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Prepared by: Jacqui Edwards[1], Eleanor Linscott[1], Jason Archer[2], Matt Wolcott[3],
Rob Banks[3], Wayne Pitchford[4] and Dorian Garrick[5]
[1]Beef + Lamb New Zealand Genetics, Dunedin, 9058, New Zealand.
[2]AbacusBio, 442 Moray Place, Dunedin, 9016, New Zealand.
[3]AGBU, University of New England, Armidale, NSW – 2350, Australia.
[4]University of Adelaide, Roseworthy Campus, SA – 5371, Australia.
[5]Massey University, Palmerston North, 4422, New Zealand.

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Optimising Temperate Cow Herd Efficiency – A Trans-Tasman Collaboration

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Abstract

This program aimed to investigate a set of questions on how to breed for improved lifetime productivity and profitability in temperate beef cows. The program comprised of 5 projects which in total collected fertility trait and related data on over 10,000 cattle. Key questions included – what genetic variation is there in heifer fertility and how best to detect it, how important is early fertility in terms of lifetime profitability, what are the genetic relationships between Australian and New Zealand for key traits, can data and/or genotypes from commercial cows be used in either generating EBVs and/or in decision-making at the commercial level, and are there key extension messages that need strengthening in this area. Data collected on heifers post-weaning was shown to be useful in estimating genetic merit for fertility, and it is recommended that early fertility and female body composition traits be included in BREEDPLAN. The program involved strong Trans-Tasman collaboration, which will be useful in future genetics R&D for temperate beef cattle.

Executive summary

This project sought to leverage investment in phenotyping and genotyping undertaken on behalf of New Zealand beef breeders to enable research which generated and investigated data from Australian temperate beef breeding herds to improve our understanding of factors influencing cow productivity in both countries, and the Trans-Tasman genetic evaluation for these traits. To achieve this, research and development across a number of rather disparate areas has been supported by this project.

Objective 1: Improving cow descriptors

The motivation for this work came from breeder's concerns that selection for low mature weight could lead to skinny rather than smaller cows, producing "poor doers" rather than those with lower maintenance feed requirements. The challenge was to develop descriptors of cow conformation and body composition that were simple to measure, heritable and genetically correlated to the breeding objective which focused on maximising steer productivity while moderating mature cow demands on finite pasture resources. The project analysed cow weights, body condition scores and hip height from cows at three key times through the annual cycle: pre-joining, pre-calving and at calf weaning. Results showed that, within traits, records from the three measurement times were highly genetically correlated showing that cows that were genetically higher weight, height or body composition at any one time of the year will be genetically higher for the same trait at other times of the year. The program also aimed to evaluate new records to describe cow "type" for both estimation of breeding values and management decision making. The value of height, body condition score and cow ultrasound scan composition traits were evaluated in addition to existing mature cow weight and heifer body composition scan data. All the traits are heritable and highly genetically correlated across ages. A new potential trait, Net Weight (weight adjusted for height) was also evaluated. This was also heritable but did not add utility beyond the inclusion of body condition score. The project also found that heifer rib and P8 fat depths were highly genetically correlated to cow body condition. It was concluded that including body condition score at time of recording mature cow weight in the genetic evaluation for temperate beef breeds would improve the capacity of breeders to select to meet cow productivity related breeding objectives while applying selection pressure to maximise steer productivity.

Objective 2: Indicators of fertility in cows and heifers

The increasing application of artificial breeding technologies in temperate seedstock beef breeding operations, means that the opportunity to record Days to Calving, and include it in the BREEDPLAN evaluation for these breeds is declining. Given the importance of female reproduction to productivity and profitability in any beef breeding enterprise, this component of the project sought to test alternative measures of female reproduction which could contribute to the genetic evaluation for the trait(s). Results from the Beef CRC showed that age at puberty was a heritable trait when evaluated in tropical beef breeds and displayed consistently favourable genetic relationships with all aspects of female and male reproductive performance. This project collected age at puberty phenotypes in Australian seedstock Hereford and Angus heifers (N = 1000 and 3200 respectively) and incorporated these with comparable measures in New Zealand seedstock and reference herds to assess the opportunities the trait may provide to the Trans-Tasman genetic evaluation of female reproduction for temperate beef breeds. A key result from this research was the low proportion of heifers which

were cycling as they entered their first mating, whether that took the form of synchronisation for artificial insemination in the Australian seed stock herds or natural mating in NZ progeny test females. Across both breeds, the proportion of Australian seedstock heifers which reached puberty at synchronisation averaged only 52%, with substantially fewer (25%) NZ progeny test heifers pubertal as they entered natural mating. This result was unexpected and reinforces the need for better understanding of the interaction between puberty traits and mating outcomes in temperate beef females. Genetic analyses of the trait for Australian Angus and Hereford heifers showed that heritability for age at puberty, when a penalised record was generated for heifers which failed to display a *corpus luteum* up to mating was moderate (h^2 = 0.42 and 0.38 respectively). These results suggest that age at puberty could be incorporated in the genetic evaluation for temperate beef breeds and that it is the trait to be improved by selection. As importantly, it would allow genetic age at puberty to be monitored as selection pressure is applied to improve other aspects of productivity. The impact of synchronisation for artificial insemination on the results obtained for this study were unexpected. There is a need to evaluate the trait, along with lactation anoestrus interval (the time from the start of mating to the recommencement of cycling in lactating first calf females) in naturally mated heifers and first calvers to improve our understanding of these aspects of female reproductive performance before they could be incorporated in the genetic evaluation for temperate beef breeds.

Objective 3: Genotype by Environment (GxE)

Objective 3 aimed to better understand the degree to which genotype by environment interaction (GxE) impacts the genetic evaluation of all traits currently analysed in the Trans-Tasman BREEDPLAN evaluation for Angus and Hereford breeders. The notion that progeny will rank differently depending on the environment in which they are managed is a common one, though extensive research into the phenomenon has demonstrated that it is far less common than many beef breeders expect. To address this question, access to data from the Trans-Tasman Angus and Hereford BREEDPLAN analyses was negotiated with the Angus Australia, Angus New Zealand, Herefords Australia Ltd., and the New Zealand Hereford Association. Analyses were run for all traits currently reported in the Trans-Tasman evaluation for each breed, which treated records collected in each country as separate traits. The genetic correlation between results from Australia and New Zealand were estimated for each trait, which allowed conclusions to be drawn about the degree to which selection on the basis or results from Australia could be applied to generate genetic progress for the trait in New Zealand (and *vice-versa*). For the vast majority of traits in both the Angus and Herefords analyses, genetic correlations between records collected in the two countries were greater than 0.80, which is accepted in the literature as indicative of no significant GxE. For a small number of traits, scanned heifer eye muscle area in Angus and scanned heifer P8 fat depth in Herefords, the correlation was slightly below 0.8 (r_g = 0.76 and 0.65 respectively). Overall, these results supported the current strategy of analysing records from the two countries as the same trait. More importantly, the results provide confirmation to breeders in both countries that the current BREEDPLAN Trans-Tasman evaluation is applying the correct analytical methods to estimate breeding values.

Objective 5: Economic level GxE (Bio-economic modelling)

The key messages for the cow economics objective were: in most systems in most years, feed costs are low during times of feed surplus, and high during times of feed deficit. How expensive depends on factors like topography, cost of making hay or silage, opportunity cost of selling hay or silage, costs associated with supplementary feeding, and opportunity and willingness to reduce stock number.

Varying the cost of feed during time of shortage was shown to have a significant impact on economic weightings generated in the development of selection indexes and, thus, the “types” of cows identified as genetically superior for those environments. Recent Australian development of BreedObject and New Zealand herd modelling research support this conclusion. It was also apparent that the increased likelihood of drought exacerbates the divergence of index trait emphases. It was also shown that industry will need different indexes for breeding systems in different environments as the genetic difference between indexes is growing as the capacity to describe environments in the development of selection indexes improves.

To improve our understanding of the impact of these factors on breeding objective and selection index development a stochastic bio-economic model was developed which simulated the implications of managing cows of different genetic makeup in different production environments. Model scenarios were run with three levels of cow genotype and two different feeding systems to investigate whether interactions could be observed. The model outputs were a good reflection of cow performance and responded in ways that would be expected based on real systems. The models demonstrated significant genotype x feeding system interactions for cow body reserve traits (weight and body condition score) but did not show any interactions for economic level parameters (profit, revenue and marginal costs). It also did not show any interactions with reproductive outcomes, suggesting that under the conditions modelled even the most extreme genotypes were still able to achieve sufficient body condition scores at mating that reproductive performance was not affected. It may be that the scenarios modelled did not create sufficient fluctuation in cow body reserves to enable an interaction on economic parameters to emerge. Currently the outcome suggests that where body condition score fluctuated by 0.66 units (on a 5-point scale) compared to approximately 0.35 units (under the supplementary feeding system modelled) there was no need to apply significantly different breeding objectives. BreedObject V6.0 is a marked improvement over the previous version, incorporating cow body condition score and more accurate modelling of feed availability and quality. There is still room to improve both how energy reserve issues are described in the models, and in communicating these issues to provide breeders with confidence that selection directions are appropriate for the energy challenges that cows deal with in the range of farm systems present in the Trans-Tasman environments where temperate beef cattle are bred.

Objective 6: Genomics

A key objective of this research was to quantify the capacity for genomic prediction in young replacement heifers to predict future performance if the animal were retained as a breeding female. This validation of genomic predictions focussed on mature cow weight and body condition score as reproductive traits tend to be lowly heritable, and are measured on less continuous scales, meaning that much larger validation populations would be required, and these would have to be measured over longer time frames than were available for this project. It was demonstrated that even without pedigree and date of birth information, phenotypes collected in commercial females were reflective of genetic merit for mature cow weight and body condition score. Timing of measurements was found to be unimportant, with strong correlations between measurements collected into mating, pre-calving and at weaning. The project also examined the extent to which predictions in the bull breeding sector can be made more accurate by collecting phenotypes in commercial cattle. Genomic predictions which relied only on the commercial data collected by Beef + Lamb Genetics NZ (BLG), a subsidiary of Beef + Lamb NZ, were of low accuracy. This was not surprising given the limited information on fixed effects (which allow environmental variation to be quantified and accounted for in the evaluation), and date of birth for the commercial animals genotyped and phenotyped for this study. This reinforces the need for collaboration of commercial breeders with breed associations, so that genomic predictions from single-step analyses can be applied to genomic selection for commercial animals. To illustrate this, a subset of the commercial animals genotyped for the project were sufficiently related to the current BREEDPLAN Trans-Tasman Hereford reference population to allow the estimation of breeding values based on those genomic relationships. The breeding values generated describe genetic merit for animals which otherwise would have no quantitative basis for selection decisions. Generally low accuracies reflected the low level of relatedness to the reference population but do create an opportunity to apply objective selection. This demonstrates the efficacy of genotyping in commercial, unrecorded herds as a means of obtaining description of genetic merit in such animals but highlights the importance of relatedness between such animals and the reference population.

Objective 7 & 8: Extension Messaging and Industry Capacity

The agreed Trans-Tasman messages were split into high level topics which did not fit under the headings of the project milestones but were grouped into more practical categories covering: Improving cow productivity across environments, heifer puberty, commercial genomics, Trans-Tasman genotype by environment interactions and extension. Conclusions were captured as recommendations for the development of the BREEDPLAN evaluation, and those for further work before the end of the program. These are action points that the program science team have taken on-board and are implementing. Necessary lines of communication with external parties have been opened to achieve these action points.

- Work towards the introduction of body condition score EBV in BREEDPLAN
- Distribute recording protocol for DTC EBV in BREEDPLAN
- Change presentation of DTC in BREEDPLAN
- Review protocol for recording of BCS in BREEDPLAN
- More economics of BCS modelling
- BREEDOBJECT provides a means of capturing GXE at the overall combination of traits level – stressing the importance of defining the production system. Science team review of different systems within standard indexes – including BreedObject
- B+LNZ Workshop pilots developed into maternal workshop
- Further papers published
- Match mating outcomes to heifer puberty – and collect more naturally mated data.

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1 Background

1.1 Project Description

The project's goal was to help bull breeders and commercial cattle producers to improve cow maternal efficiency at the same time as producing high value carcases. The aim was to develop specific resources for Australian and NZ farmers including two inter-linked extensive projects being undertaken by BLG (Beef Progeny Test (BPT) and Tier 2 Maternal Cow Project) and adding complementary data to existing Australian projects (Angus and Hereford Beef Information Nucleus herds, Hereford Black Baldy project, and appropriate seedstock herds). The combined dataset was used to: a) define the value of recording early life fertility traits in beef cattle and potentially introduce new Estimated Breeding Values (EBVs) for early life fertility traits; b) describe the economics of contrasting approaches to breeding herd management and production systems across a range of production and market environments; and c) determine the implications for breeding trait emphasis and cow type definition, including optimising balance between maternal and carcass quality traits.

Project outcomes aimed to improve the application of BREEDPLAN for temperate beef production with new EBVs (e.g. Heifer Weaning Rate, Age at Puberty, and cow Body Condition Score) along with enhanced $ Indexes in BREEDOBJECT. The result being faster genetic progress towards a more accurately defined breeding goal(s). To further enhance adoption, clear agreed and consistent messages around maternal efficiency based on scientific evidence were aimed to be developed and these messages packaged into formats appropriate for commercial cattle producers and bull breeders. The results aimed to assist breeders and producers to respond to changing climate and enhance their ability to optimise management strategies, including stocking rate and supplementation requirements.

1.2 Project Background

This project come about through consultation with industry in both Australia and New Zealand which identified concerns and opportunities common to commercial cattle producers in both countries. With similar cattle populations and production systems, the needs of the industries are well aligned and provide the opportunity of working together warranting less duplication of R&D and a greater amount of outcomes achieved. In both countries there is a strong desire to ensure that maternal productivity of the cow herd is maximised, and concern that current selection tools and breeding decisions may be detrimental to this. Specifically, there are concerns that selection is moving away from cows being able to handle environmental fluctuations which are anticipated to become more severe in many regions with climate change occurring. There is some evidence that beef breed heifers are achieving puberty later, and that this may have negative consequences for weaning rate of young cows (first and second calvers) and lifetime productivity as mature cows. Some of these issues were highlighted within the previous Beef CRC III Maternal Productivity project, as well as subsequent MLA research (MLA project B.NBP.0761) that supports these findings and shows a clear genetic basis for heifer age at puberty and longevity traits in tropically adapted beef genotypes. The ongoing need is the development of tools to address these cow efficiency issues and to implement change within temperate beef breeding herds. Furthermore, it is believed that taking similar approaches in temperate and tropical cattle will facilitate improved adoption across Australia.

At the same time, there is a need to target premium markets and ensure that finishing cattle are hitting market specifications for both grass-fed and grain-fed production. The requirement to balance finishing traits with maternal ability to optimise profit both on-farm and across the value chain is increasingly relevant. Especially as the pressure to produce high-value beef to achieve premium prices continues simultaneously with the need to have efficient cows adapted to increasing climatic variability. This is coupled with more general concerns that;

1) there are differences between production systems based on farm management style, region, country and target markets that are currently not adequately addressed, and
2) current $ Indexes in BREEDPLAN may not adequately address aspects of cow herd efficiency including cow size, condition score and body composition along with fertility.

With the beef cow as the profit driver for many commercial farmers, having the selection tools and balanced emphasis for important cow-herd traits is a necessity. Associated with these concerns was a perception among commercial farmers that data collected on animals in seedstock herds has less relevance to their operations, or that they are unable to capture the full benefit of improved genetics under their commercial conditions. The MLA Southern Beef Compliance project (B.SPB.0110) goes some way to addressing these concerns but lacks sufficient pedigreed grass-fed carcasses for robust analysis – a gap this project aimed to address.

Background R&D that has contributed to current understanding includes the Beef CRC III Maternal Productivity project, and ongoing work on breeding objectives for beef cattle in BREEDOBJECT version 6. New projects have been developed since the Maternal Productivity project. Including Beef Information Nucleus (BIN) herds in Australia where daughters are retained for at least one calving, the Hereford "Black-Baldy" Trial (both co-funded by the MLA Donor Company), and more recently in New Zealand, two new projects that include R&D into aspects of maternal efficiency. These are:

1) Beef + Lamb NZ Genetics Beef Progeny Test Project
2) Beef + Lamb NZ Genetics Beef Maternal Cow Tier 2 Project

In addition, some seedstock breeders were collecting records of cow condition score, not currently used in genetic evaluation, but which will become directly relevant with the inclusion of cow condition score as a breeding objective trait in BREEDOBJECT v. 6.

Importantly, all the research projects listed above were based on commercial cattle herds rather than bull breeding herds, and so utilising these herds with additional measurements to better describe cow type, fatness and fertility had the inherent advantage (compared to measurements in pedigreed bull breeding herds) of addressing a key inhibitor of uptake (i.e. the question of relevance to the commercial situation). Moreover, the aim of utilising genotypes alongside phenotypes from these herds within a one-step genomic BREEDPLAN analysis will automatically appropriately weight the genomic predictions towards commercially relevant traits.

During 2015, MLA and their counterpart in NZ, BLG facilitated Trans-Tasman discussions and workshops aimed at exploring opportunities for mutually beneficial collaborative R&D. One focus area that was highlighted in those discussions was maternal beef cow efficiency, with some clear gaps in data collection identified, and areas of mutually beneficial data analysis.

2 Project objectives

A set of outputs were developed to enhance the ability and confidence of producers and breeders in Australia and New Zealand to improve the maternal cow herd by balanced selection, while also improving carcase traits. More specific outputs to achieve this outcome included:

1) Approaches to improve the description of maternal cow traits in BREEDPLAN will be developed e.g. methods to better describe "cow type" beyond weight alone will be developed, including assessing the value of additional measurements such as cow condition score.

2) Potential measurements in young heifers, such as scanning for age of puberty or antral follicle count, as tools to better predict and improve cow fertility and stayability will be assessed. If these prove valuable in assisting selection for improved lifetime profitability, they would be introduced to BREEDPLAN as EBVs and included appropriately in BREEDOBJECT index procedures.

3) An assessment of Trans-Tasman genotype by environment interactions will be made on both Angus and Hereford data sets, to assess the on-going approach to joint analyses and to enhance confidence in the analysis results for both Australian and New Zealand breeders. This improved confidence will underpin breeders in both countries utilising the full gene pool available, resulting in greater Trans-Tasman flow of genes and improved genetic gain in Australia and New Zealand. This includes both between- and within-country GxE, reflecting different production systems and environments in both countries.

4) The assessment of genotype by breed interactions will be possible given the number of Angus and Hereford bulls mated to both Angus and Hereford cows, and through collection of data from appropriate seedstock operations linking across the Trans-Tasman gene pools of the two breeds.

5) New approaches to breeding objective development will be explored to compare the impact of alternative approaches to managing animals particularly during feed deficits (e.g. supplementation vs mobilising energy reserves) on the appropriate balance of maternal traits (e.g. cow size, ability to maintain or recover condition, etc). New indices will be made available, and where appropriate will differentiate genetics based on the nutritional environment experienced by breeding cows (including management approaches and physical environment). Proxy measures of environment will be explored, such as fluctuations in cow condition score using data described in 1 (above). This will build on existing work in BREEDOBJECT, and help build industry understanding of how to use BREEDOBJECT Indexes.

6) Genotypes collected on the cattle involved in the research will be used to develop accurate relationships between commercial animals (lacking traditional pedigree information), and will also contribute to enhancing the BREEDPLAN database with more genomic data collected on commercial animals (leading to improved genomic prediction of merit in breeding herds relevant to commercial conditions). The genotyping initiative in this project is significant with over 25,000 new genotypes proposed that would contribute to a one-step genomic evaluation in BREEDPLAN including commercial data. This provides a direct route to have the commercial data resource developed in this project contribute to the prediction of EBV in seedstock herds, extending the current limited extent to which this facility is used. Moreover, the quantity of genotype information available is critical to the commercial viability of the genomic evaluation (for a range of reasons). Hence this initiative will provide an important boost to the application of genomic selection in the cattle populations using the BREEDPLAN system.

7) An extension package around maternal efficiency will be jointly developed, for future delivery to Australian and New Zealand cattle farmers. This will result in common agreed, clear and consistent messages on a topic which is of significant debate among breeders and farmers in both countries. Note that this project will cover package development, while delivery will occur outside of the project.

8) Development of industry capacity. This will occur at two levels. Firstly, commercial cattle farmers and breeders will have significant involvement in the project, building their knowledge and involving them in communicating outcomes to their peers. Secondly at a scientific level, an expanded team which includes leading beef genetics researchers in both Australia and New Zealand collaborating and providing alternative perspectives will benefit the on-going development of genetic tools to support beef cattle breeding in both countries.

3 Methodology, Results and Discussion

The methodology and results for each of the objectives are presented separately in this section.

3.1 Objective 1 – Improving Cow Descriptors

3.1.1 Plan for collection of key measurements

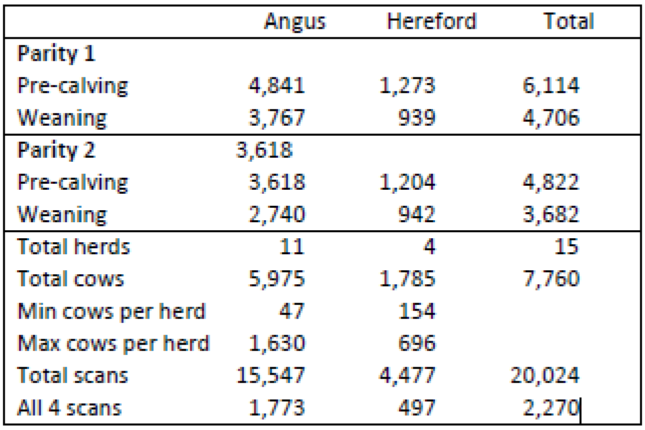
Background

The Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) ran a major project on Maternal Productivity in southern Australia. The project was initiated by concerns by breeders that too much selection emphasis has been placed on feedlot and carcass performance and this has led to cows that will be less productive, especially during periods of feed shortage. The project ran 4 lines of cattle (High-Fat, Low-Fat, High-RFI, Low-RFI) that differed in fatness and feed efficiency. They were run on two stocking rates and had group pasture feed intake measured weekly for 3.5 years on research stations in South and Western Australia.

In addition to the research station work, cows were scanned for body composition in 15 seedstock herds. The aim of this work was to quantify genetic variation in cows with changes in seasonal feed supply and physiological state (pregnancy and lactation). Breeders were also interviewed to capture in-depth concerns and beliefs about genetic improvement in maternal productivity. One of the concerns raised was that of the current BREEDPLAN EBV for mature cow weight which is designed to quantify cow feed intake on the assumption that larger cows will eat more feed. However, a problem identified with this is that cows can be lighter because they are genuinely smaller cows (expected to have lower feed intake which is good) or because they have lower body condition which is considered a bad thing as it is related to conception rate and ability to raise a live calf.

During the CRC, data was collected on weight, height, rib and rump fat depth, loin eye muscle area, intramuscular fat content and body condition score. This was done at four time points: pre-calving and weaning at first and second parity. The total number of cattle measured was 7,760 although only 2,270 had complete data on all four time points (Table 3.1.1). This data will provide valuable information for developing descriptors of cow body condition and modelling condition at different times of the year. However, a limitation of the project was that it missed data collection at joining which is often when cows are at their minimum body condition.

Table 3.1.1: Number of cattle measured by breed and time



	Angus	Hereford	Total
Parity 1			
Pre-calving	4,841	1,273	6,114
Weaning	3,767	939	4,706
Parity 2	3,618		
Pre-calving	3,618	1,204	4,822
Weaning	2,740	942	3,682
Total herds	11	4	15
Total cows	5,975	1,785	7,760
Min cows per herd	47	154	
Max cows per herd	1,630	696	
Total scans	15,547	4,477	20,024
All 4 scans	1,773	497	2,270

During the project, information was collected on cows in an attempt to provide descriptors of cow body condition and "type" that relates to Maternal Productivity or Efficiency. These included weight, height and body condition score. While body condition score seems like a sensible trait to be recording, it has been recorded at calving time in the Australian "Black Baldy" project and it lacks variation and is questionable about whether it is accurately scored. To date it has been scored on 900 cows an average of just over two times per cow (1900 scores so range 1-3 calvings). That said, a preliminary analysis of condition scores at weaning time submitted by Angus breeders to BREEDPLAN (N = 17,541), estimated the heritability as 0.15 and in Herefords a heritability of 0.24 (N=5,211).

The 900 cows that have been part of the Black Baldy project in Australia were intended to be measured for weight and height at joining in 2017 to add accuracy to the existing information on cow description. Just a subset were actually measured as intended and so these ended up being less informative than desired. In Australian seedstock herds there were almost 2300 cows measured at more than one parity (Table 3.1.2). In New Zealand project herds (Table 3.1.3: BPT and Maternal Cow projects, on commercial properties) there have been 6,974 cows and 1,146 first-calving heifers recorded, the majority of which have been measured at more than one parity. In the Australian seedstock herds 1600 of the cows have already been genotyped. A genotyping strategy was developed to enable genomic analysis of body condition in the remaining seedstock and commercial cows in the project as outlined in objective 6 of this report.

Table 3.1.2: Recording of Cow Traits in Australian Seed Stock herds

Herd	Heifer	Cow BCS				
	Number	Mating	Pre-calving	Weaning	Technician Required	Mating date
Angus						
Te Mania	631	Yes	Yes	Yes	No	15/10/2017
Knewleave	67	No	No	No	Yes	15/10/2017
Rennylea	312	Yes	No	Yes	No	01/09/2017
Bald Blair	165	Yes	No	Yes	No	10/10/2017
Straban	60	No	No	No	Yes	20/10/2017
Kennys Creek	140					14/10/2017
Pennyroyal	135	N/A	N/A	N/A	N/A	01/09/2017

Table 3.1.3: Recording of Cow Traits in NZ Project Herds

Herd	Project	No cows	No replacement heifers – cohort 1	Cow BCS			Approx. Mating date
				Mating	Weaning	Pre-calving	
Angus							
Whangara	BPT	962	134	Yes	Yes	Yes	25 Nov
Rangitaiki	BPT	950	218	Yes	Yes	Yes	20 Jan
Tautane	BPT	602	138	Yes	Yes	Yes	25 Nov
Caberfeidh	BPT	189	34	Yes	Yes	Yes	15 Dec
Mt Linton	MCP	2,643	304	Yes	Yes	Yes	15 Dec
Halden Station	MCP	118	NA				
Hereford							
Mendip Hills	BPT	646	152	Yes	Yes	Yes	15 Dec
Orari Gorge	MCP	226	81	Yes	Yes	Yes	15 Dec
Halden Station	MCP	419	NA	Yes	Yes	Yes	15 Dec
Longspur	MCP	219	85	Yes	Yes	Yes	15 Dec
Total		6,974	1,146				

3.1.2 Recommendations on better description of cow attributes (“type”) within BREEDPLAN evaluation system

The aim of this part of the program was to develop improved descriptions of cows that have greater uptake by breeders and improved description of the desired phenotype or breeding objective. Currently breeders select for improved productivity (beef production per hectare) by selecting for an index with positive weighting on growth and carcass weight but negative weighting on mature cow weight. The aim was to maximise meat production (output) per unit area where the input is feed intake and the selection criteria to reduce intake (especially in the cow herd) is mature cow weight. Mature weight is measured at the time of calf weaning. The motivation for this specific work came from breeder’s concerns that selection for low mature weight could lead to skinny rather than smaller cows, producing “poor doers” rather than those with lower maintenance feed requirements.

The challenge was to develop descriptors of cow “type”, “shape” or “size” that are simple to measure, heritable and genetically correlated to the breeding objective. The premise behind this is an assumption that the breeding objective will include a desire to select for smaller cows that are assumed to have lower feed requirements; cows in higher body condition that are assumed to be more able to cope with low feed availability often faced in the season following calf weaning (i.e. autumn in southern Australia or winter in the Australian Tablelands or New Zealand).

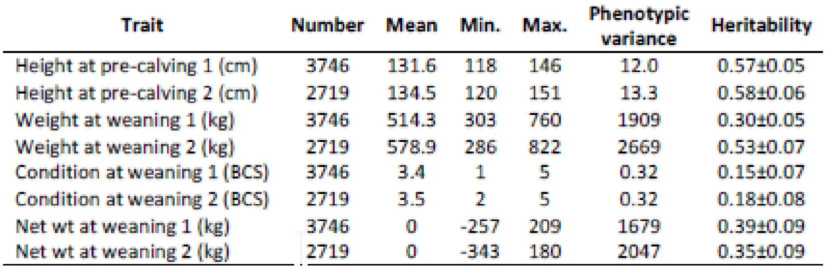
Cheap on-farm measures that could be added to mature cow weight were height and body condition score. More expensive measures included ultrasound scans of fat depth and eye muscle area. The CRC for Beef Genetic Technologies (Beef CRC III) collected data on large numbers of Angus cows in seedstock herds and this is the data utilised herein. The data has already been published by Donoghue *et al*. (2018) and De Faveri *et al*. (2018) and was analysed in a novel way for this program.

A concern with body condition score was its subjectivity, being a visual score, and its sensitivity being categorical on a 1-5 scale. Thus, an alternative was deemed to be desirable. Given that “big” cows are both tall and heavy, height data was used as an attempt to separate size from shape or condition which weight alone was unable to do. Weight adjusted for height was evaluated as a potential descriptor of cow condition and was compared to condition score as well as ultrasound scan traits. In the same way that residual or net feed intake is a measure of efficiency as intake is adjusted for mid-weight and weight gain during a feed test, weight adjusted for height is residual or net weight.

The regression of weight on height was reported as this is interpreted as a measure of size. More work will need to be conducted on economic values, but at this stage it was proposed that instead of having a negative value on mature cow weight, there may be a negative value for height and a positive value for weight adjusted for height.

The regression equation of weight at weaning on pre-calving height was weight = -614.3 (±40.0) + 8.6 (±0.3) x height for first lactation ($r_2 = 0.3$) and weight = -582.6 (±48.2) + 8.6 (±0.4) x height for second lactation ($r_2 = 0.3$). It was interesting that the regression coefficient was 8.6 kg/cm for both ages, albeit with a large intercept. Within the range of cow weights herein, if the regression went through the origin then a rough guide would be 4 kg per cm so a 130 cm cow would weight 520 kg when in good condition (3.5).

Table 3.1.2.1: Summary of data, variance and heritability estimates



Trait	Number	Mean	Min.	Max.	Phenotypic variance	Heritability
Height at pre-calving 1 (cm)	3746	131.6	118	146	12.0	0.57±0.05
Height at pre-calving 2 (cm)	2719	134.5	120	151	13.3	0.58±0.06
Weight at weaning 1 (kg)	3746	514.3	303	760	1909	0.30±0.05
Weight at weaning 2 (kg)	2719	578.9	286	822	2669	0.53±0.07
Condition at weaning 1 (BCS)	3746	3.4	1	5	0.32	0.15±0.07
Condition at weaning 2 (BCS)	2719	3.5	2	5	0.32	0.18±0.08
Net wt at weaning 1 (kg)	3746	0	-257	209	1679	0.39±0.09
Net wt at weaning 2 (kg)	2719	0	-343	180	2047	0.35±0.09

The heritability of cow weight at weaning first calf is 0.30, pre-calving of second calf 0.38 and weaning of second calf 0.53 (Donoghue *et al*., 2018). In the Beef CRC, height was measured pre-calving but not at weaning assuming that it would be highly genetically correlated and, therefore, not necessary to be recorded. Results presented by Donoghue *et al*. (2018) showed that height at weaning for parity one and two Angus females was highly heritable (h_2 = 0.57 and 0.58 respectively) and confirmed that measures at the two times were highly genetically correlated (r_g = 0.98). Thus, cow weights at weaning have been adjusted using their height pre-calving.

The heritability of body condition score was much lower than for weight or height, being 0.15 at weaning of first calf, 0.10 second pre-calving and 0.18 at weaning of second calf (Table 3.1.2.1). Even after adjustment for height, the heritability of (net) weight was 0.39 at first weaning and 0.35 at second weaning. Thus, while height was a highly significant covariate, there was still ample genetic variation in cow weight at weaning.

Table 3.1.2.2. Genetic and phenotypic correlations of height adjusted (net) weight with other traits

Trait	Net weight at weaning 1 Genetic	Net weight at weaning 2 Genetic	Net weight at weaning 1 Phenotypic	Net weight at weaning 2 Phenotypic
Weight at heifer ultrasound	0.43 ± 0.14	0.22 ± 0.15	0.33 ± 0.03	0.27 ± 0.03
Weight pre-calving 1	0.48 ± 0.12	0.49 ± 0.11	0.31 ± 0.03	0.32 ± 0.03
Weight at weaning 1	0.81 ± 0.06	0.69 ± 0.1	0.79 ± 0.01	0.45 ± 0.03
Weight pre-calving 2	0.52 ± 0.11	0.61 ± 0.1	0.46 ± 0.03	0.42 ± 0.03
Weight at weaning 2	0.64 ± 0.11	0.85 ± 0.04	0.44 ± 0.03	0.82 ± 0.01
Height pre-calving 1	0.13 ± 0.17	0.23 ± 0.15	-0.19 ± 0.03	0.07 ± 0.03
Height pre-calving 2	0.18 ± 0.16	0.22 ± 0.15	0.11 ± 0.03	-0.07 ± 0.03
Net weight at weaning 2	0.74 ± 0.11	N/A	0.45 ± 0.03	N/A
BCS pre-calving 1	0.22 ± 0.18	0.17 ± 0.17	0.14 ± 0.03	0.13 ± 0.03
BCS at weaning 1	not converged	not converged	not converged	not converged
BCS pre-calving 2	0.51 ± 0.15	0.71 ± 0.12	0.29 ± 0.03	0.3 ± 0.03
BCS at weaning 2	not converged	not converged	not converged	not converged
EMA at heifer ultrasound	-0.12 ± 0.19	0.04 ± 0.18	0.14 ± 0.03	0.11 ± 0.03
Rib fat at heifer ultrasound	not converged	not converged	not converged	not converged
P8 fat at heifer ultrasound	-0.13 ± 0.15	-0.13 ± 0.14	0.07 ± 0.04	0.04 ± 0.04
IMF at heifer ultrasound	-0.53 ± 0.20	-0.36 ± 0.22	-0.01 ± 0.03	0 ± 0.03
EMA at weaning 1	0.56 ± 0.13		0.47 ± 0.02	

IMF at weaning 1	0.30 ± 0.16		0.34 ± 0.03	
Rib fat at weaning 1	0.55 ± 0.11		0.49 ± 0.03	
P8 at weaning 1	0.50 ± 0.11		0.45 ± 0.03	
EMA at weaning 2		0.72 ± 0.09		0.51 ± 0.03
IMF at weaning 2		not converged		not converged
Rib fat at weaning 2		0.50 ± 0.10		0.42 ± 0.03
P8 at weaning 2		0.59 ± 0.09		0.43 ± 0.03

The genetic correlation between net cow weight and actual weight at weaning of their first calf was 0.81 and at second weaning was 0.85 (Table 3.1.2.2). This suggests that 66% of the genetic variation in cow weight (0.812=0.66) is independent of height. In many ways this is comforting in that more (2/3) of the variation is associated with condition than with size (1/3 associated with height). This was more than expected and suggested that the current measure may be better than expected.

As the net cow weight was a phenotypic adjustment, it is possible that the trait is still genetically correlated with height. At first weaning the correlation was 0.13 and at second weaning 0.22, both reasonably low although possibly not zero, albeit not significantly different (Table 3.1.2.2).

The net cow weight trait was genetically quite repeatable with a genetic correlation between first and second weaning of 0.74 (Table 3.1.2.2). We are still trying to estimate the genetic correlations between net cow weight and body condition score at weaning as the current models are not converging. This may be because the traits are so highly correlated given that the genetic correlation between net cow weight at first and second weaning was 0.51 and 0.71 respectively with body condition score pre second calving. A good result was that net cow weight was moderate-strongly genetically correlated with both muscle (EMA) and subcutaneous fat (Rib and P8) with values ranging from 0.50-0.72 (Table 3.1.2.2). This provides hope that the trait that is cheap to measure can provide utility as a descriptor of cow composition.

Donoghue *et al*. (2018) and De Faveri *et al*. (2018) both reported high genetic correlations between cow composition traits (fat depth and muscle area) and the same traits measured as heifers. It is of interest herein to know how net cow weight is related to heifer body composition ultrasound traits. Somewhat surprisingly, the correlations were very low at -0.13 for P8 fat depth and -0.12 for eye muscle area at first weaning. They were similarly low for second weaning being -0.13 and +0.04 respectively. It was surprising and potentially concerning that the genetic correlation with IMF was reasonably strong and negative (-0.53 and -0.36 at first and second weaning respectively).

Further work is required on developing economic values and on the genetic relationship between net cow weight and milk production as indicated by the 200d maternal or milk EBV. Unfortunately, the relationship between cow composition and maternal performance in the seedstock herds was not possible with the CRC Angus data set. There may be other data sets and some information collected in the project herein and in related proposed projects that will help with this.

3.1.3 Recommendations for any changes and additions to traits analysed in BREEDPLAN

The delivery of this work was inherently linked to the scheduled program workshop led in Central Otago, April 2019. At this workshop appropriate user input and feedback was acquired that was originally scheduled to be collected before year end 2018. With permission from MLA project manager, the delivery of the extension Milestone 7.5 was extended. This was done to allow a more natural placement of the co-operator meeting to coincide with the final analysis of program data and to allow incorporation of results from analysis of potential new cow descriptors together with the results from analysis of the heifer scanning data in conjunction with the full BREEDPLAN trait matrix.

Careful consideration of the key findings from these 2 lines of work produced the following recommendations for changes to BREEDPLAN.

- Introduce BCS EBV in BREEDPLAN
- Introduce Height EBV into BREEDPLAN
- Distribute recording protocol for DTC EBV in BREEDPLAN
- Change presentation of DTC in BREEDPLAN
- Review protocol for recording of BCS in BREEDPLAN

3.1.4 Inclusion of Body Condition Score

The Australian Cooperative Research for Beef Genetic Technologies (Beef CRC) measured body composition of Angus and Hereford cows at four time points: pre-calving as heifers, weaning of first calf, pre-calving for second calf and weaning of second calf. This was conducted in almost 5000 Angus cows and 3000 Hereford cows. The Beef CRC work demonstrated that body composition traits in cows are both heritable (Table 3.1.4.1) and highly genetically correlated across time (Table 3.1.4.2). The correlations were not as high from heifers to cows (after weaning first calf), but were very high across the three cow measurement times. The primary trait that commercial producers manage is body condition which is quantified as a score. This was less heritable than the measured composition traits, but still highly correlated across time (0.96, Table 3.1.4.2).

Table 3.1.4.1: Summary of Beef CRC data, variance and heritability estimates for live weight (WT), height (HT), body condition score (CS), net weight (NW) and ultrasound measurements of eye muscle area (EMA), fat depth at the P8 (P8) and 12/13th rib (RIB) sites and intramuscular fat (IMF).

	Number	Mean	Range	Phenotypic variance	Heritability
Yearling					
Weight				927	0.53
EMA				34.44	0.27
P8				3.59	0.64
Rib				1.95	0.71
IMF				2.21	0.19
Pre-calving 1					
Weight	4889	487.7	291-748	1184	0.50
Height	4736	131.6	116-151	12.08	0.56
CS	4601	3.3	1-6	0.232	0.12
Net weight	4735	0	-168-270	1124	0.35
Weaning 1					
Weight	3893	516.0	303-818	2082	0.37
EMA	3894	59.4	29-91	43.95	0.33
P8	3894	5.9	1-29	5.84	0.51
Rib	3894	5.0	1-24	3.52	0.49
IMF	3741	5.5	0.2-8.3	2.90	0.40
CS	3545	3.4	1-6	0.355	0.27
Net weight	3762	0	-255-212	1774	0.25
Pre-calving 2					
Height	3177	134.5	117-151	13.06	0.47
Weaning 2					
Weight	2640	582.9	208-848	2848	0.51
EMA	2641	63.1	34-97	46.88	0.28
P8	2641	8.0	1-33	10.23	0.60
Rib	2641	6.6	1-20	5.76	0.52
IMF	2631	6.1	0.2-8.3	2.68	0.24
CS	2690	3.6	2-6	0.314	0.13
Net weight	2471	0	-352-242	2121	0.32

Table 3.1.4.2: Beef CRC Genetic correlations between traits measured at weaning 2 (objective) and earlier times (criteria).

Weaning 2	Weight	EMA	P8	Rib	IMF	Height	CS	Net weight
Yearling								
Weight	0.61	0.19	0.07	0.07	-0.27	0.60	0.17	0.48
EMA	0.19	0.55	-0.04	0.01	-0.05	0.11	0.23	0.21
P8	0.07	0.21	0.67	0.58	0.34	-0.11	0.59	0.20
Rib	0.01	0.14	0.44	0.59	0.29	-0.12	0.45	0.16
IMF	-0.29	-0.12	0.15	0.17	0.56	-0.25	0.22	-0.18
Pre-calving 1								
Weight	0.85	0.33	0.05	0.08	0.06	0.69	0.14	0.69
Height	0.57	0.13	-0.09	-0.03	-0.04	0.97	-0.08	-0.03
CS	0.00	0.11	0.53	0.44	0.44	-0.48	0.44	0.42
Net weight	0.10	0.09	0.08	0.04	0.08	-0.65	0.19	0.70
Weaning 1								
Weight	0.94	0.68	0.47	0.52	0.39	0.75	0.45	0.83
EMA	0.59	0.97	0.48	0.57	0.35	0.45	0.34	0.61
P8	0.34	0.45	0.98	0.95	0.73	0.09	0.69	0.48
Rib	0.33	0.45	0.86	0.98	0.71	0.15	0.63	0.45
IMF	0.15	0.29	0.50	0.55	0.98	0.03	0.49	0.20
CS	0.31	0.59	0.72	0.77	0.73	-0.12	0.96	0.63
Net weight	0.60	0.49	0.45	0.46	0.29	0.04	0.62	0.85
Pre-calving 2								
Height	0.79	0.36	0.17	0.26	0.07	1.00	0.13	0.31
Weaning 2								
Weight	1.00	0.82	0.56	0.55	0.29	0.79	0.66	0.86
EMA	0.82	1.00	0.64	0.61	0.41	0.36	0.78	0.85
P8	0.56	0.64	1.00	0.89	0.60	0.17	0.89	0.66
Rib	0.55	0.61	0.89	1.00	0.57	0.26	0.86	0.61
IMF	0.29	0.41	0.60	0.57	1.00	0.07	0.62	0.35
CS	0.66	0.78	0.89	0.86	0.62	0.13	1.00	0.82
Net weight	0.86	0.85	0.66	0.61	0.35	0.31	0.82	1.00

Concerns raised by commercial breeders about the Beef CRC data were:

1) that many commercial cattle herds are run with cows in lower body condition that the CRC collaborating herds; and
2) that measuring at pre-calving and weaning does not capture information at the time of lowest condition of cows in an annual production cycle so other times such as pre-mating may be more important.

With this feedback taken into account, the aim of our project was to collect data body condition data on additional herds and at pre-mating as well as other key times in the annual production cycle. All animals scored were multi-parous lactating cows. In New Zealand body condition is scored on a 1-9 scale whereas in Australia it is scored on a 1-5 scale. The mean condition score at weaning was 6.9, pre-calving 5.7 and pre-joining 6.9 with distributions presented (Fig. 3.1.4.1). This is likely similar to Australian results (Table 3.1.4.1) except that in NZ they are in lower condition pre-calving.

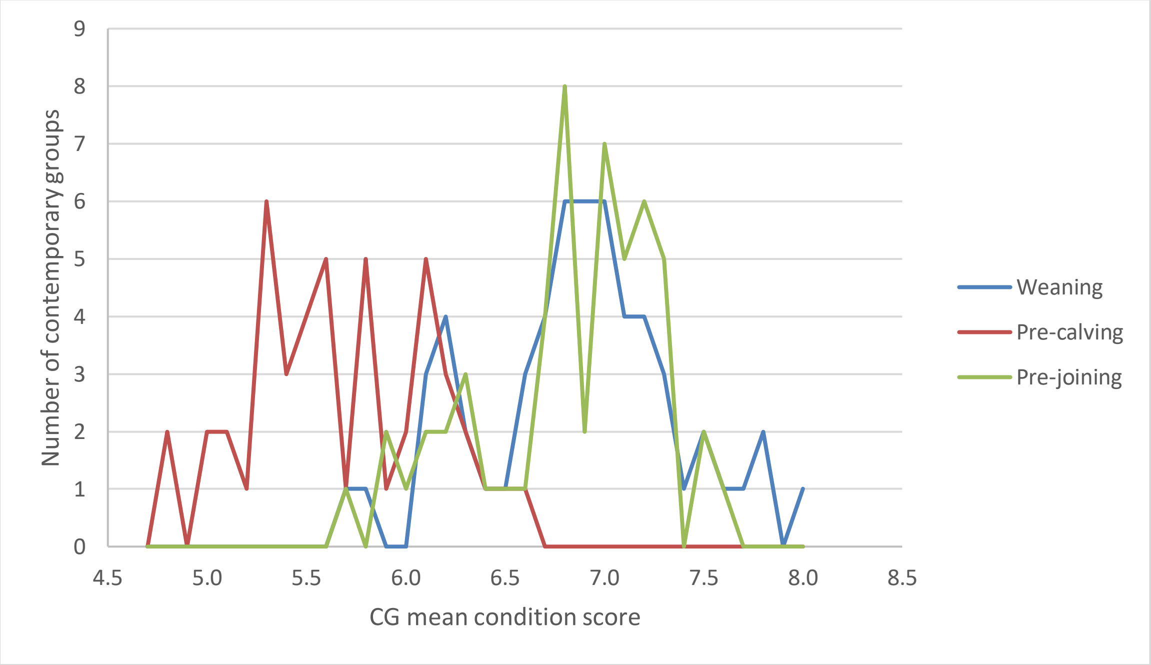


Fig. 3.1.4.1: Distribution of condition scores for contemporary groups as defined by herd, year and cow age. Only means of contemporary groups with >5 cows shown.

The heritability of body condition score was higher in New Zealand (0.38-0.41, Table 3.1.4.3) than Australian (0.13-0.27, Table 3.1.4.1). Again, the condition scores were very highly genetically correlated across time. The implications of the very high genetic correlations are twofold:

1) Selection for improved body condition throughout the annual cycle can be made by scoring at the most convenient point in time; and
2) There is negligible genetic variation in change in body condition.

The results support conclusions made from the Beef CRC analyses but add additional confidence given the additional numbers, different environmental conditions and additional measurement time (pre-joining).

Table 3.1.4.3: Heritabilities (on diagonal) and genetic correlations for body condition between time points for NZ cows.

	Weaning	Pre-calving	Pre-joining
Weaning	0.38 ± 0.06	0.93 ± 0.03	0.92 ± 0.03
Pre-calving	0.93 ± 0.03	0.42 ± 0.06	0.98 ± 0.01
Pre-joining	0.92 ± 0.03	0.98 ± 0.01	0.41 ± 0.06

3.2 Objective 2 - Indicators of fertility in cows and heifers

3.2.1 Abstract

The data collection for the project was completed with analysable puberty, antral follicle count, growth and body composition records collected in 4005 Angus and Hereford heifers in Australian seedstock herds and 1370 pubertal into mating and antral follicle count measurements for New Zealand BPT heifers. On average, each of the heifers evaluated for the Australian component of the project were scanned three times (ranging from 2 – 7). Heifer weight, height, fatness and condition score were within the ranges expected for animals of this class and stage of development, though there were clear effects of the dry conditions which prevailed in 2018 on weight and body condition, which resulted in lower percent pubertal for a proportion of herds in that year.

A key result from this research was the low proportion of heifers which were cycling as they entered their first mating, whether that took the form of synchronisation for artificial insemination in the Australian seed stock herds or natural mating in NZ BPT females. Across both breeds, the proportion of Australian seedstock heifers which reached puberty at synchronisation averaged only 52%, with substantially fewer (25%) NZ BPT heifers pubertal as they entered natural mating. This result was unexpected and reinforces the need for better understanding of the interaction between puberty traits and mating outcomes in temperate beef females. Results from the NZ component of the study showed only weak phenotypic relationships of puberty related traits with conception rates, which were consistently high (82 to 91%), or distribution of foetal ages at pregnancy testing. Calving outcomes will be available for Australian 2018 scanned seedstock heifers in the third quarter of 2019 and testing of these relationships at both the genetic and phenotypic levels will be a key area of investigating in the final phase of analyses for the project.

Genetic analyses have now been completed for the Australian Hereford and Angus data. Genetic parameters for weight and body composition traits were consistent with those in the literature. Heritability for age at puberty, when a penalised record was generated for heifers which failed to display a *corpus luteum* up to mating was moderate ($h^2 = 0.38$ and 0.42 for Hereford and Angus heifers respectively), and consistent with results reported for heifers scanned in northern Australia. These results suggest that age at puberty could be incorporated in the genetic evaluation for temperate beef breeds and that the trait to be improved by selection. As importantly, it would allow genetic age at puberty to be monitored as selection pressure is applies to improve other aspects of productivity. The high investment of time and expertise required to collect accurate age at puberty records is a limitation to large scale adoption of the serial scanning methods employed for this study. Its application in intensively recorded reference population and research herds, however, would centralise the cost of recording the trait and maximise the value of results to the industry.

The limitations of collecting puberty records in heifers which are synchronised for artificial insemination were highlighted by this project. There is a clear need to evaluate age at puberty in naturally mated females, and to expand the research to include lactation anoestrus interval in lactating, first calf temperate beef females.

3.2.2 Project objectives

The BREEDPLAN evaluation for temperate beef breeds currently analyses days to calving (DTC) and scrotal circumference to describe genetic differences in reproductive performance. In the current Angus and Hereford BREEDPLAN evaluations DTC has a heritability of 0.06. This means that, while there are opportunities to make genetic progress for the trait based on selection for DTC, rates of progress will be slower than would be the case for a more highly heritable trait. More accurate description of female reproductive performance in the evaluation would also provide better opportunities to monitor this economically important trait as selection pressure to improve other traits was applied. The female reproduction component of the Trans-Tasman Beef Cow Productivity Project was developed following consultation with researchers, seed-stock breeders and their representative bodies in southern Australia and New Zealand, who expressed an interest in better understanding the genetics of female reproduction in temperate breeds, and in an investigation of the opportunities to improve description of the trait(s) in their genetic evaluations. The aims of the project were to exploit methodologies and expertise developed in evaluating female reproduction in tropical breeds to investigate the variation in age at puberty and related traits in temperate beef females, and to determine the degree to which variation in these has a genetic basis. The project also aims to establish the genetic relationships of age at puberty and related traits with other, economically important traits currently in the evaluation for temperate breeds.

3.2.3 Methodology

3.2.3.1 Animals, pedigree and performance data

3.2.3.1.1 Australian seedstock herds

In 2017 and 2018, ultrasound scanning to detect first oestrous (and therefore age at puberty) was conducted on 3093 Angus heifers (6 seedstock herds) and 922 Hereford heifers (from 3 seedstock herds). At scanning, measurements describing growth and body composition traits were also collected. Herds selected for inclusion in the study all had a history of high quality pedigree and performance recording. This data has been used to build relationship matrices for genetic evaluation of the female body composition and reproduction traits for the animals evaluated for the study. Information describing the management of heifers involved in the study is documented in records submitted to BREEDPLAN. This forms the basis for BREEDPLAN contemporary groups, and this information was accessed for the genetic analysis of data collected to describe female body composition and reproduction in the current project.

3.2.3.1.2 New Zealand Beef Progeny Test herds

Data collection for the New Zealand BPT component of the project concluded at the end of 2017. Records for the study include data from 1370 heifers from five herds, with animals scanned to determine the presence of a CL (identifying the onset of puberty as described for Australian seedstock heifers above), antral follicle count and the size of the dominant follicle in non-cyclic ovaries. Also available on these animals was the results of pregnancy test data and foetal ages for pregnant females. Preg-tests and foetal aging were conducted at 3 to 4 months after bulls were introduced to the heifer herds. This represents the only source of puberty and associated ovarian scanned data in naturally mated heifers for the project, and allows an analysis of patterns of conception in naturally mated females which have been evaluated for ovarian function.

3.2.3.2 Measurements and trait definitions

3.2.3.2.1 Australian seedstock herds

Ovarian activity was assessed in heifers by real-time ultrasound scanning performed by one of three trained operators. At scanning, each ovary was viewed by ultrasound imaging using a Mindray M7Vet® scanner, equipped with a variable frequency 6LE5Vs transducer. While other options were available, imaging of ovaries for this project was undertaken at a frequency of 7.5Mhz for all animals, and to minimise variation between operators the same ultrasound unit was used at all sites.

Based on advice from co-operating breeders, scanning commenced when the first signs of oestrous were observed in their heifers, with date at first scans ranging from early April to early-September (all herds were spring calving). For animals scanned in 2017, this meant scanning began in June and, following observation that the earliest pubertal animals were not identified in a small proportion of herds, scanning commenced in April in 2018 for those herds. Scanning at 4 – 8 week intervals continued in all herds, with final scans collected at (or as close as was practically possible to) the heifer's maiden mating. The results of subsequent pregnancy test, foetal aging by ultrasound scanning and subsequent calving outcomes (still not available for heifers scanned in 2018 at the date of this report) will provide additional information on ages at conception and, therefore, the distribution of age at puberty. These data will also form the basis of estimating relationships of heifer puberty and reproductive outcomes for the heifer's first mating.

Scanning for ovarian function aimed to record age at puberty in beef heifers. This was achieved by the identification of a *corpus luteum* (CL), which indicates a female has recently ovulated. The presence of a *corpus albumens* (CA: a regressing CL) was also interpreted as indicative of cycling, with the date of detection used similarly to calculate age at puberty. The number of follicles greater than 2mm, (antral follicle count (AFC)), was also recorded. Higher AFC has been favourably associated with heifer pregnancy rate in cross-bred beef heifers (Cushman *et al*. 2009), and lifetime reproductive performance in dairy cows (Mossa *et al.* 2012). Both studies reported high repeatability for AFC (r = 0.65 – 0.94), within age categories and across years. If this can be borne out in beef heifers, the appeal of a single ultrasound measure to characterise early and lifetime reproductive performance is significant, when compared to the serial scanning required to determine age at puberty. Finally, the size of the largest follicle in ovaries not displaying a CL or CA was also recorded. Dominant follicle size increases as cows approach ovulation, and this may be exploited to identify heifers which are about to cycle, but are not yet displaying a CL or CA. Based on ovarian scanning results, the following traits will be defined:

> **Age at puberty (AP)** was calculated as a trait of females which displayed a CL prior to mating, and calculated as scanning date minus date of birth.
>
> **Penalised AP (APP)** generated an age at puberty record for heifers which had failed to display a corpus luteum prior to mating. APP was calculated for these animals as the maximum AP for their contemporary group plus 21 days (similar to the method employed to produce a days to calving record for cows which fail to calve in the BREEDPLAN analysis).
>
> **Pubertal into mating (PUB)** was a binary trait which identified heifers which had cycled at any time up to mating (1) or not (0).
>
> **Antral follicle count (AFC)** was the total number of follicles greater than 2mm, visible by ultrasound examination of non-cycling ovaries.

Size of the dominant follicle (FOL) for non-cycling heifers was measured (in mm) with the scanner's in-built callipers.

At each ovarian scan records of liveweight, hip height, body condition score and P8 fat depth were recorded following the protocols described by Johnston *et al*. (2009) for tropically adapted heifers involved in the Beef CRC Northern Breeding Project. These will allow characterisation of heifer weight, height and condition at puberty, and an examination of the genetic variation present for these, as well as their potential as indirect genetic indicators of the harder to measure puberty traits evaluated by ultrasound scanning for the current project.

3.2.3.2.2 New Zealand Beef Progeny Test herds

A key difference in protocols across in Australia and New Zealand was that the vast majority of NZ BPT heifers (86%) only received a single ovarian scan; as they entered mating. This was not unreasonable as scans undertaken prior to mating never identified more than 9% of females as pubertal (range = 0 to 9%). Additionally, these commercially managed females did not have dates of birth recorded, making age at puberty impossible to calculate. The 1 / 0 'pubertal into mating' trait could be generated for the heifers, however, and foetal age information provided a useful descriptor of their first reproductive outcome to evaluate the efficacy of ovarian scanned traits. The initial dataset contained 1870 records. Of these, 320 were records collected prior to the into-mating scan and were removed from these analyses. Of the remaining 1550 heifers, 180 did not have a valid pregnancy test result and were also omitted from these analyses, leaving 1370 heifers with analysable results. Finally, as the presence of a CL supresses follicular development, dominant follicle size was a trait in non-cycling females only, meaning that only 975 heifers had analysable records for the trait. Within herd and year groups, numbers of animals ranged from 63 to 298 animals.

3.2.3.3 Data Analysis

For all traits measured in the Australian Angus and Hereford heifers evaluated for the Australian seedstock component of the project, descriptive statistics were generated using proc means in SAS. Genetic analyses were undertaken using ASReml, with relationship information extracted from the Herefords Australia Ltd. or Angus Australia database to build a 3 generation pedigree separately for each breed. Univariate analyses were conducted to determine genetic parameters for growth, body composition and ovarian scanned traits, with EBVs estimated as the solutions for the random animal effect. Bivariate analyses were undertaken to estimate genetic correlations between selected puberty and growth and body composition traits.

For New Zealand BPT heifers, descriptive statistics for ovarian scanned traits were estimated using PROC MEANS in SAS. The power of antral follicle counts to predict conception and foetal age traits were also estimated in SAS using generalised linear modelling techniques.

3.2.4 Results and Discussion

Scanning for the second year of the project was completed and recording levels have met the requirements set out for the project. As important as the number of animals evaluated was the frequency with which animals were scanned. Excellent co-operation from veterinary and technical staff recruited to undertake scanning in 2017 and 2018 saw a minimum of 2 scans per herd, with some key herds getting up to 4 scans from weaning to mating (average scans per animal = 3). Negotiations around access to Angus Australia pedigree and performance data were finalised in October of 2019, two months before the completion date for the project. This limited the opportunity to conduct analyses for this component of the data until that time, and to publish results relating to Angus females, as was done for the Hereford component of the project (Wolcott *et al*. 2019). Despite this, the following sections outline key findings for both breeds which provide a basis for recommendations regarding the recording of age at puberty for genetic evaluation in temperate beef breeds.

3.2.4.1 Impact of dry conditions in 2018 on scanning program and results

The dry conditions which prevailed in much of south-eastern Australia over autumn, winter, and early summer of 2018 impacted the suitability of heifers from several co-operating herds for ovarian scanning. The NSW DPI heifers at both Trangie and Glen Innes were under significant nutritional stress over this period, leading to their transfer to a new location (Wollongbar research station) part way through the scanning program. Up to their relocation, the animals were in declining condition and on-site management reported that there was no evidence of cycling behaviour. The decision was made to remove the animals from the project and approach co-operating seedstock breeders to see if the heifer cohorts could be increased in the 6 remaining herds to meet the target of 1500 Angus and 500 Hereford heifers scanned for the year, which was achieved.

Of the cohorts remaining in the project, there was a clear impact of unfavourable seasonal conditions on heifer cyclicity rate. Percent pubertal into mating results were significantly down on those observed in 2017 in some herds, with average results 7 and 23% lower for Angus and Hereford heifers respectively. The variation in seasonal conditions over the two years of the project presents opportunities to quantify the impact of heifer condition on age and condition at puberty. The impact of this on the genetic parameters estimated from these data will be reported on in the final report.

3.2.4.2 Description of data

Table 3.2.4.2.1 presents descriptive statistics for live animal measurements (other than ovarian scanning results) from the first (post-weaning) and final (into mating) round of recording in Australian seedstock herds over both years of the project. Matings were almost exclusively by AI, and final scans took place on the first day of synchronisation programs in many herds, or as close to the date of synchronisation as was practically possible for the remainder.

Changes in weight, height and body composition traits over the scanning period can be observed by comparing post-weaning and into mating results in Table 3.2.4.2.1. These results show that, on average, Angus heifers were heavier and in better condition at their post-weaning scan than their Hereford counterparts. The initial difference (51kg LWT, 1.5cm HH and 1.4mm P8 fat) was substantially reduced by the into mating scan, with Hereford heifers only 20.2kg lighter than their Angus contemporaries, 0.7cm shorter, with comparable fat and body condition.

Table 3.2.4.2.1. Descriptive statistics for live animal measurements collected at their first (post-weaning) and final (Into mating) ovarian scan.

Trait /		Post-weaning			Into mating		
Breed	Units	Number	Mean	s.d.	Number	Mean	s.d.
Angus							
Liveweight	kg	3085	314.5	48.3	3149	364.1	51.6
Hip Height	cm	1816	116.9	4.5	3151	123.4	4.0
Condition score	1 – 5 score	3093	2.8	0.7	3150	3.3	0.6
P8 fat depth	mm	3039	5.0	2.9	3151	6.7	3.1
Hereford							
Liveweight	kg	922	262.9	35.0	870	343.9	62.9
Hip Height	cm	921	116.7	4.6	871	122.7	4.5
Condition score	1 – 5 score	922	2.8	0.6	871	3.4	0.8
P8 fat depth	mm	837	3.6	1.8	861	6.9	3.9

Table 3.2.4.2.2 presents descriptive statistics for ovarian scanned traits recorded in Angus and Hereford heifers across both years. Antral follicle counts and dominant follicle size are discrete records for the post-weaning and into mating scanning times, while the results presented for proportion of heifers pubertal into mating (PUB) identifies those animals which showed a CL at any scan up to mating.

Table 3.2.4.2.2. Descriptive statistics for ovarian scanned traits in Angus and Hereford heifers.

Trait	Measured at	Units	Records	Mean	s.d.	Min	Max
Angus							
Proportion Pubertal[1]	Cumulative	%	3093	0.52	0.50	0.27	0.74
Age at puberty	Cumulative	Days	1634	345.2	63.2	220	456
Penalised AP	Cumulative	Days	3093	395.0	70.5	220	478
Antral follicle count	Post-weaning	Count	2544	21.9	8.1	2	65
	Into Mating		2552	22.2	6.6	2	65
Dominant follicle size	Post-weaning	mm	2705	8.9	2.5	2	30
	Into Mating		1701	8.8	2.5	3	25
Hereford							
Proportion Pubertal[1]	Cumulative	%	902	0.53	0.51	0.14	0.75
Age at puberty	Cumulative	Days	481	365.8	38.3	283	433
Penalised AP	Cumulative	Days	902	396.2	44.3	283	454
Antral follicle count	Post-weaning	Count	895	23.1	7.1	0	50
	Into Mating		901	23.2	4.6	1	42
Dominant follicle size	Post-weaning	mm	422	7.9	2.1	3	15
	Into Mating		421	9.7	2.5	3	18

[1] Minimum and maximum percent pubertal results are at the herd level.

Table 3.2.4.2.3 presents the proportion of heifers identified as cycling and antral follicle counts at the post-weaning and into-mating scans by breed and herd. These results show that there was significant variation across herds for the proportion of heifers which were pubertal (displayed a CL or CA) at their first and final scans, ranging from 1 to 67% at first scanning and 2 to 89% for the into-mating scan. The low results for Hereford herds 1 and 2 were a direct result of unfavourable seasonal conditions in

2018. It is interesting to observe that the response of some breeders, to supplement heifers over this dry period, may have resulted in higher rates of puberty at both the post-weaning and into mating scans compared to those observed in 2017.

The large phenotypic variation in the proportion of heifers which were pubertal into mating was a key result of this study, and the impact of drought conditions of heifer cyclicity rates under commercial conditions present opportunities for new insight in this area. Antral follicle counts showed some variation across herds, and the average AFC of ~23 were consistent with the results of Mossa *et al*. (2012) who reported an average AFC of 16 in first parity dairy cows.

Table 3.2.4.2.3 Proportion of heifers pubertal, and antral follicle counts at post-weaning and into mating scans by breed and herd.

Herd	Heifers scanned	Percent pubertal: Post-weaning	Percent pubertal: Into mating[1]	Antral follicle count: Post-weaning	Antral follicle count: Into mating
***Angus*[2]**					
Herd1	93	36.3	54.6	26.7	22.9
Herd2	263	22.6	42.1	18.9	22.9
Herd3	298	35.2	57.8	22.2	23.0
Herd4	139	7.2	26.6	22.7	23.0
Herd5	170	40.1	53.8	20.5	22.8
Herd6	626	62.1	49.4	19.0	23.6
Herd7	122	25.2	72.2	22.4	22.0
Herd8	79	3.8	46.8	24.3	19.6
Herd9	1303	13.7	39.3	23.4	21.0
Total / Average	**3093**	**27.9**	**45.6**	**21.9**	**22.1**
Hereford					
Herd1	144	3.2	14.6	23.6	23.1
Herd2	240	6.1	22.8	21.8	23.0
Herd3	518	31.4	75.9	23.6	23.2
Total / Average	**902**	**19.8**	**51.0**	**23.1**	**23.2**

[1] Percent pubertal at the into-mating scan differs from the PUB trait as it describes results from a single scan as opposed to PUB which is cumulative across all scanning times.

[2] Angus heifers from herds 1, 4 and 8 were not scanned in 2018 due to extreme drought conditions.

Fig. 3.2.4.2.1 presents the progression of puberty across the scanning events (4 for Angus herds and 3 for Herefords) from post- weaning to into-mating. This was a period of 4 – 5 months, depending on the date of the first (post-weaning) scan, but across both breeds a reasonably constant increase in the proportion of heifers cycling can be observed.

Note that a small proportion of females which had previously recorded a CL failed to do so at the into-mating scan. This is expected, as a CL or CA is not visible throughout the entire cycle in post-pubertal females, and accounts for the small difference between the into-mating scan and the cumulative total (PUB). Note also that this experiment was not designed to be a breed comparison and the small differences between Angus and Hereford heifers can in no way be interpreted as significant or indicative of genetic or phenotypic differences between the breeds.

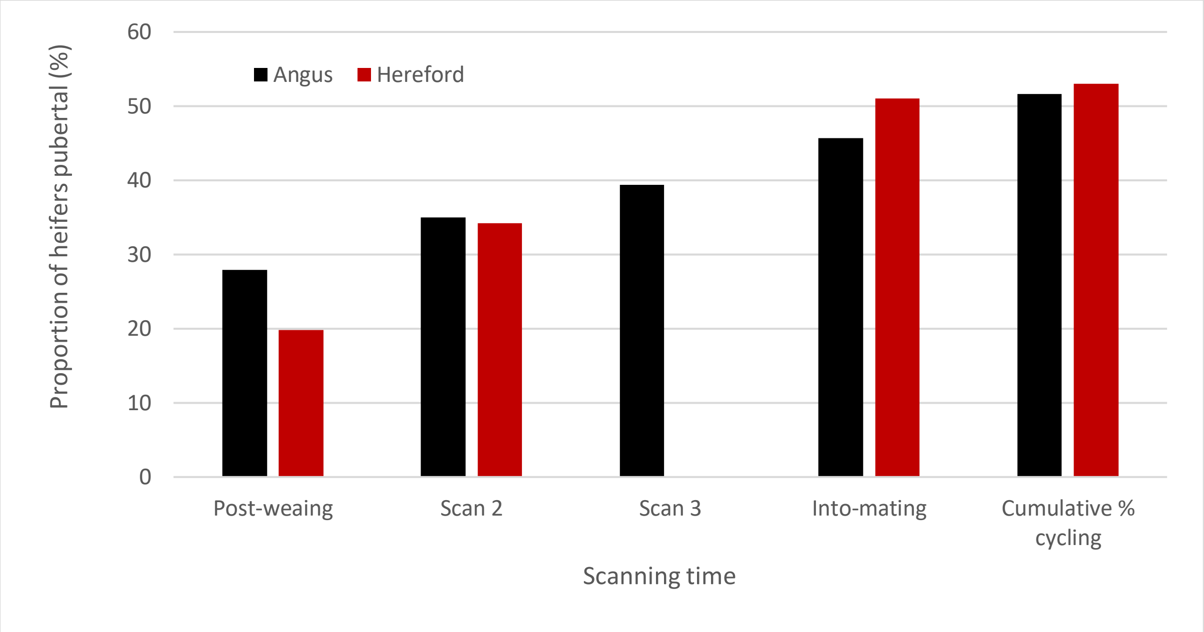


Figure 3.2.4.2.1. Proportion of Angus and Hereford heifers pubertal from post-weaning to into mating scans and final cumulative percent cycling.

3.2.4.3 Genetic analysis of ovarian scanned and related traits

Contemporary group information for genetic analyses was extracted from the Hereford Australia Ltd. and Angus Australia databases, and was built based on information supplied by participating breeders as described by Graser *et al*. (2005). The contemporary group for 200 day weight was used to analyse heifer growth, body composition and the descriptors of ovarian function evaluated for this study. For growth and body composition traits, dam age and linear animal age were fitted as covariates. Consistent with the protocols established by Johnston *et al*. (2009) heifer age was modelled for ovarian scanned traits as month of birth nested within herd and year. Variance components for each trait were estimated in univariate analyses in ASReml (Gilmour *et al*. 2009), with EBVs for all animals estimated as the solution for the random animals effect. Bivariate analyses were also run in ASReml to establish the genetic and phenotypic relationships between repeated measures of AFC.

Additive variances and heritabilities for Hereford heifer post-weaning and into-mating growth and body composition traits are presented in Table 3.2.4.3.1, and Table 3.2.4.3.2 presents the corresponding results for Angus. On average, Hereford and Angus heifers were 10.6 and 9.0 months of age at their post-weaning scan respectively, with mean ages at first scan consistent across herds, within breed. Additive variances and heritabilities for post-weaning LWT were consistent with that reported by Donoghue *et al*. (2018) for Angus and Hereford females prior to their first calving (h^2 = 0.45). The heritability for post-weaning and into-mating P8 was lower than that for either the Hereford or Angus females prior to their first calving reported for that study (h^2 = 0.64), but heritability of HH and BCS was comparable (h^2 = 0.57 and 0.29 respectively). The technicians employed to collect ultrasound data describing ovarian traits were not accredited BREEDPLAN carcass scanners and this may explain the slightly lower than expected heritability for these traits.

Table 3.2.4.3.1. Additive variance (σ_a^2) and heritability (h^2) (with standard error (s.e.)) for post-weaning growth and body composition and ovarian scanned traits in Hereford heifers.

Traits	Units	σ_a^2	h^2	s.e.
Post-weaning growth and body composition				
LWT	kg	460.4	0.35	0.11
HH	cm	6.8	0.49	0.11
P8	mm	0.6	0.30	0.10
BCS	Score (1 – 5)	0.03	0.21	0.08
Into-mating growth and body composition				
LWT	kg	502.4	0.41	0.09
HH	cm	11.9	0.62	0.09
P8	mm	1.0	0.21	0.09
BCS	Score (1 – 5)	0.03	0.20	0.08
Ovarian scanned traits				
AP	Days	363.0	0.26	0.13
APP	Days	588.7	0.38	0.10
PUB	1/0	0.05	0.36	0.11
Post Weaning - AFC	Count	21.1	0.42	0.13
Post Weaning - FOL	mm	0.32	0.17	0.08

Additive variances and heritabilities for ovarian scanned traits in Hereford and Angus heifers are also presented in Table 3.2.4.3.1 and 3.2.4.3.2. The additive variance for APP (588.7 and 1223.9 days for Hereford and Angus) were substantially lower than those reported by Johnston *et al*. (2009) for Brahman and Tropical Composite heifers, which was consistent with the much shorter scanning period in temperate breeds where maiden matings occur approximately 12 months earlier than for tropically adapted heifers. The variances were quite consistent with results of Morris *et al.* (2000), who reported an additive variance of 848 days in Angus heifers which had age at first oestrus identified by their interaction with vasectomised bulls. The moderate heritability estimated for APP in Hereford and Angus heifers (h^2 = 0.38 and 0.42) was, again, consistent with the results of Morris *et al*. (2000) (h^2 = 0.31) and suggested that opportunities exist to improve the trait by selection in these breeds. Both AP and APP were under significantly greater genetic control than days to calving (h^2 ~ 0.05) which is currently the key descriptor of female reproductive performance in the BREEDPLAN genetic evaluation for temperate beef breeds.

For Hereford and Angus sires with 8 or more progeny (N = 36 and 97 respectively), EBVs for APP ranged from -38 to +31 and -57 to +55 days respectively, with accuracies from 52 to 94%. These results suggest that sire selection could impact age at puberty in the resulting progeny by at least 35 days for Herefords and almost 60 days for Angus. With only 52% of females pubertal into their first mating, and mating periods as low as 6 weeks in commercial beef breeding herds in southern Australia, this could have implications for reproductive outcomes for naturally-mated maiden heifers.

Table 3.2.4.3.2. Additive variance (σ_a^2) and heritability (h^2) (with standard error (s.e.)) for post-weaning growth and body composition and ovarian scanned traits in Angus heifers.

Traits	Units	σ_a^2	h^2	s.e.
Post-weaning growth and body composition				
LWT	kg	339.2	0.37	0.06
HH	cm	7.1	0.57	0.08
P8	mm	0.8	0.21	0.06
BCS	Score (1 – 5)	0.04	0.29	0.06
Into-mating growth and body composition				
LWT	kg	288.2	0.30	0.06
HH	cm	4.8	0.39	0.04
P8	mm	1.6	0.36	0.05
BCS	Score (1 – 5)	0.03	0.21	0.05
Ovarian scanned traits				
AP	Days	378.1	0.33	0.08
APP	Days	1223.9	0.42	0.06
PUB	1/0	0.06	0.32	0.05
Post Weaning - AFC	Count	21.1	0.34	0.06
Post Weaning - FOL	mm	0.08	0.01	0.03

Table 3.2.4.3.3 presents genetic correlations of penalised age at puberty with antral follicle count and post-weaning and into mating growth and body composition traits in Angus heifers. Corresponding results are not presented for Hereford due to low numbers. There was a trend for lower (more favourable) APP to be genetically associated with higher LWT, HH, P8 and BCS at both post-weaning and into-mating measurement times (r_g = -0.05 to -0.45), with phenotypic relationships consistently weaker but in the same direction (r_g = -0.08 to -0.21). Age at puberty is a difficult trait to measure, and opportunities to exploit genetically related traits as indicators in the evaluation for temperate beef breeds are attractive. The magnitude of the genetic relationships presented for growth and body composition traits with APP in Table 3.2.4.3.3, however, are not high enough to suggest this could be undertaken effectively.

Table 3.2.4.3.3 Genetic (r_g) and phenotypic (r_p) correlations of penalised age at puberty with key puberty and growth and body composition traits in Angus heifers

Puberty / growth trait	r_g	se	r_p	se
Post-weaning				
Liveweight	-0.45	0.11	-0.23	0.02
Hip height	-0.14	0.14	-0.11	0.02
P8 fat depth	-0.43	0.13	-0.20	0.02
Body condition score	-0.40	0.12	-0.21	0.02
Antral follicle count*	0.06	0.15	0.02	0.03
Into-mating				
Liveweight	-0.21	0.13	-0.16	0.02
Hip height	-0.05	0.13	-0.08	0.02
P8 fat depth	-0.14	0.12	-0.13	0.02
Body condition score	-0.26	0.16	-0.11	0.02

* Genetic correlations for post weaning AFC only included animals which were not pubertal at that scan (N = 2156).

Mean and standard deviation for post-weaning AFC (Table 3.2.4.3.3, were consistent with those reported by Walsh *et al*. (2014) for dairy heifers in the US and Ireland, with heritabilities also comparable (h^2 = 0.25 and 0.31 respectively). AFC was recorded in this project to investigate their genetic associations with economically important metrics of female reproductive performance and these results will be the subject of future analyses. Genetic correlations between AFC at into-mating and subsequent scans were consistently high (r_g = 0.99 to 1.00). This is a clear indication that if AFC were shown to be a useful indicator of other, economically important aspects of female reproductive performance, a single measure of the trait would provide all necessary information. As AFC is a trait of non-cyclic ovaries, it is likely that the best time to record the trait would be at the earliest scanning opportunity.

Table 3.2.4.3.3 also presents the genetic relationship of post-weaning antral follicle count with APP. Note that any heifers which were pubertal at that scan were omitted from these analyses as the presence of a CL created inaccuracies in the recording of AFC. The low genetic relationship of AFC with APP (rg = 0.06) suggests little relationship between the traits at the genetic level and little to no expectation that the AFC could be exploited as a genetic indicator for heifer puberty. Relationships of AFC with first mating or lifetime reproductive performance are of interest, and will be examined as the data becomes available, but are beyond the scope of the current project.

This study presents an initial investigation of the genetics of age at puberty and associated traits in Australian temperate seedstock heifers. Results showed that there are opportunities to improve age at puberty by selection in the breeds evaluated and, by including the trait in the breed's genetic evaluation, to monitor this aspect of female reproduction as selection is applied to improve other economically important traits. The proportion of heifers which were not pubertal as they entered their first mating was a key result of this study. The increasing prevalence of artificial insemination and the associated treatments to synchronise (and possibly induce) first oestrous, suggest that genetic and environmental factors which impact a heifer's capacity to conceive early in their first mating season may warrant monitoring and inclusion in the genetic evaluation for temperate beef breeds.

3.2.5 New Zealand Beef Progeny Test ovarian scanning

3.2.5.1 Ovarian scanned traits in NZ Beef Progeny Test heifers

Table 3.2.5.1.1 presents summary statistics for ovarian scanned traits and those descriptive of mating outcomes for NZ BPT heifers. As observed in Australia, there was significant variation across herds in the proportion of heifers which displayed signs of oestrous as they entered their first mating, though there was a clear trend for the proportion of BPT heifers pubertal into mating to be lower than was observed in Australia (mean PUB = 0.52 and 0.53 for Australian Angus and Hereford heifers respectively). Despite this, the herds which achieved the highest proportion of heifers pubertal into mating in Australia (PUB = 74 and 75% for Angus and Hereford heifers) were only marginally higher than the herd with the highest proportion pubertal into mating observed in New Zealand (PUB = 68.7%). Results for AFC and FOL were comparable in the two countries.

Table 3.2.5.1.1. Descriptive statistics for ovarian scanned and pregnancy test traits in New Zealand Beef Progeny Test heifers collected in 2016 and 2017.

Trait		Units	Records	Mean	s.d.	Minimum[1]	Maximum[1]
Pubertal into Mating	(PUB)	%	1370	24.8	43.8	*2.1*	*68.7*
Antral follicle count	(AFC)	count	1370	22.2	8.3	3	50
Dominant follicle size	(FOL)	mm	975	12.1	2.3	2	28
Conception rate	(CON)	%	1370	86.6	41.0	*82.3*	*91.0*
Foetal age	(FAGE)	days	1090	66.8	14.7	30	97

[1] Minimum and maximum PUB and CON results are at the herd level.

Interestingly, these low levels of cyclicity into mating for NZ BPT heifers did not translate to poor conception rates, with herds averaging 86.6% conception to natural mating (ranging from 81 to 91%). Calving outcome results are not yet available for the heifers scanned in Australian in 2018, and this will be a key area of analysis in the final stages of this project.

3.2.5.2 Phenotypic relationships of ovarian scanned traits with conception and foetal age in naturally mated females

Naturally mating females in the NZ BPT project allowed variation in puberty and related traits to be expressed without the complication of artificially induced oestrous at the end of the recording period and, more importantly, for variation in maiden mating outcomes to be fully expressed.

To estimate phenotypic relationships of ovarian scanned traits with mating outcomes (conception rates and foetal age at preg-test), regression models were built in SAS which fitted either foetal age or a binary conceived (1) or not (0) trait as the dependant variable. Initially the model was run with the ovarian scanned traits (PUB, AFC and FOL), all recorded as described for their Australian equivalents above, as the sole predictor of the dependant variable. A second run was conducted with fixed effects of herd, year and breeder supplied management group also fitted to account for systematic and environmental variation. The r^2 statistic for these models describes the proportion of variation in the dependant variable explained by the ovarian scanned traits, with partial r^2 for models containing fixed effects describing the proportion of variance accounted for by the model attributable to the ovarian scanned trait under examination.

All of the models built to estimate the predictive power of ovarian scanned traits for conception rate showed consistently non-significant results, whether PUB, FA or FOL were fitted as the sole predictor of conception rate ($P > 0.10$ and $r^2 < 0.001$) or included in models with all available fixed effect information ($P > 0.17$ and $r^2 < 0.04$). The only trait which approached significance as a predictor of conception rate was AFC ($P = 0.22$), and the magnitude of the regression coefficient and its standard error was sufficiently low ($b = 0.0016 \pm 0.0013$) to indicate that no real effect was present.

Table 3.2.5.2.1 presents regression analysis results for ovarian scanned traits modelled as predictors of foetal age at pregnancy testing 3 – 4 months after bulls were introduced to the heifers for natural mating. Results were not encouraging at the phenotypic level, with models containing ovarian scanned traits as the sole predictor of foetal age accounting for consistently very low proportions of the variation observed in foetal age ($r^2 = 0.003$ to 0.028). This was despite their being consistently significant predictors of foetal age ($P < 0.05$).

Table 3.2.5.2.1. Results of regression analysis predicting foetal age at pregnancy test (3 – 4 months after bulls were introduced to the heifers for natural mating) from ovarian scanned traits.

Model	Regression statistics	Pubertal into mating	Antral follicle count	Dominant follicle size
	Number of records	1319	1319	1050
No fixed effects	Intercept	64.8	68.0	57.9
	Regression coefficient	5.85	-0.08	0.644
	Significance (P-value)	0.0001	0.043	0.003
	r^2	0.028	0.003	0.012
Fixed effects included	Intercept	77.3	78.2	69.1
	Regression coefficient	2.92	-0.046	0.69
	Significance (P-value)	0.006	0.269	0.0004
	r^2	0.27	0.28	0.25
	Partial r^2	0.003	0.014	0.011

The predictive power of the models improved significantly when fixed effects were included to describe systematic and environmental sources of variation ($r^2 = 0.25$ to 0.28). Both PUB and FOL were significant predictors of foetal age (P = 0.006 and 0.0004 respectively, though this was not the case for AFC (P = 0.27). Partial r^2, describing the proportion of variation in foetal age described by ovarian scanned traits in the presence of significant fixed effect, showed that they made only the most minor contribution to the description of variation in foetal age (Partial $r^2 = 0.003$ to 0.014).

Antral follicle count was of particular interest in this project given the favourable relationship of the trait with descriptors of female fertility reported by Mossa *et al*. (2012) and Martinez *et al*. (2016) in dairy cows. The results of this study were in contrast to those, but consistent with the results of a larger experiment described by Snelling *et al*. (2012), which reported a phenotypic correlation of 0.00 between antral follicle count and heifer pregnancy rate when estimated based on genomic relationships between crossbred beef heifers. These low phenotypic relationships support the similarly low genetic correlations of AFC with penalised age at puberty reported above for Australian seedstock Angus heifers. As stated for Australian results, data on first, second and lifetime calving outcomes will be interesting to analyse with AFC, but is beyond the scope of the current project.

3.2.6 Conclusions/recommendations

Collection of data has been completed for the female reproduction component of the project, with the exception of calving records for Australian heifers scanned in 2018, which will not be available until calves are weaned in the first quarter of 2020. The targets for numbers of animals scanned have been met, and numbers of scans for each herd were sufficient to describe variation in age at puberty, proportions of heifers pubertal at mating, and associated growth and body composition traits with the level of accuracy targeted for the study.

At the phenotypic level the results obtained for the study were within the ranges expected for the body condition traits evaluated, and genetic parameters for these traits were consistent with those previously reported in the literature.

A key result from this research was the proportion of heifers which were pubertal into mating whether by artificial insemination, as was the case for Australian seed-stock heifers, or natural mating as practiced in the New Zealand progeny test herds. Averages of 52% for Australian heifers and only 25% for their NZ counterparts were lower than expected. Once calving outcome data is available for the 2018 scanned females, the relationship, both genetically and phenotypically, of heifer puberty with first mating outcomes can be established.

These results suggest that age at puberty could be incorporated in the genetic evaluation for temperate beef breeds and allow the trait to be improved by selection. As importantly, it would allow genetic age at puberty to be monitored as selection pressure is applies to improve other aspects of productivity. The high investment of time and expertise required to collect accurate age at puberty records is a limitation to large scale adoption of the serial scanning methods employed for this study. Its application in intensively recorded reference population and research herds, however, would centralise the cost of recording the trait and maximise the value of results to the industry.

The low proportion of females identified as pubertal up to their first synchronisation for artificial insemination was unexpected and highlights the need to examine puberty and related traits in naturally mated temperate beef females. The results of this study also highlight the need to expand our understanding of female reproduction in temperate beef breeds to include lactation anoestrus interval.

3.3 Objective 3 – Genotype by environment interaction in the Trans-Tasman genetic evaluation

3.3.1 Background

In both Australia and New Zealand there are a range of views on the utility of Estimated Breeding Values (EBVs) as tools in cattle breeding, ranging from ardent supporters of the concept and science of EBVs through to some degree of scepticism. One concern which is raised from time to time is the ability of EBVs to adequately deal with the impact of variations in environment in which cattle are raised. While adjustments for contemporary groups and genetic linkage across environments are understood to remove the impacts of different management groups, there is still an underlying concern amongst some breeders that genuine GxE effects exist which would cause cattle to rank differently in different environments. This concern has been expressed for a range of different environmental variables within Australia. From time to time studies looking to detect Genotype x Environment effects, or an absence of these effects, have been undertaken to provide confidence to breeders that a single analysis of data across a range of environments and management systems is able to produce EBVs which have utility and predictive ability for cattle performance within alternative environments. For example, the Australian Co-operative Research Centre for Cattle and Beef Quality undertook a large experiment to investigate whether Genotype x Environment interactions exist in relevant traits between grass and grain-based finishing systems. More recently, Jeyaruben *et al*. (2009) reported investigations to determine whether significant Genotype x Environment interactions exist between production systems in temperate southern Australia (represented by herd located in Victoria) and tropical northern Australia (represented by herds located in Queensland).

Based on the results of these studies, which show minimal GxE interaction, BREEDPLAN has been running a single Trans-Tasman analysis for a number of breeds since the mid nineteen-nineties. While BREEDPLAN has the capacity to create and analyse different traits based on country of origin (e.g. weaning weight being a different but correlated trait depending on whether it is expressed in Australia vs New Zealand), it currently analyses the traits from the two countries as the same genetic trait (ie. the genetic correlation between countries is implied to be 1). At the time the Trans-Tasman analyses were set up, an investigation was undertaken to determine whether there was significant Genotype x Environment interactions between cattle populations in Australia vs New Zealand Meyer *et al*. (1995), and little or no genotype by environment effects were identified, suggesting that the approach used is valid. At this point, BREEDPLAN was in a much more limited format in terms of traits and models, and it has subsequently developed to include a wider range of traits, as well as having a significantly expanded database (in terms of numbers of records built from historical recording, and likely also via greater market penetration and implementation of performance recording). New traits added since that time include carcase traits (primarily informed by live ultra-sound measurements), reproductive performance, docility, net feed intake, feet scores.

Arguably beef cattle systems in New Zealand differ significantly to those in Australia, particularly in terms of breeding cow management. In New Zealand cattle are generally used in a mixed sheep-beef system with a specific role for the beef cow which includes removal of poorer quality pasture to maintain pasture quality for sheep, and as a tool to shift feed consumption from times of inadequate feed supply to times of excess feed (the mobile haystack effect where cows put on fat with excess feed and then lose weight during feed shortage which in New Zealand is typically due to a cold winter).

The contrast in Australia is that cows are generally regarded more as a profit centre by Australian beef farmers (vs New Zealand farmers who at times almost regard the beef cow as a cost centre required to maintain a more profitable sheep enterprise). Also, there is arguably a tendency within some Australian beef farmers to protect cow condition score during seasonal fluctuations – this has a sound rational basis as the greater variability of Australian climate and feed supply in many places means that deliberate weight loss is a less desirable strategy due to the uncertainty of being able to re-gain the weight loss within the annual productive cycle. The extent to which these differences in philosophy translate to real differences in feed supply to cattle is difficult to specify, particularly as there can be greater differences between neighbouring farmers in the same environment resulting from personal factors as there might be between countries.

Regardless of how different systems translate between countries, and the translation between grass and grain based finishing, or between functional requirements of cows on steep vs flatter topography, a perception has existed at least amongst some New Zealand breeders that Trans-Tasman analysis could be producing incorrect bull rankings for New Zealand conditions due to the joint analysis of data (with New Zealand data generally providing the minority of data in the analyses). To give answers to whether this concern is supported within the data, it was decided at the outset of this joint Australia-New Zealand beef research program that it a small proportion of the resources should be used to conduct an analysis of GxE between Australia and New Zealand for the two largest breeds (Angus and Hereford).

It is important to distinguish between issues of Genotype x Environment in evaluations (prediction of breeding values of biological traits, as examined here) compared to issues of Genotype x Environment interactions at the economic level. The former is concerned with whether data from different environments can be treated as equivalent traits within a genetic evaluation analysis, so that EBVs at the biological level accurately represent the performance of sires across environments. The latter is concerned with whether different environments require different genetic types of animals, and thus whether there should be a different breeding objective (index) for these environments. This topic is the subject of a separate report within this program.

3.3.2 **Other definitions of environment**

In reality, environments might differ as much due to differences in management system implemented by two farmers within very similar bio-physical environments, as it might between countries. And alternatively, there might be some bio-physical environments within each country which are more similar to each other, with greater variation between regions within countries. Hence it would be of interest to investigate further whether there are clusters of environments that are associated with GxE effects, where the environments are not determined a priori by factors such as country, state, or grass vs grain production systems. The challenge of undertaking this type of analysis is to have a technique to cluster similar herds based on the data, and to simultaneously undertake evaluation as to how important these environment clusters are in terms of Genotype x Environment effects. One such technique which has been used for similar purposes is factor-analytic modelling. This technique has recently provided some insight into GxE within New Zealand sheep centralised progeny test datasets, which is a designed program with a limited number of sites (5) and most sires used at most sites. It was decided to trial using this technique on industry data, which does not have the same designed structure as previously analysed data sets, to determine whether this approach could be applied to provide more insights into environmental clustering of herds and its impact on Genotype x Environmental interactions.

3.3.3 Methods

The analysis of breed society data was conducted by AGBU, under AGBU's general research licence with the breed societies.

3.3.3.1 Country of recording GxE analysis

A separate analysis was performed for each breed (Angus and Hereford). Within each breed, trait data was extracted from both Australia and New Zealand society databases and separate identifier for country of origin were maintained. The exact year extracts used differed between breeds, and traits within breeds, and are given in Tables 3.3.3.1 and 3.3.3.2. In general, extracts for traits measured on young animals was extracted from relatively recent years (e.g. 2013-2015 for Angus, 2006-2015 for Hereford) while a different year range was used for traits of cows (e.g. 2004 – 2011 for Angus, 2004 – 2013 for Herefords).

Datasets were edited to remove information not informative to the analysis. This involved identifying all sires with progeny recorded for a trait in both Australia and New Zealand. The progeny from these sires were retained in the analysis, along with all other animals which were in a contemporary group containing these progeny. Contemporary groups with less than 5 animals were then dropped from the analysis. The number of animals remaining for analysis are given for each trait in Tables 3.3.3.1 and 3.3.3.2. Maximum and minimum animal numbers for Trait x country groupings were 81,945 (Australia weaning weight) and 5,629 (New Zealand, Days to Calving) for Angus and 49,635 (Australia weaning weight) and 3,312 (New Zealand, Days to Calving) for Hereford.

Traits were defined as per normal BREEDPLAN trait definitions. Traits included in the analysis consisted of Birth weight (BWT), weaning weight (WWT), weight at 400 (W400) and 600 (W600) days, weight of mature cows at weaning (MCWT), Days to Calving (DTC), Scrotal Circumference (Scrotal), and ultra-sound scan traits of fat depth over the P8 site, eye muscle area (EMA) and intra-muscular fat (IMF). Ultra-sound scan traits were analysed separately for bulls vs heifers, as per usual BREEDPLAN analysis approach.

All phenotypes were pre-adjusted for age and age of dam effects. BREEDPLAN contemporary groups were fitted as fixed effect adjustments within the analysis.

An animal model was fitted for all traits. Maternal genetic and Dam permanent environmental effects were included for BWT, WWT AND W400. Permanent environmental effect of the animal was fitted for traits where repeated records on cows were available (MCWT and DTC). A sire x herd interaction (fitted as a random effect) was included for all traits.

A bivariate analysis was conducted for each trait, where the trait was defined as a different trait recorded in Australia vs New Zealand. The variance components were estimated for each trait/country and the genetic correlation between countries was estimated.

3.3.3.2 Factor analytic analysis

We attempted to investigate GxE effects using a factor analytic (FA) approach. According to Meyer (2009), FA models provide a natural framework for modelling GxE interaction problems in that they provide a computationally efficient description of covariance structures and there is scope for direct interpretation of environmental factors. This approach has been used successfully to measure differences in genetic performance of individuals across multiple environments in tree breeding (Smith and Cullis, 2018) and in multi-site sheep progeny test experiments (Santos, 2018). The statistical model is similar in form to a sire model, but the sire term is replaced with a herd by sire interaction term where an extended factor analytic term is applied to herd. In ASReml (Gilmour, 2009), the random term fitted is *xfa(herd,n).sire*, where *xfa()* is the term to fit an extended factor analytic model and *n* is the levels of the factor analytic term. As the statistical model is developed, the levels are increased until the log-likelihood does not increase any further or the model fails to converge. The statistical output from each level of the FA effect has a 'loading' for each herd which gives informative information to cluster herds into groups having similar environments. The weight traits Weight at 200 and 600 days of age were selected to test the models.

3.3.4 Results and Discussion

The outcomes of the Trans-Tasman GxE analyses are summarised in Table 3.3.3.1 (for Angus) and Table 3.3.3.2 (for Hereford). Table 3.3.4.1 contains ratios of variance component estimates for Australia: New Zealand to aid interpretation of the components.

As a generalisation across growth and reproductive traits, Australian mean performance levels tended to be slightly higher than New Zealand raw means by between 2% and 10%. The standard deviations of these traits were also higher for Australian data vs New Zealand data, and generally the co-efficient of variation was also higher for Australian data, indicating that slightly greater variation exists beyond that explained by differences in mean value at the unadjusted level.

For growth traits, the analysis tended to partition variance towards greater additive genetic variance in Australian data for Angus, and New Zealand data for Herefords, resulting in higher respective heritabilities. Reproductive traits did not show the same trends.

Genetic correlations between Australia and New Zealand for growth traits, and for scrotal circumference, were all greater than 0.9, giving confidence that the traits expressed in either country are effectively the same genetic trait. Notably it was not possible to get convergence for Days to Calving, which is likely a result of the lower heritability for this trait and overall lower level of recording. This re-enforces the opportunity or benefit which might be obtained by inclusion of additional predictors of fertility into an integrated analysis, rather than relying on Days to Calving as the sole female fertility measurement.

Scan traits showed slightly different outcomes to growth and reproductive traits, although the outcomes were not polar opposites. Fat depth scans in Australia were found to have between 15% and 35% higher raw means than in New Zealand. Similarly, for IMF Australian unadjusted means were from 6% to 23% higher than raw New Zealand means, and for EMA, raw Australian means were from 0 to 9% higher than New Zealand raw means. Phenotypic variances for EMA particularly tended to be substantially higher in Australian data than in New Zealand data, especially for heifers. For Angus, the amount of variation partitioned into additive genetic component tended to be similar between countries, leading to increased heritability in New Zealand scan measurements, while for Hereford the heritability tended to be similar across countries.

These results, compared to the 400-day weight results (a similar age to collection of scan data) which were 8% to 10% higher in Australia, are surprising. If the increases in scan data were solely due to scale of the animals (e.g. better environment or genetics leading to increased growth rates), then it might be expected that scan data would have similar relationships to 400-day weight data. However, it should be borne in mind that this analysis corrected for age, but did not adjust to a common carcase weight as occurs within BREEDPLAN. Adjusting to a weight, given the general trend for Australian cattle to be heavier in this data set than New Zealand cattle, might remove some of the differences observed.

Genetic correlations between Australia and New Zealand for scan traits were more variable than those estimated for growth and scrotal circumference. In part this might be due to higher standard errors on the correlation estimates, although the standard errors were still quite reasonable. The traits that stood out as being lower than 0.8 were heifer EMA (0.76) and bull IMF (0.78) in Angus, and heifer fat depth in Hereford (0.65). In particular, heifer P8 fat depth in Hereford is in a range where it might be defined as a different trait and treated as a correlated predictor. Accordingly, heifer fat depth at the 12th/13th rib site was also analysed to check whether similar outcomes were obtained and resulted in a genetic correlation between countries of 0.79.

While there is no hard and fast rule about when it is worthwhile breaking traits into separately defined but correlated traits, a genetic correlation of over 0.8 would suggest that there is little benefit in breaking traits down, especially given the additional complexity and computational overhead resulting from analysing double the number of traits. Differences in overall variances can be at least partially overcome by use of scaling, and given errors around parameter estimates for variance components there would be little justification for arguing that any remaining differences in variance components after scaling would be sufficiently important to implement as different traits. Overall, these results support the continued implementation of a Trans-Tasman analysis in these breeds with traits treated as the same genetic trait in both countries.

The exception to this general conclusion might be fat depth in Herefords, and possibly this could be further investigated. In New Zealand, Herefords tend to be predominantly run in the South Island hill and high country, where winters are longer than in most of the North Island and so possibly New Zealand Herefords represent a more extreme average environment (in terms of length of time on restricted feed) than New Zealand Angus (which are more evenly represented across both islands) and Australian systems. However, it still remains challenging to explain why this would impact on fat depth to a greater extent than other traits expressed at a similar age. Hence in the absence of a more in-depth explanation, and given standard errors on estimates and results from other traits, there is not a compelling case for treating fat depth in a different manner to other traits within Trans-Tasman analyses.

3.3.4.1 Factor analytics and the case for alternative definitions of environments

Factor analytic models were tested to see if they provided a better characterisation of GxE effect than the other methods reported here. Unfortunately, the FA models generally failed to converge at the lowest level (i.e. first level of the FA term) for the traits tested. The most likely cause of the failure in convergence is that there were insufficient sires used across multiple environments to be able to solve the equations, and that there were too many environments to model. FA models have worked well in the analysis of plantation trees (Smith and Cullis, 2018) where clonal populations allow the same individual to be tested in a wide range of environments (albeit with some simplification of environments), and in multi-site sheep progeny tests (Santos, 2018) where sires were deliberately used on as many of the five progeny test flocks as possible. The models were implied to include only a small number of well linked herds, but the models still did not converge. It would appear that FA models work well on highly structured datasets with many sires used across multiple environments, but the level of across herd use of sires that normally occur in industry dataset are not sufficient for the models to work well here.

3.3.5 Conclusion

This analysis has supported the approach currently used by BREEDPLAN to implement Trans-Tasman analysis assuming that traits are genetically the same in both countries. There is some evidence that genetic correlations for scanned carcass traits across the two countries deviate slightly from unity, and further investigation, as data and analytical techniques and capacity become available, may be worthwhile.

Table 3.3.3.1. Description of data used, and estimated variance components and genetic correlations for Angus cattle in Australia vs New Zealand.

Country	Statistics /	Trait												
	Variances	BWT	WWT	W400	W600	MCWT	DTC*	Scrotal	Heifer P8	Heifer EMA	Heifer IMF	Bull P8	Bull EMA	Bull IMF
AUS	Years	2013-15	2013-15	2013-15	2013 - 15	2004 - 11	2004 - 11	2013 - 15	2013 - 15	2013 - 15	2013 - 15	2013 - 15	2013 - 15	2013 - 15
	N	78843	81945	62386	33376	46808	23791	26240	28263	28376	28163	28381	28536	28596
	Mean	37.87	257.1	411.9	557.6	566.9	307.6	36.6	8.0	65.8	5.7	5.3	86.07	4.08
	s.d.	5.0	57.7	75.3	110.4	93.1	23.8	2.9	3.7	10.0	1.6	2.3	11.47	1.37
	V_a	5.6	60.8	260.2	470.3	1133.5	16.7	2.2	1.7	5.8	0.3	0.5	9.2	0.21
	V_m	1.1	73.0	55.8	-	-	-	-	-	-	-	-	-	-
	V_{pe}	0.8	103.1	338.3	-	933.6	28.7	-	-	-	-	-	-	-
	V_r	9.6	114.9	294.4	865.7	706.6	1.8	2.6	2.4	23.0	0.7	1.4	33.2	0.58
	SH	0.3	22.8	23.4	32.4	58.4	339.2	0.05	0.13	0.78	0.03	0.06	1.02	0.04
	V_p	17.4	374.6	972.1	1368.4	2832.1	386.4	4.9	4.2	29.5	1.0	1.9	43.4	0.8
	h^2	**0.32**	**0.16**	**0.27**	**0.34**	**0.40**	**0.04**	**0.45**	**0.40**	**0.20**	**0.29**	**0.25**	**0.21**	**0.25**
	s.e.	**0.00**	**0.00**	**0.00**	**0.02**	**0.01**	**0.01**	**0.03**	**0.02**	**0.04**	**0.01**	**0.02**	**0.02**	**0.02**
NZ	Years	2012-15	2013-15	2013-15	2013-15	2004-11	2004-11	2013-15	2013-15	2013-15	2013-15	2013-15	2013-15	2013-15
	N	31324	29234	22531	13014	21487	5629	10506	10229	10069	10010	12368	12359	11904
	Mean	35.85	233.4	380.5	513.4	555.8	314.9	36.0	5.9	64.2	5.0	4.5	78.8	3.9
	s.d.	4.833	44.0	64.3	103.4	84.0	26.8	2.8	2.8	7.4	1.8	1.5	8.7	1.4
	V_a	4.54	52.2	142.4	269.2	959.4	46.6	1.6	1.7	6.7	0.5	0.3	9.7	0.2
	V_m	0.93	60.9	60.0	-	-	-	-	-	-	-	-	-	-
	V_{pe}	0.86	97.8	327.6	-	828.6	35.1	-	-	-	-	-	-	-
	V_r	9.06	279.8	223.1	818.2	535.6	444.6	2.9	2.4	17.1	1.3	0.8	21.0	1.1
	SH	0.38	20.3	22.3	24.0	70.6	0.00	0.02	0.13	0.83	0.05	0.03	0.70	0.02
	V_p	15.8	511.0	775.5	1111.4	2394.2	526.2	4.5	4.2	24.6	1.8	1.2	31.4	1.4
	h^2	**0.29**	**0.10**	**0.18**	**0.24**	**0.40**	**0.09**	**0.35**	**0.40**	**0.27**	**0.28**	**0.30**	**0.31**	**0.17**
	s.e.	**0.01**	**0.02**	**0.01**	**0.03**	**0.01**	**0.03**	**0.03**	**0.03**	**0.03**	**0.02**	**0.03**	**0.03**	**0.02**
R_g	**AU:NZ**	**0.90**	**0.91**	**0.94**	**0.91**	**1.00**	**.**	**0.92**	**0.88**	**0.76**	**1.00**	**0.88**	**0.93**	**0.78**
	s.e.	**0.01**	**0.03**	**0.02**	**0.06**	**0.05**	**.**	**0.05**	**0.05**	**0.09**	**0.03**	**0.07**	**0.05**	**0.10**

*Bivariate models for Days to Calving did not converge.

Table 3.3.3.2. Description of data used and variance components and genetic correlations estimated for Hereford cattle in Australian and New Zealand.

Country	**Statistics /**	**Trait**													
	Variances	**BWT**	**WWT**	**W400**	**W600**	**MCWT**	**DTC***	**Scrotal**	**Heif. P8**	**Heif. RIB****	**Heif. EMA**	**Heif. IMF**	**Bull P8**	**Bull EMA**	**Bull IMF**
AUS	Years	2006-15	2006-15	2006-15	2006-15	2004-13	2004-13	2006-15	2006-15	2006-15	2006-15	2006-15	2006-15	2006-15	2006-15
	N	42355	49635	36702	24859	7092	6752	23175	16711	16711	16768	16661	15861	15826	15725
	Mean	41.3	251.3	394.9	561.5	658.1	316.4	35.5	7.6	5.7	63.0	4.2	5.66	86.85	3.10
	s.d.	5.7	44.5	83.4	119.1	87.9	25.6	2.6	3.5	2.4	9.2	1.6	2.32	12.03	1.33
	V_a	6.3	48.8	193.9	443.8	1389.4	48.8	2.0	1.8	0.8	10.3	0.3	0.59	9.9	0.18
	V_m	2.1	80.1	134.7	-	-	3.0	-	-	-	-	-	-	-	-
	V_{pe}	5.8	146.5	147.8	-	1154.1	82.4	-	-	-	-	-	-	-	-
	V_r	0.4	21.7	31.0	46.3	244.7	3.4	0.1	0.1	0.0	5.2	0.03	0.08	2.3	0.01
	SH	4.9	428.7	665.8	996.7	540.8	384.5	2.0	2.9	1.5	39.6	0.7	1.72	29.2	0.47
	V_p	19.5	725.8	1173.1	1486.8	3328.9	522.1	4.2	4.8	2.3	55.1	1.1	2.39	41.4	0.67
	h^2	**0.32**	**0.07**	**0.17**	**0.30**	**0.42**	**0.09**	**0.49**	**0.38**	**0.34**	**0.19**	**0.30**	**0.25**	**0.24**	**0.27**
	s.e.	**0.03**	**0.02**	**0.01**	**0.02**	**0.01**	**0.09**	**0.01**	**0.02**	**0.02**	**0.01**	**0.02**	**0.03**	**0.01**	**0.03**
NZ	Years	2006-15	2006-15	2006-15	2006-15	2004 -13	2004-13	2006-15	2006-15	2006-15	2006-15	2006-15	2006-15	2006-15	2006-15
	N	37389	39637	29440	13088	4137	3312	9074	7356	7359	7363	5483	9906	9898	6589
	Mean	38.96	247	358.5	537.4	638.6	312.2	34.9	6.5	4.4	63.2	3.4	4.9	81.7	2.7
	s.d.	5.3	42.43	70.4	111.8	82.9	26.9	3.1	2.2	1.5	7.3	1.4	1.5	11.0	1.1
	V_a	6.9	61.7	219.1	537.0	1208.2	4.7	1.7	1.1	0.3	8.0	0.21	0.4	7.8	0.1
	V_m	2.3	94.8	128.2	-	-	3.4	-	-	-	-	-	-	-	-
	V_{pe}	3.9	198.3	204.9	-	915.7	79.4	-	-	-	-	-	-	-	-
	V_r	0.5	39.8	39.4	16.2	182.5	7.5	0.12	0.10	0.03	0.73	0.04	0.02	0.95	0.00
	SH	5.4	390.5	393.5	769.2	468.7	427.2	2.5	1.4	0.8	16.9	1.28	0.87	24.9	0.91
	V_p	19.0	785.1	985.0	1322.4	2775.1	522.1	4.3	2.6	1.1	25.6	1.54	1.27	33.7	1.03
	h^2	**0.36**	**0.08**	**0.22**	**0.41**	**0.44**	**0.01**	**0.40**	**0.41**	**0.31**	**0.31**	**0.14**	**0.30**	**0.23**	**0.12**
	s.e.	**0.03**	**0.04**	**0.01**	**0.03**	**0.01**	**0.12**	**0.01**	**0.03**	**0.03**	**0.01**	**0.03**	**0.03**	**0.01**	**0.04**
R_g	**AU:NZ**	**0.93**	**0.92**	**~1.00**	**0.94**	**~1.00**	**.**	**1.00**	**0.65**	**0.79**	**~1.00**	**1.00**	**0.90**	**~1.00**	**~1.00**
	s.e.	**0.06**	**0.07**	**0.05**	**0.06**	**0.08**	**.**	**0.09**	**0.14**	**0.14**	**0.09**	**0.15**	**0.09**	**0.09**	**0.10**

*Bivariate models for Days to Calving did not converge.** Heifers fat depth over the 12/13th rib was added to check for consistency of results with fat depth at the P8 site.

Table 3.3.4.1. Ratio of Australian vs New Zealand population estimates for different genetic parameters. Ratios for variances have been converted to the standard deviation scale to facilitate comparisons in the same units as means.

	Trait													
	BWT	**WWT**	**W400**	**W600**	**MCWT**	**DTC**	**Scrotal**	**Heifer P8**	**Heifer RIB**	**Heifer EMA**	**Heifer IMF**	**Bull P8**	**Bull EMA**	**Bull IMF**
Angus														
Mean	1.06	1.10	1.08	1.09	1.02	0.98	1.02	1.35		1.02	1.14	1.17	1.09	1.06
s.d.	1.03	1.31	1.17	1.07	1.11	0.89	1.02	1.33		1.36	0.90	1.49	1.31	1.01
V_a	1.11	1.08	1.35	1.32	1.09	0.60	1.20	1.00		0.93	0.77	1.17	0.97	0.95
V_m	1.08	1.09	0.96											
V_{pe}	0.98	1.03	1.02		1.06	0.90								
V_r	1.03	0.64	1.15	1.03	1.15	0.06	0.95	1.00		1.16	0.74	1.32	1.26	0.72
SH	0.88	1.06	1.02	1.16	0.91	0.00	1.59	1.00		0.97	0.83	1.48	1.20	1.33
V_p	1.05	0.86	1.12	1.11	1.09	0.86	1.04	1.00		1.10	0.75	1.28	1.18	0.78
h^2	1.11	1.59	1.46	1.42	1.00	0.49	1.31	1.00		0.72	1.05	0.84	0.69	1.49
Hereford														
Mean	1.06	1.02	1.10	1.04	1.03	1.01	1.02	1.17	1.29	1.00	1.23	1.15	1.06	1.13
s.d.	1.06	1.05	1.18	1.07	1.06	0.95	0.85	1.58	1.66	1.26	1.13	1.58	1.10	1.18
V_a	0.95	0.89	0.94	0.91	1.07	3.23	1.08	1.30	1.48	1.13	1.22	1.24	1.12	1.21
V_m	0.95	0.92	1.02			0.94								
V_{pe}	1.22	0.86	0.85		1.12	1.02								
V_{sh}	0.94	0.74	0.89	1.69	1.16	0.68	0.91	0.90	1.05	2.69	0.84	1.80	1.55	199.21
V_r	0.95	1.05	1.30	1.14	1.07	0.95	0.91	1.41	1.39	1.53	0.74	1.41	1.08	0.72
V_p	1.01	0.96	1.09	1.06	1.10	1.00	0.98	1.35	1.41	1.47	0.83	1.37	1.11	0.80
h^2	0.88	0.86	0.74	0.74	0.96	10.42	1.22	0.93	1.10	0.60	2.17	0.82	1.03	2.26

3.4 Objective 4 - Underpinning animal resource development and measurements

Background R&D that has contributed to current understanding includes the Beef CRC III Maternal Productivity project, and ongoing work on breeding objectives for beef cattle reflected and delivered in BREEDOBJECT version 6. New projects have been developed since the Maternal Productivity project, including BIN herds where daughters are retained for at least 1 calving, the Hereford “Black-Baldy” Trial (both the BINs and the Black Baldy project are co-funded by the MLA Donor Company), and more recently in NZ, two new projects that include R&D into aspects of maternal efficiency. These are:

1) Beef + Lamb NZ Genetics Beef Progeny Test Project
2) Beef + Lamb NZ Genetics Beef Maternal Cow Tier 2 Project

In addition, some seedstock breeders were collecting records of cow condition score, not currently used in genetic evaluation.

As part of the BLG BPT and the BLG Beef Maternal Cow Tier 2 Project program phenotypic and genotypic information was collected. These projects encompassed animals from 5 and 4 commercial properties respectively. Heifers were followed right through to cows, as understanding cow maternal performance was a critical goal of the program.

The BPT used 5 sire breeds – Angus, Hereford, Stabiliser, Simmental and Charolais mated across Angus or Hereford cows (linkage in this program was generated by using the same sires over multiple years). Cows., sires and calves were DNA samples, whereas cows and calves only had phenotypes recorded. Steers from the program were grown out, killed and graded under Silver Fern Farm’s BeefEQ program and had AUSMEAT measurements collected. The majority of heifers from maternal breeds in the program were retained into the cow herd.

The Maternal Cow project collected phenotype records and DNA samples for 4 hill country beef properties. Recording and DNA samples were undertaken on cows and calves only. The aim was for 10,000 maternal cow measurements, with up to three repeat measures over each year.

Phenotypic traits were recorded at pre-determined times throughout the cows and calves’ lives (pre-calving, mating and weaning), these are included below:

- Live Weight
- Body Condition Score
- Hip Height
- Pregnancy Diagnosis
- Antral Follicle Count

DNA samples were sent to approved genotyping providers and genotyped as per the genotyping strategy established for this project. In the vast majority a 50K SNP Chip genotype was required.

Each year of the projects were devoted to collecting more phenotypes, and genotypes at time-periods when cows and calves were brought in to the yards for herd management reasons. All data was recorded on a Gallagher TSi 2 device and the data in csv-format for each recording session is transferred to Excel files. At the end of each recording year, data was checked and collated for each animal.

All relevant data from these projects have been made available to MDC, it has also been transferred to ABRI for inclusion in BREEDPLAN analyses. As BPT cohorts are completed (slaughter measurements), further data will be sent. This has been developed as a Business as Usual (BAU) process for BLG and will likely occur annually. Breed societies can access data form the BREEDPLAN analyses.

Outside of this program, the data recorded from the BLG BPT is being used for PhD research by Franziska Weik with supervision from AbacusBio Scientist Jason Archer, and three further supervisors from Massey University. This work is in the early stages and has so far been centred on describing live weight and body condition performance of mixed aged beef cows. Early results have shown a significant relationship between live weight (LWT) and body condition score (BCS), and little significance in the relationship between hip height and BCS. The interpretation taken from this is that it does not matter whether it is a small or a tall cow, you need to put on the same weight to increase one unit of BCS.

3.5 Objective 5 – Economic Level genotype by environment interaction

3.5.1 Abstract

The overall objective of this project was to examine the implications of different feeding and management strategies in response to fluctuations in feed supply, and to determine whether beef cows with different genetic makeup are best suited to alternative management systems. The study utilises bio-economic modelling to address this issue in detail and translates the outcomes into a breeding objective context. The interaction between feeding and managements strategies, i.e. supplementation strategy and stocking rate, and the type of beef cow to which such strategies are applied, is an issue broadly defined as a comparison between controlling the environment to maximise cow performance versus breeding the cow to perform under a more fluctuating environment.

This report describes the development of a stochastic bio-economic model which simulates the implications of managing cows of different genetic makeups, hereafter referred to as “cow genotype”, under distinct feeding and management farm practices. These practices include supplementation based on cow body condition score (BCS) triggers and managing pasture availability deficits via BCS fluctuation.

The model uses a number of inputs, including herd breeding values for different traits, phenotypic and genetic parameters and correlations, as well as feed availability estimates. Where appropriate, input averages and standard deviations are considered so that a stochastic approach could be introduced. The model runs simulations at both animal and herd level and, through replicates, creates average cow and herd performance outputs, including economic performance indicators typically considered by farmers.

Specific aspects considered in the model are:

1) The cow herd is simulated with individual cow variation at both the genotype and phenotype level and goes through a full annual reproductive cycle to weaning.
2) A feeding model determines the amount of feed offered to the herd each month. Feed availability and quality (energy content) was assumed to reflect variation in prevailing seasonal conditions. Thus, by accounting for month averages and variability within and between months, the model generates fluctuation in feed, i.e. pasture offered, through favourable and unfavourable seasons.
3) The feed offered to the herd will determine whether individual cows will consume feed and either gain, maintain or lose weight and body condition depending on energy requirements based on their physiological state, i.e. during early or late pregnancy, lactation, etc.
4) The performance of individual cows, and consequent herd performance, for key attributes is stochastically determined, but with probabilities depending on relevant factors. For example;
    a) The probability of a cow to become pregnant on a given day of the mating season is randomly determined (stochastically), but it is influenced by both the length of time from previous calving (lactational anoestrus) and her body condition score.
    b) Body condition is an outcome of current and prior feed availability, and energy requirements for factors such as milk production, mature size and others, all of which driven by the genetic potential of the cows in the herd.
    c) Consequently, both feed availability and animal genetics interact to determine outcomes for an individual cow, and these are accumulated over multiple individuals to

provide herd level outputs. This provides the ability to use the model to look at interactions between cow genotype and management systems.

5) The model runs multiple replicates to investigate cow genotype-environment interaction. Cow genotypes were defined as:
   a) Extreme size cow: extreme mature weight, low fat depth EBVs;
   b) Large size cow: high mature weight, low fat depth EBVs;
   c) Moderate size cow: smaller mature size, higher fat depth EBVs;

   Environments defined as:

   a) Feed supply is stable and tightly regulated via either constant pasture supply, or by providing supplements when triggered by feed availability or cow body condition;
   b) Feed supply is variable with little supplementation and cow body reserves are accumulated or mobilised according to pasture feed supply only;

6) The model generates economic outputs based on revenue generated from sales of weaned calves (and culled cows) and considering the cost of feed inputs (including supplements) and acquisition of replacement heifers.

Ultimately, the aim was to use this model to report on whether there are large differences in cow genotype response to the different environments. This outcome should aid to better understand the way in which different breeding objectives can or should be applied on farms running significantly different feeding and management systems.

A series of model scenarios were run with three levels of cow genotype and two different feeding systems to investigate whether interactions could be observed. The model outputs were a good reflection of cow performance and responded in ways that would be expected based on real systems. The models were able to show significant genotype x feeding system interactions for cow body reserve traits (weight and body condition score) but did not show any interactions at economic level parameters (profit, revenue and expenses). It also did not show any interactions in terms of numbers of calved born, suggesting that under the conditions modelled that even the most extreme genotypes were still able to achieve sufficient body condition scores at mating so that reproductive performance was not affected. It may be that the scenarios modelled did not create sufficient fluctuation in cow body reserves to enable an interaction on economic parameters to emerge. Currently the outcome suggests that where body conditions fluctuate by 0.66 units (on a 5-point scale) compared to approximately 0.35 units (under the supplemented system modelled) that there is insufficient reason to utilise significantly different breeding objectives. However, the next step is to test that conclusion by using the model as a profit function to develop test breeding objectives.

3.5.2 **Background**

This model simulates a group of mixed age beef cows under different feeding conditions and management strategies. The interaction between feeding and managements strategies, i.e. supplementation strategy and stocking rate, and the type of beef cow to which such strategies are applied, is an issue broadly defined as a comparison between controlling the environment to maximise cow performance versus breeding the cow to perform under a more fluctuating environment.

The overall objective of this project is to examine the implications of different feeding and management strategies in response to fluctuations in feed supply, and to determine whether beef cows with different genetic makeup are best suited to alternative management systems.

The model uses a number of inputs, including herd breeding values for different traits, phenotypic and genetic parameters and correlations, as well as feed availability estimates. Where appropriate, input averages and standard deviations are considered so that a stochastic approach could be introduced. The model runs simulations at both animal and herd level and, through replicates, creates average cow and herd performance outputs, including economic performance indicators typically considered by farmers.

The model has been built in R platform. Specifically, it uses the tool R-Markdown (code extension.rmd) to simultaneously run script calculations and their descriptions, as well as to “knit” a descriptive report which presents inputs and outputs to key outcomes of the model.

This report presents a complete description of the model. The report describes the inputs utilised in the different segments of the model, specifically phenotypic, genetic, environmental (feeding) and economic parameter inputs. The report also presents the rationale behind the calculations and functions used in the simulation. Finally, the report describes the herd economic performance outcomes of the model. This includes different metrics which allow comparison between feeding and management strategy and cow genotype scenarios modelled in the simulation.

3.5.3 **Model Description**

3.5.3.1 Inputs

The input parameters used throughout the model are described in this section of the report. The inputs used in the model are separated as genetic, phenotypic, environment (feed and energy) and economic. Users can update the absolute parameters presented in this report as necessary. The current values were populated for development of the model and should be appropriately input for each specific purpose.

3.5.3.2 Genetic inputs

Genetic inputs include “Genetic parameters” and “Trait parameters”. These inputs form the basis of the herd genetic potential to respond to fluctuations in the environment. Therefore, a proper representation of genetic and trait parameters is critical for the model to generate meaningful outputs.

3.5.3.3 Genetic parameters

The genetic parameters used in the simulation model are trait heritabilities, phenotypic variances and phenotypic and genetic correlations. These are presented in Table .5.3.4.1 for all traits considered in this demonstration version of the model. The model calculates trait genetic variances and standard deviations as, $\sigma_{2g}=\sigma_{2p}\cdot h_{2}$ and $\sigma_{g}=\sigma_{2g}--\surd$, respectively. Trait environmental variances were also utilised, these were calculated as, $\sigma 2g=\sigma 2p\cdot (1- h^{2})$.

3.5.3.4 Trait parameters

Trait parameters include EBVs and phenotypic trait averages. These are also presented in Table 3.5.3.4.1.

Table 3.5.3.4.1. Traits means and mean EBVS, heritabilities (h^2), and phenotypic (σ_p and σ_p^2), genetic (σ_g and σ_g^2) and environmental variances (σ_e^2) and standard deviations (σ).

Trait name	Abbrev.	h^2	Trait Mean	Herd EBV	Mean σ_p	σ_p^2	σ_g	σ_g^2	σ_e^2
Mature weight (kg)	MWT	0.41	480	80.0	46.9	2,199	30.0	901.8	1,298
Gestation length (d)	GL	0.25	281	-4.2	7.0	49.0	3.5	12.2	36.7
Weaning weight, maternal (kg)	MILK	0.10	0	15.2	22.3	499.9	7.07	49.99	449.97
Birth weight (kg)	BWT	0.39	30	3.9	3.8	14.5	2.4	5.6	8.8
Fat Depth Rib (mm)	FDRib	0.34	5	0.4	1.4	1.9	0.8	0.6	1.2
Postpartum anoestrus (d)	ANOEST	0.18	40	0.0	4.4	19.3	1.9	3.4	15.9
Conception rate (%)	CR	0.07	0.65	4.0	0.02	0.0006	0.007	0.000	0.0006
Weaning weight, direct (kg)	WWT	0.18	200	40.2	22.36	499.97	9.49	89.99	4.099

3.5.3.5 Trait correlations

Trait genetic correlations directly input into the model are presented in Table 3.5.3.5.1. These correlations are included in the model but for the purpose of this report all permanent and temporary environmental effects were assumed to be null.

Based on the inputs described above, a trait variance-covariance matrix (G) is calculated by the model as,

$$\mathbf{G} = \sqrt{\sigma_g^2 \cdot \sigma_g^{2\prime}} \cdot \mathbf{Corr_g}$$

Where $\mathrm{Corr_g}$ is the matrix of genetic correlation among traits included in the model (Table 3.5.3.5.1).

Table 3.5.3.5.1. Genetic correlations between traits included in the model.

	MWT	GL	MILK	BWT	FDRib	ANOEST	CR
MWT	1.00	0.00	0.00	0.35	0.10	0.0	0.0
GL	0.00	1.00	-0.74	-0.57	0.00	0.0	0.0
MILK	0.00	-0.74	1.00	0.00	0.00	0.5	0.0
BWT	0.35	-0.57	0.00	1.00	-0.05	0.0	0.0
FDRib	0.10	0.00	0.00	-0.05	1.00	0.0	0.0
ANOEST	0.00	0.00	0.50	0.00	0.00	1.0	0.5
CR	0.00	0.0 0.00	0.00	0.00		0.5	1.0
					0.00		
WWT	0.40	0.00	0.00	0.66	0.05	0.0	0.0

3.5.3.6 Environmental inputs

Permanent and temporary environmental effects are considered in the model as inputs. We assumed that there might be phenotypic correlations between traits that influence permanent and temporary environmental effects. If these relationships are known, the model uses those as inputs to predict performance at individual and herd levels.

Environmental inputs also include a number of herd parameters, energy requirement parameters as well as biological parameters used as key reference assumptions in the model.

3.5.3.7 Phenotypic correlations

Phenotypic correlations between traits is presented in Table 3.5.3.7.1. These correlations are dealt with in the model through the same approach applied to genetic correlations, where the permanent environmental variance-covariance is transposed and multiplied by which is the trait phenotypic correlation matrix, thus:

$$\mathbf{P_e} = \sqrt{\frac{\sigma_e^2}{2} \cdot \frac{\sigma_e^2}{2}'} \cdot \mathbf{Corr_p}$$

Temporary environmental effects are dealt with through the same method. Nevertheless, for the purpose of this report we assumed the same permanent and temporary environmental effects.

Table 3.5.3.7.1. Environmental (phenotypic) correlations between traits included in the model.

	MWT	GL	MILK	BWT	FDRib	ANOEST	CR	WWT
MWT	1.00	0.00	0.00	0.20	0.10	0.00	0.07	0.30
GL	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00
MILK	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00
BWT	0.20	0.00	0.00	1.00	-0.04	0.00	0.00	0.35
FDRib	0.10	0.00	0.00	-0.04	1.00	0.00	0.00	0.14
ANOEST	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00
CR	0.07	0.00	0.00	0.00	0.00	0.00	1.00	0.00
WWT	0.30	0.00	0.00	0.35	0.14	0.00	0.00	1.00

3.5.3.8 Herd parameters and phenotypic means

Described in this section are herd parameters such as age, structure, effect of parity and a number of energy utilization and requirement parameters, as well as biological parameters utilised as inputs in the model.

3.5.3.9 Age structure of Herd

The user defines both the size and age structure of the herd. For the purpose of this report, a 100-cow herd was assumed under the age structure presented in Fig. 3.5.3.9.1. The total number of cows and the proportion of cows in each parity group is the actual input into the model.

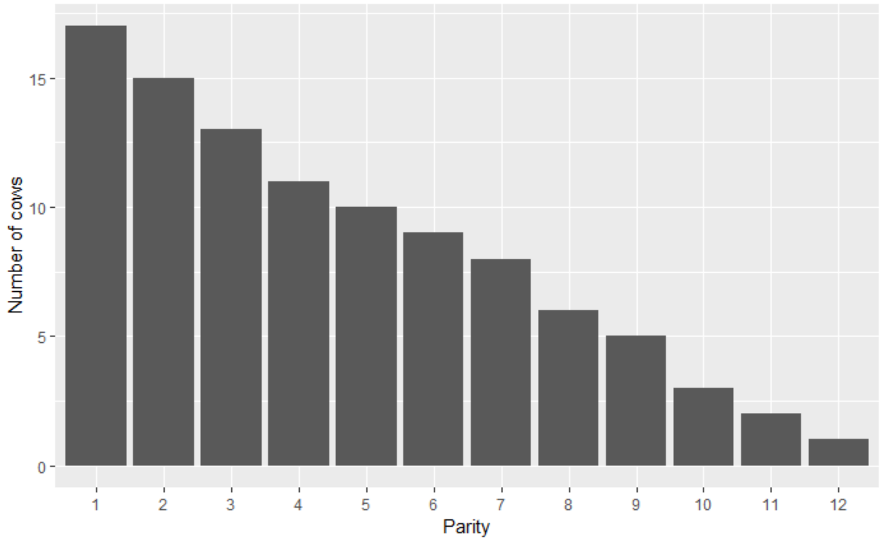


Fig. 3.5.3.9.1. Age structure of the simulation herd.

3.5.3.10 Parity effects

Cow age effects were assumed in different traits. These effects are also input into the model, and for this report, it was assumed that cows in different age groups, i.e. parities, were assumed to be affected differently in traits such as gestation length (GL), mature weight (MWT) and calf weaning weight (MILK). The age group, or parity effects, are presented in Table 3.5.3.10.1 and represent the trait expression different parities relative to each other.

Some of the assumptions were based on the literature available for such parameters and these are indicated where necessary.

Table 3.5.3.10.1. Age group effects, or parity effects, in different cow traits assumed as inputs in the model.

Parity	GL (days)	MWT (Rel. prop. by parity)	MILK (Rel. prop. by parity)
1	-2	0.77	0.71
2	0	0.89	0.89
3	0	0.95	0.97
4	0	1.00	1.00
5	0	1.00	1.00
…	…	…	…
…	…	…	…
12	0	1.00	1.00

3.5.3.11 Energetics parameters

Energy utilization and requirement parameters are input from an external file. The file named "Energetics.csv" and it is used to parameterise model assumptions such as efficiencies of live weight gain and maintenance requirements, i.e. per kg LWT$^{0.75}$. The energy related inputs used in this report are presented in Table 3.5.3.11.1.

Table 3.5.3.11.1. Energy utilization and requirement parameters.

Parameter	Description	Value
Maintenance requirement	Energy for maintenance ($K_{maintenance}$, MJME/kg^0.75)	0.62
LWT gain energy requirement	To gain 1 kg liveweight (MJ ME)	50
LWT loss energy stored	Energy saved from 1 kg liveweight loss (K_{wtLoss}, MJ ME)	30
Lactation energy efficiency (Kl)	Partial efficiency of lactation (Prop)	0.61
Energy requirement for regulation Km.hardhill	Maintenance requirement hard hill (MJ ME)	0.7
Mecon	Feed ME MJ/kg DM (MEcon)	10
EVL	EVL Energy content of milk	3.4659
Km	Km (GHG v3)	0.7
Max.intake	Max intake as % BCS 4 liveweight	2.50%
MJ fat[1]	Energy content of kg of subcutaneous	35.73
MJlean[2]	Energy content of kg of lean	0.00485
Kgain[3]	Gain efficiency	0.47

1. Food and Agriculture Organization of the United Nations (2015). Animal Production and Health http://www.fao.org/ag/againfo/themes/en/meat/backgr_composition.html (verified 2015)
2. Food and Agriculture Organization of the United Nations (2015). Animal Production and Health http://www.fao.org/ag/againfo/themes/en/meat/backgr_composition.html (verified 2015)
3. Holmes, C.W.; Roche, J.R. 2007. Pastures and supplements in dairy production systems. pp. 221-242. In: Pasture and Supplements for Grazing Animals. Eds. Rattray, P.V.; Brookes I.M.; Nicol A.M. New Zealand Society of Animal Production. Occasional Publication No 14.

The change in body condition score (BCS) per unit change in body live weight is also an important parameter in the model. This regulates mobilization and accumulation of body reserves as cow live weight fluctuates according to feed supply and physiological status. The current input assumes a change of 0.12 BCS units per kg change in live weight. Each cow had a different conversion of the number of kg to gain/lose a BCS score, depending on the mature weight of the cow, with an average of 67 kg representing one unit of BCS. The target BCS was assumed to be 3 on a 1 – 5 scale.

3.5.3.12 Biological parameters

A summary of the biological assumptions taken from the literature and utilised in the model is presented in this session. These assumptions are used mainly to predict the potential effects from changes in condition score and live weight on the reproductive performance of the herd, especially on conception rate and post-partum anoestrus interval. These parameters were input into the calculations to generate the underlying conception rate of the model. A brief description of the reference literature is presented below with the consequent conception rate prediction.

The review from Short *et al*. 1990 describes physiological mechanisms controlling anoestrus and infertility in postpartum beef cattle. This review addresses the different factors driving anoestrus, specifically how postpartum infertility is affected by several minor factors such as season, breed, parity, and carryover effects from suckling and nutrition. We utilised the references to BCS presented in this review (Fig. 3.5.3.12.1) to parameterise the conception rate prediction in the model.

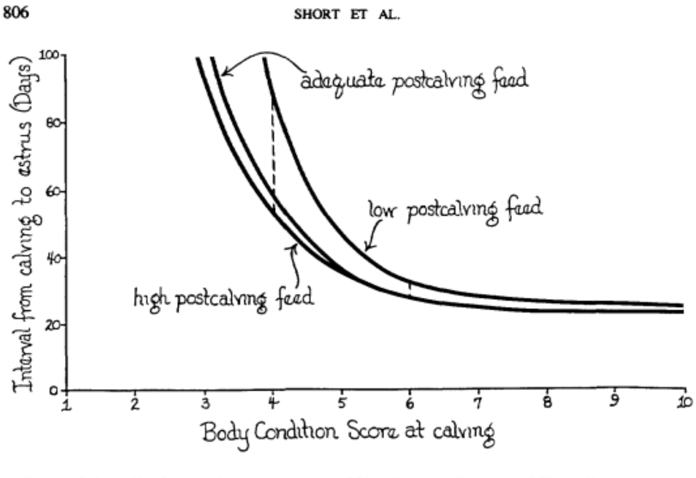


Figure 4. Relationship of interval from calving to estrus (PPI) and body condition score (BCS) as affected by levels of postpartum diets.

Fig. 3.5.3.12.1. Reference relationship between post-partum anoestrus interval and BCS, Short *et al*. 1990.

Hansen and Hauser (1983) analysed the effect of calving season on post-partum interval and other reproductive traits in suckled and non-suckled cows. Differences between seasons were greater for suckled cows, cows with genetic ability for high milk production, primiparous cows and cows fed diets low in energy. Thus, some of the findings of this paper were used to parameterise the model. For instance, as presented in Fig. 3.5.3.12.2, an average 0.22 day longer calving interval was identified for each additional day in calving date.

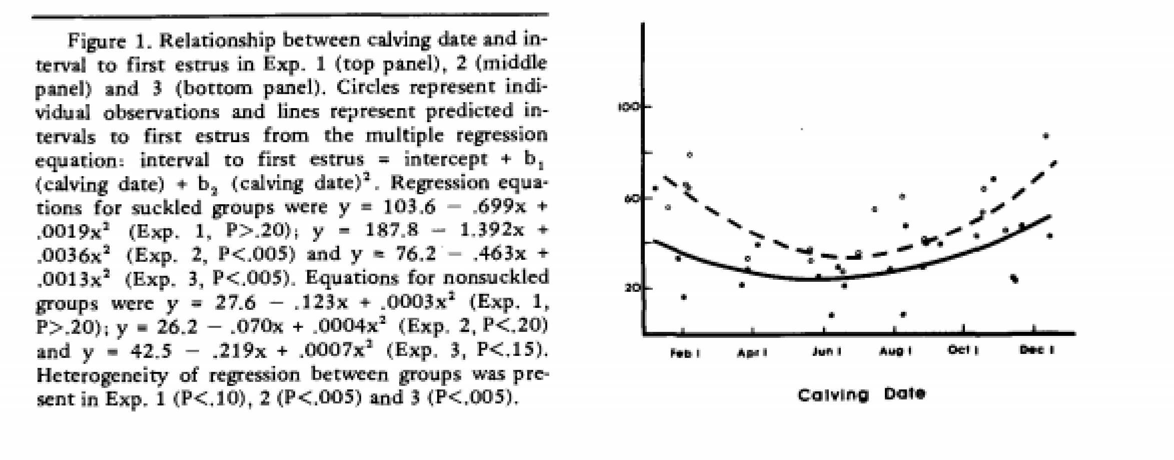
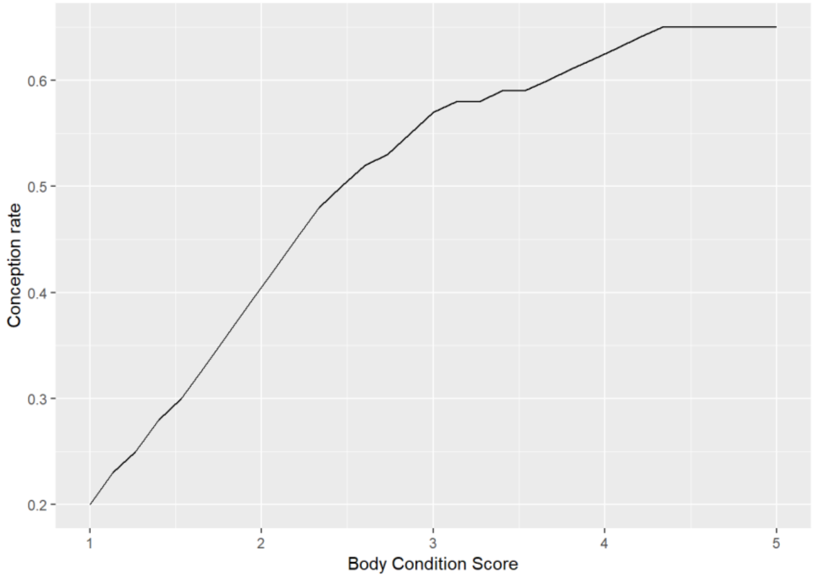


Figure 1. Relationship between calving date and interval to first estrus in Exp. 1 (top panel), 2 (middle panel) and 3 (bottom panel). Circles represent individual observations and lines represent predicted intervals to first estrus from the multiple regression equation: interval to first estrus = intercept + b_1 (calving date) + b_2 (calving date)^2. Regression equations for suckled groups were $y = 103.6 - .699x + .0019x^2$ (Exp. 1, $P>.20$); $y = 187.8 - 1.392x + .0036x^2$ (Exp. 2, $P<.005$) and $y = 76.2 - .463x + .0013x^2$ (Exp. 3, $P<.005$). Equations for nonsuckled groups were $y = 27.6 - .123x + .0003x^2$ (Exp. 1, $P>.20$); $y = 26.2 - .070x + .0004x^2$ (Exp. 2, $P<.20$) and $y = 42.5 - .219x + .0007x^2$ (Exp. 3, $P<.15$). Heterogeneity of regression between groups was present in Exp. 1 ($P<.10$), 2 ($P<.005$) and 3 ($P<.005$).

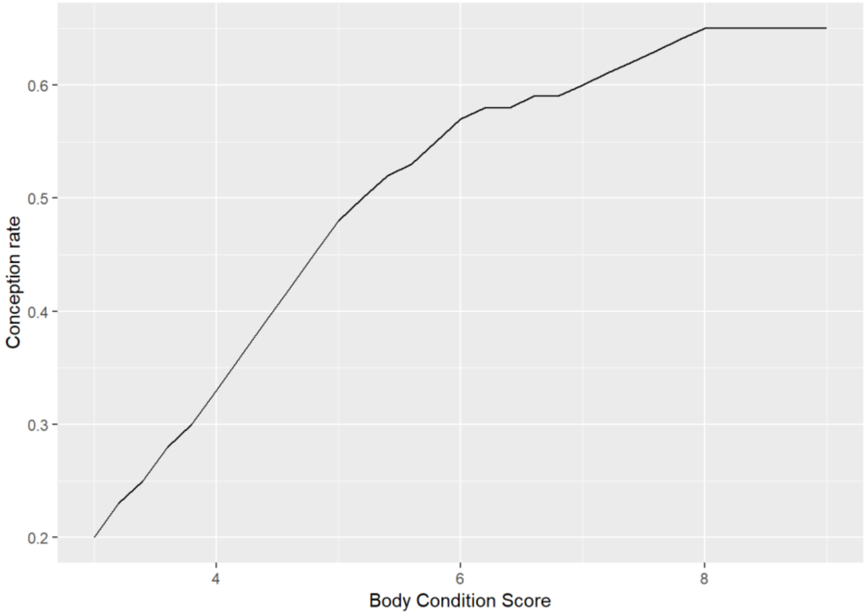
Fig. 3.5.3.12.2. Impact of calving date on average anoestrus interval in beef cows, Hansen and Hauser (1983).

On feed intake, the review from Ingvartsen (1994) has been used as reference. The study investigated different prediction models for feed management on farms as well as feed evaluation. A dynamic and mechanistic approach was needed to parameterise our model and therefore inputs might have to be adjusted for different scenarios. For this report, we assumed some insights from the review such that thinner cows eat about 24 to 27% more than fatter cows. Primiparous cows eat 13% less than multiparous cows after differences in live weight and milk yield are accounted for, and mainly that intake should sit around 2.5% of body weight.

The resulting conception rate outcome parameters used in this model report were read as an input file named “BCS vs Conception.csv”. These are presented in Fig. 3.5.3.12.3 (a) and (b) for BCS scales of 1 – 5 and 1 – 9, respectively.



(a)



(b)

Fig. 3.5.3.12.3. Conception rate of cows in different body condition score (BCS) scales, 1-5 (a) and 1-9 (b).

For conception rate and BCS content composition, the model creates specific curves for each individual cow. These curves are used as key parameters driving the probability of cows conceiving at different timepoints, given that their nutritional status will direct affect mobilization or accumulation of body reserves and consequently their reproductive performance. The average herd performance is therefore made up from the average performance of each individual cow.

3.5.3.13 Management and feeding inputs

Management and feeding inputs are a critical aspect of the model. Through these inputs the model is able to simulate stochastically live weight fluctuations and body reserves as response to feed offered for individual cows. In this session we describe the model inputs used in in the report.

3.5.3.14 Events

Event inputs represent specific dates in which mating season starts and ends, weaning date and whether the "Hill country" parameter is activated. These inputs are included directly into the model and are used as part of the functions used for energy related calculations. The current inputs used for this report are presented in Table 3.5.3.14.1.

Table 3.5.3.14.1. Main reference event dates used in the model.

Events	Input
Bull in (day of the year)	334
Bull out (day of the year)	32
Weaning (day of the year)	100
Hill Country	TRUE

3.5.3.15 Herd parameters

Herd average performance parameters are used to define critical aspects of the model such as fertility and mortality. The average herd performance indicators are presented in Table 3.5.3.15.1.

Table 3.5.3.15.1. Reference fertility and mortality parameters used in the model.

Parameter	Input
In-calf rate	0.95
Calf peri-natal mortality	0.06
Calving rate	0.89
Pre-weaning mortality	0.02
Weaning rate	0.87

3.5.3.16 Feeding regime

These inputs define the feeding regime for the cow herd. These assumptions are input directly into the model and include the average feed offered (kg of dry matter per cow per day), the variation in feed availability and the average feed composition in mega Joules of metabolizable energy per kg of dry matter (MJME per kgDM), as indicator of feed quality. The mean parameters used in the simulations of this report is presented in Table 3.5.3.16.1.

Table 3.5.3.16.1. Feed availability input parameters used for the current simulation.

Month	Pasture offered (kg DM/cow/day)	Supplement offered (kg DM/cow/day)	St. dev. feed allocation	Feed composition (MJME/kg DM)	Monthly feed price ($/kg DM)[1]
Jan	13	0	2	10	0.05
Feb	13	0	2	10	0.05
Mar	12	0	2	10	0.10
Apr	10	0	2	10	0.15
May	10	0	2	10	0.20
Jun	6	0	0.5	10	0.20
Jul	5	0	0.5	10	0.20
Aug	5	0	0.5	10	0.20
Sep	7	0	1.5	10	0.20
Oct	13	0	2	10	0.10
Nov	15	0	3	10	0.05
Dec	14	0	3	10	0.05

[1] Monthly feed price of supplements was assumed to be constant through the year at $0.40/kg.

These parameters are very important because they constitute the way in which the environment is defined in the model. The model randomly draws from the distributions above to generate the feed available for the herd on each day.

The total feed availability (kg DM per cow per day) for the cow herd throughout the production cycle is then represented in Fig. 3.5.3.16.1. Feed availability is then associated with the energy composition through the year which forms the basis through which live weight and cow body reserves are simulated.

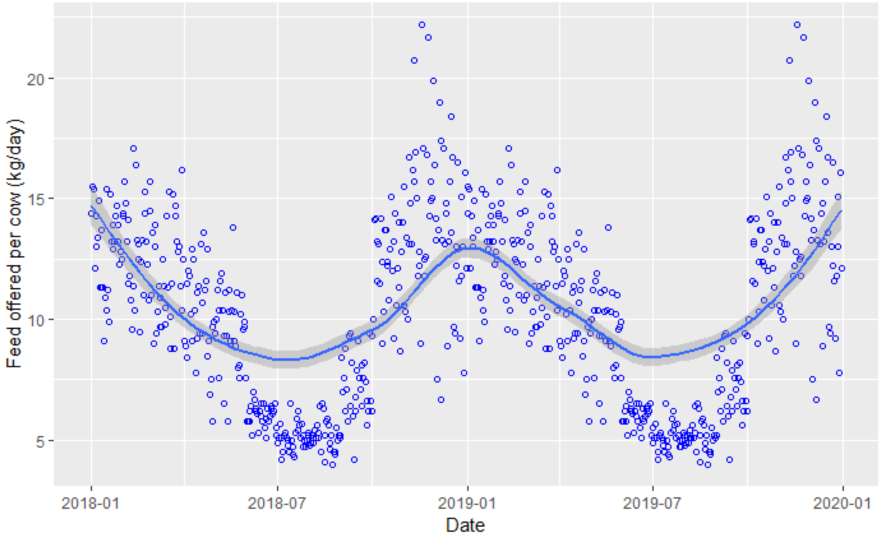


Fig. 3.5.3.16.1. Average feed availability curve (kg DM per cow per day) for the cow herd.

3.5.3.17 Economic inputs

The economic inputs include basic price reference components of revenue, considering the only cost components assumed are feed costs and replacement cost. The feed used by calves until weaning was assumed to be based on an average price from birth to weaning. These assumptions are also input directly into the model, a summary is presented in Table 3.5.3.17.1.

Table 3.5.3.17.1. Economic input parameters used for the current simulation.

Parameter	Value ($)
Weaner calf price ($/kg LWT)	3.500
Cull cow price ($/kg CWT)	3.650
Cull cow dressing (%)	0.500
Cull cow price ($/kg LWT)	1.825
Calf feed value $/kgDM	0.120
Heifer value ($)	1,500

3.5.4 **Modelling methods**

This session of the report presents the methods through which inputs and parameters are combined in tables, functions and calculations and modelled in different simulation scenarios. This session of the model simulates the functioning of the herd and its resulting performance in front of the feed availability of each environment.

3.5.4.1 Cow age and genetics

This part of the model creates and populates the "CowBV" data table. This table is formed by randomly drawing EBVs using "mvrnorm" function and the variance-covariance matrix created from the genetic correlations described above. The model uses these EBVS, the phenotypic means and the covariances to calculate starting live weights, as well as true mature live weights, and a lactation curve for each cow.

In this session of the model both genetic and phenotypic input parameters are used, including the permanent and temporary environmental effects and parity effects. Cow live weight and lactation curves are produced for each individual and account for the changes in live weight and milk production on each day of the cycle.

3.5.4.2 Cow live weight and BCS

The starting live weight is calculated based on the genetic and phenotypic parameters from the model, from where breeding values, permanent and temporary environmental effects are randomly drawn from the normal distributions described in the inputs. Parity effects were also included, to simulate age-effects in live weight. The predicted live weight at calving and live weight at target BCS across different parities is presented in Fig 3.5.4.2.1.

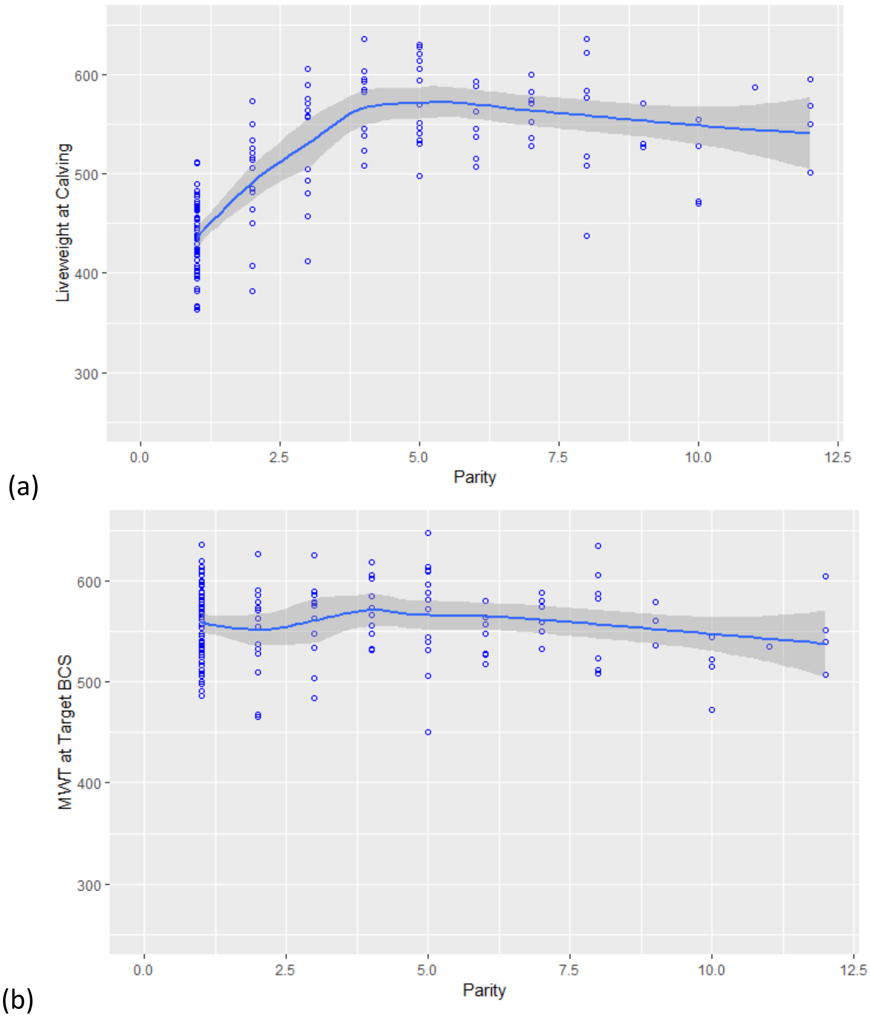


Fig. 3.5.4.2.1. Predicted cow live weights at calving (a) and at target BCS (b) across parities.

The difference between the ideal starting liveweight (adjusted for age) at calving and the liveweight simulated at target BCS (accounting for the environmental effects) was used to calculate the starting BCS at calving. For this simulation, the cow target BCS was set to 3 on a 1 – 5 scale and the distribution of cows BCs is presented in Fig. 3.5.4.2.2.

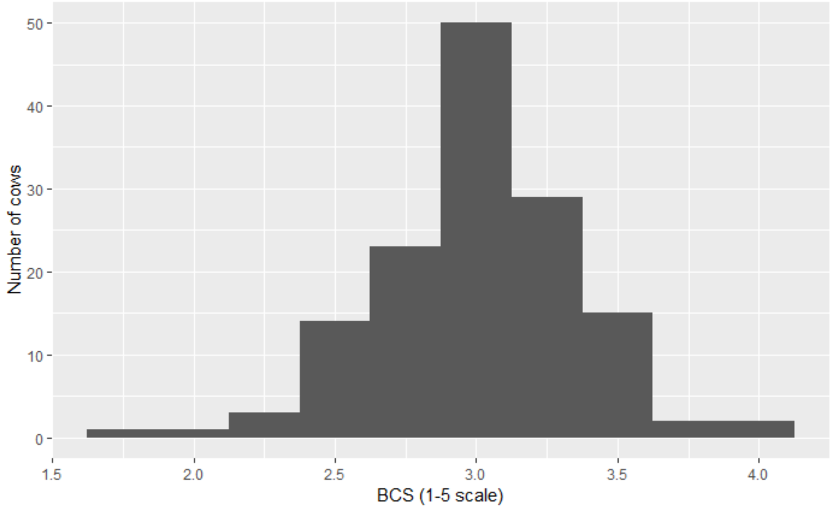


Fig. 3.5.4.2.2. Predicted cow body condition score distribution at calving.

3.5.4.3 Base lactation curve

The base lactation potential for each cow is simulated from genetic, environmental effects (temporary and permanent) and parity effects that affect milk production. This is also determined by the stage of the lactation and the total amount of milk production, both of which are inputs to the model.

As reference, we have used literature material from Fraga (2013) to understand the milk production of Angus beef cows, and for checking on model assumptions involved with lactation curves and body reserves. Nevertheless, lactation curve parameters and simulation specific inputs can be modified in different ways throughout the model - according to the needs of the scenarios investigated. The milk production related curves are presented in Figures 3.5.4.3.1, 3.5.4.3.2 and 3.5.4.3.3.

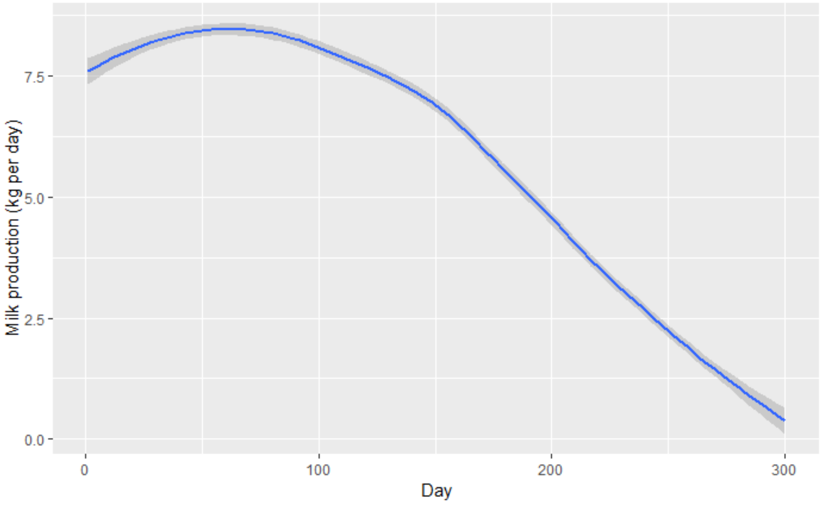


Fig. 3.5.4.3.1. Average milk production (kg per day) curve base reference for the simulation.

The model calculates the maternal weaning weight from milk potential is expressed by the calf. Based on Fraga (2013), the value of 12 kg was assumed to be the amount of milk required to produce an extra kg of weaning weight. An extra kg of milk produced approximately 0.08kg of weaning weight, depending on what stage of lactation is being measured, thus 1/0.08 = 12.5.

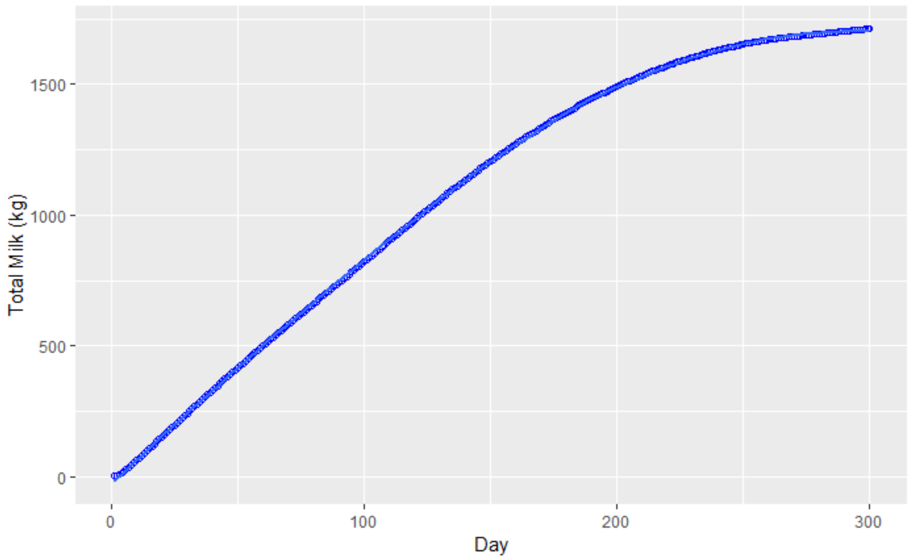


Fig. 3.5.4.3.2. Cumulative average milk production curve over a lactation.

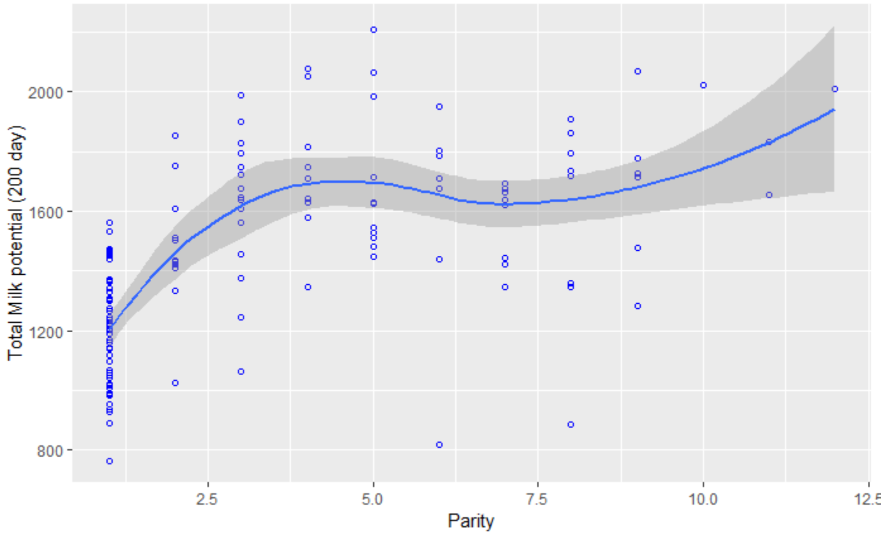


Fig. 3.5.4.3.3. Average cumulative lactation curve by herd parity age.

3.5.4.4 Calf performance

The model produces calves whose performance is a reflection of the genetic merit of the cow and bull and a mendelian sampling component based on half the additive genetic variance and sampled from a multi-variate normal distribution to maintain trait correlations. Bull EBVs were assumed to be the equivalent of the herd mean EBV, with the same bull (or bulls of equal genetic merit) used as the sire for all calves. The calf traits predicted in the model are: birth date, birth weight, weaning date, weaning weight, 200-day weight, total energy and total feed required per weaned calf. The methods used to calculate these model parameters are presented in this session.

The model starts on the first day of the calving season. Cows are randomly assigned a calving date from a distribution (mean = 39.5 days after start of calving, sd=14 days). The first day of the calving season is user-defined. Nevertheless, the model accounts for the fact that during the first mating cycle, a large number of cows get pregnant, then that number progressively reduces.

3.5.4.5 Cow calving date

Calving date is generated from the cow calving methodology which involves mating, conception and gestation length. The conception date of each cow will result in a specific calving date which will be used as reference birth date for the calf. An initial mating period of 70 days is assumed with an initial conception rate of 60% in the first cycle, i.e. assuming 21 days cycles. This creates the number of cows conceiving at each cycle given a certain probability of conception. Each cow has a conception date sampled from the resulting distribution, and variation in gestation length (sd = 5 days) is also added along with 281 days gestation length to produce a birth date. First day of calving is calculated with reference to the user-input of mating date to ensure an annual cycle is accurately represented.

3.5.4.6 Birth weight

Calf birth weight is generated from the reference average herd birth weight (BWTh), the average herd breeding value of birth weight (BWTebv) and accounts for permanent (BWTpe) and temporary (BWTte) environmental effects. Calf birth weight also accounts for the ratio between birth weight and mature cow weight (basebwt), so that the effect that bigger cows will generate bigger calves can be accounted for. Thus,

BWT (kg)=BWTh·basebwt+BWTebv+BWTpe+BWTte , where basebwt=BWThMWTh.

3.5.4.7 Weaning date and age

Age at weaning (at a user-specified fixed date) is calculated based on birth date of the calves. A random binomial distribution has been included to account for peri-natal and overall pre-weaning mortality. This assigns random loss of calves to a proportion of cows and this shortens lactation length in the corresponding mothers.

3.5.4.8 Weaning weight

Weaning weights are generated from a reference birth weight and the reference 200-day weight from which the daily average daily gain (adg_{milk}) is calculated. The 200-day weight is calculated through a similar principle as birth weight: 200d (kg)=$Milk_{h}$ + $Milk_{ebv}$ + $Milk_{pe}$ + $Milk_{te}$, where $Milk_{h}$ is the reference average herd weaning weight, $Milk_{ebv}$ is the average herd breeding value of weaning weight, $Milk_{pe}$ accounts for permanent environmental effects and $Milk_{te}$ for temporary environmental effects. The average daily gain is calculated as:

$$adg_{milk} = \frac{(200d(kg) - BWT(kg))}{200}.$$

The average daily gain is then multiplied by the age at weaning and added to the birth weight. Thus,

$$Milk\ (kg) = \left(Milk_{age}(days) \times adg_{milk}\right) + BWT(kg),$$

Where $Milk_{age}$ is the weaning age of each calf.

3.5.4.9 *Total calf energy required*

The total amount of energy required to wean a calf is determined by the live weight growth between calving and weaning and the required amount of energy per kg of growth. In this simulation, the live weight gain energy requirement per kg of gain was assumed to be 50 MJME (Table 3.5.3.11.1). Therefore,

$$\text{Energy (MJME)}=(\text{Milk(kg)}-\text{BWT(kg)})\times 50(\text{MJME/kg}).$$

3.5.4.10 *Total calf feed required*

The total amount of feed required to wean a calf is calculated from the total energy required, the proportion of that energy that is provided by the cow through milk (EVL, energy content of milk is 3.4659 MJME, Table 3.5.3.11.1), and the remaining energy supplied by pasture and or supplements ($\text{feed}_{\text{MJME}}$). The total amount of feed required is then,

$$Feed\ (kgDM) = Energy\ (MJME) - (Lact_{milk} \cdot EVL)$$

Where $\text{Lact}_{\text{milk}}$ is the cow total milk production during the lactation.

3.5.4.11 *Cow body reserves dynamics*

All cows are assigned a body fat content curve which is formed from an average reference on the fat and lean body composition of cows. The curve also uses this to calculate how much energy is stored in the body of the cow (per unit of live weight) over different BCS.

The model uses parameters to calculate the body fat and lean composition and the amount of energy necessary to sustain that as the BCS of the cow changes according to her physiological status and the feed available. The key parameters used are presented in Table 3.5.4.11.1.

Table 3.5.4.11.1. Main reference parameters used to calculate body fat and lean composition requirements.

Parameter	Acronym	Input
Energy in fat (MJME per kg)[8]	-	35.73
Energy in lean (MJME per kg)[9]	-	4.85
Efficiency of energy conversion (%)	Conv	40
Fat energy requirement (MJME per kg)	$\text{Energy}_{\text{fatkg}}$	89.32
Lean energy requirement (MJME per kg)	$\text{Energy}_{\text{leankg}}$	12.12

[8] Food and Agriculture Organization of the United Nations (2015). Animal Production and Health http://www.fao.org/ag/againfo/themes/en/meat/backgr_composition.html (verified 2015)

[9] Food and Agriculture Organization of the United Nations (2015). Animal Production and Health http://www.fao.org/ag/againfo/themes/en/meat/backgr_composition.html (verified 2015)

The contribution of fat ($\text{fat}_{\text{BCS\%}}$) and lean ($\text{lean}_{\text{BCS\%}}$) content to the BCS composition is input into the model through a reading file named “BradBCS.csv”. The curve that represents the average fat and lean content composition of BCS for the herd is presented in Fig. 3.5.4.11.1.

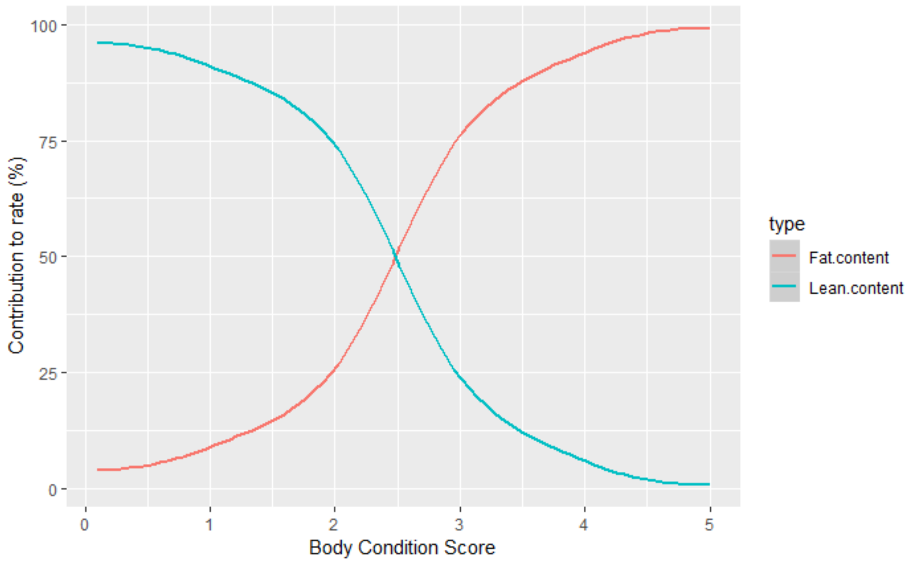


Fig. 3.5.4.11.1 . Fat and lean content composition of BCS for the average cow herd.

The resulting calculations provide the energy requirements as cows body weight dynamics occur. These dynamics depend on body composition which is driven by the cow's genetic potential (FDRibebv) to mobilise or accumulate energy (fat) reserves through the cycle. The calculations can be described as,

$$Energy_{kg}^{gain} = \left(\frac{fat_{cont}}{100} \times Energy_{kg}^{fat}\right) + \left(\frac{lean_{cont}}{100} \times Energy_{kg}^{lean}\right),$$

Where fat$_{cont}$ and lean$_{cont}$ are respectively fat content and lean content, calculated as:

$$fat_{cont} = fat_{\%}^{BCS} + FDRib_{ebv} \text{ and } lean_{cont} = lean_{\%}^{BCS} + FDRib_{ebv}$$

3.5.4.12 Pre and post first mating function

This session of the report describes the function which calculates the effect of social ranking which considers that larger and older cows are less likely to lose out on feed, the required amount of growth that cows need (younger growing cows) and body weight change over the cycle, the associated energy and feed requirements to support these dynamics.

3.5.4.13 Social ranking

The model ranks the cow herd by parity and liveweight in key events during the cycle. This is used to create a social ranking of cows which further determines the preferential access to the contestable feed available.

3.5.4.14 Feed and growth from calving to mating

The next mating event of a cow following a calving is determined by the calving date, the day of the year in which the mating starts and the duration of the mating period. The feed required for that period by day, as described before, is determined by the amount of body weight change that occurs for each cow over the cycle divided by 365 days. The feed required between calving and mating is the daily feed requirement in kg of DM multiplied by the period between calving and the end of the mating period.

3.5.4.15 Heifer energy requirements

Cow maintenance requirements are calculated based on the pre-mating live weight and the input parameter maintenance energy requirement, such that $Energy_{MaintMJME}=LWT^{0.75}_{pre.mate}\times k_{maint}$, where k_{maint} is 0.62 (Table 3.5.3.11.1). Pregnancy energy requirement for late pregnant heifers, i.e. non-lactating, during the calving season, are estimated based on the stage of pregnancy, predicted conception date, the planned start of calving and the gestation length EBV of the herd. The foetal age (Age_f) influences the amount of energy required for the growing cow and it is considered on every day during the lactation, so that pregnancy requirements are calculated as:

$$Energy^{Pregnancy}_{MJME} = 0.025 \times 10 \times \left(10^{\wedge}151.64^{-0.0000576\cdot Age_f}\right) \times \frac{0.0202^{(-0.0000576\cdot Age_f)}}{0.13}$$

The total amount of growth required to achieve the potential cow mature weight at target condition score within a cycle is calculated from the mature weight EBV, and the proportion of actual weight fluctuation relative to the potential mature weight.

$$LWT_{pre.calf}=LWT_{BCStarget}\times Rel.prop_{MWT}$$

and

$$Residual_{Growth}=LWT_{BCStarget}-LWT_{pre.calf}$$

Heifer growth energy requirements is determined based on the residual growth to achieve from the current live weight of the heifer up to its expected mature live weight daily. Growth requirements also account for the energy (K_{wtLoss}, MJME) saved from 1 kg live weight loss. Thus, $Energy_{GrowthMJME}=Residual_{Growth}\times K_{wtLoss}$

The total energy required for growing heifers is then calculated for each individual cow as

$$Energy_{TOTALMJME}=Energy_{MaintMJME}+Energy_{PregnancyMJME}+Energy_{GrowthMJME}$$

3.5.4.16 Intake

The necessary feed intake to sustain the energy required along the cow-cycle was based on the feed available for the herd considering the social interactions that account for cow size and age. This concept is referred to as contestable feed, which is the feed that can be missed by lower social ranking cows in the herd. This means that all surplus feed is shared fairly on the farm, but in a shortage situation, approximately 10% of that feed is contestable.

The contestable feed assumes that cows have a maximum daily intake which is modulated by their body condition. According to Ingvartsen (1994), leaner cows eat about 24 to 27% more than fatter cows.

3.5.4.17 Herd feed function

This function collates a number of parameters and calculates cow live weight and BCS for day 1 of the year until the start of the mating period. All data associated to this function is written to a data table called “Herdfeed” which plots feed and requirements over time.

3.5.4.18 Postpartum anoestrus interval function

Here we define the postpartum anoestrus interval which is influenced by the cows calving date, her BCS and genetic potential. The function accounts for the body condition score of the cow in the different times along the cycle, but particularly at calving. The postpartum anoestrus interval (PPAI) for each cow is calculated as:

$$\text{PPAI (days)}=\text{ANOEST}_{h}+\text{ANOEST}_{ebv}+\text{ANOEST}_{pe}+\text{ANOEST}_{te}$$

From the calculations of each cow, the average postpartum herd average anoestrus date is calculated and plotted based on the herd calving date pattern. This function also assigns a certain number of non-cycling cows at the start of mating and generates an average herd non-cycling rate.

3.5.4.19 Cow mating function

This function defines the cycling day of each cow in the herd based on a 21-day cycle. This is defined in advance so that a variable named “cownextpregnatndate” is created to predict the conception date of each cow and an average herd conception date distribution.

This function is similar to the "pre and post mating" function described above, but includes adult cows, i.e. cows from the second-mating onwards. Similarly, to the "pre and post mating" function, this also accounts for the BCS profile of the cow herd to predict conception distributions and conception rates up to 5 cycles. After mating, the function determines the cows that did not conceive and identifies those that should be culled at weaning time.

3.5.4.20 Cow weaning function

This function establishes the calves that are actually weaned and their weight at the end of the lactation period. At this point, replacements are also added to the herd and included in the data table. All replacements kept are populated with a gestation length and a calving date. The number of replacements kept is basically defined based on the number of cull cows removed from the herd in the end of the cycle, which is determined based on their live weight and body condition score at weaning and includes cows that have eventually lost calves along the cycle.

For the calculation of the predicted weaning weights, the parameters used are the feed type and amount available for the herd during the lactation period, the energy requirements for cows that are pregnant and lactating, and eventually still growing. The function produces a plot of the total herd energy needs and the total feed and energy supplied.

The output of this part of the function is the total number and a list of animals that should be culled or kept as replacements. This is then used to inform the economics part of the model.

3.5.4.21 Cow post weaning function

This function repeats the pre and post mating function to complete the simulation up until the complete 365-day cycle. The function produces a summary of herd feed for the year, which includes the total energy needs of the herd and a break down by energy allocation, feed available and also describes the number of cows fed.

3.5.4.22 Economics function

This function describes the economics of the simulations which accounts for feed costs and revenue from weaned calves and cull cows.

The economic output summary is relatively simple. The main outcomes are based on total cow and weaned calves' weights. A value is attributed to cows and calves based on total amounts and respective prices. The actual feed eaten is valued based on the month in which feed is consumed in, accounting for availability and price. The eventuality of costs related to supplementation is also accounted for considering the amount of supplements used. This cost reflects difference between the base pasture grown and feed fed for scenarios where supplementation is used. The model also adjusts economics to a steady state system, by putting a value on the difference in cow weight at the start and end of the year, i.e. if cows on average have lost 10 kg over the year, this might affect the reference price of the animal.

3.5.5 **Model outputs**

3.5.5.1 Cow calving date

The model produces a plot with the herd calving distribution from the first day of the calving season.

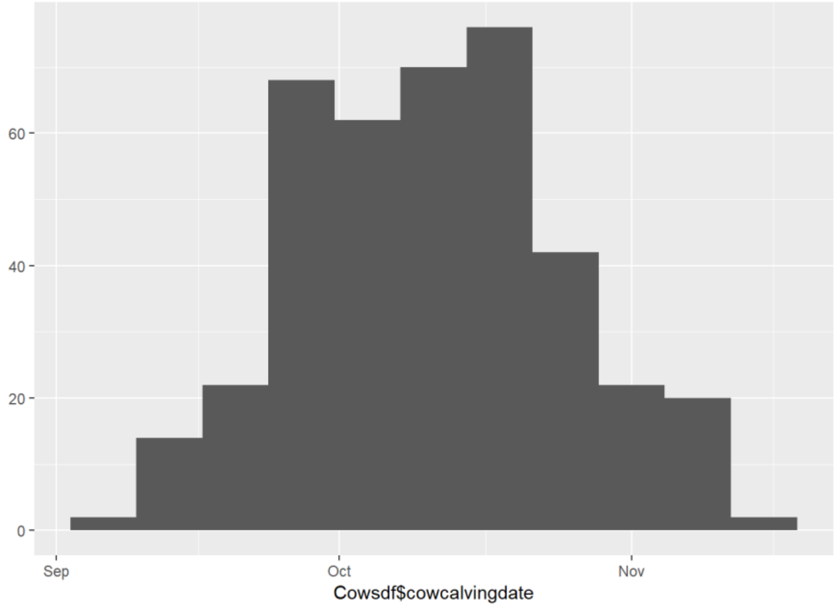


Fig. 3.5.5.1.1. Distribution of cows calving along the season.

3.5.5.2 Generate the calves

The amount of energy stored in the form of body reserves for each cow is presented as an indication of the overall herd condition.

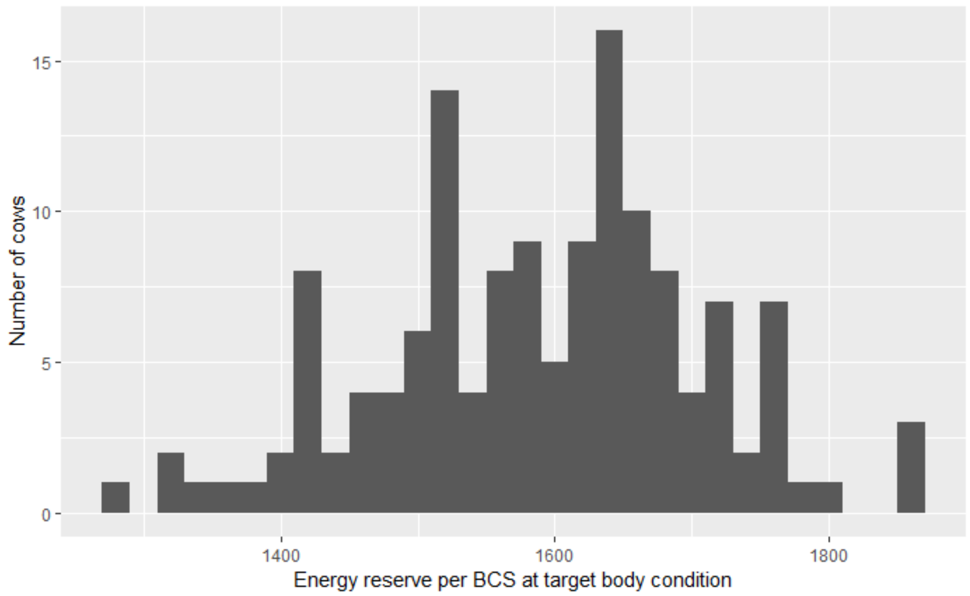
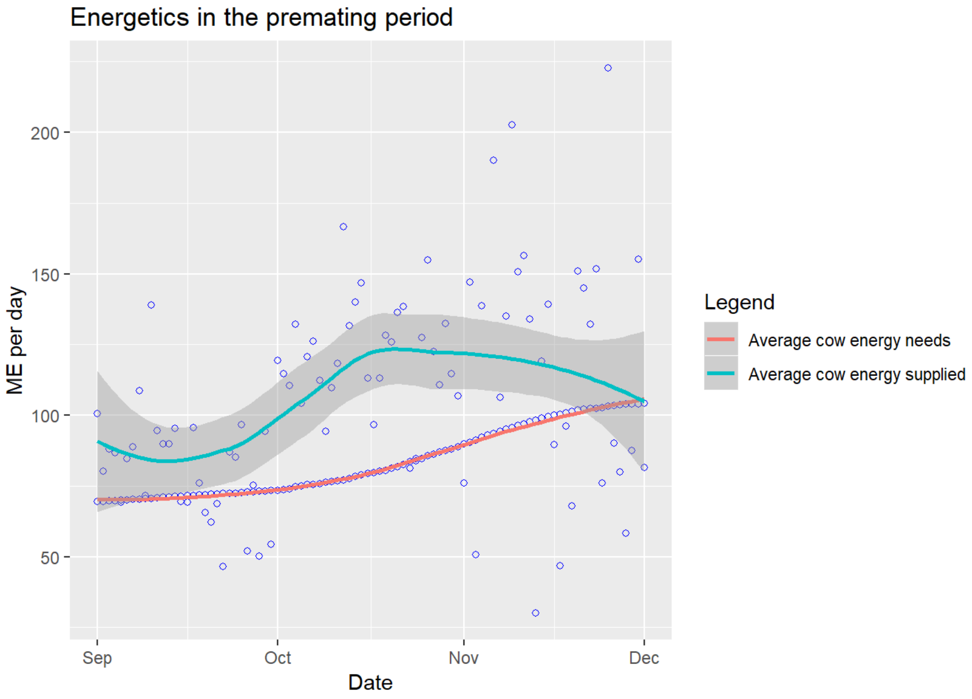
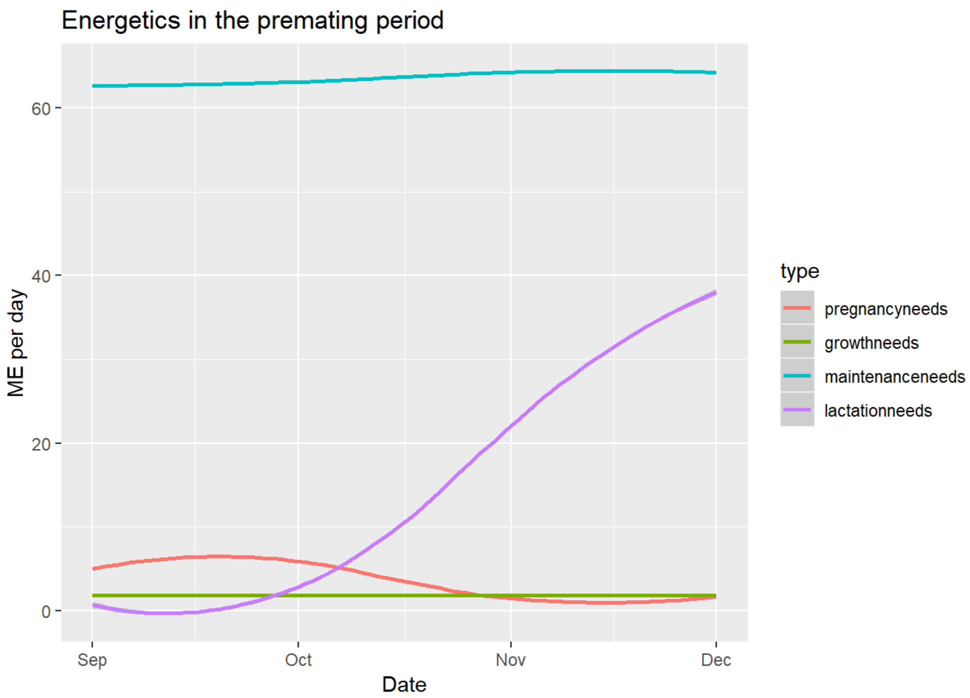


Fig. 3.5.5.2.1. Distribution of body reserves (MJME) in cow herd at target BCS 3 on a 1 – 5 scale.



(a)



(b)

Fig. 3.5.5.2.2. Cow energy balance over the pre mating period, average needs (a) and broken down needs by allocation target (b).

3.5.5.3 Postpartum anoestrus interval

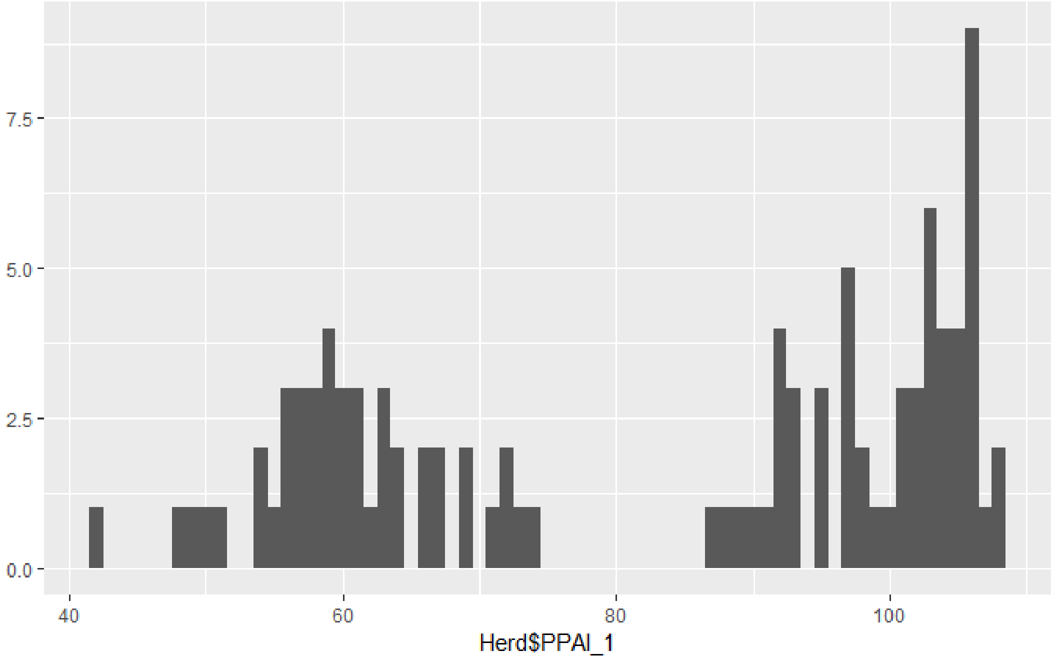


Fig. 3.5.5.3.1. Cow herd average postpartum anoestrus interval.

3.5.5.4 Cow mating

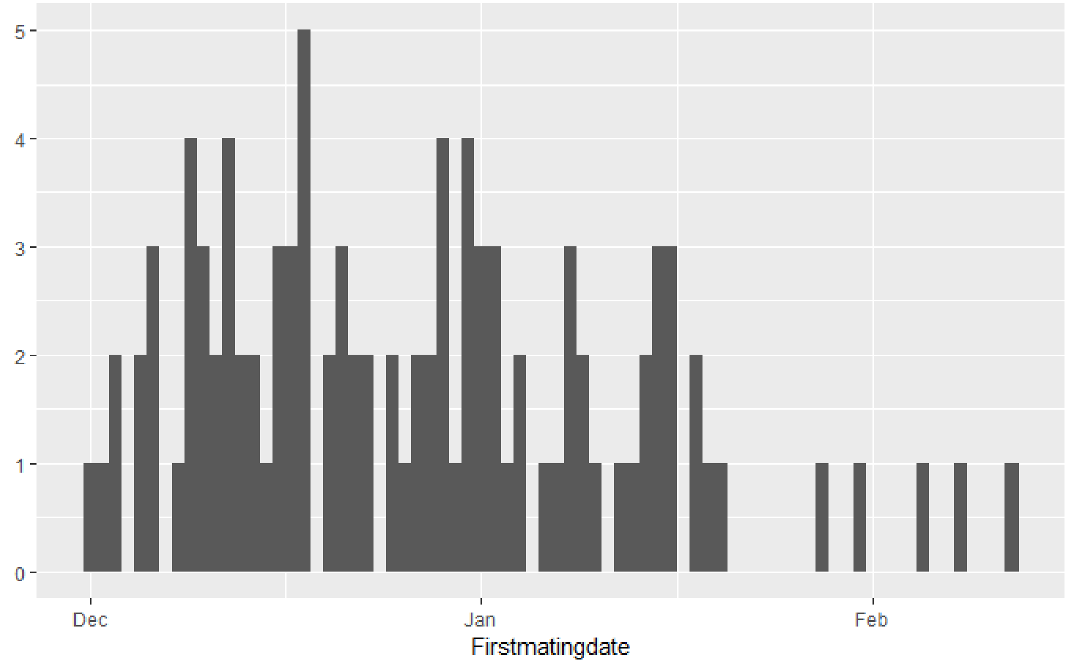


Fig. 3.5.5.4.1. Cow herd average first mating date.

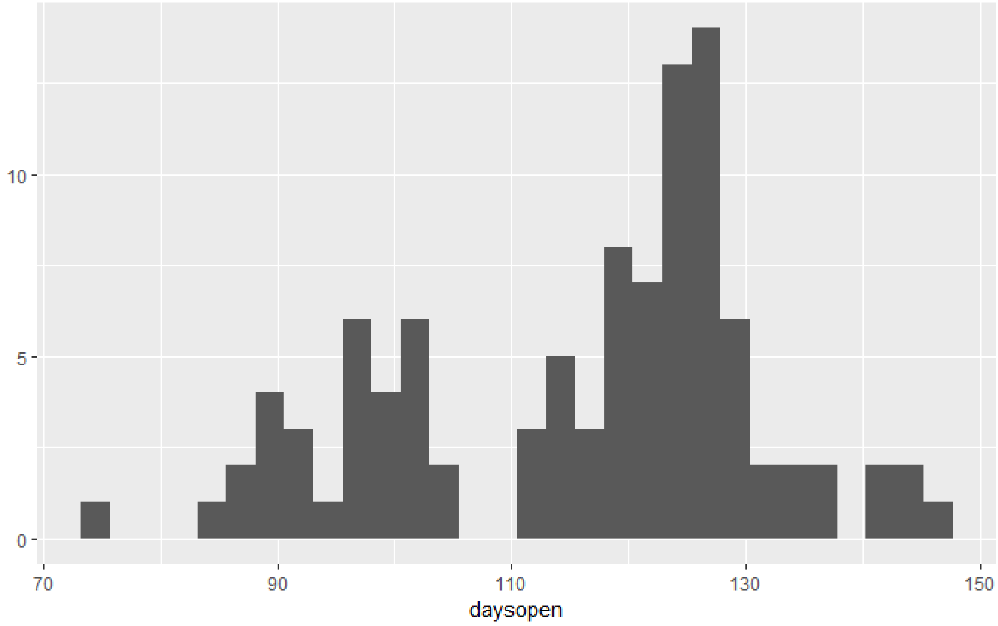


Fig. 3.5.5.4.2. Cow herd average number of days open after calving (assuming a pregnancy rate of 100% in the end of the season).

3.5.5.5 *Weaning time*

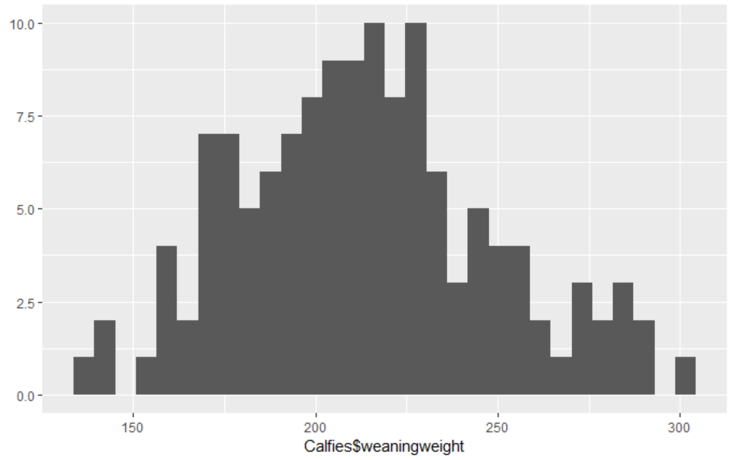


Fig. 3.5.5.4.3. Cow herd average weaning weight.

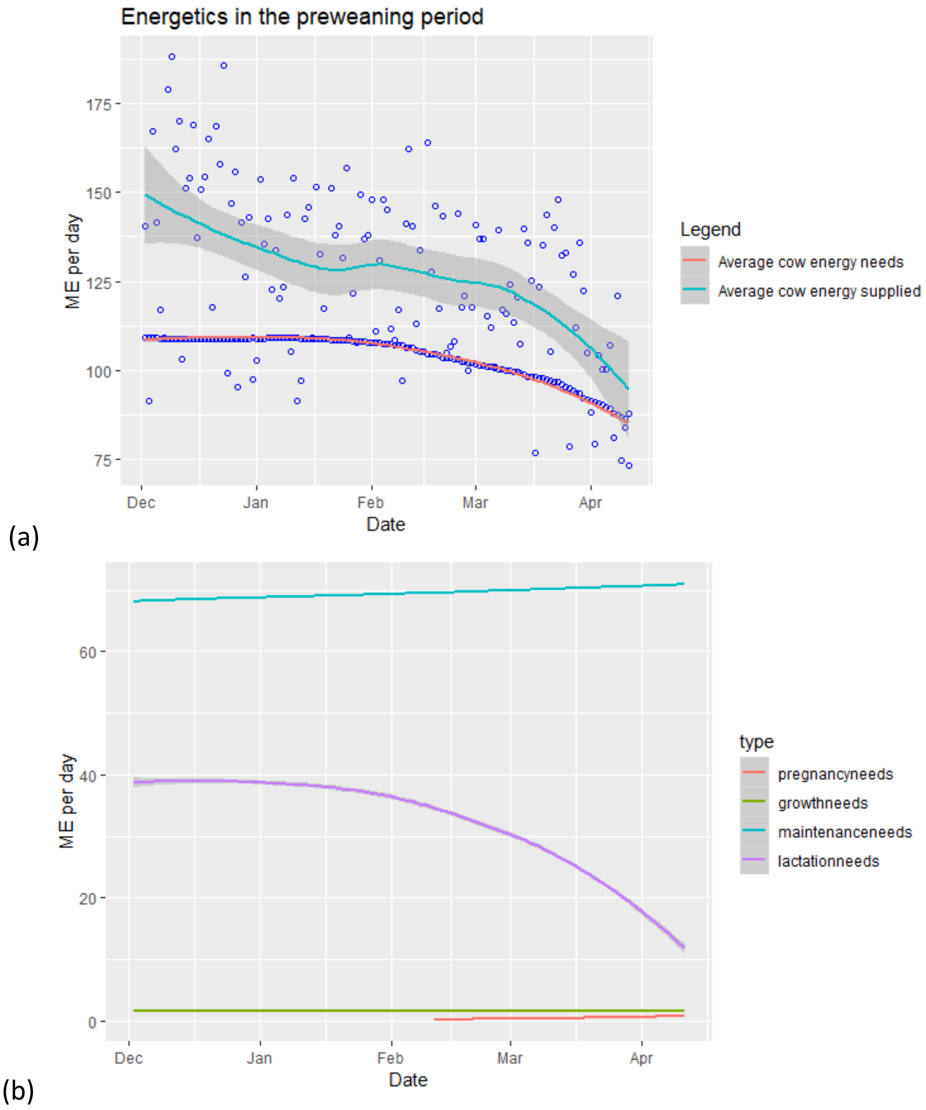


Fig. 3.5.5.4.4. Cow energy balance over the pre-weaning period, average needs (a) and broken-down needs by allocation target (b).

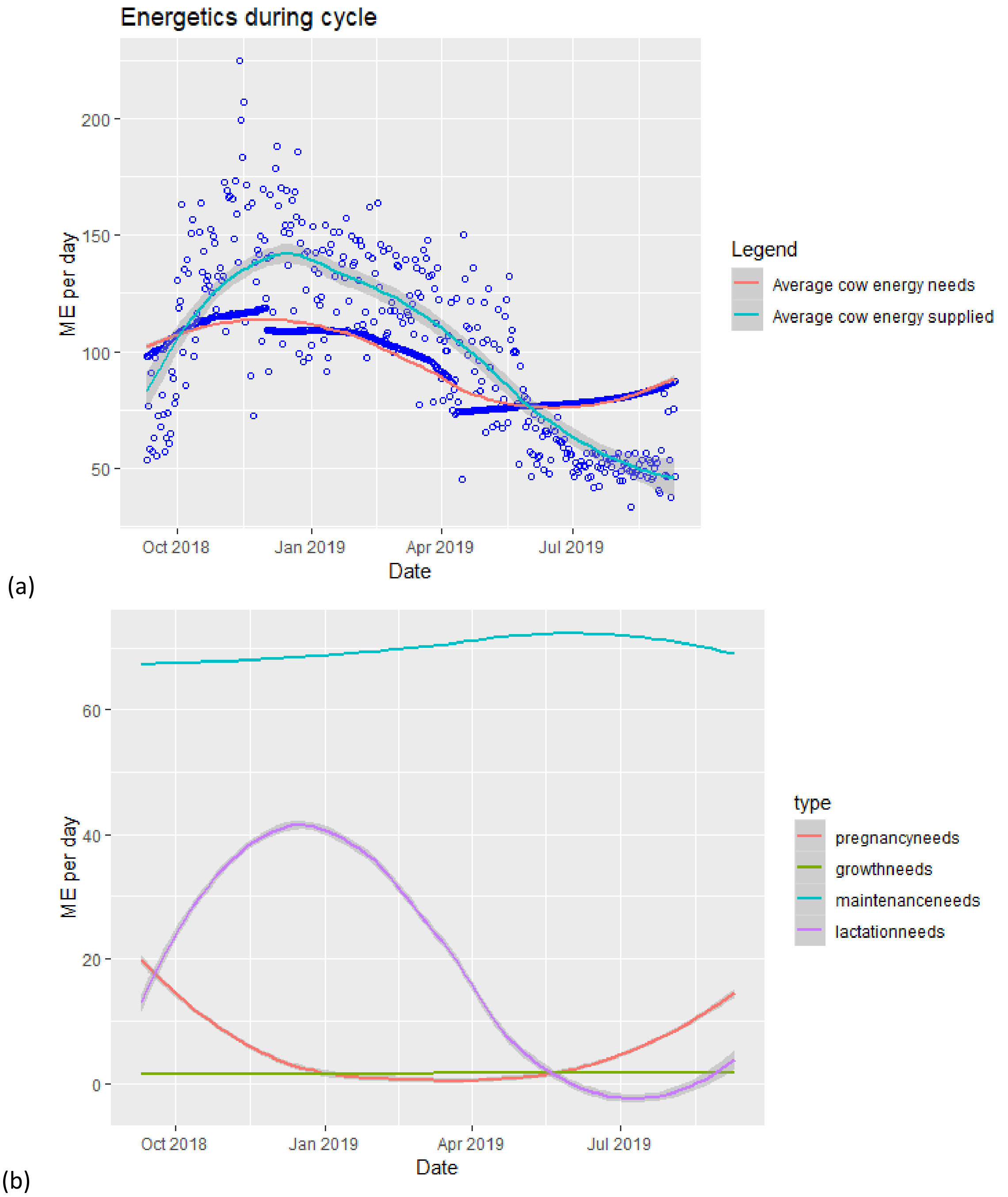


Fig. 3.5.5.4.5. Cow energy balance over the cycle, average needs (a) and broken down needs by allocation target (b).

3.5.5.6 Economic outputs

Table 3.5.5.6.1. Summary of main economic outputs of the model.

Economic Outcome Summary	results
Cull Cows	0
Total cull cow weight (kg)	0
Total cull cow value ($)	0
Replacement cost ($)	0
Calves Weaned	94
Total weaning weight (kg)	20,166
Total weaning value ($)	70,581
Average weaning weight (kg)	214.5
Average weaning value ($)	750.86
Average cow weight start (kg)	526
Average cow weight end (kg)	530.5
Max cow weight (kg)	569.6
Min cow weight (kg)	516.7
Max cow BCS (kg)	3.5
Min cow BCS (kg)	2.9
Total feed eaten MJ (MJME)	3,713,426
Total feed eaten (kgDM)	371,342.6
Total feed required (MJME)	3,464,819
Total feed required (kgDM)	346,481.9
Average feed eaten (kgDM)	3,713.426
Average feed required (kgDM)	3,464.819
Total feed difference (kgDM)	24,861
Total feed cost ($)	40,170
Feed cost per cow ($)	401.7
Revenue ($)	70,581
Expenses ($)	40,170
Cow weight adjustment ($)	821
Profit ($)	31,232

3.5.6 **Model Application**

The initial purpose of the model is to investigate whether cow genotype interacts with feeding system to provide significantly different outcomes. The hypotheses to be addressed follow on the maternal efficiency program within the Beef CRC III, and deals with real industry differences in schools of thought. In that program, research found that there was a spectrum of philosophy among breeders in terms of the way they approach variation in feed availability and their expectations of the sort of genotype that best deals with their approach. At one end of the spectrum, cows are largely un-supplemented and are left to use body reserves to get through periods of low feed availability, with the expectation that they will have other periods during the year where they have surplus feed and therefore able to re-gain body reserves. At the other end of the spectrum are breeders whose system aims to tightly control the feed available to cows, and would provide supplements to cows during shortages to maintain cow body condition score above a certain level. These philosophies are presented as extremes of a spectrum, and most breeders would fall somewhere between the two but with a tendency towards one approach or the other. Across temperate Australia and New Zealand both systems exist. While environment (e.g. degree of variability of rainfall, pasture management, and or ability to practically provide supplements due to topography) can influence which philosophy and management system a farmer chooses, it is also common to see contrasting systems on farms which are neighbouring and have a similar environment and other constraints.

There are differences of opinion among breeders as to whether different genotypes are warranted for different feeding systems. Some breeders believe that non-supplemented systems require a moderate sized cow, with a propensity to lay down subcutaneous fat so that the cow is sufficiently robust to cope with the fluctuations in feed supply. Other breeders prefer to accept a larger cow (often a consequence of selecting for post-weaning growth) and are prepared to supplement this cow where necessary so that the fluctuations in feed supply are reduced. However, it is not clear whether there a genuine genotype by environment interaction (GxE) exists such that significantly different genotypes are required for different systems, or whether a single breeding goal is able to cover both systems.

The model described in this report has been developed to assist in answering some of these questions. The flexibility of a simulation model means that it is possible to use the model in multiple ways, running “in silica experiments” to:

1) Assess the performance of different genotypes under different systems;
2) Develop “breeding objectives” under different systems to assess whether the system results in different trait balances;
3) Use the simulations to look at different evaluation issues, such as:
    a) The optimal time of the annual cycle to measure mature weight (and other cow descriptors);
    b) The value of a measure of anoestrus in cows as a selection criteria for evaluations;
    c) The implications of running cows at lower condition scores (e.g. as in many commercial enterprises) for estimates of key genetic correlations. This could be used to shed light on issues surrounding fatness and fertility.

This report will show use the model to address point 1 above. A subsequent report will take the approach outlined in point 2.

3.5.7 **Modelling Approach**

The model was set up with two different feeding systems and three genotypes.

3.5.7.1 Feeding Systems

Feeding systems were constructed based on a typical annual cycle in New Zealand beef cow systems, loosely based on a South Island summer moist winter cold situation, where key features include:

- calving is timed for early spring to take advantage of spring growth over lactation;
- pasture grows over summer and autumn, with cows building body reserves during lactation and for approximately two months after weaning;
- winter is relatively long with very little pasture growth from late May to October, during this time cows are normally eating saved feed from autumn and removing poor quality feed so that pasture quality in spring is high (normally for the benefit of other stock classes);
- Cows generally lose liveweight from the start of winter through to early spring, effectively mining the body reserves laid down earlier in the year.

While this system was chosen as a base, the key variable is how much annual fluctuation in cow live weight and body reserves occurs, and the actual base system is likely to have relatively less impact on the outcomes (although this could be checked in future work). Thus, two variations on this base system were constructed.

1) A system where there are significant seasonal fluctuations in feed supply relative to cow requirements, and rather than feed supplements the cow is expected to use body reserves to deal with these fluctuations. Under this system and overall lower stock rate is generally used, so that there are times of the year where significant surpluses exist, allowing the cow an opportunity to regain body reserves.
2) A system where supplements are fed during feed deficits to minimise the difference in feed supply relative to cow requirements. Under this scenario there is still a period of deficit and surplus, but neither period has the same differences expressed as the first system would.

The base pasture feed supply and supplementary feeds (on a kg per cow per day basis) are outlined in Table 5.13. Both systems were constructed so that when moderate cow genetics are used (outlined below), the annual start weight of the cows was similar to the final weight a year later. In this case, the system was attempted to re-create a steady state, with minor differences in cow weight accounted for by putting an economic value on this. The pasture supply actually fed was sampled from a normal distribution on a daily basis, with differences between months in standard deviations reflecting greater or less expected variability in pasture supply. While the facility exists to enter different quality of feed on a monthly basis, for this simulation all feed was considered to be 10 MJME/kg DM. Pasture had differential costs by month and price of supplements was assumed to be constant through the year or bought once a year.

Table 3.5.7.1.1. Target feed available (kg DM per cow) on a monthly basis. These values are the target means, but random variability in pasture feed supply was also built into the actual feed supplied according to the standard deviations given for each month. Costs allocated to pasture and supplement are also given.

Month	Non-supplemented system		Supplemented system		S.D. of pasture supply	Cost of pasture	Cost of supplements
	Base pasture	Supplements	Base pasture	Supplements			
Jan	13	0	10	0	2	$0.05	$0.40
Feb	13	0	10	0	2	$0.05	$0.40
Mar	12	0	10	0	2	$0.10	$0.40
Apr	10	0	9	0	2	$0.15	$0.40
May	10	0	7	2	0.5	$0.20	$0.40
June	6	0	6	3	0.5	$0.20	$0.40
July	5	0	6	3	0.5	$0.20	$0.40
Aug	5	0	6	3	0.5	$0.20	$0.40
Sep	7	0	8	3	1.5	$0.20	$0.40
Oct	13	0	11	0	2	$0.10	$0.40
Nov	15	0	11	0	3	$0.05	$0.40
Dec	14	0	11	0	3	$0.05	$0.40

3.5.7.2 Genotypes

Three different genotypes were created by selecting all published sires off the Angus NZ website which fell within a range of values for mature cow weight (MWT) EBVs. The ranges chosen were 75 to 85 kg (Moderate), 125 to 135 kg (Large) and 145 to 155 kg (Extreme). The average EBVs for these sires were then calculated and used to describe the genotypes. The Genotype EBV profiles are given in Table 3.5.7.2.1.

Table 3.5.7.2.1. Genotypes used in model simulations.

Trait	Moderate[1]	Large[1]	Extreme[1]
BWT (kg)	3.9	6.6	8.3
W200 (kg)	40.2	49.6	51.2
MILK (kg calf)	15.2	11.4	9.5
MWT (kg)	80	128	150
FDRib (mm)	0.4	-0.6	-1.5
GL (days)	-4.2	-3.8	-2.9
ANOEST (days)	0	0	0
CR (%)	4.0	3.2	1.2

[1] Genotypes based off EBV averages for selected groups of widely used Angus bulls. Traits considered were Birth weight (BWT), 200-day weight (W200), 200-day weight- maternal (MILK), mature cow weight (MWT), Fat depth at 12th/13th rib (FDRib), gestation length (GL), Post-partum anoestrus (ANOEST) and Conception Rate (CR). No EBVs were available to describe post-partum anoestrus, while Conception rate was set to the Days to Calving EBV multiplied by -1.

3.5.7.3 Other model details

The price inputs to the model are given in Table 3.5.3.5.1 A herd of 100 cows was simulated for each replicate. A combination of genotype (3 levels) x feeding system (2 levels) formed treatments, and five replicates were simulated for each treatment combination.

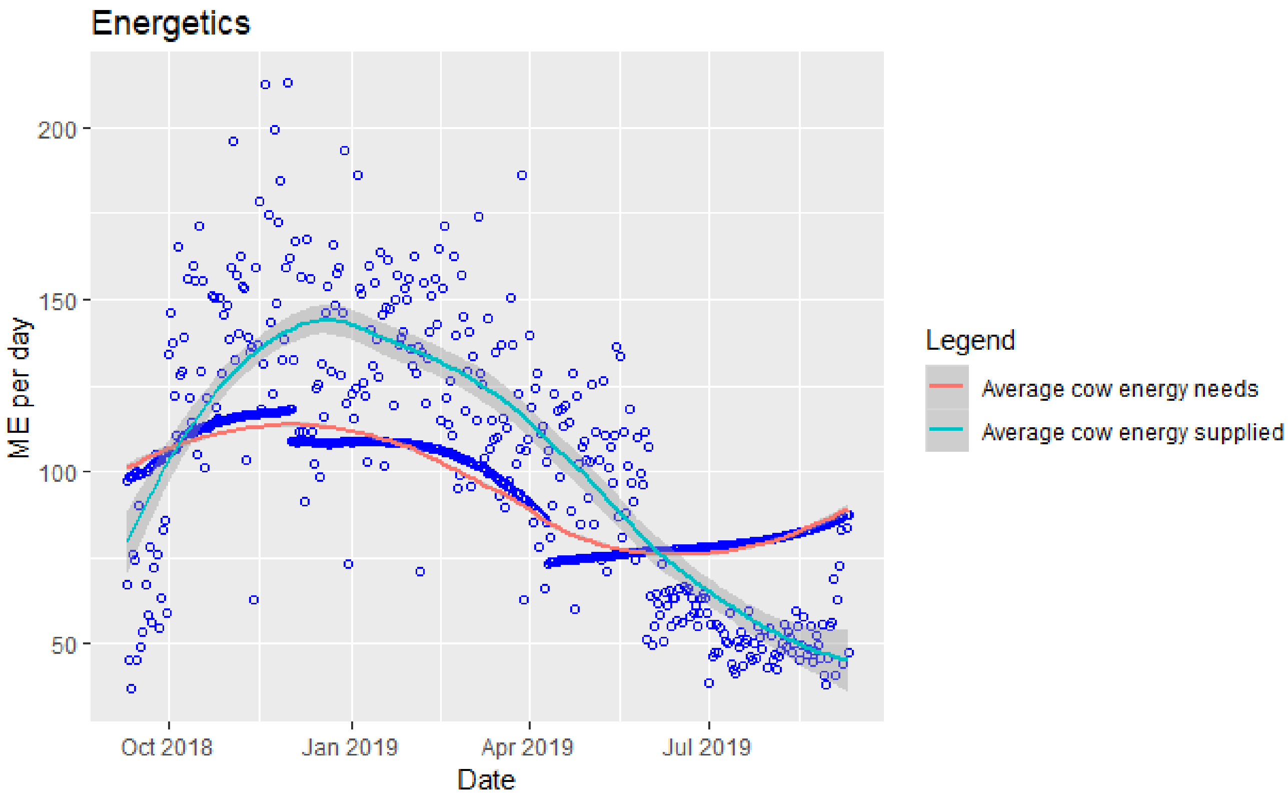
Key details were extracted from the model for each replicate, and an analysis of variance performed to test for main effects of Genetics and Feeding System, and Genetics x Feeding System interactions.

3.5.8 **Results**

The model potentially creates a very large number of outputs, so it is important to focus on the key descriptors. For this report, the first aspect is to examine some herd level means from within representative replicates to confirm that the model overall is performing as might be expected, and is a reasonable representation of real breeding cow systems. It also needs to confirm that the treatments applied are having the expected effect on the model.

Fig. 3.5.8.1 shows the difference between cow energy requirements and cow energy supplied across a 12-month cycle from start of calving (10th September), for a non-supplemented and a supplemented system. Based on the systems modelled, it would be expected that there will be a period of surplus over late spring to late autumn, and a period of deficit over winter and early spring where cows utilise body reserves. If the model achieves approximately equal deficits and surpluses, represented by the gaps between the two lines, then the system will be approximating a steady state system. The pattern shown in both the non-supplemented and the supplemented system appear to conform to those expectations. Moreover, it would be expected that both the surpluses and the deficits in the non-supplemented system would be significantly larger than in the supplemented system, so the lines will be further apart for longer periods, which also appears to be borne out in the output.

a. **Non-supplemented feeding system**



b. **Supplemented feeding system**

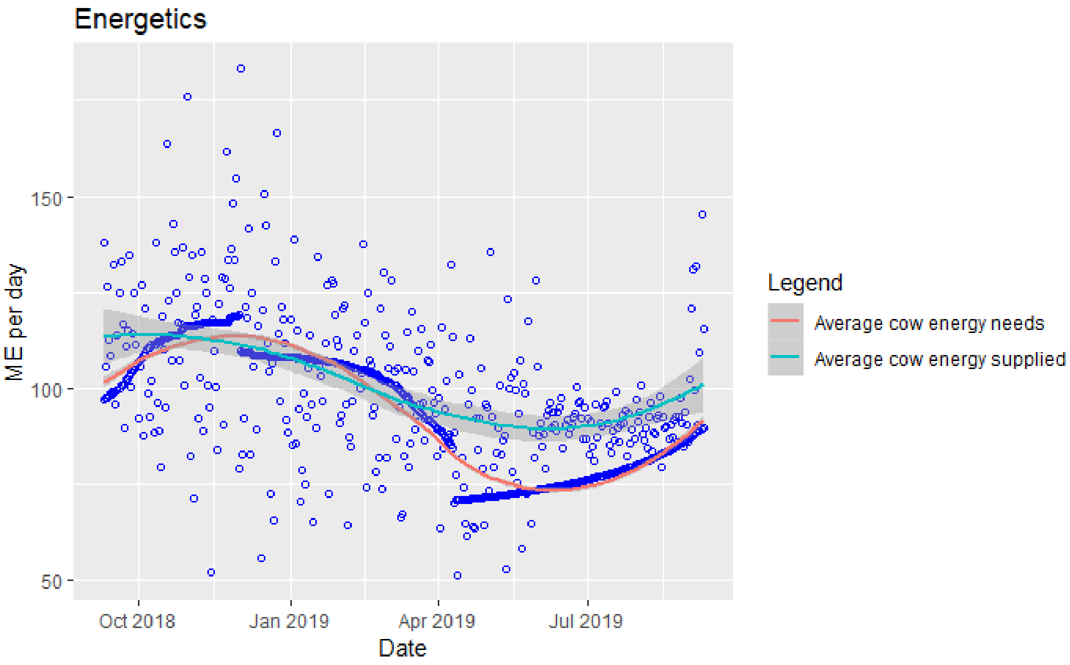
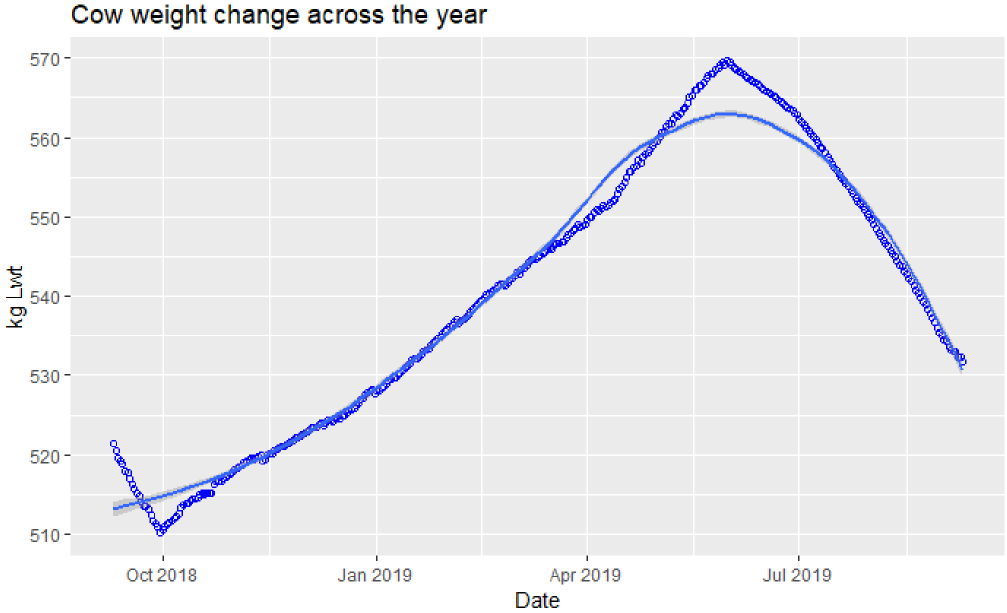


Fig. 3.5.8.1. Representation of the difference between cow energy requirements and cow energy supplied, for a non-supplemented and a supplemented system (using moderate cow genetics), showing larger surpluses and deficits in the non-supplemented system.

a. **Non-supplemented feeding system**



b. Supplemented feeding system

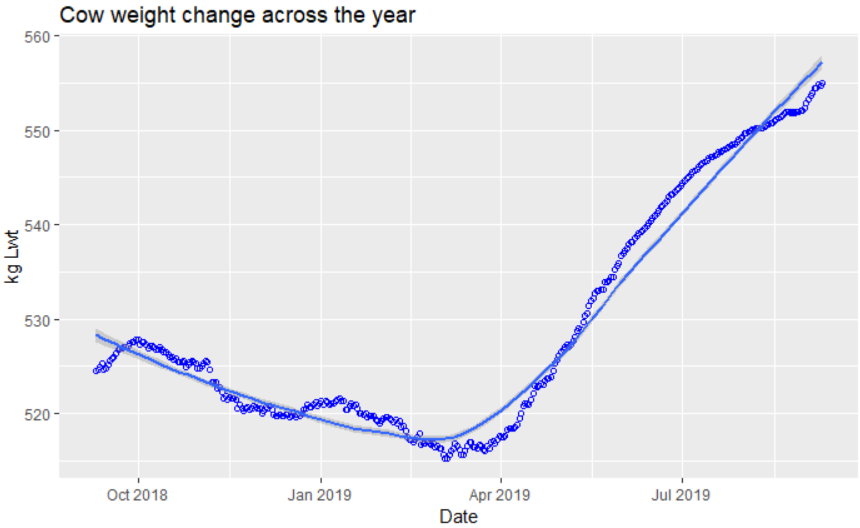
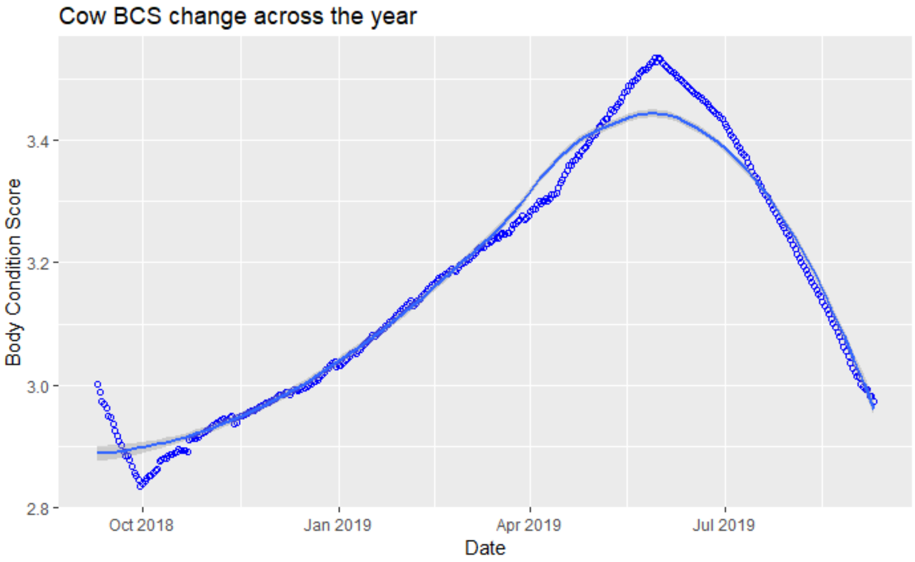


Fig. 3.5.8.2. Change in cow weight (without gravid uterus weight included) over the year, for an non-supplemented and a supplemented feeding system, showing greater fluctuation in cow weight for non-supplemented systems.

a. **Non-supplemented feeding system**



b. **Non-supplemented feeding system**

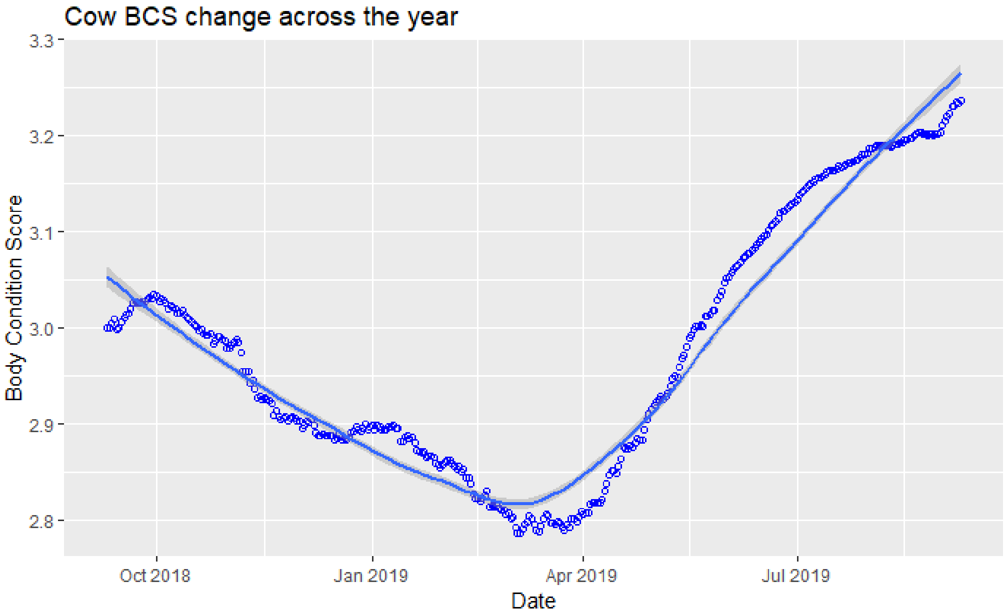


Fig. 3.5.8.3. Change in cow Body Condition Score over the year, for an non-supplemented and a supplemented feeding system, showing greater annual fluctuation in BCS for non-supplemented system.

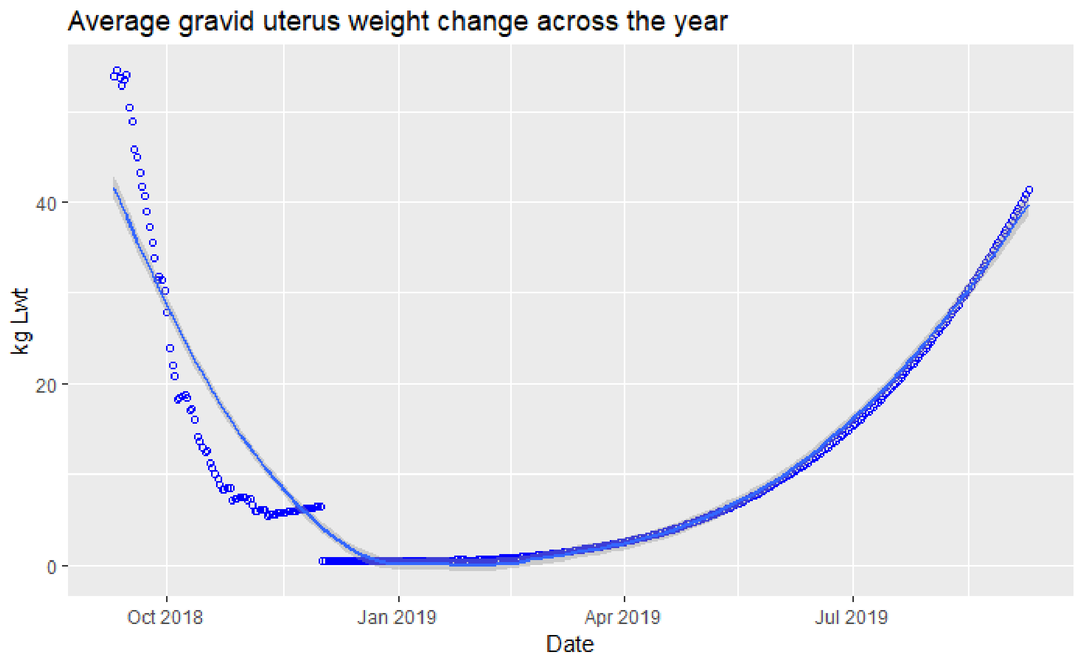


Fig. 3.5.8.4. Changes in weight of gravid uterus (average across the cow herd) occurring during the year. The average gravid uterus weight descends quickly in the spring as cows calve (accounting got the stepped pattern due to random calving events), is zero between calving and early pregnancy, and then rises again during winter as pregnancy progresses.

3.5.9 Analysis of outcomes

A statistical analysis of variance was performed on key outcomes from the model. (Appendix 8) Table 1 shows the outcomes for the financial parameters. There were significant effects of both Genetics and Feeding System on aspects of financial performance, with effects largely as expected. For example, the supplemented feeding system incurred significantly higher expenses which would be mainly due to the cost of supplementation. However, no interaction between Genetics and Feeding System was found in the financials, with the exception of the adjustments made for changes in cow weight (which may just be an artefact rather than a biologically significant occurrence. There were also few differences in calf numbers weaned and average weaning weight, and no significant interactions.

When cow weight and cow body condition score were considered (Appendix 8, table 2, and 3) there were a number of significant interactions observed. In general the results show that less fluctuation in cow weight and body condition score occurred under the supplemented system, as might be expected. Genetic effects on cow weights also followed the pattern expected. But of most interest is the Genetics x Feeding System interaction observed for most of the weight and body condition score parameters. Cows in non-supplemented systems hit higher weights, and expressed substantially greater variation between genotypes (approximately 65 kg difference) than the cows in supplemented systems which only had 45 kg difference in maximum weights. On both supplemented and non-supplemented systems cows of moderate genotypes were able to maintain slightly higher body condition scores than cows of larger genotypes, a result which agrees with generalised breeder observations that smaller cows with higher fat depth EBVs are “more robust”. This provides some further confidence that the model is behaving similarly to real-life observations.

Another observation is that moderate cows on non-supplemented systems generally had similar levels of fluctuation in both weight and body condition score to the other genotypes, while when compared on supplemented systems the moderate cows had significantly greater fluctuations in these parameters than the larger genotypes.

Under the conditions modelled the cows on the un-supplemented systems fluctuated by approximately 0.66 units of body condition (on a 5-point scale) or around 56 kg of body weight. This reflects actual cow body weight as weight of gravid uterus was not added into this parameter (to enable a clearer picture of cow energy reserves to be obtained). In reality there are many breeders (at least in New Zealand, and likely in Australia too) who manage cows to much greater bodyweight fluctuations than these levels. It would not be uncommon for cows to fluctuate by 1.5 body conditions scores between end of autumn and calving, and to lose 100 kg of liveweight (which considering an increase in gravid uterus over this time actually represents a greater loss of body-weight). Even with a quite moderate imposition of feed restrictions in this model, significant genetics x feeding system interactions were found for cow body reserves. However, these did not really translate into interactions in economic performance at this level. It is not known, but could be investigated further, as to whether a more extreme feed regime with greater variability in cow body reserves would then create a significant genotype x feeding system interaction. In this "experiment" there was no differences in number of calves weaned, suggesting that none of the treatments resulted in cows that were in lower body condition score at mating (ie. The part of the BCS vs Pregnancy rate curve where declines in body condition have a much more significant impact on overall conception rate). A more severe restriction may tip some cow genotypes into poorer reproductive rates due to body condition score at mating, which would create significant interactions.

3.5.10 **Further modelling approaches**

A model is never complete, and opportunities for improvements and additional features always exist. For this newly developed model the list of possible improvements is long. However, one improvement which could be made is to have the model itself change the feed supplied to cows in terms of supplements, based on a measure such as body condition score. This could be applied either on a herd basis or on an individual basis and would enable a situation to be modelled where the breeder is monitoring the cow herd and adjusting management practices accordingly – probably a better representation of real life scenarios for many situations. The outcome of this would be the ability to allow the model itself to determine the extent of fluctuation in cow liveweight or body condition, and to more tightly specify the degree of liveweight fluctuation rather than allowing it to be an outcome of feeding and genotype decisions set arbitrarily at the outset of the model.

Another option is to create a user-friendly interface and create an on-line application which could be made available for different users to create their own specific scenarios and eventually support decisions when researchers and industry service providers are defining breeding and management strategies. This could be implemented in a Shiny-App format (a package that provides a link between R as the programming language and html).

3.5.11 **Conclusion**

The simulation model created appears to be a good representation of cow performance and body reserves, with responses matching what is observed in reality. This observation is based on anecdotal observation and expert opinion rather than the model having been matched against real cow data (which is only just becoming available in sufficient quantities to allow this to be done).

The model was able to find significant genetics x feeding system interactions in cow weight and body reserves. However, for the situation considered it was not able to demonstrate that these interactions are important at the economic level. Possibly imposing a more severe feed fluctuation in the non-supplemented system might better reflect the quartile of industry who adopt this practice to a greater degree, and might reveal some interactions at the economic level. However, based on the scenarios run to date there is not strong evidence that difference feeding systems are suited to very different genetic types.

3.6 Objective 6 – Genomics

3.6.1 Genotyping Strategy

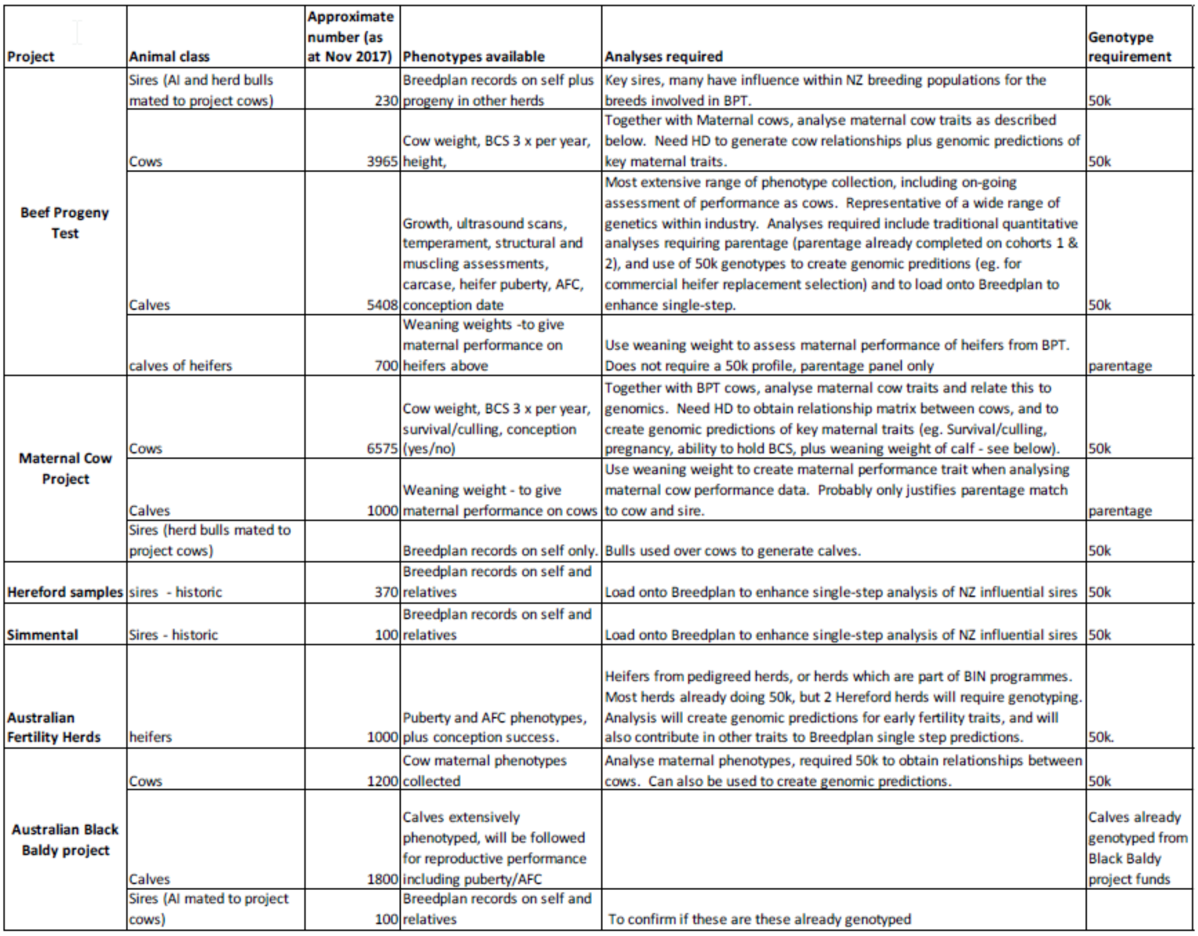
As part of this program a genotyping strategy was developed, the animal resources and phenotype information available was assessed and a proposed genotyping plan was established based on four criteria:

1) requirements for other sub projects,
2) contribution towards genomic-specific goals such as demonstration of commercial heifer selection tools;
3) value of animals for contributing to Angus and Hereford reference populations
4) budget available vs costs of genotypes.

The genotyping plan is included in Table 3.6.1.1 below. GeneSeek Australasia (University of Queensland) were used as the genotyping provider after taking into consideration factors such as price for the different genotype platforms, turn-around time, ownership of raw genotype results, and long-term storage of extracted DNA samples.

An inventory of existing industry genotypes available for R&D was developed which included information regarding animals, platform, location and whether they had been included in a genetic evaluation.

Table 3.6.1.1. Proposed Genotyping Strategy



Project	Animal class	Approximate number (as at Nov 2017)	Phenotypes available	Analyses required	Genotype requirement
Beef Progeny Test	Sires (AI and herd bulls mated to project cows)	230	Breedplan records on self plus progeny in other herds	Key sires, many have influence within NZ breeding populations for the breeds involved in BPT.	50k
	Cows	3965	Cow weight, BCS 3 x per year, height,	Together with Maternal cows, analyse maternal cow traits as described below. Need HD to generate cow relationships plus genomic predictions of key maternal traits.	50k
	Calves	5408	Growth, ultrasound scans, temperament, structural and muscling assessments, carcase, heifer puberty, AFC, conception date	Most extensive range of phenotype collection, including on-going assessment of performance as cows. Representative of a wide range of genetics within industry. Analyses required include traditional quantitative analyses requiring parentage (parentage already completed on cohorts 1 & 2), and use of 50k genotypes to create genomic preditions (eg. for commercial heifer replacement selection) and to load onto Breedplan to enhance single-step.	50k
	calves of heifers	700	Weaning weights -to give maternal performance on heifers above	Use weaning weight to assess maternal performance of heifers from BPT. Does not require a 50k profile, parentage panel only	parentage
Maternal Cow Project	Cows	6575	Cow weight, BCS 3 x per year, survival/culling, conception (yes/no)	Together with BPT cows, analyse maternal cow traits and relate this to genomics. Need HD to obtain relationship matrix between cows, and to create genomic predictions of key maternal traits (eg. Survival/culling, pregnancy, ability to hold BCS, plus weaning weight of calf - see below).	50k
	Calves	1000	Weaning weight - to give maternal performance on cows	Use weaning weight to create maternal performance trait when analysing maternal cow performance data. Probably only justifies parentage match to cow and sire.	parentage
	Sires (herd bulls mated to project cows)		Breedplan records on self only.	Bulls used over cows to generate calves.	50k
Hereford samples	sires - historic	370	Breedplan records on self and relatives	Load onto Breedplan to enhance single-step analysis of NZ influential sires	50k
Simmental	Sires - historic	100	Breedplan records on self and relatives	Load onto Breedplan to enhance single-step analysis of NZ influential sires	50k
Australian Fertility Herds	heifers	1000	Puberty and AFC phenotypes, plus conception success.	Heifers from pedigreed herds, or herds which are part of BIN programmes. Most herds already doing 50k, but 2 Hereford herds will require genotyping. Analysis will create genomic predictions for early fertility traits, and will also contribute in other traits to Breedplan single step predictions.	50k.
Australian Black Baldy project	Cows	1200	Cow maternal phenotypes collected	Analyse maternal phenotypes, required 50k to obtain relationships between cows. Can also be used to create genomic predictions.	50k
	Calves	1800	Calves extensively phenotyped, will be followed for reproductive performance including puberty/AFC		Calves already genotyped from Black Baldy project funds
	Sires (AI mated to project cows)	100	Breedplan records on self and relatives	To confirm if these are these already genotyped	

3.6.2 Utilisation of genomic and phenotypic data for selecting replacement heifers

3.6.2.1 Background

Commercial cow-calf operations need to improve their production efficiency to maintain a competitive position relative to other livestock sources of protein. There are two main approaches to achieving that end – improving the production environment via management interventions such as stocking rate, calving dates, feeding levels, reproductive and animal health management, or improving the potential productivity of the herd over successive generations by genetic improvement.

In this context a commercial cow-calf enterprise is defined as a breeding herd that generates its own female replacements, but purchases its sires from bull breeding enterprises. The national herd can be considered to comprise mostly commercial cow-calf enterprises and perhaps about 1% of herds representing bull breeding enterprises. The annual rate of genetic improvement of any commercial cow-calf operation is characterised by two factors, the annual rate of genetic improvement in the purchased sires, which is largely out of the control of the commercial cow-calf operation but is determined by the activities that occur in the bull breeding sector (i.e. BREEDPLAN evaluated purebred herds that performance record their purebred animals through their respective breed associations), and by the genetic lag between the merit of the purchased sires and the merit of each annual calf crop in the commercial cow-calf herd. That genetic lag is approximately the amount of improvement made in the bull breeding sector over two generations, but can be reduced in the commercial cow-calf herd by reducing the generation interval in the cow-calf herd, or by selecting above-average female replacements to become the parents in the next generation.

Prior to 2006 the rate of improvement in the bull breeding herds, and the ability of commercial cow-calf producers to select above-average replacement heifers was largely dictated by the ability of those producers to rank their animals on any family information (i.e. parent average merit), and any individual performance records that could be obtained on the selection candidates before the time of selection. In bull breeding herds, pedigree information was used to provide reliable family information, but in most commercial cow-calf herds, multiple sire mating is common, and calves are not typically identified to their dams, so there is no family information. Given that a balanced selection program should take due account of growth traits, reproductive traits, carcass merit, longevity, disease resistance etc, this has been problematic for the cow-calf sector because most of the indicator traits for those attributes are not available for measurement until after selection decisions have been made.

The BLG Maternal Cow Project and the BPT had three principal aims in the collection of data from commercial cow-calf producers. First, by collecting phenotypes in commercial circumstances, it could demonstrate that national EBVs as commonly used by the bull breeding sector had utility in predicting the performance of offspring in commercial cow-calf enterprises. Second, in providing information that could be utilised to improve the accuracy of prediction in the bull breeding sector by feeding information on commercial cattle back into the bull breeding information systems – this activity made possible by the use of SNP chip genotyping that can resolve the parentage of commercial cattle bred in multiple sire pastures without mothering up of offspring to dams. Third, to demonstrate that SNP chip genotyping in commercial cow-calf herds could provide more accurate prediction of those maternal traits, particularly mature cow live weight and mature cow body condition scores that could not be directly observed on selection candidates prior to their selection to be used as parents.

In this genomics related objective, milestone 6.2 quantifies the ability for a genomic prediction on a young replacement heifer to predict the future performance of that heifer if retained as an adult. In that regard, this validation of genomic predictions focussed on mature cow weight and body condition score as other reproductive traits tend to be less heritable, and are measured on less continuous scales, meaning that much larger validation populations would be required, and these would have to be measured over longer time frames than were available for this research project. Milestone 6.3 quantifies the extent to which predictions in the bull breeding sector can be made more accurate by collecting phenotypes on commercial cattle. Such phenotypes would in the past have been of no practical utility without knowledge of parentage of the commercial calves, and even then would have only increased the accuracy of EBVs of the direct ancestors of the commercial calves. In the genomics era, genomic prediction can improve accuracy in the bull breeding sector without having to know parentage of all the commercial calves, and can theoretically improve the accuracy of predicting any genotyped animal in the bull breeding sector, not just the direct ancestors. Milestone 6.1 dealt with practicalities of SNP chip genotyping, has been reported in an earlier milestone report, and provided the recommendations for the genotyping platform and density used to SNP chip genotype the animals in all these projects. The following sections report directly on the learnings from the joint collection of phenotypes from commercial cow-calf herds, and the genotyping of those individuals, when those data are used to attempt to improve predictive abilities of so-called validation animals – either cohorts in commercial herds or animals from the bull breeding sector.

3.6.2.2 Methods

Two of the key parameters of interest for selection are the heritability and the genetic correlation. Heritability reflects the strength of the relationship between genotype and phenotype. High heritability traits can easily be improved by mass selection based on individual phenotypes with little need for recording, provided they are not influenced too greatly with non-genetic fixed effects such as age at measurement, or age of the dam. In bull breeding herds information on these fixed effects is readily collected and phenotypes can be adjusted for these effects as part of a formal animal evaluation system such as BREEDPLAN.

The genetic correlation between a pair of traits indicates the strength of the relationship between the breeding value of one trait and the breeding value of another trait. This information is useful for a number of reasons; it indicates the correlated response that might be expected in one trait following selection on the other trait. It indicates the value of one trait, to predict the EBV of another trait, this information being useful to identify indicator traits that can be measured early in life and used to predict some other trait that might be more difficult or expensive to measure. Finally, it indicates if a repeated observation of the same apparent trait, such as body condition score at one age like at mating, is really controlled by the same set of genes as the trait measured at another age, such as body condition score at weaning.

These variance parameters are estimated by estimation of the components of variance and covariance between genotype and phenotype of the same or different traits. Such parameters have traditionally been measured based on pedigree data, such as can be used to compute the variance among half-sibs in relation to the variance among full siblings in relation to the variance between families. In other experimental designs the pedigree can be used to determine covariances between parents and offspring, or even more distant ancestors. Now, in the genomics era, these parameters can be estimated without any pedigree information, using SNP chip genotypes collected on animals with phenotypes. In the broader context of this study, phenotypes were collected on maternal cows and BPT animals, in an earlier experiment. These commercial animals were genotyped in the context of this experiment as part of the activities of milestone 6.1. In this milestone we first estimated variance and covariance parameters from multiple trait models that treated with body condition score (BCS) or mature cow weight (MCW) on mature cows (i.e. aged 3 or older) as different traits according to whether the phenotypic observation was measured at weaning (W; i.e. the end of the lactation period), at pre-calving (P; i.e. in non-lactating mature cows that had previously calved), or at mating (M; i.e. in mid lactation).

Generally speaking, animals that are heavier (of fatter) at one age would be expected to be heavier (or fatter) at another age. We would expect there to be a high genetic correlation between MCW measured at the same time of the year but at different ages, or for BCS measured at the same time of year but at different ages. However, there are plausible reasons why a high genetic correlation may not apply to measurements made at different times of the year for animals of the same age in years. For example, measurements taken in Spring immediately prior to calving (P) may not be so highly correlated with measurements taken near peak lactation at M, or at the end of lactation at W because cows that produce more milk tend to lose more weight and body condition by peak lactation and sometimes even more so over late lactation. Such a phenotypic effect could be manifest as a result of a reduced environmental or residual covariance between measurements at these times. Alternatively, since milk production is a heritable trait, it could be that a reduced genetic covariances between measurements at these times causes the reduced phenotypic relationship. Or it could be that both genetic covariances and residual covariances contribute to a reduced phenotypic correlation. The scientific approach to resolve this issue is to estimate these variance components from repeated measurements taken at different ages and different times of the year. Such data was available for this project based on previously undertaken maternal cow studies and BPT studies, some of these animals having been genotyped as part of the activities of milestone 6.1. Some of the animals were measured prior to their first calving, and the measurements taken on first parity animals might be considered a different trait from measurements taken on older animals that would have had to recover bodyweight and condition score after the challenges of a lactation in their previous year. Accordingly, the multiple trait analyses were limited to records on MCW and BCS that were measured on cows during their second or later parity – that is, from animals that were at least three years old.

The maternal cow project collected MCW and BCS from some 7,931 cattle on four farms over four years (2014-2017) on up to three occasions per year (P, M, W). About 80% of the animals were Angus, and the remainder were Hereford. Milestone 6.1 included the genotyping of 5,017 of the animals from the maternal cow and BPT studies using the GGP 50k chip. These data were used for the analyses that are described below.

3.6.2.3 Models

The animals in the maternal cow project included commercial cattle that do not have the level of recording that would be routine for cows in bull breeding herds. This means that for the most part, none of their pedigrees had been recorded, nor was their birthdate known beyond the resolution of birth year from a Spring calving. The models used in subsequent analyses fitted location parameters for the combined effects of herd, year of measurement, and age of cow (in years). Those parameters were fitted as fixed effects. For estimation of multiple trait variance components, the random effects included an effect for each and every segregating SNP marker, fitted concurrently using a Bayes C model with parameter pi set to 0. That is, all markers were fitted together and no markers were assumed to have 0 effect on the trait. A residual effect explained the deviation from the fitted effects and the observed phenotype, and was assumed random. The datasets included missing values as not every animal had been measured at all three occasions. Variance components for the marker and residual effects for each of the tree measurement periods, and covariance components for marker effects between measurement periods, and for residual effects between measurement periods, were estimated using single-site Gibbs sampling to construct posterior distributions of the unknown parameters using Markov chain Monte Carlo (MCMC) procedures. The chain included 50,000 plausible values for each parameter, with the first 1,000 values discarded as a burn-in period. The computing was carried out using the JWAS package that can be downloaded from github by following the links at https://qtl.rocks. That open-source package runs in the public domain Julia computing environment that can be freely downloaded for Mac OS-X, Windows and Unix computers at https://julialang.org.

Posterior distributions of genetic variance and covariance were obtained by computing the simple variances and covariance between samples of the breeding values of the animals for all of the traits, those samples of breeding values being obtained by multiplying the marker matrix by the samples of marker effects at each iteration in the Markov chain. Posterior distributions for functions of variance and covariance parameters, such as the correlations and heritabilities were obtained by creating a Markov chain of samples for those parameters from the Markov chains of samples for their constituent variance and covariance parameters.

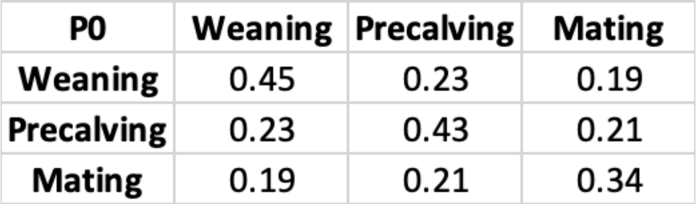
3.6.2.4 Results

3.6.2.4.1 Multiple trait analyses of body condition score at different times of the year

The results of the variance component analyses for body condition score are shown in tables 3.6.2.4.1.1 to 3.6.2.4.1.5 below. There was greater phenotypic variance among cows of the same age on the same farm at weaning then at pre-calving or mating, reflecting the variation in mature weight in itself, as well the variation in due to weight loss or gain over the lactation period. Phenotypic correlations between measurements at any pair of times were however quite similar. Residual variance was greatest at weaning, and least at mating. Heritabilities at any of the three time points were high at around 40%, and only slightly lower at weaning that at other stages. The genetic correlation between pre-calving and mating were near perfect, whereas the genetic correlation between either of those stages and weaning were slightly lower at 0.92-0.93, but still sufficiently similar that no real differences in ranking of sire merit would be expected from one stage age to another.

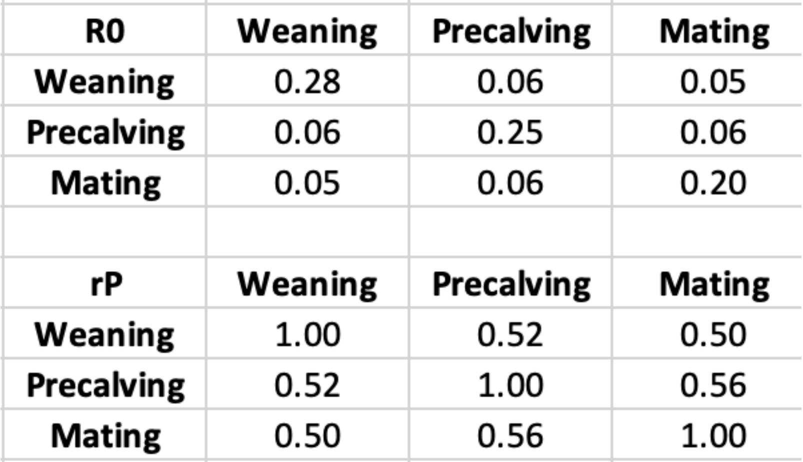
The results demonstrate that a single BCS measure at any stage of the year has a strong association with the genetic merit of the animal, since the heritabilities were high, and that merit at any stage would provide information predictive of merit at other stages, since the genetic correlations are all near perfect. The lower phenotypic correlations relative to the genetic correlations are a result of the residual covariance being much lower than the genetic covariances, and this indicates that most of the residual variance is unique to the measurement taken at a particular stage of life. This indicates that more accurate rankings of genetic merit for BCS could be obtained by using repeated measures of BCS at different stages.

Table 3.6.2.4.1.1: Phenotypic variance-covariance components for body condition score in beef cattle of at least parity two.



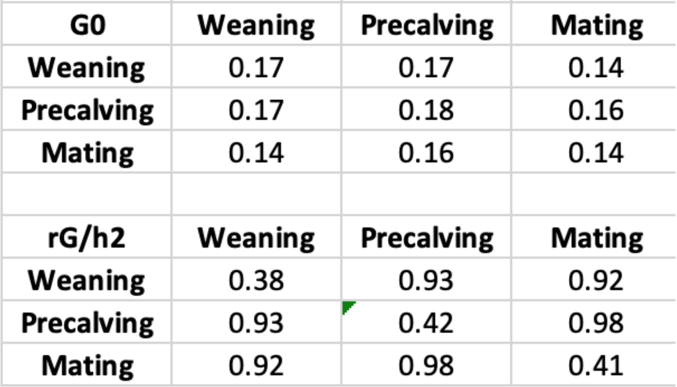
P0	Weaning	Precalving	Mating
Weaning	0.45	0.23	0.19
Precalving	0.23	0.43	0.21
Mating	0.19	0.21	0.34

Table 3.6.2.4.1.2: Residual variance-covariance components and phenotypic correlations for body condition score in beef cattle of at least parity two.



R0	Weaning	Precalving	Mating
Weaning	0.28	0.06	0.05
Precalving	0.06	0.25	0.06
Mating	0.05	0.06	0.20
rP	**Weaning**	**Precalving**	**Mating**
Weaning	1.00	0.52	0.50
Precalving	0.52	1.00	0.56
Mating	0.50	0.56	1.00

Table 3.6.2.4.1.3: Genetic variance-covariance components, genetic correlations and heritabilities for body condition score in beef cattle of at least parity two.



G0	Weaning	Precalving	Mating
Weaning	0.17	0.17	0.14
Precalving	0.17	0.18	0.16
Mating	0.14	0.16	0.14
rG/h2	**Weaning**	**Precalving**	**Mating**
Weaning	0.38	0.93	0.92
Precalving	0.93	0.42	0.98
Mating	0.92	0.98	0.41

Table 3.6.2.4.1.4: Variance-covariance components and related statistics such as; heritabilities and correlations for body condition score at three measurement occasions in beef cattle of at least parity two.

BCS	Weaning	Weaning	Weaning	Precalving	Precalving	Precalving	Mating	Mating	Mating
BCS		**Precalving**	**Mating**	**Weaning**		**Mating**	**Weaning**	**Precalving**	
Posterior-Means									
G0	0.17	0.17	0.14	0.17	0.18	0.16	0.14	0.16	0.14
R0	0.28	0.06	0.05	0.06	0.25	0.06	0.05	0.06	0.20
P0	0.45	0.23	0.19	0.23	0.43	0.21	0.19	0.21	0.34
rG	1.00	0.93	0.92	0.93	1.00	0.98	0.92	0.98	1.00
rE	1.00	0.25	0.22	0.25	1.00	0.26	0.22	0.26	1.00
rP	1.00	0.52	0.50	0.52	1.00	0.56	0.50	0.56	1.00
h2	0.38				0.42				0.41

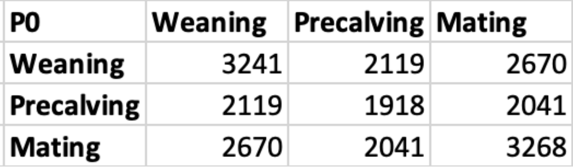
Table 3.6.2.4.1.5: Standard errors of variance-covariance components and related statistics such as heritabilities and correlations for body condition score at three measurement occasions in beef cattle of at least parity two.

BCS	Weaning	Weaning	Weaning	Precalving	Precalving	Precalving	Mating	Mating	Mating
BCS		**Precalving**	**Mating**	**Weaning**		**Mating**	**Weaning**	**Precalving**	
Posterior-SDs									
G0	0.042	0.041	0.036	0.041	0.044	0.038	0.036	0.038	0.034
R0	0.012	0.011	0.010	0.011	0.015	0.010	0.010	0.010	0.011
P0	0.041	0.041	0.035	0.041	0.043	0.037	0.035	0.037	0.033
rG	0.000	0.034	0.034	0.034	0.000	0.014	0.034	0.014	0.000
rE	0.000	0.038	0.038	0.038	0.000	0.037	0.038	0.037	0.000
rP	0.000	0.044	0.044	0.044	0.000	0.042	0.044	0.042	0.000
h2	0.057				0.058				0.060

3.6.2.4.2 Multiple trait analyses of mature cow weight at different times of the year

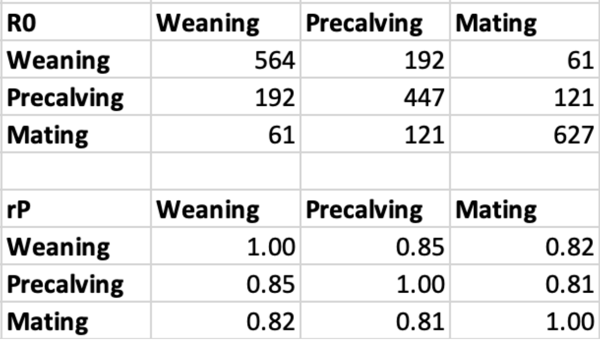
The results for MCW were a little different from those for BCS. The variation in liveweight was least pre-calving, but similar at mating or weaning.

Table 3.6.2.4.2.1: Phenotypic variance-covariance components for mature cow weights in beef cattle of at least parity two.



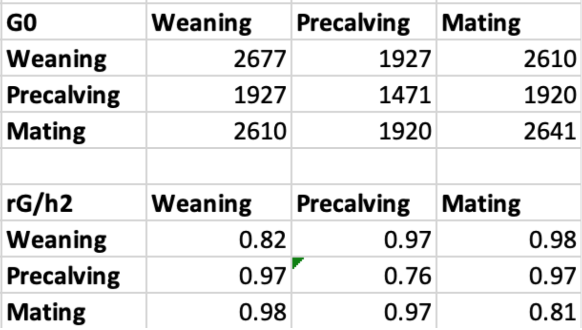
P0	Weaning	Precalving	Mating
Weaning	3241	2119	2670
Precalving	2119	1918	2041
Mating	2670	2041	3268

Table 3.6.2.4.2.2: Residual variance-covariance components and phenotypic correlations for mature cow weights in beef cattle of at least parity two.



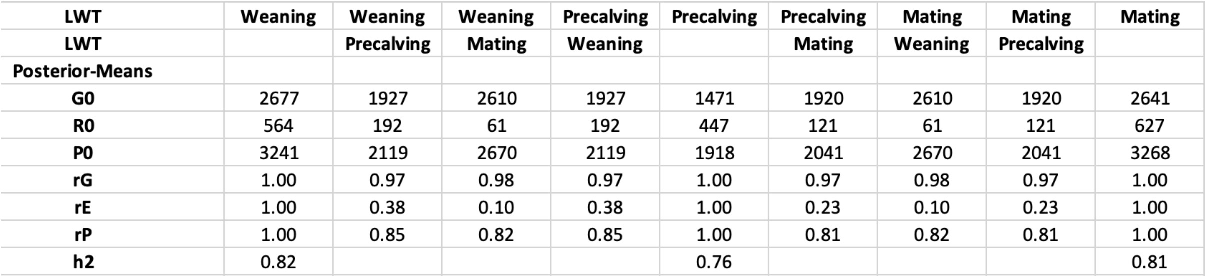
R0	Weaning	Precalving	Mating
Weaning	564	192	61
Precalving	192	447	121
Mating	61	121	627
rP	**Weaning**	**Precalving**	**Mating**
Weaning	1.00	0.85	0.82
Precalving	0.85	1.00	0.81
Mating	0.82	0.81	1.00

Table 3.6.2.4.2.3: Genetic variance-covariance components, genetic correlations and heritabilities for mature cow weights in beef cattle of at least parity two.



G0	Weaning	Precalving	Mating
Weaning	2677	1927	2610
Precalving	1927	1471	1920
Mating	2610	1920	2641
rG/h2	**Weaning**	**Precalving**	**Mating**
Weaning	0.82	0.97	0.98
Precalving	0.97	0.76	0.97
Mating	0.98	0.97	0.81

Table 3.6.2.4.2.4: Variance-covariance components and related statistics such as heritabilities and correlations for mature cow weights at three measurement occasions in beef cattle of at least parity two.



LWT	Weaning	Weaning	Weaning	Precalving	Precalving	Precalving	Mating	Mating	Mating
LWT		Precalving	Mating	Weaning		Mating	Weaning	Precalving	
Posterior-Means									
G0	2677	1927	2610	1927	1471	1920	2610	1920	2641
R0	564	192	61	192	447	121	61	121	627
P0	3241	2119	2670	2119	1918	2041	2670	2041	3268
rG	1.00	0.97	0.98	0.97	1.00	0.97	0.98	0.97	1.00
rE	1.00	0.38	0.10	0.38	1.00	0.23	0.10	0.23	1.00
rP	1.00	0.85	0.82	0.85	1.00	0.81	0.82	0.81	1.00
h2	0.82				0.76				0.81

Phenotypic correlations at around 0.8 were high between weights measured at any stage, higher than for BCS where the comparable values were around 0.5. Genetic correlations between weights at different stages were all near perfect. Residual correlations were mostly low, except between weaning and pre-calving. Heritabilities were extraordinarily high at 0.75-0.80, more so than is usually expected for MCW, but these data did exclude first parity weights. Similarly, to BCS, these data show that any single measure of adult MCW would be a good indicator of genetic merit for mature size. An additional measure at a different stage would further increase accuracy of predicting genetic merit because of the low residual covariance between stages.

Table 3.6.2.4.2.5: Standard errors of variance-covariance components and related statistics such as heritabilities and correlations for mature cow weights at three measurement occasions in beef cattle of at least parity two.

LWT	Weaning	Weaning	Weaning	Precalving	Precalving	Precalving	Mating	Mating	Mating
LWT		Precalving	Mating	Weaning		Mating	Weaning	Precalving	
Posterior-Variances									
G0	416	288	407	288	211	285	407	285	419
R0	30	24	26	24	30	28	26	28	38
P0	412	287	405	287	211	284	405	284	416
rG	0.000	0.009	0.006	0.009	0.000	0.009	0.006	0.009	0.000
rE	0.000	0.035	0.042	0.035	0.000	0.047	0.042	0.047	0.000
rP	0.000	0.017	0.021	0.017	0.000	0.020	0.021	0.020	0.000
h2	0.023				0.027				0.024

In summary, BCS and MCW, which are collectively useful descriptors of mature cows can be easily measured on commercial farms and, within farm and year, and for cows of the same age in years, are good indicators of genetic merit for these traits. However, achieving genetic change in BCS and/or MCW is much easier if predictions can be made before animal are retained and selected to be used as parents. This requires juvenile predictions of MCW or BCS. Parent average or sire-maternal grandsire average predictions at the herd level could be achieved based on BCS and MCW EBV from bull breeding herds, but selection directly in the commercial herd would require indicator traits that were useful in young animals, or the use of new technologies such as genomic prediction. The accuracy of genomic prediction is quantified in the analyses reported below.

First, single trait variance components were estimated using MCMC in a similar manner to that described previously, except that measurements at weaning, pre-calving or mating were not pooled in the same analysis, and measurements recorded during first parity were included. First parity cows are still maturing, and differences in relative maturity between breeds, ages and farms would influence results more so than measurements taken only in second and later parities.

3.6.2.4.3 Single-trait analysis of BCS and MCW at all cow ages

There are notable differences in the single-trait compared to multiple-trait analyses when first parity animals are included in the dataset and analyses are undertaken within year. First, there are large differences in phenotypic variance between years. There are many possible explanations for this heterogeneous variance, but the most likely explanation is that scoring has not been consistent across farms, years, and cow age groups. Although a 10-point scoring system was used, across all the data recorded observations were really only in the range of 4 to 8. The most common score was 7, suggesting recorders were discriminating more animals with poorer BCS and less among animals with higher BCS. Second, heritability was typically much lower than had been observed in the multi-trait analyses using only second and later parities. It is perhaps not surprising that there would be more non-genetic variance in measurements taken on animals in their first parity, and this would reduce heritability. Mature cow weight is measured objectively using electronic scales, and should therefore be measured more consistently than a subjective score. This is reflected in a lesser degree of heterogeneous variance than was observed for BCS. Heritability for MCW was about double that for BCS, bit still much less than had been observe in the multi-trait analyses that used only records from second and later parities.

Table 3.6.2.4.3.1: Variance parameters for body condition score measured in a single year.

BCS	2014		2016		
	Weaning	Mating	Weaning	Pre Calving	Mating
Number	786	1,302	1,496	1,312	1,688
Residual Variance	0.43	0.34	0.15	0.24	0.13
Genetic Variance	0.06	0.05	0.02	0.04	0.03
Phenotypic Variance	0.49	0.39	0.17	0.28	0.16
heritability	**0.12**	**0.13**	**0.17**	**0.14**	**0.16**

Table 3.6.2.4.3.2: Variance parameters for mature cow weight measured in a single year.

MCW	2014		2016	
	Weaning	Mating	Weaning	Pre Calving
Number	781	1,299	1,568	1,305
Residual Variance	1,467	1,435	1,495	982
Genetic Variance	501	405	655	380
Phenotypic Variance	1,968	1,840	2,150	1,362
heritability	**0.25**	**0.22**	**0.3**	**0.28**

3.6.2.4.4 Major gene effects

Fitting a marker effects model for genomic prediction provides, as a by-product, information that can be used for a genome-wide association study. There are a number of major gene effects that localise to particular genomic regions, known as quantitative trait loci (QTL). Many of these have been shown to be pleiotropic in cattle, influencing growth, carcass and calving ease traits. Further, most of these effects are found in many different cattle breeds (Saatchi *et al*. 2014). These analyses using commercial cow data for MCW demonstrated the presence of some of these body weight QTL on chromosome 6, at 38-39 Mb, chromosome 7 at 93 Mb, and chromosome 20 at 4 Mb.

3.6.2.4.5 Cross-validation of genomic prediction

Genomic prediction of animals on farms and years not included in the so-called training analyses that estimated marker effects were used to quantify the accuracy of genomic predictions using this commercial farm data. Goddard and Hayes (2009) have shown that ideally tens of thousands of individuals are required for reliable genomic prediction. Cross-validation was characterised by correlations less than 0.2, which was disappointing. However, the training data size was small, the training and validation datasets often comprised two breeds (Angus and Hereford), further eroding the number of training animals per breed. Further, the heterogeneous variance for BCS presented above is systematic of scoring issues that might be compromising predictive ability. Inspection of the correlation between genomic predictions and recorded phenotypes within herd-year and cow age showed that these results were very variable, from near 0 (or even negative) in some cohorts, but as high as 0.3 or 0.4 in some other cohorts (data not shown).

Table 3.6.2.4.5.1: Accuracy of cross-validation for genomic prediction of body condition score and mature cow weight

BCS numbers	Number in Training		Number in Validation*		Correlation☞	
2014 for 2016	AAN	HER	AAN	HER	**BCS**	**MCW**
Weaning	786	-	492	485	**0.00**	**0.07**
PreCalving	650	277	472	310	**0.04**	No train
Mating	996	306	501	445	**0.10**	No valid
2016 for 2014						
Weaning	1,011	485	-	267	**0.10**	**0.14**
PreCalving	839	473	284	114	**0.14**	No valid
Mating	598	1,090	407	153	**0.13**	No train

3.6.2.5 Summary

The genomic analyses of the mature cow weight and body condition score descriptors of commercial cows, demonstrate that even without pedigree recording and date of birth information, farm measured phenotypes are reflective of genetic merit for these heritable traits. Further, the stage of measurement (i.e. weaning, pre-calving or mating) is not too important, indicating that measurements can be taken at the time that is most convenient to farmers, which is probably weaning and/or pre-calving.

Genomic predictions that rely only on the commercial data collected by BLG were disappointing, but not surprising given the body of literature showing that large training populations are required for all breeds that will be targeted in the prediction. This reinforces the need for either routine measurement and genotyping of large groups of commercial cows to increase the accuracy of genomic prediction, or for collaboration, for example with breed associations, so that genomic predictions from single-step analyses can be used for commercial analyses.

3.6.3 Evaluate the impact of genomic data collected within the project on accuracy of industry single-step evaluations and the value proposition of commercial heifer selection utilising genomics.

3.6.3.1 Evaluation of Genomic data collected

3.6.3.1.1 A note on access to Angus Australia and the New Zealand Angus Association data

AGBU has been in negations with Angus Australia and the New Zealand Angus Association around access to data for research purposes. At the time of completing this report (30th September 2019), these negations were ongoing, and access to both Australian and New Zealand Angus genotypes, phenotypes and pedigree information was not available. All of these are required to analyse the impact on EBV accuracy for currently registered BREEDPLAN animals of including NZ commercial genotypes and phenotypes in the evaluation for the breed. This meant that it has only been possible to attempt to evaluate these for animals included in the Herefords Australia Limited and New Zealand Hereford Association databases. Once agreements with Angus Australia and the New Zealand Angus Association are finalised, results for that breed will be analysed and reported. It is hoped that this will be possible by final reporting for the project at the end of 2019.

3.6.3.2 Data Analysed

3.6.3.2.1 Genotypes

Genotypes were initially supplied in 13 report files. Attempts to read these into the genomic pipeline for the combined Trans-Tasman Hereford evaluation resulted in rejection of all genotypes. Investigation showed that this was due to an inability of the system to determine sex based on the SNPs provided (all animals were identified as male despite phenotypic information suggesting that they were almost exclusively female). BLG were approached to provide unedited genotypes, in the format made available by the lab, and these were supplied, with a cross reference file which allowed the SNP data to be matched to identifying information in the supplied pedigree and phenotype files.

These genotypes were processed from the final report format to the standard genotype extract format used for the BREEDPLAN genomic pipeline, and were successfully loaded to the system. This allowed a G-matrix to be built for the NZ commercial animals and for this to be incorporated into the G-matrix for the combined Trans-Tasman Hereford evaluation.

In total, 8428 genotypes were supplied. Analysis of breed composition showed that 922 were purebred Angus (AA), and 161 were purebred Herefords (HH). A further 4180 contained greater than 80% but less than 100% Angus alleles (AA80), while 1651 were at least 80% but less than 100% Hereford genetics (HH80). There were 883 animals which fell between 50 and 80% Angus (AAX) and 320 which were between 50 and 80% Hereford (HHX). The remaining 308 animals were very close to 50% Angus and Hereford, with 2 animals in this group returning results which suggested they were more than 50% Charolais, 1 animal which was more than 50% Limousine and one which was more than 50% Simmental (XX). Due to limitations around access to Australian and New Zealand Angus data, it was the 1815 animals identified as 80% or greater Hereford which could be included in subsequent genomic analyses (reported here), only 794 of which had mature cow weight or body condition score phenotypes collected as part of this project.

3.6.3.2.2 Phenotypes evaluated

3.6.3.2.2.1 Cow age at weight and body condition score measurement

Dates of birth were not available on any of the commercial females recorded for the cow weight and body condition traits recorded for this project. Information describing year of birth was made available for each animal and descriptive statistics for ages at measurement calculated on this basis are presented, by herd, in Table 3.6.3.2.2.1.1.

Protocols for the genetic evaluation which the genotypes and phenotypes on commercial NZ females were to be included in require that dates of birth for every animal be included in the analysis. This allows accurate adjustment for age, which is particularly important for mature cow traits where records are accepted for animals from 2.4 to 10.7 years old (870 to 3900 days). Based on these age requirements, just over one quarter or the records would be unsuitable for inclusion in the current evaluation, with 5421 measurements on animals which were too young and 161 from animals which were too old (based on the assumption that all animals from 3 to 11 year old were of appropriate age for inclusion in the evaluation).

Table 3.6.3.2.2.1.1. Descriptive statistics for cow age at weight and body condition score measurement (in years) for Angus and Hereford cows from four New Zealand commercial herds collected over 3.5 years from March 2014 to September 2017.

HERD	N	Mean	sd	Min	Max
6022	11803	4.5	2.5	1	14
6024	5624	4.7	2.2	1	14
6026	2112	4.2	2.6	1	15
6027	2400	4.0	2.5	1	15
All Herds	21939	4.5	2.4	1	15

Analyses of data included in the current evaluation for temperate beef breeds has also shown that the most accurate estimation of genetic merit for mature cow traits is for animals which have their first record before 6 years of age. Like all of the requirements for data to be included in BREEDPLAN, this is not a theoretical standard, but one developed as our understanding of the data improves to maximise the accuracy with which genetic differences between animals are described. Table 3.6.3.2.2.1.2 presents descriptive statistics for age (in years) at females' first record. For 376 of the 4020 females included in the NZ commercial cow dataset, the age at first weight / condition score record was 6 years of age or greater.

Table 3.6.3.2.2.1.2. Descriptive statistics for age (in years) at first cow weight for Angus and Hereford cows from four New Zealand commercial herds collected over 3.5 years from March 2014 to September 2017.

HERD	N	Mean	sd	Min	Max
6022	2117	3.6	2.4	1	13
6024	964	3.9	2.0	1	13
6026	448	3.5	2.4	1	13
6027	491	3.3	2.3	1	13
All Herds	4020	3.6	2.3	1	13

3.6.3.2.2.2 Cow weight

Phenotypes for cow weight (CWT) were supplied on 4019 females, with individual animals having between 1 and 11 weight records (a total of 21939 weight records, across both breeds and their crosses). Females were from 4 herds, with 2117, 963, 448 and 491 weights recorded from herds 6022, 6024, 6026 and 6027 respectively. Records were collected over a 3.5 year period (March 2014 to September 2017), with approximately equal representation of records, within herd, across three recording periods: February – April (Autumn), August – October (Spring) and November – January (Summer). While not universally the case, almost all animals had more than one record per year, with many having records from each recording period.

Table 3.6.3.2.2.2.1 presents descriptive statistics, by herd, for all cow weight (Angus, Hereford and crossbreds combined). Mean cow weights were reasonably similar across herds, with cows from herd 6024 slightly heavier, on average than those form the other three herds. Of the 21939 weights available for analysis, only 3746 were from females of 80% or greater Hereford content, and were recorded in 794 animals from two herds (305 from herd 6026 and 489 from herd 6027). Average weights were similar across breeds.

Table 3.6.3.2.2.2.1. Descriptive statistics for cow weights (kg) from 4019 Angus and Hereford cows, from four New Zealand commercial herds. Data includes 1 - 11 weight records per animal.

HERD	N	Mean	sd	Min	Max
6022	11803	519.9	90.5	223	896
6024	5624	563.5	85.8	293	870
6026	2112	509.0	86.2	257	754
6027	2400	509.0	113.0	187	838
All Herds	21939	528.8	94.0	187	896

To describe the number of individual animals with data, and their breed composition, Table 3.6.3.2.2.2.2 presents descriptive statistics for the first weight recorded for each animal, by the breed categories described in the previous section. The majority of animals had their first weight recorded in Autumn (N = 3745), with 88 first weighed in Spring and 186 in Summer, and these proportions were reasonably consistent across the 7 breed categories. There was significant differences in age at first record (1 – 15 years), though these were reasonably consistent across the major breed categories. A significant proportion of animals weighed (and condition scored) for the study did not have a genotype supplied (N = 1165), and breed composition (and subsequent genomic analyses) could not be undertaken for them.

Table 3.6.3.2.2.2.2. Descriptive statistics for first recorded weight, by breed category, for mature cow weights in NZ commercial females (one record per animal).

Breed Category*	N	MEAN	SD	MIN	MAX
No Genotype	1165	590.2	86.3	327	870
AA	452	520.6	85.9	272	774
AA80	1456	534.7	96.1	266	814
AAX	11	637.5	59.5	530	732
XX	17	614.4	76.4	542	850
HH	77	490.6	116.9	239	762
HH80	717	513.6	103.3	187	826
HHX	124	547.3	81.6	325	744
TOTAL	4019	545.6	98.5	187	870

* See the previous section for a description of breed composition acronyms.

3.6.3.2.2.3 Cow Body Condition Score

Phenotypes for cow body condition score (BCS) were supplied on 4020 females (essentially the same animals which had cow weight phenotypes described above), with individual animals having between 1 and 11 records for the trait. Females were from the same 4 herds, with 2118, 963, 448 and 491 from herds 6022, 6024, 6026 and 6027 respectively. As was the case for CWT, records were collected over 3.5 years from March 2014 to September 2017, with approximately equal representation of records, within herd, across three recording periods (Spring, Summer and Autumn).

Table 3.6.2.7.2.3.1 presents descriptive statistics, by herd for cow body condition score. Scores ranged from 3 to 9.5 in half score increments. Mean cow BCS was reasonably consistent across herds, with levels of variation also similar. Of the 21865 BCS available for analysis, only 3746 were from females of 80% or greater Hereford content, and were recorded in 794 animals (See Table 3.6.3.2.2.1.1 above) from two herds (305 from herd 6026 and 489 from herd 6027). The breakdown of breed composition for body condition scores was virtually identical to that described in the previous section for weights.

Table 3.6.3.2.2.3.1. Descriptive statistics for body condition scores in Angus and Hereford cows from four New Zealand commercial herds collected over 3.5 years from March 2014 to Sept. 2017.

HERD	N	Mean	sd	Min	Max
6022	11823	6.7	0.9	3	9.5
6024	5595	6.5	0.9	3	9.5
6026	2038	6.6	0.8	3	8
6027	2409	6.6	0.8	3	8
All Herds	21865	6.6	0.9	3	9.5

Fig. 3.6.3.2.2.3.1 presents the frequency of cow BCS, by score and herd. Results show that the trait was essentially normally distributed, with the most commonly assigned score being a 7.0 for all herds. While it's a little difficult to see in the Figure below, scores from 3 to 8 were recorded in all herds, with scores of 8.5, 9 and 9.5 recorded only in cows from herds 6022 and 6024. The assumption is that the results provided for these analyses were based on a 1 – 10 scoring system, with half score increments (18 levels). No records were reported for scores from 1 to 2.5, interpreted as suggesting that no females were identified in the bottom quarter (22%) of possible cow condition scores throughout the recording period for the project.

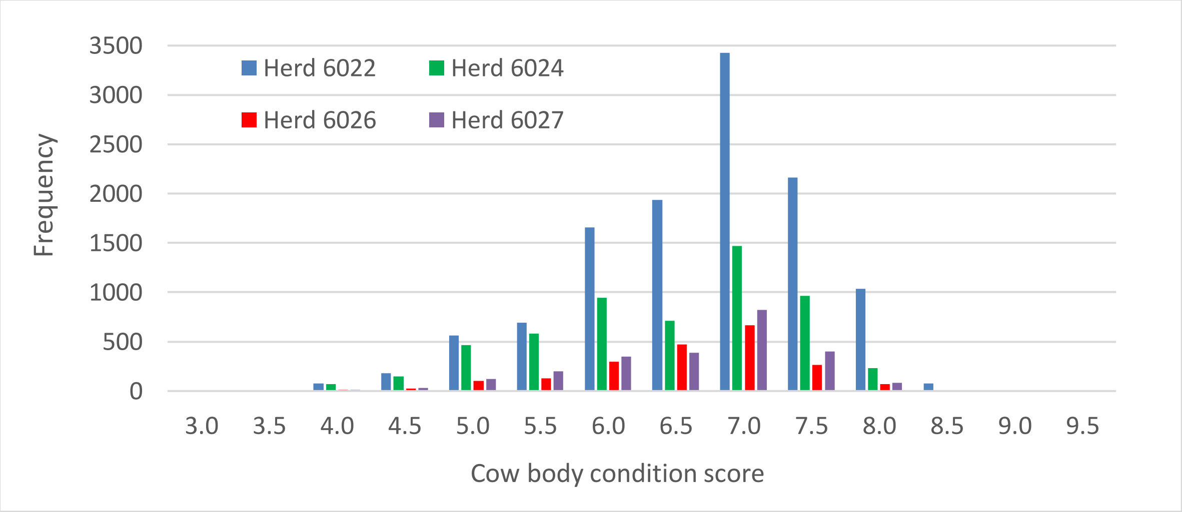


Fig. 3.6.3.2.2.3.1. Distribution of condition scores by herd for 4020 Angus and Hereford cows assessed in four commercial beef herds in New Zealand.

Cow condition score is not currently included in the traits analysed and reported in the Trans-Tasman BREEDPLAN evaluation for Angus and Hereford cattle. Records for the trait are, however being accepted and included in the database, and are currently the subject of research to establish whether cow condition score could be included in the multi-trait evaluation for temperate and tropical beef breeds.

3.6.3.3 Results

3.6.3.3.1 The impact of genomic data collected in the project on accuracy of industry single-step evaluations

There are significant limitations to the capacity of the Trans-Tasman Hereford evaluation to incorporate phenotypes of the type supplied from this study. As stated above, the lack of an accurate date of birth makes it impossible to correctly adjust cow weight and body condition score for the effect of the substantial age differences between animals. Additionally, the variation in age at first record meant that a proportion of the phenotypes would be excluded on that basis.

For both mature cow weight and body condition score, there is also a need for the records to be submitted within 14 days of the 200 day weight record for the females' calf. The lack of information about calf performance is a key limitation of the data made available from this project, and one which is almost impossible to overcome. The need for an accompanying calf record with mature cow traits ensures that records are from females in the same physiological state (i.e.: just weaned a calf). The lack of any information about the presence and performance of a calf means there is limited capacity to account for differences in lactation status among the females being evaluated.

Finally, mature cow traits are analysed as an annual record in the BREEDPLAN analysis collected at a time when females are all in the same physiological condition and, within a contemporary group, at the same time of year. Repeated measures collected throughout a year, at times other than at the weaning of their calf, will be for cows in varying stages of pregnancy or lactation and require more complex models to account for these differences. For this reason, mature cow weight has been defined as a trait recorded at the weaning of the females' calf. The current Trans-Tasman BREEDPLAN evaluation cannot analyse records taken more than 2 weeks from the weaning of a female's calf meaning that, even if one of the records collected in a year for the cows recorded for the project could be identified as that at weaning time, the remaining records, taken within a year, would have to be excluded from the analysis.

The bottom line is that, based on our understanding of the data currently included in the Trans-Tasman Hereford evaluation, the inclusion of the commercial cow weights and body condition scores collected as part of this project does not present an opportunity to more accurately describe genetic differences between animals, either those animals measured for this project or those which can be shown, via genomic relationships, to be related to them.

Before arriving at this conclusion, significant efforts were made to include the data in the current Trans-Tasman Hereford evaluation. These steps included the generation of:

- A date of birth for cows based on year of birth records supplied with the data.
- A calf identity to associate with the autumn records for females without offspring in the pedigree.
- A calf weaning weight to associate with the calf identity created to validate the cow weight.

When this was done, only 144 cow weight records (and similar numbers of BCS) could be retained from the 3746 weights collected in the 794 animals which met the minimum Hereford content for inclusion in the Trans-Tasman Hereford analysis. Attempts to run these data showed that the inaccuracies which would be introduced to the evaluation by including these invented ages and calf details out-weighed any value obtained from the cow phenotypes, and the exercise was halted. The conclusion has to be that opportunities to exploit commercial genotypes and phenotypes of this type, as a source of greater accuracy in the estimate of genetic merit for animals currently included in the Trans-Tasman Hereford evaluation, are limited. Moreover, attempts to force the data into the evaluation by ignoring or circumventing the requirements ran the risk of reducing, rather than improving, the accuracy with which genetic merit was described.

This does not mean that commercial data does not have role to play in the evaluation, and there are examples of this being done successfully. The key has always been that consideration be given to the requirements of the data which have been established to maximise the accuracy of the evaluation for its participants, when developing a commercial recording program. As our understanding of fixed effects decreases the ability to accurately partition variances declines, and the phenotypes analysed begin to lose their relationship with traits in the breeding objective. This can result in selection outcomes which are marginal or even contrary to the breeding objective.

3.6.3.3.2 The value proposition of commercial heifer selection utilising genomics

One of the opportunities that genomics presents to livestock breeders is to generate understanding of genetic merit in animals which are not a part of a current evaluation, including animals which may not have a phenotype of their own. This relies on genomic relationship between commercial animals, like those genotyped and phenotyped for this project, and those currently in an established genetic evaluation, with the Trans-Tasman Hereford evaluation the one available to analyse for this study.

When the genotypes for commercial animals were included in the BREEDPLAN Trans-Tasman evaluation, 794 were sufficiently related to the Hereford reference population to generate breeding values. This included only 448 cows which had been phenotyped and genotyped from two of herds described previously, as part of the Trans-Tasman project, though these weights were not included in the analysis which generated the results in Table 3.6.3.3.2.1.

Table 3.6.3.3.2.1 presents descriptive statistics for EBVs and accuracies for growth, reproduction and carcass traits for all animals genomically related to the Hereford BREEDPLAN reference population. Results show that estimated breeding values, based on phenotypes collected in the Hereford reference population and the genomic relationships of commercial NZ females to those animals, ranged in accuracy from 11 to 62%, with means for individual traits ranging from 14.9 to 43.1%. With the exception of DTC and RBY, both traits with very low levels of recording in the reference population, average EBV accuracies were sufficient to allow selection decisions to be made with more confidence than could be the case in the absence of this information.

The minimum accuracies presented in Table 3.6.3.3.2.1 are reflective of expectations for animals with only genomic links to the reference population. The proximity of mean accuracies to their respective minimums, as well as the low standard deviation for all trait accuracies, suggests that the majority of animals in the data analysed were in this category. Animals with significantly higher accuracies will be those which have progeny with phenotypes, or are closely related to higher accuracy animals in the reference population.

Table 3.6.3.3.2.1. Descriptive statistics for BREEDPLAN growth, reproduction and carcass EBVs, and their accuracies, for 794 commercial NZ females meeting the minimum Hereford requirement (80%) for inclusion in that analysis, with BREEDPLAN Trans-Tasman Hereford evaluation average breeding values from 2000 and 2017 presented for comparison.

Trait*	Units	EBVs				EBV accuracy (%)				2000	2017
		Mean	sd	Min	Max	Mean	sd	Min	Max	Average	Average
GL	Days	1.4	1.7	-0.8	4.4	34.9	6.9	27	58	0.1	-0.3
BWT	kg	0.5	0.7	-1.5	2.6	43.1	6.3	35	62	3.7	4.4
W200	kg	11.9	2.4	7.6	24.2	41.6	6.3	34	61	22.0	33.0
W400	kg	20.1	6.4	6.1	43.5	40.7	6.4	33	61	32.9	54.0
W600	kg	28.6	7.3	12.4	60.6	41.9	6.2	34	62	46.5	77.0
MCWT	kg	29.0	5.7	14.9	63.0	32.5	6.7	25	57	46.6	68.0
MILK	kg	11.9	0.7	10.1	15.7	21.3	7.4	14	53	8.7	16.0
SS	cm	0.9	0.6	-0.4	2.6	40.9	6.2	33	61	1.0	2.0
DTC	Days	-2.7	1.2	-4.4	-0.1	14.9	5.7	11	44	-1.0	-2.6
CWT	kg	22.3	5.5	9.7	42.6	30.0	6.8	23	55	24.9	50.0
EMA	cm^2	0.0	1.1	-1.4	2.0	23.1	6.7	17	50	2.1	3.5
P8	mm	1.5	0.2	0.7	2.4	31.2	6.4	25	55	0.2	0.5
RIB	mm	1.3	0.3	0.7	1.9	28.6	6.3	22	53	0.2	0.5
RBY	%	-0.7	0.3	-1.2	0.3	20.3	6.9	15	48	0.5	0.8
IMF	%	0.8	0.1	0.4	1.1	28.1	6.9	21	53	0.0	0.4

* EBV acronyms are: gestation length (GL), birth weight (BWT), 200 day weight (W200), 400 day weight (W400), 600 day weight (W600), mature cow weight (MCWT), maternal weaning weight (MILK), scrotal circumference (SC), days to calving (DTC), carcass weight (CWT), carcass eye muscle area (EMA), carcass P8 fat depth (P8), carcass 12/13th rib fat depth (RIB), retail beef yield (RBY) and percent intra-muscular fat (IMF).

The mean of breeding values for the traits presented in Table 3.6.3.3.2.1 suggest that, in general, genetic merit of the females evaluated for this exercise were substantially below the current New Zealand Hereford Association means. This was not an unexpected result. Many of the females evaluated for this study were older than animals included in the 2017 born bulls and heifers described in the currently published breed means. There is also a significant lag in average seedstock population performance being reflected in commercially bred animals. For this reason, average EBVs for 2000 are presented along with the current (2017) breed averages, and are likely to be a more realistic benchmark against which to assess genetic merit in these commercial animals.

Weight traits tended to show the largest difference from current (2017) and even the 2000 mean EBVs for the NZ Hereford BREEDPLAN evaluation. Interestingly, reproduction traits (SC and DTC) were reasonably consistent with average seedstock performance, and this reflected limited genetic progress for the traits in the NZ seedstock Hereford population over the last 20 years. Interestingly, EBVs describing fat traits (both P8 and RIB fat depths and IMF) were the only ones which were higher than those presented for the mean of the seedstock population.

These results demonstrate that opportunities exist to exploit the recording taking place in the structured, seedstock genetic evaluation, to estimate the genetic merit of commercial animals via their genomic relationship to the reference population. They also show, however, the importance of relatedness to that population if reliable breeding values are to be obtained. This is one of the basic concepts which underpins genomic selection, and one which is given significant consideration in the development of reference populations for a number of beef breeds in their Beef Information Nucleus (BIN) or similar progeny test based programs.

3.6.4 Conclusions

Genomic evaluation presents real opportunities to improve our understanding of genetic merit in beef cattle breeding enterprises, and this applies at both the seedstock and commercial levels. The commercial phenotypes collected for this project had real limitations when considered for inclusion in an established genetic evaluation with requirements around data quality. The conclusion that including the data was likely to result in the estimation of breeding values with extremely limited value as descriptors of actual genetic merit was not arrived at lightly. It was, however, the only reasonable position given the lack of capacity to partition variances, calculated based on these data, to systematic (environmental) and genetic sources.

The fact that genomic information is included in an evaluation does not remove the need to apply the basic components of effective genetic evaluation, which include:

- Reliable animal identification.
- Accurate and complete phenotyping.
- Accurate description of contemporary groups (both current and historical).
- The minimisation of, or at least the capacity to account for harvesting, which can be a particular issue for traits recorded in mature animals.
- Where genomics are to be the sole source of information about relationships between a group of animals and the genotyped and phenotyped reference population, an expectation that a reasonable level of genomic relatedness exist between the two.

Failure to observe some or all of these is common in recording practiced in commercial beef breeding herds, and is central to the difficulty faced when trying to incorporate such data in genetic evaluation programs.

A subset of the animals included in the project were sufficiently related to the current BREEDPLAN Trans-Tasman Hereford seedstock reference population to allow the estimation of breeding values based on those genomic relationships with the phenotyped and genotyped reference animals. Those breeding values describe genetic merit for animals which otherwise would have no quantitative basis for selection decisions. Generally low accuracies reflected the low level of relatedness to the reference population, but do create an opportunity to apply objective selection. This demonstrates the efficacy of genotyping in commercial, unrecorded herds as a means of obtaining some description of genetic merit in such animals.

3.7 Objective 7 & 8 – Extension Messaging and Industry Capacity

The agreed Trans-Tasman messages were split into high level topics which did not fit under the headings of the project milestones but were grouped into more practical categories covering: Improving cow productivity across environments, heifer puberty, commercial genomics, Trans-Tasman genotype by environment interactions and extension. Conclusions were captured as recommendations for the development of the BREEDPLAN evaluation, and those for further work before the end of the program. These are action points that the program science team have taken on-board and are implementing. Necessary lines of communication with external parties have been opened to achieve these action points.

- Work towards the introduction of body condition score EBV in BREEDPLAN including a review of recording BCS
- Distribute recording protocol for Days to Calving EBV in BREEDPLAN
- Examine changing presentation of DTC in BREEDPLAN. Examples include weaning rate, proportion of calves born early (first or second cycle), days to calving in heifers or first two parities where there is more variation.
- More economics of BCS modelling using a range of tools
- BREEDOBJECT provides a means of capturing GXE at the overall combination of traits level –stressing the importance of defining the production system. Science team review of different systems within standard indexes – including BreedObject
- B+LNZ Workshop pilots developed into maternal workshop
- Match mating outcomes to heifer puberty – and collect more naturally mated data.
- Further papers published

Milestone 7 and 8 were interlinked, and as such are reported on together. The aim of Milestone 7 was to develop an extension package around maternal efficiency for delivery to Australian and New Zealand cattle farmers. This was to include agreed, clear and consistent messages on a topic which is of significant debate among breeders and farmers in both countries. Note that the project was to cover package development only, with delivery to occur outside of the project.

Milestone 8 was to develop industry capacity at two levels. 1) Commercial cattle farmers and breeders were to have significant involvement in the project, building their knowledge and involving them in communicating outcomes to their peers. 2) At a scientific level, an expanded team which includes leading beef genetics researchers in both Australia and New Zealand collaborating and providing alternative perspectives will benefit the on-going development of genetic tools to support beef cattle breeding in both countries.

A series of workshops were held in New Zealand and Australia as part of Milestones 7 and 8. The first and second workshops held in Albury, Australia and Fielding, NZ respectively, involving 31 attendees from the Australian and New Zealand Beef Industry, ranging from breeders to scientists. From these workshops a series of action points were developed, as well as a greater understanding of the difficulties faced by commercial cattle farmers gained. The group collaboratively identified key issues for Australia and New Zealand and a draft report on agreed Trans-Tasman extension messaging and priorities was developed.

Extension materials were developed from these initial meetings, these can be grouped in to three age segments and two farm priorities within these:

Age Segments

1) Birth to First Pregnancy
2) First Pregnancy to second pregnancy
3) Cow Productivity

Priorities

1) Management on farm (phenotypes)
2) Genetics (sire selection and genotypes)

The forum in which the above messages were hoped to be extended were identified as part of the annual project workshop held in Cromwell, NZ. In order to achieve this, synergies/complementarity with other MLA and B+LNZ extension activities were assessed and opportunities for extension integration identified. In Australia this was the MLA Bred Well Fed Well (BWFW) extension package, and in New Zealand, Beef + Lamb NZ was identified as the most synergistic forum for extension. MLA is continuing to develop material as part of their next generation of awareness and adoption packages, Profitable Grazing Systems.

Prior to the extension messages being finalised they were tested at pilot workshops in New Zealand and Australia throughout 2018. In New Zealand these were held alongside the BLG BPT field days, held at Mendip Hills (South Island) and Rangitaiki Station (North Island) on 1 and 8 May 2018 respectively. In Australia the pilot workshops were presented as part of the revised MLA 'Bred Well Fed Well' delivery at Wirruna, in Holbrook Australia on July 31, 2018.

From workshops and pilots held, the following agreed messages were developed. These were split into high level topics that are not the same as the project milestone work but were more easily grouped into; Improving Cow Productivity Across Environments, Heifer Puberty, Commercial Genomics, Trans-Tasman Genotype by Environment interactions and Extension.

3.7.1 Improving cow descriptors

1) There are a range of ways of using existing and potential new records to describe cow "type" for both estimation of breeding values and management decision making.
2) The value of height, body condition score and cow ultrasound scan composition traits have been evaluated in addition to existing mature cow weight and heifer composition scan data. All the traits are heritable and highly genetically correlated across ages, especially those following first calving.
3) The project collected body condition scores pre-joining in addition to pre-calving and at calf weaning times. As expected, these all three were highly genetically correlated demonstrating that cows that are genetically in better condition at any one time of the year will be genetically better condition at other times of the year, i.e. genetically there is very little re-ranking.
4) A new potential trait Net Weight being weight adjusted for height was evaluated. This was also heritable but did not add utility beyond inclusion of body condition score.
5) Heifer Rib and P8 Rump fat depths are highly genetically correlated to cow body condition and can be used as selection criteria for an objective of improved cow condition.

6) The project team sees value in including body condition score at time of recording mature cow weight in genetic evaluation. This has value in recording cow condition and also likely in more accurately describing mature cow weight.
7) There are multiple body condition scoring systems. Pragmatically, a condition score that combines fat and muscle seems sensible rather than trying to score fat and muscle separately.

3.7.2 Economics of cows

1) In most systems in most years, feed costs are very cheap during times like spring, and very expensive during times of feed shortage. How expensive depends on factors like topography, cost of making hay or silage, opportunity cost of selling hay or silage, flexibility, cost and willingness to feed out, opportunity and willingness to reduce stock numbers.
2) Varying the cost of feed during time of shortage has a significant impact on selection index weights and, thus, the "types" of cows that will be bred. Both recent Australian work on BreedObject (version 6) and New Zealand herd modelling work support this conclusion.
3) Increased likelihood of drought exacerbates the changes in index trait emphases. This is also likely the case for systems with greater stocking rates per unit rainfall.
4) It is looking likely that industry will need different indexes for different breeding systems as the genetic difference between indexes is growing as system understanding improves. Ensuring industry understanding of the need for different indexes for different production system x market combinations, at both breeder and producer level, will be an important challenge.
5) Both BreedObject version 6 (AGBU) and a stochastic model (developed within this project) are useful tools for testing scenarios that impact on trait emphasis for selection for increased maternal productivity or efficiency. An important outcome of this parallel work is strong agreement on fundamentals of breeding objectives for beef production systems with a cow-calf component.
6) An Honours student (Kellie Wenham) at University of Adelaide in 2019 used the stochastic model (point 5) to test interactions between previous seasonal feed conditions, current feed conditions and calving time on maternal productivity (Appendix 9). She found that the combination of consecutive poor seasons had a severe impact on performance of Autumn calving herds, but much less so for Spring calving. This is the type of interaction that helps understand and communicate messages to producers and is ripe for ongoing work. Some of this will occur as part of the University of Adelaide project B.GBP.0038. Part of this could also be evaluating the impact of genetics (EBV) on the phenotypic and economic outcomes.

3.7.3 Heifer Puberty

1) There is genetic variation in age at puberty.
2) Many herds have as few as 10-50% of heifers pubertal by joining.
3) This may not be a problem as there is evidence that mating at the time of peak pasture quality and quantity as well as the effect of joining with a bull or synchronisation for AI triggers oestrus sufficiently to still achieve good results.
4) There are likely to be management approaches to improving the onset of puberty and they may only be at the low end (phenotypes).
5) For genetic improvement, it is far better to scan heifers using ultrasound than score body condition in heifers.
6) In terms of practicality of ongoing recording in studs, collars are likely to be more useful than ovarian scanning, and deciding whether to continue collecting age at puberty will depend on results from R&D on first calvers.
7) There are not strong genetic correlations between cow body composition and age at puberty.

8) MLA has funded a subsequent project on heifer development in commercial herds with University of Adelaide and Agriculture Victoria (B.GBP.0038). The project is not recording puberty attainment, but is focussed on pregnancy outcomes. The project will help with developing commercial management guidelines for heifers and first lactation cows.
9) Ongoing work:
    a. The relationships between heifer puberty and subsequent reproductive performance are important and will be reported outside of this specific project.
    b. This work should also be validated using New Zealand information being collected on heifer reproduction and on-going cow reproduction with the BPT project, where females are mated using natural service for their first two joinings
    c. Information from the Black Baldy trial (P.PSH.0716) will be included in the genomic analysis of the trial, at least purebred Angus calves and potentially crossbreds also.

3.7.4 Commercial Genomics

1) Analysis limited by size of training population.
2) Genomic h2 was as expected.
3) Poor cross validation accuracy.
4) When predictions took advantage of outside data, as expected this improved the accuracy of prediction.
5) Even within the project there was differences between years in the variance of BCS which suggests more work is needed to ensure standardisation of traits like BCS.

3.7.5 Trans-Tasman GxE

1) There is no evidence of significant GxE at the trait level in a range of production and quality traits examined, between Australia and NZ. Thus, it is sensible to continue a Trans-Tasman analysis for breeding value estimation.
2) Approaches to “drilling into” the data, to detect possible differences between specific production systems, have not so far been possible.

3.7.6 Extension

1) Bred Well Fed Well – TTBCPP messages have been integrated. We now have a MLA manager for genetics adoption and work should continue to ensure common messages across MLA supported programs. An example of this is approaches to selection indexes in bull selection workshops where current mixed messages are causing confusion. Some of this confusion is due to lack of clear explanation of the difference between genotype and phenotype.
2) B+LNZ Workshop pilots developed into maternal workshop. The responsibility for this sits with MLA and BLNZ.
3) Publication of research papers is continuing.
4) Material will be included in MLA Profitable Grazing Systems programs. The DesireBull tool being developed by NSW DPI will be useful for breeders to compare rankings of bulls when selection emphasis is changed. However, the deviation from industry indexes should be included in information reported to warn breeders of straying too far from what is considered closer to ideal.

The Final outcome from objectives 7 and 8 was the development of extension package material using the agreed messages that was appropriate for trainers and rural industry training organisations. This was completed and includes; a PowerPoint slide deck – Appendix 7.3, a summary sheet for recommendations on heifer mating and the Birth to first pregnancy segment – Appendix 7.4 titled 'Birth to first pregnancy summary' and, a summary sheet for angus bull selection, based on outcomes from the Beef CRC work – Appendix 7.6 titled 'Guideline for bull selection based on maternal productivity work'.pdf The current state of this material is adequate in that it is being used, although could benefit from further work with collaboration across diverse groups in addition to those within this current project team.

Some of these extension materials were used for the B+LNZ Genetics Virtual Beef Breeder Forum with great success. This was held In August 2018 and featured a mix of international speakers on beef genetics. There were both live and 'on demand' video sessions that had interactive features and live questions. The forum was well attended and the programs was well represented within it. TTBCPP sessions included;

- Birth to first pregnancy 'Carpool Karaoke' - with Jason Archer and Max Tweedie
- Beef Progeny Test: A frank conversation with the men at the coalface – with Jason Archer Max Tweedie and 5 BPT managers
  Beef Progeny Test: Let's cut to the chase - with Jason Archer and Max Tweedie
- Describing the ultimate cow: It's not as easy as you think -with Wayne Pitchford

Table 3.7.6.1 Virtual Beef Breeder Forum views – October 1 2018

	Conference platform			**You Tube**	**TOTAL**
	Live sessions - **Presso** - (Q&A)	On-demand sessions	Breeders: - % of views - Raw number	**Presso** (Q&A)	
Simu-live sessions					
Crossbred bulls (Cleveland & Cornell)	**83** (78)	**8**	36% (35%) (32/27 breeders)	**43** (15)	**134**
Genomics is here (Bendall & Reed)	**84** (81)	**13**	32% (38%) (31/30 breeders)	**53** (50)	**150**
So what will be for dinner? (Sowden)	**70** (60)	**13**	37% (41%) (31/24 breeders)	**13** (10)	**96**
BPT panel (BPT managers)	**59** (54)	**13**	34% (38%) (24/20 breeders)	**90** (13)	**162**
Ireland’s beef genomics (Cromie)	**63** (51)	**4**	38% (36%) (25/18 breeders)	**26** (11)	**93**
On-demand sessions					
EQ hit rates (van Bohemen)		**12**	17% (ie 2 breeders)	**131**	**143**
Bull Breeder job description (Beeby)		**10**	40% (2 breeders)	**40**	**50**
Why single step is the bomb (Byrne)		**9**	63% (5 breeders)	**43**	**52**
The Aussies are muscling up (Café)		**5**	40% (2 breeders)	**16**	**21**
Describe the ultimate cow (Pitchford)		**6**	33% (2 breeders)	**45**	**51**
BPT: let’s cut to the chase (Archer & Tweedie)		**7**	14% (1 breeder)	**42**	**49**
B+LNZ Genetics beef strategy (Alder)		**5**	20% (1 breeder)	**35**	**40**
Will Dairy and Beef still be dating? (Hickson)		**7**	14% (1 breeder)	**44**	**51**
Heifer mating (Tweedie & Archer)		**7**	14% (1 breeder)	**64**	**71**
Want 5 gold stars? (Millen & Gudex)		**5**	40% (i.e. 2 breeders)	**42**	**47**

All Virtual Beef Breeder Forum Videos can be viewed on the B+LNZ Genetics YouTube Channel below;
https://www.youtube.com/playlist?list=PLI0sUCZ_8ISDP7uBcAsc_30_fuyG6dEik

4 Conclusions/recommendations

The most important overall conclusions from the program are:

- Useful R&D can be conducted with field data, but definition of recording protocols is important
- There is genetic variation within the temperate beef breeds for key traits influencing early life fertility
- Methods are available for recording those traits, but it is likely that the intensive recording involved may be limited to key reference herds
- Early life fertility is important in overall lifetime profitability, and should be included in genetic evaluation via BREEDPLAN. Incluson of traits of cow body composition including adult cow weight and body condition score would enhance breeders' ability to improve lifetime profitability and cow robustness or resilience.
- At the trait level, there is no evidence of significant genotype-by-environment interaction between Australia and New Zealand, at least for the range of environmental and management systems applied in the herds involved in the project.
- Extension of the data collection work to include first mating calving and lactational anoestrus recording in naturally-mated females would be very valuable in understanding the relationship between age-at-puberty and second and later calving success
- Data from commercial herds can contribute to genetic evaluation, but knowledge of non-genetic effects is very valuable. Conversely, genomic breeding values can be generated on commercial animals, but the usefulness of those breeding values is very dependent on the strength of genetic relationshiup between the commmerical herd and the breed(s) reference population

Overall, the findings of the program can be summarised as that there is genetic variation in early fertility of beef cattle, it can be described through EBVs which for greatest reliability require data directly on fertility traits, and it is valuable to do so.

The most pressing need for future R&D is to collect that data on naturally mated first calving females, linking that data into the genetic evaluation along with data on puberty. Data collection on male fertility traits in parallel would enhance selection for fertility in both sexes.

More generally, the program has some useful messages in relation to beef cattle genetics R&D and industry engagement:

- The program grew out of initial MLA-BLGNZ workshops aimed at identifying common R&D and E goals and challenges, with subsequent consultation and project development by a small group of researchers, drawing on their interactions with breeders
- The program included regular face-to-face interaction, and significant workshops including the breeders – both the interaction and the workshops helped "thrash out"

some key questions, and overall helped improve mutual and shared understanding of those questions, and of some aspects of BREEDPLAN

- Applied R&D of this type is very valuable as a component of ongoing BREEDPLAN development and industry engagement. Of particular significance in this context, the program bought Australian and New Zealand researchers together, including interacting together with breeders. This has helped to build confidence in BREEDPLAN, and the industry engagement activities in NZ in particular were invaluable. Given the gene flow across the Tasman in a number of breeds, this improved communication and engagement is vital for maintaining trhe strength of the Trans-Tasman BREEDPLAN analyses in a number of breeds.
- Beef cattle genetics R&D is by nature large-scale and longer-term, and there is considerable value in industry and researchers maintaining a collaborative approach to R&D planning and funding. In particular, the genomics era increases the value of continuing R&D and data collection in hard-to-measure traits, and collaboration between Australia and New Zealand will be great benefit to both countries by increasing the scale of genomic reference populations, and the trait coverage. The relevance of this point is highlighted by the increasing focus in New Zealand on methane, which is costly and difficult to measure – collaboration in R&D and data collection in this and in feed intake data would be beneficial to both industries.

Finally, the program was innovative in terms of the approach to collaborative funding: BLG and MLA collaborated to enable a Trans-Tasman “mini-CRC”. This collaboration reflects the strong genetic links between the beef industries in the two countries, and the strong mutual interest in maximising the usefulness and adoption of BREEDPLAN.

The collaboration bought together industry levy and government funds in the two countries, enabling a level of outputs that would not otherwise have been possible, and the project management contributions from both organisations are to be commended.

The beef cow is the fundamental production unit for the beef industry, and finding ways to breed more productive and more profitable beef cows is central to sustained industry viability. The beef cow must rear calves throughout a long life, use feed efficiently rear calves that maximise profit, and all with minimal emissions. By definition therefore, genetic improvement is multi-trait, and requires knowledge of the genetics of many individual traits and of how those traits work together genetically and in different production environments. This program was multi-dimensional, multi-trait, multi-country, and very cost-effective for the investors. The program can be a model for future R&D in this particular area of R&D, and more broadly.

4.1 Recommended outcomes

The recommend outcomes were captured as both recommendations to BREEDPLAN and recommendations for further work before the end of the program. These are action points that the program science team have taken on-board and implemented where possible. Necessary lines of communication with external parties have been opened to achieve these action points.

- Introduce BCS EBV in BREEDPLAN, including reviewing the protocols for recording BCS (in the AGBU workplan for 2020)
- Introduce Height EBV into BREEDPLAN (in the AGBU workplan for 2020)
- Distribute recording protocol for DTC EBV in BREEDPLAN (in progress)
- Change presentation of DTC in BREEDPLAN (consultation on this change will be undertaken by AGBU and ABRI in 2020)
- More economics of BCS modelling (recommendation for further R&D – BREEDOBJECT v6 includes updated modelling of BCS, and the methodology for this has been published)
- BREEDOBJECT provides a means of capturing GXE at the overall combination of traits level –stressing the importance of defining the production system. Science team review of different systems within standard indexes – including BreedObject (this work will continue via BREEDOBJECT v6 roll-out)
- B+LNZ Workshop pilots developed into maternal workshop (will need new project – potential MLA-BLNZ joint activity)
- Match mating outcomes to heifer puberty – this will require data collection on naturally mated heifers.

In the absence of a direct extension of the collaborative R&D program, it is likely that the momentum for work on these recommendations will fit within the current AGBU R&D workplan under MLA funding.

There is currently no formal mechanism for continuing Beef and Lamb MZ input to priorities for either Australian industry R&D or collaborative programs. Consultation between MLA and Beef and Lamb NZ on such collaboration is recommended. This recommendation reflects the points made under Conclusions/Recommendations on the value and cost-effectiveness of such collaboration given the scale of R&D required in beef cattle (numbers of animals and timeframes), the trait coverage that will be required given anticipated changes in community expectations of industry, and the continuing gene flow between beef cattle populations in the two countries.

5 Key messages

The agreed messages are a combination of genetic and phenotypic outcomes and have been grouped into: Improving cow descriptors, Economic modelling for genetic evaluation, Trans-Tasman genotype by environment interactions, heifer puberty, commercial genomics, and extension.

5.1 Improving cow descriptors

This component of the project sought to examine existing and new descriptors of cow growth and body composition traits as descriptors of mature female productivity. This focused on an evaluation of easily measured body condition score and hip height traits to provide additional information in describing cow productivity to mature cow weight, which is currently used in the genetic evaluation for temperate beef breeds. Records for mature cow weight, body condition score and hip height collected at three key times through the females annual cycle (pre-joining, pre-calving and at weaning) were analysed, with results showing that records at all times were highly genetically correlated. This means that time of measurement time will not be of great importance in establishing measurement protocols for such traits, and that the current convention, to record them at weaning, will not ned to change if traits in addition to cow weight were considered for inclusion in the genetic evaluation for these breeds.

In response to breeder concerns that mature cow weight alone may not provide all the necessary information to quantify mature cow energy balance, a new trait was generated and analysed which adjusted cow weight for hip height records collected at the same time. The philosophy was to avoid the possibility that tall but lean females be evaluated as having similar energy reserved to shorter females of the same mature cow weight. Results showed that the height adjusted weight trait was heritable, but that it did not provide more information to that available when body condition score was included in the evaluation. This result supports the conclusion from other components of this project that mature cow body condition score be included in the genetic evaluation for temperate beef breeds, and that extension efforts include information on body condition scoring in mature beef females.

5.2 Economic modelling for genetic evaluation

A central understanding in modelling extensive livestock production systems is that feed costs fluctuate across the annual cycle through periods of surplus, and virtually no cost, to periods of feed deficit and a relatively high cost of providing the required energy to grazing animals. Recent research in Australian and New Zealand has sought to better understand these fluctuations, and how they impact cost of production in different environments, and developments in BreedObject Version 6.0 have recently been implemented which reflect this new understanding.

Work in the economic modelling component of this project sought to examine the implications of different feeding and management strategies in response to fluctuations in feed supply, and to determine whether beef cows with different genetic makeup are best suited to alternative management systems. Results showed that under a reasonable range of environmental conditions, ranking of performance for animals of the same genetic profile was not of sufficient magnitude to have significant impact at the economic level. This result was consistent with the outcomes reported below for the Trans-Tasman GxE analyses, and supports the idea that interactions of genetics and environment are unlikely to impact the accuracy of selection under the normal range of conditions. It was pointed out, however, that as environmental changes begin to impact productivity in extensive animal production systems, this may not remain the case, and the model developed as part of this research could provide the basis for better understanding these potential changes and their impact on beef breeding.

5.3 Trans-Tasman GxE

This research was undertaken in response to clear concerns from New Zealand breeders that the progeny of bulls bred in Australia, with BREEDPLAN EBVs generated based on predominantly (or exclusively) data recorded in Australia, could rank differently when mated to New Zealand females, managed under New Zealand conditions. The results of the research conducted as part of this project showed that there were almost no traits in the Hereford or Angus Trans-Tasman BREEDPLAN evaluations for which a significant genotype by environment interaction was present. This means that breeders in New Zealand can make selection decisions based on BREEDPLAN EBVs which will predict progeny performance in their environments as well as they do for animals managed under Australian conditions.

Additional work in this area examined a complex statistical method (factor analytics) which has the capacity to define environmental categories which most influenced breeding value estimation, and to allocate animals to them. It became clear that the development of a complete factor analytic model to evaluate the effect of categorical environmental effects, independent of country of origin which allocated herds (on a herd by herd basis) to groups of environmentally similar production systems, was beyond the scope of this project. It does, however, present an interesting area for future research and has the potential to provide much more accurate description of environmental factors in the genetic evaluation model.

5.4 Heifer Puberty

An increasing prevalence of artificial breeding in temperate beef seedstock herds has seen a decline in the number of records submitted for days to calving, the only descriptor of female reproductive performance in the BREEDPLAN evaluation. This research sought to describe age at puberty (assessed by serial ultrasound scanning for ovarian function) in temperate beef females and assess the degree to which variation in the trait had a genetic basis.

Variation in the proportion of heifers pubertal as they enter their first mating was significant across the herds evaluated and ranged from 15 to 76%. There was no significant effect of breed on these results, with average percent pubertal into mating almost identical for Hereford (53%) and Angus (52%) heifers. Despite these results, reproductive rates from first mating were good, whether this was from natural mating (as conducted in New Zealand herds) or artificial insemination (in Australian herds). This suggests that both natural mating and AI are stimulating puberty in heifers which were not cycling as they entered their first mating.

There was significant genetic variation in heifer age at puberty for the two temperate beef breeds evaluated for this study (Angus and Hereford), with heritability in the range of 0.26 to 0.38 depending on how the trait analysed was defined. Genetic correlations of age at puberty with heifer growth and body composition traits showed that these would not provide a useful genetic indicator for age at puberty. Understanding these relationships is, however, an important step in including the trait in the genetic evaluation for temperate beef breeds. Future research will focus on evaluating age at puberty and lactation anoestrus interval in naturally mated females.

5.5 Commercial Genomics

This research demonstrated that genotypes and phenotypes collected in a large commercial population of temperate beef cows could be analysed to generate genetic parameters for cow weight and body condition score. Consistent with Australian results from this project, the stage of measurement (weaning, pre-calving or into-mating) did not produce significantly different results, indicating that measurements could be taken at the time that is most convenient to farmers.

Heritabilities for these traits were higher than expected, when data for mature cows only (those at parity 2 or greater) was included in the analysis, which was consistent with the less accurate description of fixed effects and age which was possible for data collected under commercial conditions. A small proportion of the Hereford cows which were analysed for this study could have their genotypes included in the Trans-Tasman BREEDPLAN evaluation as commercial animals, which allowed EBVs for all traits currently published for that evaluation to be generated. While accuracies were generally low, these EBVs provided a basis for objective selection, which would not have been possible without the contribution of the single-step analyses which have recently been implemented for the BREEDPLAN Trans-Tasman Hereford evaluation.

5.6 Extension

Key messages for the extension component of this project have been summarised under the preceding headings for this section. There is clear evidence from the work carried out under a number of the sub-programs for this project that a deception of mature cow energy reserves, as body condition score, would make a valuable addition to the current genetic evaluation for temperate beef breeds. Extension efforts in this direction need to include both information about the benefits of describing cow energy balance in the genetic evaluation, and instructions on how, and when this is best done. These messages are in the process of being incorporated into the Australian 'Bred Well Fed Well' and the Beef and Lamb NZ Workshop programs and materials.

The issue of genotype by environment interaction is one which causes concern among many breeders, and this is particularly so for NZ beef breeders making selection decisions based on breeding values estimated from records collected predominantly in Australia. Research from this project shows that these concerns are almost entirely unfounded, and the inclusion of this new understanding in both the Australian 'Bred Well Fed Well' and the Beef and Lamb NZ Workshop programs and materials, is underway.

The rather unexpected results obtained as part of the heifer puberty research conducted for this project are not yet well enough understood for messages to be agreed on or for coursed of action in selection or management programs to be recommended. The results do, however, identify a real need for further research in naturally mated females, and interaction with leading breeders could seek to explain the results and highlight the importance of collecting good quality reproduction data in naturally mated heifers and first calvers.

Messages around the economic modelling and application of genomics to selection in commercial beef herds are less clear than those described above, and require better understanding before recommendations on changes to breeding and management programs in seedstock and commercial beef breeding enterprises can be made with confidence. These are areas which will be the subject of future research and development which will build on the understanding generated as part of this project.

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7 Appendix

7.1 Appendix 1 – Papers Published

7.1.1 Genetics of heifer age at puberty in Australian Hereford cattle

M.L. Wolcott[1], R.G. Banks[1], M. Tweedie[2] and G. Alder[2]

[1]Animal Genetics and Breeding Unit, University of New England, Armidale, NSW 2351 Australia
[2] Beef and Lamb New Zealand Genetics, Dunedin 9058, New Zealand

SUMMARY

Age at puberty has become a key trait in the genetic evaluation of female reproduction for tropically-adapted beef breeds in northern Australia. This study aimed to characterise the trait in Australian Hereford seedstock heifers and to determine the degree to which it, and associated traits, were under genetic control. Hereford heifers (N = 922) from three seedstock herds were serially ultrasound scanned to detect their first *corpus luteum* (indicative of age at puberty) at 4 - 6 week intervals from 10.6 to 13.2 months of age, at which time heifers were synchronised for artificial insemination. Results showed that only 52% of heifers were pubertal at synchronisation, and for these heifers, age at puberty had a heritability of 0.26. When a penalised record (equal to the maximum age at puberty for their contemporary group plus 21 days) was included for heifers which were not pubertal at mating, the heritability increased to 0.38. For sires with at least 10 progeny, EBVs for age at puberty ranged from -42 to 28 days. The ability of heifers to conceive early in their first mating season is linked to lifetime reproductive performance. These results suggest that the proportion which have reached sexual maturity as they enter their first mating is significantly less than 100% and that opportunities exist, if the trait were included in the genetic evaluation for the breed, to monitor and apply selection to improve age at puberty in Hereford heifers.

INTRODUCTION

Results from the Co-operative Research Centre for Beef Genetic Technologies' Northern Breeding Project (Beef CRC) showed that age at puberty, identified by serial ultrasound scanning to determine date at first ovulation, was heritable in tropically adapted beef genotypes (Johnston *et al*. 2009). These results have been supported by subsequent research in the Repronomics™ project (Johnston *et al*. 2019) (h^2 = 0.32 to 0.56). Associated research also demonstrated that lower age at puberty was favourably genetically correlated with lifetime reproductive outcomes (r_g = -0.29 to -0.40), and that selection to improve age at puberty would have favourable consequences for lifetime reproductive performance (Johnston *et al*. 2014). Morris *et al*. (2000) showed moderate heritability for age at puberty in Angus heifers when the trait was based on observed first oestrus (h^2 = 0.31), and a high genetic correlation with first mating pregnancy rate (r_g = -0.89). The current study aimed to exploit methods developed in the Beef CRC to characterise age at puberty in Hereford heifers, to determine the heritability of the trait, and to assess its potential to provide a means of monitoring female reproduction in the genetic evaluation for the breed.

MATERIALS AND METHODS

Animals and management. Heifers used for this study were made available by three Hereford seedstock breeders, and represented the entire cohort of females weaned in 2017 and 2018 from each herd. Herds were selected for inclusion based on a history of high quality pedigree and performance recording, and a willingness to accommodate the repeat ultrasound scanning required to identify first oestrous. Heifers were managed in accordance with standard practices for the three seedstock herds, one of which was located in the Southeast of New South Wales (N = 534) and the other two in the New England region (N = 149 and 239).

Heifers were born over a 2-month calving period at the Southern New South Wales property and over three months for the New England herds. The animals evaluated for this study were the progeny of 99 sires, with 71% from sires with at least 10 progeny, and 20% of heifers from sires used in at least two herds.

Heifers were weaned at an average of 5.4 months, with the two New England properties weaning at 6.6 months and the remaining herd weaning earlier (average 4.5 months old). Heifers weaned in 2018 were reared under significantly dryer conditions than those in 2017. This meant that more supplementary feeding was provided for heifers in 2018, but within herd and year, all animals received the same nutritional interventions. This was also the case for routine management practices (animals identification and branding, vaccination, parasite control treatments, etc.) as well as culling for conformation-related traits between weaning and syncronisation for artificial insemination. All herds routinely submit data to BREEDPLAN for genetic evaluation. For the heifers involved in this study, this included pedigree information, date of birth and weaning weight, and these data were extracted from the Hereford Australia Ltd. database for these analyses.

Scanning for ovarian function. Ultrasound scanning to detect first oestrous followed the protocols described by Johnston *et al*. (2009) for tropical beef females in the Beef CRC. Within herd and year, scanning was performed by one of three technicians using a Mindray M7Vet real-time ultrasound unit equipped with a variable frequency 6LE5Vs intra-rectal transducer, set at 8MHz. The timing of first scans to detect the presence of a *corpus luteum* (CL), was undertaken when managers at each location observed the first signs of heat in the heifer cohorts examined for this study (post-weaning). Subsequent scans were undertaken at 4 - 6 week intervals, until the first progesterone based synchronisation treatment occurred in each herd, prior to artificial insemination (into-mating). At the post-weaning and into mating measurement times all heifers in the cohort were scanned. Interim scans were only on heifers which had not previously displayed a CL. This resulted in the majority of heifers scanned three times up to synchronisation, with average number of scans per animal, within herd and year, between 2.3 and 2.8. Based on ovarian scanning results, the following traits were defined:

- **Age at puberty (AP)** was a trait in females which displayed a CL prior to mating, calculated as the scanning date at which the first CL was detected minus date of birth.
- **Penalised AP (APP)** generated an age at puberty record for heifers which had failed to display a corpus luteum prior to mating. APP was calculated for these animals as the maximum AP for their contemporary group plus 21 days. A small number of heifers which failed to display a CL prior to mating were in small contemporary groups, for which the maximum AP was based on too few records to be reliable, and no APP was generated for these animals (N = 15).
- **Pubertal into mating (PUB)** was a binary trait which identified heifers which had cycled at any time up to mating (1) or not (0).
- **Antral follicle count (FC)** was the total number of follicles greater than 2mm, visible by ultrasound examination of both ovaries at the first scan in heifers which did not have a CL.

Growth and body composition traits. At each scan, records of liveweight weight (LWT), hip height (HH) and body condition score (BCS) were collected for each heifer following the protocols for growth and body composition traits described by Johnston *et al*. (2009). P8 fat depth (P8) was also measured at each scan using the scanner's inbuilt callipers, with the exception of the first scan for heifers from one herd where the records could not be collected.

Modelling, variance component and EBV estimation. Descriptive statistics were generated using PROC MEANS in SAS. Contemporary group information was extracted from the Hereford Australia Ltd. database, and was built based on information supplied by participating breeders as described by Graser *et al.* (2005). The contemporary group for 200 day weight was used to analyse heifer growth, body composition and the descriptors of ovarian function evaluated for this study. For growth and body composition traits, dam age and linear animal age were fitted as covariates. Consistent with the protocols established by Johnston *et al.* (2009) heifer age was modelled for ovarian scanned traits as month of birth nested within herd and year. Variance components for each trait were estimated in univariate analyses in ASReml (Gilmour *et al.* 2009), with EBVs for all animals in the three generation pedigree estimated as the solution for the random animals effect.

RESULTS AND DISCUSSION

Growth and body composition traits. Summary statistics, additive variances and heritabilities for post-weaning growth and body composition traits are presented in Table 1. On average, heifers were 10.6 months of age at their post-weaning scan, with mean ages at first scan consistent across herds. Additive variances and heirtabilities for post-weaning LWT and HH were consistent with those reported by Donoghue *et al.* (2018) for Angus and Hereford females prior to their first calving ($h^2 = 0.45$ to 0.57). The heritability for post-weaning P8 was lower than that for Hereford females prior to their first calving reported for that study ($h^2 = 0.64$), but heritability fo BCS was comparable ($h^2 = 0.29$). The technicians employed to collect ultrasound data describing ovarian traits were not accredited BREEDPLAN carcass scanners, and this may explain the slightly lower thn expected heiritability for the scanned fat depth trait.

Ovarian scanned traits. Summary statistics, additive variances and heritabilities for ovarian scanned traits are also presented in Table 1. A key result from this work was the proportion of heifers which were pubertal into mating (PUB = 0.52). This reinforces the need to investigate the genetics of puberty traits in temperate breeds and for subsequent analyses which will examine relationships of the trait with first mating outcomes. The phenotypic and additive variance for APP (1549.2 and 588.7 days respectively) were substantially lower than those reported by Johnston *et al.* (2009) for Brahman and Tropical Composite heifers, which was consistent with the much

Table 1. Number of records analysed (N), mean and standard deviation (SD), with additive variance (σ_a^2) and heritability (h^2) (and standard error (s.e.)) for post-weaning growth and body composition and ovarian scanned traits in Hereford heifers.

Traits	Units	N	Mean	SD	σ_a^2	h^2	s.e.
Post-weaning growth and body composition							
AGE	Days	922	321.4	27.9	.	.	.
LWT	kg	922	262.9	35.0	460.4	0.55	0.11
HH	cm	921	116.7	4.6	6.8	0.49	0.11
P8	mm	837	3.6	1.8	0.6	0.29	0.10
BCS	Score (1 – 5)	922	2.8	0.6	0.03	0.20	0.08
Ovarian scanned traits							
AP	Days	481	365.8	38.3	363.0	0.26	0.13
APP	Days	902	396.2	44.3	588.7	0.38	0.10
PUB	1/0	917	0.52	0.50	0.05	0.36	0.11
AFC	Count	729	23.3	7.1	21.1	0.42	0.13

shorter scanning period in temperate breeds where maiden matings occur approximately 12 months earlier than for tropically adapted heifers. The moderate heritability estimated for APP ($h^2 = 0.38$) suggested that opportunities exist to improve the trait by selction in the Hereford breed. Both AP and APP were under significantly greater genetic control than days to calving ($h^2 \sim 0.05$) which is currently the key descriptor of female reproductive performance in the BREEDPLAN genetic evaluation for the breed.

For sires with 10 or more progeny, EBVs for APP ranged from -42 to 28 days. The heifers available for this study were a reasonably small sample of the breed, but these results suggest that sire selection could impact age at puberty in the resulting progeny by at least 35 days. With only 52% of females pubertal into their first mating, and mating periods as low as 2 months in commercial beef breeding herds in southern Australia, this could have implications for reproductive outcomes for naturally-mated maiden heifers.

Mean and standard deviation for post-weaning AFC were consistent with those reported by Walsh *et al*. (2014) for dairy heifers in the US and Ireland, with heritabilities also comparable ($h^2 = 0.25$ and 0.31 respectively). AFC was recorded in this project to investigate their genetic associations with economically important metrics of female reproductive performance and these results will be the subject of future analyses.

CONCLUSIONS

This study presents an initial investigation of the genetics of age at puberty and associated traits in Australian Hereford seedstock heifers. Results showed that there are opportunities to improve age at puberty by selection in the breed and, by including the trait in the breed's genetic evaluation, to monitor this aspect of female reproduction as selection is applied to improve other economically important traits. The proportion of heifers which were not pubertal as they entered their first mating was a key result of this study. The increasing prevalence of artificial insemination and the associated treatments to synchronise (and possibly induce) first oestrous, suggest that genetic and environmental factors which impact a heifer's capacity to conceive early in their first mating season may warrant monitoring and inclusion in the genetic evaluation for temperate beef breeds.

ACKNOWLEDGEMENTS

This research was supported by co-funding from Beef and Lamb New Zealand Genetics and Meat and Livestock Australia under project P.PSH.0869. The co-operation of the principals and employees of 'Wirruna' Poll Herefords, 'Yalgoo' Genetics and 'Te-Angie' Poll Herefords, as well as their breed representative body (Herefords Australia Ltd.), is also gratefully acknowledged.

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Walsh S.W., Mossa F., Butler S

7.1.2 Demonstrating BREEDPLAN estimated breeding values in New Zealand commercial beef herds

M. Tweedie[1], J. Archer[2] and L. Proctor[2]

[1]Beef + Lamb New Zealand Genetics, Level 2, Queens Gardens Court, 3 Crawford Street, Dunedin

[2]AbacusBio Ltd, 442 Moray Place, Dunedin 9058

SUMMARY

Demonstration of BREEDPLAN Estimated Breeding Values (EBVs) is important to build confidence in the value of genetic improvement for commercial farming businesses and for user trust in genetic evaluation. Work of this kind has not been completed before in a New Zealand setting. The way that this validation is presented to users is also important in order to maintain confidence. Across the 9 BREEDPLAN traits assessed to date, the responses in calf performance ranged from 25% to 151% of predicted response based on sire EBVs – giving confidence to users that selection on EBVs is translating into gains in performance under New Zealand commercial beef cattle systems.

INTRODUCTION

The uptake of Estimated Breeding Values (EBVs) and other genetic tools has been mixed in New Zealand beef breeding to date. In sheep breeding, the uptake is relatively advanced and many rams sold are first grouped on $ Index to be valued for sale. Given a vast majority of farms run both sheep and beef on the same land – this is an interesting difference.

Beef+Lamb New Zealand Genetics established the Beef Progeny Test (BPT) with a strong focus on adoption. Typically, progeny tests are formed for the purpose of evaluating sires and providing research data primarily. While the BPT also has evaluation and research goals, a strong adoption focus is a defining aspect of the BPT. Proving that the tools work and that the investment pays off from using them is a central theme for the test – it has become a platform for adoption in NZ beef genetics. The use of significant sized commercial farms is a key factor in ensuring that NZ farmers believe and relate to the outputs of the BPT.

MATERIALS AND METHODS

The BPT is an industry and government funded project that tests the genetic merit of beef sires through the performance of their progeny. The project completed its 5th cohort of joining via artificial insemination (A.I) in 2018. Approximately 2200 cows are fixed time A.I'd annually to approximately 50 sires representing Charolais, Hereford, Stabilizer, Angus and Simmental breeds.

Sires are used across 5 properties; Mendip Hills Station- Cheviot, Tautane Station- Hawkes Bay, Whangara Farms- Gisborne, Caberfeidh Station- Hakataramea Valley and Rangitaiki Station near Taupo. Not every sire is used on every property, however there is sufficient genetic linkage to compare the performance of sires across these wide ranging environments with most sires (except Stabilizers) used across at least two properties and many used across four. Maternal sires were used with the intention of achieving a rate of 25 effective progeny per sire (30 in later years), and terminal sires at a rate to achieve 12.5 effective progeny (15 in later years) - with all progeny being DNA verified to sire. International sires from other global progeny tests have been used- to provide benchmarks for New Zealand beef sire performance and to allow future collaboration with these programs. Progeny of sires are assessed for over 30 traits- including growth, carcass quality (using live ultra-sound at approximately 18 months of age, and actual carcase assessments based on the MSA measurement system), structural assessments, maternal ability, fertility, cow size and body condition. Heifers from Angus, Hereford and Stabiliser sires are mated naturally to calve at 2 years of age, with the intention of retaining them into the cow herd. All steers and heifers from Simmental and Charolais sires were slaughtered and carcase measurements collected. Animals for slaughter were drafted into groups based on weight, generally several months prior to slaughter, and all animals within the pre-allocated groups were killed on the same day.

Statistical analysis. An analysis of how calf performance related to sire EBVs was undertaken to provide a demonstration of the utility of EBVs for improving performance in commercial environments. Data was restricted to calves sired by Angus, Hereford and Simmental sires with BREEDPLAN EBVs available. Two cohorts of calves (born 2014 and 2015) were available for growth and ultra-sound scanning traits, with only one cohort available for carcase traits. For each trait a model was fitted which included effects of sex, calf age within Herd-year (estimated from conception date scanning and dam-calf DNA match), age of dam (years) and contemporary group (Herd-sex-mob), Sire EBV and Sire Breed. This model assumes the same regression slope on Sire EBV between breeds, but a previous analysis had found that EBV x Breed interaction was not significant. The EBVs used in the analysis were from Angus, Simmental and Hereford Group BREEDPLAN analyses, where the BPT data was not included in the analysis (and so were independent of this data).

RESULTS AND DISCUSSION

(Fig. 1) is an example of the graphs which were produced to summarise the analysis in a visual way. The major goal of these graphs is to give farmers confidence that a response to the different EBVs is observed in a commercial beef production setting in New Zealand, and that EBVs created largely on data collected in seedstock herds are relevant to commercial beef systems.

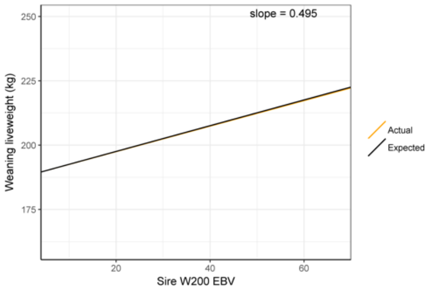

Fig. 1. Demonstrating 200 Day Weight EBV

(Table 1) gives the slope observed, and the percentage of this slope relative to what might be expected (generally expectation is 0.5 where the trait mirrors the EBV definition exactly). The impact of error in the EBVs on the expected slope is not accounted for in the calculation. Robinson (2005) showed that when the assumption that the independent variable is measured without error is violated, the expected slope is reduced and this can be predicted based on known errors. While accounting for this would be more appropriate from a scientific viewpoint to assess the utility of EBVs, communicating this to a lay audience is difficult, and it is also a “real world” factor which influences the realisation of commercial gains from use of EBVs. Consequently, for extension purposes the expected response was not adjusted to account for imperfect accuracy in sire EBVs

Table 1. Demonstrating EBVs across traits

Trait	Observed slope	% of expectation
200 Day Weight EBV	0.49	99%
400 Day Weight EBV	0.41	82%
600 Day Weight EBV	0.45	90%
Days to Calving EBV*	0.50	100%
Rib Fat EBV	0.75 (abattoir)	151%
Eye Muscle Area EBV	0.33 (abattoir)	67%
Intra Muscular Fat EBV**	8.0 (abattoir)	25%
Carcass Weight EBV	0.15 (abattoir)	32%
Rib Fat EBV	0.20 (ultrasound scanning)	40%
Rump Fat EBV	0.32 (ultrasound scanning)	65%
Eye Muscle Area EBV	0.33 (ultrasound scanning)	66%
Intra Muscular Fat EBV	0.27 (ultrasound scanning)	54%
		73%

** Conception date as recorded in the BPT is calculated similarly to DTC but doesn't include Gestation length and is based off conception.*

***MSA marble score has been scaled to relate to IMF%. So expectation is moderate.*

As a general rule, the relationships between calf performance and EBVs which were closest to expectation were for traits where EBVs are generally the most accurate (e.g. growth traits). The responses in calf performance for growth and fertility traits were generally close to expectation from Sire EBV. Responses in carcase ultra-sound measurements were generally lower than expectation (ranging from 40% to 66% of expectation) but still strongly positive.

For actual carcase measurements, the relationships between progeny performance and sire EBV for fat depth, marble score and carcase weight the relationship were positive but substantially below theoretical expectation. For these traits, the accuracy of the EBVs is affected by both the lower level of recording, and that the majority of recording is based on ultra-sound carcase predictions rather than actual carcase data. This is particularly important for marbling predictions, where ultra-sound %IMF is imperfectly correlated to actual marble scores which likely contributes to the lower than expected correlation (where the calculation of expectation does not take this into account). Responses in carcase eye muscle area were similar to those for ultra-sound scan eye muscle area, while for carcase fat depth the responses exceeded that predicted by Sire EBVs. Responses in carcase weight being much lower than expected can be explained by the impact of drafting strategy, where animals were pre-selected into groups to be killed together based on liveweight (generally several months before actual slaughter). Reverter et al. (2000) found measurements on the same cattle ultrasound scanned as yearlings and then again at the abattoir were moderate to strongly positive, suggesting that selection using yearling ultrasound measurements of seedstock cattle should result in predictable genetic improvement for abattoir carcass characteristics. This has been demonstrated anecdotally around the world with good levels of genetic gain in carcass traits using ultrasound scanning.

Across the 9 BREEDPLAN traits assessed 73% of sires EBVs turned into calf performance. This was further demonstrated by Angus Australia (2018) which showed an excellent relationship between expected difference between sires and actual differences in their progeny. The outcome was comparable to this work where the percentage of predicted difference and the actual difference averaged 120%. This was reinforced by Thrift & Thrift (2006) where the expected differences between high and low EBV sires were similar to the realised differences.

Our experience in showing these relationships to commercial farmers, with the aim of enhancing uptake of EBVs, is that the main focus of farmers tends to be on the fact that there is a positive relationship, rather than the proportion of the expected relationship actually achieved. Thus while the relationships might be lower than hoped for from a scientific perspective, the main message taken from these relationships from an extension viewpoint is that the EBVs are predictive of calf performance, and therefore selection based on EBVs will lead to gains within commercial beef production systems.

CONCLUSION

Although Sire EBVs are imperfect in terms of accuracy, it has been shown they have strongly positive relationships with the performance of their calves. Commercial farmers hope to see a positive relationship and having this visually represented assists with demonstration of the tools.

ACKNOWLEDGEMENTS

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7.2 Appendix 2 – News articles

7.2.1 Next generation selection - Focus on Traits Not Considered.

The following article is a summary of Dorian Garrick's presentation to the 'Angus through the ages' conference at Albury in May 2019. It draws from learnings from the program.

NEWS

Angus breeders urged not to overlook maternal traits

James Nason, May 30, 2019

Internationally renowned New Zealand geneticist and animal breeder Professor Dorian Garrick had some pats on the back for Australian Angus breeders at the Angus Through the Ages conference in Albury last week.

But this was followed with a sobering warning that breeders were selecting too heavily on terminal sire traits at the expense of important maternal efficiency traits.

Angus breeders had made "tremendous improvements" in terminal sire traits over the past 30 years which had led to higher weaning weights, higher yearling weights and higher carcase weights, and increased the value of their product.

An average 2017-born steer earned $103/head more than a 1980 steer. (Importantly though not all of that benefit was captured by cow-calf operators, with some captured by feedlotters and processors).

However, they were falling short on key maternal traits that are becoming increasingly important as society demands more efficient production and a smaller environmental beef hoofprint.

Professor Dorian Garrick is the Chief Scientist and Director of the AL Rae Centre at Massey University in New Zealand.

With bigger cattle has come increased feed costs. The cost of feeding the average Angus daughter in 2017 was $57/head more than the average Angus daughter in 1980.

And all of those costs are carried by the cow calf operator.

"So collectively I would say the cow calf operator, the genetic change that has occurred since 1980 has not been what I would consider to be improvement," Dr Garrick said.

"The cloud has moved, it has moved hugely, but it has moved more in a terminal sire direction and not enough in a maternal cow direction."

Dr Garrick has had a distinguished 37 year career as an animal breeder at Massey University in NZ and also at various universities in the United States including Cornell, Colarado State and Iowa State. He is a global authority on livestock improvement through pedigree selection, genetic and genomic evaluations and the development of cross breeding model predictions.

His key message to last week's audience in Albury was that the beef industry needs to improve the efficiency of beef production, which involves focusing on number of traits not being given adequate consideration at present.

Dr Garrick said improved efficiency could certainly be achieved with well-designed genetic selection programs, but had to be focus on total merit indexes.

And the change would need to be led by innovative breeders and entrepreneurs.

Dr Garrick said a rear-view mirror analysis of objective measurement data in a herd or across an entire breed provided a clear demonstration of what was being prioritised in selection decisions.

He offered the below example of data showing the genetic trend of weaning weight and yearling weight in the American Hereford industry from 1975 to 2015.

Click on chart to enlarge

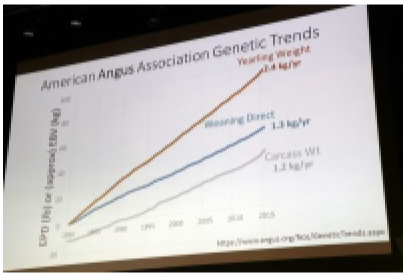
After rising sharply from 1980s through to the 1990s the rate of ascent clearly slowed somewhat.

Dr Garrick said that bend illustrated the emergence of ultrasound testing in the 1990s, which led to the prediction of merit for carcase characteristics in the American Hereford herd.

"Up until that time selection was primarily on growth, so when Hereford breeders chose to move the cloud they now had the opportunity to put more emphasis on improving the carcase merit and less emphasis on growth, and we can see that here as a bend in that curve for growth rate."

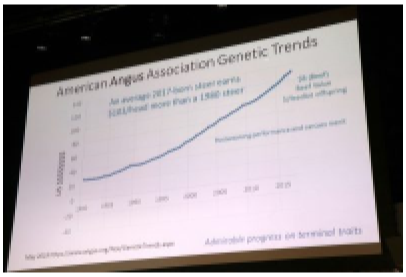
Similar data for American Angus from 1980 to 2015 demonstrated that Angus breeders had not changed their attitude about growth in the same way.

Weaning weight, yearling weight and carcase weight have gone up and up over the same period:

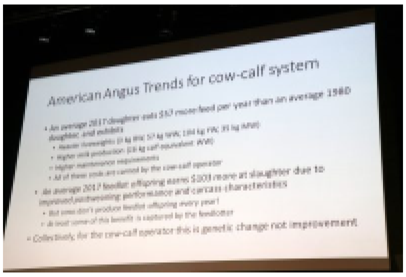


The trend toward bigger and bigger carcases was being driven not by the abattoir or processor end but way back in the bull selection process, a couple of generations animals were born.

It was being driven by American Angus Association dollar indexes such as the one below showing that average 2017 feedlot offspring earned $103 more at slaughter due to improved postweaning performance and carcase characteristics than 1980 offspring.



While that had been a fantastic performance on those terminal traits, other genetic trends showed the cost of feeding an average Angus daughter in 2017 compared to 1981 was about $57 more feed per year."



American Angus Trends for cow-calf system

Clear breeding goal essential

Dr Garrick said professional animal breeders can design a breeding program based around the goal a breeder wants to achieve. Every breeder should be able to describe their breeding goal in the time it takes an elevator to rise a single floor.

As an example one dairy breeding client in New Zealand used to have a goal defined by "profit per hectare", but now defines their goal in terms of "profit per 4.5 tonnes of dry matter". (Why 4.5 tonnes of dry matter specifically? That is the average amount of dry matter a dairy cow in New Zealand averaged across breed and her share of replacements eats in a year.)

"So they recognise we're in a pastoral production system, and some cows are bigger and eat more, and some cows are smaller and eat less, but the goal is profit per unit of food consumed," he said.

The next step is to define what needs to change to advance your animals toward your goal. This involves identifying the list of traits you want to change and the relative emphasis of each of those traits which then defines an index to summarise the merit of those animals.

That informs which individual measures are required to produce the relevant EBVs and which animals need to be measured and how the breeding program is structured.

Dr Garrick said in the US an increasing number of commercial Angus cow calf operators were now mating Hereford bulls to Angus cows, because of the view the American Angus Association has not placed enough emphasis on maternal traits. "That is why the Hereford association has seen such a success in bull sales in recent times in the US," he said.

A final step was to do an economic analysis to look at the overall benefit and costs. "I could easily double the rate of improvement in any industry I have ever had anything to do with, but the costs of implementing those improvements could be more than the benefits that flow right through the system. So in my job and probably in your jobs as well it is all about compromise, and only spending the money where we know that we get a good return on that investment."

You are doing a good job of selecting for the income traits – particularly growth and some of the things that affect eating," he said.

"What are the things you could do a better job of selecting on? Well I would argue it is everything else.

"So why aren't these other traits being adequately considered? Well I think part of the problem is that you are not selecting on the total merit indexes."

While most breeders would say they are selecting on total merit indexes, he said a rear vision mirror look often showed that was not the case.

"In particular the one that tends to get missed out a lot is the maternal system traits," he said.

"You are not measuring enough of the less tangible attributes, the things that can't be measured in a production system." This included attributes such as carcase merit on a breeding animal, or ones that were too expensive or labour intensive to measure such as age of puberty. Nor were these traits being rewarded by bull buyers, who tended to like buying the

"If you asked me about the value proposition among the bull breeding sector I would say the big problem with beef industries globally is there are too many animals being recorded and not enough traits being recorded," he said.

The changing regulatory environment was also underlining the importance of maternal traits. Cattle producers in New Zealand for example must now comply with specific urine nutrient excretion limits. It is anticipated dairy markets will increasingly ban dairy products produced from animals that are genetically horned, because they have to be dehorned in ways that social media indicates is not appropriate.

Traits producers could to be a better job of selecting included reproduction, longevity, healthfulness, feed efficiency, animal welfare and environmental hoofprint.

Social media and online forces continued to highlight a perceived lack of efficiency of beef production. Critics of beef production regularly point to figures indicating it takes 25kg of feed to produce 1kg of beef, by far the least efficient of all animal proteins. (People in the beef industry understand that much of that intake is food nothing else would eat, but consumers making a purchase decision still see it as beef being worse than any other animal protein on that score).

"You can move the cloud in anyway you like, so if you wanted to make your goal to improve to improve the protein efficiency of beef production, we could make huge improvements in this particular characteristic, but that is not what you are going to achieve by accident by selecting on things like yearling weight," Dr Garrick said.

50 years ago most people ate beef and lamb every day and chicken on special occasions. Now that trend had largely reversed. These per capita meat consumption trends highlighted the success the poultry and pig industries have achieved in using genetic selection programs to make chicken and pork production as efficient and cost effective as possible.

"One of the reasons that we haven't been able to achieve the same things here is we have been focusing too much on those terminal sire characteristics and not enough on those whole systems aspects," Dr Garrick said.

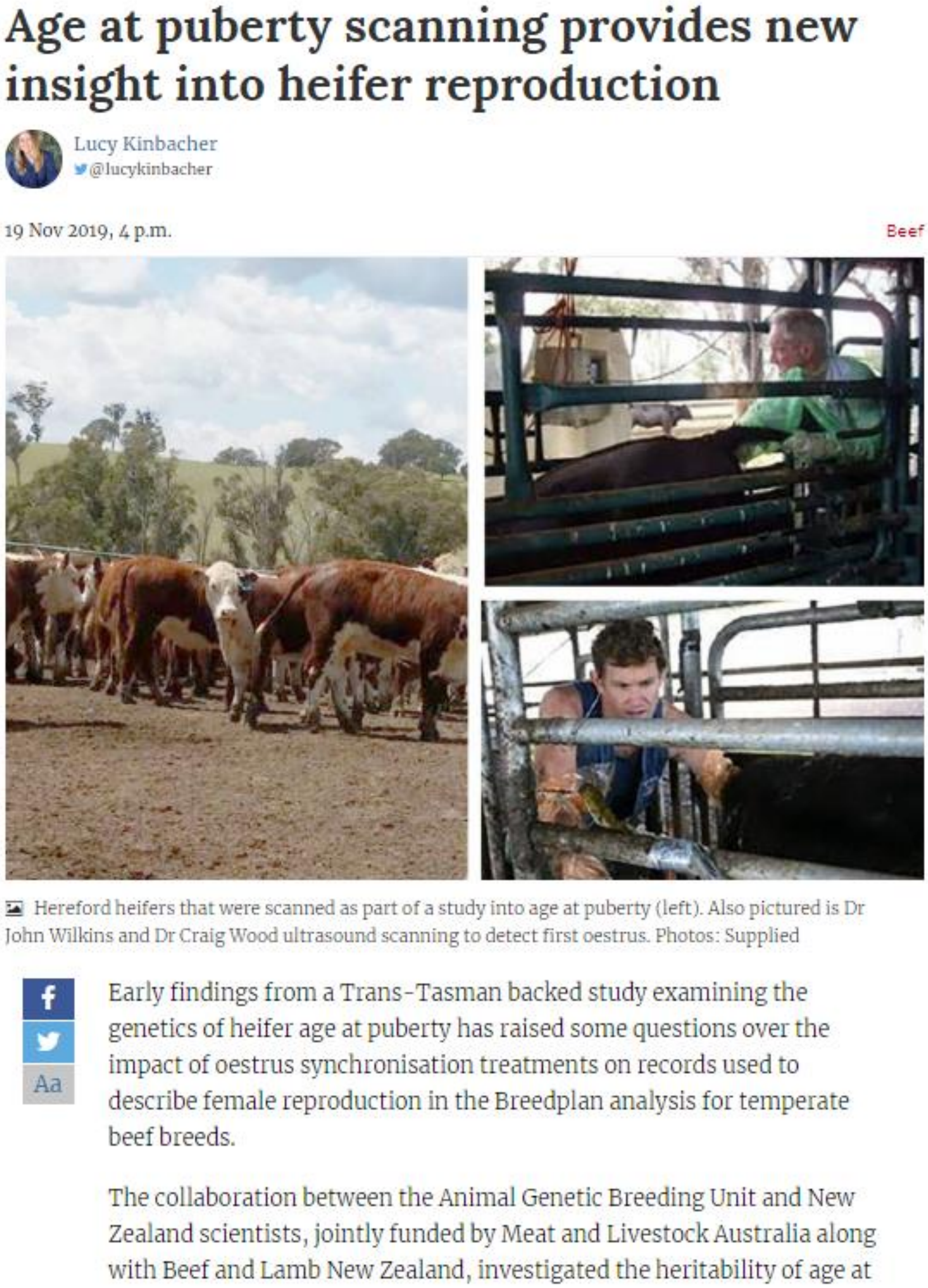
"So in summary we really need to improve the efficiency of beef production, and we need to be seen to be trying to improve the efficiency of beef production and particularly that means reproductive efficiency, birth to finish efficiency, and doing so involves a number of traits, many of which we're not adequately considering.

"Selection is a proven and cost effective mechanism for doing this, but it needs to be based on whole system indexes, not just say a feedlot index.

"Genomics allows us to get predictions of these things in all kinds of ways we couldn't do in the past, but we need to do it in a way that doesn't give us market failure, and rewards the individuals that invest in those activities.

7.2.2 Age at puberty scanning provides new insight into heifer reproduction

The following article is a summary of Matt Wolcott's presentation at the Association for the Advancement of Animal Breeding and Genetics conference in Armidale 2019.



Age at puberty scanning provides new insight into heifer reproduction

Lucy Kinbacher
@lucykinbacher

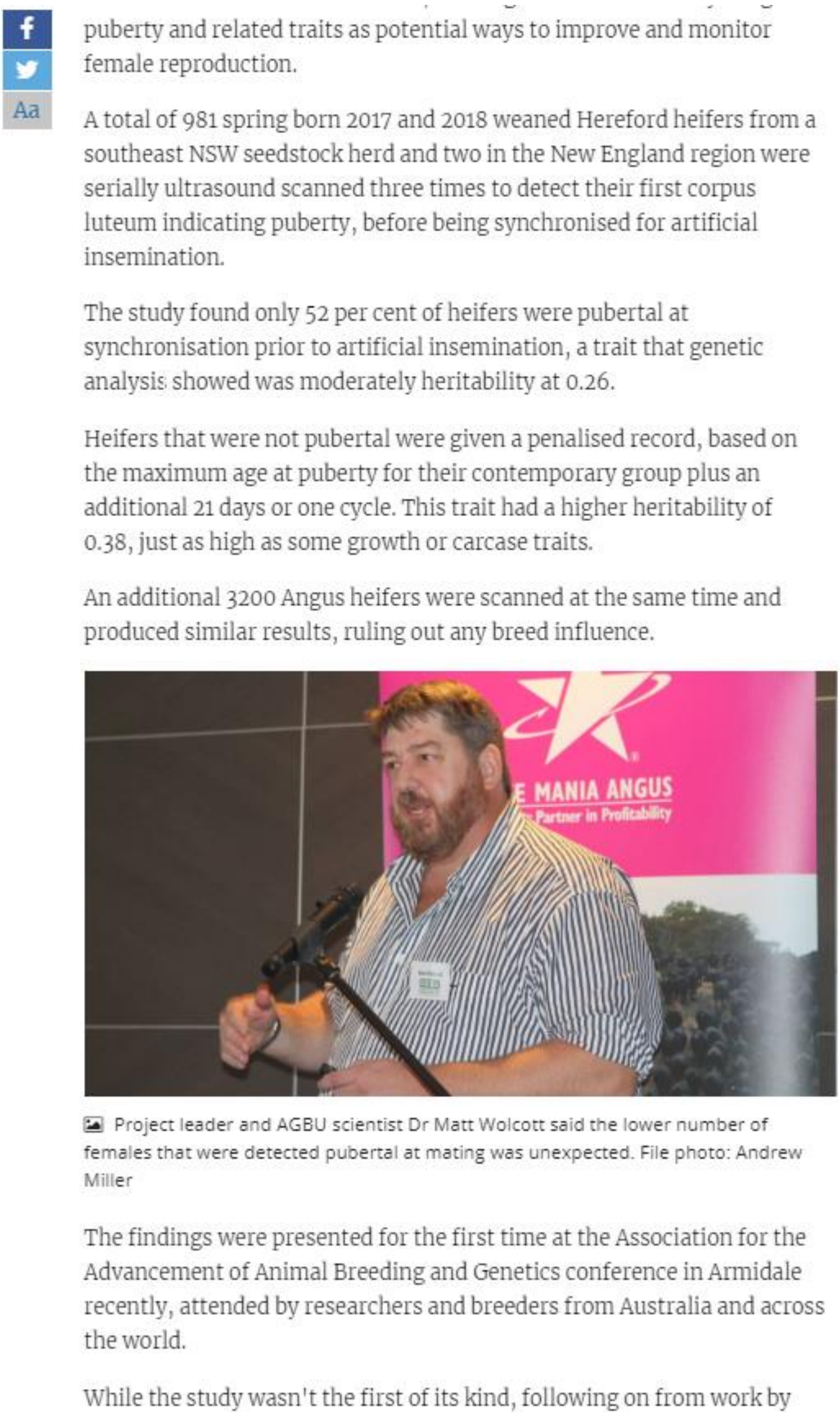
19 Nov 2019, 4 p.m.

Beef

Hereford heifers that were scanned as part of a study into age at puberty (left). Also pictured is Dr John Wilkins and Dr Craig Wood ultrasound scanning to detect first oestrus. Photos: Supplied

Early findings from a Trans-Tasman backed study examining the genetics of heifer age at puberty has raised some questions over the impact of oestrus synchronisation treatments on records used to describe female reproduction in the Breedplan analysis for temperate beef breeds.

The collaboration between the Animal Genetic Breeding Unit and New Zealand scientists, jointly funded by Meat and Livestock Australia along with Beef and Lamb New Zealand, investigated the heritability of age at



puberty and related traits as potential ways to improve and monitor female reproduction.

A total of 981 spring born 2017 and 2018 weaned Hereford heifers from a southeast NSW seedstock herd and two in the New England region were serially ultrasound scanned three times to detect their first corpus luteum indicating puberty, before being synchronised for artificial insemination.

The study found only 52 per cent of heifers were pubertal at synchronisation prior to artificial insemination, a trait that genetic analysis showed was moderately heritability at 0.26.

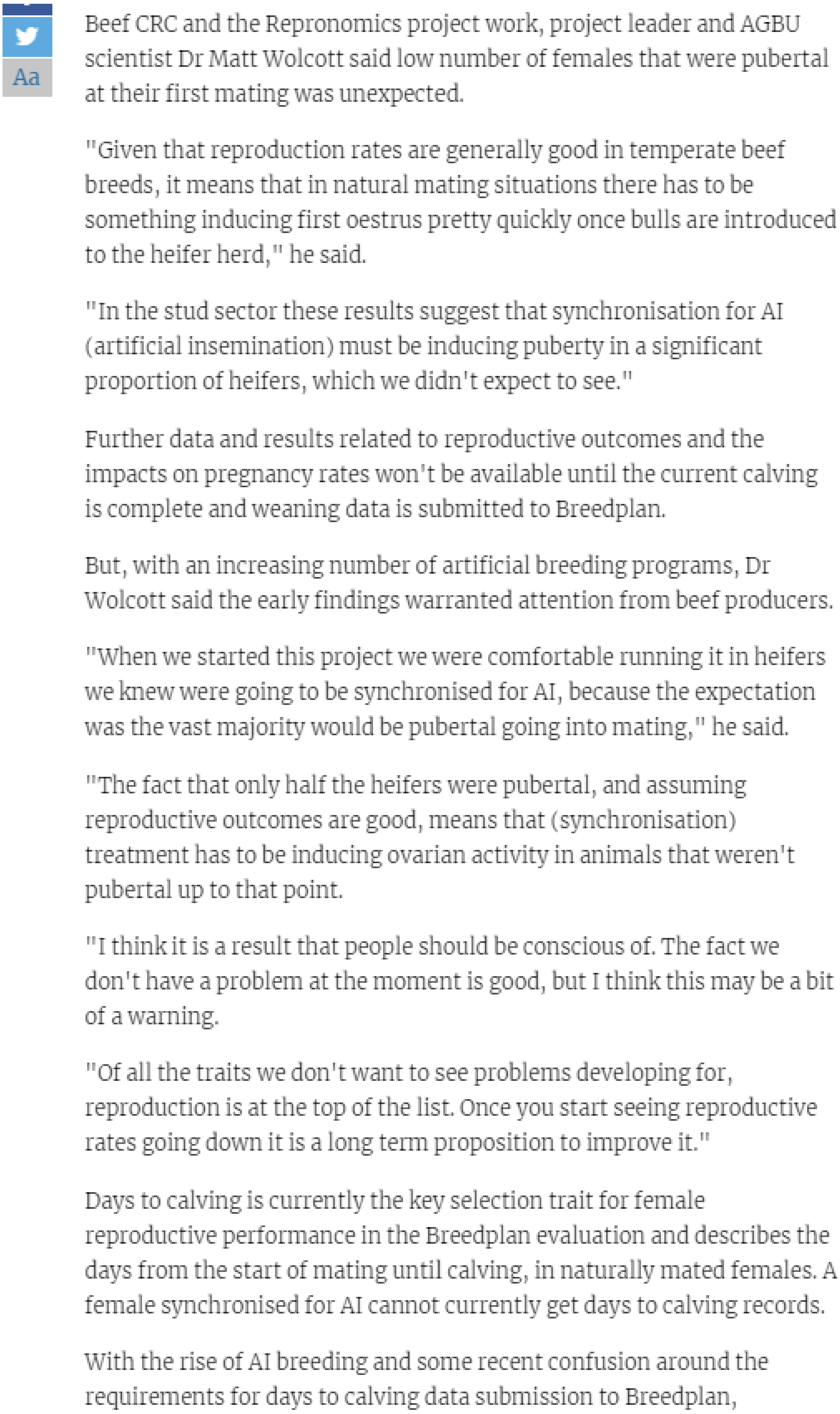
Heifers that were not pubertal were given a penalised record, based on the maximum age at puberty for their contemporary group plus an additional 21 days or one cycle. This trait had a higher heritability of 0.38, just as high as some growth or carcase traits.

An additional 3200 Angus heifers were scanned at the same time and produced similar results, ruling out any breed influence.

Project leader and AGBU scientist Dr Matt Wolcott said the lower number of females that were detected pubertal at mating was unexpected. File photo: Andrew Miller

The findings were presented for the first time at the Association for the Advancement of Animal Breeding and Genetics conference in Armidale recently, attended by researchers and breeders from Australia and across the world.

While the study wasn't the first of its kind, following on from work by



Beef CRC and the Repronomics project work, project leader and AGBU scientist Dr Matt Wolcott said low number of females that were pubertal at their first mating was unexpected.

"Given that reproduction rates are generally good in temperate beef breeds, it means that in natural mating situations there has to be something inducing first oestrus pretty quickly once bulls are introduced to the heifer herd," he said.

"In the stud sector these results suggest that synchronisation for AI (artificial insemination) must be inducing puberty in a significant proportion of heifers, which we didn't expect to see."

Further data and results related to reproductive outcomes and the impacts on pregnancy rates won't be available until the current calving is complete and weaning data is submitted to Breedplan.

But, with an increasing number of artificial breeding programs, Dr Wolcott said the early findings warranted attention from beef producers.

"When we started this project we were comfortable running it in heifers we knew were going to be synchronised for AI, because the expectation was the vast majority would be pubertal going into mating," he said.

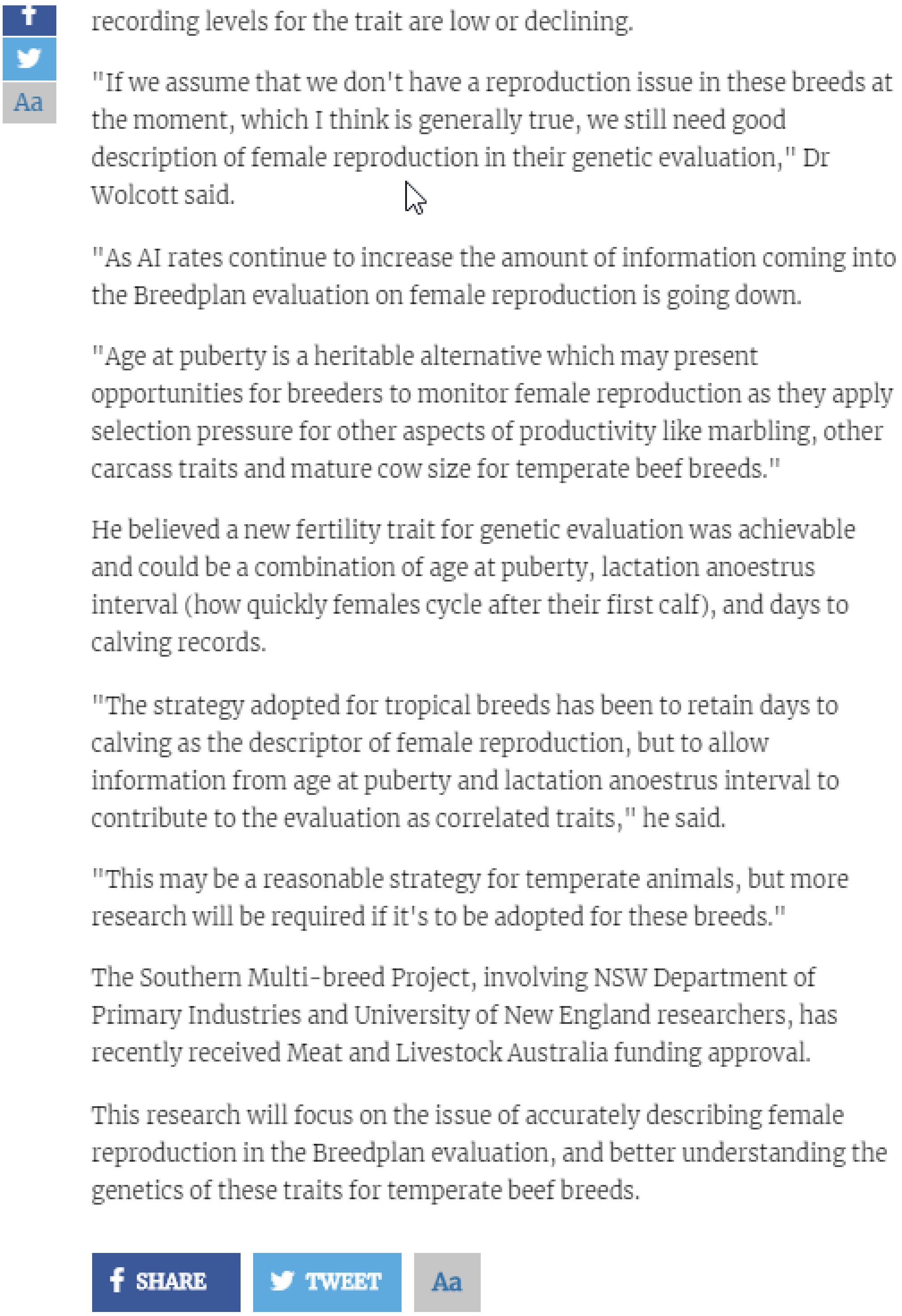
"The fact that only half the heifers were pubertal, and assuming reproductive outcomes are good, means that (synchronisation) treatment has to be inducing ovarian activity in animals that weren't pubertal up to that point.

"I think it is a result that people should be conscious of. The fact we don't have a problem at the moment is good, but I think this may be a bit of a warning.

"Of all the traits we don't want to see problems developing for, reproduction is at the top of the list. Once you start seeing reproductive rates going down it is a long term proposition to improve it."

Days to calving is currently the key selection trait for female reproductive performance in the Breedplan evaluation and describes the days from the start of mating until calving, in naturally mated females. A female synchronised for AI cannot currently get days to calving records.

With the rise of AI breeding and some recent confusion around the requirements for days to calving data submission to Breedplan,



recording levels for the trait are low or declining.

"If we assume that we don't have a reproduction issue in these breeds at the moment, which I think is generally true, we still need good description of female reproduction in their genetic evaluation," Dr Wolcott said.

"As AI rates continue to increase the amount of information coming into the Breedplan evaluation on female reproduction is going down.

"Age at puberty is a heritable alternative which may present opportunities for breeders to monitor female reproduction as they apply selection pressure for other aspects of productivity like marbling, other carcass traits and mature cow size for temperate beef breeds."

He believed a new fertility trait for genetic evaluation was achievable and could be a combination of age at puberty, lactation anoestrus interval (how quickly females cycle after their first calf), and days to calving records.

"The strategy adopted for tropical breeds has been to retain days to calving as the descriptor of female reproduction, but to allow information from age at puberty and lactation anoestrus interval to contribute to the evaluation as correlated traits," he said.

"This may be a reasonable strategy for temperate animals, but more research will be required if it's to be adopted for these breeds."

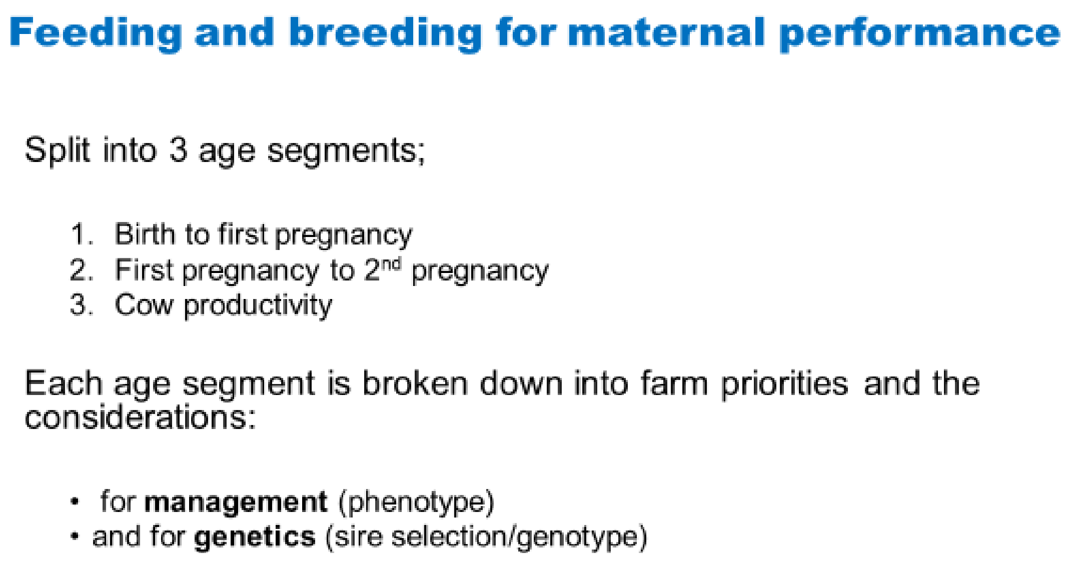
The Southern Multi-breed Project, involving NSW Department of Primary Industries and University of New England researchers, has recently received Meat and Livestock Australia funding approval.

This research will focus on the issue of accurately describing female reproduction in the Breedplan evaluation, and better understanding the genetics of these traits for temperate beef breeds.

7.3 Appendix 3 – Extension Messaging Slides

FEEDING AND BREEEDING
FOR MATERNAL PERFORMANCE

Trans-Tasman Beef Cow Profitability Programme



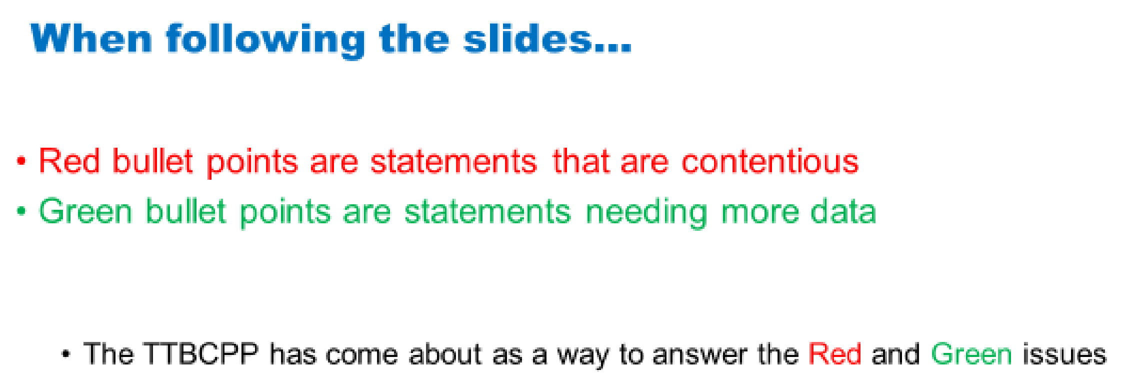
Feeding and breeding for maternal performance

Split into 3 age segments;

1. Birth to first pregnancy
2. First pregnancy to 2nd pregnancy
3. Cow productivity

Each age segment is broken down into farm priorities and the considerations:

- for **management** (phenotype)
- and for **genetics** (sire selection/genotype)



When following the slides…

- Red bullet points are statements that are contentious
- Green bullet points are statements needing more data

- The TTBCPP has come about as a way to answer the Red and Green issues

Birth to First Pregnancy

1. Hit puberty

Birth to First Pregnancy
PRIORITY 1: HIT PUBERTY

Management

- Planning, monitoring and hitting targets for BCS and liveweight at mating- as yearlings
    - *Grow heifers out well and get them fat for mating*
    - *Reach relative proportion of mature weight at mating (1*)*
    - *Get in-calf early in the season*

% heifers conceiving in 1st cycle
Industry benchmark: 65%

Genetics

- Reduced Days to Calving EBVs = increased heifer conception
    - *Although the DTC EBV doesn't directly refer to heifer puberty; the relationship is widely reinforced (BPT, Beef CRC, Dairy Industry)*
    - *Also to be considered; The Scrotal Size EBV has a moderate relationship with heifer puberty. However, this is captured within the DTC EBV*
- Sires with increased Rib Fat EBVs produce daughters that are fatter and conceive earlier (*2)

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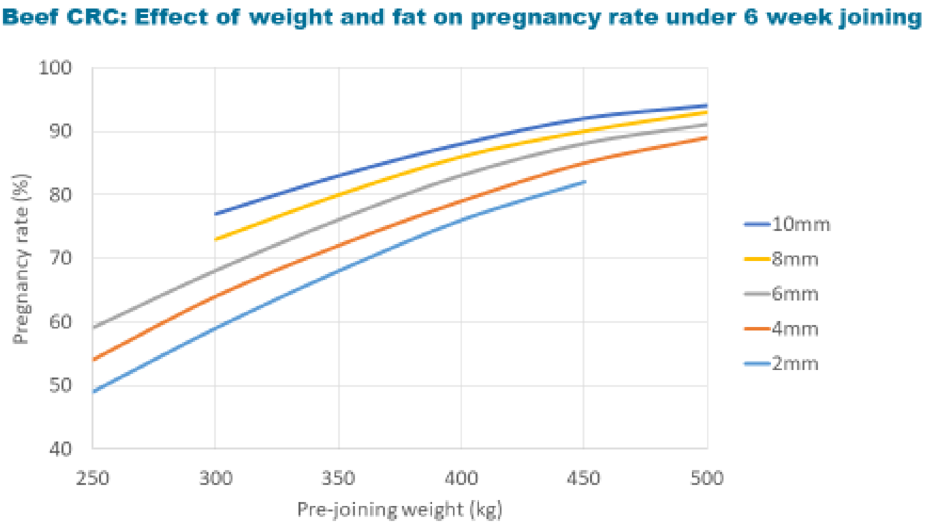
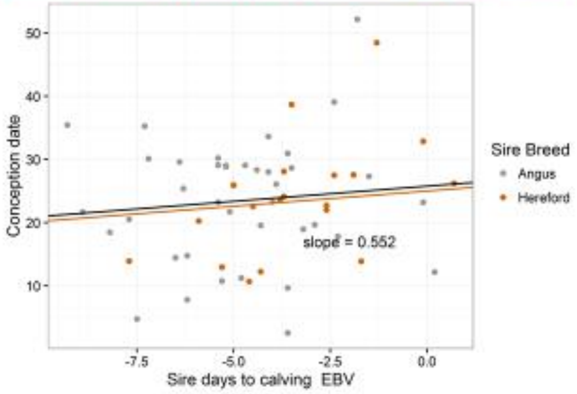
Birth to First Pregnancy
PRIORITY 1: HIT PUBERTY

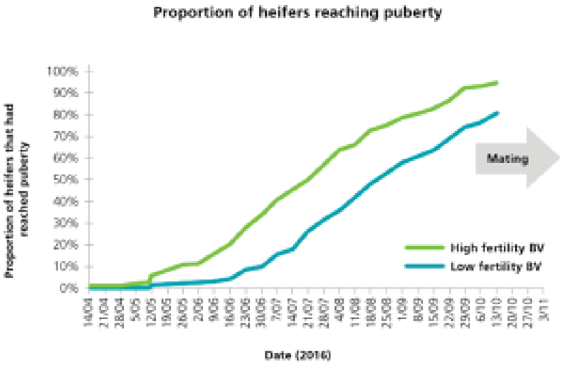

Beef CRC: Effect of weight and fat on pregnancy rate under 6 week joining

Birth to First Pregnancy
PRIORITY 1: HIT PUBERTY

BPT: Conception Date & Days2C eBV



Birth to First Pregnancy
PRIORITY 1: HIT PUBERTY
Dairy NZ

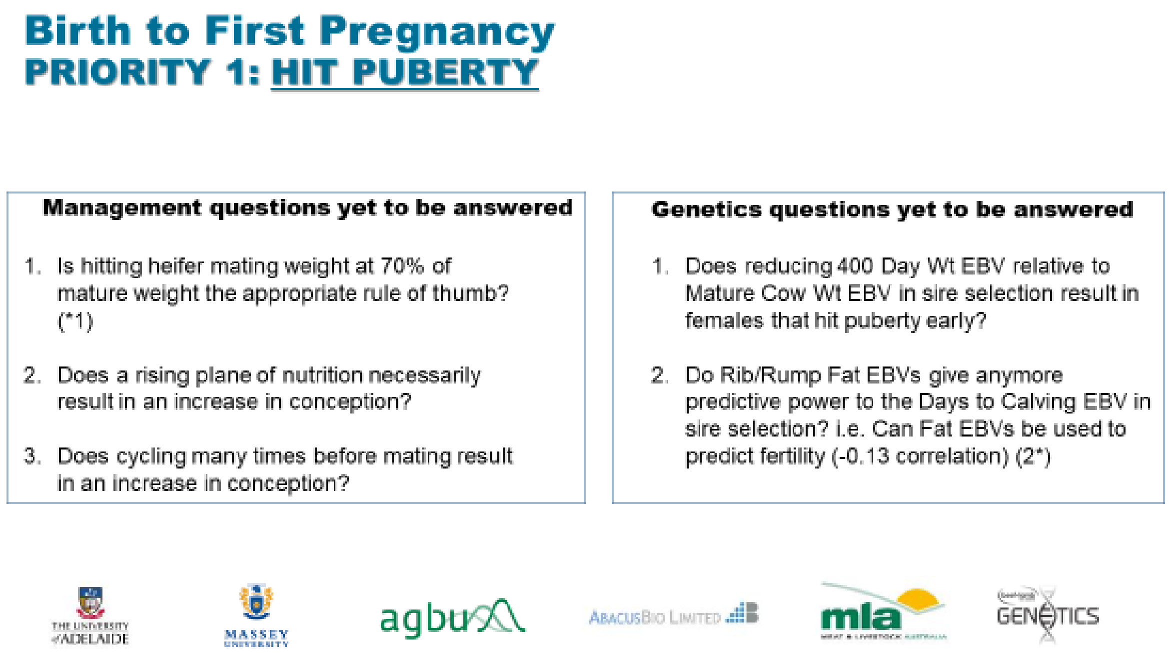


Note: Puberty is defined as 2 consecutive or 2 of 3 P4 >1 ng/ml

High Fertility relative to Low Fertility animals selected based on post pubertal reproductive performance over lactations 1-4

- reached puberty on 21 days earlier (358 vs 379 days)
- at a lighter body weight (271 vs 296 kg) despite similar expected mature weight
- so were at 51 vs 55% estimated mature live weight

Pregnancy rates after 3 weeks of mating were 74 vs 66% and after 6 weeks of mating were 91 vs 85%
Low line had slightly higher outcross embryo failure



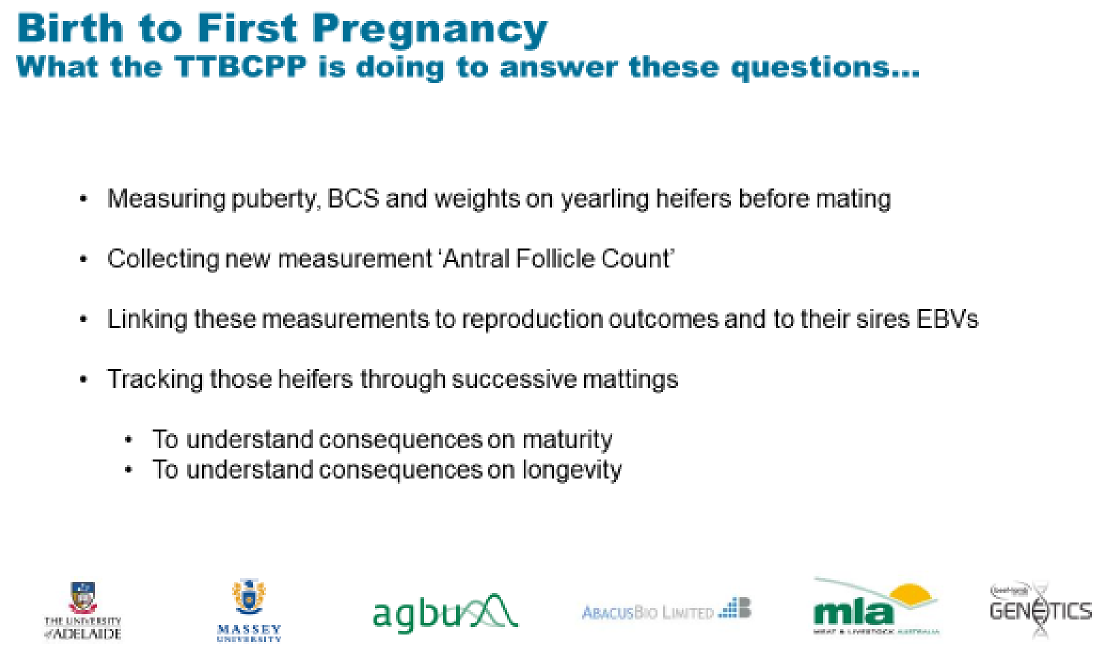
Birth to First Pregnancy
PRIORITY 1: HIT PUBERTY

Management questions yet to be answered

1. Is hitting heifer mating weight at 70% of mature weight the appropriate rule of thumb? (*1)
2. Does a rising plane of nutrition necessarily result in an increase in conception?
3. Does cycling many times before mating result in an increase in conception?

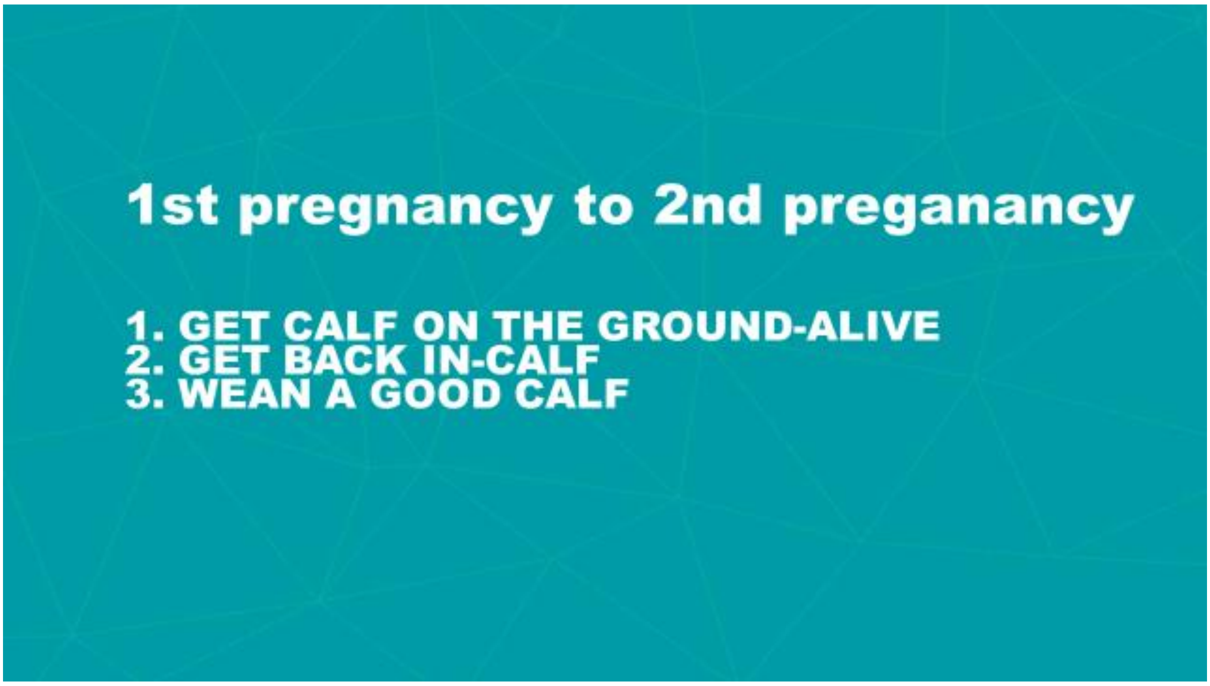
Genetics questions yet to be answered

1. Does reducing 400 Day Wt EBV relative to Mature Cow Wt EBV in sire selection result in females that hit puberty early?
2. Do Rib/Rump Fat EBVs give anymore predictive power to the Days to Calving EBV in sire selection? i.e. Can Fat EBVs be used to predict fertility (-0.13 correlation) (2*)



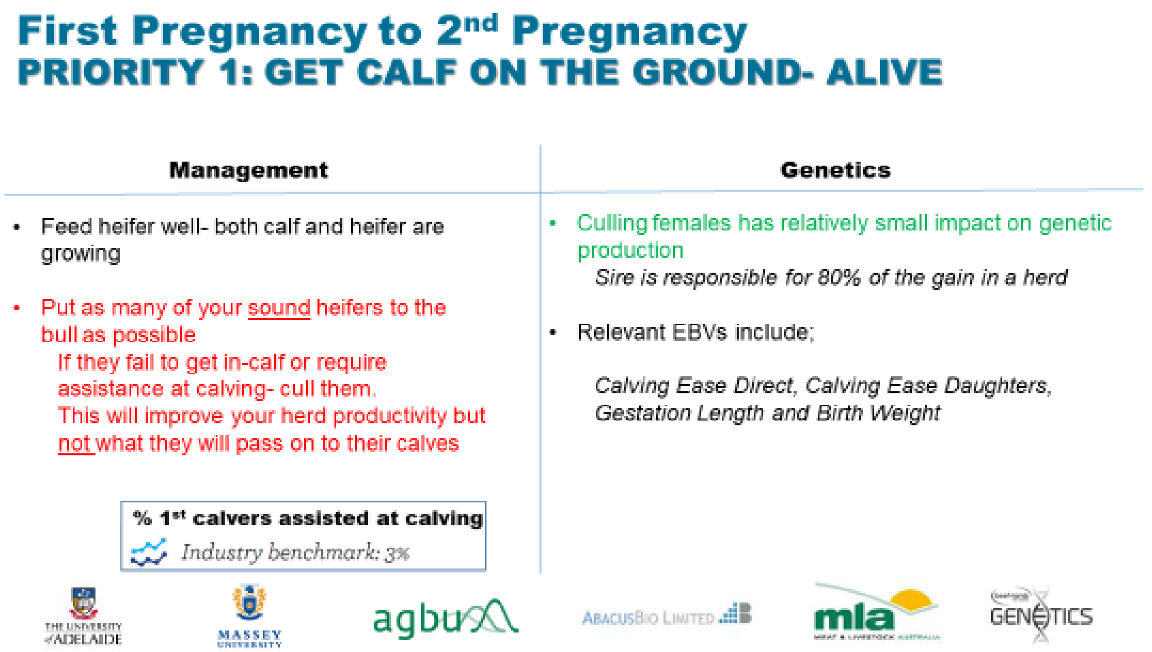
Birth to First Pregnancy
What the TTBCPP is doing to answer these questions…

- Measuring puberty, BCS and weights on yearling heifers before mating
- Collecting new measurement 'Antral Follicle Count'
- Linking these measurements to reproduction outcomes and to their sires EBVs
- Tracking those heifers through successive mattings
    - To understand consequences on maturity
    - To understand consequences on longevity



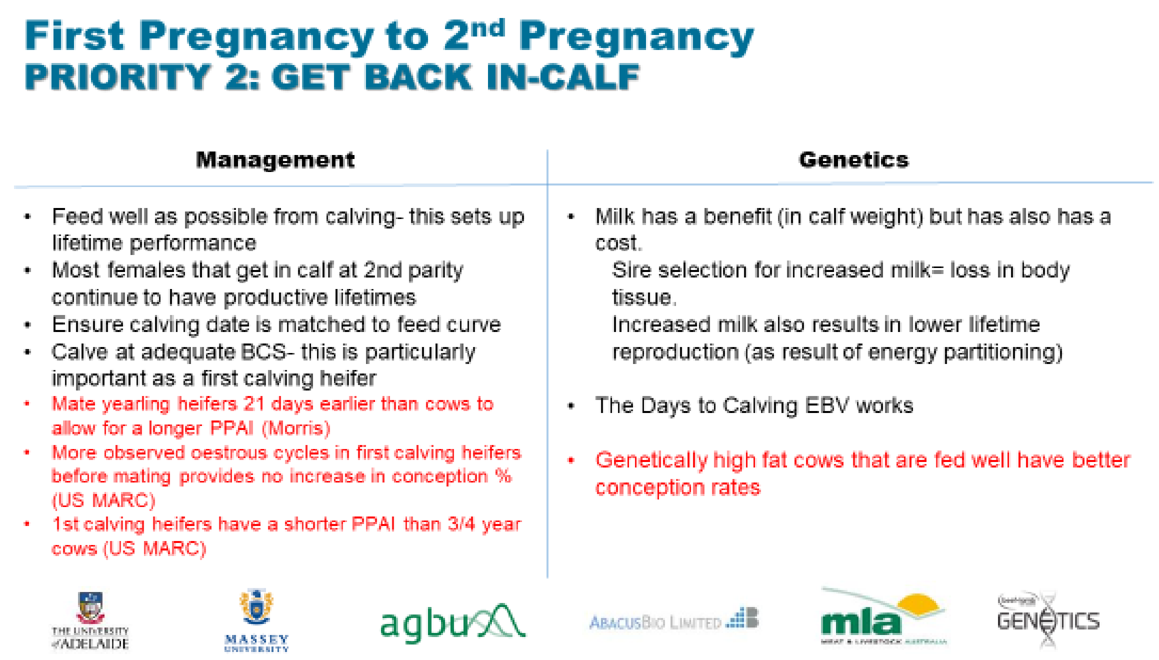
1st pregnancy to 2nd preganancy

1. GET CALF ON THE GROUND-ALIVE
2. GET BACK IN-CALF
3. WEAN A GOOD CALF



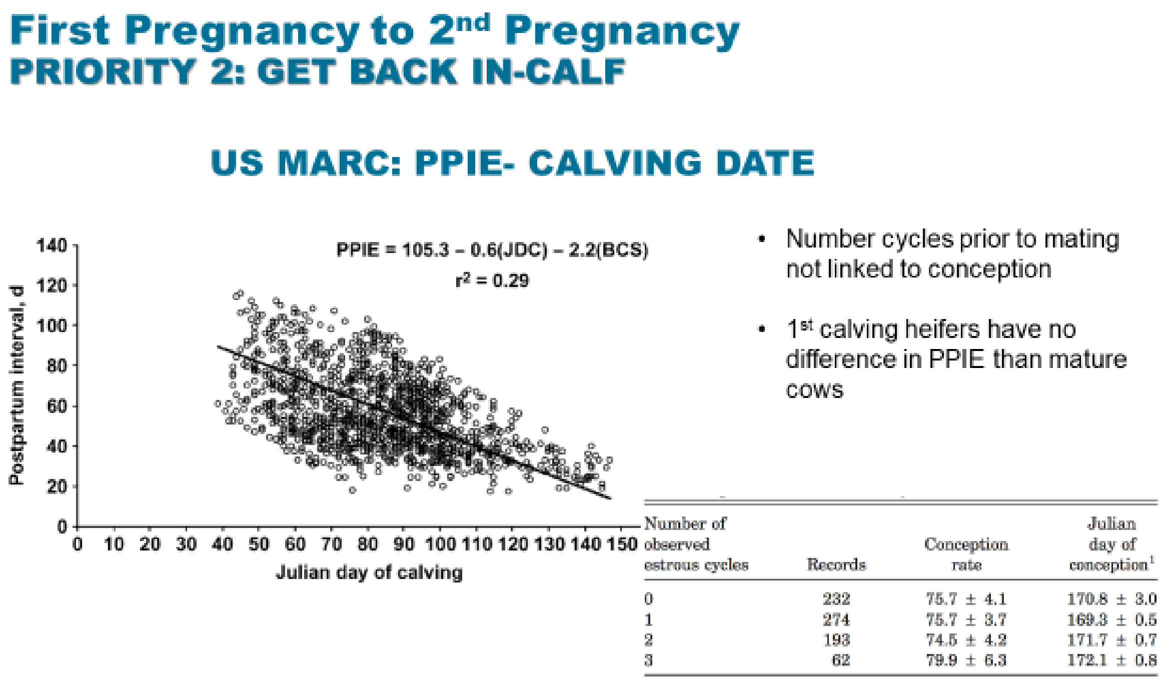
First Pregnancy to 2nd Pregnancy
PRIORITY 1: GET CALF ON THE GROUND- ALIVE

Management	**Genetics**
• Feed heifer well- both calf and heifer are growing • Put as many of your <u>sound</u> heifers to the bull as possible If they fail to get in-calf or require assistance at calving- cull them. This will improve your herd productivity but <u>not</u> what they will pass on to their calves **% 1st calvers assisted at calving** *Industry benchmark: 3%*	• Culling females has relatively small impact on genetic production *Sire is responsible for 80% of the gain in a herd* • Relevant EBVs include; *Calving Ease Direct, Calving Ease Daughters, Gestation Length and Birth Weight*



First Pregnancy to 2nd Pregnancy
PRIORITY 2: GET BACK IN-CALF

Management	**Genetics**
• Feed well as possible from calving- this sets up lifetime performance • Most females that get in calf at 2nd parity continue to have productive lifetimes • Ensure calving date is matched to feed curve • Calve at adequate BCS- this is particularly important as a first calving heifer • Mate yearling heifers 21 days earlier than cows to allow for a longer PPAI (Morris) • More observed oestrous cycles in first calving heifers before mating provides no increase in conception % (US MARC) • 1st calving heifers have a shorter PPAI than 3/4 year cows (US MARC)	• Milk has a benefit (in calf weight) but has also has a cost. Sire selection for increased milk= loss in body tissue. Increased milk also results in lower lifetime reproduction (as result of energy partitioning) • The Days to Calving EBV works • Genetically high fat cows that are fed well have better conception rates



First Pregnancy to 2nd Pregnancy
PRIORITY 2: GET BACK IN-CALF

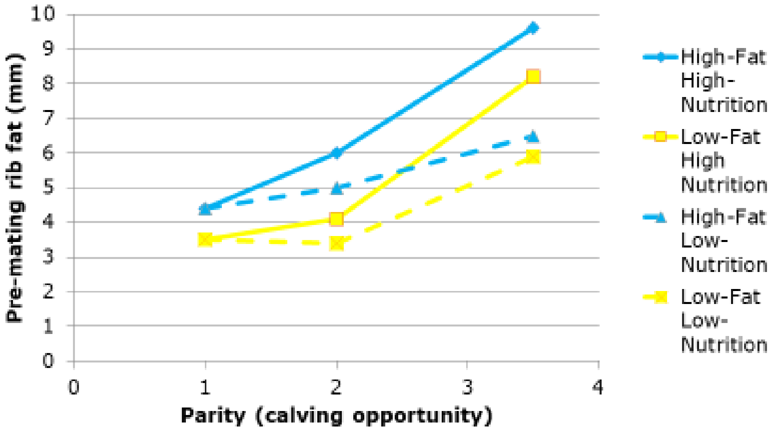
US MARC: PPIE- CALVING DATE

- Number cycles prior to mating not linked to conception
- 1st calving heifers have no difference in PPIE than mature cows

Number of observed estrous cycles	Records	Conception rate	Julian day of conception[1]
0	232	75.7 ± 4.1	170.8 ± 3.0
1	274	75.7 ± 3.7	169.3 ± 0.5
2	193	74.5 ± 4.2	171.7 ± 0.7
3	62	79.9 ± 6.3	172.1 ± 0.8

First Pregnancy to 2nd Pregnancy
PRIORITY 2: GET BACK IN-CALF

Beef CRC: Effect of Feed and Fat EBV



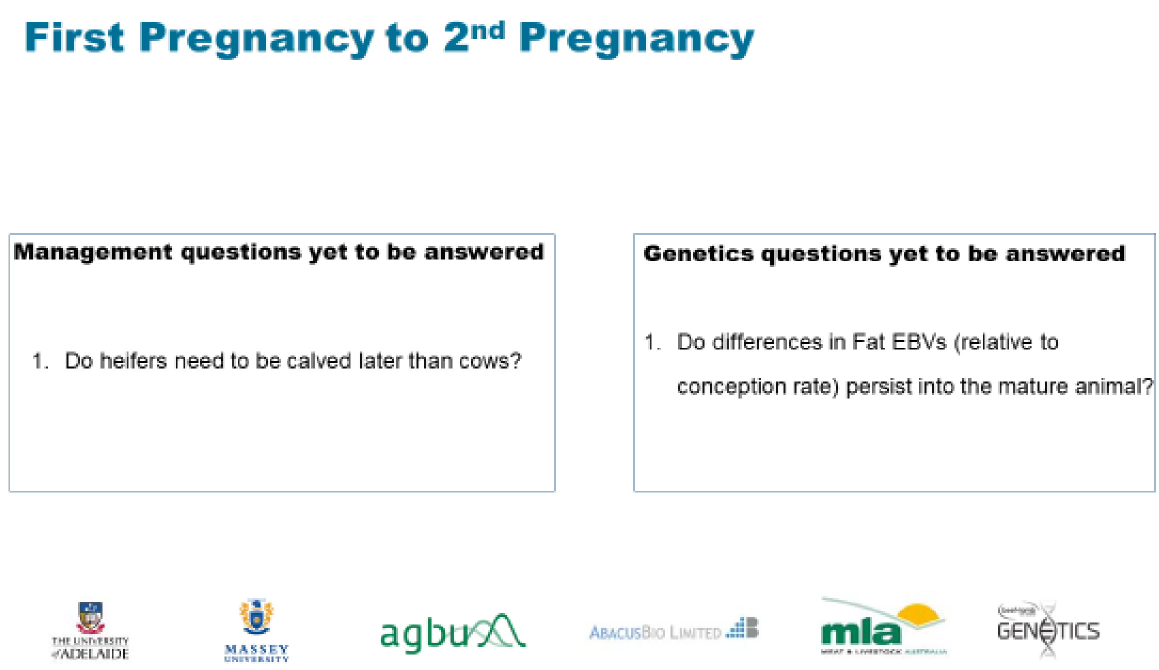
First Pregnancy to 2nd Pregnancy
PRIORITY 3: WEAN A GOOD CALF

Management

- Feed the heifer well
- Milk the heifer well
- Breed her early. Early born calves are heavier
- Calve her at adequate BCS

Genetics

- Select sires for calf growth.
  Use the 200 Day Weight EBV
- Select sires to breed daughters that milk well.
  Use the Milk EBV
- Select sires to breed daughters that conceive early and have heavier calves at weaning.
  Use the Days to Calving EBV



First Pregnancy to 2nd Pregnancy

Management questions yet to be answered

1. Do heifers need to be calved later than cows?

Genetics questions yet to be answered

1. Do differences in Fat EBVs (relative to conception rate) persist into the mature animal?

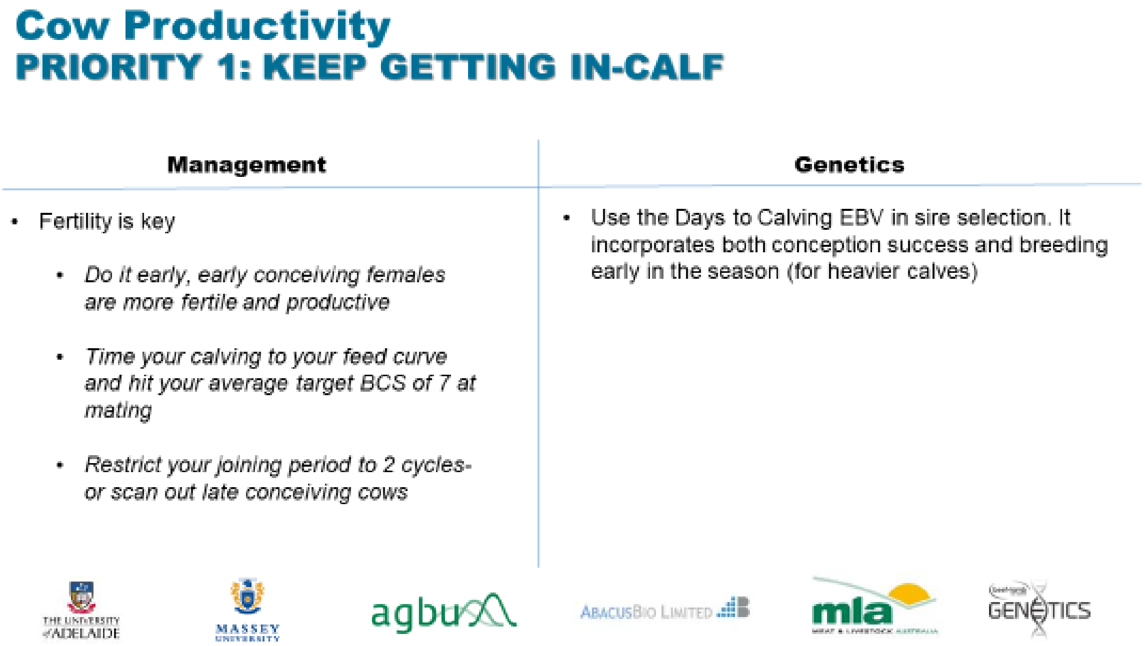
First to 2nd Pregnancy

What the TTBCPP is doing to answer these questions...

- Recording conception dates from natural mating on all properties
    - To investigate PPAI of heifers against cows
- Will compare fat EBVs against ongoing reproductive outcomes

COW PRODUCTIVITY

1. Keep Getting in-calf
2. Turn Grass into calf- efficiently
3. Stay in the herd

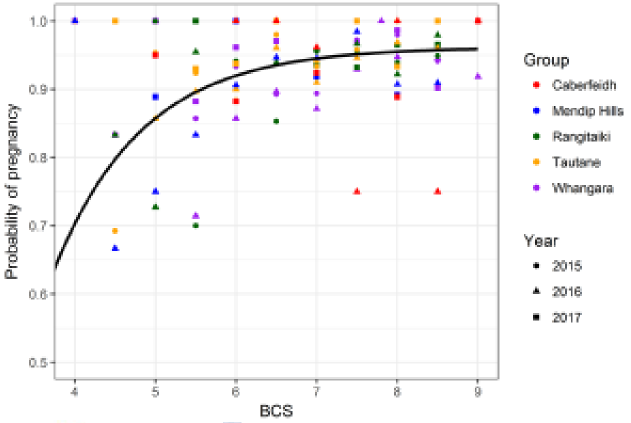


Cow Productivity
PRIORITY 1: KEEP GETTING IN-CALF

Management	Genetics
• Fertility is key • *Do it early, early conceiving females are more fertile and productive* • *Time your calving to your feed curve and hit your average target BCS of 7 at mating* • *Restrict your joining period to 2 cycles- or scan out late conceiving cows*	• Use the Days to Calving EBV in sire selection. It incorporates both conception success and breeding early in the season (for heavier calves)

Cow Productivity
PRIORITY 1: KEEP GETTING IN-CALF

BPT: Body condition score and pregnancy



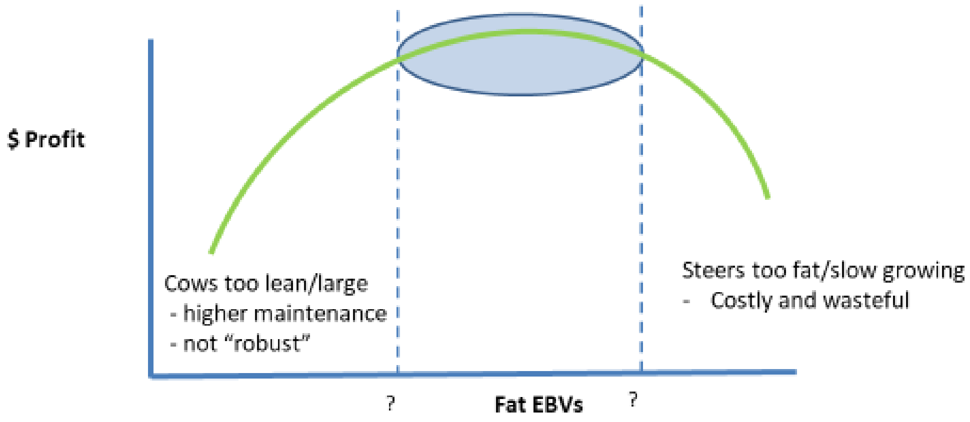
- Cow management practices (should) aim to achieve the cow herd being at sufficiently high condition score to achieve economically optimal conception rate.

Note that this is economically optimal rather than maximum biologically possible, due to the law of diminishing returns for conception vs increased feed requirements – but there is no objective analysis of what is economically optimal

Cow Productivity
PRIORITY 2: TURN GRASS INTO CALF-EFFICIENTLY

Management	**Genetics**
• High milk cows have high maintenance feed requirements. Even when not milking • Heavier mature weight cows have high maintenance feed requirements • *To note; smaller cows with less milk typically produce calves of less value* *Industry benchmark: 530 kg cow (weaning 240 kg calf)*	• Consider Mature Cow Weight and Milk EBVs in sire selection as they determine the maintenance feed requirements of your herd • Choose a bull breeder that matches your farm system and environment

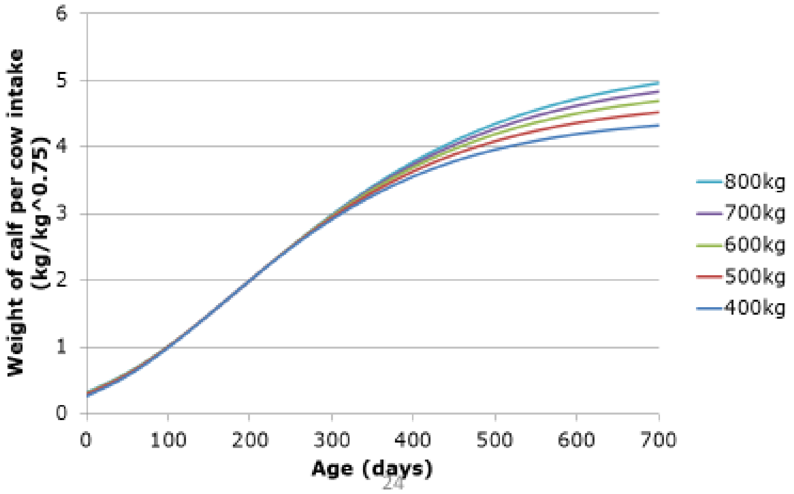
What are optimal cattle genetics for hill country systems?



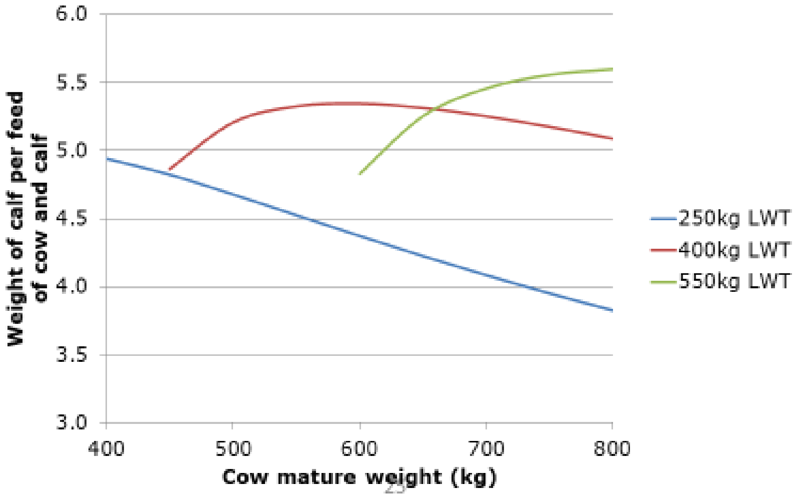
Cows too lean/large
- higher maintenance
- not “robust”

Steers too fat/slow growing
- Costly and wasteful

Effect of size on maternal productivity - marketed at constant age



Effect of size on maternal productivity - effect of market endpoint



Cow Productivity

PRIORITY 3: STAY IN THE HERD

Management	Genetics
- Continue to achieve priority 1: Keep getting in-calf	- Use the Days to Calving EBV in sire selection

Cow Productivity

Management questions yet to be answered

1. How is cow type defined?
2. Are certain cow types suited to certain systems/ environments?
3. How is maternal productivity and calf productivity balanced?

Genetics questions yet to be answered

1. How do you use current Breedplan EBVs to select for maternal efficiency?
2. How do you use current Breedplan EBVs to select for stayability?
3. How do you use current Breedplan EBVs to select for feed efficiency?

Cow Productivity

What the TTBCPP is doing to answer these questions…

- Recording ongoing cow mature weights, BCS and fates (reasons for leaving the herd), reproductive outcomes. Across many farms and environments
- Explore maternal GxE
    - To understand longevity/stayability
    - To characterise cow types and develop better maternal descriptors

7.4 Appendix 4 – Birth to First Pregnancy pdf

Birth to First Pregnancy. Heifer mating – *how to get there.*

PRIORITY: GET IN-CALF EARLY IN THE SEASON

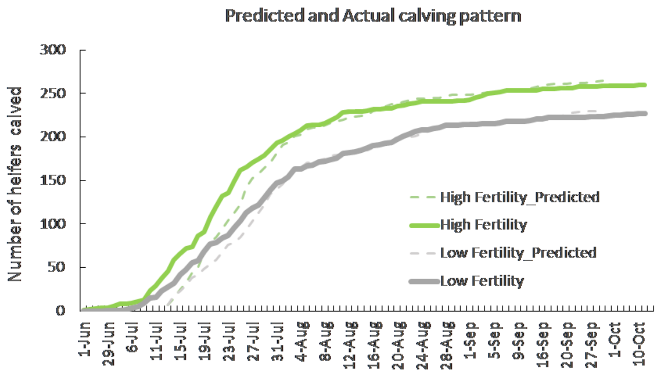
Why?

- Sets her up for lifetime performance *Australian Beef CRC research*
- Longer time to get back into calf *US MARC research*
- Will stay longer in the herd
- Wean a heavier calf

Evidence?

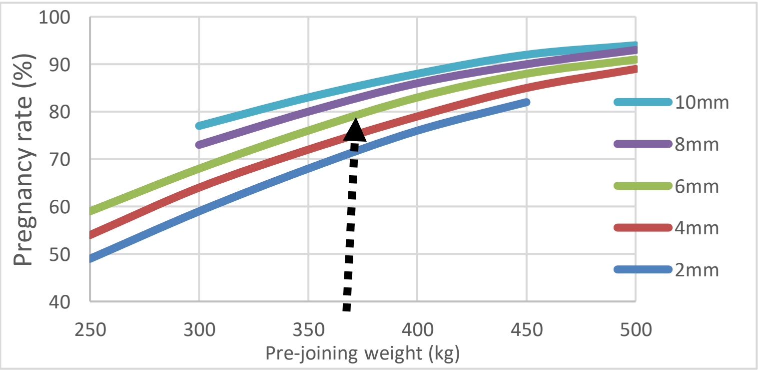
Dairy NZ high v low line fertility research

'Heifers predicted to be more fertile reached puberty earlier and conceived earlier'



Australian Beef CRC- High & Low fat lines

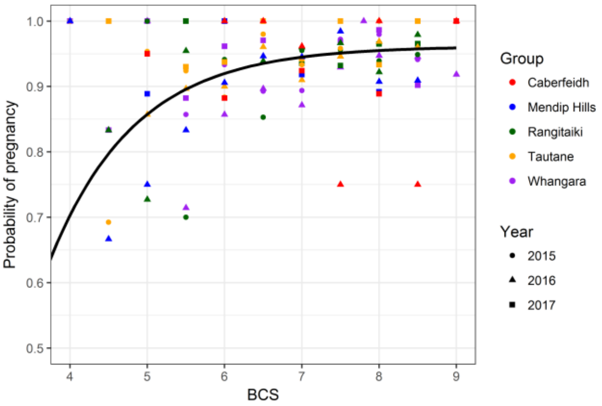
'Heavier and fatter heifers achieve puberty and conception earlier'



How? Management

- Grow heifers out well and get them to sufficient condition for mating and through it: *Beef CRC*
- Don't have a rule of thumb with mating weight i.e. different systems and genetics will impact

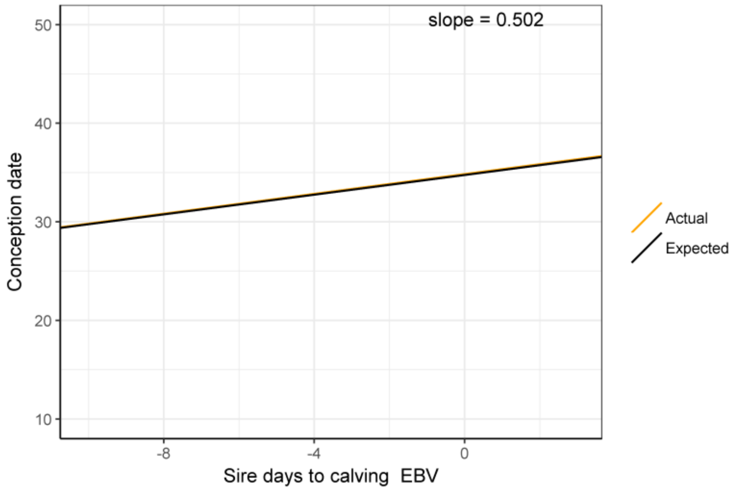
- Reach relative proportion of mature weight at mating
        - Rule of thumb used to be 70% of mature weight. *US MARC* data suggests that modern cattle can be as low as 55% of mature weight at mating
    - Mate lots of them and restrict to keeping those that conceive in 42 days by foetal age scanning



1 Increased Cow Body Condition score increases probability of pregnancy. B+LNZ Genetics Beef Progeny Test

How? Genetics

- Reduced Days to Calving (DTC) EBVs = increased heifer conception
    - Use the DTC EBV (although doesn't directly refer to) improves heifer puberty: *BPT, Beef CRC, Dairy Industry*
    - Use the Scrotal Size EBV- already in DTC
    - Sires with increased Rib Fat EBVs produce daughters that are fatter and conceive earlier: *AUS Beef CRC*



2 Reduced Days to Calving EBV means cows get in calf earlier. B+LNZ Genetics Beef Progeny Test

7.5 Appendix 5 – Guideline for bull Selection

Guideline for bull selection based on maternal productivity work

Prof Wayne Pitchford, University of Adelaide, Australia

Max Tweedie, Beef and Lamb Genetics, New Zealand

The following are general guidelines based on work that has been undertaken or is underway. Estimated breeding values (EBVs) are estimated and on young bulls this is not with 100% accuracy. They are better than visual appraisal of the bulls and the average EBVs of a team of 5 bulls will be highly accurate, but individual bulls can change a little with more information.

- A selection index is the best overall measure of the economic performance of a bull relative to others of the same age. For some traits, extreme EBVs could be treated like a structural fault. For others, extreme EBVs could be treated as an outstanding attribute.
- Days to calving is the best EBV for improving maternal productivity and should be as short as possible. The genetic relationships with fat and scrotal size are accounted for in calculating this EBV.
- Carcass value is a function of maximum weight, eye muscle area, intramuscular fat and optimum fat cover. Simply put, more is better for weight, muscle and intramuscular fat. The EBV to achieve optimum fat cover depends on the finishing system where long feedlot regimes can get over fat but short feedlot or pasture finished are rarely overfat. Also with very light stocking rates it is likely that cattle will be fatter and so genetic fat (high fat EBVs) is not important.
- Fat EBVs are related to fatness of heifers and cows and there has some relationship with reproductive performance and ability to maintain body condition. This should be treated as avoiding very lean animals (perhaps <-1mm rib fat EBV for Angus) rather than focusing on maximising fat EBV.
- Very high fat EBVs are rarely associated with cattle with high growth EBVs and growth is important for maximising income. Thus, by focussing on traits of high importance rarely will this lead to cattle that are too fat.
- The selection index places appropriate weightings on calving ease and mature cow weight but some breeders may want to place additional emphasis on these for their systems. Gestation length and birth weight both impact on calving ease and the relationships are accounted for already in the calving ease EBV. That said, as calving difficulties in many herds are so low, this is based on little information and so some additional focus on gestation length and birth weight could be warranted.
- While most producers and scientists don’t want cows to get bigger, often this is an inevitable outcome and most economic modelling shows this is more profitable.

Once you have selected bulls using EBVs, check to make sure they are structurally correct before making purchase decisions. It is also important to ensure bulls have had appropriate vaccination protocols. We also encourage Bull Breeding Soundness Examinations.

PS Implicit in this document is that commercial producers will look at the Fig.s before the visual appraisal. Too many times highly productive bulls are overlooked due to overemphasis on a minor visual trait. By looking at Fig.s first, this is less likely to occur and breeders can still avoid buying structural faults into their herd.

7.6 Appendix 6 - MLA Bred Well Fed Well Workshop Slides

Breeding Profitable Cattle

1. Fit for farm
2. Suitable for market
3. Adopt strategies for ↑ genetic gain
   - Select better bulls
   - Cow/heifer joining pressure

Fit for farm

Females – of paramount importance!

- Reproductive capacity
- Ease of calving
- Maintenance requirements in your environment

The female is the foundation of your herd

Her fitness for farm needs to compliment target market requirements of progeny

Fit for Farm = ↑ Reproduction (genetic drivers)

Fertility

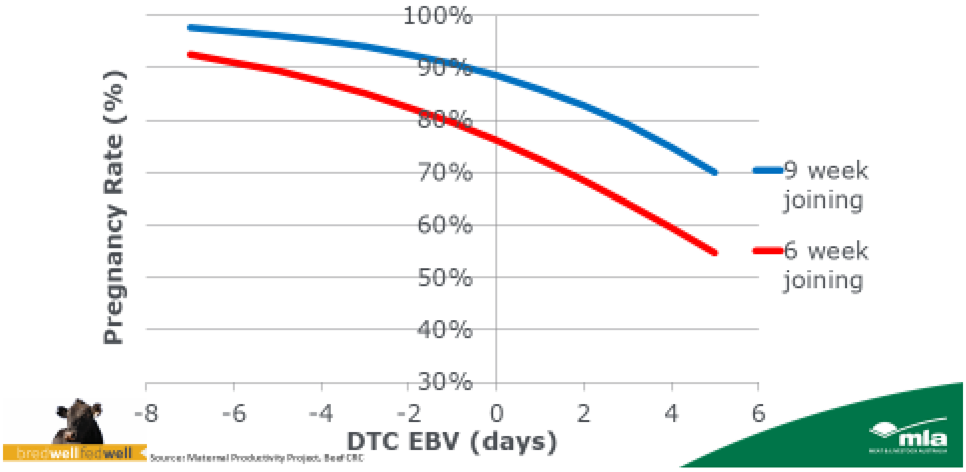
1. ↓ Days to calving EBV
2. ↑ Scrotal Size EBV

Influencers

- Rib and Rump fat
- Gestation length
- Birth weight

Target: 95 calves weaned per 100 cows joined

Days to Calving EBV = Higher pregnancy rates



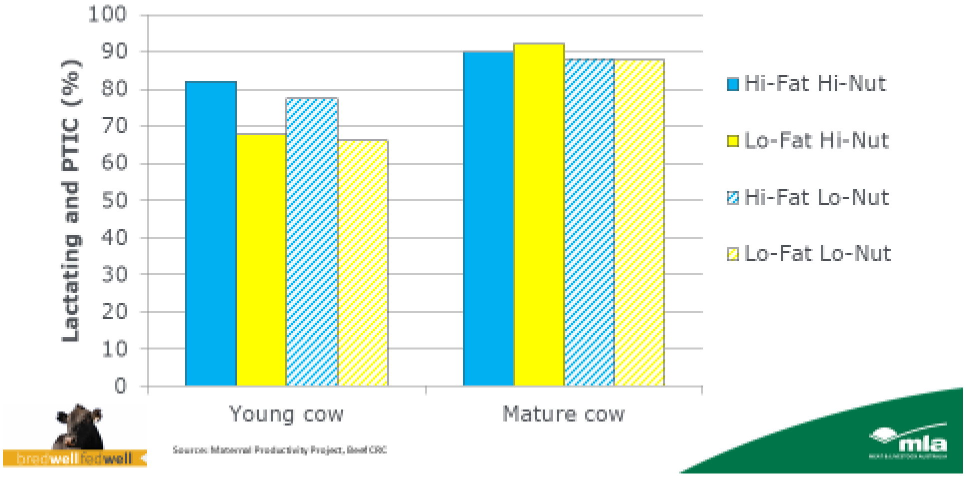
Source: Maternal Productivity Project, Beef CRC

↑ scrotal size EBV ≈ improved reproductive performance

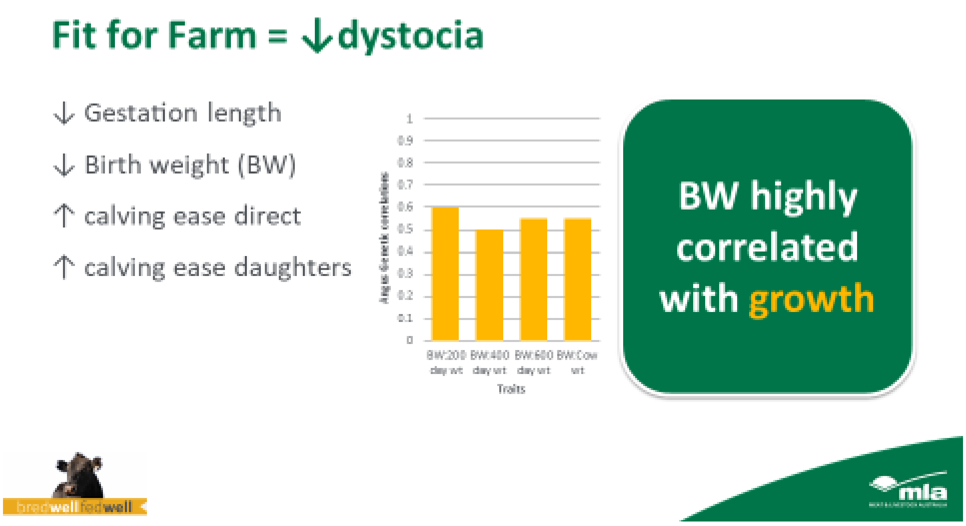
Does anyone have a graph on: impact of selection for increase scrotal size EBV on reproductive performance of daughters?

This would be particularly helpful to refer to for breeds that don't have a Days to Calve EBV.

Fat and nutrition influence reproductive performance



Source: Maternal Productivity Project, Beef CRC



Fit for Farm = ↓dystocia

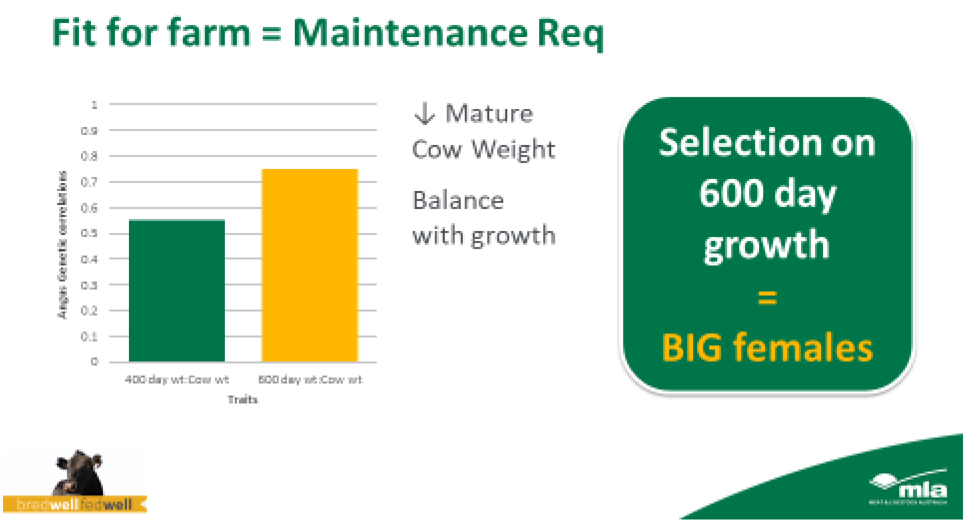
↓ Gestation length

↓ Birth weight (BW)

↑ calving ease direct

↑ calving ease daughters

BW highly correlated with growth

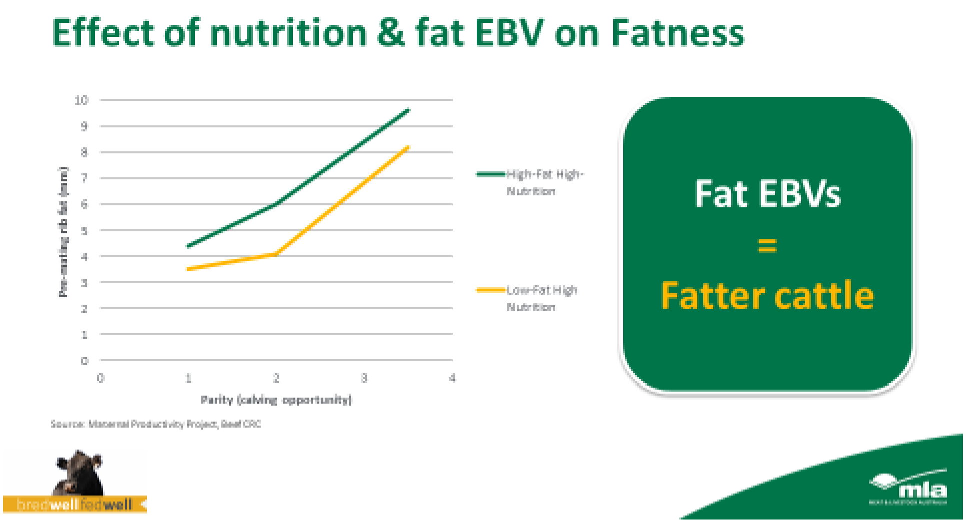


Fit for farm = Maintenance Req

↓ Mature Cow Weight

Balance with growth

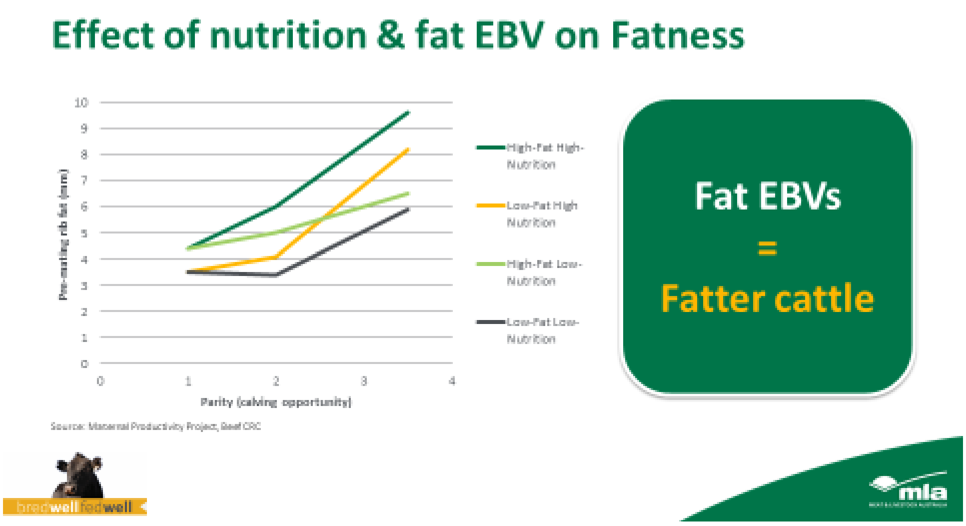
Selection on 600 day growth = BIG females



Effect of nutrition & fat EBV on Fatness

Source: Maternal Productivity Project, Beef CRC

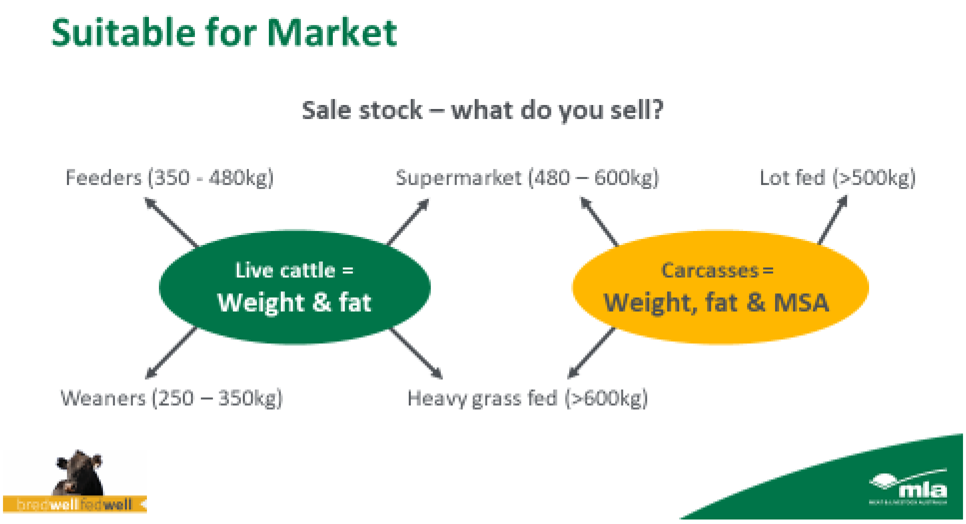
Fat EBVs = Fatter cattle



Effect of nutrition & fat EBV on Fatness

Fat EBVs = Fatter cattle

Source: Maternal Productivity Project, Beef CRC



Suitable for Market

Sale stock – what do you sell?

Feeders (350 - 480kg)

Supermarket (480 – 600kg)

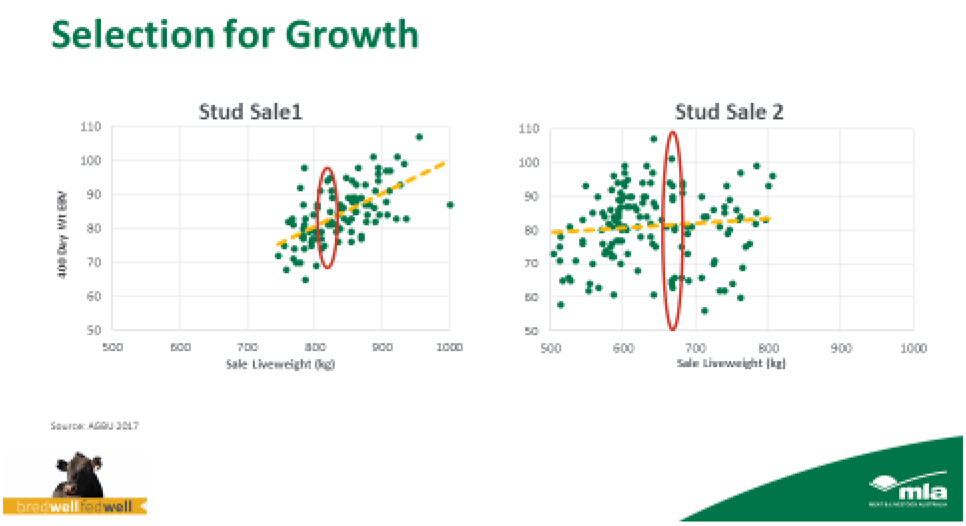
Lot fed (>500kg)

Live cattle = Weight & fat

Carcasses = Weight, fat & MSA

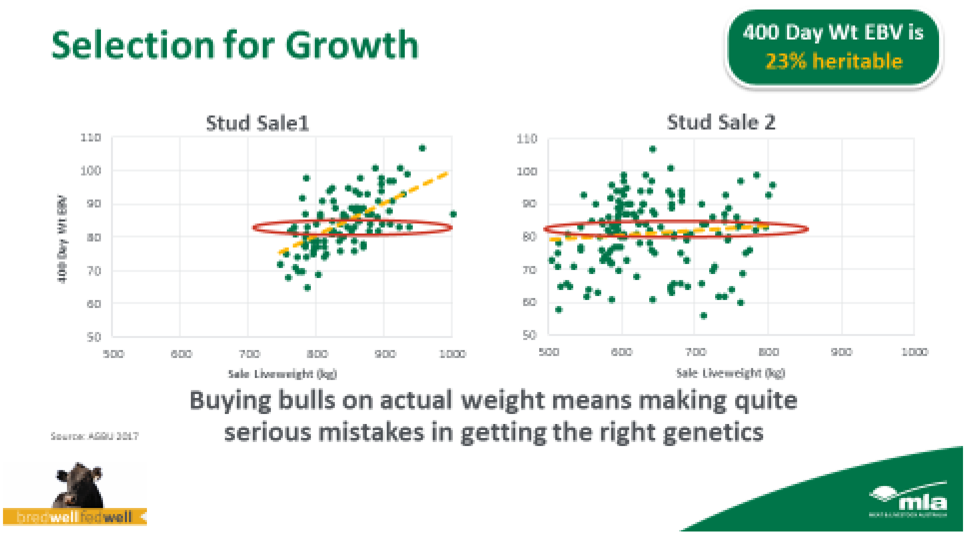
Weaners (250 – 350kg)

Heavy grass fed (>600kg)



Selection for Growth

Source: ABBU 2017



Selection for Growth

400 Day Wt EBV is 23% heritable

Buying bulls on actual weight means making quite serious mistakes in getting the right genetics

Source: AGBU 2017

Suitable for market = Growth

- ↑ 200 day wt
- ↑ 400 day wt
- ↑ 600 day wt

What age do
YOU
sell your cattle?

When would producers improve the quality of their beef?

- Price premiums for higher quality carcasses or MSA grids
- More satisfied consumers
- Targeting a new market opportunity
- To improve compliance to a market specification
- Improve the lot feeder rank of your cattle

5 genetic traits to ↑ eating quality

↑ IMF (marbling)

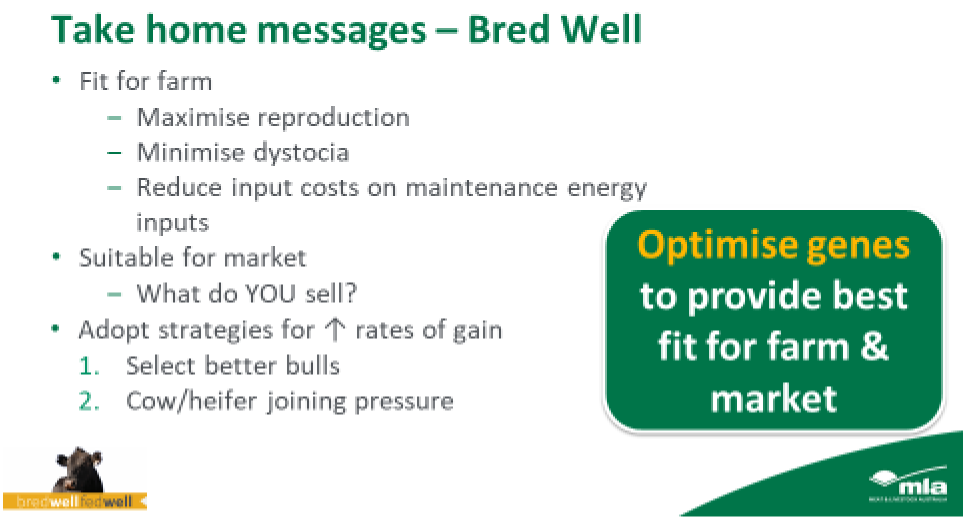
↑ Rib Fat

↓ Bos Indicus % (Hump height)

↑ Carcass Wt

Optimise Growth (reduce Ossification)

Within carcass specs



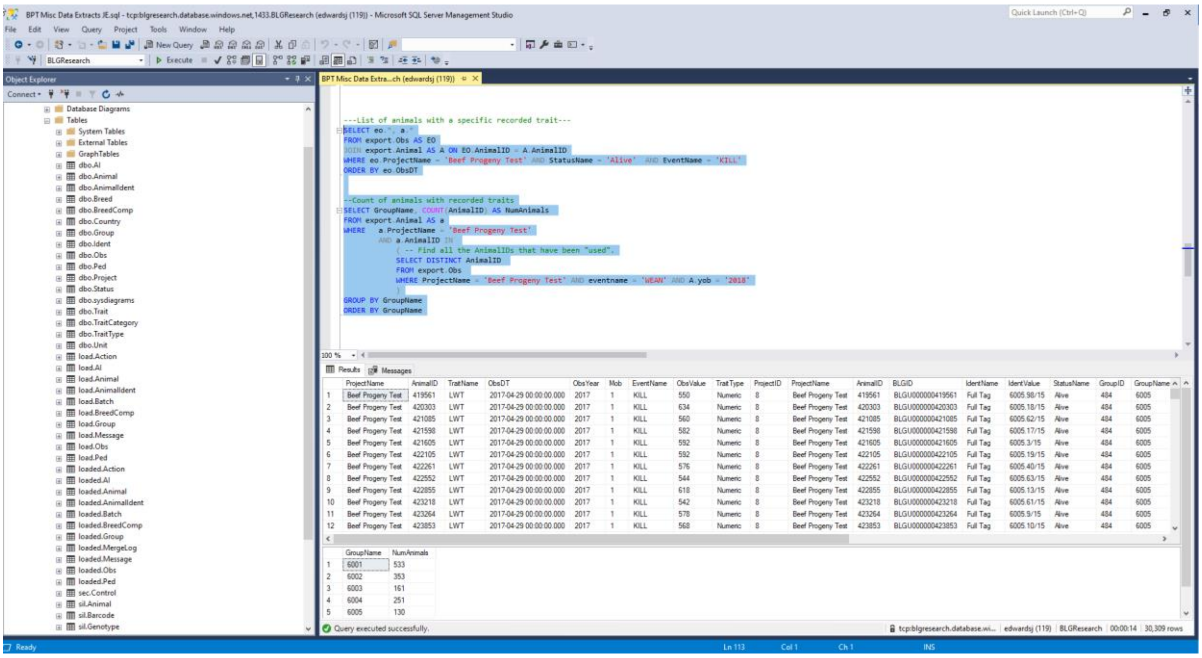
Take home messages – Bred Well

- Fit for farm
  - Maximise reproduction
  - Minimise dystocia
  - Reduce input costs on maintenance energy inputs
- Suitable for market
  - What do YOU sell?
- Adopt strategies for ↑ rates of gain
  1. Select better bulls
  2. Cow/heifer joining pressure

Optimise genes to provide best fit for farm & market

7.7 Appendix 7 – Data Management

To facilitate the MDC project, BLG invested in research data management infrastructure which included the capability to export data formatted for ABRI. This infrastructure enables BLG's ongoing research projects to include ABRI export and evaluation as a standard process moving forward. Included below is a screenshot of the database itself and well as a relational schema diagram.



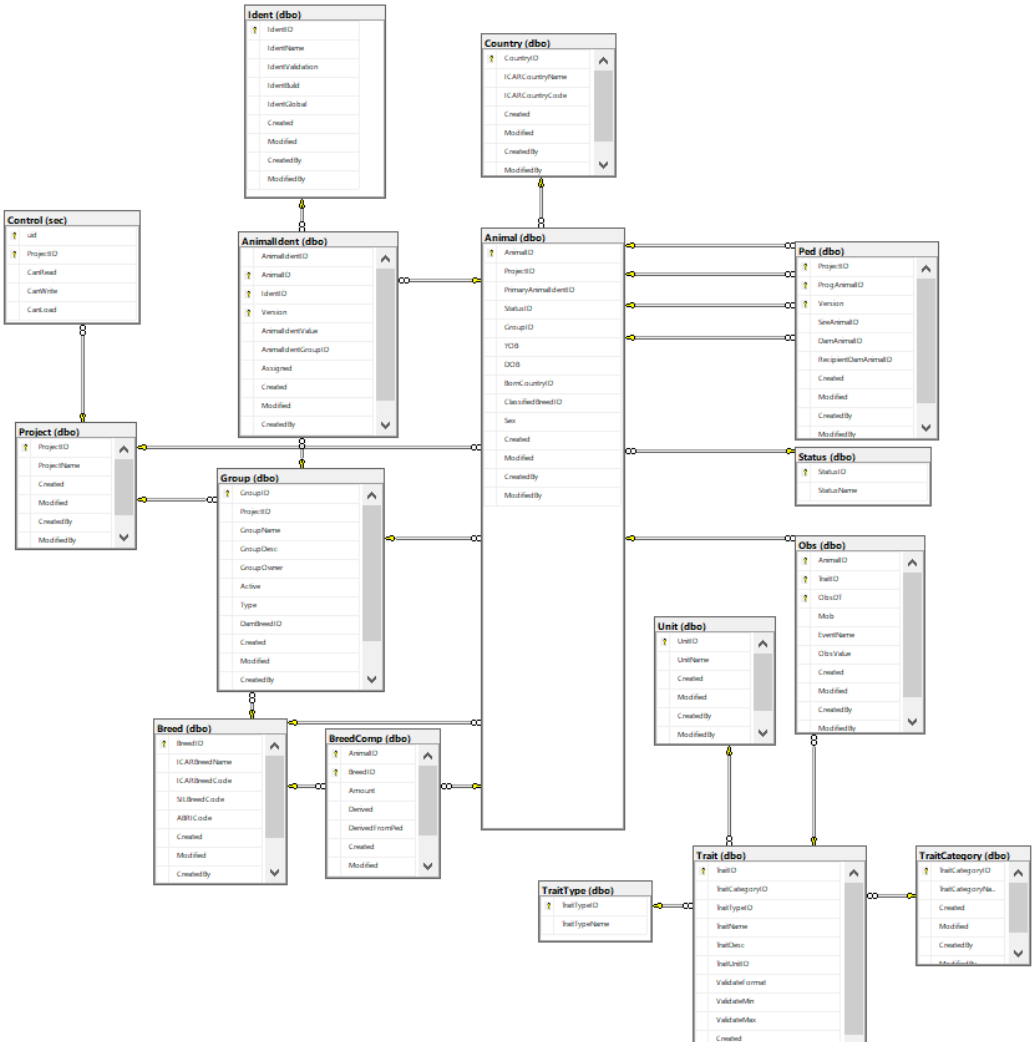
```sql
---List of animals with a specific recorded trait---
SELECT eo.*, a.*
FROM export.Obs AS EO
JOIN export.Animal AS A ON EO.AnimalID = A.AnimalID
WHERE eo.ProjectName = 'Beef Progeny Test' AND StatusName = 'Alive'  AND EventName = 'KILL'
ORDER BY eo.ObsDT


--Count of animals with recorded traits
SELECT GroupName, COUNT(AnimalID) AS NumAnimals
FROM export.Animal AS a
WHERE   a.ProjectName = 'Beef Progeny Test'
      AND a.AnimalID IN
          ( -- Find all the AnimalIDs that have been "used".
          SELECT DISTINCT AnimalID
          FROM export.Obs
          WHERE ProjectName = 'Beef Progeny Test' AND eventname = 'WEAN' AND A.yob = '2018'
          )
GROUP BY GroupName
ORDER BY GroupName
```

	ProjectName	AnimalID	TraitName	ObsDT	ObsYear	Mob	EventName	ObsValue	TraitType	ProjectID	ProjectName	AnimalID	BLGID	IdentName	IdentValue	StatusName	GroupID	GroupName
1	Beef Progeny Test	419561	LWT	2017-04-29 00:00:00.000	2017	1	KILL	550	Numeric	8	Beef Progeny Test	419561	BLGU000000419561	Full Tag	6005.98/15	Alive	484	6005
2	Beef Progeny Test	420303	LWT	2017-04-29 00:00:00.000	2017	1	KILL	634	Numeric	8	Beef Progeny Test	420303	BLGU000000420303	Full Tag	6005.18/15	Alive	484	6005
3	Beef Progeny Test	421085	LWT	2017-04-29 00:00:00.000	2017	1	KILL	560	Numeric	8	Beef Progeny Test	421085	BLGU000000421085	Full Tag	6005.62/15	Alive	484	6005
4	Beef Progeny Test	421598	LWT	2017-04-29 00:00:00.000	2017	1	KILL	582	Numeric	8	Beef Progeny Test	421598	BLGU000000421598	Full Tag	6005.17/15	Alive	484	6005
5	Beef Progeny Test	421605	LWT	2017-04-29 00:00:00.000	2017	1	KILL	592	Numeric	8	Beef Progeny Test	421605	BLGU000000421605	Full Tag	6005.3/15	Alive	484	6005
6	Beef Progeny Test	422105	LWT	2017-04-29 00:00:00.000	2017	1	KILL	592	Numeric	8	Beef Progeny Test	422105	BLGU000000422105	Full Tag	6005.19/15	Alive	484	6005
7	Beef Progeny Test	422261	LWT	2017-04-29 00:00:00.000	2017	1	KILL	576	Numeric	8	Beef Progeny Test	422261	BLGU000000422261	Full Tag	6005.40/15	Alive	484	6005
8	Beef Progeny Test	422552	LWT	2017-04-29 00:00:00.000	2017	1	KILL	544	Numeric	8	Beef Progeny Test	422552	BLGU000000422552	Full Tag	6005.63/15	Alive	484	6005
9	Beef Progeny Test	422855	LWT	2017-04-29 00:00:00.000	2017	1	KILL	618	Numeric	8	Beef Progeny Test	422855	BLGU000000422855	Full Tag	6005.13/15	Alive	484	6005
10	Beef Progeny Test	423218	LWT	2017-04-29 00:00:00.000	2017	1	KILL	542	Numeric	8	Beef Progeny Test	423218	BLGU000000423218	Full Tag	6005.61/15	Alive	484	6005
11	Beef Progeny Test	423264	LWT	2017-04-29 00:00:00.000	2017	1	KILL	578	Numeric	8	Beef Progeny Test	423264	BLGU000000423264	Full Tag	6005.9/15	Alive	484	6005
12	Beef Progeny Test	423853	LWT	2017-04-29 00:00:00.000	2017	1	KILL	568	Numeric	8	Beef Progeny Test	423853	BLGU000000423853	Full Tag	6005.10/15	Alive	484	6005

	GroupName	NumAnimals
1	6001	533
2	6002	353
3	6003	161
4	6004	251
5	6005	130

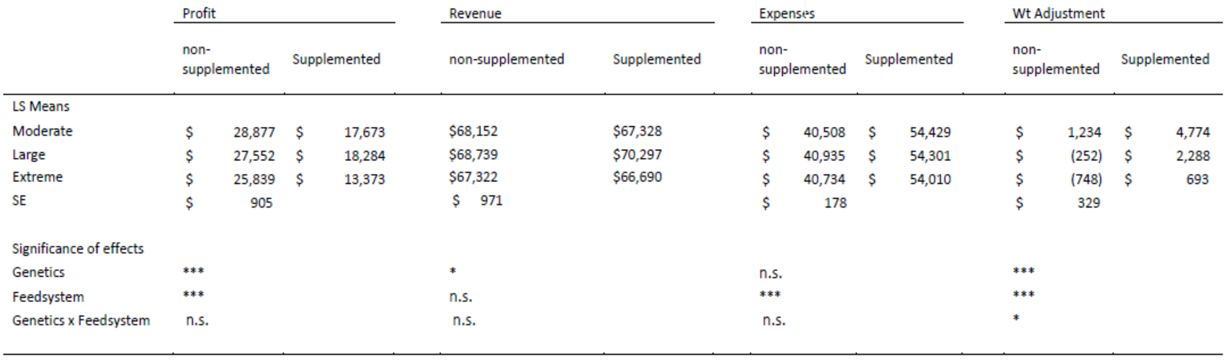
Query executed successfully.

tcp:blgresearch.database.wi... | edwardsj (119) | BLGResearch | 00:00:14 | 30,309 rows


Ident (dbo)
IdentID
IdentName
IdentValidation
IdentBuild
IdentGlobal
Created
Modified
CreatedBy
ModifiedBy
Country (dbo)
CountryID
ICARCountryName
ICARCountryCode
Created
Modified
CreatedBy
ModifiedBy
Control (sec)
uid
ProjectID
CanRead
CanWrite
CanLoad
AnimalIdent (dbo)
AnimalIdentID
AnimalID
IdentID
Version
AnimalIdentValue
AnimalIdentGroupID
Assigned
Created
Modified
CreatedBy
Animal (dbo)
AnimalID
ProjectID
PrimaryAnimalIdentID
StatusID
GroupID
YOB
DOB
BornCountryID
ClassifiedBreedID
Sex
Created
Modified
CreatedBy
ModifiedBy
Ped (dbo)
ProjectID
ProgAnimalID
Version
SireAnimalID
DamAnimalID
RecipientDamAnimalID
Created
Modified
CreatedBy
ModifiedBy
Project (dbo)
ProjectID
ProjectName
Created
Modified
CreatedBy
ModifiedBy
Status (dbo)
StatusID
StatusName
Group (dbo)
GroupID
ProjectID
GroupName
GroupDesc
GroupOwner
Active
Type
DamBreedID
Created
Modified
CreatedBy
Obs (dbo)
AnimalID
TraitID
ObsDT
Mob
EventName
ObsValue
Created
Modified
CreatedBy
ModifiedBy
Unit (dbo)
UnitID
UnitName
Created
Modified
CreatedBy
ModifiedBy
Breed (dbo)
BreedID
ICARBreedName
ICARBreedCode
SILBreedCode
ABRICode
Created
Modified
CreatedBy
BreedComp (dbo)
AnimalID
BreedID
Amount
Derived
DerivedFromPed
Created
Modified
Trait (dbo)
TraitID
TraitCategoryID
TraitTypeID
TraitName
TraitDesc
TraitUnitID
ValidateFormat
ValidateMin
ValidateMax
Created
TraitType (dbo)
TraitTypeID
TraitTypeName
TraitCategory (dbo)
TraitCategoryID
TraitCategoryNa...
Created
Modified
CreatedBy

7.8 Appendix 8 – Objective 5 analysis of outcomes

Table 1. Outcomes for financial parameters from cow herd

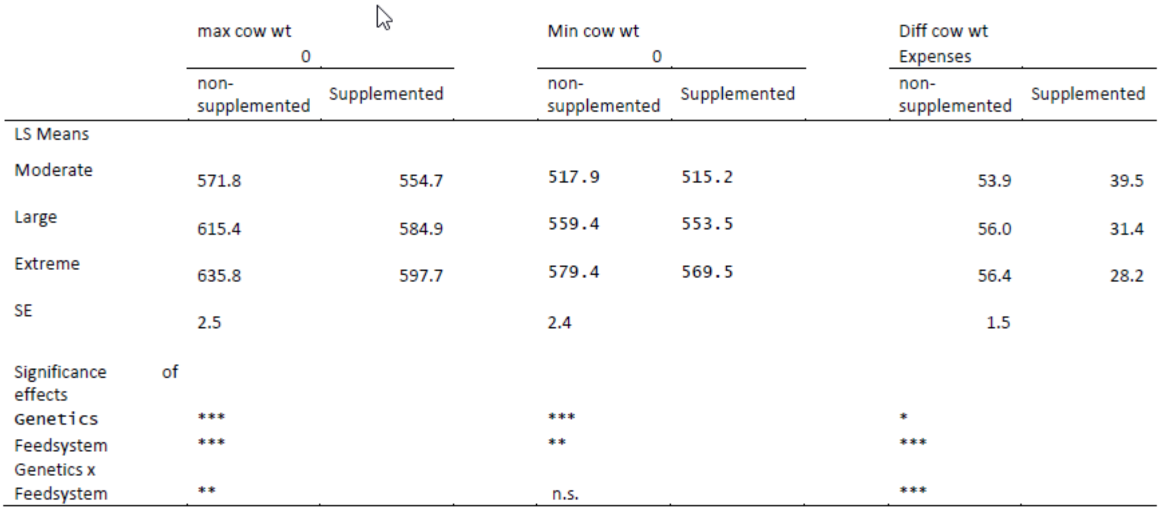


	Profit		Revenue		Expenses		Wt Adjustment	
	non-supplemented	Supplemented	non-supplemented	Supplemented	non-supplemented	Supplemented	non-supplemented	Supplemented
LS Means								
Moderate	$ 28,877	$ 17,673	$68,152	$67,328	$ 40,508	$ 54,429	$ 1,234	$ 4,774
Large	$ 27,552	$ 18,284	$68,739	$70,297	$ 40,935	$ 54,301	$ (252)	$ 2,288
Extreme	$ 25,839	$ 13,373	$67,322	$66,690	$ 40,734	$ 54,010	$ (748)	$ 693
SE	$ 905		$ 971		$ 178		$ 329	
Significance of effects								
Genetics	***		*		n.s.		***	
Feedsystem	***		n.s.		***		***	
Genetics x Feedsystem	n.s.		n.s.		n.s.		*	

Table 2. Calf weaning outcomes

	No Calves weaned		Calf weaning Weight	
	non-supplemented	Supplemented	non-supplemented	Supplemented
LS Means				
Moderate	92.0	92.2	211.6	208.7
Large	92.6	94.6	211.3	212.3
Extreme	92.8	91.8	207.2	207.6
SE	1.2		1.1	
Significance of effects				
Genetics	ns		**	
Feedsystem	ns		ns	
Genetics x Feedsystem	ns		ns	

Table 3. Outcomes for cow weight. Note that these are based on the average of all cows in the herd, not on individual cows, and represent the degree of fluctuation in cow weight across the year.



	max cow wt 0		Min cow wt 0		Diff cow wt Expenses	
	non-supplemented	Supplemented	non-supplemented	Supplemented	non-supplemented	Supplemented
LS Means						
Moderate	571.8	554.7	517.9	515.2	53.9	39.5
Large	615.4	584.9	559.4	553.5	56.0	31.4
Extreme	635.8	597.7	579.4	569.5	56.4	28.2
SE	2.5		2.4		1.5	
Significance of effects						
Genetics	***		***		*	
Feedsystem	***		**		***	
Genetics x Feedsystem	**		n.s.		***	

7.9 Appendix 9 – Stochastic Model Presentation

Earnscleugh Station
Alexandra, Central Otago, New Zealand
April 2019

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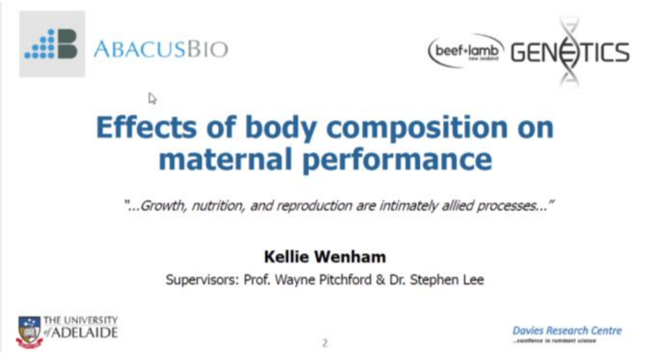

ABACUSBIO

beef+lamb new zealand GENETICS

Effects of body composition on maternal performance

"...Growth, nutrition, and reproduction are intimately allied processes..."

Kellie Wenham

Supervisors: Prof. Wayne Pitchford & Dr. Stephen Lee

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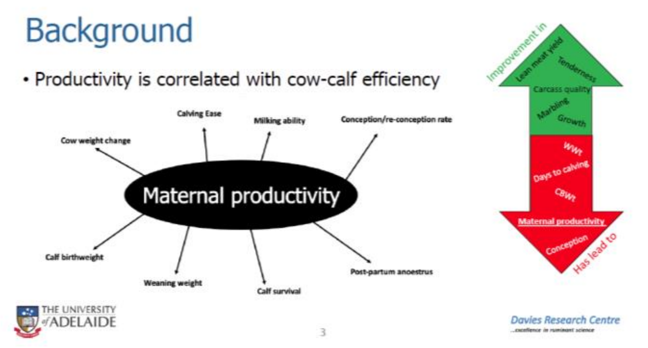

Background

- Productivity is correlated with cow-calf efficiency

Maternal productivity

Cow weight change
Calving Ease
Milking ability
Conception/re-conception rate
Calf birthweight
Weaning weight
Calf survival
Post-partum anoestrus

Improvement in
Lean meat yield
Tenderness
Carcass quality
Marbling
Growth
WWt
Days to calving
CBWt
Maternal productivity
Conception
Has lead to

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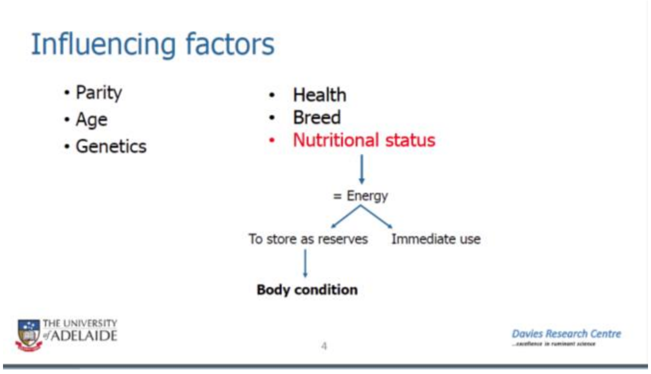

Influencing factors

- Parity
- Age
- Genetics

- Health
- Breed
- Nutritional status

= Energy

To store as reserves
Immediate use

Body condition

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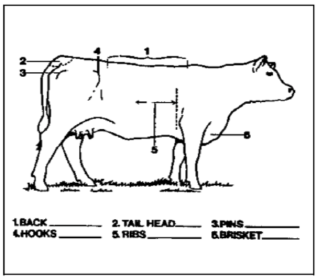
Body condition scoring (BCS)

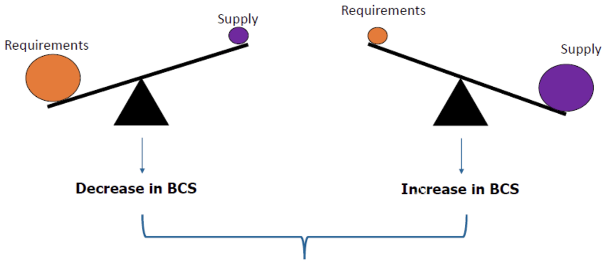
0	Emaciated
1	The individual processes are sharp to the touch, no tail head fat. The hip, bones and ribs are prominent
2	The individual processes can easily be felt, but feel rounded, rather than sharp. There is some tissue cover around the tail head. Individual ribs are no longer visually obvious
3	The short ribs can only be felt with firm thumb pressure. Areas either side of tail head have fat cover which can be easily felt
4	The processes cannot be felt and fat cover around the tail head is easily seen as slight mounds, soft to touch. Folds of fat are beginning to develop over ribs and thighs.
5	The bone structure of the animal is no longer noticeable and the tail head is almost completely buried in fatty tissue.

(Graham 2003)



(Knuckle et al. 1998)

Managing BCS



Decrease in BCS

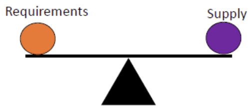
Increase in BCS

Implications for maternal productivity

Managing BCS

Variable climate = variable feed quality and quantity
Differences in management and location

No single solution to assist producers



Beef CRC Maternal productivity project

- Walmsley and Oddy (2018)
  1. The development of heifers to reach puberty
  2. The reproductive consequences of the relationship between cow herd requirements and nutrient availability
  3. The phenotypic changes within the herd as a result of breeding decisions

Aim

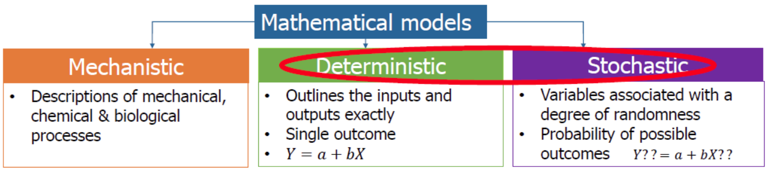
Model the relationship between pasture growth, cow body condition and calving time and their effect on maternal productivity

Hypothesis

Cows in sub-optimal condition (< BCS 3) at the start of a nutritionally poor season will have poorer maternal outcomes

Modelling

- Designed to mimic real world systems
- Predict how a system will behave under specified conditions
- Model type depends on inputs and outputs required

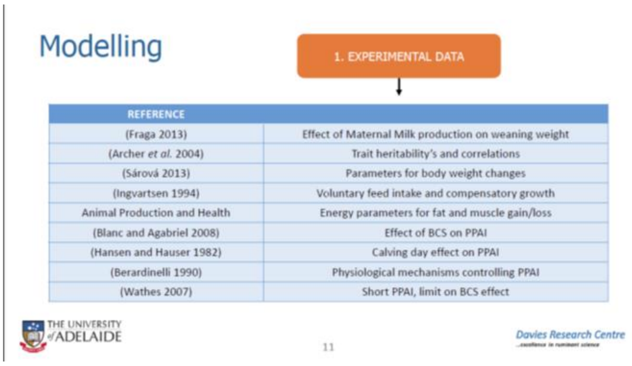


Mathematical models

Mechanistic
- Descriptions of mechanical, chemical & biological processes

Deterministic
- Outlines the inputs and outputs exactly
- Single outcome
- $Y = a + bX$

Stochastic
- Variables associated with a degree of randomness
- Probability of possible outcomes $Y ?? = a + bX ??$



Modelling

1. EXPERIMENTAL DATA

REFERENCE	
(Fraga 2013)	Effect of Maternal Milk production on weaning weight
(Archer *et al.* 2004)	Trait heritability's and correlations
(Sárová 2013)	Parameters for body weight changes
(Ingvartsen 1994)	Voluntary feed intake and compensatory growth
Animal Production and Health	Energy parameters for fat and muscle gain/loss
(Blanc and Agabriel 2008)	Effect of BCS on PPAI
(Hansen and Hauser 1982)	Calving day effect on PPAI
(Berardinelli 1990)	Physiological mechanisms controlling PPAI
(Wathes 2007)	Short PPAI, limit on BCS effect

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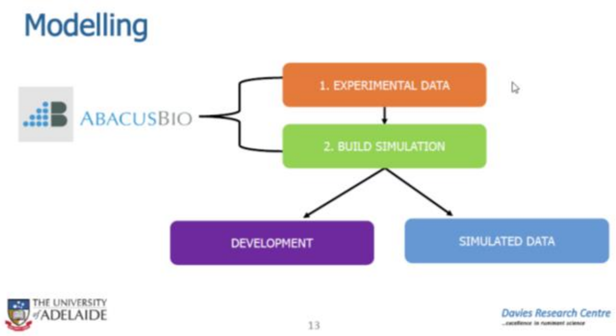

Modelling

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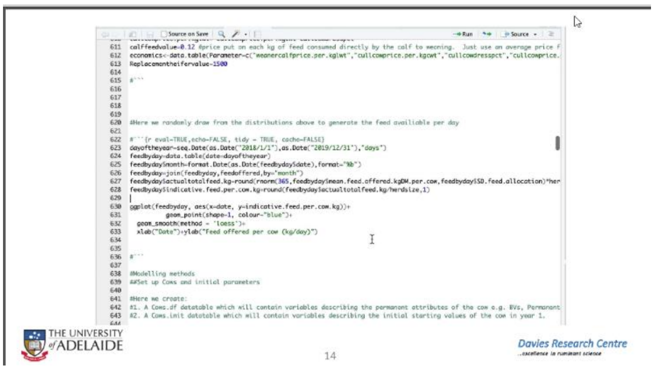

```
calffeedvalue=0.12 #price put on each kg of feed consumed directly by the calf to weaning.  Just use an average price f
economics<-data.table(Parameter=c("weanercalfprice.per.kglwt","cullcowprice.per.kgcwt","cullcowdresspct","cullcowprice.
Replacementheifervalue=1500

#```




#Here we randomly draw from the distributions above to generate the feed availiable per day

#```{r eval=TRUE,echo=FALSE, tidy = TRUE, cache=FALSE}
dayoftheyear=seq.Date(as.Date("2018/1/1"),as.Date("2019/12/31"),"days")
feedbyday=data.table(date=dayoftheyear)
feedbyday$month=format.Date(as.Date(feedbyday$date),format="%b")
feedbyday=join(feedbyday,feedoffered,by="month")
feedbyday$actualtotalfeed.kg=round(rnorm(365,feedbyday$mean.feed.offered.kgDM.per.cow,feedbyday$SD.feed.allocation)*her
feedbyday$indicative.feed.per.cow.kg=round(feedbyday$actualtotalfeed.kg/herdsize,1)

ggplot(feedbyday, aes(x=date, y=indicative.feed.per.cow.kg))+
          geom_point(shape=1, colour="blue")+
  geom_smooth(method = 'loess')+
  xlab("Date")+ylab("Feed offered per cow (kg/day)")


#```

#Modelling methods
##Set up Cows and initial parameters

#Here we create:
#1. A Cows.df datatable which will contain variables describing the permanent attributes of the cow e.g. BVs, Permanent
#2. A Cows.init datatable which will contain variables describing the initial starting values of the cow in year 1.
```

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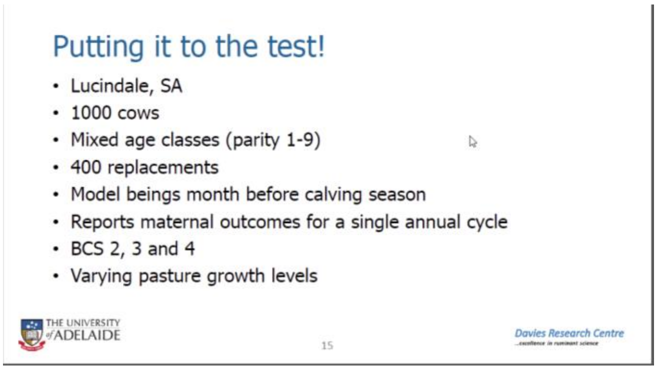

Putting it to the test!

- Lucindale, SA
- 1000 cows
- Mixed age classes (parity 1-9)
- 400 replacements
- Model beings month before calving season
- Reports maternal outcomes for a single annual cycle
- BCS 2, 3 and 4
- Varying pasture growth levels

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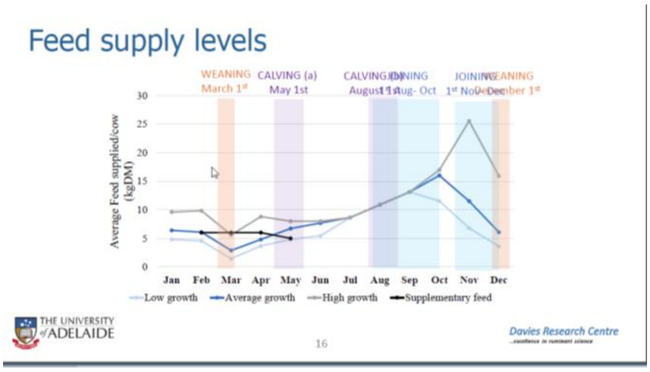
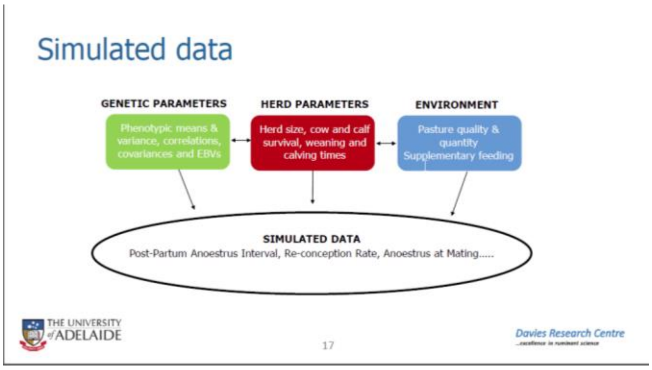


Feed supply levels



Simulated data

GENETIC PARAMETERS

Phenotypic means & variance, correlations, covariances and EBVs

HERD PARAMETERS

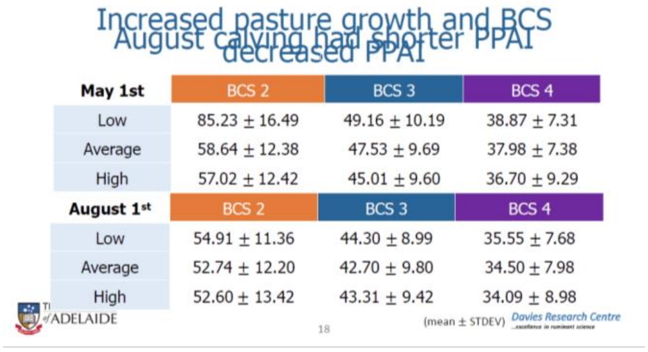
Herd size, cow and calf survival, weaning and calving times

ENVIRONMENT

Pasture quality & quantity
Supplementary feeding

SIMULATED DATA

Post-Partum Anoestrus Interval, Re-conception Rate, Anoestrus at Mating.....

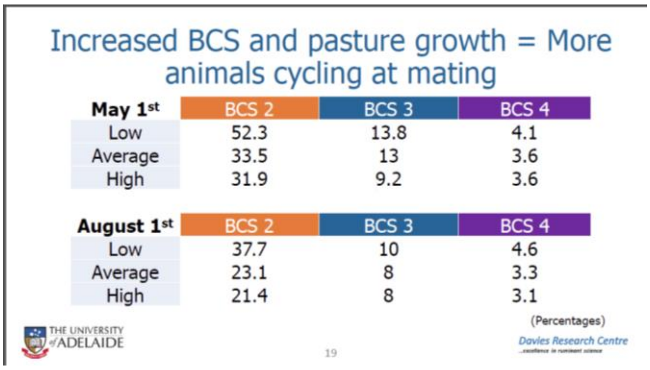


Increased pasture growth and BCS decreased PPAI

August calving had shorter PPAI

May 1st	BCS 2	BCS 3	BCS 4
Low	85.23 ± 16.49	49.16 ± 10.19	38.87 ± 7.31
Average	58.64 ± 12.38	47.53 ± 9.69	37.98 ± 7.38
High	57.02 ± 12.42	45.01 ± 9.60	36.70 ± 9.29
August 1st	**BCS 2**	**BCS 3**	**BCS 4**
Low	54.91 ± 11.36	44.30 ± 8.99	35.55 ± 7.68
Average	52.74 ± 12.20	42.70 ± 9.80	34.50 ± 7.98
High	52.60 ± 13.42	43.31 ± 9.42	34.09 ± 8.98

(mean ± STDEV)

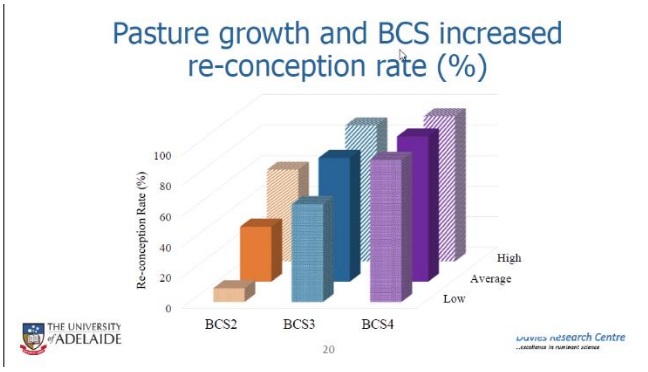


Increased BCS and pasture growth = More animals cycling at mating

May 1st	BCS 2	BCS 3	BCS 4
Low	52.3	13.8	4.1
Average	33.5	13	3.6
High	31.9	9.2	3.6

August 1st	BCS 2	BCS 3	BCS 4
Low	37.7	10	4.6
Average	23.1	8	3.3
High	21.4	8	3.1

(Percentages)



Pasture growth and BCS increased re-conception rate (%)

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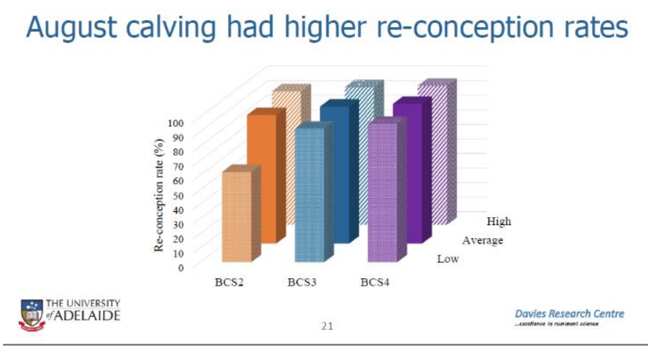

August calving had higher re-conception rates

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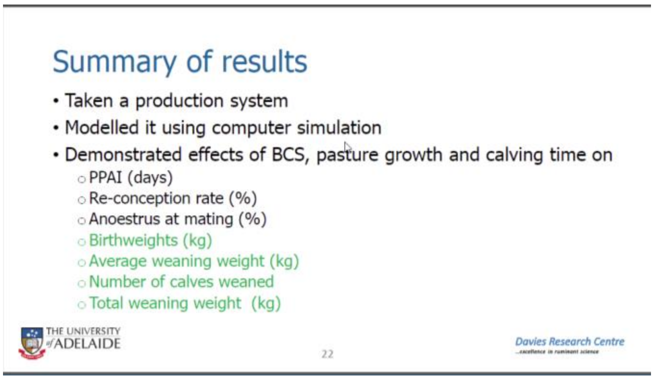

Summary of results

- Taken a production system
- Modelled it using computer simulation
- Demonstrated effects of BCS, pasture growth and calving time on
  - PPAI (days)
  - Re-conception rate (%)
  - Anoestrus at mating (%)
  - Birthweights (kg)
  - Average weaning weight (kg)
  - Number of calves weaned
  - Total weaning weight (kg)

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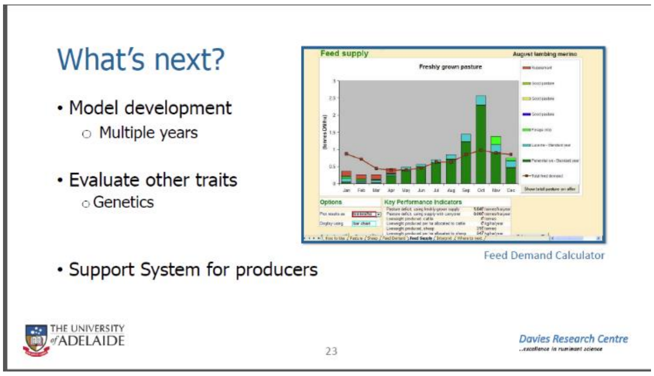

What's next?

- Model development
  - Multiple years
- Evaluate other traits
  - Genetics
- Support System for producers

Feed Demand Calculator

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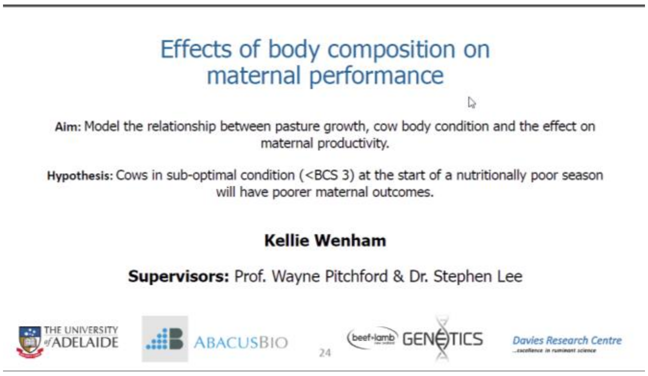


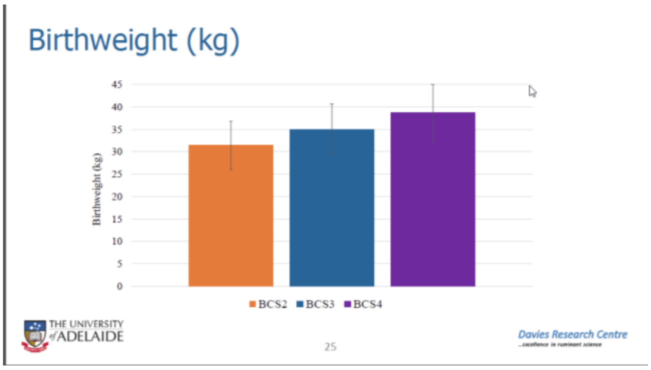
Effects of body composition on maternal performance

Aim: Model the relationship between pasture growth, cow body condition and the effect on maternal productivity.

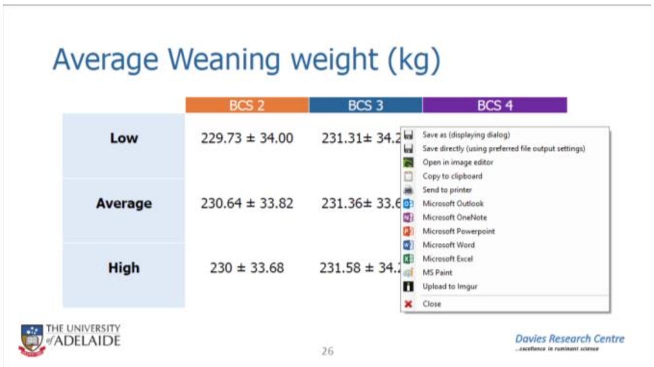
Hypothesis: Cows in sub-optimal condition (<BCS 3) at the start of a nutritionally poor season will have poorer maternal outcomes.

Kellie Wenham

Supervisors: Prof. Wayne Pitchford & Dr. Stephen Lee

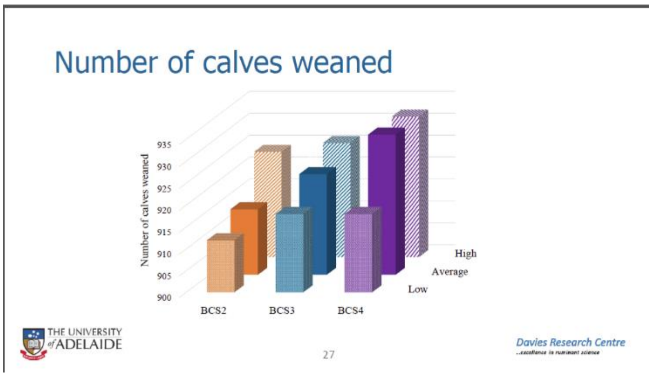


Birthweight (kg)

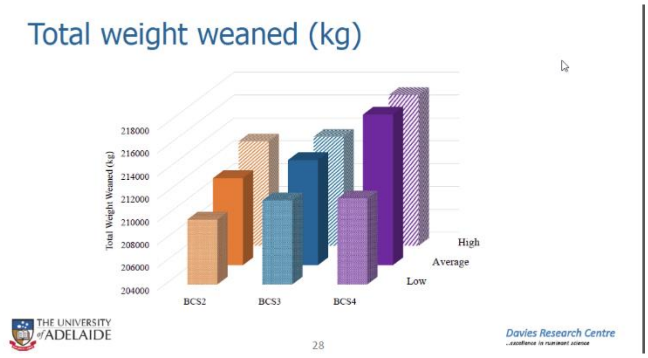


Average Weaning weight (kg)

	BCS 2	BCS 3	BCS 4
Low	229.73 ± 34.00	231.31± 34.2	
Average	230.64 ± 33.82	231.36± 33.6	
High	230 ± 33.68	231.58 ± 34.	



Number of calves weaned



Total weight weaned (kg)