate analysis 0.38 ( $\pm 0.07$ ) (Chapter 4). It was also much higher than the estimate by Ball *et al.* (2001) using a sub-set of the same data but different filtering (0.19 $\pm$  0.04). The low heritability of weaning weight at 0.11 ( $\pm 0.03$ ) was higher than that of the univariate analysis of 0.05 ( $\pm 0.03$ ) (Chapter 4). This was likely because the univariate analysis included a maternal genetic component but the bivariate analysis did not. The heritability of 0.11 was still lower than previous published estimates of between 0.18 and 0.32 (Schoeman *et al.* 1997; Ball *et al.* 2001; Zhang *et al.* 2009b). Post-weaning weight heritability was not different to the univariate estimate, at 0.12 ( $\pm 0.03$ ) it was much lower than Ball *et al.* (2001) at 0.37 ( $\pm 0.06$ ). This difference was likely due to the data filtering removing a large number of records and questions the reliability of the data. More and



accurate data is needed to improve the confidence in the heritability estimate of both weaning and post-weaning weight. Yearling weight was the only growth trait to have similar heritability estimates for the bivariate analysis at  $0.35 (\pm 0.06)$ , univariate analysis  $0.34 (\pm 0.09)$ , and the previous published estimate of Ball *et al.* (2001) at  $0.45 (\pm 0.07)$ .

The composition traits (EMD and FAT) heritabilities were not different to the univariate analysis at  $0.11 (\pm 0.05)$  and  $0.06 (\pm 0.05)$  respectively. Ball *et al.* (2001) used post-weaning and yearling eye muscle depth for heritability estimates of  $0.10 (\pm 0.06)$  and  $0.05 (\pm 0.05)$ . The heritability estimate for EMD was lower compared to Merino sheep which ranges between 0.21 and 0.27 (Fogarty *et al.* 2003; Huisman *et al.* 2008; Fogarty *et al.* 2009). Ball *et al.* (2001) in Table 3 was also the only previous published estimate of C-site fat depth heritability for goats between 0.11 and 0.13 which was slightly higher than the heritability estimate of this analysis but compared to sheep at  $0.25 (\pm 0.02)$  goats are much lower due mostly to the small amount of variation and are much leaner than sheep (Table 1, Safari *et al.* 2005).

### 5.5.2 Genetic correlations

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  $0.19 (\pm 0.19)$ , the high standard error was of some concern however the positive correlation indicates there is a relationship. Rosati *et al.* (2002) in Table 5 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 3-7), increasing birth weight is likely to increase the survival of multiples which have lower birth weights (3.2 kg) (Figure 3-7) but increasing birth weight of singles (4.1 kg) could lead to higher rates of dystocia which is not currently an issue for goats (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.

The main cause of dystocia and hypoxia in sheep is fetal-pelvic disproportion (Brounts *et al.* 2004; Brien *et al.* 2010; Hinch and Brien 2014). Dystocia and difficult births in goats are not common (2-3% prevalence) and the cause was normally due to large litter sizes with more than one kid entering the birth canal at a time, rather than fetopelvic disproportion such as in sheep (Braun 2007; Zahraddeen *et al.* 2011; Sofi *et al.* 2012).

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  $-0.04 \pm 0.61$ . 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 (2016b) reported in Table 3 across breeds the genetic correlation of PFAT was negative for BWT ( $-0.27 \pm 0.02$ ), WWT ( $-0.24 \pm 0.03$ ), PWT ( $-0.19 \pm 0.02$ ), and YWT ( $-0.27 \pm 0.08$ ). 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 (Chapter 4).

### 5.5.3 Phenotypic correlations

The phenotypic correlations were mostly positively correlated or not different to zero. The moderate to high phenotypic correlations for the growth traits (between 0.32 and 0.81) were similar to those reported in Table 2 by Ball *et al.* (2001) of between 0.35 and 0.78. The number of records was a concern for the accuracy of the phenotypic correlations

between the scanned traits (EMD and FAT) and growth traits, it appears that these correlations were low and generally not different to zero. The positive phenotypic correlation between EMD and FAT of 0.27 ( $\pm 0.03$ ) suggests that more muscled animals are also fatter.

## 5.6 Conclusion

Kid survival was positively genetically correlated with birth weight and there was no genetic correlation with other production traits. The correlations between growth traits were similar to previous estimates on Boer goats and with the same dataset. The genetic correlations of scanned traits with other production traits has not previously been reported for goats, the strong negative relationships even with high standard errors indicates selecting for high weights could possibly decrease muscularity and increase fat deposition. Better recorded data is needed to improve the confidence in the genetic variance and covariance estimates for scanned traits as a large amount of data is removed due to the data cleaning.

6 Kid survival should not be treated as a separate trait for different birth types.



## 6.1 Abstract

The biological processes for the survival of kids born as singles, twins or multiples had 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. The three kid survival traits were heritable;  $0.08 \pm 0.05$  for singles,  $0.12 \pm 0.03$  for twins, and  $0.13 \pm 0.04$  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.

## 6.2 Introduction

The estimates from the univariate and bivariate analyses of kid survival showed it to be variable, heritable, and positively correlated with production traits which makes it ideal for improving reproductive rate in Boer goats (Chapter 4 and Chapter 5). This chapter further investigated the relationships between birth type and birth weight with kid survival. There were three reasons to continue the analysis of kid survival; the higher than expected variation in kid survival, the significant difference in survival due to the fixed

effect of birth type in the univariate analysis, and the positive genetic correlation between birth weight and kid survival (Figure 3-7, Chapter 4 and Table 5-2).

Differences in reproductive performance between yearling, hogget, and adult ewes were investigated for phenotypic and genetic differences (Bunter and Brown 2013; Newton *et al.* 2014). For Merino hoggets and adults there were no differences in the heritability of lamb survival as a trait of the ewe,  $0.02 \pm 0.03$  and  $0.00 \pm 0.00$  respectively (Newton *et al.* 2014). Similar for maternal crosses there was no difference in heritability between yearling, and hogget lamb survival,  $0.11 \pm 0.09$  and  $0.00 \pm 0.03$  respectively (Newton *et al.* 2014). Also for maternal crosses, there was no difference in lamb survival between yearlings and adults at two or over two years of age between 0.06 and 0.07 (Bunter and Brown 2013). The most relevant result from Bunter and Brown (2013) was the genetic correlation for lamb survival between the age groups was between  $0.38 \pm 0.20$  and  $0.65 \pm 0.22$ , significantly less than unity. The significant difference from unity supported the reasoning that reproductive traits could be treated as genetically different traits for yearling and adult ewes. The results from the literature where reproductive traits are treated differently based on a factor supported treating kid survival as a different trait based on birth type.

Differences in kid survival due to birth type have been explored by Snyman (2010), with singles, twins, and multiples having survival rates of 89%, 86%, and 78% respectively. These differences were due to different physiological effects. Treating lamb survival as a trait of the ewe Bunter *et al.* (2017) did support that it should be treated as separate traits for single and twin/multiple births. Treating lamb survival as three separate traits and as

a trait of the lamb, was found to be different traits with different genetic relationships with birth weight (Kelly *et al.* 2016; Kelly *et al.* 2017)

The aim of this chapter was to determine if kid survival is a different trait for single, twin, and multiple born kids where the birth type is treated as a different environment. Due to the relationship between birth weight and kid survival, further investigation was needed to determine the relationship between birth weight and survival separately for singles, twins, and multiples and what effect selecting for different survival traits will have on birth weight of each birth type.

## 6.3 Materials and Method

### 6.3.1 Dataset and trait definitions

Australian national performance recording data (KIDPLAN) was provided by Sheep Genetics. Sires, dams, and sites with inaccurately recorded birth types were filtered (as described in Chapter 3 and Chapter 4). Contemporary groups were based on sex, year of birth, site, and conception method. Any contemporary group with fewer than ten animals were removed. The number of records remaining was 6,863. The two traits of interest are birth weight and kid survival.

Both birth weight and kid survival were separated into three separate traits based on birth type, where each birth type was treated as a different environment in a genotype x environment interaction. The new birth weight traits included birth weight of singles (BWT\_S) with 522 records, birth weight of twins (BWT\_T) with 2,293 records, and birth



weight of multiples (BWT\_M) with 1,099 records. For kid survival the birth type traits included kid survival of singles (KSV\_S) with 1,235 records, kid survival of twins (KSV\_T) with 3,772 records, and kid survival of multiples (KSV\_M) with 2,006 records. An animal could only have one of each of the birth weight and kid survival birth type traits as there could be no residual covariance between the birth type traits.

### 6.3.2 *Statistical analysis*

In previous models both birth weight and kid survival models included birth type as a fixed effect. In this case birth type was confounded with the definition of the new traits so it was not fitted in any of the following models unless specified. The fixed effects included for each analysis were doe age and contemporary group (year of birth, sex, conception type, and site). Each model included a maternal permanent environmental effect, for each analysis both a sire and animal model were tested. All of the statistical analyses were conducted using ASREML version 3 (Gilmour *et al.* 2009).

The first method was separate univariate analyses for each birth type trait for birth weight and kid survival with a sire model. The estimated breeding values (EBV) of sires were extracted and plotted against the EBV's for the other traits. This analysis was repeated with an animal model. As KSV is a binomial trait and there was a chance of non-normal distribution each sire and animal model were also run with a binomial logistic transformation. The variance of the underlying scale was the default 3.3 for a logistic distribution (Gilmour *et al.* 2009).

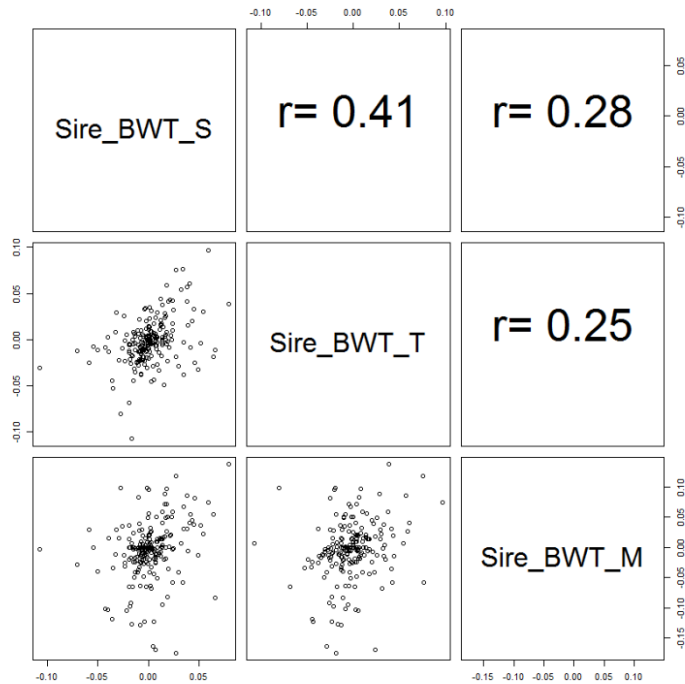
The second analysis was separate tri-variate analyses of the three birth weight traits and the three kid survival traits. As animals could only have one of each of the birth type traits for birth weight and kid survival the residual covariance were fixed at zero between traits. Both tri-variate analyses were tested using a sire and then animal model. The sire and animal models were compared with CORGH which parameterises the unstructured model differently and was generally more difficult to fit but would not converge. Current limitations of ASREML version 3 prevents more than one trait to be logistically transformed in a model and therefore survival data was only analysed as untransformed for the bivariate or tri-variate models (Gilmour *et al.* 2009).

The third analysis was a series of multivariate and bivariate analyses to estimate the genetic correlation between each of the kid survival traits with the other production traits. A single multivariate model of the six traits for birth weight and kid survival was attempted but was too complex to reach convergence. Birth weight was highly genetically correlated between birth types and was returned to being treated as a single trait with birth type fitted as a fixed effect. A multivariate analysis of BWT and the three kid survival traits also did not reach convergence. Bivariate analyses were used to estimate the genetic correlation between each of the three kid survival traits and each of the production traits (BWT, WWT, PWT, YWT, EMD, and FAT).

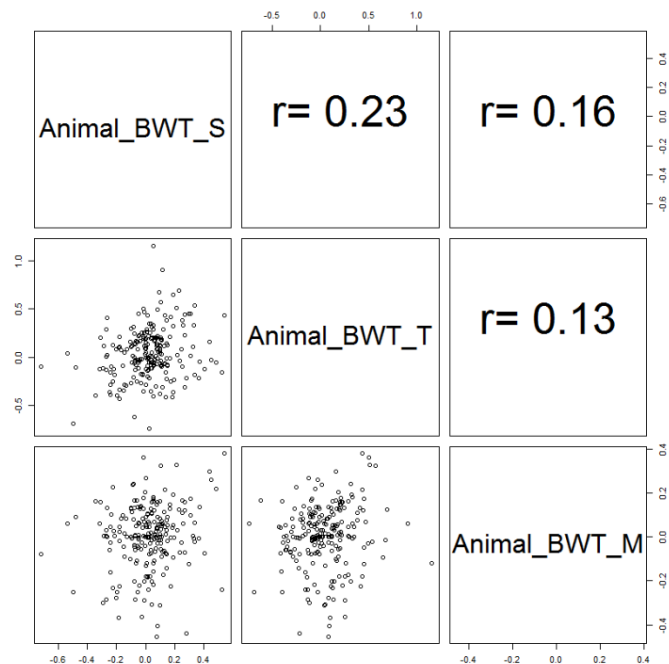
## 6.4 Results

The univariate analyses were used to determine if the birth type traits could be separated, to determine preliminary genetic correlations using EBVs, and to determine the suitability of logistic transformation for the kid survival traits. The correlation between EBVs for

the birth weight traits were lower than expected. The correlations were all positive for birth weight, higher for the sire model (0.25 to 0.41, Figure 6-1) compared to the animal model (0.13 and 0.23, Figure 6-2).



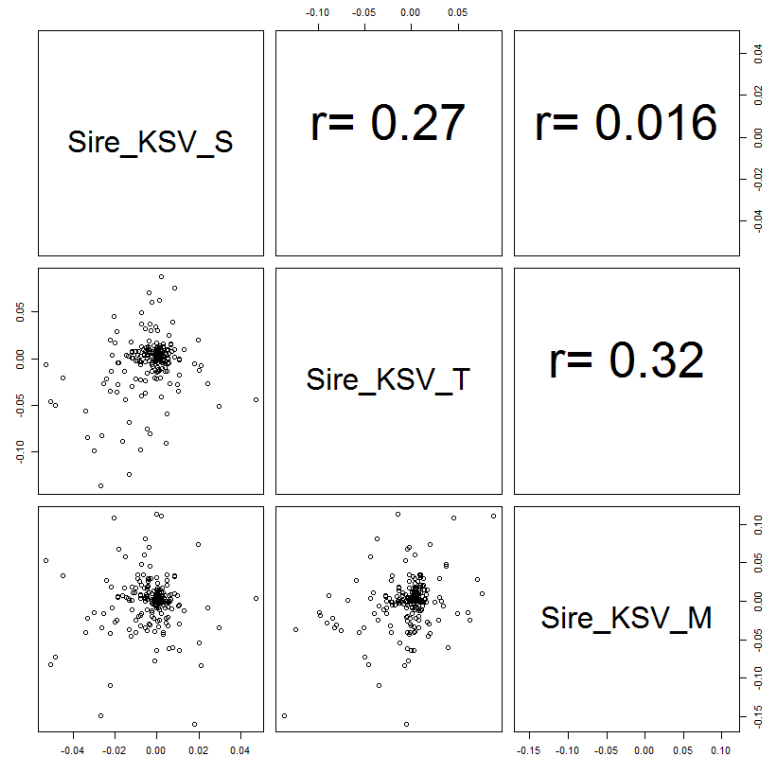
**Figure 6-1: Correlation of EBVs for birth weight traits separated by birth type, with a sire model.**



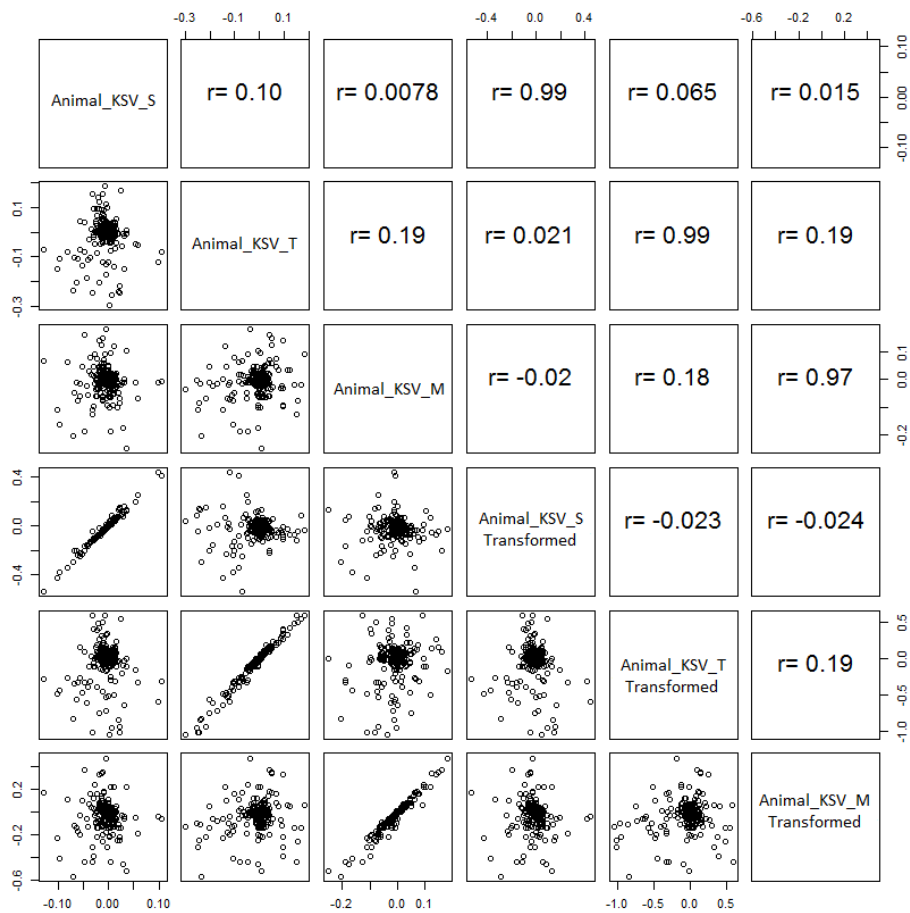
**Figure 6-2: Correlation of EBVs for birth weight traits separated by birth type, with an animal model.**

For kid survival each of the traits had higher phenotypic variances compared to a single survival trait. For both the sire and animal model the phenotypic variance was higher for multiples than for singles and twins. The heritability for each of the kid survival birth type traits tended to be higher compared to a single trait (0.09), increasing from singles ( $0.07 \pm 0.06$ ), twins ( $0.12 \pm 0.04$ ) to multiples ( $0.14 \pm 0.07$ ). The log-transformed data tended to have higher heritability estimates but the standard error also increased for all kid survival traits; singles ( $0.18 \pm 0.18$ ), twins ( $0.21 \pm 0.09$ ), and multiples ( $0.18 \pm 0.12$ ).

The correlation between EBVs for the kid survival traits were also lower than those for birth weight and also lower than expected for both the normal and logistically transformed models. The correlations were higher for the sire model (0.016 to 0.32, Figure 6-3) compared to the animal model (0.0078 to 0.19, Figure 6-4). The low correlations for the KSV traits could have been due to the high standard errors for the EBVs and low accuracies of between 0.39 and 0.51 for the animal model. Correlations between EBVs of transformed and non-transformed KSV traits were between 0.97 and 0.99 (Figure 6-4).



**Figure 6-3: Correlation of EBVs for kid survival traits separated by birth type, with a sire model.**



**Figure 6-4: Correlation of EBVs for kid survival traits separated by birth type, without and with logistic transformation, using animal models.**

To determine if the covariance between the kid survival traits could be estimated for an animal model, three bivariate models were used. The parameter estimates for the three survival traits were not different to the univariate analysis. For the bivariate analysis, the genetic correlation between the three kid survival traits was  $0.54 \pm 0.33$  between KSV\_S and KSV\_T, higher for KSV\_S and KSV\_M at  $0.77 \pm 0.47$ , and lower between KSV\_T and KSV\_M at  $0.42 \pm 0.30$ . There were also no significant differences between sire and animal models determined by a  $\chi^2$  difference in log-likelihood test, and no difference in parameter estimates. Logistic transformation had no significant difference to parameter estimates of the univariate model. There were no differences in parameter estimates for the univariate, bivariate, and multivariate analyses.

The ability to estimate the covariance between the three kid survival traits with the bivariate animal model gave support to attempt a tri-variate analysis. Both the three birth weight traits and three kid survival traits were analysed with a sire and then animal model. There was a trend for lower heritabilities with increasing birth type traits for birth weight (0.32 to 0.24) and an increasing trend for kid survival (0.10 to 0.19) (Table 6-1). Based on the standard errors, the differences in heritability between the three birth weight or three kid survival traits were not significant. There was also no difference between either of the sire and animal model heritabilities.

**Table 6-1: 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	<b>0.34 ± 0.18</b>		<b>0.10 ± 0.18</b>		
	Twin	0.86 ± 0.14	<b>0.29 ± 0.10</b>	0.77 ± 0.31	<b>0.15 ± 0.11</b>	
	Multiple	0.35 ± 0.27	0.74 ± 0.17	<b>0.25 ± 0.15</b>	0.83 ± 0.27	<b>0.19 ± 0.15</b>
Animal model	Single	<b>0.49 ± 0.08</b>		<b>0.08 ± 0.05</b>		
	Twin	0.91 ± 0.08	<b>0.41 ± 0.04</b>	0.46 ± 0.34	<b>0.12 ± 0.03</b>	
	Multiple	0.63 ± 0.15	0.87 ± 0.09	<b>0.32 ± 0.05</b>	0.72 ± 0.45	<b>0.53 ± 0.29</b>

Sire multivariate models were fit originally, but variance estimates were not significantly different to the animal models (Table 6-1). The tri-variate KSV model had lower standard errors for the heritability of KSV traits (0.03 to 0.05 for KSV animal model, Table 6-1) than when treating the birth types as three separate traits with no genetic correlation (0.04 to 0.07 for KSV animal models, not presented). Thus the tri-variate analysis also had higher EBV accuracies (0.53 to 0.58 for KSV animal model) than the univariates (0.39 to 0.51 for KSV animal models), calculated based on standard errors of EBVs and selection index theory. When kid survival was analysed as a univariate trait (Table 4-4), the log-likelihood was 3,537.82 and when analysed as a tri-variate (Table 6-1), it was 2239.68, a difference of 1,298.14. Using a  $\chi^2$  test, this difference was significant ( $P < 0.001$ ) indicating the univariate model was superior, this was also the case for BWT.

To further validate the results of the tri-variate the same method was used for weaning weight (WWT) and post-weaning weight (PWT). For both WWT and PWT the genetic correlations were predicted to be higher than those for BWT but were in fact lower (Table 6-2). For WWT the genetic correlation between singles, twins, and multiples was between 0.38 and 0.76 with standard errors of between 0.19 and 0.60. For post-weaning weight the genetic correlations were between 0.37 and 0.77 with standard errors between 0.21 and 1.06. The standard errors on these correlations were much higher compared to BWT. The largest concern was the estimates of heritability of the multiples for WWT\_M ( $0.06 \pm 0.04$ ), and PWT\_M ( $0.03 \pm 0.05$ ).

To estimate the covariances between the three birth weight traits and the three kid survival traits a series of bivariate were used (Table 6-3). There were very large standard errors



associated with all of the estimates and were higher for the sire model compared to the animal models. For the sire model KSV of singles was negatively correlated with birth weight but positive for the animal model.

**Table 6-2: Tri-variate analysis for separate birth type traits of weaning weight (WWT) and post-weaning weight (PWT) with an animal model. The heritability is on the diagonal and genetic correlation below the diagonal.**

	WWT			PWT		
	Single	Twin	Multiple	Single	Twin	Multiple
Single	<b>0.25 ± 0.06</b>			<b>0.34 ± 0.08</b>		
Twin	0.76 ± 0.19	<b>0.20 ± 0.03</b>		0.43 ± 0.21	<b>0.21 ± 0.03</b>	
Multiple	0.38 ± 0.60	0.58 ± 0.51	<b>0.06 ± 0.04</b>	0.37 ± 0.92	0.77 ± 1.06	<b>0.03 ± 0.05</b>

**Table 6-3: Genetic correlations between birth weight (BWT) and kid survival (KSV) birth type traits with a sire and animal model.**

	Sire model			Animal model		
	BWT			BWT		
	Single	Twin	Multiple	Single	Twin	Multiple
Single	-0.26 ± 1.08			0.17 ± 0.56		
Twin		0.02 ± 0.51			0.22 ± 0.22	
Multiple			-0.46 ± 0.41			-0.43 ± 0.33

Various multivariate analysis were attempted but would not converge. The first was with all six traits for birth weight and kid survival. To simplify the model the original birth weight trait and the three kid survival traits were used. After also attempting the analysis with a sire model, it was evident that the data was not suitable for further multivariate analysis.

The final analysis was to determine the relationship between the three kid survival traits and the other production traits. This was achieved through a series of bivariate analyses of the three kid survival traits and the original production traits. 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 6-4). All of the genetic correlations had large standard errors associated with them. For KSV\_1 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\_2 with production traits were higher and significantly different from zero compared to KSV\_1 and KSV\_3. There were convergence issues for several of the KSV\_3 bivariate models. Both weaning weight and post-weaning weight were positively correlated with KSV\_3.

**Table 6-4: Genetic correlations with animal model between kid survival birth type traits and individual production traits.**

	Kid survival			
	Single	Twin	Multiple	<sup>b</sup> 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	*	<sup>a</sup> 0.48 ± 0.18	*	0.05 ± 0.03
FAT	0.45 ± 0.60	0.67 ± 0.32	<sup>a</sup> 0.45 ± 0.60	0.05 ± 0.03

<sup>a</sup> - Log likelihood converged but parameters not converged

<sup>b</sup> - Values from Table 5-2

\* - Did not converge.

## 6.5 Discussion

It was possible to separate lamb survival as a trait of the ewe into separate biological traits based on birth type (Bunter *et al.* 2017), but the ability to do so with goats and as a trait of the kid was limited. The parameter estimates from the univariate analysis, correlations between EBVs, the ability to estimate covariances with bivariate and tri-variate models all supported treating kid survival as different trait based on birth type as different environments in a G x E interaction. With the available data, the method is not recommended for use in breeding programs, until the recording practices in the KIDPLAN database have improved and more accurate estimates can be made with confidence.

Both the sire and animal models had no significant difference between the phenotypic variance, heritability or maternal permanent environmental effect of the individual kid survival traits and the original KSV trait. This was a small amount of support for the hypothesis as each of the traits were variable and heritable. The parameter estimates for the logistically transformed kid survival traits for both the sire and animal models were

higher but not different to zero with large standard errors. This was some evidence for there being no benefit in performing the logistic transformation. This was further demonstrated with the bivariate analysis, by the fact that ASREML could only fit one logistically transformed trait at a time (Gilmour *et al.* 2009). It is not expected, that if it were possible, that it would provide better estimates, as it did not improve them for the univariate analysis from Chapter 4 nor the univariate analyses of separate birth type traits.

The univariate EBVs for the three kid survival traits had low to moderate correlations which indicate they have a low genetic correlation, however the EBVs have high standard errors and low accuracy. For birth weight it was anticipated that the three traits and their EBVs would have a moderate to high correlation. The reason for the low correlations could be due to the high standard errors of the EBV's, the small number of sires with adequate numbers of progeny for each trait, or the suitability of the methodology.

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 (Chapter 4) compared to the tri-variate

analysis were not significantly different however the standard errors were much higher with the tri-variate analysis. The  $\chi^2$  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 and the assumption in the  $\chi^2$  test for random effects is that the same fixed effects model is fitted. That said, in the tri-variate 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.

Tri-variate analysis of weaning weight and post-weaning weight suggested that further investigation is warranted. For weaning weight the heritability decreased from 0.25 for singles to just 0.06 for multiples while post-weaning weight dropped from 0.34 to 0.03. Once more the genetic correlations were predicted to be moderate to high. For weaning

weight the genetic correlation was between 0.38 and 0.76 and for post-weaning weight between 0.37 and 0.77. While the standard errors were high, if these results are correct it could have a major effect with a breeding index that could place a higher selection pressure of weights for twins.

Another major issue was estimating the covariances between the separate birth weight and kid survival traits for multivariate analysis. 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 (Chapter 5).

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.

## 6.6 Conclusion

The probability of kid survival was different depending on birth type. This was evident in the fact that singles and multiples had lower survival rates than twins. It was hypothesised that kid survival could be treated as a different trait for different birth types. While it was possible to treat them as separate traits and the models converged, the accuracy of the results was not suitable for them to be used practically in a breeding objective. With more and precise data it should be re-considered for the implementation in national performance recording as it has the potential to increase the rate of genetic gain.





## 7 Australian goat producers say they want to sell more meat.



## 7.1 Abstract

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.

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 will be developed (Chapter 8). Such an index is likely to have a large emphasis on reproduction and body weight.

## 7.2 Introduction

The Australian meat goat industry is undergoing some major changes and there is a need to update the breeding objectives and economic values for important production traits. There is a growing global demand for goat meat, with the price per kilogram at record highs (MLA 2016). To capitalise on this growing market, Australian goat breeders said they want an index that is specifically designed for producing goat meat in self-replacing herds instead of using Carcase Plus (CPLUS) which is a terminal sire index for sheep (BCS Agribusiness 2012; Sheep Genetics 2016).

Ponzoni (1988) outlined five steps for a breeding program; 1) define the breeding objective, 2) identify the selection criteria, 3) develop a performance recording system, 4) present the information for making selection decisions, and 5) use the selected animals. The Australian sheep and beef industries have worked extensively on developing economic values and breeding objectives. Both industries have considered the income and expenses for those production systems, as well as the objectives of the breeders (Hazel 1943; Morris 1981; Ponzoni 1988; Butler *et al.* 1995). The sheep industry has undergone major changes with an increasing demand for meat and a premium for wool quality (Swan *et al.* 2007; Swan *et al.* 2009). By communicating with producers and analysing these market changes, Sheep Genetics have developed a number of indexes for wool and lamb production (Swan *et al.* 2007; Swan *et al.* 2009; Swan *et al.* 2015).

The index currently used by KIDPLAN breeders is Carcase Plus (CPLUS) (Sheep Genetics 2016). This index was one of the indexes developed by Sheep Genetics for terminal sire sheep. It places 65% of the selection emphasis on growth (originally 60%),

30% on muscling (originally 20%), and 5% on decreasing fat (originally 20%) (Sheep Genetics 2016). The issue raised by Australian meat goat breeders, is the suitability of using a sheep index for goats and the need to develop an index that uses goat breeding objectives (BCS Agribusiness 2012).

There were a number of stakeholders that need to be considered when designing such an index for the Australian meat goat industry. There are the rangeland harvesters, which are the largest production group (90%) and are opportunistic, but don't use KIDPLAN (MLA 2013). Commercial producers that farm rangeland goats in fenced paddocks and often have a breeding program that incorporates crossing with Boer goats. Seedstock breeders, either currently use or could potentially use the national performance recording scheme. Finally, processors providing the goat meat to meet the domestic and global demand.

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.

## 7.3 Materials and Method

### *7.3.1 Industry surveys*

Three targeted surveys were developed for Australian goat producers to complete (Appendix 7-1, 7-2, and 7-3). Specific questions were included about herd size, management practices, reproduction, marketing, and breeding objectives. The surveys were available online (via the Meat and Livestock Australia website) for three months and had a total of 44 responses. In regards to the rangeland, commercial, and seedstock

surveys, there were 5, 24, and 15 responses respectively. A survey was also sent to goat processors, however the three respondents were small boutique operators processing their own stock and were not representative of the wider industry (Appendix 7-4).

To determine if there was a difference in responses between commercial producers, they were split into Pure Boer, Boer Cross Rangeland, and Other Meat Breeds with 10, 6, and 8 responses respectively.  $\chi^2$  tests were conducted to test if there was a significant difference in responses between the commercial producer categories. As there was a large range in herd size, the responses were split by the number of does joined (either less than or greater than 200). There were nine small producers with less than 200 does (<200 does) and 12 large producers with more than 200 does (>200 does), respondents that did not farm a meat breed were not included in the analysis.  $\chi^2$  tests were also used to test if there was a significant difference in responses between the <200 does and the >200 does data groups. The Pearson's  $\chi^2$  test-statistic was used to determine if there was a significant difference in responses between rangeland, commercial, and seedstock producers.

Within the seedstock breeder survey there were three groups; breeders using KIDPLAN (all of whom are Boer breeders), Meat Breeders (predominantly Boer breeders), and Other Breeders. For the KIDPLAN group there were five responses and Meat Breeders had seven. Other Breeds included one Angora and one unidentified dairy breed, these two responses were not included in the analysis as they are not representative of the Australian meat goat industry. A summary of the number of responses and size of the response groups are provided in Table 7-1.

**Table 7-1: Summary of the number of responses and annual herd size for each survey by production system and survey group.**

Survey Group	Number of responses	Mean number of does	Median number of does	Mean number of bucks used / year	Median number of bucks used / year
Rangeland	5	240	200	-	-
Commercial	24	372	200	-	-
Commercial (Boer)	10	332	128	-	-
Commercial (Boer x Rangeland)	6	380	60	-	-
Commercial (Other Meat Breeds)	8	430	370	-	-
Commercial (<200)	9	38	29	-	-
Commercial (>200)	13	692	510	-	-
Seedstock	15	101	75	5	4
Seedstock (KIDPLAN)	5	135	80	5	3
Seedstock (Meat breeders)	7	83	65	5	4

- Relevant question not asked

There were some questions which asked their opinion on a statement. These questions were on a 5 point Likert scale of Strongly Disagree, Disagree, Neutral, Agree, and Strongly Agree which were coded as -2 to +2. The average was used to determine the opinion of the respondents.

There were also questions on economic values in relation to income. Following advice from Meat and Livestock Australia, there was an understanding that producers within these systems had different depths of knowledge of their business (Julie Petty, MLA Goat officer, personal communication). Not all of the surveys asked the same questions of

producers in relation to income, particularly the rangeland harvesters. Only seedstock producers were expected to keep detailed trait records, questions about recording practices were excluded from the rangeland and commercial surveys.

### 7.3.2 Economic Values

Economic values were calculated using SheepObject2, a breeding objective software program developed by Andrew Swan (AGBU). The program requires inputs regarding herd structure, reproductive performance, sales of surplus males and females, and the annual management costs. The values used for this input were extracted from the industry surveys, market reports, and previous literature. The output from SheepObject2 is in dollars per unit gain. Using the estimates from the bivariate analysis (Chapter 5) these were converted to relative economic values, calculated as dollars per genetic standard deviation ( $\sigma_G$ ).

SheepObject2 calculated the total profit as: Total profit = Sale weight returns - management costs - sale weight costs - feed costs. Base profits and feed costs are determined for surplus males, surplus females, and breeding ewes. The base profit and feed costs were then adjusted for sex, weight, birth type, and rearing type. Economic values were then calculated for litter size, number of kids weaned, fertility rate, kid survival, sale weight, mature weight and dressing percentage. These economic values were functions of the herd structure, base profit and base feed cost.

## 7.4 Industry Surveys

### *7.4.1 Management practices*

The management practices section of the survey, included questions about supplement feeding, internal parasites, weight recording, and goat fencing. A summary of the categorical questions asked and the results of the  $\chi^2$  tests of these questions are provided in Table 7-2.



**Table 7-2: Summary of management questions asked and the results of tests of significant difference for those questions.**

Question	Majority response	$\chi^2$ tests of significant difference
What month does the 'limited feed period' normally start?	March	NS
What month does the 'limited feed period' normally end?	May	NS
Do you supplement feed?	Yes	Commercial producers (59%) had a lower rate of supplement feeding than Seedstock breeders (92%).
If you supplement feed, what is the primary feed base?	Hay	NS
Do you monitor internal parasites?	Yes	Commercial producers (50%) had a lower rate of monitoring than Seedstock breeders (91%).
Do you control internal parasites?	Yes Drenching	NS
What proportion of the current drop males and females will have Worm egg count's (WEC) tested?	>50%	NS
Do you have improved fencing designed for goat management?	-	NS
Please tick the body weights you currently record for females.	BWT, WWT, PWT	NS
Please tick the body weights you currently record for males.	BWT, WWT, PWT	NS

Birth weight (BWT), weaning weight (WWT), and post-weaning weight (PWT)

NS – Not significant

One of the key requirements for calculating the economic values (7.5 Economic Values) is the cost of supplement feeding. Commercial, and seedstock producers were asked “what month does the limited feed period start/end”. There was no significant difference in when supplement feeding starts and ends between production systems or production groups (Table 7-2). For the majority of producers the limited feed period started in March and ended in May. The limited feed period lasted a mean of 3.5 months. As to whether respondents supplement feed, there was no significant difference between commercial groups, nor was there a difference between seedstock groups. On average 59% of commercial producers supplement feed compared to 92% of seedstock breeders.

The main type of supplement feed for seedstock producers in both KIDPLAN and meat breed groups was hay, although grain was also reported to be fed. Three commercial producers reported a known amount of feed fed over the limited feed period, but the large range (0.5 to 150 kg/head/year) indicated a misunderstanding of the question and was not useful to generate an average annual amount fed. Of the seedstock breeders, only one knew how much hay they fed (32 kg/head/year). There were four seedstock breeders with a known amount of grain fed. The range of values reported (0.3 to 20 kg/head/year) again indicated a misunderstanding of the question. The two breeders feeding under 2 kg of grain per head/year were likely in preparation of a show competition or misinterpreted the question. It is possible that the low outliers answered in terms of kg/day, kg/head or kg/live weight, without clarification it was not sensible to use these values. Excluding these low outliers the mean amount of grain fed was 20 kg/head/year.

For seedstock breeders, the average cost of supplement feed was \$2.57/kg for hay and \$1.07/kg for grain. Additional comments from the surveys suggested, that the high prices for both hay and grain was likely a misinterpretation of the question, incorrect units or included pelleted and processed feed. Three commercial producers responded to “what is the average cost of feed in \$/kg?” with values of \$0.55, \$1.00, and \$30.00. It is possible that the \$1.00 was for pelleted feed or in units of \$/live weight kg. If \$/live weight, this would be approximately \$47 per doe fed for 90 days giving a final feed cost of \$0.42/kg. The \$30.00/kg was very high, suggesting the responder misinterpreted the question as \$/head instead of \$/feed kg (which when converted for the average doe gives a value of \$0.14/kg). The average cost of supplement feed for the three commercial producers, after these adjustments and assumptions, was \$0.37/kg of feed. The conclusion for feed costs was that the predominant system is mixed pasture with limited supplement feeding.

Commercial and seedstock producers were asked if they monitor internal parasites, but were not asked to describe their monitoring practice. Significantly more seedstock breeders (91%), monitor for internal parasites, compared to commercial producers (50%). There was no difference between groups within commercial producers or within seedstock breeders. While commercial producers had a lower rate of monitoring, both commercial and seedstock producers had some form of parasite control. For both commercial producers (67%) and seedstock breeders (73%), drenching was the predominant control method. Some seedstock breeders also reported “off-label” use of Barbervax®, a vaccination for *Haemonchus contortus* (Barber’s Pole Worm). Of the seedstock breeders, 44% recorded worm egg counts (WEC) in more than 50% of the current drop male and females. The high rate of monitoring of WEC was not consistent with the low number of WEC records submitted to KIDPLAN (Chapter 3 and 4).

Seedstock breeders were asked if male and female progeny had weights recorded corresponding to the KIDPLAN weight traits (Birth, weaning, post-weaning, yearling, hogget, and adult weights). There was no significant difference in weight recording practices, between the KIDPLAN group and the Meat breed group. Of the seedstock respondents, 60% to 67% recorded birth weight, weaning weight, and post-weaning weight, for both males and females. For yearling, hogget, adult, and repeat adult weights of males, the number of respondents dropped to 40%, 13%, 33%, and 27% respectively. Similarly for the females; yearling, hogget, adult, and repeat adult weights were recorded by 40%, 20%, 40%, and 27% of respondents respectively.

Commercial producers were asked if they had improved fencing designed for goats and what proportion of the property used such fencing. There was no difference between the different groups, with 91% of commercial properties using such fencing. The mean proportion of the property enclosed by improved fencing was 63%.

#### *7.4.2 Reproduction*

On all surveys, the reproduction questions had few responses and there were some difficulties with respondents' misinterpretation of the questions. The categorical questions related to joining and weaning, and the  $\chi^2$  tests for these questions are summarised in Table 7-3.

**Table 7-3: Summary of categorical reproductive questions and the  $\chi^2$  tests of significant difference production systems and groups.**

Question	Majority response	$\chi^2$ tests of significant difference
Do you routinely join Doe kids less than 12 months of age?	No	NS
Please tick the months when you join.	Feb-May	NS
Do you control joining?	Yes	Large Commercial producers had a lower rate of controlled joining (46%) than Small Commercial producers
Do you control weaning?	Yes	Commercial producers had a lower rate of controlled weaning (59%) than Seedstock breeders (92%)
Please tick the Months when you wean.	Dec-Mar	NS

NS – Not significant

Producers were asked about the age of first joining. The first was “Do you routinely join Doe kids less than 12 months of age?”, both commercial and seedstock producers agreed that joining doe kids less than 12 months of age was not common. As commercial producers were expected to be less likely to know an accurate mean age of does first joining, they were asked to select a 3 month age period (Table 7-4). There was no significant difference between the commercial groups with the majority of does being joined after 18 months of age. This result was unexpected as it was originally thought that the majority of joining occurred at 18 months of age. This result was likely due to an error in creating the category ranges which should have included 17-20 months.

**Table 7-4: Summary of the proportion of producers for the age which does are first joined.**

	12-15 Months	15-18 Months	18-21 Months	21-24 Months	24+ Months
Pure Boer	0%	20%	20%	50%	10%
Boer X Rangeland	33%	33%	0%	33%	0%
Other meat breeds	43%	0%	29%	14%	14%
Total	22%	17%	17%	35%	9%

The seedstock breeders were asked at what age (in months) their does and bucks are first joined (Table 7-5). There was no significant difference in the age of does or bucks joined between the seedstock groups. However, there was a trend for the KIDPLAN group to join animals later (older than 16 months of age) compared to other Meat breeders who typically join before 16 months. The average weight of does at joining for seedstock breeders was 50.0 kg  $\pm$  4.3 kg, with no significant difference between KIDPLAN and other Meat breeders. Commercial producers were joining at an average body weight of 47.2 kg  $\pm$  3.4 kg, which was not significantly different to the seedstock breeders.

**Table 7-5: Summary of the age (months) that does and bucks are first joined.**

	Doe mean age	Doe median age	Buck mean age	Buck median age
KIDPLAN	17 $\pm$ 2	18	16 $\pm$ 2	18
Meat	15 $\pm$ 1	15	13 $\pm$ 2	10
Seedstock total	16 $\pm$ 1	17	13 $\pm$ 1	16

To determine the rate of genetic progress, commercial producers were asked at what age they sell cast for age does (CFA), and seedstock breeders were asked how many kiddings does are retained for. On average commercial producers and seedstock breeders retained does for seven years. Only seedstock breeders were asked how many years bucks are used for, which was an average of four years. The length these animals were retained for was much longer than expected.

None of the commercial or seedstock groups had a significant difference between the month in which does and bucks are joined. As expected, the majority of joining occurred between February and May. The main reason for this was that goats are highly seasonal (Papachristoforou *et al.* 2000, 2007; Arrebola *et al.* 2010). A small number of producers reported additional joining in spring, these responders had post codes in Queensland where seasonality is reduced and explains the large number joined during the potential anoestrus of 21-24 months (Table 7-4). This also helped explain the unexpected results with the majority of joining occurring after 18 months instead of the category ranges (Table 7-4).

Both commercial producers and seedstock breeders were asked for their average fertility rate (does pregnant as percentage of does joined), scanning rate (percentage of fetuses scanned as a percentage of does joined), number of kids born alive (commercial breeders excluded), and the average weaning rate (kids weaned as percentage of does joined). The average fertility rate for both commercial producers and seedstock breeders was very high at 94% and 95% respectively. For scanning rate there was only one response each for commercial producers (200%) and seedstock breeders (156%). The average number of kids born alive for seedstock breeders was 1.8 kids per doe, compared to 1.6 kids per doe in KIDPLAN (Chapter 3, Table 3-1). The average weaning rate for the commercial and seedstock systems were 130% and 144% respectively, similar to KIDPLAN which is 143%.

When asked “Do you control joining”, the only significant difference was between commercial groups with less than 200 and more than 200 does. However, in both groups the majority of respondents did control joining. Both groups had a majority of respondents that controlled weaning, but there was a significant difference between commercial producers (59%) compared to seedstock breeders (92%).

For the time of weaning, there was no difference between any of the groups. The majority of respondents were weaning between December and March. This was likely a result of the high seasonality of goats, so joining occurred at the same time for most producers, as well as the limited feed period starting shortly after these dates for weaning.

All but one seedstock breeder reported that they record full reproductive data. The question also stated “Must include recording of Dead at Birth and Dry animals, pedigree information, accurate Birth Type, Rearing Type, and Birth Date.” 12 positive responses is an overestimate, as there was an under-reporting for the reproductive questions.

#### *7.4.3 Marketing and income*

Questions on marketing and income were included in all of the survey groups. In this part of the survey there were fewer categorical questions. Categorical questions that were asked related to how animals were selected (Table 7-6). The majority of these questions were based on the dollar value of the animals sold.



**Table 7-6: Summary of marketing questions asked and the results of tests of significant difference for those questions.**

Question	Majority response	Tests of significant difference
Do you sell cast for age Does based on live weight, dressed weight or per head?	Dressed weight	NS
For animals sold to slaughter are they sold based on \$/kg live, dressed or head.	Dressed weight	NS
Do you sell your bucks to other seedstock breeders?	Yes	NS

NS – Not significant

Commercial producers were asked what method cast for age does were sold, with the majority replying they were sold based on dressed weight (Table 7-6). All of the surveys also asked what method was used for animals sold for slaughter. Again, across all of the surveys, the majority of respondents sold their animals based on dressed weight. Rangeland harvesters had 50% of respondents selling based on live weight, but this difference was not significant, due to the low number of responders. The seedstock breeders were also asked if they sold their male progeny to other seedstock breeders, with 80% reporting that they did sell their males to other breeders.

Respondents were then asked to report sale prices based on the method of sale (Table 7-7). The majority of animals for each of the production systems were sold based on dressed weight. The groups within production systems had no significant difference in price for cull for age does and male progeny, which suggests that there are no price premiums for goat meat quality. The slaughter price between production systems had a small but not significant difference, with values of \$5.12/kg (Commercial), and \$5.56/kg (Rangeland).

Animals in rangeland systems were sold at a younger age and lighter weight compared to commercial and seedstock breeders.

**Table 7-7: Summary of age and value of animals sold.**

Question	Rangeland	Commercial	Seedstock
What is the average sale price of CFA does in \$/kg dressed?	\$5.56	\$5.13	-
What is the sale price of male progeny in \$/kg dressed?	\$5.56	\$5.12	\$5.35
What is the sale price in \$/kg live?	\$1.89	\$2.50	-
What is the sale price in \$/head live?	-	\$68.00	\$67.50
Age CFA sold	3 Years	7 Years	-
Weight CFA sold (Live)	31.5 kg	47.3 kg	-
Weight CFA sold (Dressed)	17.0 kg	-	-
Age male progeny sold	3-6 Months	9 Months	11 Months
Weight male progeny sold (Live)	17.0 kg	28.9 kg	35.8 kg
Weight male progeny sold (Dressed)	5.0 kg	15.8 kg	17.7 kg

#### *7.4.4 Breeding objectives*

A small number of questions were asked in regards to the MLA (2012) research and development strategy (Table 7-8). The first was, if they considered reducing adult doe weight to be of importance as larger does eat more feed. Both commercial producers and seedstock breeders disagreed with this statement. When asked if they consider internal parasites an issue, all respondents tended to agree with the statement. Both commercial producers and seedstock breeders were neutral or slightly disagreed with the statement on the importance of increasing fat (an issue when cooling carcasses). Only the seedstock

breeders were asked if increasing meat yield was of importance to their breeding objective, which respondents agreed or strongly agreed with.

**Table 7-8: Summary of breeding objective questions asked and the results of tests of significant difference for those questions.**

Question	Mean response	$\chi^2$ tests of significant difference
Reducing adult doe weight is of high importance to my breeding objective.	Disagree (-1.2)	NS
Do you consider internal parasites to be a significant issue for you?	Agree (+0.4)	NS
Increasing carcass fat is of importance to my breeding objective.	Neutral (-0.2)	NS
Increasing carcass meat yield is of importance to my breeding objective.	Strongly Agree (+1.6)	NS

NS – Not significant

## 7.5 Economic Values

The surveys indicated there were very few differences between production systems or groups within those systems. In most cases when there were differences, the majority still agreed with each other. Only one set of economic values were calculated, as there was only a small number of differences between the production systems, and groups within those systems.

Where possible, values from the survey were used for the economic value calculations. The majority of the values used for the reproductive components were calculated from the survey responses (Table 7-9). The kidding date (August 28) and weaning age (156 days) used the mean from both commercial and seedstock responses. The mean number

of does joined for the commercial and seedstock producers was 280 does. The median (80 does), was also used in the calculations, because it was of concern that 280 was an overestimate. As both values are relatively low for a breeding program, using either number of does, had no significant effect on the economic values calculated. The age at first kidding was calculated from the mean of the commercial producers and seedstock breeders. The number of kiddings was determined from the age of cull for age does with an assumption that there was a kidding each year after the first kidding. For the traits: doe mortality, fertility rate, litter size, and survival from yearling to adult, values from previous literature and the currently used values from SheepObject2 were used. Survival from birth to weaning was calculated from the KIDPLAN database for the birth types single, twin, and multiple (Chapter 3).

**Table 7-9: Summary of reproductive inputs, from survey responses and KIDPLAN data, for SheepObject2.**

Parameter	Value
Kidding date	August 28
Weaning age	156 days
Number of does	280
Age at first kidding	1.5 years
Number of kiddings	7
Doe mortality rate for age (2yo, 3yo, 4yo, 5yo, 6yo, 7yo, 8yo)	0.05, 0.04, 0.03, 0.02, 0.01, 0.01, 0.01
Fertility rate for parity (1 <sup>st</sup> , 2 <sup>nd</sup> , 3 <sup>rd</sup> , 4 <sup>th</sup> , 5 <sup>th</sup> , 6 <sup>th</sup> , 7 <sup>th</sup> )	0.80, 0.84, 0.88, 0.92, 0.96, 0.98, 0.96
Litter size for parity (1 <sup>st</sup> , 2 <sup>nd</sup> , 3 <sup>rd</sup> , 4 <sup>th</sup> , 5 <sup>th</sup> , 6 <sup>th</sup> , 7 <sup>th</sup> )	1.9, 2.1, 2.2, 2.4, 2.3, 2.3, 2.3
Survival birth to weaning (Single, Twin, Multiple)	0.71, 0.83, 0.72
Survival yearling to adult	0.97

The values used for surplus male and female progeny sold are summarised in Table 7-10 from the survey responses. Both males and females are sold at approximately 300 days

old. The only difference for the male and female progeny sold was the mean carcass weight (16 kg for males and 12 kg for females). From the survey responses of rangeland harvesters, commercial producers, and seedstock breeders the mean dressing percentage was 51% which is similar to the mean of 52% reported by Dhanda *et al.* (2003) in Table 2. The mean price for all carcasses sold in the survey was \$5.35/kg. The skin value was assumed to be \$1 due to the lower demand compared to sheep (SheepObject2). The weight for age was calculated from the raw weights of age provided in the KIDPLAN database and adjusted for doe age, birth and rearing type. The weight for age is used in determining feed costs per animal. The sale cost per animal (\$1.50) also uses the current SheepObject2 value for Merino lambs and includes marketing and transport costs.

**Table 7-10: Summary of survey responses for male and female progeny sold, as inputs used for SheepObject2.**

Parameter	Value
Sale age	300 Days
Carcass weight	16 kg males / 12 kg females
Dressing %	51%
Carcass price \$/kg	\$5.35
Skin value	\$1.00
Weight for age	Body weight adjustment
Sale cost per animal	\$1.50

The cull for age does, unlike cull for age ewes, do not have a price penalty and were sold at \$5.35/kg. The recovery period and animal sale cost, were an oversight and not asked in any of the surveys, so the values used the current provided values of SheepObject2 for Merino ewes culled for age. The management costs for kids, hoggets, and adults paid annually for labour, drenching, vaccination, and tagging was estimated at \$4.00/head. For a mixed pasture system with minimum inputs and limited supplementation (supplement

feed cost \$21.20/head/year, based on survey results) a cost of \$0.005/MJ was calculated (CSIRO 2007).

The above income and costs were used as input for SheepObject2 and the results are summarised in Table 7-11. Body weight had the largest economic value, with an increase of one kilogram at 300 days of age, increasing the value of the individual by \$2.53. This is higher than reported for sheep at \$1.83 (Table 2, Swan *et al.* 2015). A percentage point increase for dressing percentage had a \$1.78 increase, lower than sheep which was reported as \$2.04 (Table 2, Swan *et al.* 2015). Fertility rate and kid survival had a \$0.66 and \$0.87 increase per percentage point respectively. The value for kid survival was higher compared to the economic value for lamb survival of between \$0.23 and \$0.35 (Amer *et al.* 1999). Mature weight had a lower economic value due to the higher costs for maintenance at \$0.46 per kilogram increase. Increasing litter size and number of kids weaned had the lowest economic values of \$0.11 and \$0.30 per percentage respectively. The economic value for litter size was similar to sheep reported between \$0.15 and \$0.24 (Amer *et al.* 1999).

**Table 7-11: Summary of meat goat economic values from SheepObject2.**

Component	Economic value / Unit	Economic value / $\sigma_G$
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

The economic values from SheepObject2 are required for the development of an Australian meat goat index. Previously, a sensitivity analysis of key lean meat production traits indicated that fertility would have a significant effect on selection (Chapter 2). The inconsistent recording of dry does and the high fertility rate of goats, means that the  $\$5.94/\sigma_G$  could be unattainable (Chapter 3). The low economic value of  $\$0.33/\sigma_G$  for litter size and the higher value of  $\$9.79/\sigma_G$  for kid survival reaffirms the high fecundity of goats. It also showed that kid survival is more important than to just increase the number of kids born as demonstrated earlier (Table 2-7) and reported by others (Husain *et al.* 1995; Snyman 2010). One of the most encouraging results, is the same conclusion was made between the calculated economic values for the index, compared to the original sensitivity analysis of the literature review (Table 2-7), with decreasing importance placed on reproductive traits, growth traits, and carcass traits.

Post-weaning weight was consistently recorded in KIDPLAN and with body weight at 300 days having a large economic value of  $\$3.94/\sigma_G$ . Therefore an index incorporating

bodyweight could be acted upon using current data recording practices. Dressing percentage also had a large economic value, there was not a consistent recording practice for carcass traits and will be a limitation if a large emphasis is placed on it without a change to recording practices in KIDPLAN. Mature weight had a low economic value compared to body weight at 300 days, few producers' record weight after yearling age, and the survey responses indicate it was not important to the breeding objective which will also limit the emphasis placed on mature weight within an Australian meat goat index.

## 7.6 Conclusion

The main message from the producer groups surveyed was that the main goal of the industry is to increase meat production of Australian meat goats. Body weight at sale age had the highest economic value as calculated with SheepObject2. A new Australian meat goat index needs to place a large amount of selection pressure on body weight. There was a large amount of discussion by producers on parasite resistance and increasing the dressing percentage. The limitation of producers not recording or submitting this data, remains an issue and will limit their selection pressure in an index. Increasing fertility and kid survival will improve the reproductive performance, which was a limiting component of production for many of the producers that were surveyed.

The results from the survey on herd structure, reproduction, management, and marketing were used as input in the breeding objective software SheepObject2 (Andrew Swan, personal communication). Increasing weight at sale age, had a large economic value with an increase of \$2.53/kg and \$3.94/ $\sigma_G$ . The economic values for kid survival of \$0.87/%



and  $\$9.79/\sigma_G$ , was significant and supportive of its inclusion in the breeding objective. With clear breeding objectives from the surveys and the calculated economic values, an index for Australian meat goats will be developed (Chapter 8). Such an index is likely to have a large emphasis on body weight and reproduction



## 8 An Australian meat goat selection index to increase growth and reproductive rates.



## 8.1 Abstract

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 was 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 these traits in the breeding objective.

## 8.2 Introduction

Selection indexes are used to measure the net merit of animals in a breeding program, accounting for the genetic parameters of correlated traits and the relative economic values for each trait (Hazel 1943). Not considering sources of income and expenses, or other important traits based on economic grounds, reduces the selection efficiency or overestimate the genetic improvement (Ponzoni 1988). Goat breeders using the national performance recording scheme (KIDPLAN) have been using the Carcase Plus (CPLUS) selection index which was designed for Australian terminal sire sheep (Sheep Genetics

2016). The CPLUS index puts a large emphasis on increasing growth and eye muscle depth while maintaining leanness. There are several issues with the use of this index when applied to KIDPLAN. The main issue with CPLUS is the 20% emphasis on decreasing post-weaning fat depth (FAT) and 20% on increasing post-weaning eye muscle depth (EMD). There are not enough breeders consistently recording and submitting data for eye muscle depth or fat depth to justify the emphasis placed on these traits. The CPLUS index also places a negative economic value on fat depth to decrease fat depth, but goats are already very lean and have a small amount of variation in fat depth (Chapter 4). Another issue with the CPLUS index is that large changes have occurred in the Australian goat industry. The value of goat meat continues to increase with a growing demand globally (MLA 2016). The values used in CPLUS are based on lamb economic values and are not representative of the Australian meat goat market.

The final issue with the CPLUS index, is that the genetic and phenotypic covariance, and variance matrices rely on values estimated from Terminal sheep breeds, which have been somewhat modified to suit the KIDPLAN dataset. Australian goat producers have a growing demand for the development of an index built specifically for Australian meat goats (BCS Agribusiness 2012). The aim of this project was to develop the first Australian meat goat specific index. From the previous sensitivity analysis (Chapter 2), the bivariate analysis (Chapter 5), and the results of the surveys and economic values (Chapter 7), an Australian meat goat index will place emphasis on body weight and kid survival, and a small amount on carcass and health traits.

## 8.3 Materials and Method

### *8.3.1 Trait genetic and phenotypic parameters*

There were nine traits of interest used in the analysis; birth weight (BWT), weaning weight (WWT), post-weaning weight (PWT), maternal weaning weight (MWWT), number of kids born (NKB), number of kids weaned (NKW), kid survival (KSV), eye muscle depth (EMD), fat depth (FAT), and worm egg count (WEC). Body weight was defined as 50% emphasis of WWT and PWT. For EMD and FAT the previous sheep parameter estimates were for post-weaning but the parameter estimates in this analysis used the combined post-weaning and yearling traits (Chapter 4; Chapter 5). There was insufficient data in KIDPLAN or published literature for genetic and phenotypic correlations of maternal weaning weight or worm egg count, any analysis that included these traits used the previous covariance estimates from CPLUS for Terminal sheep or literature.

The genetic correlations between traits were from the previous bivariate analysis (Chapter 5). Due to the large standard errors and low number of records for EMD and FAT, genetic correlations from Brown and Swan (2016b) have been used. The genetic variance, residual variance and maternal permanent environmental variances were means of the bivariate analysis, which were not significantly different to estimates of the univariate analysis (Chapter 4). Number of kids born and weaned were treated as traits of the doe and used means from previous goat literature (Chapter 2). This high estimate for permanent environmental variance was likely an over estimate and requires updating if number of kids weaned is evaluated using KIDPLAN data. Kid survival was treated as a trait of the kid, with a maternal permanent environmental effect. Previous estimates for

maternal heritability were not different to zero, or not estimable, and supported treating survival as a trait of the kid (Chapter 4). The genetic correlations did not include the three additional birth type traits for kid survival due to the inaccuracy of the estimates (Chapter 6). The variances and covariances used for the analysis are summarised in Table 8-1.

**Table 8-1: Summary of parameter estimates. Genetic variance ( $\sigma_A^2$ ), residual variance ( $\sigma_e^2$ ) and maternal permanent environmental variance (MPE). The genetic correlations are below the diagonal the phenotypic correlations above.**

	BWT	WWT	PWT	MWWT	EMD	FAT	WEC	NKB	NKW	KSV
$\sigma_A^2$	0.21	1.17	2.45	1.00	0.25	0.014	1.40	0.012	0.013	0.013
$\sigma_e^2$	0.12	8.28	15.56	9.20	2.01	0.206	5.39	0.300	0.307	0.133
MPE	0.07	1.56	2.42	1.00	0.09	0.005	7.00	0.030	*0.321	0.007
BWT		0.35	0.32	0.20	0.01	-0.02	-0.03	0.00	0.00	0.01
WWT	0.53		0.81	0.11	0.03	-0.06	0.00	0.00	0.00	0.00
PWT	0.50	0.88		0.08	0.06	-0.04	0.03	0.08	0.06	0.00
MWWT	0.48	0.50	0.50		0.00	0.00	0.00	0.00	0.00	0.00
EMD	-0.22	-0.21	-0.26	-0.38		0.27	-0.06	-0.07	0.01	0.00
FAT	-0.27	-0.24	-0.19	-0.27	0.26		-0.11	-0.29	0.01	0.00
WEC	0.11	-0.03	-0.24	-0.12	<0.01	<0.01		-0.02	0.04	0.00
NKB	0.10	0.08	0.12	0.15	<0.01	<0.01	<0.01		0.41	0.00
NKW	0.01	0.18	0.29	0.33	<0.01	<0.01	<0.01	0.90		0.00
KSV	0.19	0.05	0.03	-0.06	0.05	0.05	<0.01	0.57	0.63	

Estimates from Table 5-2 or literature.

\*Animal permanent environmental variance

### 8.3.2 Indexes, economic values and recording practices

There were six indexes of interest; two of which were terminal sire indexes, the CPLUS which is the current index used for KIDPLAN and Lamb 2020 (LP2020). The LP2020

index was designed to increase worm resistance and was included for comparison because of comments by producers (Chapter 7) where internal parasites were identified as an industry issue. Both the CPLUS and LP2020 used values calculated for prime lamb production. The CPLUS includes economic values for WWT, PWT, EMD, and FAT but LP2020 had lower economic values for these traits with additional values on BWT and WEC. The maternal sheep index, Self-replacing Carcase (SRC) index, was also included to make a comparison with the new KIDPLAN indexes, which also included reproductive traits. The SRC index included economic values on birth weight, WWT and PWT, mature weaning weight (MWWT), EMD, WEC, and importantly NKW. Economic values for three KIDPLAN indexes were determined from industry surveys and calculated using SheepObject2 (Chapter 7). The first KIDPLAN index is a Lean Meat Goat index (LMG) that included economic weights for the body weights (WWT and PWT) and for carcase traits (EMD and FAT). The second KIDPLAN index was a Maternal Meat Goat index (MMG), which added values for NKB and NKW. The final KIDPLAN index Kid Plus (K+), was a dual purpose index for lean meat production and reproduction which included a weight for KSV. No economic value was placed on MWWT for the KIDPLAN indexes but was included to determine the trait direction change for milk production. The economic values that were used are summarised in Table 8-2.



**Table 8-2: 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 (Table 8-3). The first scenario was for Growth which assumed the only traits recorded were BWT, WWT, and PWT. The second scenario was Carcase which added EMD and FAT to the previous Growth scenario. Reproduction was the third scenario which included growth traits (BWT, WWT, and PWT) and reproductive traits (NLB, NLW, and KSV). Standard practice and Best practice were two scenarios which include all the traits in Growth, Carcase, and Reproduction. Best practice assumed all siblings and own traits are recorded, but Standard practice has a reduced number of records for EMD, FAT, and reproductive traits. Finally the Gold standard recording scenario is with full recording of all traits, including WEC.

**Table 8-3: Summary of own / half-sib traits recorded for each scenario.**

	Growth	Carcase	Reproduction	Standard practice	Best practice	Gold standard
BWT	1 / 30	1 / 30	1 / 30	1 / 30	1 / 30	1 / 30
WWT	1 / 30	1 / 30	1 / 30	1 / 30	1 / 30	1 / 30
PWT	1 / 30	1 / 30	1 / 30	1 / 30	1 / 30	1 / 30
EMD	0 / 0	1 / 30	0 / 0	1 / 7	1 / 30	1 / 30
FAT	0 / 0	1 / 30	0 / 0	1 / 7	1 / 30	1 / 30
WEC	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	1 / 30
NLB	0 / 0	0 / 0	0 / 7	0 / 7	0 / 7	0 / 7
NLW	0 / 0	0 / 0	0 / 7	0 / 7	0 / 7	0 / 7
KSV	0 / 0	0 / 0	1 / 7	1 / 7	1 / 7	1 / 7

A herd of 280 does was used to model the indexes as per the calculations for the average herd size of commercial and seedstock producers (Chapter 7). The proportion of males selected was 5%, and 50% for females. Generation intervals of 3 and 4 years were used for males and females respectively. The selection emphasis for EBVs was 65%. To address the Bulmer effect (Bulmer 1971) for a reduction in genetic variance caused by genetic selection, an adjustment for males and females was calculated using Normal distribution theory.

### 8.3.3 Matrix calculation and selection response

The index calculations were done using R (R Core Team 2016). The index selection theory of Hazel (1943) was used with the variances and covariances in Table 8-1. The economic values of Table 8-2 were used for an economic weights vector (a). The index weights (b) were then calculated (Eq. 8.1). The genetic gain (Eq. 8.2) and the total economic gain (Eq. 8.3) of the index response for one standard deviation of selection was calculated for each of the indexes under different recording scenarios.

$$\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{a} \quad (\text{Eq. 8.1})$$

$$\mathbf{R} = \mathbf{b}'\mathbf{G}(\mathbf{b}'\mathbf{P}\mathbf{b})^{-0.5} \quad (\text{Eq. 8.2})$$

$$\sigma_I = (\mathbf{b}'\mathbf{P}\mathbf{b})^{0.5} \quad (\text{Eq. 8.3})$$

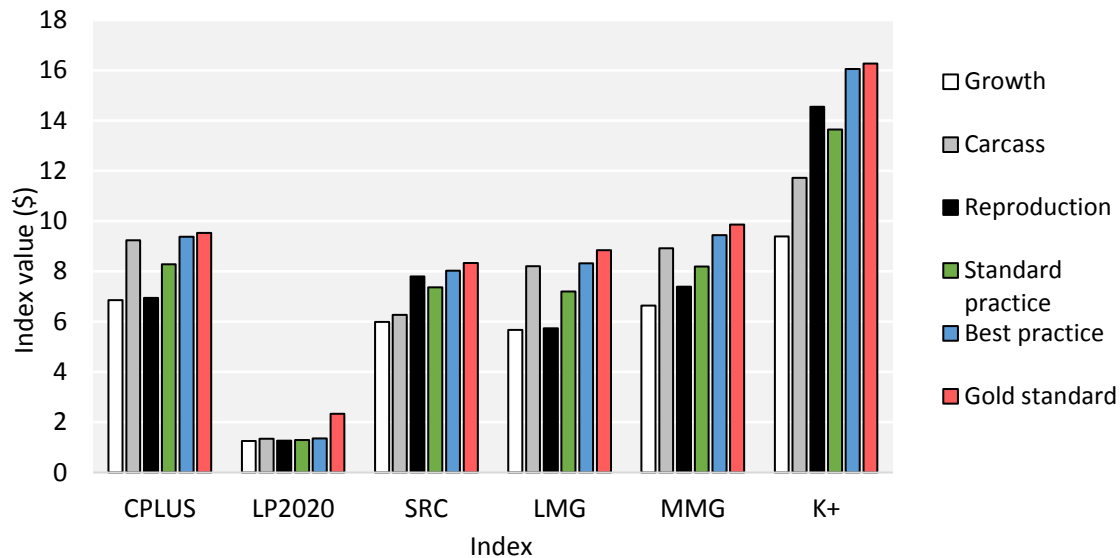
Results from the index calculations were summarised in five parts. Which included the index dollar value, selection emphasis, 10 year gain for each trait, selection differential, and sensitivity analysis of economic values. The selection differential was a function of index weights and EBVs for recent sires (used after the year 2000) compared to recent sires in the top 10%, determined by the index calculation. A sensitivity analysis of economic values adjusted by up to 50%, was used to determine the response for the K+ index.

## 8.4 Results

### 8.4.1 Index \$ Value

The index dollar value is the \$AUD of additional income per doe joined, per generation, with 5% of males selected and 50% of females, and using the index for the Australian market (Figure 8-1). The CPLUS index had an index dollar value of between \$6.86 and \$9.53 across recording scenarios, and was similar to the LMG, which was between \$5.67 and \$8.84. Both indexes had an increasing value under the following recording scenarios; Growth, Reproduction, Standard practice, Carcase, Best practice, and Gold standard. The maternal index SRC had index dollar values of between \$5.99 and \$8.33. In comparison, MMG had a value of between \$6.64 and \$9.86 and K+ had the highest values of between \$9.39 and \$16.27. Indexes SRC, MMG and K+ increased for the recording scenarios from Growth, Carcase, Standard practice, Reproduction, Best practice to Gold standard.

LP2020 had the lowest index dollar values of \$2.34 for the recording scenario Gold standard and between \$1.25 and \$1.35 for the remaining recording scenarios.



**Figure 8-1: Summary of index values (\$ / doe joined / generation) for each index type and under Growth (white), Carcass (grey), Reproduction (black), Standard practice (green), Best practice (blue) and Gold standard (red) recording scenarios.**

#### 8.4.2 Predicted trait change

For each index and recording scenario, the change in each trait was calculated for a ten year response (Table 8-4). 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

*Genetic improvement of Australian Meat goats*

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 8-4: 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
<i>Growth recording scenario</i>								
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
<i>Carcase recording scenario</i>								
CPLUS	1.01	0.89	0.26	-0.07	0.09	0.01	0.02	0.03
LP2020	0.92	0.50	0.11	-0.02	-0.25	0.01	0.03	0.02
SRC	1.23	0.71	0.03	-0.04	-0.13	0.01	0.03	0.03
LMG	0.90	0.86	0.31	-0.07	0.07	0.01	0.02	0.03
MMG	0.97	0.84	0.27	-0.07	0.03	0.01	0.02	0.03
K+	1.06	0.92	0.20	-0.07	0.07	0.02	0.02	0.04
<i>Reproduction recording scenario</i>								
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
<i>Standard practice recording scenario</i>								
CPLUS	1.14	0.77	0.10	-0.06	0.03	0.01	0.02	0.03
LP2020	0.99	0.41	0.02	-0.02	-0.27	0.01	0.03	0.02
SRC	0.99	0.49	0.03	-0.02	-0.11	0.05	0.06	0.08
LMG	1.06	0.74	0.14	-0.06	0.00	0.01	0.02	0.03
MMG	1.08	0.66	0.10	-0.05	-0.04	0.02	0.04	0.04
K+	0.93	0.55	0.03	-0.04	0.00	0.04	0.05	0.07
<i>Best practice recording scenario</i>								
CPLUS	1.02	0.88	0.26	-0.08	0.10	0.01	0.02	0.03
LP2020	0.93	0.49	0.12	-0.02	-0.24	0.01	0.03	0.02
SRC	1.00	0.51	0.04	-0.02	-0.37	0.05	0.06	0.07
LMG	0.91	0.85	0.31	-0.07	0.08	0.01	0.02	0.03
MMG	0.94	0.77	0.26	-0.06	0.04	0.03	0.04	0.05
K+	0.82	0.60	0.16	-0.04	0.05	0.05	0.06	0.09
<i>Gold standard recording scenario</i>								
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

#### *8.4.3 Index economic selection emphasis*

The Growth recording scenario placed the majority of selection pressure on body weight for all of the indexes (Table 8-5). The sheep maternal index SRC, was the only index to place an economic value on maternal weaning weight, and was the only index to place selection emphasis on the trait, for any of the recording scenarios. The CPLUS, LP2020, and SRC indexes place 29%, 12%, and 6% on EMD, and between 0 to 2% on FAT, which is similar to the new KIDPLAN indexes. With the large economic values on WEC for LP2020, correlated traits were used to place emphasis on WEC, even when the trait was not recorded. Similarly, there was emphasis placed on the reproductive traits of NKB, NKW for MMG, and KSV for K+, without records being submitted. There was emphasis placed on traits with large economic values, but without data being submitted for them the response to this selection pressure was very low.

The Reproductive recording scenario was the most similar to current recording practices. As CPLUS, LP2020, and LMG did not have any reproductive traits with economic values, there was no difference between the emphases placed on traits with the Growth or Reproductive recording scenarios. Importantly, MMG greatly reduces the emphasis placed on the growth traits and adds it to NKW (24%), and a small amount on NKB (6%). This was similar to the SRC index which moved a large amount of the selection emphasis to NKW (68%). The K+ index was similar but removes more emphasis from the growth traits and placed it on KSV (58%), NKW (14%), and NKB (4%). Due to the extra emphasis and the reproductive traits recorded, the response to these traits was substantially improved.



The Gold standard recording scenario, was the best practice recording for all traits, including WEC. There were some important differences for the CPLUS and LP2020 but not the new KIDPLAN or SRC indexes. The CPLUS index placed more emphasis on EMD (46%) by removing emphasis from body weight (49%). With the addition of recording for WEC, LP2020 placed the majority of selection emphasis on WEC (79%). The small differences observed between the recording scenarios for the new KIDPLAN indexes was due to removing emphasis from body weight to EMD.

**Table 8-5: 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+
<i>Growth recording scenario</i>						
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%
<i>Reproduction recording scenario</i>						
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%
<i>Gold standard recording scenario</i>						
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%

#### *8.4.4 Selection differential*

The index means were calculated for each recently used sire (after the year 2000) and compared to the top 10% of the sires in that group (Table 8-6). The index means ranged between 98.24 (LP2020) and 100.86 (CPLUS). There was more variation for LP2020 with a standard deviation of 7.84 compared to a range of 1.89 and 2.89 for the other indexes. The top 10% of sires for each index was superior compared to the population mean, increasing for K+ (3.98), MMG (5.53), LMG (5.65), CPLUS (5.63), SRC (7.12) to LP2020 (10.71).

The mean sire EBV for each trait was calculated and compared to the mean EBV of the top 10% of sires. The top 10% of sires for the CPLUS index had the greatest superiority for body weight, with a mean EBV 2.65 kg heavier than the population mean of 0.47 kg. The top 10% of sires from new KIDPLAN indexes ranged from between 2.06 kg and 2.44 kg greater than the mean EBV. The SRC index was lower with a superiority of 1.01 kg. The top 10% of sires from LP2020 had the lowest superiority with a 0.18 kg difference to the mean EBV. For MWWT the top 10% of sires for CPLUS, LMG, MMG, and K+ were between 0.06 and 0.10 kg heavier than the mean of -0.26 kg. The LP2020 and SRC indexes were lighter at -0.03 kg and -0.02 kg respectively.

**Table 8-6: Trait and index superiority of the top 10% of KIDPLAN sires selected on each index.**

Index	Index Mean	Index SD	Superiority	Body Weight (WWT & PWT)	MWWT	EMD	FAT	WEC	NKB	NKW	KSV
CPLUS	100.86	2.51	5.63	2.65	0.10	0.78	0.20	1.67	0.031	0.032	-0.004
LP2020	98.24	7.84	10.71	0.18	-0.03	0.15	0.15	-12.28	-0.027	-0.036	-0.028
SRC	100.82	3.44	7.12	1.01	-0.02	0.23	-0.02	19.61	0.022	0.029	0.013
LMG	100.17	2.89	5.65	2.06	0.06	0.74	0.25	-7.39	0.015	0.013	-0.011
MMG	100.19	2.82	5.53	2.22	0.09	0.72	0.26	-6.67	0.019	0.018	-0.009
K+	100.31	1.89	3.98	2.44	0.08	0.73	0.24	-4.65	0.027	0.027	0.000
Mean				0.47	-0.26	0.04	0.01	2.12	-0.012	-0.017	-0.007

The mean EBV for the top 10% of sires were all greater than the population means for EMD (0.04 mm) and FAT (0.01 mm). For EMD, the top 10% of sires from CPLUS, LMG, MMG, and K+ indexes were between 0.72 mm and 0.78 mm greater than the population, while LP2020 and SRC were only 0.15 mm and 0.23 mm greater respectively. For FAT, each of index top 10% of sires were between 0.15 mm and 0.26 mm greater than the population mean, except for SRC which was the only index to have a lower superiority (-0.02 mm).

The population mean EBV for WEC was 2.12%, compared to the mean EBV of the top 10% of sires of CPLUS and SRC which had an unfavourable differences relative to the population of 1.67% and 19.61% respectively. The new KIDPLAN indexes were favourable for the selection of WEC and ranged between -4.65% and -7.39%. The LP2020 has the largest difference relative to the mean at -12.28%.

For the reproductive traits, the recent sires had a mean EBV of -0.012 for NKB, -0.017 for NKW, and -0.007 for KSV. There was no difference between CPLUS and K+ with the top 10% of sires having mean EBVs for NKB (0.031 and 0.027 respectively), and NKW (0.032 and 0.027 respectively) greater than the population. Importantly the top 10% of sires for the K+ index had no difference in mean EBV compared to the population mean of -0.007 and for CPLUS it was -0.004 less than the population mean. Both LMG and MMG had smaller differences of between 0.013 to 0.019 kids for NKB and NKW, and -0.009 to -0.011 for KSV. The top 10% of sires from the LP2020 index had lower EBVs compared the population mean for NKB (-0.027), NKW (-0.036), and KSV (-0.028). The SRC index had the greatest superiority for NKB (0.022), NKW (0.029), and KSV (0.013).

#### 8.4.5 *Sensitivity analysis of economic values*

The results from the sensitivity analysis of economic values showed that the response was relatively insensitive to the specific economic value. This has been demonstrated for the additional traits included in the K+ index that are not in the CPLUS index (including; NKB, NKW, KSV, and WEC). For each of these selected traits and economic value changes, the change to the index value, the 10 year change to all traits, selection emphasis for the selected trait and superiority of EBVs for the selected trait were described. The Gold standard recording scenario was used for this analysis.

For number of kids born, the economic value calculated from SheepObject2 and used for the index analysis was \$11.00 (Chapter 7). This was adjusted down to \$5.50 and up to \$16.50 (Table 8-7). This 50% change to the economic value changed the index value from \$16.28, to between \$16.06 and \$16.60 (approximately a 2% change). It appears that the \$11.00 value for NKB is the optimum value for the index, as there was no significant differences to the 10 year trait change for each trait except for a decrease in body weight. The selection emphasis changed from 3.8%, to between 1.9% and 5.6%. There was a concern for the top bucks having a lower EBV superiority with an increase to the economic value. This was due to the highly genetically correlated traits KSV and NKW having lower index weights as a result of the economic value change.

The sensitivity analysis for number of kids weaned had similar results to NKB. The original economic value of \$30.00 (Chapter 7) was decreased to \$15.00 and increased to \$45.00 (Table 8-8). This 50% change to the economic value changed the Index value by

between \$0.74 and \$0.87 (approximately a 5% change). There was no significant change to the 10 year trait changes, but with a decrease to the economic value the superiority of bucks also decreased, from 0.027 to 0.022.

There were some changes with the sensitivity analysis of the economic value for kid survival (Table 8-9). The original economic value of \$87.00 (Chapter 7) was adjusted by 10%, 25%, and 50%, this tested economic values of between \$43.50 and \$130.50. There were some significant differences compared to the original index value of \$16.28, which had an average change of \$0.77 for 10%, \$1.91 for 25%, and \$3.78 for 50%. There were small differences for bodyweight, MWWT, EMD, WEC, NKB (between 0.041 and 0.052), NKW (between 0.050 and 0.058), and importantly for KSV (between 0.076 and 0.094). This was caused by the large change to the selection emphasis for KSV which was originally 54%, but changed to between 32 and 67%. The reduction of the selection emphasis to 32% reduced the EBV superiority of top bucks for KSV to -0.006, but increased it to 0.009 for the increase to selection emphasis.

Worm egg count had the lowest economic value of -\$1.71 (Chapter 7). The sensitivity analysis changed it by up to \$0.85 (Table 8-10). There was no significant change to the index value (less than 1% change from \$16.28) or any of the 10 year trait changes except for WEC. The original trait change for WEC was -0.11% which changed to between -0.05 and -0.18, but still did not compare to LP2020, originally -0.95%. Selection emphasis changed from 1.4%, to between 0.3% and 3.2%. The EBV superiority of the top bucks was originally -4.65, but ranged between -0.24 and -7.48 for the sensitivity analysis. This was the largest change for the WEC sensitivity analysis.

**Table 8-7: Sensitivity analysis of economic values for number of kids born**

NKB economic value		Index value	Trait change							NKB selection emphasis	NKB top bull EBV superiority	
% Change	\$ value		Body weight	MWWT	EMD	FAT	WEC	NKB	NKW			KSV
-50%	\$5.50	\$16.06	0.79	0.63	0.18	-0.05	0.15	0.048	0.053	0.088	1.9%	0.023
-25%	\$8.25	\$16.19	0.78	0.63	0.18	-0.05	0.14	0.049	0.054	0.089	2.8%	0.023
0%	\$11.00	\$16.28	0.84	0.61	0.16	-0.04	-0.11	0.049	0.056	0.088	3.8%	0.027
25%	\$13.75	\$16.46	0.78	0.62	0.18	-0.05	0.14	0.049	0.054	0.089	4.7%	0.023
50%	\$16.50	\$16.60	0.78	0.62	0.18	-0.05	0.14	0.050	0.054	0.090	5.6%	0.023

**Table 8-8: Sensitivity analysis of economic values for number of kids weaned**

NKW economic value		Index value	Trait change							NKW selection emphasis	NKW top bull EBV superiority	
% Change	\$ value		Body weight	MWWT	EMD	FAT	WEC	NKB	NKW			KSV
-50%	\$15.00	\$15.54	0.79	0.65	0.19	-0.05	0.16	0.047	0.051	0.088	5.7%	0.022
-25%	\$22.50	\$15.93	0.79	0.64	0.19	-0.05	0.15	0.048	0.053	0.088	8.5%	0.023
0%	\$30.00	\$16.28	0.84	0.61	0.16	-0.04	-0.11	0.049	0.056	0.088	11.8%	0.027
25%	\$37.50	\$16.74	0.78	0.61	0.17	-0.05	0.14	0.050	0.055	0.090	14.0%	0.027
50%	\$45.00	\$17.15	0.77	0.60	0.17	-0.04	0.13	0.051	0.056	0.090	16.6%	0.027

**Table 8-9: Sensitivity analysis of economic values for kid survival**

KSV economic value		Index value	Body weight	Trait change							KSV selection emphasis	KSV top bull EBV superiority
% Change	\$ value			MWWT	EMD	FAT	WEC	NKB	NKW	KSV		
-50%	\$43.50	\$12.68	0.91	0.70	0.21	-0.05	-0.17	0.041	0.050	0.076	32%	-0.006
-25%	\$65.25	\$14.41	0.87	0.65	0.18	-0.04	-0.14	0.046	0.053	0.083	44%	-0.003
-10%	\$78.30	\$15.52	0.85	0.63	0.17	-0.04	-0.12	0.047	0.055	0.086	54%	-0.002
0%	\$87.00	\$16.28	0.84	0.61	0.16	-0.04	-0.11	0.049	0.056	0.088	54%	0.000
10%	\$95.70	\$17.05	0.82	0.60	0.16	-0.04	-0.1	0.049	0.056	0.089	57%	0.000
25%	\$108.75	\$18.22	0.80	0.58	0.15	-0.04	-0.09	0.051	0.057	0.091	61%	0.007
50%	\$130.50	\$20.24	0.78	0.55	0.13	-0.03	-0.08	0.052	0.058	0.094	67%	0.009

**Table 8-10: Sensitivity analysis of economic values for worm egg count**

WEC economic value		Index value	Body weight	Trait change							WEC selection emphasis	WEC top bull EBV superiority
% Change	\$ value			MWWT	EMD	FAT	WEC	NKB	NKW	KSV		
-50%	-\$0.86	\$16.21	0.83	0.62	0.17	-0.04	-0.05	0.049	0.055	0.089	0.3%	-0.24
-25%	-\$1.28	\$16.23	0.83	0.62	0.17	-0.04	-0.08	0.049	0.055	0.088	0.7%	-2.11
0%	-\$1.71	\$16.28	0.84	0.61	0.16	-0.04	-0.11	0.049	0.056	0.088	1.4%	-4.65
25%	-\$2.14	\$16.33	0.84	0.61	0.16	-0.04	-0.15	0.048	0.056	0.087	2.2%	-5.96
50%	-\$2.57	\$16.40	0.84	0.61	0.16	-0.04	-0.18	0.048	0.055	0.087	3.2%	-7.48



## 8.5 Discussion

From the results of this chapter and previous chapters in this thesis, it is recommended that the current carcass focused (CPLUS) index be replaced with the balanced (K+) index. The main reasons for this were it uses updated goat parameter estimates and goat economic values, and better describes the breeding objective. Each of the new KIDPLAN indexes demonstrated the importance of updating the parameter estimates and economic values with a better described breeding objective. This resulted in larger index dollar values, and increased reproductive performance and growth traits.

Economically, the LMG index was similar to CPLUS which had slightly greater index dollar values. There were two reasons for CPLUS having a larger index dollar value; a larger economic value for PWT (\$3.50 compared to \$2.53), and no value for WEC. From the results of the surveys and economic values (Chapter 7), the values used for PWT with CPLUS were overestimated. Producers did not consider EMD or FAT to be of high importance, or didn't consistently record the traits (Chapter 7). What the LMG demonstrated, is that a KIDPLAN index that included commonly recorded growth traits with industry relevant economic values, will have a similar but more realistic outcome than CPLUS.

The importance of including reproductive traits was identified from the results of a sensitivity analysis in the literature review (Chapter 2, Table 2-7), and was illustrated by MMG. The sensitivity analysis of the literature review calculated a change in one genetic standard deviation for fecundity, survival, and weaning weight would increase lean meat production by 35%, 30%, and 13% respectively. With the addition of economic values

on number of kids born (\$11.00) and number of kids weaned (\$30.00), MMG had larger index dollar values compared to both CPLUS and LMG (Chapter 7). Having additional goats for sale was more profitable than larger goats, and as such, a small increase in reproduction had a larger increase on profits. Further work is still required on the dam traits of NKB and NKW. Previously the parameter estimates were calculated from sheep and did not include economic values for reproductive traits. The KIDPLAN indexes used parameter estimates calculated from the KIDPLAN database and previous literature, and the economic values calculated from the industry surveys (Chapters 2, 4, 5 and 7). It was also important to note that KSV was treated as a binary trait for the parameter estimates (Chapters 4 and 5), but the indexes analysis assumed the phenotypes to be continuous and that all animals are available for selection. In practice this is not the case as all animals that are selected must be living. This means that the gains in KSV, NKB and NKW could be overestimated and should be further investigated.

There are a number of reasons why the index K+ should replace the current CPLUS for KIDPLAN users. Most importantly, it better described profit for the breeding objective of Australian meat goat producers. This was illustrated by the higher index dollar values for all recording scenarios. This was primarily due to the inclusion of KSV, which was a result hypothesised by the previous literature review sensitivity analysis (Chapter 2) and the high economic value calculated with SheepObject2 (Chapter 7). Even under the Growth and Carcase recording scenarios, K+ was similar to CPLUS due to the high economic value placed on body weight and the positive genetic correlations those traits have between each other and KSV (Chapter 5). The higher heritability and variation of survival compared to sheep was another reason why KSV is a suitable trait to be included in a KIDPLAN index (Chapter 4). The fact that producers must submit the required birth

type and rearing types for the KSV calculation improves the accuracy of estimates (Chapter 3, Chapters 4 and 5). Producers need to have further education on the importance of accurate pedigree and birth type recording. If that is accomplished and more accurate estimates of separate survival traits for different birth types are calculated, K+ should be re-evaluated with the additional KSV traits (Chapter 6).

If more producers record EMD and FAT, or a premium is offered instead of all sales based on hot carcass weight, then the parameters should be updated again and economic values for goats recalculated, instead of using the current sheep values. There are currently not enough producers consistently recording post-weaning or yearling EMD and FAT (Chapters 3 and 7). As goats are smaller than sheep and very lean, there is not much variation in EMD and in particular FAT, which limits their response to selection and the ability to estimate the genetic correlations (Chapters 4 and 5). There is some concern that the new KIDPLAN indexes cause a negative change to EMD but that can be avoided if carcass traits are recorded. The change in EMD is at the given carcass weight, so if the carcass weight also increases, this change should not be an issue.

An index like LP2020 is not useful until more producers record WEC. Only three sites are currently recording WEC, with a total of 267 records. There was not enough data to include the trait in a genetic evaluation (Chapter 3). The inability to estimate any genetic parameter estimates for this trait was previously demonstrated (Chapter 4), so sheep estimates were used from CPLUS. From the producer responses it was concluded that internal parasites remain an issue which they want to include in their breeding objective (Chapter 7). It was possible to include WEC in a breeding objective, but there will be

little to no response until producers record the trait. With the current sheep parameter estimates and economic values, all of the indexes have a change to WEC in the desired direction, or have no change. There was not a significant difference to the WEC trait change, comparing LP2020 to the new KIDPLAN indexes, even under the Gold standard recording scenario.

Currently, the Reproductive recording scenario was most representative of the data submitted to KIDPLAN. The majority of producers are recording growth traits and the required birth and rearing type traits (Chapters 3 and 7). Improving the submitted data and the recorded traits is necessary so that less data cleaning is required, and the index can include a value for EMD and WEC (Chapter 4). The Standard practice recording should be the first goal, where producers are recording each of the Growth, Carcase, and Reproduction traits. Producers should be educated on the benefits of better recording practices so that the Best practice scenario can be achieved. The Gold standard recording scenario which includes WEC should be the long term goal for goat breeders. If the producers submitting data to KIDPLAN begin meeting these requirements, then the genetic parameters from the univariate and bivariate analyses, industry surveys, and economic values should be re-analysed.

There were large differences comparing Growth, Reproductive, and Gold standard recording scenarios with differences in trait changes and selection emphasis. 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.

The differences in index means and superiority between indexes can be explained by the differences in variation. It was encouraging that the top 10% of sires had desirable differences across traits for the majority of indexes. The three new KIDPLAN indexes had no significant differences in selection differentials or in sires selected. It was expected that the K+ index would have a greater variation index values, as it had a larger economic value, which was not the result observed. It can be explained by the large economic values placed on NKB, NKW, and KSV which best describes the breeding objective.

The MMG and K+ indexes showed that by adding economic values for reproductive traits, the index dollar value changes significantly. The reason for conducting the sensitively analyses was to determine how sensitive the indexes are to changes in the economic values. Including parameter estimates and economic values, had a greater change to the index, than the response to changes in economic values. This was demonstrated by the changes to economic values for NKB and NKW, and the differences in 10 year trait changes and EBV superiority, as a result of high genetic correlations. Compared to the change in economic values, the change in index value was comparatively small. The change on the economic value for kid survival was extreme at \$43.50 but the

change to the index value and trait changes were relatively small. The K+ index was not only more balanced, but also fairly insensitive to the specific economic values. Finally the results from the Self-replacing Carcase index (SRC) were similar to those for MMG and K+. This indicates that KIDPLAN should have been using a maternal index instead of CPLUS all along. However without breeders recording reproductive traits accurately when KIDPLAN was first adopted it may not have had a significant impact using a maternal index, but it may have encouraged breeders to improve their recording practices in which case it would have been very useful.

## 8.6 Conclusion

Goats are different to sheep and there are some important genetic differences that have been investigated. The main differences included; higher heritabilities for kid survival which were positively genetically correlated to birth weight, greater variation in number of kids born and weaned, less variation for eye muscle and fat depth, and genetic correlations between production traits were significantly different from sheep. The differences in genetic and phenotypic parameters, recording practices, economic values, and breeding objectives of goat breeders led to the creation of new Australian meat goat indexes for KIDPLAN users. It is recommended that the K+ index be adopted by KIDPLAN users. This places selection pressure on growth and reproductive traits, including the kid survival trait calculated from existing birth and rearing type data. The K+ index is based on the best defined breeding objective. Future testing of the index is recommended to compare the theoretical response to the real world and to demonstrate to producers that it is better than the current CPLUS index. Producers are also strongly recommended to record key traits for WEC and carcase traits.

## 9 General discussion: Genetic improvement of Australian meat goats



## 9.1 Introduction

The best tool for the genetic improvement of goats in Australia is KIDPLAN, it is the only tool to provide a benchmark for breeders and EBVs for a range of production traits (BCS Agribusiness 2012; Sheep Genetics 2016). As the industry develops it is important that KIDPLAN is in a position to respond to the growing demands of the industry to help make greater gains. This project was a good starting point to achieve that. From discussion with breeders and the sensitivity analysis in the literature review, the importance of various traits on lean meat production were determined (Table 2-7). The results suggested the largest potential improvement could be made with reproductive traits. 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 overall number of kids weaned.

## 9.2 Key findings

The most important result from the thesis was that a kid survival trait treated as a trait of the kid (KSV) can be calculated using KIDPLAN data. When adjusted for birth type, it was heritable ( $0.09 \pm 0.02$ ), and had significant phenotypic variation ( $\sigma_p^2 = 0.15 \pm 0.01$ , Table 4-4 and 5-2). Fitting birth weight did not significantly change the results for the univariate, and bivariate models would not converge with birth weight fitted as a covariate. When kid survival was treated as a trait of the doe (RT/BT), the heritability was low and not different to zero ( $0.02 \pm 0.02$ ). This difference demonstrates the individual additive genetic variation in kid survival rather than the maternal effect. The heritability estimate for KSV was similar to previous estimates by Singh *et al.* (1990) which treated kid survival as a trait of the doe (0.06 to 0.10). Both estimates for KSV and RT/BT were within the range of previous estimates for lamb survival as a trait of the ewe,



between 0.00 and 0.12 (Fogarty *et al.* 1994; Rosati *et al.* 2002; Afolayan *et al.* 2008a; Bunter and Brown 2013; Newton *et al.* 2014). The higher heritability for KSV, the high correlation of EBVs between KSV and RT/BT (0.90, Figure 4-1), the variation in KSV, and similar estimates to previous literature, meant it was decided it is most appropriate for kid survival to continue to be analysed as a trait of the kid.

A novel result was from a multivariate analysis of three KSV traits based on birth type (single, twin, multiple). The genetic correlations between birth types ranged from  $0.46 \pm 0.34$  to  $0.72 \pm 0.45$  (Table 6-1). This was similar to previous genetic correlations for lamb survival traits based on birth type (-0.08 and 0.60) (Kelly *et al.* 2016). Given the data limitations, improved model fit with the original trait, and relatively high genetic correlations, it was concluded the most sensible method to analyse kid survival is as a single trait with litter size fitted as a fixed effect.

Kid survival is an economically important trait as evidenced by the calculated economic values per genetic standard deviation being \$9.79 for kid survival compared to \$0.33 for number of kids born, \$3.00 for number of kids weaned and \$3.94 for body weight (Table 7-11). This was the first time an index for Australian meat goats has been developed using parameter estimates and economic values of goats not sheep. The Lean Meat Goat index more accurately addresses the breeding objectives than the current Carcase Plus index (Table 8-2). The only difference between the Maternal Meat Goat and Kid Plus (K+) index, was that K+ included an economic value for KSV. This one difference resulted in a greater 10 year trait change for the reproductive traits; number of kids born (3% to 5%), number of kids weaned (4% to 6%) and kid survival (5% to 9%) (Table 8-4). Selecting

for number of kids born and number of kids weaned will improve the reproductive traits, but it is important to include kid survival. This supported reasoning by Bunter and Brown (2013) who reported that component traits such as fertility, litter size (fecundity) and lamb survival might be more accurate for genetic evaluation than for number of lambs born or weaned. It also supported a report by Bunter *et al.* (2017) who suggest it is possible to select for higher litter sizes and lower lamb losses at the same time.

## 9.3 Future genetic research for Australian meat goats

### 9.3.1 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 (Chapter 5) and the multivariate analysis of kid survival (Chapter 6) 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. Ideally future research on kid survival would include genomics as it would provide better pedigree information and more accurately describe the additive relationship between animals, increasing the accuracy of EBVs, and potentially the heritability as a trait of the kid is likely to be even higher than currently estimated.

Future research on kid survival should continue to treat kid survival as trait of the kid rather than the doe for several reasons. In sheep the main issue has been focused on mismothering but in goats there is a need to improve the animals own ability to survive (Luff 1980; Snyman 2010; Brown *et al.* 2014). While in sheep the focus has also been to

increase the number of lambs born, the goat industry needs to address keeping the larger number of kids born alive.

There is a large gap in the goat literature compared to sheep. 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 (Brien *et al.* 2010; Plush *et al.* 2011; Brien *et al.* 2014; Brown *et al.* 2014; Young *et al.* 2014; Brien *et al.* 2015; Li and Brown 2016).

A correlated trait for kid survival needs to be easily measured in the paddock, as it has already been demonstrated that data accuracy in KIDPLAN is an issue. In sheep, rectal temperature is moderately correlated to number of lambs weaned (0.56) but lowly heritable (0.10) (Brien *et al.* 2010). Breeders could be apprehensive about measuring rectal temperature, as it is invasive it could raise animal health and welfare concerns. Time to bleating has a lower and negative genetic correlation (between -0.25 and -0.43) and similar heritability (between 0.04 and 0.11) (Brien *et al.* 2014; Brien *et al.* 2015). Time to bleating is also easier to record and can be incorporated into current practices. Lamb vigour and maternal behaviour score have higher heritabilities (between 0.11 and 0.16 for lamb vigour and between 0.09 and 0.35 for maternal behaviour) but lower genetic correlations with survival (-0.25 for lamb vigour and between -0.09 and -0.29 for maternal behaviour) (Plush *et al.* 2011; Brien *et al.* 2014; Brien *et al.* 2015; Brown *et al.* 2016c). They are also subjective measures that can be difficult to incorporate into current on-farm practices. Time to bleating would be the preferred trait to be investigated as a potential

correlated trait for kid survival, because it is non-invasive and has been demonstrated to be a useful correlated trait in sheep.

Another result that should be further explored is treating traits separately based on a factor, such as birth type. The genotype x environment interaction tested for kid survival, with different birth types treated as different environments, were shown to be different traits (Table 6-1). This supported the earlier work of Kelly *et al.* (2016) in lambs. What was surprising, was that weaning weight and post-weaning weight also appeared to be different traits depending on birth type as a G x E interaction (Table 6-2). This result should not only be further explored for goats but also in sheep.

Another option would be to combine two of the three kid survival traits in a similar way to the combine traits EMD and FAT. Some additional modelling using selection index theory was done to test this. Using the mean survival rates, proportion of progeny of each birth type, and the parameter estimates from the genetic analysis of kid survival (Chapters 3, 6 and 8), the economic response to selection was estimated. 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. This result should be further explored in the future. The issue is that implementing the results in a selection index is currently too difficult for several reasons, there is only information on one trait for each animal as an animal can only be a single, twin or multiple, residual co-variances with other production traits are not currently estimable and the low confidence caused by the high standard errors for genetic correlations. Using the original survival trait would mean there are fewer EBV's to report

to breeders and using the component trait of KSV is still better than selecting just for number of kids weaned (Chapter 8).

Other traits (including litter size, number of kids weaned, and fertility rate) and other factors (such as dam age) could be investigated. Unfortunately the current data in KIDPLAN is not sufficient for such an analysis. Doe age is a potential factor already recorded in KIDPLAN, it has previously been shown in sheep to have different genetic expressions for number of lambs born and weaned for yearlings, hoggets and adults. For both number of kids born and weaned, genetic correlations of 0.64 to 0.72 between yearling and hoggets, and 0.68 to 0.70 between hoggets and adults have been reported, with higher heritabilities for younger animals (Bunter and Brown 2013; Newton *et al.* 2014). In KIDPLAN there are only 29 animals with a yearling dam but it could still be useful to investigate the difference between hoggets, adults and older does.

The multivariate analysis of kid survival as separate traits and the higher survival rate of twins compared to singles and multiples has led to the development of another question. That is, is it possible to select for more twin litters without increasing the incidence of multiples? This would be a trait for the proportion of dams that have twins and treated as a trait of the dam. It could be achieved with a binary trait where twins are assigned 1, and 0 for singles or multiples, and treated as a repeated measure with one record per litter. 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  $0.44 \pm 0.50$  (SD). The phenotypic variance was  $0.24 \pm 0.01$ , the heritability was  $0.03 \pm 0.02$ , maternal permanent environmental variance

was  $0.01 \pm 0.02$ , and service sire variance of  $0.04 \pm 0.01$ . This suggests that selecting for twins without increasing the number of triplets is theoretically possible but progress would be very slow and the result indicates little encouragement biologically as it is likely driven by ovulation rate and it could be naïve to expect a clear biological optimum.

Fertility, fecundity and survival rates have been identified as key traits with the greatest potential to increase lean meat yield (Chapter 2 and 7). However, the project predominantly focused on kid survival with the justification that there is an under reporting of dry does in KIDPLAN (502 does). This is essential information for the analysis of fertility and fecundity which require number of does joined for their calculation. It was also raised that goats have a high fertility (mean of 0.82 and  $\sigma_p^2 = 0.41$ ) and fecundity rate (mean of 1.67 and  $\sigma_p^2 = 0.59$ ) and there is potential for selection with heritabilities of 0.05 (sheep estimate) and 0.22 respectively (Fogarty *et al.* 1994; Odubote 1996; Walkden-Brown and Bocquier 2000; Rosati *et al.* 2002; Matika *et al.* 2003; Hanford *et al.* 2005; Hanford *et al.* 2006; Safari *et al.* 2007; Afolayan *et al.* 2008a; Zhang *et al.* 2009a; Mellado *et al.* 2011). Increasing the number of kids born without increasing kid survival is an animal welfare issue (Table 2-7). With the new kid survival trait, this issue is addressed, which means fertility and fecundity should be further investigated if breeders report dry does.

### 9.3.2 *Production trait research*

This was the first time genetic correlations between a kid survival trait and other production traits have been reported. There are no antagonisms between KSV and production traits as they were either negligible or favourably genetically correlated (between  $-0.06 \pm 0.03$  and

0.19 ± 0.19, Table 5-2). The positive genetic relationship between birth weight (BWT) and KSV (0.19 ± 0.19) has also been observed in sheep with a phenotypic curvilinear correlation of 0.34 (Rosati *et al.* 2002). Selecting for a larger BWT could potentially increase neonatal survival in goats. The bivariate analysis was limited by the number of records for the scanned carcass traits, with large standard errors and higher than expected negative genetic correlations (Brown and Swan 2016b; Table 5-2). If more data becomes available for the scanned carcass traits then they should be re-analysed to update the genetic parameters in KIDPLAN. There is also still a gap in the literature on carcass traits which have been partially covered for scanned traits but a large gap remains for eating quality traits. The largest issues that need to be addressed for the carcass 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 carcass traits are not consistently recorded.

Breeders should continue or begin recording ultrasound EMD and FAT traits to enable genetic selection towards greater meat yields. This suggestion is made based on the results from all of the indexes having an undesirable decrease in eye muscle area (-0.08 mm to -0.17 mm over 10 years) when EMD is not recorded and body weight fitted as a covariate (Table 8-4). From a production aspect breeders should first focus on improving recording practices of dam identification, birth and rearing type information first. Breeders should also begin collecting data on carcass weight where possible, as a key production trait. Unfortunately, currently there is limited justification for breeders to record carcass quality traits until other recording practices are improved.

Finally genomic testing has potential to address these gaps. Genomic testing has two major potential uses for rangeland and Boer goats. The first potential use is for the genomic selection of rangeland animals. It is not currently logistically possible to collect phenotypic records of production traits on rangeland animals. Genomic prediction could potentially be used to select animals in rangeland systems similar to the use of genomic selection for reproductive traits in tropical beef cattle or identifying phenotypic variation in wild sheep populations (Johnston *et al.* 2011; Zhang *et al.* 2014). This has broader implications as it could be a fundamental change to the current harvesting practices and could limit the use of Boer bucks for improvement. This could be achieved by genotyping rangeland goats removing the need for pedigree information, tagging females to collect longevity data and making selections within the wild population. Logistically the most suitable animals to be recorded to develop genomic prediction would be a nucleus herd that includes, Boer, rangeland and crossed animals. Maintaining these herds in a commercial system with improved fencing would be easiest. This would also have the added benefit of providing starting the process of linking between rangeland systems and intensive breeding systems.

Implementation within rangeland systems would be easiest at mustering when young does could have a hair follicle sample taken. The two greatest limitations would then be the majority of selection is placed on females, determining which animals to sample and the cost. This could be mitigated as the cost of genomic prediction continues to decrease and male selection could be improved by the release of Boer bucks. This would be most useful for growth traits as rangeland harvesters don't record live weights except at point of sale, and reproductive traits which is currently limited to an estimate of number of does on the property (Tables 7-1 and 7-7). Both reproductive and growth traits would rely on the



previously mentioned nucleus herds. The other potential use for genomics, is for lean meat yield and eating quality traits which are difficult to measure and could be implemented in both intensive (Boer) and extensive (Rangeland) systems with (Fogarty *et al.* 2007; Daetwyler *et al.* 2010; Warner *et al.* 2010). These traits have the added benefit that recording can be made at point of slaughter on all animals. There are issues that this potential research would face; limitations in accuracy caused by the number of phenotyped animals, rangeland systems are used because of their low input and low costs which would require a cost benefit analysis and finally the gap in literature for genomic testing of Australian meat goats.

### 9.3.3 *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.

The first step in identifying what traits could be genetically improved with a selection index was with a sensitivity analysis of the literature. There was a weakness in the sensitivity analysis, which was that parameter estimates for fertility, dressing percentage, survival and lean meat production utilised sheep literature (Fogarty *et al.* 1994; Moreno *et al.* 2001; Rosati *et al.* 2002; Fogarty *et al.* 2003; Matika *et al.* 2003; Safari *et al.* 2005; Ingham *et al.* 2007; Safari *et al.* 2007; Afolayan *et al.* 2008a; Fogarty *et al.* 2009; Mortimer *et al.* 2010; Bunter and Brown 2013; Newton *et al.* 2014). This further demonstrated the gap in goat literature on reproductive and carcass traits. Furthermore, multiplying these components is over simplistic and would have been better if selection index theory was used instead. Selection index theory would also account for genetic and phenotypic covariances between traits, however this information was not available in the published literature. This is important as “The simultaneous equations can be solved only if estimates of the various correlations can be calculated.” (Hazel 1943). The work in the project demonstrated that not including NKB, NKW and KSV in the breeding objective results in limited genetic progress of goats, and there is still room for more improvement by investigating these other traits when data becomes available.

## 9.4 Extension of genetic evaluation in the meat goat industry

### 9.4.1 Engage with seedstock breeders

The results from this thesis will have a direct impact for Australian meat goat breeders. Comments made by breeders about the need for a kid survival trait have been addressed by answering the main hypotheses. It has been shown that kid survival is an economically important trait. The KIDPLAN database can be used to derive a kid survival trait. Finally selecting for kid survival as a component trait of number of kids weaned is useful to

breeding programs. This will lead to goats produced by seedstock breeders having higher survival rates, increased profitability and new marketing opportunities with commercial and rangeland managers. However, the potential gains made for KSV could be overestimated as the index analysis assumed KSV to be continuous not binary and that all animals are available for selection (including dead animals). Clearly only those animals which have survived are actually available for selection which is why response could have been overestimated. Future work should further test the impact of this assumption to determine the impact on future indexes.

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. Updating of the parameters used in the KIDPLAN analysis and the indexes developed should be adopted. 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). The meat goat industry can also distinguish itself by adopting the K+ index. There is real opportunity to improve the amount and the quality of meat goat production, with index dollar values for animal gains of between \$9.39 and \$16.27 for the new K+ compared to the current \$6.86 to \$9.53 for Carcase Plus. 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.

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. This is for two main reasons; to increase the number of active users and to improve the accuracy of the data submitted. One of the issues is that there is a group of breeders that currently don't meet the KIDPLAN user requirements or they do not understand the value in engaging with KIDPLAN. The main aspects contributing to why producers are not meeting Sheep Genetics quality assurance include herd size, identity records, ear tagging, and managing mating (Sheep Genetics 2017b). These groups should be engaged with and supported to improve management practices so that they meet the requirements and can benefit from KIDPLAN. The development and promotion of KIDPLAN would represent a large step to breaking those boundaries.

The results from this thesis are directly applicable to Australian meat goat breeders but it is significant for other meat goat industries globally and for other production systems domestically. Boer goats are the predominant meat breed internationally and these results could improve kid survival in other countries. The Australian Angora goat industry is focused on fibre production and use MERINOSELECT, which means they are using sheep parameter estimates. It is possible that by using a Merino index they are placing too much emphasis on fibre and not enough on reproductive traits such as kid survival. The dairy goat industry does not use a national performance recording scheme but instead use their own analysis and private consultants. There is an opportunity that with the improvements to KIDPLAN for meat goats that dairy breeders could be encouraged to join a national performance recording scheme. Having breeders help develop a breeding objective and index specific for Australian dairy goats could avoid issues the Australian meat goat breeders have faced using Carcase Plus.

#### 9.4.2 *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.

One of the motivations for the project was the anecdotal evidence of Boer bucks being released in the rangeland during the early 1990's, then not competing with the rangeland bucks or the progeny having lower survival rates. Before breeders can market to the

rangeland they need to address their own survival issues related to kid survival. 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.

Control of bucks could be achieved with traditional methods including shooting and mustering. With advances in technology since the 1990's methods to control rangeland bucks such as tracking with GPS equipped "Judas" goats, and automated drafting systems at water points that utilise imaging software should also be investigated. It is hypothesised that Boer bucks should be conditioned to the environment before release into the rangeland, this will make a marked difference in their competitiveness and survival compared to the original practice. Identifying the optimum time for release also needs to be investigated. This is likely to be before the mating season begins and should be avoided during drought years to maximise the effectiveness of release. Finally releases should be done collaboratively amongst local rangeland managers, as genetically superior animals will potentially move between properties unless improved fencing for goat management is installed and also to stop Boer bucks from being harvested by other managers. However, with the value of goat meat increasing and the goat meat industry moving from the fringes of livestock production to a key production system, this will likely see a move to more carefully managed systems. This was evidenced by the discussion from producers at the 2017 Goat Industry Council of Australia annual general meeting, and recent articles published Meat and Livestock Australia and Sheep Central (GICA 2017; MLA 2017; Sheep Central 2017). If that scenario is true then genetic improvement will have the

largest benefit for more intensive commercial systems based on rangeland crosses with Boer goats.

#### 9.4.3 *What the industry needs to address*

There will always be errors with data recording and there are some errors that producers cannot address with current technology and production systems. Where possible it is important for producers to limit the errors and have some quality control over the data provided for evaluation. 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. As the cost of pedigree testing and automated software for pedigree matchmaking continues to decrease, this will hopefully become less of an issue (Morris *et al.* 2012; Swan *et al.* 2012), but ideally this would not be an issue as it would be solved with genomic testing. KIDPLAN needs to use a maternal self-replacing index not a terminal sire index, which in hindsight should have been the original choice. Now KIDPLAN should adopt one of the indexes developed as part of this project, ideally that would be Kid Plus. Following those improvements, selection of animals based on the EBVs and indexes from KIDPLAN should be made using the updated parameter estimates. Finally this work is another step to improving the productivity of Australian rangeland goats. This requires engagement and uptake of KIDPLAN by seedstock breeders and commercial producers.

## 9.5 Conclusion

The two key outcomes of this thesis are 1) including reproduction traits in the industry selection program (KIDPLAN), and 2) including kid survival as a trait of the kid as a

selection criteria rather than just using number of kids weaned. As with the majority of datasets, there are issues with the industry recorded KIDPLAN database in that there are some errors due to recording practices and there is currently insufficient data for key traits such as fertility rate, growth traits of animals older than yearlings, scanned carcass traits and health traits for parasite resistance. 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.



# Appendices

## Appendix 7.1 Rangeland survey

### Rangeland \$ index evaluation

1. What is your postcode?\*

2. Please tick the boxes on how do you decide when to harvest?

- Live weight  
 Estimated number of goats  
 Time of year  
 Age  
 Available feed  
 Price  
 Other, please specify

3. If you ticked any of the boxes in QUESTION 2 please specify the value for each box ticked.

#### Insert Number

Live weight [insert live weight in kg]

Estimated numbers of goats [Insert number of goats]

Time of year [insert time in the Month number (1-12) when harvest begins]

Age [insert age in 0.5 years]

Available feed

Price [insert \$/kg dressed weight]

Other [insert factor]

4. Tick which animals you select to be harvested?

Select no more than 1.

- Everything  
 Any Adult over 24kg live weight  
 Only Bucks, over 24kg live weight  
 Only Bucks but of any weight  
 Only kids  
 Other, please specify

5. If known, what is the average age of Does before they are harvested? If unknown leave blank.

6. If known, what is the average age of Bucks before they are harvested? If unknown leave blank.

*Genetic improvement of Australian Meat goats*

7. If known what is the average age of kids that are harvested? If unknown leave blank.

8. What is the average LIVE weight of Bucks at harvest? If unknown leave blank.

Insert Buck live weight in kg. The value must be between 0 and 100, inclusive.

9. If known, what is the average CARCASS weight of Bucks at slaughter? If unknown leave blank.

Insert Buck carcass weight in kg. The value must be between 0 and 100, inclusive.

10. What is the average LIVE weight of Does at harvest? If unknown leave blank.

Insert Doe live weight in kg. The value must be between 0 and 100, inclusive.

11. If known, what is the average CARCASS weight of Does at slaughter? If unknown leave blank.

Insert Doe carcass weight in kg. The value must be between 0 and 100, inclusive.

12. What is the average LIVE weight of Kids at harvest? If unknown leave blank.

Insert Kid live weight in kg. The value must be between 0 and 100, inclusive.

13. If known, what is the average CARCASS weight of Kids at slaughter? If unknown leave blank.

Insert Kid carcass weight in kg. The value must be between 0 and 100, inclusive.

14. For animals sold to slaughter, is your predominant sale method; per head, per kg live or per kg dressed?

15. Referring to your answer in QUESTION 14, what is the average sale price for these animals in the past 12 MONTHS?

Insert value in \$/kg or \$/head. The value must be between 0 and 1000, inclusive.

16. Referring to your answer in QUESTION 14, what is the average sale price for these animals in the past 5 YEARS?

Insert value in \$/kg or \$/head. The value must be between 0 and 1000, inclusive.

17. Do you consider internal parasites a significant issue for you?

18. Do you monitor any body weights in addition to pre-sale weight?

19. How many Does do you estimate are on your property? The value must be between 0 and 100000, inclusive.

20. Referring to your answer to QUESTION 19, how accurate do you think this estimate is?

21. Over the past five years has the local unmanaged rangeland population been increasing or decreasing?

22. If known, at what age do the Does have their first kid? If unknown leave blank.

23. Please tick the following relevant boxes

- 1. Would you like to be entered in the draw for a \$100 fuel voucher?
- 2. Would you like to be provided a summary of the project results?
- 3. Are you happy to be contacted if we require clarification on an answer?

24. If you ticked any of the boxes in QUESTION 23 please provide your NAME, EMAIL ADDRESS and CONTACT PHONE NUMBER

## Appendix 7.2 Commercial survey

### Commercial \$ index evaluation

1. What is your postcode?\*

2. Are you a commercial producer or a seedstock breeder answering on behalf of your average client?\*

3. What is the main breed within your managed herd?

4. If you answered OTHER in QUESTION 3, please specify your main breed.

5. Do you have improved fencing designed for goat management?

6. If you answered YES to QUESTION 5, what percentage of your property does this apply to? The value must be between 0 and 100, inclusive.

7. If you know the accurate number of Does on your property, how many do you have? If you don't know please leave the value blank.

8. If you know the accurate number of Bucks on your property, how many do you have? If you don't know please leave the value blank.

9. Do you control joining between Bucks and Does?

10. If you answered YES to QUESTION 9, please tick the months when you join.

- January
- February
- March
- April
- May
- June
- July
- August
- September
- October
- November
- December

12. What is the average number of Does joined? If unknown leave blank.

13. What proportion of your Does, are mated to pure Boer Bucks? If unknown leave blank. The value must be between 0 and 100, inclusive.

14. Do you routinely join Does at less than 12 months of age?

15. On average, what age do Does have their first Kid?

16. In kg, what is the average mature live weight (at joining) of your Does? If unknown leave blank.

17. On average, what age in years do you sell cast for age (CFA) Does? If unknown leave blank.

18. Do you sell cast for age Does based on live weight, dressed weight or per head? If unknown please leave blank.

19. Based on your sale method for cast for age Does what is the average sale price in \$/kg or \$/head. If unknown please leave blank.

20. What is the average conception (fertility) rate achieved in your production system when they are joined?

If unknown leave blank.

Insert Does pregnant as percentage of Does joined. The value must be between 0 and 100, inclusive.

21. If known what is the average scanning rate achieved in your production system?

If unknown leave blank.

Insert percentage of Fetuses scanned as a percentage of Does joined. The value must be between 0 and 300, inclusive.

22. If known, what is the average weaning percentage achieved in your production system?

If unknown leave blank.

Insert Kids weaned as percentage of Does joined. The value must be between 0 and 300, inclusive.

## Genetic improvement of Australian Meat goats

24. If you answered YES to QUESTION 23. Please tick the Months when you wean.

- January
- February
- March
- April
- May
- June
- July
- August
- September
- October
- November
- December

25. What month does the 'limited feed period' normally start?

*Limited feed period: when developing a breeding objective it is important to account for the cost of feed. The concept of the "limited feed period" is required when designing an index, feed is costed only at times of the year when it is in short supply. There is no need to cost feed at other times when it is in surplus.*

26. What month does the 'limited feed period' normally end?

27. Do you supplement feed?

28. If you answered YES to QUESTION 27, do you know how much feed you use per head or per ha? If unknown please leave blank.

29. Referring to your answer in QUESTION 28. How much feed in kg do you use per head or ha in an average year? If unknown leave blank.

30. Referring to your answer in QUESTION 29, what is the average cost of feed in \$ per kg. If unknown, please leave blank.

31. It is known that, on average, larger Does consume more feed. Based on this, what is your response to the following statement? "Reducing adult doe weight is of high importance to my breeding objective."

32. Do you consider internal parasites to be a significant issue for you?

33. Do you monitor internal parasites?

34. If you answered YES to QUESTION 33 please briefly describe which animals get tested, how frequently they are tested and which test you use.

If you answered NO to QUESTION 33 please continue to QUESTION 35.

35. Do you control internal parasites?

- No control
- Drenching
- Paddock rotation
- Cross grazing with another species such as cattle
- Other, please specify

36. What is your response to the following statement: "Increasing carcass fat is of importance to my breeding objective".

--None-- ▾

37. Only answer this question if you cross with Pure Boer Bucks. In MONTHS what is the slaughter age of the progeny from Boer Bucks? If unknown leave blank.

38. Only answer this question if you cross with Pure Boer Bucks. Referring to the progeny sold in the previous question what is the average LIVE WEIGHT in kg at the age mentioned? If unknown leave blank.

39. Only answer this question if you cross with Pure Boer Bucks. Referring to the progeny sold in the previous question what is the average CARCASS WEIGHT of these animals? If unknown leave blank.

40. Only answer this question if you cross with Pure Boer Bucks. For animals sold to slaughter are they sold based on \$/kg live, dressed or head. If unknown please leave blank.

--None-- ▾

41. Only answer this question if you cross with Pure Boer Bucks. Again, referring to the progeny and your answer to QUESTION 40. What is the sale price in \$/kg or \$/head for these animals.

42. Please tick the following relevant boxes.

- Would like to be entered in the draw for a \$100 fuel voucher
- Would like to be provided with a summary of the project results
- Are you happy to be contacted if we require clarification on an answer

43. If you ticked any of the boxes in QUESTION 40, please provide your NAME, EMAIL ADDRESS and CONTACT PHONE NUMBER.

## Appendix 7.3 Seedstock survey

### Intensive / Seedstock \$ index evaluation

If you sell any of your bucks to other breeders or commercial producers, when you complete this survey please also answer the commercial producer survey on behalf of your average clients. Thank you.

1. What is your postcode?\*

2. Are you a member of KIDPLAN?

3. If you answered YES in QUESTION 2, what is your flock number?

If you answered NO in QUESTION 2, what is the main reason for not using KIDPLAN?

4. Do you sell your bucks to other seedstock breeders?

5. What is the average number of Does joined each year?

6. What is the average number of Bucks joined each year?

7. Do you routinely join Doe kids less than 12 months of age?

8. What is the average age in Months of Does at first joining?

9. What is the average age in Months for Bucks at first joining?

10. In kg, what is the average mature weight (at joining) of your Does? If unknown leave blank.

11. On average how many KIDDINGS are Does retained for?

12. On average how many YEARS are stud Bucks used for?



13. What time of year do you join your Bucks and Does for mating?

- January
- Febraury
- March
- April
- May
- June
- July
- August
- September
- October
- November
- December

14. What is the average conception (fertility) rate achieved in your production system when they are joined?

If unknown leave blank.

Insert Does pregnant as percentage of Does joined. The value must be between 0 and 100, inclusive.

15. If known what is the average scanning rate achived in your production system?

If unknown leave blank.

Insert percentage of Fetuses scanned as a percentage of Does joined. The value must be between 0 and 300, inclusive.

16. What is the average number of Kids born alive per Doe? If unknown leave blank.

17. If known, what is the average weaning percentage achieved in your production system?

If unknown leave blank.

Insert Kids weaned as percentage of Does joined. The value must be between 0 and 300, inclusive.

18. Do you control weaning?

19. If you answered YES to QUESTION 19. Please tick the Months when you wean.

- January
- February
- March
- April
- May
- June
- July
- August
- September
- October
- November
- December

## Genetic improvement of Australian Meat goats

20. What month does the 'limited feed period' normally start?

*Limited feed period: when developing a breeding objective it is important to account for the cost of feed. The concept of the "limited feed period" is required when designing an index, feed is costed only at times of the year when it is in short supply. There is no need to cost feed at other times when it is in surplus.*

--None-- ▾

21. What month does the 'limited feed period' normally end?

--None-- ▾

22. Do you supplement feed?

--None-- ▾

23. If you supplement feed, what is the primary feed base?

Select no more than 1.

- Hay
- Silage
- Grain
- Other, please specify

24. If you answered YES to QUESTION 22, do you know how much feed you use per head or per ha in an average year?  
If unknown please leave blank.

--None-- ▾

25. Referring to your answer in QUESTION 24. How much feed in kg do you use per head or ha. If unknown please leave blank.

26. Referring to your answer in QUESTION 25, what is the average cost of feed in \$ per kg. If unknown please leave blank.

27. On average bigger Does eat more. What is your response to the following statement: "Reducing adult doe weight is of high importance to my breeding objective".

--None-- ▾

28. Are internal parasites a significant issue for you?

--None-- ▾

29. Do you monitor internal parasites?

--None-- ▾

30. Do you control internal parasites?

- No control
- Drenching
- Paddock rotation
- Cross grazing with another species such as cattle
- Other, please specify

31. In MONTHS what is the slaughter age of the progeny from your Bucks? If unknown leave blank.

32. Referring to the progeny sold in the previous question what is the average LIVE WEIGHT in kg at the age mentioned? If unknown leave blank.

33. Referring to the progeny sold in the previous question what is the average CARCASS WEIGHT of these animals? If unknown leave blank.

34. For animals sold to slaughter are they sold based on \$/kg live, dressed or head?

35. Again, referring to the progeny and your answer to QUESTION 34. What is the sale price in \$/kg or \$/head for these animals. If unknown please leave blank.

36. What is your response to the following statement: "Increasing carcass fat is of importance to my breeding objective."

37. What is your response to the following statement: "Increasing carcass meat yield is of importance to my breeding objective."

38. Do you record complete reproductive data? *Must include recording of Dead at Birth and Dry animals, ensuring linkage for reproduction data, accurate Birth Type , Rearing Type and Birth Date.*

39. What proportion of males get Scrotal Circumferences recorded? The value must be between 0 and 100, inclusive.

40. Please tick the body weights you currently record for females.

- Birth Weight - Within 24 hours of birth
- Weaning Weight - 6 to 16 weeks
- Post-weaning weight - 4 to 10 months
- Yearling weight - 10-13 months
- Hogget weight - 13 to 18 months
- Adult weight > 18 months
- Repeat adult weight

41. Please tick the body weights you currently record for males.

- Birth Weight - Within 24 hours of birth
- Weaning Weight - 6 to 16 weeks
- Post-weaning weight - 4 to 10 months
- Yearling weight - 10-13 months
- Hogget weight - 13 to 18 months
- Adult weight > 18 months
- Repeat adult weight

*Genetic improvement of Australian Meat goats*

41. Please tick the body weights you currently record for males.

- Birth Weight - Within 24 hours of birth
- Weaning Weight - 6 to 16 weeks
- Post-weaning weight - 4 to 10 months
- Yearling weight - 10-13 months
- Hogget weight - 13 to 18 months
- Adult weight > 18 months
- Repeat adult weight

42. Please tick the boxes of the current recording practices for carcass traits.

- Weaning eye muscle depth
- Weaning C-site fat depth
- Post-weaning eye muscle depth
- Post-weaning C-site fat depth
- Yearling eye muscle depth
- Yearling C-site fat depth
- Carcass weight

43. Referring to your answer in Question 42 on carcass traits, which animals do you record carcass traits for?

--None-- ▼

44. What proportion of the current drop males and females will have Worm egg count's (WEC) tested?

--None-- ▼

45. Please tick the following relevant boxes.

- Would like to be entered in the draw for a \$100 fuel voucher
- Would like to be provided with a summary of the project results
- Are you happy to be contacted if we require clarification on an answer

46. If you ticked any of the boxes in QUESTION 40, please provide your NAME, EMAIL ADDRESS and CONTACT PHONE NUMBER.

## Appendix 7.4 Processor survey

### Goat Processor \$ index evaluation

If you sell any of your bucks to other breeders or commercial producers, when you complete this survey please also answer the commercial producer survey on behalf of your average clients. Thank you.

1. What is your postcode?\*

2. What is the average number of goats you process in a year?

3. What is your ideal carcass weight? Please insert carcass weight in kg dressed.

4. What is your ideal dressing percentage? The value must be between 1 and 100, inclusive.

5. What is your average dressing percentage? The value must be between 1 and 100, inclusive.

6. Do you ever pay based on animal Live Weight?

7. If known, what is the average age of Bucks before slaughter? If unknown leave blank.

8. If known, what is the average carcass weight of Bucks at slaughter? If unknown leave blank.

Insert Buck carcass weight in kg. The value must be between 0 and 100, inclusive.

9. For Bucks, are they sold based on whole carcass, broken down or bone out?

Please answer in relation to the average animal that you process.

10. Again, referring to the Bucks and your answer to QUESTION 9. What is your average sale price in \$/kg for these animals. If unknown please leave blank.

11. If known, what is the average age of Does before slaughter? If unknown leave blank.

12. Referring to the Does in the previous question what is the average CARCASS WEIGHT of these animals? If unknown leave blank.

Insert Doe carcass weight in kg.

*Genetic improvement of Australian Meat goats*

13. For Does, are they sold based on whole carcass, broken down or bone out?

Please answer in relation to the average animal that you process.

14. Again, referring to the Does and your answer to QUESTION 13. What is your average sale price in \$/kg for these animals. If unknown please leave blank.

15. Do you regularly process Kid goats? (less than 12 months old)

16. In MONTHS what is the average slaughter age of Kids? If unknown leave blank.

17. Referring to the Kids in the previous question what is the average CARCASS WEIGHT of these animals? If unknown leave blank.

18. For Kids, are they sold based on whole carcass, broken down or bone out?

Please answer in relation to the average animal that you process.

19. Again, referring to the Kids and your answer to QUESTION 18. What is your average sale price in \$/kg or \$/head for these animals. If unknown please leave blank.

20. Do you regularly process Capretto goats? (Kids not weaned with carcass weights between 5-12kg)

21. If known, what is the average \$ value for each hide? If unknown leave blank.

22. What percentage of animals processed are male? The value must be between 0 and 100, inclusive.

23. What percentage of males processed are castrated? If unknown leave blank. The value must be between 0 and 100, inclusive.

24. If known what percentage of animals are processed halal? If unknown leave blank. The value must be between 0 and 100, inclusive.

25. On average what percentage of products are destined for export markets? The value must be between 0 and 100, inclusive.

26. What is your response to the following statement: "Increasing carcass fat should be of importance to my suppliers".

-None- ▼

27. What is your response to the following statement: "Increasing carcass meat yield should be of importance to my suppliers."

-None- ▼

28. Are internal parasites a significant issue for your suppliers? If unknown leave blank.

-None- ▼

29. Would you value more improvement in; improving carcass traits or an increase of rangeland animals processed?

-None- ▼

30. Would you prefer an increase in % of meat on carcass or an increase in carcass size?

-None- ▼

31. Please tick the following relevant boxes.

- Would like to be entered in the draw for a \$100 fuel voucher
- Would like to be provided with a summary of the project results
- Are you happy to be contacted if we require clarification on an answer

32. If you ticked any of the boxes in in the previous question, please provide your NAME, EMAIL ADDRESS and CONTACT PHONE NUMBER.

# Reference List

- Afolayan, R, Fogarty, N, Gilmour, A, Ingham, V, Gaunt, G, Cummins, L (2008a) Reproductive performance and genetic parameters in first cross ewes from different maternal genotypes. *Journal of animal science* **86**, 804-814.
- Afolayan, R, Fogarty, N, Gilmour, AR, Ingham, V, Gaunt, G, Cummins, L (2008b) Genetic correlations between reproduction of crossbred ewes and the growth and carcass performance of their progeny. *Small Ruminant Research* **80**, 73-79.
- Al-Shorepy, S, Alhadrami, G, Abdulwahab, K (2002) Genetic and phenotypic parameters for early growth traits in Emirati goat. *Small Ruminant Research* **45**, 217-223.
- Alade, N, Dilala, M, Abdulyekeen, A (2010) Phenotypic and genetic parameter estimates of litter size and body weights in goats. *International Journal of Science and Nature* **1**, 262-266.
- Amer, PR, McEwan, JC, Dodds, KG, Davis, GH (1999) Economic values for ewe prolificacy and lamb survival in New Zealand sheep. *Livestock Production Science* **58**, 75-90.
- Arrebola, F, Pérez-Marín, C, Santiago-Moreno, J (2010) Limitation of seasonality in reproductive parameters of Mediterranean bucks, using photoperiod treatment. *Small Ruminant Research* **89**, 31-35.
- Atkins, K, Murray, J, Gilmour, A, Luff, A (1991) Genetic variation in liveweight and ultrasonic fat depth in Australian Poll Dorset sheep. *Australian Journal of Agricultural Research* **42**, 629-640.
- Australian Bureau of Statistics (2013) Agricultural Commodities, Australia, 2012-2013. *Australian Bureau of Statistics* **7121.0**,
- Ball, A, Brown, D, Spiker, S, Field, S, Banks, R (2001) Opportunities for genetic development of the Boer Goat in Australia using Kidplan. *Proc. Assoc. Adv. Anim. Breed. Gen* **14**, 445-448.
- Barazandeh, A, Moghbeli, SM, Vatankhah, M, Mohammadabadi, M (2012) Estimating non-genetic and genetic parameters of pre-weaning growth traits in Raini Cashmere goat. *Tropical animal health and production* **44**, 811-817.
- BCS Agribusiness (2012) Goat Seedstock Industry Stocktake. *Meat and Livestock Australia*
- Boujenane, I, Hazzab, AE (2008) Genetic parameters for direct and maternal effects on body weights of Draa goats. *Small Ruminant Research* **80**, 16-21.
- Brash, L, Fogarty, N, Gilmour, A, Luff, A (1992) Genetic parameters for liveweight and ultrasonic fat depth in Australian meat and dual-purpose sheep breeds. *Australian Journal of Agricultural Research* **43**, 831-841.
- Braun, W (2007) Parturition and dystocia in the goat. *Current Therapy in Large Animal Theriogenology 2nd edition. Missouri Saunders Elsevier* 555-558.
- Brien, F, Hebart, M, Smith, D, Edwards, JH, Greeff, J, Hart, K, Refshauge, G, Bird-Gardiner, T, Gaunt, G, Behrendt, R (2010) Opportunities for genetic improvement of lamb survival. *Animal Production Science* **50**, 1017-1025.
- Brien, F, Cloete, S, Fogarty, N, Greeff, J, Hebart, M, Hiendleder, S, Edwards, JH, Kelly, J, Kind, K, Kleemann, D (2014) A review of the genetic and epigenetic factors affecting lamb survival. *Animal Production Science* **54**, 667-693.



- Brien, FD, Hebart, ML, Hatcher, BS, van der Werf, JHJ (2015) Can indicator traits aid genetic improvement of lamb survival? 2. Predictions of genetic gain. *Unpublished*
- Brounts, SH, Hawkins, JF, Baird, A, Glickman, LT (2004) Outcome and subsequent fertility of sheep and goats undergoing cesarean section because of dystocia: 110 cases (1981-2001). *Journal of the American Veterinary Medical Association* **224**, 275-281.
- Brown, D, Jones, R, Hinch, G (2014) Genetic parameters for lamb autopsy traits. *Animal Production Science* **54**, 736-744.
- Brown, D, Swan, A (2016a) Genetic importance of fat and eye muscle depth in Merino breeding programs. *Animal Production Science* **56**, 690-697.
- Brown, D, Swan, A (2016b) Genetic parameters for liveweight, wool and worm resistance traits in multi-breed Australian meat sheep. 2. Genetic relationships between traits. *Animal Production Science* **56**, 1449-1453.
- Brown, D, Fogarty, N, Iker, C, Ferguson, D, Blache, D, Gaunt, G (2016c) Genetic evaluation of maternal behaviour and temperament in Australian sheep. *Animal Production Science* **56**, 767-774.
- Browning, R, Leite-Browning, M (2011) Birth to weaning kid traits from a complete diallel of Boer, Kiko, and Spanish meat goat breeds semi-intensively managed on humid subtropical pasture. *Journal of animal science* **89**, 2696-2707.
- Bulmer, M (1971) The effect of selection on genetic variability. *The American Naturalist* **105**, 201-211.
- Bunter, K, Brown, D (2013) Yearling and adult expressions of reproduction in maternal sheep breeds are genetically different traits. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **20**, 82-85.
- Bunter, KL, Swan, AA, Brown, DJ, Brien, FD, Smith, J (2017) Litter size at lambing influences genetic evaluation of maternal rearing ability. *Animal Production Science* Online early access.
- Butler, L, Corkrey, S, Knox, I, Hannan, G, Thomson, R (1995) Perceptions and knowledge of measurement in selection programs: a survey of stud Merino breeders in Australia. *Animal Production Science* **35**, 681-692.
- Carl, GR, Robbins, CT (1988) The energetic cost of predator avoidance in neonatal ungulates: hiding versus following. *Canadian Journal of Zoology* **66**, 239-246.
- CSIRO (2007) Nutrient requirements of domesticated ruminants. *CSIRO publishing, Australia* 16-19.
- Daetwyler, H, Hickey, J, Henshall, J, Dominik, S, Gredler, B, Van Der Werf, J, Hayes, B (2010) Accuracy of estimated genomic breeding values for wool and meat traits in a multi-breed sheep population. *Animal Production Science* **50**, 1004-1010.
- Davis, G, Morris, C, Dodds, K (1998) Genetic studies of prolificacy in New Zealand sheep. *Animal Science* **67**, 289-297.
- Dhanda, J, Taylor, D, Murray, P (2003) Part 1. Growth, carcass and meat quality parameters of male goats: effects of genotype and liveweight at slaughter. *Small Ruminant Research* **50**, 57-66.
- Fogarty, N, Brash, L, Gilmour, A (1994) Genetic parameters for reproduction and lamb production and their components and liveweight, fat depth and wool production in Hyfer sheep. *Australian Journal of Agricultural Research* **45**, 443-457.
- Fogarty, N, Safari, E, Taylor, P, Murray, W (2003) Genetic parameters for meat quality and carcass traits and their correlation with wool traits in Australian Merino sheep. *Australian Journal of Agricultural Research* **54**, 715-722.

- Fogarty, N, Banks, R, Van Der Werf, J, Ball, A, Gibson, J (2007) 'The information nucleus—a new concept to enhance sheep industry genetic improvement, Proceedings of the Association for the Advancement of Animal Breeding and Genetics.'
- Fogarty, N, Safari, E, Mortimer, S, Greeff, J, Hatcher, S (2009) Heritability of feed intake in grazing Merino ewes and the genetic relationships with production traits. *Animal Production Science* **49**, 1080-1085.
- Gebrelul, S, Sartin III, LS, Iheanacho, M (1994) Genetic and non-genetic effects on the growth and mortality of Alpine, Nubian and crossbred kids. *Small Ruminant Research* **13**, 169-176.
- GICA (2017) Latest News *Goat Industry Council of Australia*. Available at <http://www.gica.com.au/news-and-events> [Accessed 15/09/2017].
- Gilmour, AR, Gogel, B, Cullis, B, Thompson, R, Butler, D (2009) ASReml user guide release 3.0. *VSN International Ltd, Hemel Hempstead, UK*
- Gunia, M, Phocas, F, Arquet, R, Alexandre, G, Mandonnet, N (2011) Genetic parameters for body weight, reproduction, and parasite resistance traits in the Creole goat. *Journal of animal science* **89**, 3443-3451.
- Gunia, M, Phocas, F, Gourdine, J-L, Bijma, P, Mandonnet, N (2013) Simulated selection responses for breeding programs including resistance and resilience to parasites in Creole goats. *Journal of animal science* **91**, 572-581.
- Hamed, A, Mabrouk, M, Shaat, I, Bata, S (2009) Estimation of genetic parameters and some non-genetic factors for litter size at birth and weaning and milk yield traits in Zaraibi goats. *Egyptian Journal of Sheep and Goat Sciences* **4**, 55-64.
- Hanford, K, Van Vleck, L, Snowden, G (2005) Estimates of genetic parameters and genetic change for reproduction, weight, and wool characteristics of Rambouillet sheep. *Small Ruminant Research* **57**, 175-186.
- Hanford, KJ, Van Vleck, LD, Snowden, G (2006) Estimates of genetic parameters and genetic trend for reproduction, weight, and wool characteristics of Polypay sheep. *Livestock Science* **102**, 72-82.
- Hazel, LN (1943) The genetic basis for constructing selection indexes. *Genetics* **28**, 476-490.
- Hinch, G, Brien, F (2014) Lamb survival in Australian flocks: a review. *Animal Production Science* **54**, 656-666.
- Huisman, A, Brown, D, Ball, A, Graser, H-U (2008) Genetic parameters for bodyweight, wool, and disease resistance and reproduction traits in Merino sheep. 1. Description of traits, model comparison, variance components and their ratios. *Animal Production Science* **48**, 1177-1185.
- Husain, S, Horst, P, Islam, A (1995) Effect of different factors on pre-weaning survivability of Black Bengal kids. *Small Ruminant Research* **18**, 1-5.
- Ingham, V, Fogarty, N, Gilmour, AR, Afolayan, R, Cummins, L, Gaunt, G, Stafford, J, Edwards, JH (2007) Genetic evaluation of crossbred lamb production. 4. Genetic parameters for first-cross animal performance. *Australian Journal of Agricultural Research* **58**, 839-846.
- Johnston, SE, McEWAN, J, Pickering, NK, Kijas, JW, Beraldi, D, Pilkington, JG, Pemberton, JM, Slate, J (2011) Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. *Molecular Ecology* **20**, 2555-2566.
- Kadim, I, Mahgoub, O, Al-Ajmi, D, Al-Maqbaly, R, Al-Saqri, N, Ritchie, A (2004) An evaluation of the growth, carcass and meat quality characteristics of Omani goat breeds. *Meat Science* **66**, 203-210.

- Kelly, O, Hebart, M, Brien, F, Pitchford, W (2016) Lamb survival should be considered separate genetic traits across different birth types. *31st Conference of the Australian Society of Animal Production*
- Kelly, O, Hebart, M, Brien, F, Pitchford, W (2017) Genetic correlations between lamb survival, birth weight, and gestation length differ between birth types. *Proc. Assoc. Adv. Anim. Breed. Gen* **22**, Available online.
- Li, L, Brown, D (2016) Estimation of genetic parameters for lambing ease, birthweight and gestation length in Australian sheep. *Animal Production Science* **56**, 934-940.
- Lickliter, RE (1984) Hiding behavior in domestic goat kids. *Applied Animal Behaviour Science* **12**, 245-251.
- Luff, A (1980) A service for all seasons. *Final Report Australian Wool Corporation Project K/1/1051, Melbourne*
- Mahgoub, O, Lodge, G (1996) Growth and body composition in meat production of Omani Batina goats. *Small Ruminant Research* **19**, 233-246.
- Mandonnet, N, Aumont, G, Fleury, J, Arquet, R, Varo, H, Gruner, L, Bouix, J, Khang, J (2001) Assessment of genetic variability of resistance to gastrointestinal nematode parasites in Creole goats in the humid tropics. *Journal of animal science* **79**, 1706-1712.
- Maniatis, N, Pollott, G (2002) Maternal effects on weight and ultrasonically measured traits of lambs in a small closed Suffolk flock. *Small Ruminant Research* **45**, 235-246.
- Marai, I, Abou-Fandoud, E, Daader, A, Abu-Ella, A (2002) Reproductive doe traits of the Nubian (Zaraibi) goats in Egypt. *Small Ruminant Research* **46**, 201-205.
- Marichal, A, Castro, N, Capote, J, Zamorano, M, Argüello, A (2003) Effects of live weight at slaughter (6, 10 and 25 kg) on kid carcass and meat quality. *Livestock Production Science* **83**, 247-256.
- Matika, O, Van Wyk, J, Erasmus, G, Baker, R (2003) Genetic parameter estimates in Sabi sheep. *Livestock Production Science* **79**, 17-28.
- Mellado, M, Meza-Herrera, CA, Arévalo, JR, De Santiago-Miramontes, MA, Rodríguez, A, Luna-Orozco, JR, Veliz-Deras, FG (2011) Erratum to: Relationship between litter birthweight and litter size in five goat genotypes. *Animal Production Science* **51**, 490-490.
- Meyer, H (2002) Genetic and Environmental Impacts on Prenatal Lamb Loss1. *Sheep and Goat Research Journal* **17**, 11-14.
- MLA (2004a) The Breeder's Guide. *Meat and Livestock Australia*
- MLA (2004b) The role of the Boer goat in the development of the Australian goat meat industry. *Meat and Livestock Australia*
- MLA (2012) Australian Goat Industry RD&E Strategy – 2012. *Meat and Livestock Australia*
- MLA (2013) Fast facts 2013, Australia's goatmeat industry. *Meat and Livestock Australia*
- MLA (2015) Australian goat Industry summary 2015. *Meat and Livestock Australia*
- MLA (2016) Australian goat Industry summary 2016. *Meat and Livestock Australia*
- MLA (2017) News and Events. *Meat and Livestock Australia* Available at <https://www.mla.com.au/news-and-events/> [Accessed 15/09/2017].
- Moreno, C, Bouix, J, Brunel, J, Weisbecker, J, François, D, Lantier, F, Elsen, J (2001) Genetic parameter estimates for carcass traits in the inra401 composite sheep strain. *Livestock Production Science* **69**, 227-232.
- Morris, C (1981) Economic values of net reproduction and weight-for-age for use in genetic calculations applied to Australian beef cattle herds. *Animal Production Science* **21**, 464-473.

- Morris, JE, Cronin, GM, Bush, RD (2012) Improving sheep production and welfare in extensive systems through precision sheep management. *Animal Production Science* **52**, 665-670.
- Mortimer, S, Van der Werf, J, Jacob, R, Pethick, D, Pearce, K, Warner, R, Geesink, G, Edwards, JH, Gardner, G, Ponnampalam, E (2010) Preliminary estimates of genetic parameters for carcass and meat quality traits in Australian sheep. *Animal Production Science* **50**, 1135-1144.
- Mourad, M (1996) Estimation of repeatability of litter size of common African goats and crosses with Alpine in Rwanda. *Small Ruminant Research* **19**, 263-266.
- Mourad, M, Anous, M (1998) Estimates of genetic and phenotypic parameters of some growth traits in common African and Alpine crossbred goats. *Small Ruminant Research* **27**, 197-202.
- Mousa, E, Van Vleck, LD, Leymaster, K (1999) Genetic parameters for growth traits for a composite terminal sire breed of sheep. *Journal of animal science* **77**, 1659-1665.
- Mugambi, J, Wakhungu, J, Inyangala, B, Muhuyi, W, Muasya, T (2007) Evaluation of the performance of the Kenya Dual Purpose Goat composites: Additive and non-additive genetic parameters. *Small Ruminant Research* **72**, 149-156.
- Neser, F, Erasmus, G, Van Wyk, J (2001) Genetic parameter estimates for pre-weaning weight traits in Dorper sheep. *Small Ruminant Research* **40**, 197-202.
- Newton, J, Brown, D, Dominik, S, van der Werf, J (2014) Genetic and phenotypic parameters between yearling, hogget and adult reproductive performance and age of first oestrus in sheep. *Animal Production Science* **54**, 753-761.
- Odubote, I (1996) Genetic parameters for litter size at birth and kidding interval in the West African Dwarf goats. *Small Ruminant Research* **20**, 261-265.
- Ozcan, M, Ekiz, B, Yilmaz, A, Ceyhan, A (2005) Genetic parameter estimates for lamb growth traits and greasy fleece weight at first shearing in Turkish Merino sheep. *Small Ruminant Research* **56**, 215-222.
- Papachristoforou, C, Koumas, A, Photiou, C (2000) Seasonal effects on puberty and reproductive characteristics of female Chios sheep and Damascus goats born in autumn or in February. *Small Ruminant Research* **38**, 9-15.
- Papachristoforou, C, Koumas, A, Photiou, C (2007) Initiation of the breeding season in ewe lambs and goat kids with melatonin implants. *Small Ruminant Research* **73**, 122-126.
- Perez-Razo, M (1998) Factors affecting kid survival in five goat breeds. *Canadian journal of animal science* **78**, 407-411.
- Plush, KJ, Hebart, ML, Brien, FD, Hynd, PI (2011) The genetics of temperament in Merino sheep and relationships with lamb survival. *Applied Animal Behaviour Science* **134**, 130-135.
- Plush, K, Brien, F, Hebart, M, Hynd, P (2016) Thermogenesis and physiological maturity in neonatal lambs: a unifying concept in lamb survival. *Animal Production Science* **56**, 736-745.
- Pollott, G, Greeff, J (2004) Genotype× environment interactions and genetic parameters for fecal egg count and production traits of Merino sheep. *Journal of animal science* **82**, 2840-2851.
- Pollott, G, Karlsson, L, Eady, S, Greeff, J (2004) Genetic parameters for indicators of host resistance to parasites from weaning to hogget age in Merino sheep. *Journal of animal science* **82**, 2852-2864.

- Ponzoni, RW (1988) Accounting for both income and expense in the development of breeding objectives. *Proc. Assoc. Advmt. Breed. Genet* **7**, 55-66.
- Portolano, B, Todaro, M, Finocchiaro, R, Van Kaam, J (2002) Estimation of the genetic and phenotypic variance of several growth traits of the Sicilian Girgentana goat. *Small Ruminant Research* **45**, 247-253.
- R Core Team (2016) R: A Language and Environment for Statistical Computing. *R Foundation for Statistical Computing*
- Rao, S, Notter, D (2000) Genetic analysis of litter size in Targhee, Suffolk, and Polypay sheep. *Journal of animal science* **78**, 2113-2120.
- Robertson, A, (1959) The sampling variance of the genetic correlation coefficient. *Biometrics*, **15**: 469-485.
- Rosati, A, Mousa, E, Van Vleck, L, Young, L (2002) Genetic parameters of reproductive traits in sheep. *Small Ruminant Research* **43**, 65-74.
- Safari, A, Fogarty, NM (2003) Genetic parameters for sheep production traits. *Estimates from the literature. NSW Agriculture, Orange Agricultural Institute, Orange, NSW* **49**, 13-21.
- Safari, E, Fogarty, N, Gilmour, AR (2005) A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. *Livestock Production Science* **92**, 271-289.
- Safari, E, Fogarty, N, Gilmour, AR, Atkins, K, Mortimer, S, Swan, A, Brien, F, Greeff, J, Van der Werf, J (2007) Across population genetic parameters for wool, growth, and reproduction traits in Australian Merino sheep. 2. Estimates of heritability and variance components. *Australian Journal of Agricultural Research* **58**, 177-184.
- Schoeman, S, Els, J, Van Niekerk, M (1997) Variance components of early growth traits in the Boer goat. *Small Ruminant Research* **26**, 15-20.
- Sheep Central (2017) Goat Central *Nascon Media*. Available at <https://www.sheepcentral.com/goat-central/> [Accessed 15/09/2017].
- Sheep Genetics (2016) 'ASBVS and Indexes explained.' Available at <http://www.sheepgenetics.org.au/Getting-started/ASBVs-and-Indexes> [Accessed 05/05/2017].
- Sheep Genetics (2017a) 'Case studies.' Available at <http://www.sheepgenetics.org.au/Resources/Case-studies> [Accessed 22/08/2017].
- Sheep Genetics (2017b) SGA Breeder's Quality Assurance Manual. *Sheep Genetics, Australia*
- Singh, D, Mishra, H, Singh, C (1990) Genetic and non-genetic factors affecting pre-weaning survivability in kids. *Animal Production* **51**, 559-564.
- Snyman, M (2010) Factors affecting pre-weaning kid mortality in South African Angora goats. *South African Journal of Animal Science* **40**, 54-64.
- Sofi, K, Makhdoomi, D, Ahmed, T, Dar, S (2012) Management of dystocia in a goat: a case report. *North-East Veterinarian* **12**, 23.
- Swan, A, Van der Werf, J, Atkins, K (2007) Developments in breeding objectives for the Australian sheep industry. *Proc. Assoc. Advmt. Breed. Genet* **17**, 483-490.
- Swan, A, Brown, D, Banks, R (2009) Genetic progress in the Australian sheep industry. *Proc. Assoc. Advmt. Breed. Genet* **18**, 326-329.
- Swan, AA, Johnston, DJ, Brown, DJ, Tier, B, Graser, H-U (2012) Integration of genomic information into beef cattle and sheep genetic evaluations in Australia. *Animal Production Science* **52**, 126-132.
- Swan, A, Pleasants, T, Pethick, D (2015) Breeding to improve meat eating quality in terminal sire sheep breeds. *Proc. Assoc. Advmt. Breed. Genet* **21**, 29-32.

- Tosh, J, Kemp, R (1994) Estimation of variance components for lamb weights in three sheep populations. *Journal of animal science* **72**, 1184-1190.
- Turner, H (1969) Genetic improvement of reproduction rate in sheep. *Animal Breeding Abstracts* **37**, 545-563.
- Turner, HN (1972) Genetic interactions between wool, meat and milk production in sheep. *Animal Breeding Abstracts* **40**, 621-643.
- Walkden-Brown, S, Bocquier, F (2000) Nutritional regulation of reproduction in goats. *Proceedings of the 7th International Conference on Goats* **1**, 389-395.
- Warner, RD, Greenwood, PL, Pethick, DW, Ferguson, DM (2010) Genetic and environmental effects on meat quality. *Meat Science* **86**, 171-183.
- Webb, E, Casey, N, Simela, L (2005) Goat meat quality. *Small Ruminant Research* **60**, 153-166.
- Young, J, Trompf, J, Thompson, A (2014) The critical control points for increasing reproductive performance can be used to inform research priorities. *Animal Production Science* **54**, 645-655.
- Zahraddeen, D, Butswat, I, Naibi, S, Yande, D, Rahman, S (2011) Multiple births and reproductive problems in West African dwarf ewes and does in southern Guinea Savannah zone of Nigeria. *Journal of Commonwealth Veterinary Association* **27**, 218-222.
- Zhang, C-Y, Yang, L, Shen, Z (2008) Variance components and genetic parameters for weight and size at birth in the Boer goat. *Livestock Science* **115**, 73-79.
- Zhang, C-Y, Chen, S-L, Li, X, Xu, D-Q, Zhang, Y, Yang, L-G (2009a) Genetic and phenotypic parameter estimates for reproduction traits in the Boer dam. *Livestock Science* **125**, 60-65.
- Zhang, C-Y, Zhang, Y, Xu, D-Q, Li, X, Su, J, Yang, L-G (2009b) Genetic and phenotypic parameter estimates for growth traits in Boer goat. *Livestock Science* **124**, 66-71.
- Zhang, YD, Johnston, D, Bolormaa, S, Hawken, R, Tier, B (2014) Genomic selection for female reproduction in Australian tropically adapted beef cattle. *Animal Production Science* **54**, 16-24.