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Causal factors affecting variation in liveweight gain in north Australian beef herds

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Abstract

This project investigated the reasons for the large within-herd variation in steer growth identified in extensive beef herds in northern Australia, and the scope for targeted improvement of the performance of the tail of the annual steer or heifer crop, either by better selection or improved management.

Eleven study groups of steers on different commercial cattle properties were inducted at weaning and observed in one of three 12-month periods: 2008/09 (n=1); 2009/10 (n=5); and 2010/11 (n=5). In addition to liveweight, individual animal measurements included hip height, body condition, flight speed, tick score, buffalo fly count, lesion score, HGP (timing and retention), internal parasite status, and disease status. Data analysis did not show any of the measured factors to be major drivers of the observed variation in growth rates within a mob, so no factors emerged to explain the 'poor doers' or tail that typically occur in mobs. Note that this does dismiss the importance of factors such as tick, flies, internal parasites and disease as being able to cause production losses from time to time at the mob level.

Weaning weight and hip height at weaning appeared to be associated with dry season ADG. The largest dry season weight gains were observed in animals that were taller at weaning and animals that were lighter at weaning. It is important to note that while annual growth rate was higher in those animals that were lighter at weaning, the increased growth rate in lighter weaners was not enough to overcome the weight advantage conferred on those animals that were heavier at weaning. Pen studies found that variability in post-weaning growth rate is not related to the nutrient status of the animals. It is unlikely that the variability in post-weaning growth rate is genetic or a genotype x diet quality interaction given that the animals responded similarly when provided with identical diets under pen feeding conditions.

This project, therefore, has shown little practical scope for improving performance of the 'tail' of steer, or heifer, mobs in extensive production systems. Additional and more detailed research may reveal some key causes of variation within a mob and, perhaps, some practical solutions. In the meantime, improvements in productivity will arise from improving the average performance of the whole mob through genetic selection and improved nutrition.

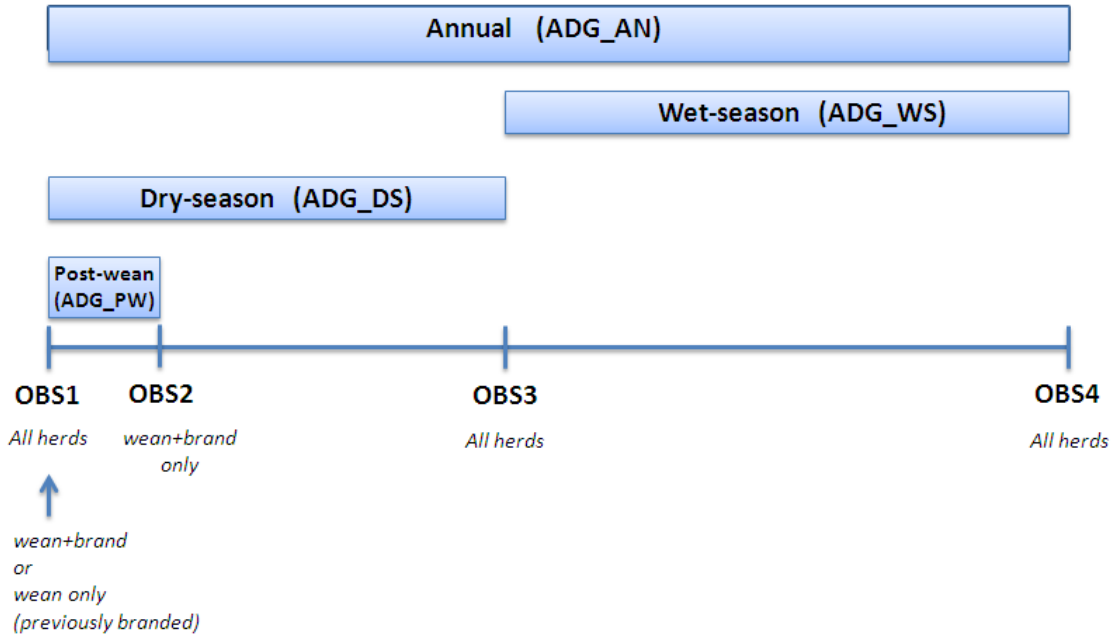
Executive Summary

This project investigated the reasons for the large within-herd variation in steer growth identified in extensive beef herds in northern Australia. The underlying premise was that a cost effective way of improving liveweight gain would be to address variation in performance within the herd and reduce the number of poor performing cattle, rather than only focussing on the performance of the leading animals or the mob as a whole.

The objectives were as follows:-

1. Analyse data from Beef CRC herds and stud herds from two major pastoral companies in northern Australia and determine the amount of variation in liveweight gain in growing animals that can be attributed to genetic and environmental influences.
2. Estimate the proportion of variance in liveweight gain explained by a specific set of determinants under study, within and between selected study mobs in the Northern Territory.
3. Identify the influence of other difficult-to-measure causal factors such as foraging behaviour and feed efficiency, from a series of smaller-scale nested experiments.
4. Report the potential impacts of studies of high and low growth animals identified in Objective 2 in pen studies at Katherine Research Station.
5. Develop a practical analytical toolkit and determine data requirements for investigating and identifying the drivers of live weight growth performance in individual herds.
6. Develop strategies that can be identified using an analytical toolkit to reduce the number of poor performing animals and increase average herd performance.

Eleven study groups of steers on different commercial cattle properties were inducted at weaning and observed in one of three 12-month periods: 2008/09 (n=1); 2009/10 (n=5); and 2010/11 (n=5).



Data collected on individual animals within each mob included weight, hip height, flight speed, castration and dehorning information, tick and buffalo fly counts, dung samples for internal parasites and diet quality and serum samples for various diseases (Pestivirus, Anaplasmosis and Bovine Ephemeral Fever) and liver function tests. In addition nested studies were performed on weighing techniques and calf production by sires.

Data analysis did not show any of the measured factors to be major drivers of the observed variation in growth rates within a mob, so no factors emerged to explain the 'poor doers' or tail that typically occur in mobs. Note that this does dismiss the importance of factors such as tick, flies, internal parasites and disease as being able to cause production losses from time to time at the mob level.

Weaning weight and hip height at weaning appeared to be associated with dry season ADG. The largest dry season weight gains were observed in animals that were taller at weaning and animals that were lighter at weaning. It is important to note that while annual growth rate was higher in those animals that were lighter at weaning, the increased growth rate in lighter weaners was not enough to overcome the weight advantage conferred on those animals that were heavier at weaning. When looking at final liveweight as an outcome, the heaviest animals were those that were heavier at weaning even though they had lower dry season and annual growth rates than their cohorts that were lighter at weaning.

Pen studies tested for relationships between insulin-like growth factor-1, and metabolites associated with growth and nutrient status of animals, and post-weaning liveweight gain. Variability in post-weaning growth rate within a mob was not related to the nutrient status of the animals, as there were no differences in plasma albumin, creatinine, glucose or urea concentrations between the fastest and slowest growing steers at weaning or 91 days later. It is unlikely that the variability in post-weaning

growth rate is genetic or a genotype by diet quality interaction given that the animals responded similarly when provided with identical diets under pen feeding conditions.

This project, therefore, has shown little practical scope for improving performance of the 'tail' of steer, or heifer, mobs in extensive production systems. Additional and more detailed research may reveal some key causes of variation within a mob and, perhaps, some practical solutions. In the meantime, improvements in productivity will arise from improving the average performance of the whole mob through genetic selection and improved nutrition.

In the conduct of the study and analysis of the data, several other relevant findings included:

- The significant number of non performing sires in extensive multiple sired herds
- The improvement in the precision of liveweight measurements by use of a weighing box;
- The need to ensure proper hygiene techniques when implanting HGP's to maximise retention rates;
- Incidence and prevalence data for common diseases in beef herds in the NT;
- Relatively high internal parasitic levels in some herds still at 18 months of age – the significance of which remains unclear.

There is a need for best practice information on how best to implement regular liveweight weighing into routine animal management procedures in order to maximise the accuracy and precision and the value of measurements for producers.

Further R&D on the following areas may benefit industry:

- Factors influencing liveweight and hip height at weaning.
- Further studies on the use of faecal NIRS or other methods that might allow exploration of grazing behaviour, diet selection and net energy measures associated with grazing (energy costs vs energy gains at the animal level associated with different grazing behaviours), and associated impacts on liveweight performance.
- Further demonstration of performance response to genetic selection.
- Further studies on parasite burdens in young beef cattle and their potential impacts on health and performance under routine management conditions.

Contents

1 Background

This project was motivated by interest in improving liveweight gain (LWG) in young growing beef cattle in extensive, northern pastoral areas of Australia. The underlying premise was that a cost effective way of improving liveweight gain would be to address the variation in performance within the herd, rather than focussing on the performance of the leading animals. In many cases the limiting factor for growth of animals appears to be the digestibility of their diet and any major change to that may be relatively expensive. Inspection of LWG data within extensively managed herds in the Northern Territory (NT) has shown wide variation in rates of LWG within herds, even within mobs that had little or no variation in breed, and this variation was considered to represent an opportunity for significant improvement.

While there has been a considerable amount of research investigating aspects of beef cattle production in northern Australia, there is a relative scarcity of detailed data on LWG and in particular relatively few refereed publications that report estimates of mean LWG and variance or standard deviation.

There has been a considerable amount of research designed to provide information to producers through a variety of reports and extension activities. This information is not always easy to access as evidenced by the periodic production of summative reports that in turn collate and present the findings of other research (Holroyd and O'Rourke, 1989, Hasker, 2000), and these sources also tend not to provide estimates of variance which were of particular interest for this project.

A large-scale survey of 375 participating properties from 8 northern regions of Australia did provide estimates of annual LWG and variance, over a period from 1991-1995 (Bortolussi *et al*., 2005a, Bortolussi *et al*., 2005b, Bortolussi *et al*., 2005c, Bortolussi *et al*., 2005d, Bortolussi *et al*., 2005e). The regions incorporated in this survey included 6 regions from Queensland and one each from the Northern Territory and Western Australia. Regions relevant to this review included the North West Queensland region (NT border to the Gulf and Winton and Boulia shires to the south), the Northern Territory (Barkly, Katherine, Darwin and Victoria River districts), and the Western Australian region (northern part of the state, Kimberley and Pilbara).

Estimates of annual liveweight gain from Bortolussi *et al.* (2005c) are presented here for the three regions most relevant to this review.

Table 1: Estimated annual liveweight gain (kg/head) for the NW Queensland region (Bortolussi *et al*., 2005c). n=number of properties contributing data, sd=standard deviation, cv=coefficient of variation.

Pasture community	Status	n	Mean	sd	cv	Min	Max
Black speargrass	Native	65	116	25.5	22.0	80	140

Bluegrass roundtop	Native	3	137	41.5	30.3	100	182
Gidgee	Improved	7	129	19.4	15.0	105	155
Gidgee	Native	7	141	25.2	17.9	105	175
Mitchell grass	Native	68	145	30.2	20.8	98	240
Spinifex	Native	3	93	15.3	16.5	80	110
Overall weighted average			130.6				

Table 2: Estimated annual liveweight gain (kg/head) for Northern Territory properties (Bortolussi *et al*., 2005c). n=number of properties contributing data, sd=standard deviation, cv=coefficient of variation.

Pasture community	Status	n	Mean	sd	cv	Min	Max
Annual sorghum/tallgrass	Native	7	114	24.4	21.4	80	150
Blue bush	Native	4	103	39.6	38.4	50	146
Bluegrass (NW Australia)	Native	7	108	22.3	20.6	64	125
Mitchell grass	Native	34	111	27.2	24.5	50	182
Perennial tallgrass & other	Native	8	87	14.6	16.8	67	110
Ribbongrass	Native	4	110	10	9.1	96	120
Overall weighted mean			107.4				

Table 3: Estimated annual liveweight gain (kg/head) for Western Australian properties (Bortolussi *et al*., 2005c). n=number of properties contributing data, sd=standard deviation, cv=coefficient of variation.

Pasture community	Status	n	Mean	sd	cv	Min	Max
Acacia woodland	Native	6	91	14.9	16.4	71	111
Bluegrass (NW Australia)	Native	7	120	14.7	12.3	100	135
Mitchell grass	Native	20	136	27.8	20.4	100	185
Mulga	Native	3	146	17.4	11.9	126	158
Ribbongrass	Improved	9	169	41.5	24.6	125	240
Ribbongrass	Native	5	133	31.9	24.0	104	176
Spinifex	Improved	5	114	33.8	29.6	83	152
Spinifex	Native	13	114	27.4	24.0	75	160
WA short tussock grass	Improved	3	111	47.5	42.8	63	158
WA short tussock grass	Native	7	136	41.2	30.3	83	201
Overall weighted mean			129.1				

During the preparation phase for this project staff from the Northern Territory Department of Primary Industry and Fisheries obtained data on liveweight measurements of steers and heifers from a number of properties in the Katherine, Barkly and Victoria River Downs regions. Within each property animals were generally of the same type (breed, sex, age). These were then analysed to produce crude summary

statistics similar to those estimated by Bortolussi *et al.* (2005c). Estimates of gain were based on the difference between two weight measures. Where weigh dates were recorded, the number of days between the two weight measures were noted and an estimate made of the average daily gain (ADG) for the period. Data from an additional two properties in the Barkly region were obtained from the 2010-2011 year and have been added to this table.

Table 4: Estimates of liveweight gain (kg/head) from Northern Territory properties. n=number of cattle measured on each property, sd=standard deviation, cv=coefficient of variation.

Region	Period	Class	n	Mean	sd	cv	Min	Max	days	ADG
Barkly	Nov 04 to June 05	heifers	432	112	23.91	21.3	-1	174	203	0.55
Barkly	2010-11 wet season	steers	202	76	18.12	0.24	23	173	111	
Barkly	2011 dry season	steers	208	13	9.28	0.73	-39	43	83	
Katherine	June 93 to Apr 94	steers	50	88	19.47	22.1	50	156		
Katherine	June 95 to May 96	steers	45	152	23.74	15.6	94	206		
Katherine	July 05 to May 06	heifers	211	77	25.21	32.7	-55	126	320	0.24
Katherine	Sept 05 to May 06	heifers	464	86	19.76	23.0	-2	138	254	0.34
Katherine	Feb 05 to Sept 05	heifers	309	97	18.51	19.1	31	169	201	0.48
Katherine	Nov 04 to Apr 05	heifers	387	84	26.81	31.9	-24	157		
Top End	Jan 05 to May 05	heifers	233	62	23.3	37.8	-18	154		
VRD	Oct 05 to June 06	heifers	97	119	17.34	14.6	85	164	223	0.53

The coefficient of variation (cv) is calculated as the standard deviation divided by the mean and expressed as a percentage. It provides a measure of variation that is expressed relative to the mean and allows direct comparisons of different estimates of variability. Assessment of the minimum and maximum values relative to the mean also provides an indication of the variability.

In discussions contributing to the design of this project there was particular interest in understanding the amount of variation in key outcome measures such as LWG and determining factors that might influence variability in LWG. This information might then be used to try and improve the performance of the herd through reducing variability and in particular if measures could be identified that might allow improvement in the worst performing animals in the herd.

Multiple factors have the potential to influence liveweight gain in beef cattle in a complex causal pattern. The major factors operating in northern Australia have been identified by (Bortolussi *et al*., 2005c).

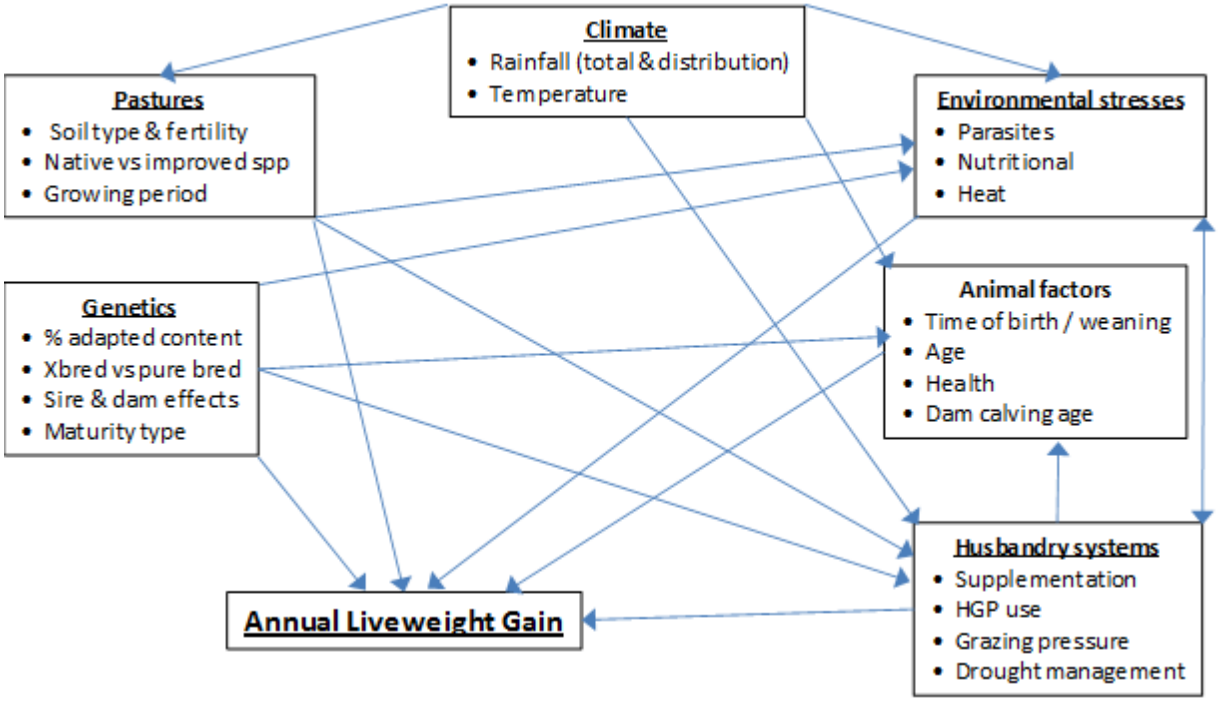


Figure 1: Major factors affecting annual liveweight gain in beef cattle in northern Australia (Bortolussi *et al.*, 2005c).

A detailed literature review of factors influencing LWG in north Australian beef herds has been completed as a separate report in association with this project and is available from the Meat and Livestock Australia website.

This project was designed to investigate variation in liveweight gain and to identify reasons for the variation in order to reduce the number of poor performing cattle.

2 Project Objectives

1. Analyse data from Beef CRC herds and stud herds from two major pastoral companies in northern Australia and determined the amount of liveweight gain variation in growing animals that can be attributed to genetic and environmental influences.

2. Estimate the proportion of variance in liveweight gain explained by a specific set of determinants under study, within and between selected study mobs in the Northern Territory.

3. Identify the influence of other difficult-to-measure causal factors such as foraging behaviour and feed efficiency, from a series of smaller scale nested experiments.

4. Report the potential impacts of studies of high and low growth animal identified in Objective 2 in pen studies at Katherine Research Station.

5. Develop a practical analytical toolkit and determined data requirements for investigating and identifying the drivers of live weight growth performance in individual herds.

6. Develop strategies that can be identified using an analytical toolkit to reduce the number of poor performing animals and increase average herd performance.

3 Analyses of industry datasets

3.1 Introduction

Two types of historical datasets were identified as relevant to the aims and objectives of this study: the Beef Cooperative Research Centre (Beef CRC) and either commercial or research properties within the NT.

This component of the study was developed to access historical datasets and analyse these data to assess LWG variability and attribute variability to various explanatory factors.

3.2 Objectives

1. Document the levels of variation in weaning weight and post weaning ADG attributed to: 1) sire; and 2) other effects i.e. weaning age, weaning weight, birth year, season at weaning, in three datasets (Beef CRC and two industry stud datasets).

2. Identify consistencies and discrepancies in outcomes between datasets, and discuss possible explanations and relevance to northern Australian beef herds

3. Discuss outcomes, in context of measuring factors affecting variation in weight gain under commercial conditions

3.3 Methods

Following discussions with Dr David Johnston, Senior Scientist at the Animal Genetics and Breeding Unit UNE Armidale, and Dr Heather Burrow, Chief Executive Officer at Beef CRC UNE Armidale, the Beef CRC 1 dataset was identified as a potential data source. A subset of records limited to tropically adapted cattle over a set time period was extracted from the dataset. A detailed description of the design of the Beef CRC 1 program can be found in Upton et al. (2001).

The Beef CRC 1 dataset contained animal measurements from weaning to a point about 500 days post-weaning. Animals were bred from commercial cow herds, and sires of the same breed were used. The CRC was not responsible for selection of any specific sires. Breeding herds were situated throughout much of eastern Australia, South Australia and Victoria and also one property in each of western NT and gulf region of QLD. At weaning calves were relocated to various CRC collaborating properties and were

managed in cohort groups, which were defined by season of birth (autumn or spring joining for southern cattle), average weaning age, weight and property of origin.

The dataset provided by the Beef CRC included two separate, linked tables. The first table (animal records) contained animal level data for 5,625 individual animals born over a six-year period (1993-1998). The second table (traits) contained measurements recorded on the 5,625 animals at weaning or varying periods post-weaning. Traits that were measured included body weight, condition score, frame score, hip height and muscle score.

Measures other than body weight were not measured as frequently as body weight and they were not always measured at the same time as body weight. As a result it was not possible to incorporate all ancillary parameter measurements as explanatory variables into statistical models using repeated measures analyses to assess the impact of explanatory variables on body weight over time.

The Beef CRC dataset was restricted to those animals which were grown on pastures in central Queensland post-weaning, and where the post-weaning measurements for each animal covered a period of no less than 300 days post-weaning(Upton et al., 2001). These eligibility criteria resulted in an analytical dataset that contained 15,620 records and 1,690 animals (individual animals had between 2–16 separate weight records with 99% animals having >6 separate weight records).

In addition to the Beef CRC data, historical datasets were obtained from two northern beef properties including the NT Government Douglas Daly Research Farm (data courtesy of Gehan Jayawardhana), and a commercial enterprise (data courtesy of Dr Matt Bolam).

The Douglas Daly Research Farm (DDRF) is located in the subtropical Douglas Daly region, approximately 220 km south of Darwin. This dataset was derived from the stud herd and was considered relevant to the current study because the property is located in northern Australia, and the records involved multiple post-weaning measurements from more than 10 birth-years on animals with known birth dates and known sires. The method of selection and management of this herd has been detailed in Schatz (2010).

The DDRF dataset contained records from a total of 2,221 animals, and included records from animals born over a 21-year period (1986-2006). Various specific weight measures were recorded including weaning weight (labelled 200d_LWT) and post-weaning weights (400d_LWT and 600d_LWT). Additional variables in the dataset included sex (male, female), sire, birth year, branding year, and dates for each weighing.

The commercial enterprise (CE) dataset was sourced from a Brahman stud operated by a pastoral company in the Barkly region of the Northern Territory. This dataset had similar benefits to those identified for the DDRF data. The CE dataset contained records from a total of 2,927 animals born over a 14-year period (1994-2007). Individual animals were weighed on up to four occasions though most animals only had two weights recorded. The dataset included variables for animal identity, date of measurement, body weight, sex (male/female), year of birth, weaning season (summer, autumn, winter, spring) and sire identity. A subset of the animals in this dataset were produced from single sire matings to a known sire and these animal records were used for analyses aimed at identifying sire contribution to variance in weight or growth.

Analyses involved a similar general pattern for all three datasets with initial exploratory analyses followed by descriptive statistics and plots to produce summary measures for key outcomes of interest. Multivariable mixed linear models were then used to explore explanatory factors that may explain variability in bodyweight or average daily gain (ADG). Separate analyses were conducted for each dataset (CRC, DDRF, RS) because the different datasets did not contain the same explanatory variables. Each analysis followed the same pattern. Candidate explanatory variables were considered based on what was available in the dataset. A backwards model building process was used with explanatory variables omitted from the model if they were associated with a non-significant p-value ($p>0.05$). This produced final models that contained only significant fixed effects. A random effect was included in all models that accounted for sire identity (sire_id). An intercept only model (no fixed effects) was used to estimate the proportion of variance in the outcomes that was associated with sire_id. Variance estimates from the final models were then used to estimate the proportion of total variance that was explained by the fixed effects portion of the model and the proportion of unexplained variance that was left at the sire and residual levels. Model checking was conducted by inspection of plots of standardised residuals vs fitted values. All analyses were conducted in Stata (Version 10 to 12; www.stata.com), using alpha=0.05.

3.4 Results

3.4.1 Weaning weight

Table 5: Summary statistics for weaning age (days) and weaning weight (kg) from Beef CRC, Douglas Daly Research Farm (DDRF) and a commercial enterprise (CE).

	Beef CRC		DDRF		CE	
	Wean age (d)	**Wean wt (kg)**	**Wean age (d)**	**Wean wt (kg)**	**Wean age (d)**	**Wean wt (kg)**
Number of records	5096	5019	2221	2215	1373	1373
mean	203.1	199.3	196.02	187.1	192.18	195.34
se	0.566	0.605	0.68	0.72	1.46	1.29

95% CI Lower	202	198.1	194.7	185.7	189.32	192.82
95% CI Upper	204	200.4	197.4	188.5	195.03	197.87
Min	52	80	81	75	60	72
25th %	177	169	176	166	156	161.5
50th % (median)	204	198	197	188	188	192
75th %	233	228	218	210	221	224
Max	334	384	285	315	399	384

Table 6: Variance estimates from mixed models with weaning weight as the outcome. Data from Beef CRC, Douglas Daly Research Farm (DDRF) and a commercial enterprise (CE).

	Beef CRC		**DDRF**		**CE**	
	Intercept only model	**Full model**	**Intercept only model**	**Full model**	**Intercept only model**	**Full model**
Variance at Sire level	838.3	88.1	547.76	34.14	742.75	222.85
Variance at residual level	1150.7	505.1	774.71	396.55	1663.55	713.06
Total Variance	1989.05	593.2	1322.47	430.69	2406.3	935.91
Reduction in variance (explained by full model)		1395.85		891.78		1470.39
% of intercept only total variance at sire level		4.4%		2.6%		9.3%
% of intercept only total variance explained by:						
Full model		70.2%		67.4%		61.1%
Each factor in the full model						
Wean age (days)		27.8%		39.5%		32.3%
Animal sex		2.0%		5.1%		7.1%
Breed (CRC only)		2.7%		NA		NA
Season of birth (CRC only)		0.6%		NA		NA
Year of birth		1.0%		9.0%		7.1%
Property of origin (CRC only)		18.8%		NA		NA

Season at weaning	NA	0.0002%	7.30%

Season at weaning was not recorded in the Beef CRC dataset.

Table 6 provides results from separate linear models run with each dataset that each had weaning weight as the outcome or y-variable. All models had sire_id added as a random effect.

The intercept only model provides a starting estimate of variance at the level of sire (level 2) and at the level of the observation (residual variance). The sum of these two estimates provides an estimate of the total variance in weaning weight for each model.

The full model has fixed effects added to each model coding for weaning age in days, sex of the weaner, breed, season of birth (summer, autumn, winter, spring), birth year, property of origin (where the weaner was bred and raised up until weaning), and season at weaning.

When fixed effect terms are added to the model the expectation is that these factors will explain some of the variability in the outcome. The total variance in an outcome for a given dataset may be considered to be constant and is represented by the total variance in the intercept only model. The impact of adding fixed effects will be to reduce the unexplained variance, represented by the variance estimates for sire and residual. Adding fixed effects can reduce variance estimates at either level (residual or sire). The explaining power of a model or an individual factor within a model can be represented as a percentage of the total variance (intercept only variance).

In the full model, the variance at the sire level can be expressed as a percentage of the unexplained variance for that model, or as a percentage of the total variance (derived from the intercept only model).

The full models explained between 61 and 70% of the total variance in weaning weight and the explanatory effects of the full models were associated with reductions in residual and sire level variances. This also means that 30 to 39% of the variance in the outcome has not been explained. Perhaps there are other as yet unmeasured variables or fixed effect terms that could potentially be measured and added to the model and increase the ability of the model to explain variance.

Age at weaning was the most important explanatory variable in all three models.

In the Beef CRC dataset where animals were sourced from 13 different properties of origin, **property of origin was the next most important fixed effect** with respect to the amount of total variance explained and year of birth accounted for relatively little variance.

In contrast **year of birth and animal sex were similarly important in the other two datasets**. There was an interesting difference in the importance of season of weaning as an explanatory factor for weaning weight. Season at weaning had almost no effect for the DDRF dataset, perhaps suggesting that supply of feed to animals around the time of weaning may be less influenced by seasonal variation in climate.

3.4.2 Average daily gain (ADG)

Average daily gain (ADG) estimates were based on a numerator formed by the difference in two weight measures and a denominator formed by the number of days between the two weighing dates (kg per head per day).

The Beef CRC data provided a relatively large number of weights recorded for each animal (up to 16 weights per animal with 99% of all animals having more than 6 separate weight records). Preliminary modelling of body weight and age indicated that while the best statistical fit between weight and age was produced by a non-linear model, a simple linear regression was almost as good. Given that the linear model did provide a good fit to the body weight data, it was considered reasonable to produce ADG estimates using weaning weight and an end-weight measure to allow additional statistical analyses to be performed.

Multivariable models were then developed with the outcome being a single estimate for each animal of ADG from weaning to either 500 days post-weaning (Beef CRC and CE datasets) or to 400 and 600 days post-weaning (DDRF), depending on availability of data.

Table 3 provides summary data describing the body weight and age of animals at the measurement defining the end of each ADG period, and the ADG estimate from weaning to that end point. Table 8 then provides the output from multivariable models used to estimate variance.

The intercept only model provides a starting estimate of variance at the level of sire (level 2) and at the level of the observation (residual variance). The sum of these two estimates provides an estimate of the total variance in ADG.

The full models have had fixed effects added to the model for various explanatory factors depending on what measures were available in the datasets. When fixed effect terms are added to the model the expectation is that these factors will explain some of the variability in the outcome. Since the total variance may be considered to be constant, then the impact of adding fixed effects will be to reduce the unexplained variance, represented by the variance estimates for sire and residual. Adding fixed effects can reduce variance estimates at either level (residual or sire).

Table 7: Summary statistics for end weight (kg), end age (days) and ADG (kg/hd/day) from the three datasets, using the final weight measurements from all animals included in each dataset. Data then used in a multivariable model to assess variance for ADG. n=number of records, se=standard error, CI=confidence interval. Data from Beef CRC, Douglas Daly Research Farm (DDRF) and a commercial enterprise (CE).

	Beef CRC			DDRF			CE			DDRF		
	500d weight	500d age	ADG (wean to 500d)	400d weight	400d age	ADG (wean to 400d)	500d weight	500d age	ADG (wean to 500d)	600d weight	600d age	ADG (wean to 600d)
	kg	days	kg/hd/d	kg	days	kg/hd/d	kg	days	kg/hd/d	kg	days	kg/hd/d
n	1609	1609	1609	1439	1441	1439	1196	1196	1196	1331	1337	1331
mean	385.2	673.6	0.3945	222.7	394.88	0.16	299.3	531.66	0.321	332.0	582.23	0.37
se	1.07	1.23	0.002	1.01	1.08	0.004	2.38	4.25	0.0053	1.18	1.3	0.002
95%CI Lower	383.1	671.2	0.39	220.7	392.8	0.15	294.6	523.3	0.31	329.7	579.7	0.37
95%CI Upper	387.3	676	0.398	224.7	397.0	0.16	304.0	540	0.33	334.3	584.8	0.38
Min	234	499	0.174	117	221	-0.31	110.5	218	-0.29	196	443	0.06
25th %	358	640	0.34	197	374	0.037	246	410.5	0.197	304	553	0.32
Median	386	677	0.388	219	396	0.141	295	539	0.28	332	581	0.36
75th %	414	708	0.445	246	419	0.262	339.5	627	0.404	358	607	0.43
Max	526	809	0.656	408	538	0.738	598	890	1.58	479	911	0.73

Table 8: Variance estimates derived from Beef CRC data using ADG from weaning to about 500 days post-weaning. All models included a random effect for sire identity.

	Beef CRC ADG to 500 days		DDRF ADG to 400 days		CE ADG to 500 days		DDRF ADG to 600 days	
	Intercept only model	Full model	Intercept only model	Full model	Intercept only model	Full model	Intercept only model	Full model
Variance at Sire level	0.002947	0.00034	0.00994	0.0003	0.03124	0.0109	0.00242	0.0004
Variance at residual level	0.003719	0.00220	0.01111	0.006	0.01953	0.0164	0.00452	0.0036
Total Variance	0.006666	0.0025385	0.02105	0.0063	0.05077	0.0273	0.00694	0.004
Reduction in variance (explained by full model)		0.0041275		0.01475		0.02347		0.00294
% of intercept only total variance at sire level		5.0%		1.5%		21.4%		6.30%
% of intercept only total variance explained by:								
Full model		61.9%		69.8%		46.4%		41.3%
Each factor in the full model								
Wean weight (kg)		5.8%		5.7%		2.1%		0.7%
Animal sex		0.9%		1.8%		3.6%		1.6%
Breed (CRC only)		0.6%		NA		NA		NA
Year of birth		5.7%		40.4%		15.3%		40.9%

HGP implant (CRC only)	1.0%	NA	NA	NA
Property of origin (CRC only)	15.6%	NA	NA	NA
Hip height (CRC only)	3.9%	NA	NA	NA
Season at weaning	NA	1.90%	25.00%	1.3%

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In summary, the full models have explained between 41 and 70% of the total variance in ADG, and this explanatory impact of the fixed effects has reduced both residual and sire level variances.

The effect of sire accounted for between 1.5 and 21% of the total variance in ADG, after adjusting for other fixed effects included in the models.

The most important explanatory variables based on how much of the variance in ADG that is explained, were property of origin for the CRC data (accounted for 15.6% of the total variance in ADG) and year of birth (DDRF) and season at weaning (CE) for the other two datasets. It is important to note that the Beef CRC study involved animals selected from multiple properties over a shorter time frame while the other two datasets involved animals born on a single property over a much large time period.

Other fixed effect terms account for relatively little of the variability in ADG.

3.4.3 Animal age as an explanatory variable for body weight

There was interest in trying to determine how much of the variance in body weight may be attributed to animal age using CRC data, given that the CRC dataset had accurately recorded birth dates for most animals in the dataset.

The CRC data were restricted to a single observation per animal in each of two age ranges. The first age range was between the ages of 301 days and 500 days, to produce a dataset equivalent to animals measured at an average of about 400 days of age. The second age range was between 501 and 700 days to produce a dataset equivalent to about 600 days of age. The main criteria used to select any one observation each animal in the dataset was to select the measurement closest to the ideal age (400 or 600 d).

Another dataset was then created by randomly selecting one measurement per animal from all measurements collected over the age range from 301-700 days. This produced a separate dataset with a much broader age range to assess the effect of age and wean weight on body weight.

These data were then analysed using a general linear models approach as for CRC data in earlier sections of the report.

A full model was then run that included variables coding for wean_wt, age and other fixed effects. Variables coding for wean_wt and age were then omitted and models re-run to generate variance estimates. These were used to determine the impact of animal age, wean_wt and both of these combined on amount of explained variance.

Three separate models were run:

- 400d age group: restricted to animal ages between 301-500d to simulate a controlled group of animals with average age of around 400d. The outcome was body weight measured on a single occasion for each animal.
- 600d age group: restricted to animal ages between 501-700 d to simulate a controlled group of animals with average age of around 600d. The outcome was body weight measured on a single occasion for each animal.
- Broad age range group with ages ranging from 301-700 days. The outcome was body weight measured on a single occasion for each animal. Where any animal had more than one measurement in this period, one measure was randomly selected for each animal.

Table 9: Summary statistics for body weight and age at weighing for each of the three datasets described above.

	301-500d		**501-700d**		**301-700d**	
	weight	**age**	**weight**	**age**	**weight**	**age**
N	1607	1607	1608	1608	1609	1609
Mean	244.17	398.48	356.93	597.62	298.45	490.93
Se	1.04	0.53	1.04	0.48	1.73	2.82
95% CI Lower	242.13	397.44	354.9	596.7	295.05	485.4
95% CI Upper	246.2	399.51	358.9	598.6	301.85	496.5
Min	108	316	234	211	108	301
25th %	218	384	328	586	244	389
50th % (median)	242	396	356	597	300	491
75th %	270	414	386	612	352	586
Max	400	490	484	663	500	700

Table 10: Variance estimates derived from Beef CRC data using a model with the outcome being a single weight measurement per animal at ages between 300 to 500 days, 500 to 700 days and 300 to 700 days. All models included a random effect coding for sire.

Dataset	**Beef CRC**		**Beef CRC**		**Beef CRC**	
Body weight at:	**301-500d**		**501-700d**		**301-700d**	
Model	**Intercept only model**	**Full model**	**Intercept only model**	**Full model**	**Intercept only model**	**Full model**
Variance at Sire level	734.9	60.7	712.1	34.4	510.5	20.2
Variance at residual level	1155.5	343.3	1129.3	506.0	4399.7	661.7
Total Variance	1890.5	404.0	1841.4	540.3	4910.2	681.9
Reduction in variance (explained by full model)		1486.5		1301.1		4228.4
% of intercept only total variance at sire level		3.2%		1.9%		0.4%
% of intercept only total variance explained by:						
Full model		78.6%		70.7%		86.1%
Each factor in the full model						
Wean weight (kg)		20.3%		14.6%		5.8%
Wean age (d)		3.9%		2.2%		26.7%

The purpose of these analyses was to assess the association between animal age and weight. The outcome of interest in the model was body weight.

All three models contained additional explanatory variables (sex, breed, birth year, property of origin, HGP implant and year of measurement) that are not shown in the Table because of the focus on the association between weight and age at weaning and subsequent body weight. The models explained between 70-86% of total variance in body weight at older ages.

The first two models contained data from a more tightly constrained age range, and in these models, weaning weight accounted for more of the variance in subsequent body weight than weaning age. In

contrast, when a dataset was produced that had a wider range in animal ages (as represented by the third model), weaning age accounted for more of the variance in subsequent body weight than weaning weight. These findings suggest that in extensively managed beef herds with wide expected ranges in animal age at weaning, it seems likely that weaning age is likely to be the more important driver of post-weaning body weight.

In addition, as animals aged (moving from the model at 301-500 days to 501-700 days), the proportion of variance attributable to wean weight is reduced, suggesting that as animals increase in age, the strength of wean weight as a predictor of body weight seems to be weakening.

In the third model where there is a larger age range in the data, the effect of age on the model is more substantial and age accounts for about 27% of the total variance in body weight. In a population of animals where age is unknown and may vary over a pretty wide range, this final estimate is arguably a better indication of the importance of age as an explanatory variable for body weight. This indicates that for observational studies such as the current liveweight gain study, **inability to measure animal age is an important disadvantage when modelling body weight.**

3.4.4 Property level contribution to variance

There was also interest in comparing the variance in body weight between CRC properties and the other two properties for which historical data had been obtained (DDRF and CE), as an indication of data spread and amount of variance that statistical models may have to work with. Data on body weights for two age ranges were compared (301-500 days and 501-700 days).

Table 11: Summary statistics and crude variance estimates for each property within the CRC dataset and for all CRC data combined and for each of the two other properties (CE=commercial enterprise, DDRF=research property). Limited to animals around 400 days of age (301-500 days).

Property	Obs	Age			Weight	
	n	Ave	Min	Max	Ave	Variance
CRC_1	402	410.3	301	500	238.6	2490.0
CRC_2	133	404.6	302	498	248.3	2728.3
CRC_3	292	388.6	301	499	256.0	1601.1
CRC_4	811	391.8	301	500	245.8	1567.5
CRC_5	807	390.2	301	500	203.4	2642.6
CRC_6	286	388.2	302	499	244.2	1957.7
CRC_7	147	391.1	302	500	242.3	2216.7
CRC_8	261	387.5	301	500	236.6	1580.1
CRC_9	490	396.1	301	500	259.4	1588.0
CRC_10	453	397.5	301	500	260.0	1963.9
CRC_11	684	404.5	301	500	251.6	1742.9
CRC_12	1506	402.5	301	500	272.5	2240.4
CRC_All	6272	397.3	301	500	249.0	2468.9
DDRF	1439	394.9	221	538	222.7	1480.3
CE	736	396.5	301	500	243.6	4758.9

Table 12: Summary statistics and crude variance estimates for each property within the CRC dataset and for all CRC data combined and for each of the two other properties (CE=commercial enterprise, DDRF=research property). Limited to animals around 600 days of age (501-700 days).

Property	Obs	Age	Weight

	n	Ave	Min	Max	Ave	Variance
CRC_1	378	589.8	501	700	317.9	1501.3
CRC_2	108	592.9	502	696	342.0	1781.7
CRC_3	236	601.9	501	699	354.6	1511.4
CRC_4	787	596.8	501	700	353.3	1391.8
CRC_5	680	595.6	501	700	317.0	1394.7
CRC_6	260	599.6	501	700	355.7	1272.7
CRC_7	126	597.9	505	692	308.9	1298.0
CRC_8	257	602.7	502	699	360.0	1730.1
CRC_9	461	591.9	501	700	371.2	1779.3
CRC_10	435	589.1	501	699	360.2	1465.6
CRC_11	628	596.0	502	700	357.2	1894.2
CRC_12	1340	589.3	501	700	373.8	1865.4
CRC_All	5696	593.9	501	700	353.1	2039.4
DDRF	1331	582.2	443	911	332.0	1841.7
CE	805	592.9	501	699	320.1	6402.5

The values in the row labelled CRC_All are slightly different to those presented in Table 7 because the observations contributing to this summary table were limited to animals with ages between 501 and 700 days whereas Table 7 included the final weight measurement for all animals meeting eligibility criteria from the Beef CRC data and included animals with ages ranging from 499 to 809 days.

The summary statistics indicate that the properties all have similar averages for both age and weight for the two age classes and that variance for weight does vary between properties.

The CE property had considerably higher variance estimates for weight than do the CRC properties or RS There is a 3 to 5 – fold difference between the property with the smallest variance and the property with the largest variance in each table. The findings are considered likely to reflect property level factors including management decisions concerning animal selection and husbandry as well as property factors associated with climate and soil/pasture quality.

3.5 Discussion for Beef CRC and industry datasets

The datasets used in these analyses were sourced from three different organisations: the Beef CRC, the Douglas Daly Research Farm, and a commercial beef enterprise incorporating a Brahman stud.

Datasets comprised weight measurements on cattle around the time of weaning and for the first year or so after weaning. A variety of additional information was included in the datasets (breed, sire, year, date of measurement) and for the CRC data there were measurements on a range of ancillary parameters (hip height, frame score, muscle score, crush score, and condition score).

Statistical analyses were used to assess the contributions of various explanatory variables on weight and growth outcomes. Estimates were made of means and standard errors for weaning weight and ADG measured over broadly similar periods. Mixed linear models were used to analyse data with a random effect added to models to account for the effect of sire on outcomes. This approach allowed estimation of the amount of unexplained variance in the outcomes that may be attributed to various effects, as a measure of the relative importance of various factors on weight and growth.

It is important to understand some of the assumptions underpinning this approach. It was assumed that the total variance in the outcomes of interest (body weight and ADG) was able to be estimated from the intercept only models and that these variance totals would remain constant. The genetics of individual animals (genes inherited from sire and dam) will contribute to this measured variance and in theory genetics will explain the heritable component of the outcomes being measured. It is expected that the sire and dam will each account for about one quarter of the total genomic variance in the outcomes and that the remaining 50% is accounted for by Mendelian variance.

Mendelian variance can be explained simply as the variance that is due to random genetic reassortment within the same genotype. If an experiment was designed that allowed recording of the identification of both sire and dam and the dataset contained records from multiple full siblings (same sire and same dam), then the variability measured between full siblings (same sire and same dam) would be a measure of the Mendelian contribution to variance.

In experimental studies it is possible to account for up to about 90% or more of the total variance in growth in young cattle to various measured effects (fixed effects and random effects such as sire and dam). Such studies are generally difficult and expensive to manage because they require control and measurement of so many factors. For example, it would be important to accurately identify sire and dam (and potentially earlier ancestors), and to use the same sires across multiple properties to avoid confounding of sire with property effects. In addition a range of other effects that are known to contribute at some level to variability in growth would need to be controlled for and/or measured. Under such conditions it is expected that about 5-10% of total variance in post-weaning cattle

growth may be able to be allocated to sire effects. These findings are consistent with a heritability (total genetic contribution to variance) of 20-30% (estimated as about four times the sire level variance component). Examples of attempts to measure genetic contribution to growth and other parameters under Australian conditions can be found in CRC publications (Barwick *et al*., 2009a, Barwick *et al*., 2009b).

The findings from the different datasets were broadly similar.

Age at weaning was the single biggest driver of weaning weight in all three datasets, accounting for between 28 to 40% of total variation in weaning weight in statistical models containing all significant explanatory factors that were available (full models). This is understandable given the large range in age at weaning and the generally close relationship between age and weight in young growing calves. Additional factors that were important included herd of origin (only assessed in the CRC dataset since the other two datasets involved only a single property), birth year and season. All of these factors are considered to be proxies for a range of environmental/climatic and management factors. **The effect of sire was important in all models, accounting for between 3 and 9% of total variance in weaning weight.**

Post weaning growth rate estimates were also similar. Models assumed a linear growth rate over the period of interest which is likely to be a simplification of a growth pattern that may be more complex and actually non-linear relationship. However, where additional data were present (CRC dataset), a linear relationship was found to fit the data well. In the other two datasets, there were too few measuring points to fit anything other than a linear relationship. The ADG estimates from the 3 datasets varied from 0.31 to 0.39 for the period from weaning to about 500-600 days of age. Some of the differences may have been due to differences in the period under assessment as well as variability due to various animal, property and other factors.

Weight at weaning was an important driver of post weaning ADG, accounting for between 1 and 6% of variance in the outcomes. Age and weaning weight appeared to be less important as drivers of post weaning growth compared with the importance of age in models where weaning weight was the outcome**. Herd of origin, birth year and season were also important**, again indicating the importance of environmental/climatic and management factors.

The effect of sire was variable, accounting for 1 to 21% of the total variance in full models. Estimates of the contribution of sire from the CRC and the RS datasets were similar, while the CE dataset tended to have higher proportions of total variance at the sire level. **It is not clear why sire explains more of the variance in the CE data**. All ADG estimates were based on two weight measures and datasets were limited in the fixed effects information that was available to be

modelled. It is possible that the CE dataset may have had fewer explanatory variables and it also had more variability in general as indicated by crude measures of variance for each property.

One of the major reasons for completing these analyses was to use the information to guide design of the prospective study (the subject of the remainder of this report). The key time period of interest for the prospective study was the 12 to 18 month period after weaning. Given that it was known that the current study would not be able to collect accurate data on animal birth dates or ages, it was important that an attempt be made to record weaning weight where possible and that weaning weight could potentially be included as a covariable in statistical models.

In addition in the commercial environment it was expected to be difficult to identify sires for individual animals. Properties participating in the proposed study would be managing mating under routine commercial conditions meaning that sires would be likely to be used in multiple sire groups and that individual sires would be almost certain to be used only within one property. It would not be possible to use the same sires across all properties in the study, as might be considered when specifically attempting to measure genetic impact of sires on some phenotypic outcome such as weight or growth. **From a statistical sense where a sire is only used on one property the effect of sire will be completely confounded with property.**

These issues (unknown animal age, identification of sire, number of animals per sire and total sample size) were all identified as having the potential to impact statistical analyses in the current study.

4 Liveweight gain in Northern Territory cattle herds

4.1 Introduction

The remainder of this report relates to the prospective study completed over a two to three year period on commercial properties covering multiple regions of the NT. The study investigated genetic, conformation, early management, behavioural and disease factors. One property was enrolled as a pilot herd in 2008 to test data collection procedures. Additional properties were then enrolled in the study during 2009 (five properties) and 2010 (five properties).

Participating properties were required to perform a minimum of two mustering rounds per year, to have appropriate yards and crush facilities for handling and weighing cattle, and to have management systems in place to ensure confidence in mustering efficiency so the same animals could be yarded and examined at each mustering round. All study activities were intended to be integrated with routine commercial operations though some properties did modify management slightly on occasion to facilitate yarding of study animals. The need for limited enrolment of properties each year was based on the logistics and labour requirements for visiting properties to collect data and it was not possible to enrol all properties in the first year.

Each participating property was involved in the study for 12 to 15 months, starting with the first round muster in the year in which they were enrolled and ending with the second round muster of the following year (providing a minimum of four observation points).

4.2 Methods

This study was conducted in accordance with the Australian Code of Practice for the Care and Use of Animals for Scientific Purposes and was approved by the Charles Darwin University (CDU; A07038).

4.2.1 Site Descriptions

4.2.1.1 Location

A total of eleven herds were enlisted in the study, running on properties located across seven regions of the NT and owned by both private and company enterprises (Figure 2, Table 22).

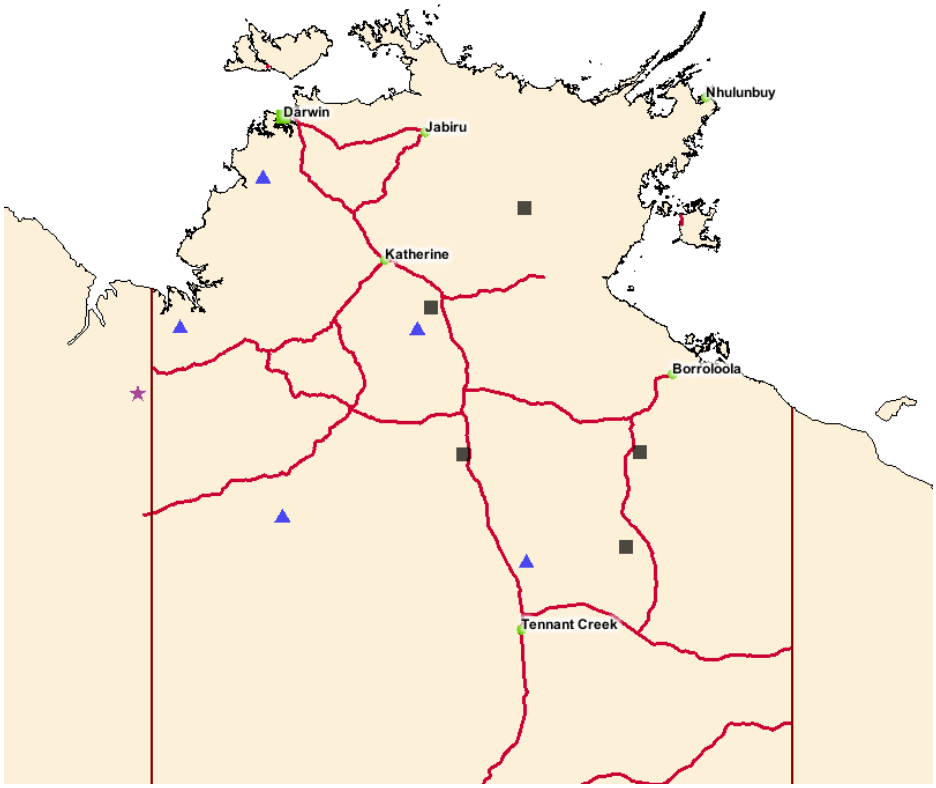


Figure 2: Location of study sites. ★ 2008/09; ■ 2009/10; ▲ 2010/11

Table 13: Descriptive summary of participating properties

Property	Year	Region	Property size (km^2)	Ownership structure
1	2009/10	Barkly	12212	Company
2	2009/10	Barkly	1701	Private
3	2009/10	Katherine	590	Company
4	2009/10	East-Arnhem	1315	Private
5	2009/10	Barkly	3580	Company
6	2010/11	Floodplain (north)	200	Private
7	2010/11	Barkly	5062	Company
8	2010/11	Floodplain (west)	3060	Company
9	2008/09	Katherine (1) VIC-Ord (2)	3794 (1) 1000 (2)	Company
10	2010/11	VRD	5493	Company
11	2010/11	Katherine	431	Private

4.2.1.2 Paddock and pasture descriptions

Table 14 provides paddock descriptions for study sites. Information includes total area, area within a 5 km radius of watering points, and land system breakdown within respective grazing radii. The general grazing period (dry-season, wet-season or annual) for paddocks is also provided. Study animals were often managed as part of a larger steer mob, and on most sites there was shifting of the mob between paddocks during the study period for management purposes.

Table 14: Paddock descriptions by property, with grazing period, watered area and land system components of watered area. DS=dry-season; WS=wet-season; AN=annual; 5WtrArea=area within 5km of water.

Property code	Year	Paddock name	Grazing period	Total Area (km^2)	5WtrArea (km^2)	5WtrArea % Total Area	5WtArea Land system %
1	2009-10	North Breeder	DS	45	41	92%	Austral (42%) Barky2 (41%) Sylvester (17%)
1	2009-10	X2	DS	65	54	84%	Austral (49%) Sylvester (30%) Drylake (21%)
1	2009-10	No 1 Lake	WS	761	445	58%	Drylake (50%) Barkly2 (28%) Sylvester (22%)
2	2009-10	Sturt Plain North	DS	20	19	97%	Atlas_II6 (100%)
2	2009-10	Bullock	WS	200	158	79%	Atlas_II6 (49%) Beetaloo (44%) Birrimbah (8%)
3	2009-10	Emu Apple	DS	3	3	100%	Banjo (43%) Larrimah (40%) Merring (17%)
3	2009-10	Cabbage Gum	DS	23	23	98%	Banjo (64%) Merring (36%)
3	2009-10	Stringybark	WS	58	44	77%	Banjo (100%)
4	2009-10	Steer	AN	39	39	100%	Favenc (50%) Cliffdale (36%) McArthur (14%)
5	2009-10	Lagoon	AN	34	32	94%	Cresswell (87%) Joanundah (13%)
6	2010-11	Multiple - Rotation system	DS				Improved
6	2010-11	Multiple - Rotation system	WS				Improved
7	2010-11	Bluebush	DS	532	269	51%	Drylake (43%) Barkly1 (42%) Sylvester (13%) Elliot (2%)
7	2010/11	New Paddock	WS	93	46	50%	Barkly1 (100%)

8	2010-11	Maidens	AN	11	11	97%	Legune (73%) Pinkerton (27%)
9	2008-09	Dick's Creek	DS	14	14	99%	Argyle (100%)
9	2008-09	River	WS	8	8	99%	Argyle (100%)
10	2010-11	Stallion	AN	8	8	96%	Franklin (88%) Wavehill (12%)
11	2010-11	Front	AN	40	23	57%	Banjo (100%)

4.2.1.3 Rainfall

Rainfall data was summarised for all properties and included seasonal conditions for both the year prior to the animals being weaned and inducted into the study, and the observation year.

A combination of methods was used for collecting rainfall data on 2009/10 properties: rain gauges installed at the experimental site (paddock); property rainfall records; and Bureau of meteorology (BOM) data. No rain gauges were installed at the experimental site for 2010/11 herds. Interpolated SILO daily data (Data Drill) was generated for 2009/10 and 2010/11 properties. Wet season onset (WSO) was determined by the date when a threshold of 50mm was reached after 1 September. Wet season retreat (WSR) was determined by the date when a threshold of 50mm was yet to fall working back from 30th April. Definitions of WSO and WSR were based on (Lo et al., 2008). Duration of wet season (WSD) was calculated as number of days from WSO to WSR. Total rainfall (mm) was calculated as the total rain which fell between 1st September and 30th April.

4.2.2 Animal descriptions and measures

4.2.2.1 Experimental animals

Eleven study groups of steers on different commercial cattle properties were inducted at weaning and observed in one of three 12-month periods: 2008/09 (n=1); 2009/10 (n=5); and 2010/11 (n=5), with the first year corresponding to the weaning year for the group. Animals were selected at random from a larger mob at weaning and inducted into the study. Table 15 provides a description of the experimental animals, including breed, sire breed, breeder/dam age structure, and branding status of animals at weaning (study induction). One group of weaners were sourced from a first-calf breeder mob (breeder age structure=3 years), while all remaining groups were from mature breeder mobs (>3 years). All weaners were sourced at first-round weaning muster on all properties.

Table 15: Description of experimental animals, with breed, sire breed, breeder (dam) age structure and branded status at weaning. Tcomp=Tropical composite; Bra=Brahman; BraX=Brahman-cross

Property	n	Breed	Sire breed	Breeder age structure	Branded status
1	231	Tcomp	Tcomp	>3 years	Unbranded
2	254	Bra	Bra	>3 years	Unbranded
3	224	Bra	Bra	>3 years	Unbranded
4	250	Bra	Bra, BraX	>3 years	Unbranded
5	289	Bra	Bra	>3 years	Unbranded

6	186	Bra	Bra	>3 years	Branded
7	250	Bra, BraX	Bra, BraX	3 years	Branded
8	207	Bra	Bra	>3 years	Mixed
9	155	Bra	Bra	>3 years	Unbranded
10	239	Bra	Bra	>3 years	Branded
11	241	Bra, BraX	Bra, BraX	>3 years	Mixed

4.2.2.2 Timing of observations

Experimental animals were yarded on four occasions for observation over the 12-month study period: Obs1, Obs2, Obs3 and Obs4 (see Figure 3). Where branding occurred as calves prior to weaning, animals were yarded for observation on only three occasions: Obs1, Obs3 and Obs4. In these cases, Obs2 did not occur as the purpose of this observation was primarily to record healing of wounds associated with husbandry procedures carried out at branding. Animals were yarded as close as possible to the end of the dry-season for Obs3, and as soon after the end of the wet-season for Obs4. Timing of observations was dependant on the availability of property staff to carry out musters, and in some cases was postponed for a considerable time after the end of the wet season to fit in with a muster to process sale cattle.

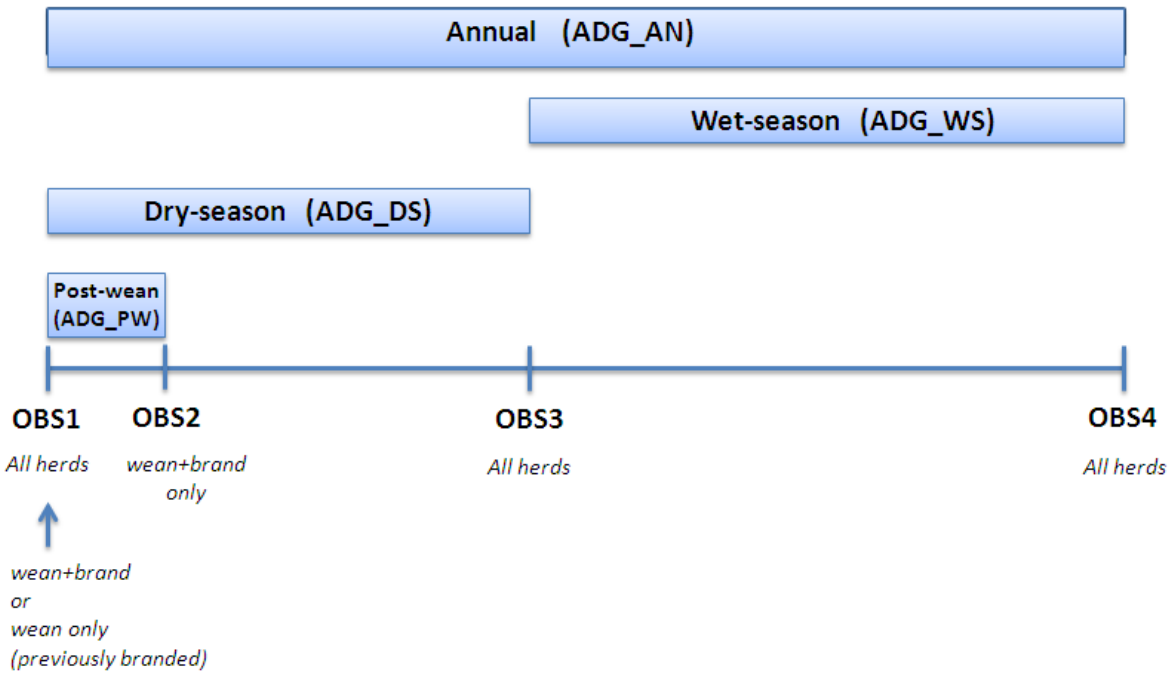


Figure 3: Sequence of observations on study herds and calculated average daily gain (ADG) periods

Table 16: Summary of dates for each observation by property

Property	Total animals	Obs1	Obs2	Obs3	Obs4
1	231	27/05/2009	16/06/2009	30/10/2009	13/08/2010
2	254	1/08/2009	23/08/2009	24/11/2009	26/06/2010
3	224	9/04/2009	1/05/2009	14/01/2010	24/05/2010
5	250	29/07/2009	22/08/2009	16/12/2009	15/05/2010
4	289	31/05/2009	30/06/2009	11/09/2009	
6	186	18/05/2010	.	26/10/2010	12/04/2011
7	250	7/08/2010	.	24/11/2010	9/05/2011
8	207	31/05/2010	15/06/2010	2/11/2010	6/06/2011
9	155	6/06/2008	27/06/2008	22/10/2008	29/04/2009
10	239	5/05/2010	.	5/11/2010	11/05/2011
11	241	7/06/2010	1/07/2010	29/10/2010	20/05/2011

4.2.2.3 Mob-level measures

A series of mob-level data was recorded for study herds and these are described in Table 26. This included information about the property the animals were located in (PIC), animal breed (BREED) and year of birth (YEAR), age structure of the Dam herd (DAM_AGE), vaccination schedule (VACC), health treatments schedule (TRT), supplementation strategy used (SUPPLEMENT) and method of supplementation delivery (SUPP_METHOD).

Table 17: Description of mob level variables that were recorded for each participating property

Code	Trait	Description
PIC	Property Identification Code	Unique property/mob identification code
YEAR	Year brand number	Year brand number
BREED	Breed	Breed. Bra=Brahman; BraX=Brahman-cross; TComp=Tropical composite

DAM_AGE	Dam age structure	Classification of dam herd age structure (3=3year old/first calf-heifer group; >3=older than 3 years/aged breeder group)
VACC	Vaccination	Vaccination, timing and disease prevention
TRT	Treatment	Health treatment, timing and classification of treatment
SUPPLEMENT	Supplement timing	Supplementation strategy. DS=dry season; WS=wet season; AN=annual/year-round
SUPP_METHOD	Supplement method	Supplementation delivery method. L=loose mix; B=block; L/B=combination of loose mix and block; W=water medicator

4.2.2.4 Animal measures

All observations and measurements recorded for individual animals over the 12-month study period are detailed in Table 18. Where data were measured on multiple occasions, the trait code is followed by a numerical prefix that can be mapped to the observation (e.g. LWT1, LWT2). Date, and, in most cases, time, of observation was recorded for all observations. Measurements of liveweight (LWT), body condition score (BCS) and flight speed (FS) were recorded at four observations (unless Obs2 did not occur, in which case these were measured at three observations over the study period). Hip height (HIP) was measured on three occasions, with the first record occurring at either Obs1 or Obs2. Tick counts (converted to a score) (TICK), buffalo fly counts (FLY) and fly lesion score (LESION) were recorded at Obs2, Obs3 and Obs4. Where animals had been implanted with hormone-growth promotant (HGP), timing of implantation and product was recorded, and a visual assessment made at subsequent observations of whether the pellet was retained.

Table 18: Abbreviation and definition of traits recorded on experimental animals

Code	Trait	Description
BREED	Breed	Bra=Brahman; BraX=Brahman-cross; TComp=Tropical composite
BRANDED_STATUS	Branded status	Branding status at weaning (branded; unbranded)
Growth traits		
LWT1	Liveweight (kg)	Weaning weight (kg)

LWT2	Liveweight (kg)	Weight (kg) post-weaning, recorded only on study groups where all or some of the animals required branding at weaning
LWT3	Liveweight (kg)	Weight (kg) end dry-season
LWT4	Liveweight (kg)	Weight (kg) end wet-season
HIP	Hip height (cm)	Hip height of the animal, when standing squarely on a level surface
BCS	Body condition score (1-9 scale)	Visual assessment of body condition
Temperament		
FS	Flight speed (m/second)	Electronically recorded exit speed from crush (meters/second).
Adaptive traits		
TICK	Tick score	Count of number of engorged (4.5-8mm) ticks on one side of animal [6], converted to a score[7]. Score 0= no ticks; 1=≤10; 2=11-30; 3=31-80; 4=81-150; 5=>150
FLY	Fly count	Count of number of buffalo flies [8] on the whole body [9] by one Observer. Converted to a categorical variable: 0=0; 1=1 to 30; 2=31 to 80; 3=≥81.
LESION	Lesion score	Total estimated area of lesion on one side of animal converted to a score [10]. Lesion classified as being *active* (erythematous hairless area sometimes raised and generally with slight serous exudation) or *chronic* (hairless areas covered with grey flaky material) [11]. Score 0=no lesion; 1=<2cm^2; 2=2-5cm^2; 3=5-10cm^2; 4=>10cm^2. Prefix of 1=active or 2=chronic
HGP_TIMING	Timing of HGP implant	Timing of implantation of HGP. Not implanted; calf only; calf+; weaning; pre-wet season.
HGP_RETENTION	HGP implant status	Visual observation of presence or absence of HGP implant (implanted animals only)
FEC	FEC	Count of number of worm eggs per gram of faeces . Measured on random selection of 10% of animals from study group only
FEC_B	FEC burden	Description of burden as not detected, detected, significant, acute
FOC	FOC	Count of number of oocysts per gram of faeces . Measured on random selection of 10% of animals from study group only

FOC_B	FOC burden	Description of burden as not detected, detected, significant, acute
Calculated traits		
ADG_DS	Dry season average daily gain (kg/day)	LWT3 – LWT1
ADG_WS	Wet season average daily gain (kg/day	LWT4 – LWT3
ADG_W	Annual average daily gain (kg/day)	LWT4 - LWT1

4.2.2.4.1 Weight and average daily gain (ADG) measures

Liveweight (kg) was recorded on up to four occasions for individual animals over the 12-month study period (Obs1_LWT, Obs2_LWT, Obs3_LWT, Obs4_LWT). Liveweight was measured using either a weigh box system or a portable platform. In some cases, the weighing system used differed within property, between observation events. The type of system used (weigh box or portable platform) was recorded for all weighing events, and the repeatability of liveweight measurement on the two types of weighing systems was assessed in a separate nested study. Weighing protocol (curfew) was recorded at each observation event, and was classified as: dry ($\geq$12 hours off feed and water); wet ($\geq$12 hours off feed, on water); full (no curfew); or combination (more than one type of curfew within observation event).

Liveweight and observation date was used to generate three defined periods of average daily gain (ADG; kg/day): dry-season (ADG_DS); wet-season (ADG_WS) and annual (ADG_AN), with the sequence of gain periods shown in Figure 3 and defined in Table 18

Consideration was given to estimation of a fourth ADG for the period just following weaning. After review of preliminary data this measure was discarded because it was considered to be of little value due to the short gain period, and the possibility that estimates could be affected by short-term shrinkages in bodyweight from disruption to feeding and watering over the weaning period.

4.2.2.4.2 Flight speed

The method of measuring flight speed was an adaptation of the method outlined by Radunz (1992). The method used in this study measured the time taken for the animal to cross two sensors (usually spaced between 1.7—2.2 m) after exiting the crush. The exact distance between beams was measured and used to

calculate exit speed (meters per second), where higher values indicate faster or 'flightier' animals. This method was adopted as it allowed for some variation in distance between beams, giving flexibility for setting up the sensor apparatus in different commercial cattle yards.

4.2.2.4.3 Husbandry practices and wound observations

A number of observations were recorded for the husbandry practices carried out at branding (where 'branding' refers to the practices of branding, castration, dehorning). Branding occurred within 7-10days after weaning, during which time weaners were generally yard-fed and weaner education was carried out. A description of traits recorded in relation to husbandry practices is given in Table 19. These observations were only made on animals which were unbranded, and subsequent observations were also made at Obs2 for wound healing.

Table 19: Abbreviation and definition of measurements of husbandry procedures on experimental animals

Abbreviation	Trait	Description
Procedure		
D_OPERATOR	Dehorning operator	Dehorning operator code (property code + unique number).
D_TOOL	Dehorning tool	Dehorning tool code. C=cup; S=scoop; DK=dehorning knife; K=knife; I=hot iron; O=other.
D_STERIL	Sterilisation (dehorning tool)	Dehorn tool sterilisation code. 1=antiseptic solution; 2=water; 3=no rinsing of tool.
D_WOUNDSIZE	Dehorning wound size (cm^2)	Total dehorn wound size area. Calculated using area of an oval (pi x ½ length x ½ width), and summing area for each side of the head.
SINUS_EXPOSED	Sinus exposed	Observation of opening of frontal sinus from dehorning wound, recorded as Y=exposed or N=not exposed. Where score differed between two dehorning wounds on one animal, the most severe score (Y) was recorded.
D_DRESSING	Dehorning wound treatment	Dehorning wound treatment applied, e.g. antiseptic solution, insecticidal treatment.
C_OPERATOR	Castration operator	Castrating operator code. Recorded as a code (property code + unique number).
C_TOOL	Castration tool	Castration tool code. S=scalpel; K=pocket knife; O=other.
C_STERIL	Sterilisation (castration tool)	Castration tool sterilisation code. 1=antiseptic solution; 2=water; 3=no rinsing of tool.

TESTES_REMOVED	Number of testes removed	Count of testes removed.
C_HIGH_LOW	Testes cut high or low	Method of removing testes. H= testes pulled out or cord cut high; L= cut low through spermatic cord.
D_BLEED	Dehorning bleed	Dehorn bleed score. 0=dehorned but no bleeding; 1=drip/slow bleed; 2=steady stream/moderate bleed; 3=spurt/rapid bleed.
C_BLEED	Castration bleed	Castration bleed score. 0=no bleed; 1=drip/slow bleed; 2=steady stream/moderate bleed; 3=rapid bleed.
TEMP	Temperature (°C)	Ambient temperature at time of procedure.
HUMIDITY	Relative humidity (%)	Relative humidity at time of procedure
Healing observations		
HORN_HEAL	Horn heal	Dehorning wound healing score. Score 0-5 with increasing signs of infection/poor healing.
CAST_HEAL	Castration heal	Castration wound healing score. Score 0-5 with increasing signs of infection/poor healing.

4.2.3 Sire identification

A subset of property managers were contacted and asked to describe the method they used for sourcing herd sires and criterion for selection (Table 20). While limited the information does provide an indication of the range of approaches used for selecting sires and indicated that properties are using a combination of selection criteria that include use of EBVs and other measurements. These findings supported the investigation of further exploration of opportunities for increased use of sire selection in northern beef breeding enterprises.

Table 20: Summary description of selection criteria used by properties for selection of bulls. Limited to those properties that provided this information.

		Selection based on		
Property	**Source**	**Appearance**	**Raw data**	**EBV**
1	Homebred nucleus	Yes	Yes	No
2	Stud auction, stud paddock	Yes	Yes	Yes
3	Homebred nucleus, commercial bull breeder	Yes	No	No
6	Stud paddock, commercial bull breeder	Yes	Yes	No
7	Stud auction, stud paddock	Yes	Yes	Yes

Participating properties were asked to yard sires when breeder mobs were yarded the year prior to weaning those animals that would be potentially enrolled in the longitudinal study, for collection of hair samples from sires for subsequent DNA analyses. This was timed so that samples could be collected from all candidate sires that may have been present in the breeder paddock at that time. This muster occurred as early in the year (thus as close to the mating period) as practical for property management. Where progeny were to be sourced from multiple breeder paddocks, bulls were sampled across all paddocks, and paddock of origin recorded for sires and progeny.

A similar hair sample was collected from all experimental animals at Obs1. All progeny and sire samples for 2008/09 and 2009/10 study groups were submitted to the University of Queensland Animal Genetics Laboratory. Sire assignment was performed using microsatellite genotyping of bulls and calves, with parentage assignment by exclusion (Gopinath and Kitts, 1984).

Computational methods for reconstructing groups of half-sibs were explored to determine whether accuracy of groupings was at an acceptable level to use these methods for assigning theoretical paternity in the absence of sire genotype. Sire assignment data from 2008/09 and 2009/10 study groups (paternity assignment by exclusion where sire genotype is known) was used to test the accuracy of grouping of half-sibs

using two models, COLONY v.2 and KINGROUP v.2.08. Where sires and progeny were sampled from multiple paddocks, each paddock was treated as a separate study site for this analysis.

4.2.4 Biological samples

Venous blood samples were collected from all animals at Obs1 and Obs4. Serum was extracted and stored frozen for later analysis of liver function measures, and disease testing (antibody detection).

Rectal faecal samples were collected from all animals at Obs2 (where observation occurred), Obs3 and Obs4. Samples were individually labelled and stored for later analysis for diet quality (diet selection) parameters.

Rectal faecal samples were also collected from a random sample of approximately 10% of animals at Obs2 (where observation occurred), Obs3 and Obs4 for measuring internal parasite burdens.

4.2.5 Statistical analyses

Data were entered into spreadsheet files, linked by unique animal ID (electronically recorded NLIS number and visual tag number) and property ID fields. Definitions were developed for variables and standardised naming conventions used to ensure that datasets could be managed effectively between different team members.

Nested studies were defined as those where samples or measurements were made on a subset of animals from participating properties. Examples of this included biochemistry and serology testing on serum samples, parasite testing on faecal samples and faecal NIRS testing on faecal samples.

Datasets were inspected to detect data entry errors and implausible values. Errors and implausible values were generally replaced with missing values and were only corrected if a valid value was identified in another source.

Analyses generally followed a standardised format. Descriptive analysis was based on plots and summary statistics including mean and confidence intervals for continuous data and proportions and percentages for nominal data.

The major outcomes of interest were the three average daily gain measures (ADG_DS, ADG_WS, ADG_AN). In most cases analyses were also conducted using the liveweights recorded at each measurement opportunity as outcomes (Obs1_LWT, Obs3_LWT, Obs4_LWT).

For each outcome of interest, regression analyses were used to assess the importance of explanatory factors on these outcomes. In some cases analyses were conducted at the property level, mainly where observations were not made on the same variables at the same time across all properties (data could not easily be combined). In other cases it was possible to combine data from multiple properties into a single analysis, and in these cases, property ID was included as a random effect to adjust for clustering at the property level.

All analyses were conducted in Stata, version 11 (www.stata.com) with alpha=0.05.

4.3 Results

The results section presents brief summaries of the main findings from completed analyses. More detailed results for many sections are presented in appendices to this report.

4.3.1 Multivariable analyses using ADG measures as outcomes

This section describes the results from a set of multivariable analyses that aimed to utilise all available data from multiple properties in analyses to explore factors that might explain variance in liveweight gain.

Univariable screening of variables associated with dehorning, castration, tick scores and fly scores did not identify any associations that were significant and biologically plausible. These variables were not considered for inclusion in multivariable models.

HGP use and HGP retention were associated with effects on liveweight and ADG measures, but unfortunately there was no consistent pattern of use that allowed effects to be analysed in multivariable analyses with combined data from multiple properties. HGP use was therefore unable to be incorporated into multivariable models.

There was an apparent association between dry season duration and ADG_DS and ADG_AN. The dry season duration appeared to be confounded completely with year of enrolment with all those properties enrolled in 2008 and 2009 being associated with long and severe dry seasons in the period following weaning. In contrast those properties enrolled in 2010 had a short and comparatively wetter dry season. A variable coding for enrolment year was created with two values: (0 coding for the 2008-2009 years and 1 coding for 2010). This variable was added to multivariable models to account for unmeasured effects of year and incorporating effects of rainfall patterns that were closely associated with year.

It was not possible to incorporate sire identity into any multivariable modelling because sires were only identified for some animals and on some properties.

Multivariable models were then developed separately for each of the ADG measures, using a linear modelling approach, and incorporating a random effect for property to account for clustering at the property level. All models included a variable coding for year of enrolment. A backwards stepwise model building process was applied with variables removed from the model if they were not statistically significant. This produced a final model including only significant explanatory variables. All omitted variables were then re-considered for

inclusion. When a final main effects model had been produced that contained only significant explanatory variables, biologically plausible two-way interactions were then considered from those terms contained in the final model. Interactions were only retained if they were statistically significant.

Because there was relatively large variation in weaning weight between properties, models included a standardised form of weaning weight. Standardisation of a variable produces a variable that has a mean of zero and a standard deviation of one, allowing unit-less comparisons of effects.

Standardisation was implemented separately within each property again because of the variability between properties with relation to weaning weight. The result was a variable where values of zero represent animals of average weaning weight for that property, negative values represent animals that have a lower weaning weight than average for that property (-1 means an animal that has a weaning weight that is one standard deviation below the average for that property), and positive values represent animals that have a weaning weight greater than the average for that property (+2 means an animal that has a weaning weight that is two standard deviations above the average for that property). Incorporating a standardised variable for weaning weight provides a way of adjusting for variability in weaning weight in those models attempting to explain post weaning weight gain.

Body condition score was not considered for inclusion in multivariable models because it was considered to be highly correlated with weight at any one measure.

Flight speed and hip height were considered for inclusion in the multivariable models. Flight speed was the average of all flight speed measures for any individual animal.

Hip height was coded as a binary variable reflecting whether animals were less than or equal to the median hip height for a given property, or greater than the median hip height for a given property. This approach was taken to account for the variation between properties in hip height while still retaining the ability to measure an association that reflected the effect of being shorter or taller for those animals within any property.

Table 21: Results from a multivariable model with ADG_DS (kg/hd/day) as the outcome. Coef=coefficient, se=standard error, z=z-statistic, CI=confidence interval.

				95% CI	

Variable	Level	Coef	se	z	p-value	Lower	Upper
Enrolment year	2008-2009	reference					
	2010	0.132	0.038	3.5	<0.001	0.058	0.206
Weaning weight		-0.028	0.003	-10.36	<0.001	-0.034	-0.023
Obs1 hip height	Up to median	reference					
	Taller than median	0.015	0.005	2.7	0.007	0.004	0.025
Intercept		-0.020	0.023	-0.87	0.385	-0.066	0.025

Random effects		Variance	se	95% CI Lower	95% CI Upper
Variance	Property	0.003	0.001	0.001	0.007
	Residual	0.007	0.000	0.006	0.007

The final model for ADG_DS incorporated explanatory variables coding for enrolment year, weaning weight and Obs1 hip height (Table 21). The interaction between hip height and weaning weight was considered (reflecting possible distinctions between the various combinations of height and weight) but was not significant and was not retained in the final model.

The coefficients displayed in the final model output represent the predicted change in the outcome (ADG_DS) based on a one-unit change in the explanatory variable. The interpretation of the coefficient depends on whether the explanatory variable is continuous or categorical (categorical means a name distinguishing one level or category from another). The final model contained three explanatory variables. Two of these were coded as categorical variables (enrolment year and Obs1 hip height).

For categorical variables the coefficient measures the change in one level of the variable compared to the reference level. For enrolment year, those animals that were enrolled in 2010 had an increase of 0.132 in ADG_DS compared to the reference level for this variable (animals enrolled in 2008-2009). For Obs1 hip height, those animals that were taller than the median hip height (as determined within each property) had a ADG_DS that was increased by 0.015 kg/day compared to those animals that were less than or equal to the median hip height for that property.

For continuous variables (weaning weight) the coefficient measures the impact of a one unit increase in the explanatory variable. In this case a 1 kg increase in weaning weight was associated with a -0.028 change in ADG_DS. Animals that were heavier at weaning had a lower ADG_DS.

The variance estimates can be compared to those from an intercept only model run on the same data retained for the final model above to allow comparisons (data not shown).The multivariable model was associated with a 34% reduction in total variance compared to the intercept only model and a 61% reduction in the property-level variance, reflecting the explanatory power of the variables incorporated into the model. The multivariable model has a residual ICC estimate of 0.28. The ICC is an estimate of the correlation between two randomly selected animals from the same property and may also be interpreted as the proportion of the overall variance in the outcome that is not explained by the fixed effects in the model and that is attributable to property-level effects. The value of 0.28 reported for this model is still relatively high, meaning a high residual correlation between measurements from the same property, and reflecting unmeasured explanatory factors at the property level that could if measured and included in the model, explain more of the variation between properties. This is an indication that further work to identify property level explanatory variables might identify additional important drivers of variability in the outcome.

Predicted mean ADG_DS values were generated from the multivariable model and are produced below.

Weaning weight was included in the multivariable model as a continuous, standardised variable (mean=zero and standard deviation =1). Predicted means for ADG_DS were generated for five specified values of weaning weight (-2, -1, 0, 1, 2), providing predicted ADG_DS for animals that are two or one standard deviations below the mean weaning weight for any property, animals that have a mean weaning weight for any property and animals that are 1 or 2 standard deviations above the mean weaning weight for any property. The predicted overall ADG_DS across those animals that represent the average weaning weight for each property was 0.037 kg/hd/d. The highest ADG_DS values were seen in those animals with a lighter than average weaning weight, and as weaning weight increased, the ADG_DS values declined.

As indicated in the discussion above on the coefficients displayed for the final model, there was a significant association between hip height at weaning and ADG_DS, with animals that were taller at weaning having a higher ADG_DS.

There was a comparatively large effect of enrolment year with animals from properties that were enrolled in 2010 having a significantly higher ADG_DS compared to those properties enrolled in either 2008 or 2009. This effect is presumed to be due largely to the seasonal conditions with 2008 and 2009 being dry years and 2010 being a very wet year.

Table 22: Predicted ADG-DS (kg/hd/day) derived from the multivariable model above, at specified levels of the explanatory variables.

		Predicted		95% CI	
Variable	**Level**	**ADG_DS**	**se**	**Lower**	**Upper**
Weaning weight	2 SD below mean	0.094	0.019	0.057	0.132
	1 SD below mean	0.066	0.018	0.029	0.102
	Mean for each property	0.037	0.018	0.001	0.073
	1 SD above mean	0.009	0.018	-0.027	0.045
	2 SD above mean	-0.020	0.019	-0.057	0.018
Obs 1 hip height	Up to median hip height	0.029	0.018	-0.008	0.065
	Greater than median	0.043	0.018	0.007	0.079
Enrolment year	2008-2009	-0.015	0.023	-0.060	0.031
	2010	0.117	0.030	0.059	0.176

Table 23: Results from a multivariable model with ADG_WS (kg/hd/day) as the outcome.

						95% CI	
Variable	**Level**	**Coef**	**se**	**z**	**p-value**	**Lower**	**Upper**
Weaning weight		-0.001	0.006	-0.23	0.82	-0.012	0.010
Obs1 hip height	Up to median						
	Taller than median	0.018	0.008	2.3	0.021	0.003	0.034
Interaction: wean weight * hip height	hip1_bin#c.c_obs1_weight						
	Up to median						
	Taller than median	0.015	0.008	1.82	0.069	-0.001	0.031
Intercept		0.426	0.040	10.64	<0.001	0.347	0.504

				95% CI	
Random effects		**Variance**	**se**	**Lower**	**Upper**
Variance	Property	0.011	0.006	0.004	0.032
	Residual	0.011	0.000	0.010	0.012

The final model for ADG_WS included variables for weaning weight and hip height and the interaction between weaning weight and hip height. Enrolment year and flight speed were considered and were dropped from the model because they were not significant.

Predicted mean ADG_WS values were generated from the multivariable model and plotted to display the association. For animals that were less than or up to median hip height at Obs1 measurement, there was no significant association between weaning weight and ADG_WS (p=0.6). This is displayed as the dashed line in Figure 4. In contrast there was a significant association between weaning weight and ADG_WS in those animals that were taller than the median hip height for any property. In these animals, as weaning weight increased relative to the average in any property, ADG_WS also increased (an increase of one standard deviation unit in weaning weight within any property was associated with an increase of 0.0137 kg/hd/day in the ADG_WS).

There was a high correlation between hip height measurement at Obs1 and Obs3 (r-squared=0.84) and therefore only Obs1 hip height was considered for inclusion in the final model.

The variance estimate from the final model was compared to a variance estimate derived from an intercept only model applied to the same dataset that was retained in the final model. **The multivariable model only reduced the intercept only variance by about 1% indicating that the multivariable model was not providing much additional explanatory power.** The multivariable model did not reduce property level variance and the residual intra-class correlation for the final model remained at 0.5, **suggesting that there remained a significant amount of unexplained variance in ADG_WS that was at the property level**. As discussed for the ADG_DS model the presence of a relatively high residual ICC indicates that further work aimed at identifying property-level explanatory variables may be useful if additional important drivers were able to be identified that explained a meaningful proportion of the residual variance. If one or more drivers could be identified that both explained relatively large proportions of the residual variance (resulting in a reduction in the residual ICC in a multivariable model) and that were amenable to management or intervention in some way, then these drivers may potentially be manipulated by producers to influence the outcome (increase ADG).

There was no effect of enrolment year on ADG_WS, suggesting that wet season growth in liveweight may be less variable from year to year. Caution is urged in interpreting this finding given that the datasets used in these analyses only covered a relatively short period of time.

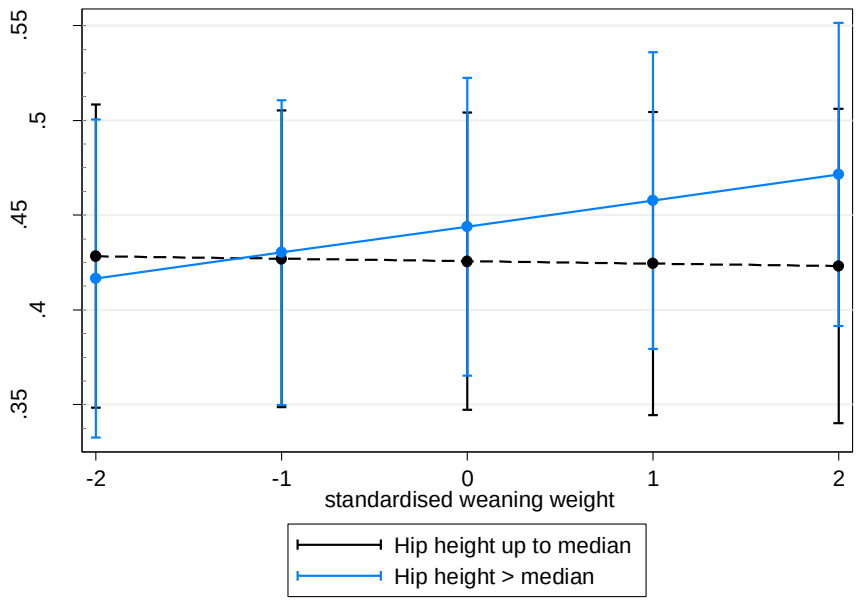


Figure 4: Plot of predicted mean ADG_WS values for each combination of Obs1 hip height (up to median, greater than median) and standardised weaning weight.

Table 24: Results from a multivariable model with ADG_AN as the outcome.

						95% CI	
Variable	**Level**	**Coef**	**se**	**z**	**p-value**	**Lower**	**Upper**
Enrolment year	2008-2009	reference					
	2010	0.065	0.030	2.21	0.027	0.007	0.123
Weaning weight		-0.013	0.002	-5.42	<0.001	-0.018	-0.008
Obs1 hip height	Up to median	reference					
	Taller than median	0.020	0.005	4.17	<0.001	0.010	0.029
Flight speed	slowest third						
	middle third	-0.002	0.005	-0.45	0.656	-0.012	0.007
	fastest third	-0.013	0.005	-2.4	0.017	-0.024	-0.002
Intercept		0.219	0.020	11.09	<0.001	0.180	0.257

				95% CI	
Random effects		**Variance**	**se**	**Lower**	**Upper**
Variance	Property	0.0015	0.001	0.001	0.004
	Residual	0.004	0.000	0.004	0.005

The final model included variables for enrolment year, standardised weaning weight, hip height measured at weaning and flight speed. Flight speed was coded as a 3-level categorical variable, using the average flight speed (metres per second) to cut the data into equal thirds (slower animals have a smaller numeric value).

The impacts of each explanatory variable on ADG_AN can be interpreted by considering the predicted mean ADG_AN values derived from the multivariable model (Table 25).

Table 25: Predicted ADG-AN (kg/hd/day) derived from the multivariable model above, at specified levels of the explanatory variables.

		Predicted	95% CI

Variable	Level	ADG_AN	se	Lower	Upper
Weaning weight	2 SD below mean	0.277	0.015	0.247	0.308
	1 SD below mean	0.264	0.015	0.235	0.293
	Mean for each property	0.251	0.015	0.222	0.280
	1 SD above mean	0.238	0.015	0.209	0.267
	2 SD above mean	0.224	0.015	0.194	0.254
Obs 1 hip height	Up to median hip height	0.241	0.015	0.212	0.270
	Greater than median	0.261	0.015	0.232	0.290
Enrolment year	2008-2009	0.223	0.019	0.185	0.261
	2010	0.289	0.022	0.245	0.332
Flight speed	Slowest third	0.255	0.015	0.226	0.284
	Middle third	0.253	0.015	0.224	0.282
	Fastest third	0.242	0.015	0.213	0.271

There was a small but significant negative association between weaning weight and ADG_AN, indicating that animals that were heavier at weaning, had a reduced ADG_AN. This overall effect as represented by the annual weight gain measure is comprised of the two season-specific components represented in the earlier models. During the dry season, heavier animals had a reduced ADG_DS, while in the wet season this effect was reversed but only in the taller animals.

There was no interaction between weaning weight and weaning hip height in the model with ADG_AN as the outcome (the interaction term was considered but was not retained because it was not significant).

There was a significant overall effect of hip height with taller animals having a higher ADG_AN.

There was a significant effect of year of enrolment with those properties enrolled in 2008-2009 having lower ADG_AN values. This appeared to be largely due to the effect on dry season growth since there was no effect of year on wet season growth.

There was a small but significant effect of flight speed. Those animals which had flight speed values in the highest third had a significant reduction in ADG_AN when compared to the animals in the lower third. There was no difference in ADG_AN between the slowest animals and those in the middle third.

When the multivariable model was compared to an intercept only model based on the same data, comparisons of variance estimates indicated that **the multivariable model was associated with an 18% reduction in total variance (explanatory power of the model) and a 42% reduction in property level variance. The residual ICC estimate in the multivariable model was 0.26 indicating that there remained a relatively large proportion of unexplained variance at the property level that can be attributed to factors other than those included in the model.**

4.3.2 Descriptive analyses for liveweight and ADG

The following tables show simple descriptive summaries (mean, standard deviation, minimum and maximum and count) for each observation period. These are presented for each property.

Table 26: Summary statistics by property, showing count of animals enrolled at the start, dates of each observation, number of records at each observation and summary statistics for liveweight (LWT). n enrolled=number of cattle enrolled, n=number of observations contributing to any one measurement, SD=standard deviation.

Obs1_LWT	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
n enrolled	**231**	**254**	**224**	**250**	**289**	**186**	**250**	**207**	**155**	**239**	**241**
month	May-09	Aug-09	Apr-09	May-09	Jul-09	May-10	Aug_10	May-10	Jun-08	May-10	Jun-10
dates	27 & 28	01	09	31/5 & 1/6	29 & 30	18 & 19	7th	31/5 & 1/6	6th	5/5 & 31/5	7/6 & 4/8
n	208	252	221	283	248	184	218	205	148	237	239
Mean (kg)	214.39	211.33	133.19	159.9	212.96	224.5	180.76	171.49	161.1	217.53	177.02
SD	51.2	43.833	19.9	29.38	35.86	35.37	26.07	39.01	39.71	30.14	35.68
min	91	104	88	87.5	131	134	95.5	84	101	136.5	60.5
max	303	338	190	246	307	321	290	348	334	313	269
Obs3_LWT	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
month	Oct-09	Nov-09	Jan-10	Sep-10	Dec-09	Oct-10	Nov-10	Nov-10	Oct-08	Nov-10	Oct-10
dates	30	24/11 & 7/12	14	11	16	26th	24th	2nd	22nd	5th	29&30
n	207	237	207	177	223	182	196	178	134	207	227
Mean (kg)	259.95	218.32	148.3	162.51	204.93	252.5	191.93	202.03	150.7	231.9	179.9
SD	53.08	43.97	20.87	24.82	33.23	32.8	24.7	42.25	35.5	28.9	33.3

min	138	111	88	109	132	137.5	120	114	101	147.5	72.5
max	360	361	210	260	309	334	298	370	310	317	257
Obs4_LWT	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
month	Aug-10	Jun-10	May-10		May-10	Apr-11	May-11	Jun-11	Apr-09	May-11	May-11
dates	13 & 14	24 & 26	24		15	21&13&14	9th	6th	29th	11th	20th
n	196	227	194	no data	211	179	221	186	85	107	209
Mean (kg)	386.55	278.15	207.1		286.47	300.5	265.76	301.26	244.88	334.69	261.64
SD	48.03	45.93	28.18		38.62	34.14	36.8	45.66	41.67	23.33	45.57
min	256	179.5	126		195	184	179	208	168	271	131.5
max	498	429	296		386	393	382	492	408	416	374

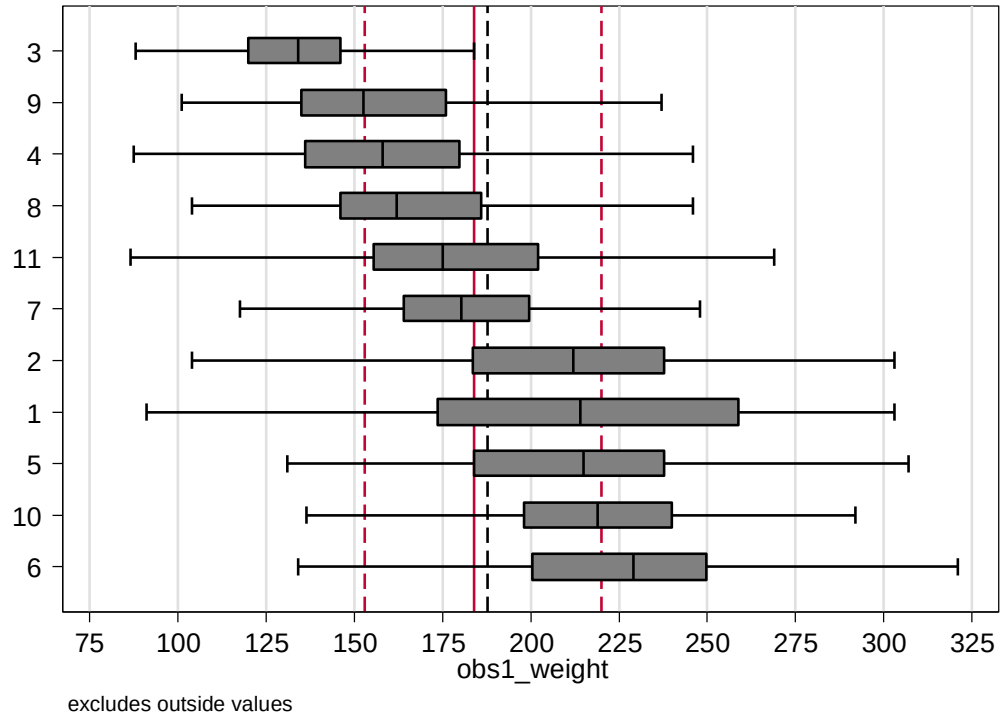


Figure 5: Box plot showing summary statistics for Obs1_LWT for each property, presented in ascending order. Outlier values are omitted. The left and right edges of each box mark the 25th percentile and 75th percentile for that property, and the vertical line inside the box marks the median (50th percentile) for each property. The vertical solid red line shows the overall median value across the entire dataset (184kg) and the vertical dashed red lines show the overall 25th (153 kg) and 75th (220 kg) percentile values for Obs1_LWT. The vertical dashed black line shows the overall mean Obs1_LWT across the entire dataset (187.7 kg).

Table 27: Intercept only model output with Obs1_LWT as the outcome and incorporating a random effect coding for property. se=standard error, CI=confidence interval, ICC=intra-class correlation coefficient, Var=variance.

			95% CI	
	Coef	**se**	**Lower**	**Upper**
Intercept	187.65	8.64	170.72	204.58
			95% CI	
	Variance	**se**	**Lower**	**Upper**
Var(property)	814.81	349.99	351.11	1890.92
Var(residual)	1278.44	36.66	1208.57	1352.36

Total variance	2093.25
ICC	0.389

Obs1_LWT is a measure of weaning weight. The striking feature of the summary information presented in Table 26 and Figure 5 is the variation between property-specific mean (and median) weaning weight measures. Figure 5 displays a relatively large amount of summary information in a single visual layout. The box for each property represents 50% of the observations for that property and shows the range between the lower and upper 25th percentiles (lower and upper edge of the box) and the median (vertical line within the central area of the box) which separates the lower and upper half of the values for each property. The vertical red lines display the same information across the whole dataset (ignoring property).

Table 27 presents results of a random effects linear model to generate estimates of variance. The intercept value displayed in Table 27 is the overall mean weaning weight in kg (averaged across all properties). The two variance estimates represent the clustered nature of the data. Animal measurements are clustered within each property. Animals from the same property are more similar than animals from different properties because of similarities in factors operating at the level of each property (topography, climate, pasture, soil, rainfall, management factors, and animal factors that may be similar within any one property such as genetics). The two variance estimates may be described as the within property variance (residual variance or variance at the observation level), and the between property variance (property-level variance).

The intra-class correlation coefficient (ICC) is a measure of the correlation between observations within the same cluster-unit; in this case, property. Values of ICC may range from zero (0) to one (1).

Values that are equal to or very close to zero indicate that the property-level variance is negligible relative to the residual variance. This is the same as saying that there is little correlation between any two measurements from the same property and that each measurement may be considered to be independent to any other measure regardless of whether they come from the same property or not (indicating there is no clustering in the dataset).

Values of ICC that are rising above zero, are indicative of clustering with increasing ICC values providing a direct measure of the strength of the correlation or level of clustering.

In this dataset, the ICC values were consistently high (0.389 for Obs1_LWT and higher for other measures) indicating that there is a high level of correlation between any two measurements from the same property.

The ICC is also a measure of the proportion of variance in the outcome that exists at the cluster level. In the case of weaning weight, 39% of the variance in weaning weight exists at the level of the property and the balance (61%) lies at the level of the observation made on an individual animal.

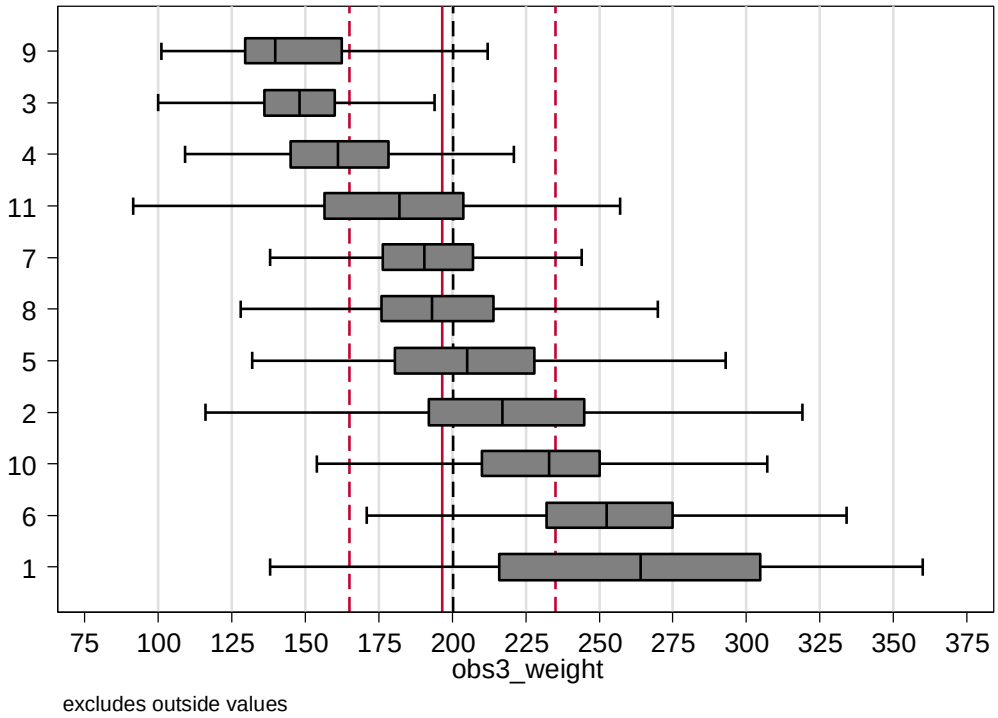


Figure 6: Box plot showing summary statistics for Obs3_LWT for each property, presented in ascending order. Outlier values are omitted. The left and right edges of each box mark the 25th percentile and 75th percentile for that property, and the vertical line inside the box marks the median (50th percentile) for each property. The vertical solid red line shows the overall median value across the entire dataset (196.5 kg) and the vertical dashed red lines show the overall 25th (165 kg) and 75th (235 kg) percentile values for Obs3_LWT. The vertical dashed black line shows the overall mean Obs3_LWT across the entire dataset (200.28 kg).

Table 28: Intercept only model output with Obs3_LWT as the outcome and incorporating a random effect coding for property. se=standard error, CI=confidence interval, ICC=intra-class correlation coefficient, Var=variance.

			95% CI	
	Coef	**se**	**Lower**	**Upper**
Intercept	200.28	11.02	178.67	221.89
			95% CI	
	Variance	**se**	**Lower**	**Upper**

Var(property)	1330.50	570.22	574.39	3081.91
Var(residual)	1247.80	37.93	1175.62	1324.41
Total variance	2578.30			
ICC	0.516			

Obs3_LWT represents liveweight towards the end of the dry season. Figure 6 shows a graphical summary of the spread of values within each property and the overall median and mean values. **More than 50% of the variation in liveweight at this point (Obs3_LWT) was at the property level.**

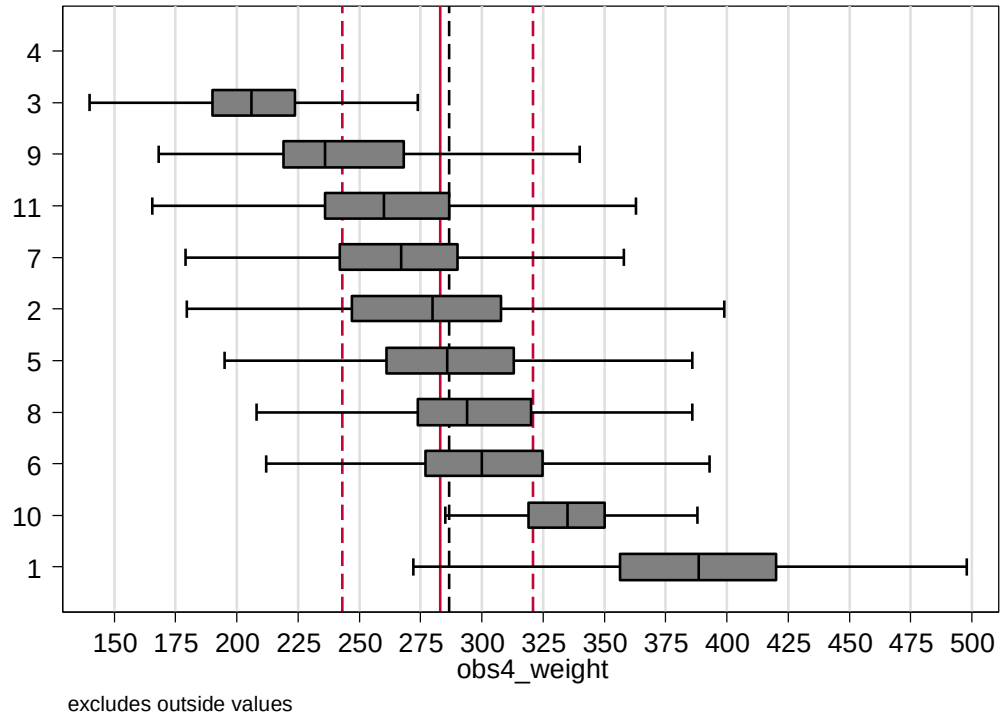


Figure 7: Box plot showing summary statistics for Obs4_LWT for each property, presented in ascending order. Outlier values are omitted. The left and right edges of each box mark the 25th percentile and 75th percentile for that property, and the vertical line inside the box marks the median (50th percentile) for each property. The vertical solid red line shows the overall median value across the entire dataset (283 kg) and the vertical dashed red lines show the overall 25th (243 kg) and 75th (321 kg) percentile values for Obs4_LWT. The vertical dashed black line shows the overall mean Obs4_LWT across the entire dataset (286.7 kg).

Table 29: Intercept only model output with Obs4_LWT as the outcome and incorporating a random effect coding for property. se=standard error, CI=confidence interval, ICC=intra-class correlation coefficient, Var=variance.

			95% CI	
	Coef	**se**	**Lower**	**Upper**
Intercept	286.70	14.80	257.70	315.70
			95% CI	
	Variance	**se**	**Lower**	**Upper**
Var(property)	2179.96	979.29	903.79	5258.11
Var(residual)	1617.55	53.84	1515.39	1726.60
Total variance	3797.51			
ICC	0.574			

Obs4_LWT represents liveweight towards the end of the wet season. Figure 7 shows a graphical summary of the spread of values within each property and the overall median and mean values. **More than 50% of the variation in liveweight at this point (Obs4_LWT) was at the property level.**

Table 30: Summary statistics by property, showing count of animals enrolled at the start, days between observations, number of records at each observation and summary statistics for three separate Average Daily Gain (ADG) measures. ADG_DS= dry season ADG, ADG_WS=wet season ADG, ADG_AN=annual ADG.

ADG_DS	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
n enrolled	**231**	**254**	**224**	**250**	**289**	**186**	**250**	**207**	**155**	**239**	**241**
days: 1 to 3	155, 156	115,128	280	102,103	140	160,161	109	154,155	138	158,184	86,145
n	202	236	207	177	225	182	201	177	133	207	228
mean (kg/d)	0.290	0.056	0.053	-0.042	-0.057	0.174	0.0972	0.196	-0.086	0.082	0.019
SD	0.109	0.118	0.039	0.079	0.106	0.084	0.081	0.078	0.072	0.077	0.076
min	-0.058	-0.352	-0.093	-0.233	-0.357	-0.130	-0.17	-0.040	-0.3	-0.260	-0.22
max	0.494	0.406	0.179	0.233	0.328	0.430	0.28	0.400	0.11	0.310	0.23
ADG_WS	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
days: 3 to 4	287,288	199,214	130	no data	150	168,170	166	216	189	187	202,203
n	201	220	191		202	178	214	173	82	88	206
mean (kg/d)	0.443	0.283	0.456	no data	0.545	0.286	0.455	0.484	0.506	0.554	0.405
SD	0.100	0.071	0.103		0.113	0.075	0.17	0.075	0.0967	0.076	0.118
min	0.188	0.084	0.200		0.167	0.070	0.1	0.280	0.29	0.360	0.17
max	0.700	0.533	0.746		0.800	0.560	0.85	0.810	0.75	0.700	0.79
ADG_AN	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
days: 1 to 4	423,424	305,307	388	no data	266,267	328,331	275	370,371	317,327	345,371	289,347

n	192	226	194		215	178	223	185	86	107	212
mean (kg/d)	0.389	0.200	0.180	no data	0.260	0.232	0.301	0.355	0.247	0.331	0.253
SD	0.066	0.056	0.045		0.055	0.060	0.105	0.059	0.056	0.060	0.075
min	0.138	0.033	0.068		0.128	0.080	0.06	0.150	0.1	0.170	0.09
max	0.512	0.365	0.293		0.431	0.380	0.53	0.520	0.35	0.500	0.46

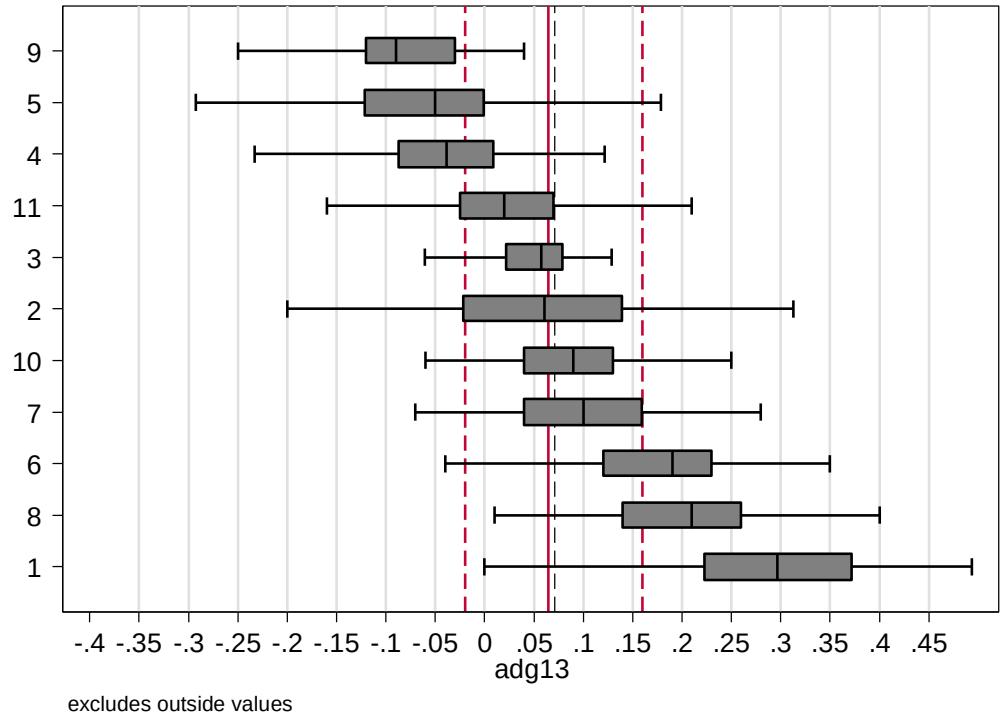


Figure 8: Box plot showing summary statistics for ADG_DS for each property, presented in ascending order. Outlier values are omitted. The left and right edges of each box mark the 25th percentile and 75th percentile for that property, and the vertical line inside the box marks the median (50th percentile) for each property. The vertical solid red line shows the overall median value across the entire dataset (0.06 kg/hd/day) and the vertical dashed red lines show the overall 25th (-0.02 kg/hd/day) and 75th (0.16 kg/hd/day) percentile values for ADG_DS. The vertical dashed black line shows the overall mean ADG_DS across the entire dataset (0.07 kg/hd/day).

Table 31: Intercept only model output with ADG_DS as the outcome and incorporating a random effect coding for property. se=standard error, CI=confidence interval, ICC=intra-class correlation coefficient, Var=variance.

			95% CI	
	Coef	**se**	**Lower**	**Upper**
Intercept	0.07	0.03	0.007	0.136
			95% CI	
	Variance	**se**	**Lower**	**Upper**
Var(property)	0.012	0.005	0.005	0.028
Var(residual)	0.008	0.000	0.007	0.008

Total variance	0.02
ICC	0.611

The results for ADG measures are similar to those reported above for liveweight measures in that there is a large amount of variance that is attributed to property-level effects.

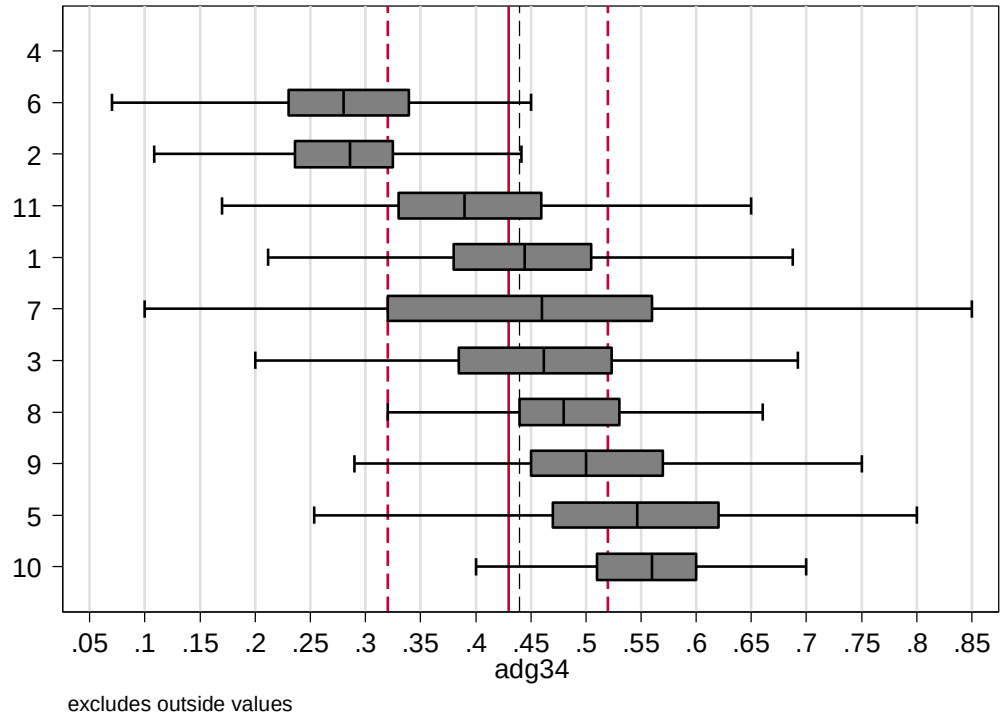


Figure 9: Box plot showing summary statistics for ADG_WS for each property, presented in ascending order. Outlier values are omitted. The left and right edges of each box mark the 25th percentile and 75th percentile for that property, and the vertical line inside the box marks the median (50th percentile) for each property. The vertical solid red line shows the overall median value across the entire dataset (0.43 kg/hd/day) and the vertical dashed red lines show the overall 25th (0.32 kg/hd/day) and 75th (0.52 kg/hd/day) percentile values for ADG_WS. The vertical dashed black line shows the overall mean ADG_WS across the entire dataset (0.44 kg/hd/day).

Table 32: Intercept only model output with ADG_WS as the outcome and incorporating a random effect coding for property. se=standard error, CI=confidence interval, ICC=intra-class correlation coefficient, Var=variance.

			95% CI	
	Coef	**se**	**Lower**	**Upper**
Intercept	0.44	0.03	0.386	0.497
			95% CI	
	Variance	**se**	**Lower**	**Upper**
Var(property)	0.0080	0.0036	0.0033	0.0193
Var(residual)	0.0114	0.0004	0.0107	0.0122

Total variance	0.02
ICC	0.411

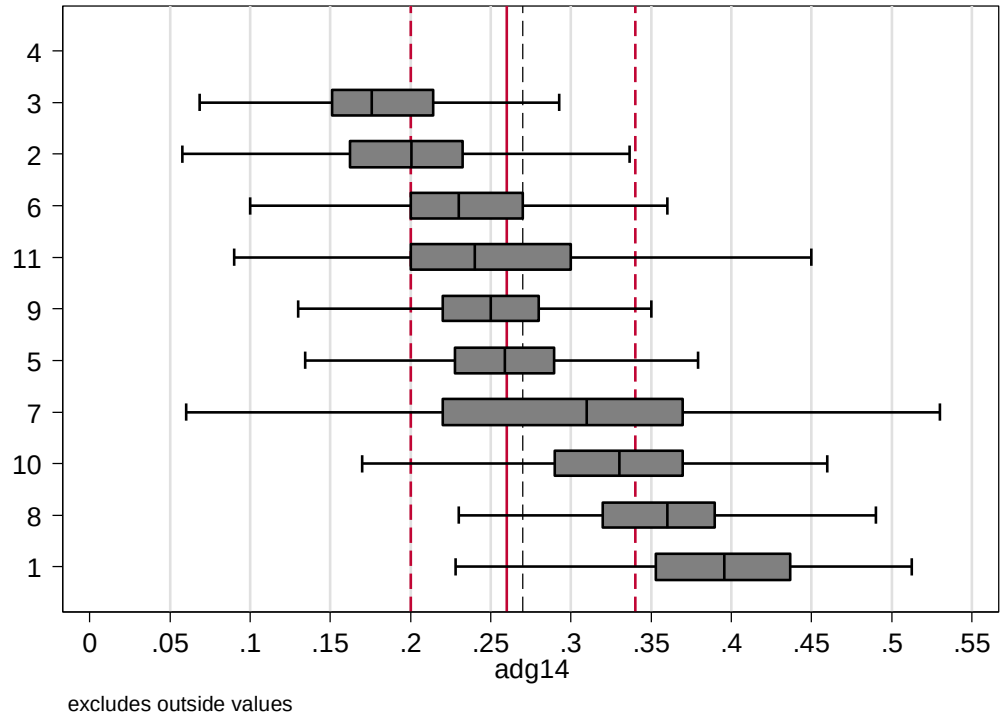


Figure 10: Box plot showing summary statistics for ADG_AN for each property, presented in ascending order. Outlier values are omitted. The left and right edges of each box mark the 25th percentile and 75th percentile for that property, and the vertical line inside the box marks the median (50th percentile) for each property. The vertical solid red line shows the overall median value across the entire dataset (0.26 kg/hd/day) and the vertical dashed red lines show the overall 25th (0.2 kg/hd/day) and 75th (0.34 kg/hd/day) percentile values for ADB_AN. The vertical dashed black line shows the overall mean ADG_AN across the entire dataset (0.27 kg/hd/day).

Table 33: Intercept only model output with ADG_AN as the outcome and incorporating a random effect coding for property. se=standard error, CI=confidence interval, ICC=intra-class correlation coefficient, Var=variance.

			95% CI	
	Coef	**se**	**Lower**	**Upper**
Intercept	0.27	0.02	0.235	0.314
			95% CI	
	Variance	**se**	**Lower**	**Upper**
Var(property)	0.0041	0.0018	0.0017	0.0099
Var(residual)	0.0045	0.0001	0.0042	0.0048

Total variance	0.01
ICC	0.477

4.3.3 Repeatability of bodyweight measures

There was interest in collecting repeated measures of liveweight on a sample of animals in order to assess repeatability of weighing systems. A sample of animals (184 animals from a total of four properties) were weighed twice on the same day by running the animals back over the scales immediately following the first weight measurement. A detailed description of the approach and results of analyses is provided in the appendices.

In general there was good agreement or repeatability. The 95% limits of agreement for successive weight measures were within plus or minus 10 kg when data from both weighing systems (fixed weigh boxes, and portable weigh platform) were combined.

There were differences between weighing systems. The fixed weigh boxes provided a tighter level of agreement, with the mean difference between the two successive measurements being -0.11 kg (close to zero) and the 95% limits of agreement were between plus or minus 7.5 kg.

In contrast the results for portable platforms showed less agreement. The mean difference was -1.9 kg and the 95% limits of agreement ranged from -12.6 kg to 8.8 kg.

These results were in line with expectations in that the fixed weigh boxes performed more effectively than portable platforms as mechanisms for generating repeatable weight measures. Both systems had individual animals with low repeatability as indicated by large differences between successive measures. The portably platform had a wider limit of agreement and more measures that were close to the margins of agreement or outside the margins.

The findings provided reassurance for the project that weight measures were broadly repeatable while also confirming that studies where weight measures are important, should attempt to use fixed scale systems rather than portable platforms to ensure higher levels of repeatability.

4.3.4 Impact of day and time on liveweight measures

There was interest in the possible effects of the time period animals may have spent in the yards before they were weighed, particularly since there was some variation in how long animals had spent in the yards between properties and also between observations at the same property. These effects were potentially exacerbated by variation in weighing protocols (curfews) between and sometimes within an observation event.

An attempt was made initially to have all study mobs dry-curfewed (off feed and water >12 hours) prior to weighing. It was noted that non-compliance occurred for a number of reasons: 1) property managers concerned about further stress on freshly weaned cattle; 2) weighing of cattle carried over into second day and cattle were returned to water and feed on the second night; 3) holding yards without water were not fully secure and animals could put heads through fencing rails into troughs to drink; and 4) property managers who were trucking experimental animals to market soon after weighing refused any curfew to prevent unnecessary shrinkage.

A decision was made part-way through the project to change the protocol to a wet curfew (on water, off feed >12 hours) because this was considered most likely to be adopted under commercial conditions, and attempts were made to have all groups curfewed with this protocol for 2010/11 study groups.

A summary of weighing protocols by property within observation event is provided below.

Table 34: Summary of weighing protocols (curfew), by property within observation event. D, dry curfew; W= wet curfew; F= full weight (no curfew); C= combination; NA= observation event did not occur.

Prop	Obs1	Obs2	Obs3	Obs4
1	C	D	D	D
2	D	D	W	W
3	W	W	W	W

4	W	D	W	NA
5	D	D	D	D
6	F	NA	W	F
7	D	NA	W	W
8	W	W	D	F
9	D	D	D	F
10	W	NA	W	W
11	W	W	W	F

For most animal records, the crush-side system recorded time of day as well as weight. In order to use a standardized approach to assessing the potential impact of time of day, a 4-level categorical variable was developed to code for time of day by dividing the time into bins that ranged from early morning (less than 10 am), late morning (10 am to midday), early afternoon (12 to 2 pm) and late afternoon (>2 pm). These bins were selected based in part on an initial inspection of the ranges of times. The first measurements on any given day were recorded between 5 am and 7 am and the last measurements ranged from 2 pm to 6 pm. The bins used ensured that there were a reasonable number of measurements in each category on most measuring occasions and allowed comparative assessment between measuring occasions.

Simple regression analyses were performed within each property to compare body weights between the categories of time of measurement for each day. On some occasions where weights were recorded over two consecutive days it was possible to look for a general effect of day (comparing mean weight on the first day to the mean weight on the second day).

The hypothesis in performing these analyses was that if there were a systematic effect of time of day as a proxy for time that animals spent waiting in the yard before they were weighed, then analyses would demonstrate a gradual and progressive decline in average LWT as time progressed, or at least see some decline in those animals that were weighed last when compared to those that were weighed first. This was based on the expectation that animals would slowly lose weight over time from dehydration and from lack of access to feed.

Table 35: Summary of change in LWT over time during the day of measurement. Summarised as NC=no change, rise=increase in LWT from one time period to another, fall=decrease in LWT from one time period to another. Rise and fall changes mean that the change was statistically significant (p<0.05) based on pairwise comparison of LWT measures. NC=no change. Numbers in the body of the table refer to time periods (1=before 10 am, 2= between 10 am & midday, 3= between midday & 2 pm, 4= after 2 pm).

Prop_n	Obs1_LWT	Obs2_LWT	Obs3_LWT	Obs4_LWT
1	NC	NC	-	-
2	Fall from1,2&3 to 4	Rise from 2 to 4	NC	NC
3	NC	Rise from 1 to 2	Fall from 1 to 2,3&4	Rise from 2 to 3
4	Fall from 2 to 3&4	NC	NC	-
5	NC	NC	Rise from 2 to 3&4	-
6	-	-	-	NC
7	NC	-	Fall from 1 to 2&3	Fall from 1 to 3&4
8	-	-	NC	NC
9	-	-	-	-
10	Fall from 1&3 to 3&4	-	NC	-
11	-	NC	-	NC

Detailed summary statistics of mean LWT by four categories of time during the day when animals were processed are presented in an appendix to this report.

Table 35 provides an overview summary of the direction of change for those changes that were significantly different. It is apparent from this table that there was no consistent pattern of change.

Time of measurement was recorded on 26 occasions. On 16 (62%) of occasions there was no statistical difference in mean body weight over the course of the day. On 6 occasions (23%), there was a significant fall in mean LWT during the course of the day but it was not always in association with the highest LWT being observed in the first time category of the day or the lowest LWT being observed in the last time category. On 4 occasions (15%), there was a rise in LWT from earlier in the day to later in the day.

There were also concerns that there may have inadvertently been some bias in the ordering of processing through the day. For example, if larger animals were processed first or last then this would potentially impact the liveweight results. On some processing occasions hip height was also measured and this provided another opportunity to explore this issue since hip height represents another measure of animal size. There is generally a very good correlation between hip height and weight measured at the same occasion (r-squared=0.72).

Regressions were run using hip height as the outcome and the categorical variable representing time of day as the predictor (the same analyses as had been done with LWT), to see if there was any evidence for the hypothesis that taller (or shorter) animals might have been processed first or last. The results suggested that on occasion both of these situations appeared to be happening. By and large, when the LWT regressions suggested that there was an association between time of day and LWT, the same analyses repeated with hip height suggested that there was an association between hip height and time of day.

When the LWT data suggested that animal weight was declining through the day (from first level of time to last level of time), the hip height data indicated that the tallest animals had been weighed first. There were also situations where the LWT data suggested that the heaviest animals had been processed last and this was consistent with the hip height data suggesting that the tallest animals had been processed last.

When the findings of these two separate assessments (LWT by time of day and hip height by time of day), were considered together, there was no consistent evidence to suggest that animals were losing weight over the course of a day as a result of shrinkage associated with time. There were occasions when there were associations between time of day and LWT, but these were generally associated with the same patterns with hip height. The findings are consistent with the hypothesis that there was actually little effect of time of weighing on LWT, and that any observed changes were likely to correspond to when taller/heavier animals were processed relative to others. This is likely to be the result of the care and attention being paid by the project team to managing curfew in the cattle to ensure little likelihood of large variation in body weight as a result of time of day when the animals were weighed.

4.3.5 Hip height

In those properties enrolled in the 2009-2010 year, hip height was measured initially at Obs2. In contrast for those properties enrolled in the 2010-2011 year, hip height was measured initially at Obs1 for several herds and at Obs2 for two herds.

A categorical variable was created to code for the quartiles of hip height (1st quartile represents the bottom or smallest 25% and 4th quartile represents the largest or tallest 25%) in an attempt to look for differences between the shortest and tallest animals.

A ratio of body weight to hip height was also created to try and facilitate assessment of different growth patterns in animals. This was an attempt to see if it might be possible to discern subtle differences in relative growth of weight or height at different times post weaning.

Hip growth was also assessed by creating variables for change in hip height per unit time (similar to ADG for change in body weight per day). These variables generally involved estimation of the change in hip height between two defined observation periods, expressed as growth in cm per 100 days.

Data were inspected for outliers by comparing the observed number of values lying outside 3 standard deviations from the mean to the expected number of observations using a standard normal distribution. If there were more values than expected then outliers were removed from the dataset. Using this approach a small number of values were removed. More detail is provided in the appendices.

Table 36: Summary statistics for hip height measurements across all properties and observations. SD= standard deviation, n=number of observations contributing to any one measurement, SD=standard deviation.

Obs1_hip height	**1**	**2**	**3**	**4**	**5**	**6***	**7***	**8**	**9***	**10***	**11**
n	220	242	217	238	212	183	241	198	153	234	207
mean (cm)	113.62	119.86	106.11	111.3	117.5	123.21	114.1	112.63	109.28	119.51	112.87
sd	7.11	6.67	4.499	5.5	5.48	4.79	5	6.14	7.24	4.68	5.31
min	92.1	93.2	95	96	105	107	97	99	97	109	95
max	131.6	138.2	120	126.5	134	135	131	134.5	133	137	125.5
Obs3_hip height	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
n	no data	232	212	175	215	179	218	173	139	208	230
mean (cm)		123.6	111.5	114.3	123.7	124.91	119.04	119.24	110.93	124.5	116.91
sd		6.16	4.83	5.1	5.11	4.97	4.66	5.42	6.63	4.25	5.34
min		102	99.5	101	110.5	110	102.5	103.5	96.5	114.5	97
max		141	127	127	138	137	135.5	137	132.5	136	128
Obs4_hip height	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
n	209	226	198	no data	196	180	224	180	no data	106	212
mean (cm)	134.84	128.81	119.9		130.2	128.3	128.19	129.38		130.35	122.22

sd	4.723	5.691	4.89	4.7	4.41	4.53	4.23	4.47	5.19
min	122	113.5	107	119.3	114	116	119	117	105
max	148	146	134	143.3	138.5	142	141	140	137

* hip height measured at Obs1, remainder measured at Obs2

There was interest in the possible relationships between hip height, LWT and ADG at different time intervals, reflecting underlying growth patterns ie do animals grow in height before adding LWT, do shorter animals have more LWT per unit height and so on.

There was an association between hip height and LWT at weaning as shown in a simple scatter plot – taller animals weighed more. Preliminary inspection of scatter plots indicated that a simple linear regression was a reasonable fit to the relationship between hip height and liveweight.

Table 37: Slope terms from separate regression analyses performed within each property, using Obs1_LWT as the outcome and Obs1-HipHeight as the predictor. The final row provides model output from a model with all property data combined and that contained a random effect for property to adjust for clustering.

			95% CI			
prop_n	**coef**	**se**	**Lower**	**Upper**	**p-value**	**r-sq**
1	6.32	0.21	5.9	6.74	<0.001	0.82
2	5.33	0.24	4.86	5.79	<0.001	0.68
3	3.4	0.2	3.01	3.79	<0.002	0.58
4	4.32	0.21	3.92	4.73	<0.003	0.66
5	5.16	0.25	4.66	5.65	<0.004	0.67
6	5.22	0.39	4.44	5.99	<0.005	0.5
7	3.99	0.24	3.52	4.46	<0.001	0.57
8	5.44	0.23	5	5.89	<0.002	0.75
9	4.88	0.23	4.41	5.34	<0.003	0.75
10	4.47	0.31	3.86	5.07	<0.004	0.48
11	5.42	0.24	4.94	5.9	<0.005	0.71
All*	5.06	0.08	4.91	5.21	<0.001	

*model included herd group & random effect for prop_n

Using the data from the first row (prop_n=1) as an example, the R-squared value is 0.82 and the coefficient for hip height is 6.32, indicating that a **1 cm increase in hip height is associated with a 6.32 kg increase in Obs1_LWT.**

The slope terms in Table 37 provide a measure of the change in Obs1_LWT when hip height increases by 1 unit (1 cm). The numeric variation in slope terms between properties suggests that the association between hip height and Obs1_LWT is not uniform across all properties.

A linear mixed model was used to test this and confirmed that the association between hip height and Obs1_LWT was well represented by a linear relationship but there was significant variation in slopes between properties. This is shown graphically in Figure 11. The plot on the right side of Figure 11 is a representation of the association between hip height and Obs1_LWT when the slopes are constrained to be the same (assumes that a 1 unit increase in hip height will produce the same change in body weight across all properties). The plot on the left side of Figure 11 provides an illustration of the association between hip height and Obs1_LWT when the slope is allowed to vary between properties. A 1-unit increase in hip height is capable of producing a different level of change in Obs1_LWT depending on which property is being assessed.

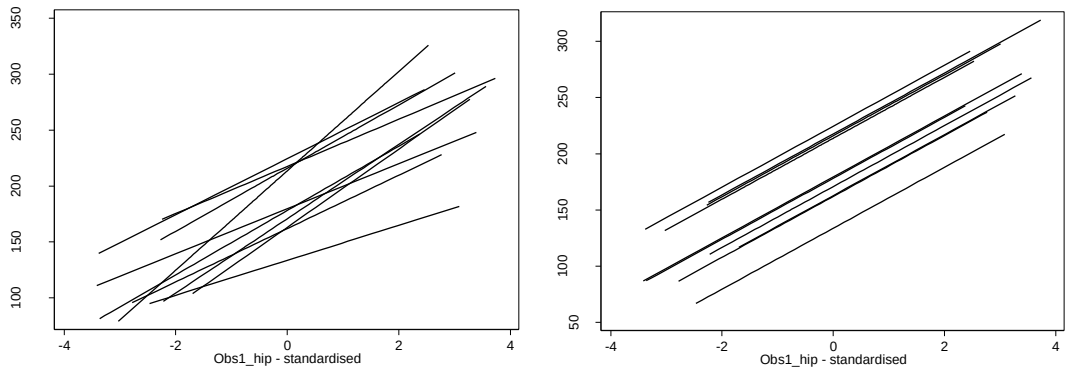


Figure 11: Plot of predicted Obs1_LWT vs standardised hip height (mean=0 and units=1 standard deviation). Left plot incorporates a random slope term for hip height allowing the effect of hip height on Obs1_weigh to vary between properties. Right plot does not have a random slope term for hip height so that the association between hip height and Obs1_LWT is forced to be the same for all properties.

Table 38: Slope values from separate regressions performed within each property and using all data combined using Obs3_LWT as the outcome and Obs3_hip as the predictor.

			95% CI			
prop_n	**coef**	**se**	**Lower**	**Upper**	**p-value**	**r-sq**
1	no data					
2	6.26	0.23	5.82	6.71	<0.001	0.77
3	3.44	0.18	3.08	3.8	<0.001	0.63

4	4.06	0.22	3.64	4.49	<0.001	0.67
5	5.11	0.26	4.59	5.63	<0.001	0.64
6	5.12	0.31	4.5	5.74	<0.001	0.6
7	4.11	0.25	3.62	4.6	<0.001	0.59
8	6.21	0.33	5.57	6.6	<0.001	0.68
9	4.63	0.23	4.17	5.09	<0.001	0.75
10	5.05	0.33	4.41	5.7	<0.001	0.54
11	5.09	0.23	4.62	5.55	<0.001	0.68
ALL*	5.05	0.08	4.88	5.21	<0.001	

* model included herd group & a random effect for prop_n

Table 39: Slope values from separate regressions performed using Obs4_LWT as the outcome and Obs4_hip as the predictor.

			95% CI			
prop_n	**coef**	**se**	**Lower**	**Upper**	**p-value**	**r-sq**
1	7.2	0.51	6.19	8.2	<0.001	0.51
2	6.35	0.33	5.69	7.01	<0.001	0.62
3	4.65	0.26	4.14	5.16	<0.001	0.63
4	no data					
5	2.26	0.57	1.15	3.38	<0.001	0.08
6	5.94	0.37	5.21	6.68	<0.001	0.59
7	4.16	0.5	3.16	5.15	<0.001	0.24
8	7.17	0.55	6.09	8.25	<0.001	0.49
10	2.98	0.42	2.14	3.81	<0.001	0.32
11	5.7	0.46	4.8	6.61	<0.001	0.42
ALL*	5.39	0.15	5.09	5.69	<0.001	

*Model included herd group & a random effect for prop_n

As the animals increased in age (from Obs1 to Obs4), the r-squared values appear to decline suggesting that in older animals the strength of the association between hip height and liveweight is reduced.

4.3.6 Association between hip height and ADG measures

Scatter plots and regression analyses were used to assess whether hip height had any association with ADG measures. An example of scatter plots between ADG_DS and Obs1_hip is shown in the Appendices.

Inspection of scatter plots and fitted lines showed little evidence of a linear association between any ADG (DS, WS, AN) and Obs1_hip. In some scatterplots there were occasions where patterns appeared but these tended to be inconsistent and were interpreted as being associated with sparse data (on the margins of plots) or influenced by property-level effects.

4.3.7 Differential growth – height vs weight

Animals within each property were classified as less than or up to the median weaning weight or greater than the median weaning weight for that property. The same approach was used to classify animals by hip height at weaning (up to median or greater than the median hip height for that property).

Statistical models were then used to explore comparisons, using combined data from all properties. A brief summary of key findings is provided here.

The highest ADG_DS was seen in the lighter animals and the smallest ADG_DS in the heavier animals. There was no effect of weaning hip height on ADG_DS. When mean Obs1_LWT was compared to mean Obs3_LWT using the same method, the groups were seen to be either maintaining their LWT over the dry or changing by less than 10 kg in total (either up or down). These findings were broadly consistent with most animals appearing to maintain their body weight through the dry since a change in body weight of less than 10 kg in either direction over the course of the dry seems like a biologically small change.

The highest dry season increase in hip height was seen in the shorter animals at weaning compared to animals that were taller at weaning. There was also an effect of weaning weight on growth in hip height over the dry season with faster growth in hip height seen in those animals that were heavier at weaning.

For wet season growth there was relatively little effect of weaning weight or weaning height on ADG_WS (when weaning weight and hip height were classified as less than or greater than the median). This is in contrast to the findings reported in Section 4.3.1 that reported better ADG_WS figures in animals that were taller and heavier at weaning. The difference is likely to be due to the different coding systems used in the two analyses (one using binary classifications for both weaning weight and hip height and the other using the same classification for hip height but a continuous standardised measure of weaning weight).

The average wet season ADG estimates were markedly higher than the dry season ADG estimates.

For annual ADG (ADG_AN), the highest ADG_AN was seen in the light/short animals at weaning, and the worst performance in the heavy/short animals at weaning.

The highest annual hip growth was seen in the shorter animals with no apparent modifying effect of Obs1_LWT.

The ratio of LWT to hip height at weaning was very closely correlated to Obs1_LWT (r-squared=0.9) and less related to hip height (r-squared=0.54). This measure does not seem to provide a great deal of value in trying to separate out growth in LWT from growth in skeletal structure (height).

These findings suggested that dry season growth had relatively little overall association with annual growth or final LWT, meaning that weaning weight (Obs1_LWT) appeared to be a major driver of final weight (Obs4_LWT).

It is interesting to note that at the property level, the property with the heaviest animals based on the final weight measure (Obs4_LWT), did not have the heaviest weaners and did not have the best ADG_WS measures but did have the best ADG_DS measures. In contrast, the property with the second best average final LWT, had the best average ADG_WS and mid-level ADG_DS performance compared to other properties (see Section 4.3.2).

It is also important to note the distinction between body weight at Obs4 and ADG measures.

Based on final body weight (Obs4_LWT), weaners that were heavy/tall (higher than the median height and heavier than the median weight), appeared to be the best performed over the following year, followed by heavy/short weaners.

Within the heavy weaners, those that were taller than average appeared to be significantly better over the following year ie there was a long term weight benefit of having additional height at weaning.

Animals with the lightest Obs4_LWT were those that had been the light/short weaners. Within the light weaners, those that were taller at weaning did increase their weight advantage by Obs4_LWT over those animals that were shorter at weaning.

Notice that some of these findings for Obs4_LWT are not the same as the findings for ADG_AN. The light/short weaners tended to have the best ADG_AN but the higher ADG did not overcome the disadvantage in body weight. Animals that were heavier at weaning were also heavier at Obs4 even though they did not have the highest ADG between Obs1 and Obs4.

4.3.8 Flight speed

Flight speed was recorded on 4 observation periods but inspection of the data indicated that there were few animals with a flight speed measure recorded on all four occasions. Animals mostly had

one, two or three separate flight speed recordings. A numerical average was created for each animal based on the average of all available flight speed records for that animal.

Summary statistics for overall average flight speed were used to develop upper and lower plausible thresholds (based on 99% Confidence Limits). There were zero (0) records that were lower than the lower threshold and 16 records that were higher than the highest record. All 16 outlier records were replaced with missing values.

Table 40: Summary statistics for Obs1, 3 and 4 flight speed measures (metres per second). The final two rows report the mean change in flight speed from Obs1 to either Obs3 or Obs4, and a p-value indicating whether or not this change was significantly different to zero.

Flight speed			95% CI		
	mean	se	low	up	p-value
Obs1	2.4	0.18	2.05	2.75	
Obs3	2.13	0.18	1.77	2.49	
Obs4	1.57	0.16	1.25	1.89	
Diff (3 - 1)	-0.26	0.18	-0.61	0.09	0.14
Diff (4 - 1)	-0.55	0.28	-1.1	0.01	0.054

An initial series of regression models were run with all data combined (including year of enrolment as a fixed effect and property as a random effect), to generate mean estimates for both individual flight speed measures and also for differences over time.

The mean flight speed reduced over time. Flight speed is measured as metres per second, meaning that smaller numbers indicate that an animal is moving at a lower speed. A reduction in mean flight speed over time may be consistent with an expectation that animals become acclimatised to handling with each successive exposure. The change from Obs1_flight speed (reported above as the last two rows in the table), to Obs3 or Obs4 measures represented a reduction in the mean flight speed but the changes were not statistically different to zero, although the difference between Obs4 and Obs1 was close to significant. These findings do support the approach taken which was to assume that flight speed would be constant within each animal and then to generate an average flight speed from all available measurements for each individual animal.

Regression models were used to assess statistical associations between flight speed and ADG measures. Separate models were run with outcomes for each ADG measure (ADG_DS, ADG_WS, ADG_AN) and each model included the animal-average flight speed measure as the predictor. All models included a random effect coding for property. Detailed findings are presented in the Appendices. There was no statistical association between flight speed and dry season ADG but there was a small negative association between flight speed and wet season ADG and annual growth (ADG_AN).

These findings indicate that animals that were more flighty may have a slightly lower wet season and annual growth performance. The low r-squared values (less than 3%) indicate that flight speed accounted for a very small proportion of the variability in ADG estimates and that these findings may represent the impact of relatively large sample sizes that are capable of producing results that may be statistically significant while they may not necessarily be biologically meaningful.

4.3.9 Body condition score (BCS)

There was a close association between BCS and liveweight at each measuring occasion with increasing BCS associated with increasing liveweight.

Counts of animals by body condition score at different measuring occasions are presented in the Appendices.

There was some movement of animals between scores over time. Between Obs1 and Obs3, there was more downward movement than upward movement and the mean difference (Obs3 – Obs1) was -0.2 score units. This finding is consistent with a trend for animals to lose condition over the dry season.

In contrast from Obs1 to Obs4, there was a general upward trend in BCS and the mean difference was 0.23 score units. This reflects the wet season growth.

Regression analyses were run using ADG measures as outcomes and BCS as a categorical predictor. Models also included a fixed effect coding for year of enrolment and a random effect coding for property. There was a significant negative association between Obs1_BCS and ADG_DS. Animals in the highest BCS score levels had lower ADG values over the dry.

In contrast there was no association between Obs1_BCS and ADG_WS or ADG_AN.

4.3.10 Dehorning method

The two main forms of dehorning are amputation and cautery disbudding with amputation being more commonly applied in northern beef areas of Australia.

While there are a number of specific techniques that may be classified as amputation, the three main tools used in northern Australia include dehorning knives, scoop dehorners and cup dehorners. A dehorning knife is curved in shape and has a blunted tip and is the preferred instrument for use on younger calves up to about 2-3 months of age (La Fontaine and Dde Witte, 2002, Laing, 2009). There are different types of scoop dehorners though they all operate on the same general principle. The dehorner is placed over the horn and the handles pushed/pulled apart to 'scoop' out the horn and surrounding tissue. Scoop dehorners are generally used on slightly older animals (2-6 months of age) (La Fontaine and Dde Witte, 2002). Cup dehorners are large instruments that are opened and placed over the horn and then closed to remove the horn base in a scissor action. Cup dehorners may be used on animals up to 12 months of age. Other tools are available such as the parrot beak dehorner, saws or surgical wire, all of which are generally used for tipping of older animals rather than attempting to remove all of the horn material and adjacent tissue to prevent regrowth.

Cautery disbudding involves the destruction of the horn bud with the use of a hot iron. The iron is heated either in a furnace or by an electrical element and is placed on the horn bud of the animal. The hot iron is held in place until all the horn and surrounding tissue is destroyed. The cauterising effect minimises blood loss and may reduce risk of wound infection. Cautery should only be used on young calves (up to about 2 months of age) (Irwin and Walker, 1998).

Management of cattle in northern Australia often means that animals are only mustered during the dry season. Under these conditions properties may conduct one or two rounds of mustering each year (April to June, and August to November depending on the season).

It is common under northern conditions for branding, castration and dehorning to all take place at the same time as weaning, and for these procedures to be applied to a wide range of size and age of animals. It was expected that there would be a range of different methods being applied given that animals may range widely in size at the time of dehorning.

In the current study, the most common dehorning methods (in decreasing order of the number of animals dehorned by each method) were dehorning knife, knife, cup dehorners, hot iron, scoop dehorners and parrot beak dehorners.

There was a significant association between weaning weight and tool type. Animals dehorned with a hot iron had the lowest weaning weight and were significantly lighter than animals dehorned with cup dehorners ($p=0.02$) but not different to any other tool. In contrast animals dehorned with cup dehorners were significantly heavier than those dehorned with other tools ($p<0.05$) with the exception of Parrot beak dehorners ($p=0.8$).

A series of regression equations were performed within each property where dehorning data were collected to look for an effect of dehorning tool. In an attempt to try and separate out effects associated with property level variability in weight and effects due to weaning weight (Obs1_LWT), regression models were run with property as a random effect and with Obs1_LWT as a covariate. Models had ADG measures as outcomes and dehorning tool as a categorical predictor. There were some differences between tool categories for ADG_DS and ADG_WS but **there was no association between tool type and annual ADG**. Some of these associations are considered likely to be due to the association between animal weight at weaning and not necessarily due to the dehorning tool type, given that there are relationships with animal weight at weaning and various growth measures.

4.3.11 Dehorning wound size

Wound size (cm^2) of the dehorning wound was recorded for some cattle.

For cattle dehorned by hot iron the recorded wound size was assumed to be the same as the area of the hot iron itself and all entries were therefore recorded as a constant value (14.372 cm^2). These values were not based on a measurement of the actual wound but were based on a measurement of the iron dimensions. As a result, wound size measures for irons were removed from the dataset for analytical purposes.

There was a significant and positive association between Obs1_LWT and dehorning wound size, and the association appeared linear. Larger animals had a larger wound size.

Regressions were run to assess for any evidence of an association between wound size and ADG outcomes. Models incorporated Obs1_LWT to adjust for the effect of body weight and also a random effect for property. Three models were run with outcomes representing dry, wet and annual ADG. Each model incorporated all available data (from all eleven properties).

There was no evidence for any association between wound size and any ADG measure (p>0.05).

4.3.12 Exposure of the frontal sinus

Animals were inspected as they were dehorned and the wound assessed as either exposing the frontal sinus or not (recorded as a binary variable – yes, no). These measurements were recorded for each tool type (cup dehorners, dehorning knife, knife, dehorning iron, parrot beak, and scoop dehorners). The percentage of animals with sinus exposure ranged from 8% (dehorning iron) to 99% (scoop dehorners) and the overall average was 55% of all animals dehorned (regardless of tool) had an exposed sinus.

For all tools except the dehorning knife, there was no difference in Obs1_LWT between animals that had an exposed sinus and those that did not.

There was a significant association between sinus exposure and Obs1_LWT for dehorning knife only ($p<0.05$). There were a total of 396 animals that were dehorned with the dehorning knife and that had Obs1_LWT and sinus exposure recorded (251 had no sinus exposure and 145 had an exposed sinus). Animals with an exposed sinus were significantly heavier at dehorning (200.7 kg), compared with animals that did not have an exposed sinus (171.5 kg). These findings suggest that heavier animals that are dehorned with a dehorning knife have a higher risk of sinus exposure.

There was no statistical association between exposure of the sinus and any ADG outcome (DS, WS or AN; $p>0.05$).

4.3.13 Bleeding after dehorning

Bleeding was assessed visually soon after dehorning and animals were classified into 4 levels (0=no bleeding, 1=drip, 2=steady stream, 3=rapid spurt). For analytical purposes the lower two categories were combined.

Bleeding was assumed likely to have a short term effect primarily and therefore assessment focused on possible associations between bleeding score and dry season ADG (ADG_DS). If there was evidence that bleeding was associated with ADG_DS then it may be reasonable to look for possible associations with wet (ADG_WS) or annual ADG (ADG_AN).

There was an association between bleeding score and wound size with increased wound size being associated with more bleeding. Each of the 3-level categories of bleeding was significantly different to the other two categories (in a model with Obs1_LWT fitted as covariate and property as a random effect).

Animals in combined bleed category 0 and 1 had a mean wound size of 49 cm^2 (sem= 8.0) while animals in category 2 of bleeding had a mean wound size of 54.5 cm^2 (sem=8.01), and animals with the highest bleeding score had the largest mean wound size (60 cm^2, sem =8.02).

There was little evidence for an association between bleeding score and tool category with the exception of hot iron which was significantly less likely to produce bleeding scores of 2 and 3 combined than any other tool type.

One property recorded temp and humidity at about the time of dehorning and castration. Animals in the highest category of bleeding score (score=3) were associated with a higher environmental temperature recording (28.9 C) and a lower humidity recording (34.4%), when compared with animals in the lowest bleeding score category (combined 0 and 1 scores: temp=27.5C and humidity= 36.5%). These differences were significant in regression modelling ($p<0.05$).

There was no effect of bleeding score on dry season ADG ($p>0.05$).

There was a significant difference in ADG_WS between bleed score 0 and 2 ($p=0.04$) while other comparisons were not different ($p>0.05$). Animals with bleed score = 2 had a lower ADG_WS than animals with bleed score=0.

There was a significant difference in ADG_AN between bleed score 0 and 3 ($p=0.04$) while other comparisons were not different ($p>0.05$). Animals in the highest bleed score had a lower ADG_AN than animals in the lowest bleed score category.

These findings suggest that there could be an association between increased bleeding and reduced growth, but caution is urged in interpreting these findings. Bleeding is correlated to other factors such as wound size and body weight and may be linked to tool type and other factors that were not measured. The effect of bleeding is considered likely to be largest in the shortest time frame since animals that recover from a bleeding episode are likely to have regenerated red blood cells quite quickly. The fact that there was no statistical association between bleeding and dry season growth is suggestive that there may not be a real association. However, increased bleeding may also be an indication of risk of other events such as infection which may in turn have a longer lasting adverse effect. Further work is necessary to understand the details of this possible association.

4.3.14 Dehorn wound healing

A wound healing score was produced at the first observation after dehorning. The original score was on a scale of 0 to 5 with larger numbers indicating wounds of worsening severity or that were not healing as well.

There was initial interest in the category zero level of wound healing score since this was considered to be representing polled animals. A specific comparison of ADG measures between the zero category and other categories was performed to check whether there was any advantage in polledness vs horned.

There was no difference in any ADG measure between the zero category (polled animals) and any other wound healing score. The zero and one categories of wound healing score were then combined for further analysis.

Because there were relatively few observations in the lowest and highest categories these were collapsed into the adjacent categories to produce a 3-level score (1, 2, 3) with lower numbers representing better healing.

Regression models were run with each ADG measure as separate outcomes and with fixed effects coding for healing score (1,2,3) and Obs1_LWT. Models also included a random effect for property. There was no statistical association between wound healing scores and any growth measure (ADG_DS, ADG_WS, ADG_AN).

There was a significant association between dehorning wound size and wound healing score. Each healing score level was significantly different to each other level ($P<0.05$). Wounds with higher healing scores had a larger wound area than wounds with lower healing scores.

4.3.15 Castration tool

There was no association between castration tool and weaning weight. This suggests that choice of castration tool may be more influenced by personal preference since the above table indicates that most properties use a single type of tool. The most commonly used tool was a scalpel.

There was no association between castration tool and any measure of ADG (DS, WS or AN).

4.3.16 Castration sterilisation

Summary findings from statistical analyses are presented in the Appendices.

Choice of sterilisation method was not associated with weaning weight.

There was no association between type of sterilisation and any measure of ADG (DS, WS, AN).

4.3.17 Castration type

The approach to castration was classified as high or low based on where the spermatic cord was severed.

Most castrations were classified as high.

There was a significant association between castration type (high vs low) and weaning weight. Animals that were classified as being castrated high, had a significantly smaller weaning weight than animals recorded as being castrated low (high=177 kg, low=193 kg; $p<0.001$).

Regression models were performed to look for associations between castration type and ADG measures. Each model had fixed effects coding for Obs1_LWT and castration type, and a random effect coding for property. There was an apparent association between castration type and ADG_DS.

Animals recorded as having a high castration, had a lower ADG_DS than animals recorded as having a low castration ($p=0.001$). This effect may be due to confounding with LWT rather than a real effect due to castration type.

There was no association between castration type and either ADG_WS or ADG_AN.

4.3.18 Bleeding at castration

Bleeding at castration was recorded visually soon after animals were released from restraint. Animals were scored on a 4-point scale (0=no bleed, 1=drip, 2=steady stream, 3=rapid spurt).

Scores were aggregated into a two-level scale (0=no bleed or drip, 1=stream or spurt).

Animals with a worse bleeding score at castration were significantly heavier at weaning than animals with a better bleeding score ($p<0.001$).

There was no statistical association between castration bleeding score and any ADG measure.

Animals that were castrated low were 2.6 times more likely to have a higher bleeding score compared to animals that were castrated high (relative risk=2.6, 95% CI from 1.9 to 3.7, chi-squared p-value <0.001).

There was no association between castration bleed score and environmental temperature or humidity measured around the time of castration.

4.3.19 Scrotal healing score

There was no association between scrotal healing score and castration bleeding score.

There was also no association between scrotal healing score and any measure of ADG.

There was an association between healing score and weaning weight. Animals in healing score 1 were lighter (Obs1_LWT=170 kg) than all other levels ($p<0.05$) and animals in healing score 4 were heavier than all other levels (Obs1_LWT=190 kg; $p<0.05$). There was no difference in weight between scores 2 and 3.

4.3.20 Tick scores

Tick scores were recorded using a 6-point scale described by (Corbet et al., 2007). There were so few animals with scores greater than 2 that the score was refined to a 3-level score (0=no ticks, 1=<10 ticks and 2=>10 ticks). Properties that were not in the tick zone were excluded and properties that did not record any ticks were excluded from analyses, meaning that analyses looking for an association between tick score and other measures (such as ADG) were limited to those properties that recorded any ticks at all.

Ticks were only observed on three properties at Obs2 and there was no association between Obs2 tick score and any measure of ADG.

The same approach was then taken for Obs3 tick score. Tick scores were recorded for ten properties and 7 of the 10 recorded some ticks. Properties with no ticks recorded were excluded and tick scores were coded into a 3-level score (0=none, 1<10 and 2>10 ticks).

Regressions with run with ADG measures as outcomes. Each model incorporated Obs1_LWT as a fixed effect along with tick score, and each model also included a random effect coding for property.

There was no association between Obs3 tick score and ADG_DS, ADG_WS or ADG_AN.

The same approach was then taken for Obs4 tick scores.

There was no association between a 3-level tick score and ADG_DS (in a model that included a fixed effect coding for Obs1_LWT and a random effect for property).

There was a significant association between Obs4 tick score and ADG_WS. Animals without any observed ticks had a significantly smaller ADG_WS than both groups of animals with any ticks ($p<0.05$).

Table 41: Mean ADG_WS (kg/hd/d) for each level of Obs4 tick score

Obs4 Tick score	ADG_WS mean	sem	95% CI Low	Up
None	0.385	0.057	0.273	0.497
<10	0.425	0.058	0.312	0.539
>10	0.425	0.059	0.310	0.540

A similar association was also seen between Obs4 tick scores and ADG_AN. **Animals without any observed ticks had a significantly lower ADG-AN than animals with <10 ticks (p=0.005)** and tended to be lower than animals with >10 ticks (p=0.066). There was no difference between the two groups with any ticks.

Table 42: Mean ADG_AN (kg/hd/d) for each level of Obs4 tick score

Obs4 Tick score	ADG_AN mean	sem	95% CI Low	Up
None	0.234	0.029	0.178	0.290
<10	0.253	0.029	0.197	0.310
>10	0.253	0.030	0.194	0.311

It is important that this finding be interpreted with caution. There is substantial evidence in the scientific literature of adverse effects of cattle ticks on cattle health and performance with effects attributable to blood loss and reduction in feed intake, digestibility, metabolism and host immunity (O'Kelly et al., 1971, Inokuma et al., 1993, Jonsson, 2006). In addition ticks have the potential to transmit agents that cause tick fever diseases (Anaplasmosis and Babesiosis)(Callow, 1984). *Bos indicus* cattle are relatively more resistant to ticks and tick-borne diseases than *Bos taurus* cattle.

It is not clear why our results do not show any negative association between ticks and measures of ADG. It may be that the combination of genetics (*B. indicus* bloodlines) and property level management factors (including animal treatments) may have prevented tick burdens from reaching levels capable of causing adverse effects. The apparent association between higher tick scores and improved ADG is likely to represent confounding with seasonal factors (rainfall) that may favour tick survival and at the same time produce better pasture quality and availability.

Our findings should not be interpreted as suggesting that tick burdens are not a serious potential threat to animal health and productivity in northern Australia.

4.3.21 Buffalo fly score

Buffalo fly were counted and recorded at three periods (Obs2, Obs3 and Obs4). Fly counts were recoded into a 4 category score: 0=no fly, 1=1 to 30 and 2=31 to 80, 3= 81+.

Regression analyses were run with each ADG measure as an outcome and with fixed effects coding for fly score and Obs1_LWT. A random effect was added to code for property.

There was no association between fly score for the lower categories and any ADG measure.

There were significant associations between Obs3 fly scores and ADG measures but generally these were not consistent with an adverse effect of flies. Increasing fly score (more flies) was associated with an increase in ADG_DS, ADG_WS and ADG_AN, though the effect was only significant for some levels and not others.

There was no association between fly score at Obs4 and any measure of ADG. It is interesting to note that the highest ADG_AN was seen in the heaviest fly score category (though there was no statistical difference between any level).

The findings with respect to Buffalo fly should be interpreted with caution. Previous reports have described reduced weight gain in cattle in association with buffalo fly infestation though the authors did suggest that there may be little adverse impact when fly counts were below a threshold of around 30 flies per beast (Jonsson and Mayer, 1999). Others have suggested an aggravation and economic threshold of 200 horn flies per animal (Schreiber *et al*., 1987).

The apparent association between increased fly burdens in our study and improved LWG is likely to be due to confounding with seasonal factors (rainfall) that may favour fly survival and at the same time produce better pasture quality and availability. Our findings should not be interpreted as suggesting that buffalo fly are not a potentially serious problem for beef producers.

4.3.22 Lesions attributed to Buffalo fly

A visual assessment was made of skin lesions attributed to flies. Lesions were scored by size and whether they were acute or chronic in appearance.

There were no associations between lesion score and ADG measures.

Hide lesions are often associated with buffalo fly, and are thought to be caused by the combination of direct fly damage and by the animal rubbing against hard objects to relieve irritation either due to the fly bites or to irritation caused by a nematode *Stephanofilaria* spp., for which the fly is a vector (Sutherst *et al*., 2006). Some studies have suggested that presence or size of skin lesions are not correlated with fly numbers (Holroyd et al., 1984), whereas Sutherst and colleagues (2006) reported that number of flies was significantly correlated to the presence and size of skin lesions.

The lack of any association between fly lesions and adverse effects on weight gain reported in our findings should not be interpreted as suggesting that buffalo fly may not be a serious problem for extensive beef producers. As indicated above, there is a body of scientific evidence and anecdotal reports confirming that heavy fly burdens have the potential to cause serious adverse effects on livestock health and production and on hide quality.

4.3.23 Hormonal growth promotants (HGP)

Preliminary discussions with properties indicated that it would be difficult or impossible to enrol cattle that had not been treated with HGP because of widespread use of implants in northern beef cattle. An attempt was then made to try and ensure that all participating properties were administering HGP to their young cattle. While there was interest from the project team in trying to ensure that all enrolled cattle were treated with similar products in a similar manner (timing of administration, type of product, and number of treatments), it became apparent that there was considerable variation between properties with respect to these characteristics. Information was collected from properties about their HGP use and summary findings from statistical analyses are presented below with additional findings presented in the Appendices.

HGP data were re-structured to try and simplify the representation of when and how often animals received HGP. Initial inspection of data indicated:

- some animals never received HGP;
- some animals received implants once as calves;
- some received an initial HGP as a calf and then a follow up HGP at the end of the dry period;
- some animals received HGP at weaning or branding or second round muster.

The fact that not every property had all categories and that some properties only had one category meant that it was not possible to combine data from multiple properties into one analysis to look for associations between HGP usage and growth measures. Other property level effects (pasture, season, management, genetics, etc) may also be confounded with HGP, meaning that it was difficult to compare data for different uses of HGP when data may be completely confounded with property.

As a result analyses were done within individual properties to try and tease out some inferences concerning HGP.

Obs1_LWT was added to models to try and account for weaning weight when assessing effect of HGP.

- Comparison of no HGP vs use at weaning
    - Animals receiving HGP at weaning had a lower ADG_DS than animals that did not receive HGP
        - HGP at weaning: mean ADG_DS=0.093, sem=0.006
        - never: mean ADG_DS=0.14, sem=0.019
        - significantly different p=0.02
    - Animals receiving HGP at weaning had a higher ADG_WS.
        - weaning: mean ADG_WS= 0.46, sem=0.012
        - never: mean ADG_WS=0.35, sem=0.04
        - p-value=0.018
    - Animals receiving HGP at weaning had higher ADG_AN but the effect was not significant.
        - weaning: mean ADG_AN=0.31, sem=0.007
        - never: mean ADG_AN=0.27, sem=0.023
        - p-value=0.083

- Comparison of HGP administered to calves only vs at weaning
    - Animals receiving HGP as calf only had a higher ADG_DS than animals that received it at weaning only.
        - calf only: mean ADG_DS=0.039, sem=0.007
        - weaning: mean ADG_DS=0.015, sem=0.007
        - p-value=0.001
    - There was no difference between HGP at calf vs at weaning for ADG_WS or ADG_AN ($p>0.05$).

- Comparison of single administration to calves vs animals receiving one implant as a calf and a subsequent implant at a later muster (any second administration)
    - There was no difference between groups for ADG_DS or ADG_WS (p>0.05).
    - Animals receiving a single implant as a calf had a higher ADG_AN than those animals that received an implant as a calf and a second implant at a later date.
        - calf only: mean ADG_AN=0.36, sem=0.012
        - calf+: mean ADG_AN=0.33, sem=0.006
        - never used: mean=0.26, sem=0.03 (5 animals)
        - p-value = 0.048

- Comparison of animals receiving a single implant as calves to those receiving a single implant as weaners
    - **Animals implanted as a calf had a higher ADG_DS than those implanted at weaning.**
        - calf: mean ADG_DS=0.28, sem=0.021
        - weaning: mean ADG_DS=0.19, sem=0.006
        - p-value<0.001
    - There was no effect on ADG_WS
    - **Animals implanted as a calf had a higher ADG_AN than those implanted at weaning.**
        - calf: mean ADG_AN=0.39, sem=0.017
        - weaning: mean ADG_AN=0.35, sem=0.005
        - p-value=0.044

Caution is urged in interpreting these findings because they were based on relatively small numbers and each analysis could effectively only be done within single property datasets. However, the findings do pose some interesting questions concerning use of HGP and timing of administration in extensive northern herds where there are large seasonal effects on growth. More work is needed to resolve these issues.

4.3.24 Impact of loss of HGP implants

HGPs are used by a large proportion of cattle enterprises and are regarded as an effective means of improving liveweight gain by 10-15% in northern Australia, provided that they are used correctly (Hunter, 2010). In extensive cattle herds, animals are not usually inspected after implantation and it is assumed that the implant remains in place although this may not be the case. Industry reports from the USA feedlot industry indicate that abscesses are the most common complication of HGP use and that missing implants occur in about 1.7% of cases (Lehman and Rains, 1996).

Preliminary inspection of animals post-weaning indicated that there were some properties that were experiencing a higher than expected rate of complications associated with HGP implant sites. Loss rates on three properties ranged from 56% (126 of 227 animals) to 12.2% (28 of 229), to 2.2% (4 of

184 animals), based on observations made at Obs3 or 4 with animals having been implanted at a range of different times (mostly at branding or weaning).

A small nested study was then performed on four properties where animals were implanted as calves and loss rates were recorded at weaning.

Table 43: Summary count of HGP implant losses on properties that implanted animals as calves, with losses determined at weaning

Property	Animals examined (n)	lost implants (n)	(%)
A	175	9	5.1
B	224	78	34.8
C	239	29	12.1
D	181	3	1.7
Combined (all)	819	119	14.5
B, C & D (excl B)	595	41	6.9

The most common reason for implant loss or complication was infection, noted by a purulent discharge or abscess present at the implant site. While it is difficult to identify reasons for the variation in loss rates, it was noted that Property A provided training in implant techniques and dipped the applicator into an antiseptic solution between each animal, while Properties B, C and D did not.

These data indicate that loss rates might average around 7% (range from 2 to 12%) and that in extreme cases loss rates may be very high (approaching 50%).

Data on HGP retention from one property in the study were then analysed in more detail to look for an association between HGP implantation and measures of growth. These analyses were restricted to one property because almost all animals on all other properties were implanted and loss rates were relatively low, precluding comparisons between HGP implanted and non-implanted animals. Results from the single property are presented below.

- ADG_DS: Animals that retained their implants had a higher ADG
    - implants retained: mean=0.31, sem=0.012
    - implants lost: mean=0.27, sem=0.01
    - p-value=0.019
- ADG_WS: no difference
    - implants retained: mean=0.45 , sem=0.01
    - implants lost: mean=0.43, sem=0.009
    - p-value=0.3
- **ADG_AN: Animals that retained their implants had a higher ADG**
    - implants retained: mean=0.40, sem=0.007
    - implants lost: mean=0.38, sem=0.006
    - p-value=0.023

4.3.25 Sire contribution to variance in growth

Sire identification data were used in random effects models to partition variance in ADG measures to sire and other effects.

Because this project enrolled commercial properties and involved animals that were being managed under routine management for each property, there was no opportunity to assign a uniform set of experimental sires to generate offspring across all properties for genetic comparisons. As a result each property used different sires. There were also no records identifying which sires might have sired which weaners because mating involved moving multiple sires into paddocks containing females. Hair samples were collected from eligible sires and from enrolled animals on each property and were subjected to genetic analysis to identify a sire for each enrolled weaner.

Table 44: Estimates of percentage of total variance attributable to sire for models using weaning weight as the outcome. Properties 1 to 11 represent data drawn from the longitudinal study while historical datasets from Beef CRC, Douglas Daly Research Farm (DDRF) and a commercial enterprise (CE).

	% Total variance at sire level	
Property	**Intercept only model**	**Full model**
1	29.5	-
2	3.0	-
3	0.0	-
5	8.4	-
6	5.5	-

7	11.4	-
11	7.8	-
Beef CRC	42.1	4.4
DDRF	41.4	2.6
CE	30.9	9.3

The above table provides an estimate of the percentage of total variance in weaning weight that can be attributed to sire. The first column represents estimates drawn from intercept only models (containing no fixed effect terms) that included a random effect coding for sire. The column labelled *Full model* presents estimates from the models described for the historical datasets where additional fixed effects were added to the model. The three models did not necessarily contain the same fixed effects because it depended on what variables were available in these datasets. For more information, refer to Chapter 3 of this report and to the Appendices

Table 45: Estimates of percentage of total variance attributable to sire for models using annual ADG as the outcome. Properties 1 to 11 represent data drawn from the longitudinal study while historical datasets from Beef CRC, Douglas Daly Research Farm (DDRF) and a commercial enterprise (CE).

	% Total variance at sire level	
Property	**Intercept only model**	**Full model**
1	11.1	-
2	6.8	-
3	14.5	-
5	18.4	-
6	8.4	-
7	0.0	-
11	6.9	-
Beef CRC	44.2	5
DDRF	47.2	1.5
CE	61.5	21.4

It was not possible to run similarly specified full models in the property specific datasets derived from the longitudinal study mainly because of the relatively small sample sizes that limited the number of factors that could be considered, and the short time frame of the longitudinal study relative to the industry datasets.

It is notable that for the intercept only variance estimates, the percentage of total variance attributable to sire in the industry datasets (Beef CRC, DDRF and CE) appear to be higher than those values derived from this study.

There are a number of potential explanations for this.

The historical datasets either involved animals from many properties (CRC) or from one property but over many years (DDRF and CE). A number of factors (herd of origin in CRC and year or season or birth in the DDRF and CE datasets) were important contributors to variance and were effectively eliminated in the Liveweight Gain project because of the design effects (analyses involved one year of data and were performed separately within each property).

The Liveweight Gain project also involved considerably smaller datasets. These effects may have reduced the total variance in the outcome of interest and therefore it is understandable that the proportion of variance attributable to sire may have reduced in our models.

4.3.26 Rainfall

Rainfall data were generated from one of three sources (rain gauge at paddock where enrolled cattle were maintained, property records, or Bureau of Meteorology records) from 2009/10 properties were compared with interpolated SILO output for these property locations. There was some difference in rainfall data from SILO compared to the three primary sources in Total Rainfall (mm), and calculated WSO and WSR. A general trend was that SILO data tended to under-predict Total Rainfall at the average end of the scale (Total Rainfall= 300-600 mm) and over-predict at the upper end of the scale (Total Rainfall= 1200-1400 mm). However, the SILO data was considered sufficient for seasonal descriptive purposes, and in order to keep methods consistent between properties and years, SILO data has been exclusively used to summarise rainfall data for this report.

Rainfall and wet season descriptors for study sites are provided below.

Table 46: Rainfall records for study sites for year prior and year of study, with wet season descriptors (source: SILO[a]). WSO, wet season onset; WSR, wet season retreat; WSD, wet season duration.

Property	**9**
Total rainfall 2007-08 (mm)	915.7
WSO 2007-08	8/11/2007
WSR 2007-08	2/03/2008
WSD 2007-08 (days)	115
Unseasonal rainfall (mm)	8
Total rainfall 2008-09 (mm)	987.7
WSO 2008-09	28/11/2008
WSR 2008-09	26/02/2009
WSD 2008-09 (days)	90

Property	**1**	**2**	**3**	**4**	**5**
Total rainfall 2008-09 (mm)	621	856	1101	895	891
WSO 2008-09	29/12/2008	26/11/2008	26/11/2008	29/11/2008	26/11/2008
WSR 2008-09	10/02/2009	13/02/2009	2/03/2009	13/03/2009	10/02/2009
WSD 2008-09 (days)	43	79	96	104	76
Unseasonal rainfall (mm)	0	0	0	0	0
Total rainfall 2009-10 (mm)	524	586	703	1106	582
WSO 2009-10	22/12/2009	19/12/2009	14/12/2009	23/11/2009	24/12/2009
WSR 2009-10	14/03/2010	27/02/2010	25/03/2010	18/04/2010	1/04/2010
WSD 2009-10 (days)	82	70	101	146	98

Property	**6**	**7**	**8**	**10**	**11**
Total rainfall 2009-10 (mm)	1896	515	1044	645	790
WSO 2009-10	10/11/2009	25/12/2009	1/12/2009	18/12/2009	13/12/2009
WSR 2009-10	15/04/2010	28/02/2010	10/04/2010	11/04/2010	2/03/2010
WSD 2009-10 (days)	156	65	130	114	79
Unseasonal rainfall (mm)	85	50	87	84	45

[a] http://www.longpaddock.qld.gov.au/silo/

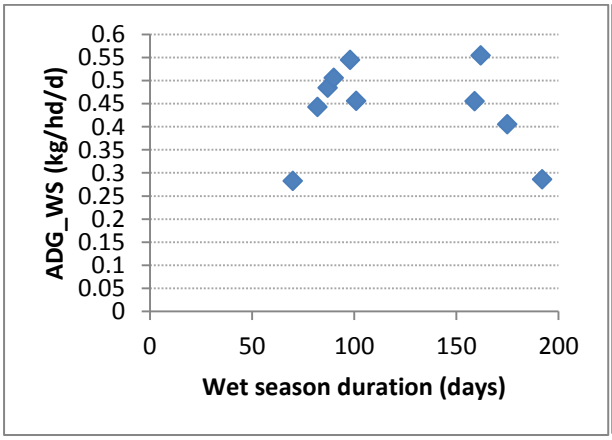
Total rainfall 2010-11 (mm)	2890	943	1873	915	1501
WSO 2010-11	29/09/2010	15/10/2010	11/10/2010	13/10/2010	13/10/2010
WSR 2010-11	9/04/2011	23/03/2011	4/04/2011	24/03/2011	6/04/2011
WSD 2010-11 (days)	192	159	175	162	175

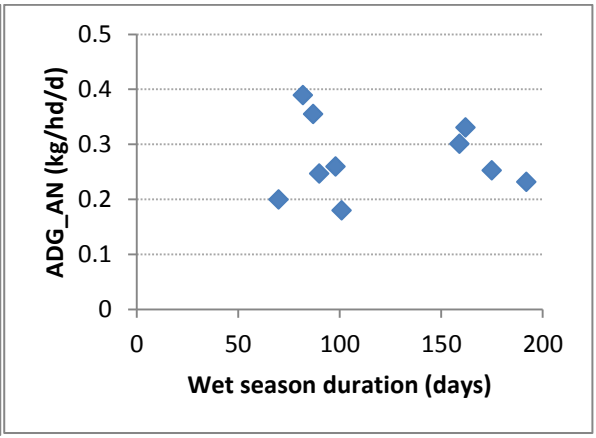
Review of the records displayed in Table 46 indicates that the 2008-2009 year was relatively dry and 2009 was noted as being hot and dry with the southern part of the NT recording the lowest annual rainfall on record. There was generally an early end to the 2008-2009 wet season and a late start to the 2009-2010 wet season.

In contrast the 2010 year was one of the wettest on record with the 2009-2010 wet season providing average or above average rain and then heavy rain continuing through the middle months of the year, producing the second-wettest dry season on record for the NT[b]. The 2010-2011 wet season was another record wet that was then followed by a severe dry season with very little rain.

In general, records suggested that the time period of the study was associated with unusual and relatively extreme weather patterns and included both record dry periods and record hot periods.

Rainfall records were used to generate an estimate of wet season duration in days. Simple scatter plots were then used to explore possible associations between wet season duration and liveweight or ADG measures. There was little evidence of a clear association between wet season duration and ADG_WS or ADG_AN.





[b] www.bom.gov.au

Figure 12: Scatter plots showing wet season duration in days (X-axis) and either ADG_WS (left side) or ADG_AN (right side).

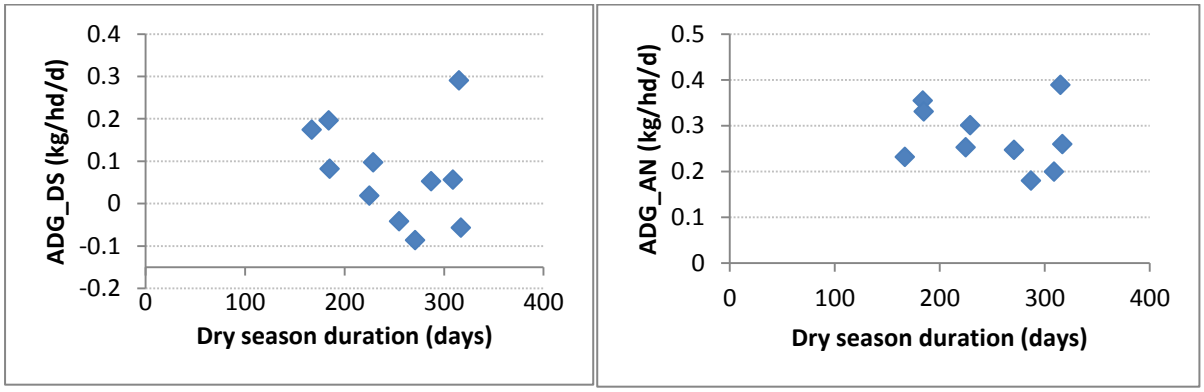


Figure 13: Scatter plot showing dry season duration in days (X-axis) and either ADG_DS (left side) or ADG_AN (right side).

There was a suggestion of an association between dry season duration and ADG_DS and ADG_AN, with increasing length of the dry season associated with a reduction in weight gain.

The properties with longer dry season duration were all those that were enrolled in 2008 (one pilot property) and 2009 (five properties), reflecting the fact that these years were comparatively dry. Those properties enrolled in 2010 were all associated with shorter dry seasons, reflecting the unseasonally wet conditions through the middle of 2010.

5 Use of faecal NIRS to study diet selection

5.1 Introduction

Near Infrared Reflectance Spectroscopy (NIRS) is widely used for analysis of the nutritive value of stock feed, and more recently this technology has been applied to determine the dietary characteristics of herbivore faecal samples (Coates, 2004, Dixon and Coates, 2005, Dixon and Coates, 2010, Coates and Dixon, 2007).

Faecal NIRS (F.NIRS) was utilised in this study to measure selected attributes of a grazing ruminant's diet, as LWG is primarily influenced by dietary intake and quality.

The NIRS process involves measurement of spectra which relate to the concentration of feed constituents using samples of known composition to generate calibration equations; which are then used to predict the composition of unknown samples.

F.NIRS provides the capability to assess diet in grazing ruminants under extensive commercial systems, allowing assessment of diet quality in situations where it may not have been possible prior to this technique being made available. It is still considered to be an emerging technology with inherent prediction errors and with variable levels of calibration for different regions and pasture systems.

F.NIRS was used in this study on a subset of properties and animals in an attempt to explore possible associations between ADG measures and diet quality. There was particular interest in the hypothesis that the grazing behaviour of better performing animals may be different to that in the less well performing animals, perhaps seeking a better diet or walking out a different distance from water.

5.2 Methodology

This study was performed on a subset of properties and animals from the main longitudinal study, involving properties 1, 2, 3, 4, 5, and 7.

The decision to restrict the NIRS study to a smaller subset of properties was mainly because of the relatively high analytical cost for performing the NIRS analyses. Properties were mainly from those

enrolled in the first year of enrolment in the main part of the study with the addition of one property (property=6) from the 2010/11 enrolment group. Property 7 was chosen because animals on this property were grazing a paddock with a proportion of Dry Lake land system which contained *Chenopodium auricomum* (Northern Bluebush/Swamp Bluebush). Northern bluebush is a high-protein (2-20%) shrub readily eaten by stock, and was considered to be a grazing situation which presented a notable opportunity for variation in diet selection compared to other pasture types. A description of the paddocks and pastures from the properties can be found in Table 14.

5.2.1 Animal measures and faecal sampling

Animal liveweight was recorded and average daily gain (ADG) (kg/head/day) calculated as reported for the main project.

Faecal samples were collected from individual animals when presented for three mustering events: Obs2 (2 weeks post-weaning); Obs3 (end of dry-season); and Obs4 (end of wet-season), unless the mustering event did not occur. In one case (property=6), the first sampling occurred at Obs1.

Faecal samples were collected by sampling per rectum, and samples were then individually bagged and labelled. Samples were placed in an insulated container at 4°C as soon as possible after sampling and during transport. After receipt at the Katherine Research Property, samples were usually stored frozen, then defrosted in batches at room temperature and placed in a forced draft oven at 65^0C until completely dried. Dried samples were then stored in a cold room.

5.2.2 Selection of animals for F.NIRS testing

The aim of this part of the study was to determine whether diet quality)as measured by F.NIRS) was associated with liveweight gain outcomes (LWT or ADG). Cost constraints meant that it was not possible to analyse F.NIRS outcomes on samples from every animal on each participating property.

The selection process therefore involved measuring LWT and ADG outcomes on animals and selecting animals from the upper and lower extremes based on ADG_AN (ADG_AN classification= High or Low). Faecal samples from selected animals were then identified and submitted for laboratory analysis for F.NIRS outcomes.

Because it was not possible to calculate ADG_AN until after Obs4, this meant that faecal samples were collected from all animals on participating properties and stored until animals could be assigned to ADG_AN class (High or Low).

Sample size estimations were used to inform the final sampling strategy which involved selection of 40 animals in each of the Low and High annual growth rate groups from each property.

There were two properties where the approach varied slightly from the protocol above.

Property 4 withdrew from the study before Obs4 and for this property, ADG_DS was used instead as the basis for classifying animals into ADG Low and ADG High.

Property 1 had additional data on whether or not animals had lost or retained their HGP implants. Sampling was altered on this one property to 30 animals to be selected from each combination of HGP status (yes=retained, no=implant lost) and ADG_AN class (Low, High), for a total sample of 120 animals (30 where HGP=No and ADG_AN=Low, 30 where HGP=No and ADG_AN=High, 30 where HGP=Yes and ADG_AN=Low, 30 where HGP=Yes and ADG_AN=High).

Once animals were selected, identification details were used to retrieve stored, dried faecal samples from those animals and these samples were submitted for F.NIRS analysis in accordance with methods outlined by (Coates and Dixon, 2007).

A series of t-tests were used to determine whether there was any difference in diet quality parameters: faecal nitrogen (Fec_N%); total crude protein (CP%); dry matter digestibility (DMD%); and dietary non-grass proportion (DNG%), between groups based on ADG_AN class (low vs high) within property, within observation (sampling) date.

5.3 Results

Table 47 provides the sampling dates for observation events by property, and the paddocks from which animals were mustered (usually the day prior to sampling). Additional description of the paddocks can be found in Table 14.

Table 47: Summary description of property and paddock where animals were housed at the time that faecal samples were collected and the observation number and date that animals were yarded for sampling.

Property	Obs	Sample date	Paddock
1	3	30/10/2009	North Breeder
1	4	13/08/2010	No. 1 Lake
2	2	23/08/2009	Unknown (holding pdk)
2	3	24/11/2009	Sturt Plain North
2	4	26/06/2010	Bullock
3	2	1/05/2009	Emu A
3	3	14/01/2010	Cabbage Gum
3	4	24/05/2010	Stringybark
4	2	30/06/2009	Unknown (holding pdk)
4	3	11/09/2009	Steer
5	2	22/08/2009	Lagoon
5	3	16/12/2009	Lagoon
5	4	15/05/2009	Lagoon
6	1	7/08/2010	Unknown (breeder pdk)
6	3	24/11/2010	Bluebush
6	4	9/05/2010	New

Table 48: Count of number of faecal samples submitted for F.NIRS analysis arranged by property, HGP status (for property=1 only), ADG_AN class and observation

			observation where F.NIRS sample was collected			
property	HGP status	ADG_AN class	2	3	4	Total
1	No	High	0	22	20	42
	Yes	High	0	20	17	37
	No	Low	0	27	29	56
	Yes	Low	0	27	26	53
2		High	36	37	37	110
		Low	39	40	38	117

3	High	38	34	34	106
	Low	39	39	39	117
4*	High	39	39	0	78
	Low	40	35	0	75
5	High	36	37	37	110
	Low	39	41	40	120
7	High	38	36	39	113
	Low	36	33	33	102
Total		380	467	389	1236

* property=4 used ADG_DS

5.3.1 Faecal nitrogen %

Table 49: Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP retention (YES=retained, NO=lost) and ADG_AN. Data from property =1 and Obs3.

Faecal N%		ADG_AN			95% CI	
Property	**Obs=3**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	1.42	0.027	1.37	1.48
		High	1.36	0.03	1.3	1.42
	HGP=YES	Low	1.29	0.27	1.24	1.34
		High	1.34	0.03	1.28	1.4

Comparisons	**Level of other factor**	**p-value**
HGP=no vs HGP=yes	ADG_AN=Low	0.001
HGP=no vs HGP=yes	ADG_AN=High	0.7
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.009
ADG_AN=Low vs High	HGP=No	0.098
ADG_AN=Low vs High	HGP=Yes	0.24
ADG_AN=Low vs High	Averaged over both levels of HGP	0.75

There was no difference in Faecal Nitrogen % between ADG_AN classes ($p>0.05$) for property=1 and Obs3 samples.

Within ADG_AN=Low and when averaged over both ADG_AN classes, there was a significant difference in Faecal Nitrogen % between HGP groups. Animals that had lost their HGP implant (HGP=No) had higher Faecal Nitrogen % than animals that had retained their HGP implant (HGP=Yes).

Table 50: Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP and ADG_AN. Data from property =1 and Obs4.

Faecal N%	**ADG_AN**	**95% CI**

Property	Obs=4	Group	Mean	se	lower	upper
1	HGP=NO	Low	1.02	0.03	0.96	1.08
		High	1.17	0.04	1.1	1.24
	HGP=YES	Low	1.02	0.03	0.96	1.08
		High	1.15	0.04	1.07	1.23

Comparisons	Level of other factor	p-value
HGP=no vs HGP=yes	ADG_AN=Low	0.98
HGP=no vs HGP=yes	ADG_AN=High	0.74
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.78
ADG_AN=Low vs High	HGP=No	0.003
ADG_AN=Low vs High	HGP=Yes	0.013
ADG_AN=Low vs High	Averaged over both levels of HGP	<0.001

There was no effect of HGP status on Faecal Nitrogen % at Obs4 in property=1.

There was an effect of ADG_AN class with animals in the high class of ADG having higher Faecal Nitrogen % than those animals in the low ADG_AN class.

Table 51: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Faecal Nitrogen (%). Data from property=2, 3, 5 & 7 and Obs=2, 3 & 4. Within each observation and property, t-tests were used to compare mean Faecal Nitrogen % between ADG_AN classes, and p-values are reported in the last column.

Faecal N%		ADG_AN			95% CI		
Property	Obs	Group	Mean	se	lower	upper	p-value
2	2	Low	1.312	0.018	1.28	1.35	
		High	1.32	0.019	1.28	1.36	0.6
	3	Low	1.04	0.013	1.018	1.07	
		High	1.05	0.014	1.02	1.08	0.9
	4	Low	1.35	0.041	1.26	1.43	
		High	1.44	0.05	1.34	1.55	0.14
3	2	Low	1.102	0.022	1.06	1.15	
		High	1.14	0.05	1.035	1.24	0.5
	3	Low	1.7	0.035	1.63	1.77	
		High	1.7	0.03	1.65	1.76	0.9
	4	Low	1.214	0.021	1.17	1.26	
		High	1.24	0.022	1.19	1.28	0.5
5	2	Low	1.26	0.023	1.21	1.31	
		High	1.4	0.06	1.27	1.54	**0.043**
	3	Low	1.12	0.018	1.08	1.15	
		High	1.15	0.023	1.11	1.2	0.19
	4	Low	1.57	0.04	1.49	1.64	
		High	1.59	0.04	1.51	1.67	0.7
7	2	Low	1.02	0.02	0.98	1.06	
		High	0.99	0.02	0.95	1.04	0.4
	3	Low	2.15	0.07	2.02	2.28	
		High	2.14	0.052	2.03	2.24	0.9
	4	Low	2.14	0.05	2.05	2.24	

High	2.11	0.06	1.99	2.22	0.6

There was a single occasion where mean Faecal Nitrogen % was statistically different between classes of ADG (property=5, Obs2). On this occasion animals in the ADG_AN=High class had a higher Faecal Nitrogen % than animals in the ADG_AN=Low class. **All other comparisons were not different.**

5.3.2 Dietary crude protein (CP%)

Table 52: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for Dietary Crude Protein (CP%). Data from property =1 and Obs3.

Diet CP%		ADG_AN			95% CI	
Property	**Obs=3**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	8.03	0.19	7.66	8.41

		High	8.22	0.21	7.8	8.64
	HGP=YES	Low	7.94	0.19	7.56	8.31
		High	8.02	0.22	7.58	8.46

Comparisons	**Level of other factor**	**p-value**
HGP=no vs HGP=yes	ADG_AN=Low	0.7
HGP=no vs HGP=yes	ADG_AN=High	0.5
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.5
ADG_AN=Low vs High	HGP=No	0.5
ADG_AN=Low vs High	HGP=Yes	0.8
ADG_AN=Low vs High	Averaged over both levels of HGP	0.5

None of the comparisons were significant. There was no difference between ADG_AN=Low vs ADG_AN=High, and there was no difference between HGP=Yes vs HGP=No.

Table 53: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for Dietary Crude Protein (CP%). Data from property =1 and Obs4.

Diet CP%		**ADG_AN**			**95% CI**	
Property	**Obs=4**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	5.71	0.2	5.32	6.1
		High	6.37	0.24	5.9	6.84
	HGP=YES	Low	5.51	0.21	5.09	5.92
		High	5.97	0.26	5.46	6.48

Comparisons	**Level of other factor**	**p-value**
HGP=no vs HGP=yes	ADG_AN=Low	0.5
HGP=no vs HGP=yes	ADG_AN=High	0.3
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.2
ADG_AN=Low vs High	HGP=No	0.035
ADG_AN=Low vs High	HGP=Yes	0.2

ADG_AN=Low vs High	Averaged over both levels of HGP	0.015

There was a significant association between ADG_AN class and Obs4 CP%. Animals in the ADG_AN=High class had a higher CP% when averaged over both levels of HGP and this difference was also significant in the HGP=No group.

Table 54: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dietary Crude Protein (CP%) from property=2, 3, 5 & 7 and Obs=2, 3 & 4. Within each observation and property, t-tests were used to compare mean CP% between ADG_AN classes, and p-values are reported in the last column.

Diet CP%		ADG_AN			95% CI		
Property	Obs	Group	Mean	se	lower	upper	p-value
2	2	Low	4.46	0.11	4.23	4.69	
		High	4.2	0.09	4.02	4.38	0.07
	3	Low	3.85	0.07	3.7	4	
		High	3.7	0.07	3.57	3.83	0.13
	4	Low	5.1	0.09	4.91	5.29	
		High	5.23	0.19	4.84	5.61	0.5
3	2	Low	5.31	0.14	5.02	5.6	
		High	5.29	0.23	4.83	5.76	0.9
	3	Low	10.64	0.2	10.24	11.05	
		High	10.52	0.2	10.12	10.91	0.7
	4	Low	5.23	0.14	4.96	5.51	
		High	5.34	0.13	5.08	5.6	0.6
5	2	Low	6.18	0.12	5.94	6.43	
		High	6.73	0.22	6.27	7.18	**0.04**
	3	Low	4.69	0.12	4.45	4.94	
		High	4.45	0.13	4.19	4.71	0.16
	4	Low	6.23	0.13	6.35	6.9	
		High	6.73	0.13	6.48	6.99	0.6
7	2	Low	4.72	0.13	4.45	4.98	
		High	4.53	0.13	4.26	4.79	0.31
	3	Low	11.22	0.32	10.58	11.86	
		High	10.6	0.18	10.23	10.97	0.1
	4	Low	8.82	0.21	8.39	9.24	

High	8.33	0.29	7.75	8.92	0.17

There was only one significant association (property=5, Obs2). Animals in the ADG_AN=High class had higher CP% than those in the ADG_AN=Low class.

5.3.3 Dry matter digestibility (DMD)

Table 55: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for Dry Matter Digestibility (DMD). Data from property =1 and Obs3.

In Vivo DMD		ADG_AN			95% CI	
Property	**Obs=3**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	58.51	0.34	57.83	59.18
		High	58.12	0.38	57.38	58.87
	HGP=YES	Low	58.37	0.34	57.7	59.04
		High	58.24	0.4	57.46	59.02

Comparisons	**Level of other factor**	**p-value**
HGP=no vs HGP=yes	ADG_AN=Low	0.8
HGP=no vs HGP=yes	ADG_AN=High	0.8
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.9
ADG_AN=Low vs High	HGP=No	0.5
ADG_AN=Low vs High	HGP=Yes	0.8
ADG_AN=Low vs High	Averaged over both levels of HGP	0.5

None of the comparisons were significant. There was no difference between ADG_AN=Low vs ADG_AN=High, and there was no difference between HGP=Yes vs HGP=No.

Table 56: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for Dry Matter Digestibility (DMD). Data from property =1 and Obs4.

In Vivo DMD		ADG_AN			95% CI	
Property	**Obs=4**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	52.69	0.35	52	53.39
		High	52.52	0.43	51.68	53.35
	HGP=YES	Low	52.17	0.37	51.43	52.9
		High	52.62	0.46	51.71	53.52

Comparisons	Level of other factor	p-value
HGP=no vs HGP=yes	ADG_AN=Low	0.31
HGP=no vs HGP=yes	ADG_AN=High	0.9
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.6
ADG_AN=Low vs High	HGP=No	0.8
ADG_AN=Low vs High	HGP=Yes	0.5
ADG_AN=Low vs High	Averaged over both levels of HGP	0.7

None of the comparisons were significant. There was no difference between ADG_AN=Low vs ADG_AN=High, and there was no difference between HGP=Yes vs HGP=No.

Table 57: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dry Matter Digestibility (DMD%). Data from property=2, 3, 5 & 7 and Obs=2, 3 & 4. Within each observation and property, t-tests were used to compare mean DMD% between ADG_AN classes, and p-values are reported in the last column.

In Vivo DMD		ADG_AN			95% CI		
Property	Obs	Group	Mean	se	lower	upper	p-value
2	2	Low	56.8	0.18	56.44	57.16	
		High	56.62	0.19	56.23	57	0.5
	3	Low	56.2	0.22	55.74	56.64	
		High	56.38	0.2	55.97	56.79	0.5
	4	Low	50.06	0.25	49.46	50.56	
		High	50.74	0.34	50.05	51.42	0.1
3	2	Low	49.69	0.27	49.13	50.25	
		High	50.15	0.33	49.48	50.81	0.3
	3	Low	59.4	0.44	58.5	60.31	
		High	59	0.24	58.5	59.49	0.4
	4	Low	53.46	0.36	52.73	54.2	
		High	53.91	0.24	53.43	54.39	0.3
5	2	Low	53.01	0.23	52.55	53.48	
		High	53.7	0.45	52.8	54.61	0.2
	3	Low	54.99	0.27	5445	55.53	
		High	55.12	0.38	54.35	55.9	0.8
	4	Low	54.21	0.25	53.7	54.71	
		High	54.58	0.25	54.07	55.07	0.3
7	2	Low	52.33	0.31	51.7	52.95	
		High	52.57	0.2	52.16	52.97	0.5
	3	Low	60.15	0.35	59.43	60.87	
		High	59.32	0.24	58.83	59.81	0.062

4	Low	56.59	0.22	56.15	57.04	
	High	55.98	0.29	55.39	56.57	0.092

There were no significant associations between DMD% and ADG_AN measures.

5.3.4 Ratio of DMD: CP

Table 58: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for the ratio of Dry Matter Digestibility (DMD) to Crude Protein (CP). Data from property =1 and Obs3.

Ratio: DMD/CP		ADG_AN			95% CI	
Property	**Obs=3**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	46.23	0.92	44.42	48.04
		High	44.95	1.02	42.95	46.96
	HGP=YES	Low	46.28	0.92	44.47	48.09
		High	45.82	1.07	43.72	47.93

Comparisons	**Level of other factor**	**p-value**
HGP=no vs HGP=yes	ADG_AN=Low	0.97
HGP=no vs HGP=yes	ADG_AN=High	0.56
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.64
ADG_AN=Low vs High	HGP=No	0.36
ADG_AN=Low vs High	HGP=Yes	0.75
ADG_AN=Low vs High	Averaged over both levels of HGP	0.38

None of the comparisons were significant. There was no difference between ADG_AN=Low vs ADG_AN=High, and there was no difference between HGP=Yes vs HGP=No.

Table 59: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for DMD/CP ratio. Data from property =1 and Obs4.

Ratio: DMD/CP		ADG_AN			95% CI	
Property	**Obs=4**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	59.07	2.20	54.77	63.37
		High	53.26	2.64	48.08	58.44
	HGP=YES	Low	61.84	2.32	57.30	66.38
		High	57.47	2.87	51.85	63.09

Comparisons	Level of other factor	p-value
HGP=no vs HGP=yes	ADG_AN=Low	0.39
HGP=no vs HGP=yes	ADG_AN=High	0.28
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.17
ADG_AN=Low vs High	HGP=No	0.094
ADG_AN=Low vs High	HGP=Yes	0.24
ADG_AN=Low vs High	Averaged over both levels of HGP	0.047

There was a single significant comparison. Animals in the ADG_AN=Low group had a higher overall average ratio of DMD:CP when compared to animals in the ADG_AN=High group (p=0.047).

Table 60: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for the ratio of DMD:CP. Data from property=2, 3, 5 & 7 and Obs=2, 3 & 4. Within each observation and property, t-tests were used to compare mean DMD% between ADG_AN classes, and p-values are reported in the last column.

Ratio: DMD/CP		ADG_AN			95% CI		
Property	Obs	Group	Mean	se	lower	upper	p-value
2	2	Low	85.86	1.78	82.25	89.46	
		High	81.29	1.86	77.51	85.07	0.08
	3	Low	96.33	1.6	93.1	99.56	
		High	92.55	1.55	89.4	95.69	0.09
	4	Low	63.58	2.29	58.93	68.22	
		High	62.15	0.98	60.15	64.15	0.57
3	2	Low	61.82	1.77	58.24	65.39	
		High	59.88	1.44	56.96	62.79	0.4
	3	Low	35.5	0.62	34.24	36.75	
		High	35.15	0.46	34.21	36.09	0.66
	4	Low	64.66	1.39	61.23	68.09	
		High	64.34	1.77	61.74	68.94	0.78
5	2	Low	51.11	1.03	49.12	53.21	
		High	54.26	1.02	52.19	56.34	0.034
	3	Low	80.2	2.5	75.14	85.26	
		High	75.01	1.96	71.04	78.99	0.11
	4	Low	51.29	0.86	49.56	53.03	
		High	51.78	0.85	50.04	53.51	0.7
7	2	Low	74.5	1.92	70.61	78.39	
		High	71.62	2.15	67.26	75.97	0.3
	3	Low	35.29	0.53	34.21	36.36	
		High	34.28	0.79	32.68	35.87	0.3
	4	Low	43.34	1.29	40.73	45.97	

High	41.01	1	38.99	43.03	0.15

There was a single significant comparison. Within property = 5 and Obs2, animals in the ADG_AN=High group had a higher average DMD:CP ratio than animals in the ADG_AN=Low group (p=0.034).

5.3.5 Non-grass %

Table 61: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for Non-Grass %. Data from property =1 and Obs3.

Non-grass%		ADG_AN			95% CI	
Property	**Obs=3**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	25.92	1.13	23.71	28.12
		High	27.57	1.13	25.36	29.78
	HGP=YES	Low	26.8	1.25	24.35	29.24
		High	29.15	1.31	26.59	31.72

Comparisons	**Level of other factor**	**p-value**
HGP=no vs HGP=yes	ADG_AN=Low	0.3
HGP=no vs HGP=yes	ADG_AN=High	0.2
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.1
ADG_AN=Low vs High	HGP=No	0.6
ADG_AN=Low vs High	HGP=Yes	0.4
ADG_AN=Low vs High	Averaged over both levels of HGP	0.3

None of the comparisons were significant. There was no difference between ADG_AN=Low vs ADG_AN=High, and there was no difference between HGP=Yes vs HGP=No.

Table 62: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests for Non-Grass %. Data from property =1 and Obs4.

Non-grass%		ADG_AN			95% CI	
Property	**Obs=4**	**Group**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	Low	25.03	1.2	22.68	27.38
		High	27.27	1.27	24.78	29.75
	HGP=YES	Low	26.23	1.44	23.4	29.06
		High	28.54	1.57	25.47	31.61

Comparisons	Level of other factor	p-value
HGP=no vs HGP=yes	ADG_AN=Low	0.2
HGP=no vs HGP=yes	ADG_AN=High	0.3
HGP=no vs HGP=yes	Averaged over both levels of ADG_AN	0.1
ADG_AN=Low vs High	HGP=No	0.5
ADG_AN=Low vs High	HGP=Yes	0.5
ADG_AN=Low vs High	Averaged over both levels of HGP	0.4

None of the comparisons were significant. There was no difference between ADG_AN=Low vs ADG_AN=High, and there was no difference between HGP=Yes vs HGP=No.

Table 63: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Non-Grass%. Data from property=2, 3, 4, 5 & 7 and Obs=2, 3 & 4. Within each observation and property, t-tests were used to compare mean Non_grass% between ADG_AN classes, and p-values are reported in the last column.

Non-grass%		ADG_AN			95% CI		
Property	Obs	Group	Mean	se	lower	upper	p-value
2	2	Low	9.14	0.45	8.23	10.06	
		High	10.11	0.42	9.26	10.96	0.12
	3	Low	9.34	0.4	8.54	10.14	
		High	9.89	0.44	8.99	10.79	0.4
	4	Low	9.16	0.48	8.18	10.15	
		High	9.96	0.46	9.02	10.91	0.24
3	2	Low	12.7	0.81	11.05	14.35	
		High	10.84	0.96	8.9	12.78	0.15
	3	Low	11.88	0.91	10.02	13.73	
		High	10.84	0.96	8.9	12.78	0.44
	4	Low	12.12	0.95	10.19	14.05	
		High	10.84	0.96	8.9	12.78	0.35
5	2	Low	18.87	0.75	17.35	20.39	
		High	19.35	0.91	17.52	21.19	0.7
	3	Low	18.75	0.74	17.26	20.25	
		High	19.2	0.88	17.42	20.99	0.7
	4	Low	18.75	0.74	17.26	20.25	
		High	19.16	0.9	17.33	20.99	0.7
7	2	Low	17	1.07	14.82	19.17	
		High	14.55	1.14	12.25	16.86	0.12
	3	Low	16.53	1.16	14.18	18.88	
		High	15.28	1.43	12.37	18.19	0.5

4	Low	16.73	1.08	14.54	18.92	
	High	13.53	0.95	11.59	15.47	**0.032**

There was one significant association (property=7, Obs4). Animals in the ADG_AN=High class had higher NonGrass% than those in the ADG_AN=Low class.

5.3.6 Summary

F.NIRS measures were obtained from 33-40 animals in each of the low and high ADG_AN groups for five of the six properties. The sixth property had 17 to 29 animals in each of four groups representing a factorial combination of ADG_AN (low and high) and HGP retention (no and yes).

Four separate F.NIRS measures were generated: faecal nitrogen %, dietary crude protein % (CP), dry matter digestibility % (DMD), and non-grass %. An additional summary measure was created by calculating the ratio of DMD:CP. Comparisons were made between the mean F.NIRS measures for each of the two ADG_AN groups (low vs high) in order to test the hypothesis that grazing behaviour and diet selection might be an explanation for the difference in ADG between the low and high groups.

The results generally showed little or no relationship between LWG groups (lowest and highest quartiles) and faecal dietary parameters measured using F.NIRS.

With respect to faecal nitrogen % and dietary crude protein %, there were two properties where the high ADG_AN group had significantly higher F.NIRS measures than the low ADG_AN group (one at Obs2 and the other at Obs4). All other comparisons were not significant.

There were no significant associations between dry matter digestibility and ADG_AN group.

There was a single property where the non-grass % was lower in the high ADG_AN group compared to the low ADG_AN group (based on F.NIRS measures on samples at Obs4). All other comparisons were not significant.

There was a single property where the DMD:CP ratio was higher in the high ADG_AN group compared to the low ADG_AN group and another property where the comparison was reversed and the DMD:CP ratio was lower in the high ADG_AN group compared to the low ADG_AN group.

The findings are considered preliminary because they were based on a relatively small number of sampled properties. In addition faecal samples were collected at a point in time and then related to weight gain over a much longer time period.

The findings do not support the hypothesis that diet selection and grazing behaviour are major contributors to variation in annual weight gain.

However, more work is required to conclusively test this hypothesis, presumably involving more frequent sampling of both faeces and pasture to describe patterns of change over time and relate these to LWG measures.

6 Disease seroprevalence and liver function in study herds

6.1 Introduction

Livestock diseases have the potential to adversely affect body weight and liveweight gain and were considered potentially capable of contributing to poor weight gains in affected animals. The interest for this study was mainly focused on endemic diseases likely to be present in the regions where participating properties were located (Bovine Ephemeral Fever, Bovine Anaplasmosis and Bovine Virus Diarrhoea Virus or pestivirus).

Bovine ephemeral fever (BEF) (commonly called 'three day sickness) has been regarded as the most important viral disease of cattle in Australia (Uren, 1989), and others have estimated losses due to the disease to be about $83 million per annum for northern herds (Holmes *et al*., 2006). The disease is endemic in northern Australia, with sporadic waves of morbidity occurring in localized outbreaks during the wetter months in some years. Mosquitoes and biting midges (*Culicoides brevitarsus*) are believed to be vectors of the virus. BEF is characterised by a sudden onset of fever and lameness and severely affected animals may become recumbent though most generally recover after 2-5 days. Mortality associated with BEF is generally low, occurring in approximately 1% of cases (Uren, 1989). The disease most often affects naïve cattle between 6 months and 2 years of age (Uren, 1989). However, adult cattle especially bulls, heavy bullocks and fat cows may be more severely compromised than younger animals because of their heavier body weight and the higher likelihood of complications arising if recumbency occurs (Hungerford, 1990, Nandi and Negi, 1999).

A recent study compared effects of BEF vaccination to no vaccination in northern Australia herds over the period 2003-2009 and found no significant effect of vaccination on average daily gains of steers during either the back grounding or feedlot stage (McGown, 2010). While it may be unlikely that BEF would commonly contribute to long-term weight loss in northern Australia beef herds, localized outbreaks of the disease in some years could cause considerable short-term losses. Depending on the timing of outbreaks in relation to weight measurements or marketing, these losses could either be reflected in recorded poor weight performance, or be undetected.

The disease anaplasmosis is due to infection with a rickettsial organism *Anaplasma marginale* which is usually spread by the cattle tick in Australia. This infection is widespread in areas infested by the cattle tick in Australia (Callow, 1984). The main clinical signs of anaplasmosis are fever, depression and anaemia and severely affected animals may become recumbent and die while less severe cases may gradually recover but rate of growth would be depressed in this period. In northern Australia the high *B. indicus* content is thought to confer both tick resistance and resistance to the babesial tick borne diseases (Bock *et al*., 1999a, Bock *et al*., 1999b) and should reduce the likelihood of these diseases being a major problem in northern regions. Both *indicus* and *taurus* cattle are considered susceptible to anaplasmosis and therefore this form of tick fever continues to pose a risk to northern

beef producers and may be a cause of reduced weight gain in cattle greater than 1 year of age (Callow, 1984).

Bovine pestivirus is regarded as endemic in northern Australian beef herds (Taylor and Rodwell, 2001, Schatz et al., 2008). When a naïve herd of pregnant cows is exposed to pestivirus, there can be substantial losses due to foetal infection. These losses are commonly reported in reduced pregnancy rate, losses between pregnancy testing and branding, and ill thrift and deaths in weaners. Reports of weaning weight and post-weaning performance of calves persistently infected with pestivirus are consistently low, and survival rates beyond 12 months of age are poor.

It is important to note that cost constraints limited the amount of disease testing that could be done. This component of the study was developed as a nested study with the aim being to measure antibodies to selected disease agents in high and low growth rate animals to assess whether there was any association between evidence of prior exposure (seropositive status) and poorer weight gain. The aim was to determine whether any or all of these three diseases were present across the participating properties such that they may be expected to be contributing to widespread reduced LWG.

In addition a smaller sample of animals had blood samples collected and sent for biochemistry analysis with a particular focus on liver function tests. The focus on liver function was based on the fact that a number of potential insults (infectious conditions, poisonous plants, environmental toxins etc) may have long term adverse impacts on live function. In addition it is known that cattle with compromised liver function have decreased feed intake, growth weights, slaughter weight, carcass weight, fat thickness, and dressing (Epperson, 1999).

As indicated above for disease testing, cost constraints also meant that liver function testing was only applied to a small sample of the enrolled animals. The purpose of this sampling strategy was to determine whether or not compromised liver function (likely to be due to exposure to poisonous plants) might be occurring across relatively large numbers of animals in Northern Australia and therefore acting as a major whole-of-industry cause of reduced LWG. The sampling strategy was not expected to tell whether individual animals or individual properties might have problems with compromised liver function or with specific poisonous plants.

6.2 Methodology

The major components of the study design have been presented earlier in this report (see Section 3.3).

Blood samples were collected from the tail or jugular vein from all animals presented at Obs1 (weaning) and Obs4 (post wet-season).

There were three properties where blood sampling did not occur from all animals at both periods (property = 8, 10, 11), because there were where inadequate facilities or insufficient time to allow for sampling from all animals. In these cases, a selection of animals was sampled to allow for an indication of mob-level disease status only, where the first animals presented at the crush for observation had blood collected until about 40 samples had been collected.

Blood was collected into 8.5ml BD Vacutainer® tubes, labelled and immediately stored in insulated containers at 4°C, before being transported to Berrimah Veterinary Laboratory. The samples were centrifuged and serum then stored at -20°C until analysis.

A similar approach was taken to selecting animals for serology testing as was used in selecting animals for F.NIRS testing. Within each property, animal records were sorted on ADG_AN and then between 30 and 40 animals were selected from the top and bottom of the rankings. Selected animals were then classified as ADG_AN=low or high, depending on whether they were selected from the bottom or top of the rankings for ADG_AN. For those properties where F.NIRS testing was performed on stored faecal samples, the same animals were selected for serology testing. In some cases, all stored serum samples from individual properties were tested without regard for ADG_AN classification, while in others testing was limited to those animals selected on the basis of ADG_AN classification as described above.

A smaller subset of animals (five each randomly selected from the low and high groups based on ADG_AN) were then identified for biochemistry analysis to screen for live function testing.

All serology and biochemistry testing was performed by laboratory staff at the Berrimah Veterinary Laboratory.

Testing for antibodies to Bovine Pestivirus (Bovine Virus Diarrhoea Virus or BVDV) was performed on serum from Obs1 and Obs4, using the agar gel immunodiffusion (AGID) test (Kirkland and MacKintosh, 2006). Antibody reaction was measured and classified as: 0= Negative/susceptible; 1 = weak positive; 2 = positive; 3 = strong positive (recent infection); >3 = very strongly positive (recent infection) (BVDV Technical Advisory Group, 2006).

Testing for Bovine Ephemeral Fever (BEF), was performed on serum samples collected at Obs4 only because it was felt that testing was best performed after the wet-season period when animals were at greater risk of exposure to biting insects (potential vectors of the virus). Diagnosis of BEF was by serology using the virus neutralisation (VN) test (Uren, 1993). To classify results for the purpose of statistical analysis, a titre of less than or equal to 10 was considered not indicative of a significant infection, or possibly due to a cross reaction, and was classed as '*negative*'. A titre of 10-19 was classed as '*indeterminate'*, and a titre of greater than 20 was considered an indication of infection in the last 6 months and classified as '*positive'* (L Melville, personal communication 2010). It is acknowledged that there is no absolute criterion for interpretation of test results for the purpose of diagnosis. The limitations of the use of VN test results for diagnosis are discussed in detail by (Uren, 1993).

Testing for Bovine Anaplasmosis was limited to those properties in the Northern Territory that were located within cattle tick 'infected' and 'control' zones only were tested for anaplasmosis (property id= 2, 3, 5, 6 & 10). A map of the Northern Territory Cattle Tick Zones is provided in the Appendices. Testing for antibodies to Bovine Anaplasmosis was performed on serum samples from Obs4 only, using a competitive enzyme-linked immunosorbent assay (C-ELISA). Samples with <30% inhibition were classed as '*negative'*, while samples with $\geq$30% inhibition were classed as 'p*ositive'* using criteria outlined by(Office International Des Epizooties (Oie), 2008).

Serum biochemical tests were performed according to company instructions on an automated analyser (Konelab 20i 981800, Thermo Fisher Scientific, Vantaa, Finland). Prior to analysis of test serum, controls supplied by Thermo Fisher Scientific were analysed under routine quality assurance procedures. The following factors were measured: total bilirubin (umol/L), alanine aminotransferase (ALT, units/L), alkaline phosphatase (units/L), aspartate aminotransferase (AST, units/L), gamma-glutamyltransferase (GGT, units/L), total protein (g/dL), albumin (g/dL), gamma globulins (g/dL), total globulins (g/dL), and the albumin/globulin ratio.

A brief description of test methodology is presented here for each of the tests: total bilirubin (acid diazo method), alanine aminotransferase and aspartate aminotransferase (both using the Infinity ™ reagent based on enzymatic reactions of L-Alanine or L-Aspartate, respectively, in the presence of nicotinamide adenine dinucleotide and lactate dehydrogenase), gamma-glutamyltransferase (based on enzymatic conversion of L-gamma-glutamyl-3-carboxy-4-nitroanilide), alkaline phosphatase (based on enzymatic conversion of 4-nitrophenylphosphate), total serum protein (biuret method), albumin (bromcresol green dye binding method) and globulin (calculated by subtraction of albumin from total protein).

Seroprevalence is reported as proportion or percent positive and prevalence between ADG_AN classes (low vs high) were compared using chi-square tests.

There was also interest in assessing whether disease status might possibly be related to other measures of growth. Using animal identification records, measures for the three ADG values (ADG_DS, ADG_WS and ADG_AN) were matched to each animal in the disease output file. Regression analyses were then run with ADG measures as outcomes and disease status as a predictor in models with property as a random effect to account for clustering.

6.3 Results

6.3.1 Bovine Ephemeral Fever (BEF)

Table 64: Summary count of animals arranged by growth category (ADG_AN=low or high) and BEF status, by property

		Property									
ADG_AN	**BEF category**	**1**	**2**	**3**	**5**	**6**	**7**	**8**	**10**	**11**	**Total**
Low	negative	21	23	26	38	26	35	6	19	7	201
	indeterminate	6	2	1	0	1	0	0	0	0	10
	positive	30	15	12	3	12	3	2	1	0	78
	% positive	52.6	37.5	30.8	7.3	30.8	7.9	25.0	5.0	0.0	27.0
High	negative	26	27	23	37	26	32	5	20	5	201
	indeterminate	6	2	2	1	1	2	0	2	1	17
	positive	25	11	14	1	12	5	4	1	0	73
	% positive	43.9	27.5	35.9	2.6	30.8	12.8	44.4	4.3	0.0	25.1
Unknown	negative					64		23	15	25	127
	indeterminate					7		2	0	1	10
	positive					31		5	2	2	40
	% positive					30.4		16.7	11.8	7.1	22.6

The four properties with results presented for ADG_AN class = unknown, were those properties where all available serum samples were submitted for testing instead of just those samples from animals in the low and high categories based on ADG_AN.

BEF test results were coded by the laboratory as negative, indeterminate and positive.

For these analyses, BEF status was coded as either:

- BEF_posneg: 0=negative test, 1=positive test (indeterminate test results were coded as missing)
- BEF_posother: 0=negative, 1=indeterminate or positive

There was no association between BEF status and ADG_AN category, based on chi-squared tests performed on 2x2 tables. For BEF_posneg the test result returned a p-value of 0.7 and for BEF_posother, the p-value was 0.9,

Separate analyses were then conducted to compare the mean growth outcomes between BEF disease categories using regression analyses. There was no significant difference between BEF negative animals and either BEF positive or the combination of BEF positive and indeterminate animals for any of the three growth outcomes (ADG_DS, ADG_WS, ADG_AN) using multivariable regression.

6.3.2 Bovine Anaplasmosis

Table 65: Summary count of Anaplasma test results by property and arranged by category of growth based on ADG_AN (low, high).

		Property							
ADG_AN	**Anaplasma**	**2**	**3**	**5**	**6**	**8**	**10**	**11**	**Total**
Low	negative	0	14	39	0	0	2	4	59
	positive	40	24	1	39	8	18	3	133
		100.0	63.2	2.5	100.0	100.0	90.0	42.9	69.3
High	negative	0	21	37	0	0	5	6	69
	positive	40	18	2	39	9	18	0	126

		100.0	46.2	5.1	100.0	100.0	78.3	0.0	64.6
Unknown	negative				1	0	1	23	25
	positive				98	30	16	5	149
					99.0	100.0	94.1	17.9	85.6

There was no association between test status for Bovine Anaplasmosis (negative vs positive) and growth category for ADG_AN (low vs high) when analysed using a chi-squared test (p=0.2).

There was also no significant difference between Anaplasma negative animals and Anaplasma positive animals for any of the three growth outcomes (ADG_DS, ADG_WS, ADG_AN) using multivariable regression (p>0.05).

When the anaplasmosis results were compared to results for tick scores from the same properties, there appeared to be a direct relationship between Obs3 tick scores in particular and the anaplasmosis results reported above in that those properties with a higher prevalence of positive anaplasmosis results were also the properties with large numbers of animals with higher tick scores.

6.3.3 Bovine Virus Diarrhoea Virus (BVDV)

Table 66: Summary count of BVD test results for samples collected at Obs1 arranged by property and growth category

	Obs1	**Property**							
ADG_AN	**BVD category**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	Total
Low	negative	55	40	35	40	38	40	31	279
	weak pos	2	0	3	0	0	0	5	10
	positive	2	0	0	0	0	0	0	2
	strong positive	0	0	1	0	1	0	0	2
	% positive	6.8	0.0	10.3	0.0	2.6	0.0	13.9	4.8
High	negative	38	39	37	38	38	39	32	261
	indeterminate	6	0	2	1	0	0	5	14
	positive	3	1	0	0	1	0	1	6

	strong positive	0	0	0	0	0	0	0	0
	% positive	19.1	2.5	5.1	2.6	2.6	0.0	15.8	7.1

BVD status at Obs1 was coded as a binary variable (0=negative, 1=weak positive, positive or strong positive). Binary BVDV status was used as the outcome for statistical analyses.

An initial analysis was run just using data from one property (property id=1) where there was additional information on HGP status for individual animals. HGP status was coded as 0=implant lost and 1=implant retained. There was no association between BVDV outcome and either HGP status, ADG_AN classification or the interaction between HGP and ADG_AN ($p>0.05$).

A second analysis used data from all properties as shown in the above table. There was no association between BVD status and ADG_AN category ($p=0.24$).

There was also no difference in the mean ADG measures (ADG_DS, ADG_WS and ADG_AN) between BVD status (negative vs positive) ($p>0.05$).

Table 67: Summary count of BVD test results for samples collected at Obs4 arranged by property and growth category

	Obs4	**Property**						
ADG_AN	**BVD category**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	Total
Low	negative	1	40	31		40	38	4	154
	weak pos	9	0	4		0	0	1	14
	positive	44	0	4		1	0	23	72
	strong positive	3	0	0		0	0	10	13
	% positive	98.2	0.0	20.5		2.4	0.0	89.5	39.1
High	negative	1	39	33		38	37	2	150
	indeterminate	6	0	4		0	1	3	14
	positive	44	1	2		1	0	20	68

strong positive	5	0	0	0	0	14	19
% positive	98.2	2.5	15.4	2.6	2.6	94.9	40.2

The same approach was then used for BVD status at Obs4. There was a noticeable increase in the percentage of animals that tested positive at Obs4 relative to Obs1 for some properties, reflecting the increased opportunity for exposure on properties where BVD virus was circulating. In contrast some other properties continued to have very low percentages of positive animals suggesting that there was little or no active infection on those properties.

There was no association between Obs4 BVD status and class of ADG_AN (low vs high; $p>0.05$).

Using regression analyses with each of the three ADG measures as outcomes there was also no association between ADG_DS, ADG_WS or ADG_AN and Obs4 BVD status ($p>0.05$).

6.3.4 Liver function tests

Blood samples were collected from 5 to 10 animals from each combination of property and ADG_AN class (low and high) and submitted for biochemistry testing to measure liver function characteristics.

Detailed results are presented in the appendices.

Individual animals had results that were either lower than normal or higher than normal but there was little evidence of a consistent pattern that might have contributed to an explanation for lower ADG values. It seems more likely that these results might be consistent with a small proportion of animals having extreme values without pathology and a small proportion of individual animals that may be suffering from some insult (disease or toxin) at any point in time. The findings of these tests suggest that these situations are likely to be sporadic findings and not contribute to overall group changes in growth.

7 Parasite burdens in study herds

7.1 Introduction

The aim of this nested component of the study was to investigate the prevalence of internal parasites and influence on live weight gain variation on commercial properties in the Northern Territory.

The combination of high temperatures, prolonged dry periods and low stocking density in northern Australian beef regions mean that helminth parasitism of cattle is likely to be of major significance in northern regions only in the wet coastal and tableland areas of Queensland, the Top End of the Northern Territory and the northern fringes of the Kimberley region of Western Australia (Winks et al., 1983, de Witte and Jubb, 1998). However, microenvironments of favourable climatic conditions and high stocking rates in more inland regions could allow for otherwise unlikely proliferation of cattle worms burdens.

With a summer rainfall pattern in northern Australia, it is generally agreed that the predominant helminth species are *Haemonchus placei* (Barbers pole worm), *Oesophagostomum radiatum* (Nodular worm), *Cooperia punctata* and *Cooperia pectinata* (Small intestinal worms) (Winks *et al*., 1983, Hungerford, 1990, Love and Hutchinson, 2003). The Paramphistoma species *Calicophorum calicophorum* (rumen/stomach flukes) has been occasionally recorded in significant numbers in cattle in northern Australia (Kelly and Henderson, 1973, Brontowidjoys and Chapman, 1979). A recent study has described has produced data on 644 faecal sample submissions to the Veterinary Health Research Laboratory from the summer rainfall areas of Northern Australia which showed that *Cooperia* spp. accounted for 71% of the positive submissions, *Haemonchus* spp. 18%, *Oesophagostomum* spp 8% and others 3% (Chambers, 2009).

Weaner cattle are those most at risk from gastro-intestinal nematodes, with species-specific resistance developing by around 18months of age, given that animals are exposed to the particular species during this time (Roberts, 1951). In most cases, maximum infestations are recorded between 4-12months of age for many of the discussed species of helminths (Roberts, 1951). Such levels are rarely retained in cattle for more than 3 months, although can continue to occur until immunity develops. It is rare to see clinical conditions in cattle older than 2 years of age. Occasionally a small number of adult cattle showing consistent clinical signs with helminth infection have had a large number of *Haemonchus* species present, which has been attributed to depressed immunity in individual animals rather than an indication of total burden of the cattle population (B. Radunz, pers. comm.). A number of factors can affect the ability of an older animal to combat infections even after earlier exposure: 1) exposure to such a high number of larvae early in life that the development of resistance is delayed, or animal develops a chronic state of parasitism; 2) where exposure is at a greater level than earlier exposure, and resistance level is overwhelmed; or 3) a decrease in nutritional status, resulting in greater parasitism (Roberts, 1951).

There are few reports clearly showing beneficial impacts of anthelmintic treatments on weight gain measures in northern beef cattle. One study found no liveweight benefits in a branding or weaning anthelmintic treatment of Brahman cattle, although mortalities were less in the group treated at both branding and at weaning (Eggington *et al*., 1984). Radunz (1983) failed to demonstrate a significant liveweight response to branding or weaning or branding+weaning treatment in Brahman-cross weaners on improved pastures in the Katherine Region. Acute worm burden outbreaks were identified on two Northern Territory properties, although one study concluded that it would not be economically feasible to apply anthelmintic therapy (Henderson and Kelly, 1978). Others reported significant faecal egg counts in 30% of weaners sampled on a Central Australian property as part of a case study (Coventry, 2006). Even in an arid/semi-arid environment there may be periods where a combination of factors, particularly at weaning (nutritional and psychological stress, yard feeding etc.), could result in outbreaks of significant burdens in these areas.

Breed content may also be an important factor. High worm burdens in *B. indicus* and *B. indicus*-cross cattle may have less adverse effect on production measures than in *B. taurus* (Seifert, 1971, Turner and Short, 1971a, Wesley-Smith, 1972). Breed content of cattle in northern Australia has moved towards a predominantly pure *B. indicus* or high *B. indicus* content herd.

Bovine coccidiosis is a serious diarrhoeal disease caused by the protozoan parasite Eimeria (most commonly *E. zuernii* and *E. bovis*). Similar to gastrointestinal nematodes, young animals are usually those most affected, with adult cattle generally unaffected due to immunity acquired from early infections (Daugschies and Najdrowski, 2005). Severe scouring with mucous and bloodstained faeces is a typical clinical sign of bovine coccidiosis (Hungerford, 1990). Calves which survive acute coccidiosis can have retarded growth (ill-thrift) and may never reach full production potential (Fox, 1985, Parker *et al*., 1986, Daugschies and Najdrowski, 2005). Daugschies and Najdrowski (2005) suggested that herd production losses due to subclinical infections could be even more significant than acute clinical cases, as these occur more frequently and can still impair intestinal physiology, feed conversion and growth.

It is well documented that clinical coccidiosis is most common in calves soon after the weaning period (Parker *et al*., 1984, Daugschies and Najdrowski, 2005). Quite often, calves will ingest coccidial oocysts while on their dams, without experiencing clinical disease. The physiological stress associated with weaning can result in immune-suppression and therefore increased susceptibility to pathogenic infections (Watson, 1991). Clinical coccidiosis is usually only seen in a proportion of calves, however it is assumed that all animals within a group have the same level of exposure (Daugschies and Najdrowski, 2005). While a high level of exposure increases an animal's likelihood to acquire the parasite, the individual animal's inability to withstand factors that impose stress may predispose them to clinical disease (Daugschies and Najdrowski, 2005).

There are few reports on the prevalence of this disease in north Australian beef cattle herds. As with gastrointestinal worms, this is likely due to the assumption that conditions are rarely favourable for proliferation or spread of the parasite, and more attention has been given to diagnosis and measuring production effects in more intensive industries in temperate regions. However, it has been noted that coccidiosis is a more common cause of health problems in cattle in Northern Territory herds than worms (Fitzpatrick, 2006).

Detailed studies in northern Australia are confined to those conducted on Swan's Lagoon in the sub-tropics of north Queensland in the 1980s with *B. taurus* cattle. The prevalence of coccidiosis was reported on the research station under hot, dry and dusty conditions (Parker *et al*., 1984, Parker and Jones, 1990, Parker and Jones, 1987). These conditions were previously regarded as unsuitable for survival of the parasite in the free-living stage. Weight loss due to coccidiosis was recorded in up to 10 percent of *B. taurus* weaners every year over the four-year study (Parker and Jones, 1987). Three percent of calves died on the research station in 1980 from suspected coccidiosis, with severe diarrhoea post-weaning (Parker *et al*., 1984). Sampling of weaners from a central Australian cattle herd recorded significant oocyst counts (up to 45,000 oocysts) in 15 percent of weaners (Coventry, 2006), although the author did not record whether there were signs of clinical disease. This does however suggest that significant burdens may occur in northern Australian conditions.

The prevalence of helminth and coccidial parasites in northern Australia is believed to be limited by environmental factors due to the reliance of these parasites on suitable conditions during free living stages to survive. Under extensive grazing conditions in Northern Australia where weaner cattle are raised at low stocking density and are often weaned onto pastures at the start of or during the dry season period, it could be expected that there should not be large challenges from heavy pasture contamination of helminth larvae or coccidial oocysts. Exceptions could be where weaners are yarded for extended periods at weaning with associated yard feeding or where animals are likely to congregate for long periods around watering points or supplement troughs. There are reports to suggest that significant burdens can occur, most likely due a combination of the risk factors discussed. Animals may experience varying levels of burdens and clinical disease, most likely due to the individual level of resilience, immunity and/or level of immune-suppression associated with stress factors.

For the purposes of this project, internal parasites were considered in two groups: gastrointestinal helminths/worms; and coccidian. With a summer rainfall pattern in northern Australia, the expected predominant helminth species were *Haemonchus placei, Oesophagostomum radiatum,* and *Cooperia* spp.

7.2 Methodology

Faecal sampling for parasite determination occurred as part of the larger study. Animals were sampled for testing for internal parasites at Obs2, Obs3 and Obs4. Where Obs2 did not occur (branding occurred prior to weaning), animals were sampled at Obs1.

Approximately 10% of animals presented at each muster were systematically randomly sampled by collecting a faecal sample from every 10th animal as they were presented at the crush. No attempt was made to collect from the same animals at different observation periods. Samples collected for faecal egg testing could not be stored for long periods so it was not possible to relate FEC sampling to high or low ADG groups of animals. The FEC samples therefore were based on a small, random sample collected from different animals at different observation periods.

Faecal samples were collected from the rectum using a gloved arm and placed into a sealed 70ml specimen jar with all air excluded, and stored immediately in an insulated container at 4°C, for subsequent determination of faecal egg count (FEC) and faecal oocyst count (FOC). A second sample was collected for helminth larval culture for species identification by part-filling a 70ml specimen jar and storing the jar with a loosely closed lid at room temperature. Faecal samples were transported to the Berrimah Veterinary Laboratory for analysis, most often within 38 hours of collection.

Faecal egg counts and faecal oocyst counts were measured using methods outlined by (Roberts and O'Sullivan, 1950). Species of helminths present and percentage of burden attributed to species were determined by larval culture (Roberts and O'Sullivan, 1950).

7.3 Results

A total of 544 faecal samples were submitted for faecal egg counts (FEC) and 511 for faecal oocyst counts (FOC). One property (property = 7) submitted the first samples for FEC from Obs1 and all others submitted their first samples from Obs2. Since both Obs1 and Obs2 were in the dry period and the two observation periods were only about a month apart, the samples from property =7 have been coded as Obs2 for the purposes of analysis. In most cases faecal samples from the same animals were submitted for both FEC and FOC. Some animals did not have sufficient faeces for both tests and in these cases FEC was prioritised over FOC.

Table 68: Summary count of number of samples submitted for FEC from each property and observation.

	Observation

Property	2	3	4	Total
1	21	20	21	62
2	25	23	22	70
3	14	20	21	55
4	28	17	0	45
5	25	22	21	68
6	0	17	8	25
7	25	25	20	70
8	19	17	11	47
9	0	0	6	6
10	0	23	10	33
11	23	22	18	63
Total	180	206	158	544

Table 69: Summary count of number of samples submitted for FOC from each property and observation.

	Observation			
Property	**2**	**3**	**4**	**Total**
1	21	20	21	62
2	25	20	22	67
3	13	19	21	53
4		17		17
5	25	22	21	68
6		17	8	25
7	25	25	20	70
8	19	17	11	47
9			6	6
10		23	10	33
11	23	22	18	63

Total	151	202	158	511

FEC and FOC data were not normally distributed. There was a peak of animals with zero counts and then a second group of animals that had non-zero counts with a right skew (small number of animals with higher counts). The data were not able to be normalised by transformation.

Egg counts (eggs per gram of faeces, epg) were categorised into a five level variable (zero epg, 10 to 190, 200 to 500, >500 to 1000, >1000). Burdens of 200 or more epg were considered potentially meaningful, while Radunz (1992) has indicated that the percentage of animals with epg greater than 500 may be a useful indicator of clinical disease (Radunz, 1992).

It is recognised that faecal epg counts may not necessarily reflect internal worm burdens and that animals could have clinical impacts associated with high worm burdens with very low epg when the majority of the parasites are immature.

Between 8 and 100% of animals on any one property had zero counts of eggs per gram of faeces (epg) at any one measurement period (see following table). Between 0 and 80% of animals in any one property and at any one observation, had epg counts that were 200 or higher (classified as potentially meaningful burdens). While there appeared to be variation between properties with respect to epg, when the percentage of animals with epg >=200 were considered across all properties there was little evidence for any change from Obs2 to Obs3 while there was a general trend for higher FEC in the observations after the wet (Obs 2 and 4). We expected that higher worm counts would be observed during or shortly after the wet. The generally higher level of worms still present at Obs4 was unexpected and may have reflected local conditions in some years associated with rain on properties during the late wet and early dry seasons.

A series of regression analyses were conducted to explore the hypothesis of an association between FEC and measures of growth. Separate models were run for each of the three ADG measures (ADG_DS, ADG_WS and ADG_AN). Each model incorporated a fixed effect coding for weaning weight (Obs1_LWT) to adjust for variation in starting weight, and a random effect coding for property to adjust for clustering at the property level. Models then included either the 5-level categorical variable coding for FEC burden or a binary variable (0= epg <200, 1=epg greater than or equal to 200). Models were repeated for each observation and then with all observations combined and with selected combinations ie Obs2 and 3 combined with ADG_DS as the outcome.

There was no statistical association (p>0.05) between measures of worm burden and any ADG measure. While sample sizes were small, the evidence is suggestive of a lack of significant adverse impact of worm burdens on liveweight gain in northern beef cattle.

There were relatively few animals with epg >500. Inspection of individual liveweight and weight gain measures for these animals did not provide any clear association between high epg and adverse growth measures. ADG measures were not consistently different to those for animals with no or few epg from the same properties.

FOC were classified into categories as follows: zero (no oocysts identified), 10 to <1000 opg, 1000 to <5000 opg, and 5000 or greater opg. Published recommendations suggest that counts greater than 5000 opg may be associated with clinical disease. While counts below 5000 may not be associated with clinical disease they may indicate a potential source of severe infection if conditions favourable for spread are experienced (overcrowding of young, susceptible animals, with opportunity for faecal contamination of water or feed). Severely affected animals may have oocyst counts of 100,000 per gram faeces or higher.

Coccidiosis was present in all herds that were sampled. As expected, coccidial oocyst burdens only reached significant levels shortly after weaning (Obs2) when animals were most stressed, and had spent time within yards.

A series of regression analyses were then conducted to explore the hypothesis of an association between FOC and measures of growth, as was describe above for FOC.

There was no statistical association (p>0.05) between measures of FOC and any ADG measure. While sample sizes were small, the evidence is suggestive of a lack of significant adverse impact of coccidiosis on LWG in young northern beef cattle.

Caution is required in interpreting these results because of the small sample sizes and because of the design of our sampling strategy. Our results did not show any association between internal parasite burdens and post-weaning LWG in the herds that were participating in our study.

Our study design focused on post-weaning growth and involved LWG measures based on observations that were each separated by several months. It is possible that individual animals may have had parasite burdens at an earlier age and recovered from these before our study started. It is also possible that individual animals may have suffered adverse effects from worm burdens where

the effects were relatively short term and therefore not detected through our study. It is acknowledged that under favourable conditions internal parasites have the potential to have serious adverse effects on animal health and production in northern cattle herds.

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Table 70: Summary statistics for results of faecal egg count (FEC). Data presented as counts of animals in each category of FEC, arranged by property and observation period.

Count of animals in each category		Property											
Obs	**FEC category (epg)**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
Obs2	0	3	5	10	19	2		2	17			4	62
Obs2	10 to 190	7	13	4	8	11		9	2			6	60
Obs2	200 to 500	11	6	0	1	9		10	0			11	48
Obs2	500 to 1000	0	1	0	0	3		4	0			2	10
Obs2	>1000	0	0	0	0	0		0	0			0	0
Obs2 Total		21	25	14	28	25		25	19			23	180
% with zero epg at Obs2		14.3	20.0	71.4	67.9	8.0		8.0	89.5			17.4	34.4
% with epg= 200+ at Obs2		52.4	28.0	0.0	3.6	48.0		56.0	0.0			56.5	32.2
Obs3	0	8	7	5	6	12	1	0	12		0	22	73
Obs3	10 to 190	6	11	6	9	8	5	5	5		17	0	72
Obs3	200 to 500	4	3	6	2	2	5	11	0		5	0	38
Obs3	500 to 1000	2	2	3	0	0	2	7	0		1	0	17
Obs3	>1000	0	0	0	0	0	4	2	0		0	0	6
Obs3 Total		20	23	20	17	22	17	25	17		23	22	206
% with zero epg at Obs3		40.0	30.4	25.0	35.3	54.5	5.9	0.0	70.6		0.0	100.0	35.4

% with epg= 200+ at Obs3		30.0	21.7	45.0	11.8	9.1	64.7	80.0	0.0		26.1	0.0	29.6
Obs4	0	10	3	5		3	2	4	2	1	2	1	33
Obs4	10 to 190	9	4	6		3	4	7	6	1	4	8	52
Obs4	200 to 500	2	9	6		8	2	5	1	3	2	5	43
Obs4	500 to 1000	0	6	2		4	0	4	1	1	0	4	22
Obs4	>1000	0	0	2		3	0	0	1	0	2	0	8
Obs4 Total		21	22	21		21	8	20	11	6	10	18	158
% with zero epg at Obs4		47.6	13.6	23.8		14.3	25.0	20.0	18.2	16.7	20.0	5.6	20.9
% with epg= 200+ at Obs4		9.5	68.2	47.6		71.4	25.0	45.0	27.3	66.7	40.0	50.0	46.2
Grand Total		62	70	55	45	68	25	70	47	6	33	63	544
% with zero epg - all Obs combined		33.9	21.4	36.4	55.6	25.0	12.0	8.6	66.0	16.7	6.1	42.9	30.9
% with epg= 200+ - all Obs combined		30.6	38.6	34.5	6.7	42.6	52.0	61.4	6.4	66.7	30.3	34.9	35.3

Table 71: Summary statistics for results of faecal oocyst count (FOC). Data presented as counts of animals in each category of FOC, arranged by property and observation period.

Count of animals in each category		Property											
Obs	**FOC category (opg)**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
Obs2	0	6	1	1		1		13	11			3	36
Obs2	10 to <1000	13	8	5		9		12	8			10	65
Obs2	1000 to <5000		12	5		9						9	35
Obs2	5000+	2	4	2		6						1	15
Obs2 Total		21	25	13	0	25	0	25	19	0	0	23	151
% with zero count		28.6	4.0	7.7		4.0		52.0	57.9			13.0	23.8
% with count 1000+		1.0	6.4	5.4		6.0		0.0	0.0			4.3	3.3
Obs3	0	20	20	19	5	17	4	7	13		15	16	136
Obs3	10 to <1000				11	5	13	13	4		8	6	60
Obs3	1000 to <5000				1			5					6
Obs3	5000+												0
Obs3 Total		20	20	19	17	22	17	25	17	0	23	22	202
% with zero count		100.0	100.0	100.0	29.4	77.3	23.5	28.0	76.5		65.2	72.7	67.3
% with count 1000+		0.0	0.0	0.0	0.6	0.0	0.0	2.0	0.0		0.0	0.0	0.3
Obs4	0	19	18	6		16	3	7	4	2	1	4	80

Obs4	10 to <1000	2	4	11		5	5	13	6	4	6	11	67
Obs4	1000 to <5000			4							3	3	10
Obs4	5000+								1				1
Obs4 Total		21	22	21		21	8	20	11	6	10	18	158
% with zero count		90.5	81.8	28.6		76.2	37.5	35.0	36.4	33.3	10.0	22.2	50.6
% with count 1000+		0.0	0.0	1.9		0.0	0.0	0.0	0.9	0.0	3.0	1.7	0.7
Grand Total		62	67	53	17	68	25	70	47	6	33	63	511
% with zero count		72.6	58.2	49.1	29.4	50.0	28.0	38.6	59.6	33.3	48.5	36.5	49.3
% with count 1000+		3.2	23.9	20.8	5.9	22.1	0.0	7.1	2.1	0.0	9.1	20.6	13.1

7.3.1 Results of larval culture

A total of 83 faecal samples were selected for further inspection using larval culture to identify worm types to one of four categories: *Oesophagostomum* spp, *Cooperia, Haemonchus,* and *Trichostrongylus*. Animals were selected for larval culture based on initial results of fec (higher fec) and on sufficient and suitable faecal samples for further testing.

No *Trichostrongylus* larvae were identified in any samples.

Table 72: Summary count of samples based on identification of larvae from larval culture

	total count	***Oesophagostomum***	***Cooperia***	***Haemonchus***
Obs = 2				
Total samples	27			
Number of samples with:				
0% larvae		14	23	0
<20%		10	1	0
20-50%		3	1	3
>50% larvae		0	2	24
Max %		49%	52%	100%
Obs = 3				
Total samples	23			
Number of samples with:				
0% larvae		14	11	2
<20%		3	0	0
20-50%		6	7	8
>50% larvae		0	4	13
Max %		50%	100%	100%
Obs = 4				
Total samples	33			
Number of samples with:				

0% larvae	8	25	3
<20%	12	5	0
20-50%	9	2	4
>50% larvae	4	1	26
Max %	100%	100%	100%

Natural worm burdens are expected to be made up of mixed species of parasites with the relative importance of any particular species then dependent on a range of animal, management and environmental factors. All three of the identified genera are capable of causing clinical disease and weight loss in young cattle (calves and weaners) (Radunz, 1992).

As expected the percentage of worms identified under any one genera was inversely related to the percentages identified for the other genera. If animals had no or very few worms identified as *Cooperia* or *Oesophagostomum*, then they were likely to have 100% identified as *Haemonchus* for example.

Larvae were identified as belonging to all three nematode genera. There were relatively few *Oesophagostomum* spp (roundworms) identified in samples with a single animal (property=5, Obs4) having 100% of all larvae identified as being roundworms.

There were also relatively few animals identified with *Cooperia* worm burdens with most animals recording no larvae of this genera. There were two animals at Obs3 (both from property=3) and one animal at Obs4 (property=1) where 100% of larvae were identified as *Cooperia* indicating that individual animals may have a higher proportion of worms from this genera.

Almost all animals had *Haemonchus* burdens at all measuring occasions and there was a higher percentage of animals where *Haemonchus* appeared to be the dominant worm genera (of the identified genera).

8 Pen trial to explore factors associated with divergent post-weaning liveweight gain[c]

8.1 Introduction

This study was planned as an intensive, pen trial to complement the larger, field study investigating factors that contribute to variation in post-weaning liveweight gain in northern beef cattle.

Preliminary work on a small number of animals in two groups based on post-weaning growth (moderate post-weaning growth, n=8; low post-weaning growth, n=8) was conducted within the MLA project NBP.350. Animals were grazed on low CP, dry season pastures for 100d and then exposed to varying diets under experimental conditions. Results suggested that there was little observable difference between the two groups in feed intake or rumen function when offered a low CP diet alone, or when offered non-protein nitrogen (NPN) or protein (cottonseed meal) supplements under controlled experimental conditions (Turnbull et al., 2008). In the preliminary study, LWG was not measured under controlled conditions. These results suggested that factors, other than intake driven by rumen conditions, may contribute to the variation in growth evident in cattle grazing low CP forages after weaning in northern Australia. These factors may include stress responses during the marking and weaning process, access to and willingness to consume supplements, grazing behaviour and range, disease or parasite burden and genetics.

The preliminary study in NBP.350 did identify a difference in the concentration of circulating insulin-like growth factor-1 (IGF-1), 100 days after weaning between the two groups (Turnbull, *pers*. *comm*.). However, this was a single point measurement taken 100 days after weaning and does not provide information as to whether this difference was apparent at weaning and how circulating IGF-1 concentration responds to post-weaning nutrition, or if circulating IGF-1 concentration is determined by genotype of the animal.

A further pen trial was then planned to make additional use of the existing animal resources and samples available within the current NBP.0390 project, to continue to investigate post-weaning growth, by investigating the concentration of specific growth factors and metabolites both at weaning and 100 d after weaning in cattle grazing low CP pastures, and investigate how those growth factors and metabolites then respond to high or low CP diets.

[c] Published as a separate MLA report. Quigley S and Poppi D. Factors associated with divergent post-weaning liveweight gain in northern Australian beef cattle B.NBP.0629, 2012.

A range of circulating factors have been used to indicate nutritional and metabolic status of animals and/or are key regulators of animal LWG. Insulin-like growth factor-1 acts in an autocrine, paracrine and endocrine manner on a range of cell types (muscle, bone, fat, mammary tissue and reproductive organs), mainly to enhance cellular proliferation and differentiation, as well as stimulating glucose and amino acid uptake. The primary site of IGF-1 production is the liver. IGF-1 binds to specific binding proteins in the circulation and these maintain its stability and regulate its activity. Circulating IGF-1 has been reported to be moderately heritable (0.35) (Moore et al., 2005) and has been previously implicated with residual feed intake (Moore et al., 2005) and post-weaning feed:gain of cattle (Bishop et al., 1989). Infusion of IGF-1 decreased protein degradation and increased protein gain in sheep (Oddy and Owens, 1996) and reduced the concentration of 3-methylhistidine in the plasma of cattle fed low protein diets (Hill et al., 1999). The concentration of circulating IGF-1 responds to energy intake but not the form of energy in the diet (Houseknecht et al., 1988).The concentration of IGF-1 in the circulation is also responsive to compensatory LWG after a restriction in energy intake (Hayden et al., 1993), feed deprivation (Wu et al., 2008), dietary protein supply (Liu et al., 1997),the administration of hormonal growth promotants (Pampusch et al., 2003) and bovine somatotropin (BST)(Lemal et al., 1989). The response of circulating IGF-1 to BST is itself dependent on the nutritional status of the animal (Elsasser et al., 1989, Rausch et al., 2002).

3-methylhistidine (3MH) is a product of muscle catabolism which is not reutilized by the animal. The concentration of 3MH in plasma (Yambayamba et al., 1996) and urine (McCarthy et al., 1983) have previously been used to estimate protein degradation rates in cattle (Gopinath and Kitts, 1984) and body protein loss in dairy cows (Phillips et al., 2003). Plasma albumin concentration typically reflects chronic protein status of an animal. Plasma creatinine concentration is associated with kidney filtration and muscle mass; creatinine is a breakdown product of muscle catabolism and the concentration typically reflects muscle mass. Glucose is the main energy substrate for all tissues in ruminants. The primary objective of most metabolic responses is maintaining a constant supply of glucose. Plasma urea concentration is an indicator of the response of ruminants to immediate dietary protein supply. Excess rumen ammonia is converted to urea in the liver and this then circulates before being excreted in urine, recycled back to the rumen or incorporated into milk (in the case of lactating animals). Plasma urea may also be elevated when muscle proteins undergo catabolism to supply amino acids for gluconeogenesis.

It was hypothesised that the variation in post-weaning LWG of cattle in northern Australia is related to variations in serum IGF-1, 3MH, albumin, creatinine, glucose and urea concentration in response to individual animal stress levels at weaning and the protein accretion in the skeletal muscle of those animals when grazing low CP diets post-weaning.

8.2 Objectives for the pen trial

1. Quantify relationships between insulin-like growth factor-1 and metabolites associated with growth and nutrient status of animals and post-weaning liveweight gain of cattle grazing low and high crude protein pastures.

2. Improve understanding of the reasons for the divergence in post-weaning liveweight gain which exists in northern Australian cattle herds.

3. Provide data and results to the NBP.0390 project team for inclusion in their conclusions with regards to herd management to increase the liveweight gain of the tail of grower cattle.

8.3 Methodology

This project was completed as a component or nested study within the larger current project.

8.3.1 Experimental design and animals

The experiment was conducted in accordance with the Australian Code of Practice for the Care and Use of Animals for Scientific Purposes and was approved by the Charles Darwin University (CDU; A07038) and University of Queensland (UQ; CDU/SAS/233/10) Animal Ethics Committees.

The experiment involved 3 phases:

- a post-weaning grazing phase (*Phase 1*),
- a pen study (*Phase 2*) and
- a wet season grazing phase (*Phase 3*),

8.3.1.1 Phase 1

Male calves (n=203) from three calving mobs on one of the properties participating in the larger study (property=3), were weighed (after an overnight feed curfew), measured for hip height (HH) , marked and then weaned in April 2010. Only Brahman type calves were included in the trial. Charbray type calves were removed from the mob.

After weaning the calves were fed cavalcade (*Centrosema pascuorum*) hay and a mixture of calf pellets (Riverina Stockfeeds), copra meal and cracked sorghum in the yards for one week. The weaners then grazed native pastures (consisting of a mixture of *Sorghum plumosum* (perennial sorghum), *Chrysopogon fallax* (ribbon grass), *Dichanthium sericum* (Queensland bluegrass), *Aristida latifolia* (feather-top wiregrass) and *Themeda triandra* (kangaroo grass) as a single mob in the same paddock for 91 days. The paddock consisted of the Banjo (40%), Larrimah (40%) and Mering (20%) land systems.

During the 91 day grazing period the weaners were offered the same concentrate as offered in the yards (described above) for two weeks and then a loose lick mix (10% urea, 26% salt, 15% kynofos, 10% gran-am, 15% copra meal, 20% limestone and 4% trace mineral mix) at 120 g/hd/day for the remainder of the 91 day grazing period.

Ninety one days after weaning the steers (n=183) were weighed (after an overnight feed curfew) and post-weaning average daily liveweight gain (ADG) was determined. Blood samples were collected from steers at weaning and 91 days post-weaning. Faecal NIRS estimated a dietary CP content of 6.3% and a dry matter digestibility of 49.8%, approximately one week before completion of *Phase 1*.

8.3.1.2 Phase 2

After 91 days of post-weaning grazing on dry season pastures (*Phase 1*), 72 steers divergent in liveweight were selected for inclusion in a pen study. Steers were ranked on ADG over the 91 day grazing period and steers with the highest (n=5) and lowest (n=5) ADG were removed from the data set. Thirty six pairs of steers divergent in post-weaning ADG were selected for the pen study by pairing steers with the highest post-weaning ADG (H-ADG) with steers with the lowest post-weaning ADG (L-ADG), that were of similar liveweight at weaning. If there were no steers in the H-ADG group within 10 kg weaning liveweight of steers in the L-ADG, they were omitted from the study. The selected steers were then transferred to the Katherine Research Property (KRS; Katherine, NT) and grazed as one mob on Sabi grass (*Urochloa mosambicensis*) dominant pasture, with cavalcade hay provided, for three weeks. The steers were then allocated to one of 24 pens with n=3 steers/pen (based on paired weaning liveweight) with diets randomly allocated to pens.

The treatment diets were a low protein Mekong grass hay (*Brachiaria brizantha*) (30 g CP and 931 g OM/kg DM) and a higher protein cavalcade hay (108 g CP and 939 g OM/kg DM), both fed *ad libitum*. Urea and ammonium sulphate (US) (20 g/hd/day) and 200 g/hd/day of copra meal (240 g CP and 940 g OM/kg DM) were added to the Mekong grass to provide a diet with a final CP content of approximately 70 g/kg DM. The animals were adapted to treatment diets and pen feeding over the

first three weeks, and data over this period has been omitted from the data analysis. The steers were fed in their group pens at the same time each day. Supplements were offered to the Mekong grass treatments by mixing thoroughly through the hay when offered each morning (US supplement was dissolved in water and sprayed over and mixed through the hay). Hay residues were collected from the feed trough every seven days or more frequently on some occasions depending on the amount of residue and weather.

At the commencement of the pen experiment all steers were weighed, HH measured and blood samples collected. Rumen fluid was collected from one animal from each pen, selected at random, to determine rumen ammonia (NH_3N) concentration and the microbial genetic profile. The steers were weighed once each week for 10 consecutive weeks, with hip height recorded at the same time, and blood and rumen fluid samples (same animals as at the commencement of the experiment) were collected after 10 weeks of treatment feeding. Liveweight and HH data at week 10 were omitted from the data analysis due to rain affecting intakes during that week. Liveweight and HH change were determined by regression over weeks 3 to 9 and 0 to 9 of the experiment, respectively.

8.3.1.3 Phase 3

On completion of Phase 2, the steers were transferred to Berrimah research farm (Darwin, NT) and grazed *Digitaria eriantha* dominant pastures for six months, from October 2010 to April 2011. Liveweight and HH were recorded once each month, with animals mustered and measured within one morning each month.

8.3.2 Analytical

Serum albumin, creatinine, glucose, and urea concentrations were determined on an Olympus AU400 auto-analyser (Beckman Coulter Diagnostic Systems Division; Melville, NYC, USA) using Beckman Coulter Diagnostic Systems kits. Insulin-like growth factor-1 concentration in serum was determined using the Bioclone IGF-1 radioimmunoassay kit according to the manufacturer's instructions (Bioclone; NSW, Australia), with radioactivity counted on a Perkin Elmer 2470 gamma counter. Ammonia-N concentration in rumen fluid was determined by titration with 0.01 M HCl using a TIM 840 Titration workproperty manager (Radiometer Analytical SAS; Villeubanne, Cedex, France) after distillation (Büchi 321 distillation unit Flawil, St Gallen, Switzerland). Dry matter content of feeds offered and residues was determined each week by drying bulked samples to a constant weight at 65^{o}C.

8.3.3 Statistical analysis

Change in liveweight and HH during each of the three phases of the experiment was determined by linear regression. The data were analysed using the GLM procedure in SAS (SAS v9.2) within each

phase of the experiment. The model included Growth (H- or L-ADG) in *Phase 1* and *Phase 3*, and Growth, Diet (Mekong or cavalcade) and their interaction in *Phase 2*.

Concentration of IGF-1 and metabolites was analysed within each Phase of the experiment using the GLM procedure in SAS (SAS v9.2). The model included Growth and Stage (weaning or post-weaning) and their interaction in *Phase 1*, and Growth and Diet and their interaction in *Phase 2*. Correlations between metabolites and liveweight, HH and rate of change of both were determined using the CORR procedure in SAS, and partial correlations were also conducted between metabolite concentration and average daily LWG, controlling for liveweight. In all cases, significant differences, or correlations, were accepted at $P<0.05$.

8.4 Results

8.4.1 Phase 1

The average liveweight of the entire mob of steers at weaning was 138.7 $\pm$ 1.8 kg (ranging from 78 to 206 kg). The average liveweight of the mob 91 days after weaning was 152.4 $\pm$ 1.7 kg (ranging from 88 to 222 kg).

Average daily LWG of steers in the entire mob over this period was 0.12 $\pm$ 0.01 kg/d (ranging from -0.22 to 0.44 kg/d).

The average liveweight of the steers selected for *Phase 2* of the experiment was 144.8 $\pm$ 2.7 at weaning, which was similar to the average liveweight of the entire mob from which they were selected.

The average liveweight of H-ADG and L-ADG steers 91 days after weaning was 163.0 $\pm$ 3.8 and 147.8 $\pm$ 3.7 kg, respectively, with an ADG of 0.21 $\pm$ 0.01 and 0.03 $\pm$ 0.01 kg/d, respectively, over this period.

The change in HH of the steers selected for *Phase 2* of the experiment was 28.2 and 24.7 $\pm$ 0.04 mm/100 d for L-ADG and H-ADG steers, respectively, between weaning and the commencement of *Phase 2* (112 d), with no significant difference between the two groups.

There was no difference in the concentration of IGF-1, albumin, creatinine, glucose or urea, or the urea:creatinine (U:C), in the serum of L-ADG and H-ADG steers at weaning or 91 days post-weaning (

Table 73). Serum concentration of IGF-1, albumin and urea and the U:C were all higher at weaning than 91 days post-weaning and the serum creatinine concentration was higher 91 days after weaning than at weaning.

There was a positive correlation between liveweight and HH at weaning (r=0.70; P<0.001) and 112 days after weaning (r=0.68; P<0.001). Serum IGF-1 was positively correlated with liveweight at weaning (r=0.49; P<0.001) and 91 days after weaning (r=0.47; P<0.001). There was no relationship between serum albumin, creatinine, glucose and urea and liveweight or LWG over the post-weaning period. Change in IGF-1 concentration between weaning and 91 days post-weaning was positively correlated with liveweight change over that period (r=0.27; P<0.05) with a stronger relationship evident when controlling for liveweight 91 days after weaning (r=0.38; P<0.05).

Table 73: Concentration of insulin-like growth factor-1 (IGF-1), 3-methylhistidine (3MH), albumin, creatinine, glucose and urea concentrations and the urea:creatinine (U:C) of weaner steers of the lowest (L-ADG) and highest (H-ADG) liveweight gain after 91 days of post-weaning grazing (Phase 1) at weaning and 91 days after weaning. Values are least-square means and pooled standard error of the mean (SEM). Columns with a different alphabetical superscripts are significantly different (P < 0.05). The interaction between Stage*Growth was not significant (P>0.05) and was removed from the model.

Parameter	Weaning		91 days after weaning			P-value	
	L-ADG	H-ADG	L-ADG	H-ADG	SEM	Stage	Growth
IGF-1 (ng/mL)	46.7[b]	38.8[b]	14.5[a]	14.6[a]	3.1	0.001	0.21
3MH (μmol/L)							
Albumin (mmol/L)	36.5[b]	36.4[b]	33.7[a]	34.4[a]	0.4	0.001	0.44
Creatinine (mmol/L)	148.4[a]	147.6[a]	162.7[b]	159.1[b]	3.2	0.001	0.5
Glucose (mmol/L)	0.98	1.13	1.19	1.27	0.1	0.18	0.39
Urea (mmol/L)	4.72[b]	4.53[b]	3.89[a]	3.96[a]	0.1	0.001	0.66
U:C	0.032[b]	0.031[b]	0.024[a]	0.025[a]	0.001	0.001	0.97

8.4.2 Phase 2

Between the end of *Phase 1* and the commencement of *Phase 2*, there was no change in liveweight of L-ADG steers (147.8 vs. 147.3 kg, respectively) however, H-ADG steers lost liveweight (163 vs. 155.2 kg, respectively) over the three week period. There was no difference in LWG between L-ADG and H-ADG steers (0.37 and 0.39 $\pm$ 0.02 kg/d, respectively) during the pen study (weeks 3 to 9) (Table 74).

Steers fed the higher protein cavalcade hay had greater LWG than steers fed the lower protein Mekong grass treatment (0.47 and 0.28 $\pm$ 0.02 kg/d, respectively) over weeks 3 to 9 of the pen study.

Change in HH was almost 2-fold higher for H-ADG steers compared to L-ADG steers when fed the Mekong grass based diet but there was no difference in HH change between L- and H-ADG fed cavalcade hay.

Serum albumin, creatinine, glucose and urea concentration and U:C were not significantly different between H-ADG and L-ADG steers at the commencement of the pen study. At the end of the pen study there was no difference in the concentration of IGF-1, metabolites and the U:C in the serum of steers of different post-weaning growth rates (Table 74).

The concentration of IGF-1 (27.3 $\pm$ 3.2 and 42.3 $\pm$ 3.1 ng/mL), albumin (31.2 and 34.1 $\pm$ 0.3 mmol/L), glucose (1.23 and 3.49 $\pm$ 0.11 mmol/L) and creatinine (116.1 and 128.3 $\pm$ 2.01 mmol/L) in the serum was lower at the start compared to the end of the pen study. The concentration of urea (6.43 and 3.97 $\pm$ 0.19 mmol/L) and the U:C (0.056 and 0.032 $\pm$ 0.002) were higher at the start compared to the end of the pen study.

At the end of the pen study, steers fed cavalcade hay had higher serum IGF-1, glucose and urea concentration and higher U:C than steers fed Mekong grass. In contrast, the serum creatinine concentration was higher in steers fed Mekong grass compared to those fed cavalcade. Serum albumin concentration did not differ between steers fed either cavalcade or Mekong grass diets.

Rumen ammonia-N concentration was not significantly different between H-ADG (86.9 $\pm$ 4.6 mg/L) and L-ADG (83.2 $\pm$ 4.6 mg/L) steers at the commencement of the pen study. At the end of the pen study rumen ammonia-N concentration was greater for steers fed cavalcade hay (84.1 $\pm$ 3.8 mg/L) compared to the Mekong grass treatment (29.9 $\pm$ 3.8 mg/L) and was greater for H-ADG (63.0 $\pm$ 3.8 mg/L) compared with L-ADG (51.0 $\pm$ 3.8 mg/L) steers.

Table 74: Liveweight gain (LWG), change in hip height (HH change) and the concentration of serum insulin-like growth factor-1 (IGF-1), albumin, creatinine, glucose, urea and the urea:creatinine (U:C) ratio and the concentration of rumen ammonia-N of steers of the lowest (L-ADG) and highest (H-ADG) average daily gain after 90 days of post-weaning grazing (Phase 1) fed either low protein Mekong grass (Mek) or higher protein cavalcade (Cav) hay ad libitum in pens (Phase 2). Values are least-square means and pooled standard error of the mean (SEM). Different alphabetical superscripts across a row indicate significances between treatments (P<0.05). The interaction between Diet*Growth was not significant (P>0.05) and was removed from the model.

Parameter	Treatment						
	L-ADG Mek	H-ADG Mek	L-ADG Cav	H-ADG Cav	SEM	Diet (D)	Growth (G)
Animal measurements							

LWG (kg/d)	0.291[a]	0.274[a]	0.447[b]	0.499[b]	0.03	0.001	0.49
HH change (mm/100 d)	24.9[a]	42.6[b]	35.1[ab]	41.1[ab]	6.1	0.056	0.42
Serum IGF-1 and metabolites							
IGF-1 (ng/mL)	36.0[ab]	29.4[a]	55.0[b]	48.7[ab]	7.1	0.009	0.36
Albumin (mmol/L)	34.1	34.7	33.8	34	0.63	0.53	0.37
Creatinine (mmol/L)	134.8[b]	139.0[b]	119.6[a]	119.7[a]	4.09	0.001	0.6
Glucose (mmol/L)	3.1[a]	2.9[a]	4.0[b]	3.9[b]	0.27	0.001	0.63
Urea (mmol/L)	1.8[a]	2.2[a]	6.0[b]	5.8[b]	0.21	0.001	0.63
U:C	0.014[a]	0.016[a]	0.051[b]	0.049[b]	0.002	0.001	0.87
Rumen ammonia-N (NH_3N)							
Rumen NH_3N (mg/L)	22.9[a]	36.9[a]	79.0[b]	89.1[b]	5.5	0.001	0.038

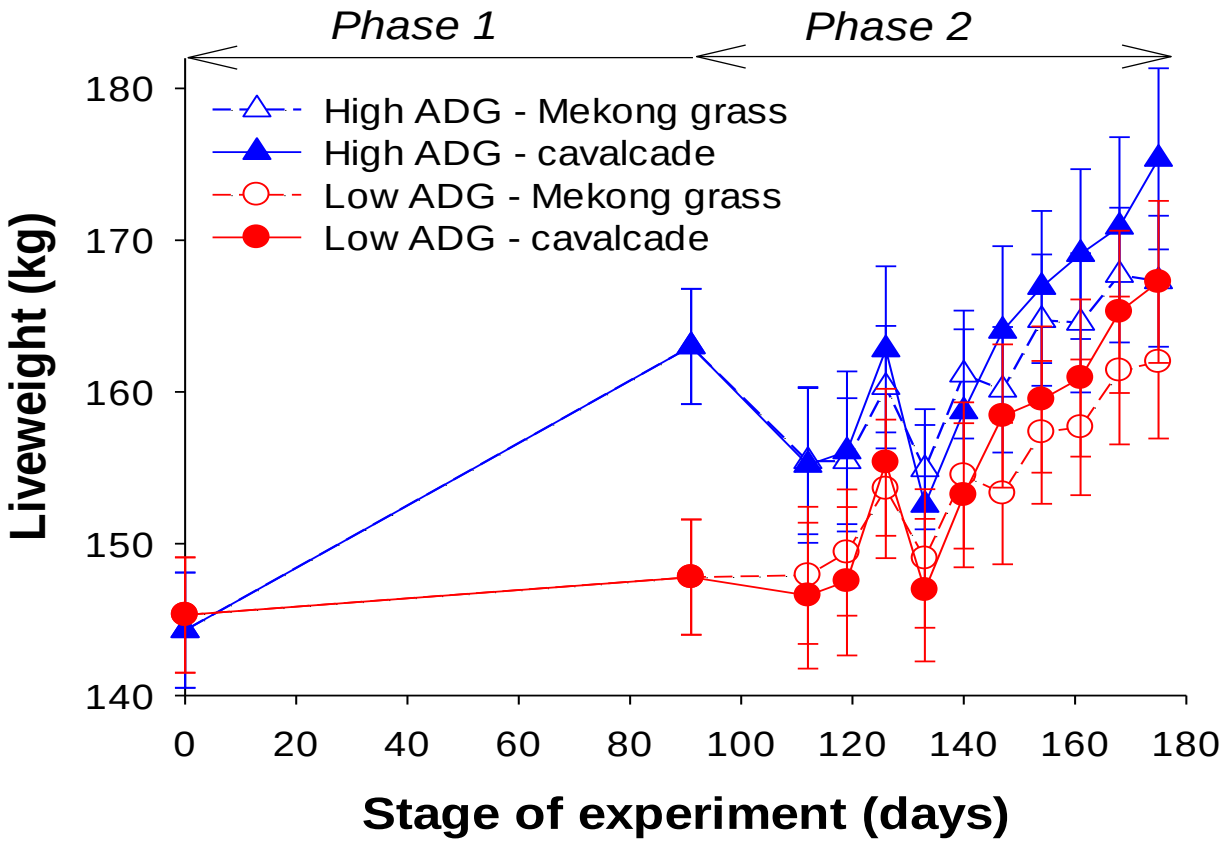

Figure 14: Liveweight of weaner steers of the lowest (Low) and highest (High) average daily liveweight gain (ADG) grazing dry season pastures for 91 days post-weaning (Phase 1) and then fed low protein Mekong grass or higher protein cavalcade hay in pens (Phase 2) for 63 days.

8.4.3 Phase 3

Steers that had higher LWG during *Phase 1*, had higher LWG than L-ADG steers when grazing wet season pasture as a single mob during *Phase 3* although the difference was quite small (0.58 and 0.55 ± 0.01 kg/d, respectively; $P<0.05$).

Steers fed the Mekong grass diet during *Phase 2* tended to have a higher LWG than steers fed cavalcade hay, when subsequently grazing wet season pasture as a single mob during *Phase 3* (0.58 and 0.55 ± 0.01 kg/d, respectively; $P=0.066$), once again the difference being quite small.

Over the wet season (early October to early April) H-ADG tended to gain more liveweight than L-ADG steers (99.6 and 94.4 ± 2.1 kg liveweight; $P=0.09$).

At the end of the experiment, H-ADG steers were approximately 12 kg heavier than L-ADG steers (271.6 and 259.8 ± 4.5 kg, respectively; *P*=0.07).

The final average liveweight of steers at the end of the experiment was 258.5, 261.0, 267.8 and 275.3 kg for L-ADG Mekong grass, L-ADG cavalcade, H-ADG Mekong grass and H-ADG cavalcade, respectively (Figure 15). There was no significant difference in HH change between L-ADG and H-ADG steers grazing wet season pastures (71.2 and 75.7 ± 2.0 mm/100 d, respectively).

There was positive correlation between liveweight and HH of steers at the end of the wet season grazing period (*r*=0.63; *P*<0.001). Liveweight at the end of *Phase 3* was positively correlated with liveweight (*r*=0.74; *P*<0.001) and HH (*r*=0.49; *P*<0.001) at weaning. Serum IGF-1 concentration at weaning was positively correlated with liveweight (*r*=0.40; *P*<0.001) but not HH at the end of *Phase 3*.

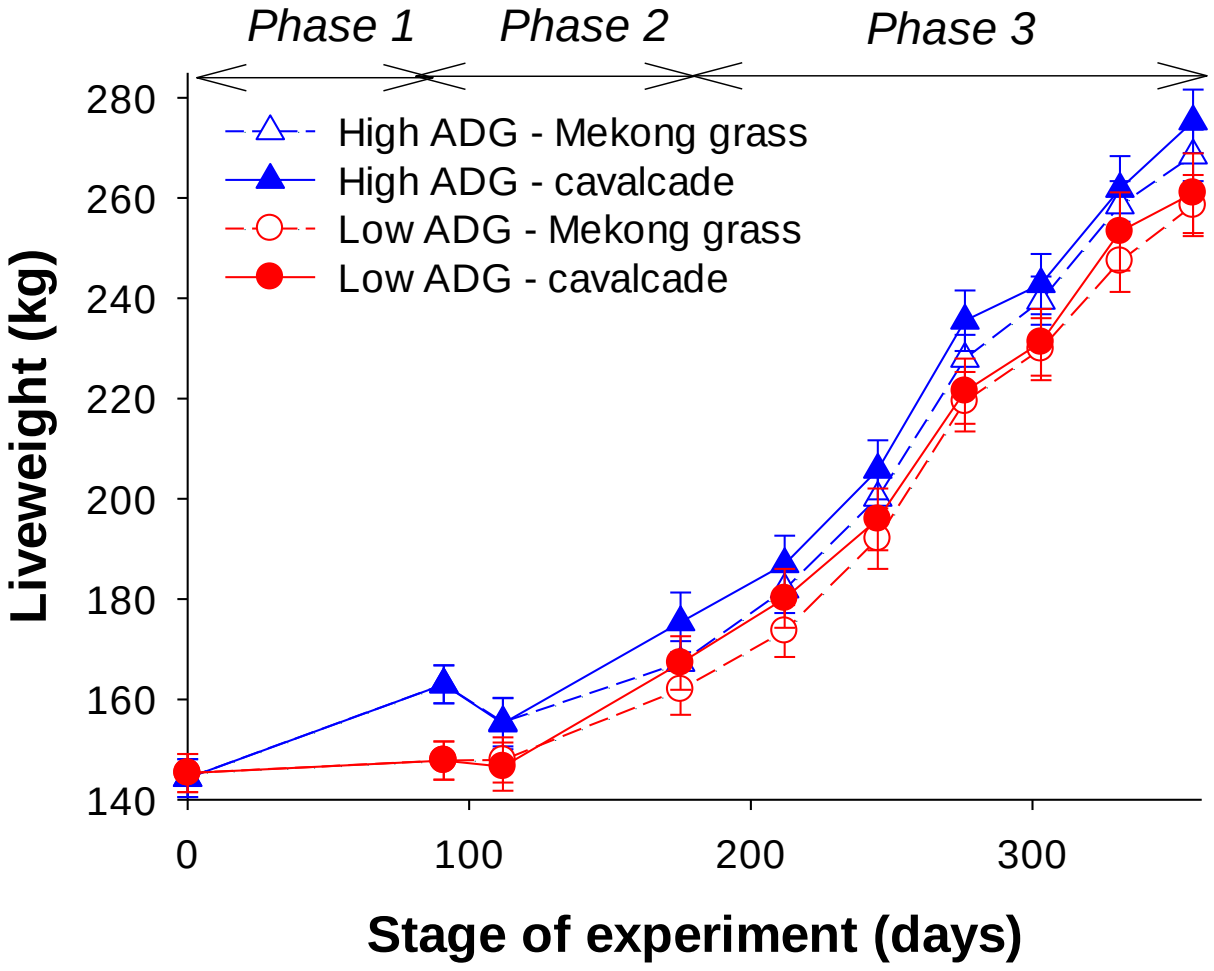

Figure 15: Change in liveweight of weaner steers of the lowest (Low) and highest (High) average daily liveweight gain (ADG) grazing dry season pastures for 91 days post-weaning (Phase 1), followed by a 63 day

period in pens fed low protein Mekong grass or higher protein cavalcade hay (Phase 2) and a 180 day period grazing wet season pastures (Phase 3).

8.5 Discussion

The results confirm that within a mob, *Bos indicus* weaner growth rates in commercial beef herds in northern Australia may be highly variable. This variability does not appear to be related to the nutrient status of the animals, as there were no differences in plasma albumin, creatinine, glucose or urea concentrations between the fastest and slowest growing steers at weaning or 91 days later. A response to dietary protein was evident regardless of growth rate during the post-weaning grazing period. Possible reasons for the variation in post-weaning growth may include stress responses to the weaning and marking processes, which result in negative impacts on weaner performance in the period immediately after weaning setting up a weight difference which is never regained completely in the subsequent periods. It is unlikely that the variability in post-weaning growth rate is genetic or a genotype x diet quality interaction given that the animals responded similarly when provided with identical diets under pen feeding conditions.

8.5.1 Change in liveweight and hip height

Steers that grew at higher (0.21 kg/d) and lower (0.03 kg/d) growth rates over the 91 day period after weaning, grew at similar rates when fed a higher protein cavalcade hay (0.47 kg/d) or moderate protein Mekong grass based diet (0.28 kg/d) in pens. This suggests that the variability in LWG 91 days after weaning is not permanent.

When the animals subsequently grazed wet season pastures as a single mob, they tended to separate into their post-weaning growth rate groups but these small differences would not be practically important.

While a genetic reason for the difference in growth rates post-weaning and over the wet season grazing period cannot be ruled out, it appears unlikely and is probably not related to differences in intake, maintenance energy requirements or the efficiency of use of energy *per se*, as the animals performed the same when fed two different diets under controlled experimental conditions. There is a possibility that the differences observed between the two groups over the two grazing periods are related to grazing behaviour and energy expenditure associated with that, albeit to achieve a similar metabolic status either through differences in grazing activity (i.e. some animals may expend less energy grazing to achieve the same nutrient intake as other animals in the mob), or differences in the energy substrates used to maintain a similar metabolic state. Another possible factor responsible for the immediate divergence after weaning could be the variable response to the weaning process and also in supplement intake, both of which are known to vary between animals. Nevertheless, during the wet season grazing period a difference of only 30 g/head/d was detected between the

two groups and by the end of the experiment (~12 months) there was only approximately 12 kg (i.e. <5%) difference in liveweight between steers that were of higher and lower growth rates during the post-weaning period. This 12 kg at the end of 12 months is comparable to the 15 kg difference in liveweight evident in the extreme divergent liveweight steers selected 91 days after weaning. This suggests that while those slower growing weaners do not catch up to the faster growing weaners, they do not continue to diverge. While this difference of 12 kg over 12 months tended to be statistically different (P<0.07), it is unlikely to be biologically or economically meaningful under commercial scenarios.

Skeletal size is linked to liveweight in cattle. In the present study HH was correlated to liveweight at each stage of the experiment, in addition HH at weaning was correlated with both liveweight and HH of animals approximately 12 months after weaning. A strong genetic correlation has been reported between HH and liveweight at weaning, and HH at 18 months of age in Brahman cattle (Vargas et al., 2000), suggesting that manipulations of HH at an early age (around weaning) will result in greater liveweight approximately 12 months later.

Interestingly, change in HH was similar for L- and H-ADG steers over the 91 day post-weaning period, despite the difference in LWG, and the rates measured here (26 mm/100 d for the entire group) are comparable to the low change in HH measured for *Bos indicus* steers fed a low P diet (27 mm/100 d; Quigley, *unpublished*).

Similarly, there was no difference in HH between the L- and H-ADG steers during the wet season grazing period (73 mm/100 d for the entire group). The rate of skeletal elongation during the wet season was almost 3-fold higher than that in the dry season. Given that it appears that there are no compensatory gains in HH change in cattle (Quigley, *unpublished*) and the strong link between liveweight and HH, strategies that can increase HH change during the post-weaning period may increase LWG over the subsequent wet season. The reason for the difference in HH change between L- and H-ADG steers fed Mekong grass during *Phase 2* is unknown. This is in contrast to the result during *Phase 1*, where no difference was measured between the L- and H-ADG steers when grazing a similarly low protein basal diet.

8.5.2 Change in metabolites

Serum concentration of albumin, creatinine, glucose and urea and the U:C did not differ between L-ADG and H-ADG steers, either at weaning or 91 days post-weaning. The results suggest that the L-ADG and H-ADG animals were metabolically similar at both time points, and indicate that there was no difference in the animal's nutritional status, or at least the ability of the two groups of animals to maintain relatively similar metabolic states. As measurements and samples were collected 91 days after weaning, rather than closer to weaning, we cannot say what the immediate effects of weaning and marking were on the performance of these animals over the 91 day period after weaning.

Steers fed the Mekong grass diet had lower rumen ammonia concentrations and lower serum urea concentrations indicative of an immediate dietary protein deficiency, which was unable to be overcome through muscle catabolism, decreased urinary N excretion or increased urea recycling. The lack of a difference in the plasma albumin concentration between steers fed the two diets suggests that these differences are not chronic and could be overcome through provision of additional protein in the diet. A reduction in serum albumin was only detected after 13 weeks of feeding a protein deficient diet to sheep(Sahoo et al., 2009), suggesting that albumin may be a suitable indicator of longer-term protein status of ruminants, rather than immediate protein status. The elevated creatinine concentration in steers fed the Mekong grass based diet would suggest that these animals were undergoing muscle catabolism to meet energy requirements, or alternatively that kidney filtration and urinary excretion of creatinine was decreased in these animals, in an attempt to recycle urea back into the rumen in response to the lower protein content and intake of the diet. Despite the increased serum creatinine concentration, serum glucose concentration was lower in steers fed the Mekong grass based diet, suggesting that not only was energy intake lower for these animals but they were also unable to maintain energy homeostasis from alternate pathways (e.g. gluconeogenesis).

8.5.3 Insulin-like growth factor-1

Insulin-like growth factor-1 concentration did not differ between animals that were divergent in LWG during the post-weaning period, at any stage of the experiment, which is in contrast to the findings of Turnbull (2008). The result of Turnbull was based on a single sample collected 100 days after weaning and on a small number of animals only, which may account for the different findings between the experiments. Differences in IGF-1 concentration were measured between weaning and 91 days after weaning, and also in response to the higher and lower protein content diets and were positively correlated with steer liveweight at each stage of the experiment at which it was measured.

The actual IGF-1 concentration measured in this experiment was lower than most other values reported in the literature, which are typically greater than 100 ng/mL (Moore et al., 2005, Barwick et al., 2009b, Wu et al., 2008). Although this is variable and is influenced by genotype (*Bos indicus* tend to have higher IGF-1 concentration than *Bos taurus*) (Caldwell et al., 2011), age (IGF-1 concentration tends to increase with increasing age) (Plouzek and Trenkle, 1991), sex (IGF-1 concentration is higher in bulls than castrated males and females) (Plouzek and Trenkle, 1991) and nutritional status (Houseknecht et al., 1988, Liu et al., 1997) of the animals. The concentration measured in the current experiment was similar to that measured for a similar class of cattle (Turnbull, *pers*. *comm*.), *Bos indicus* and *Bos taurus* cows during the post-partum period(Spicer et al., 2002), 18 month old *Bos indicus* heifers(Hill et al., 1999) and Holstein calves less than 3 months of age(Graham et al., 2010).

In the present study, circulating IGF-1 concentration decreased between weaning and 91 days post-weaning. Serum IGF-1 concentration in cattle generally increased with age prior to weaning and then decreased at weaning and returned to pre-weaning concentration when previously fed calves were re-fed milk replacer (Breir et al., 1988).

The decrease in IGF-1 concentration post-weaning is likely to be temporary and may be related to a change in diet, colostrum and milk (Elfstrand et al., 2002) contain high and low concentrations of IGF-1 respectively, or more likely to a reduction in feed intake that occurs immediately after weaning. However, this does not appear to be the case in the present experiment with the concentration remaining lower 91 days after weaning, compared with at weaning. It is likely that this decrease is related to protein status or dry matter intake of the animals (Houseknecht et al., 1988, Liu et al., 1997), as indicated by lower serum albumin and urea concentrations evident 91 days post-weaning and the response of circulating IGF-1 to the higher protein cavalcade hay during *Phase 2*. The response of IGF-1 to dietary protein content of the diet was evident during *Phase 2* of this experiment, where steers fed cavalcade hay had higher circulating IGF-1 concentration than steers fed the Mekong grass based diet. The results emphasise the importance of dietary protein supply to weaned calves over the dry season to increase serum IGF-1 concentration and LWG. It is unclear if IGF-1 concentration is affected differently by the form of dietary N (i.e. true protein vs non-protein-N), and this warrants further investigation, as do other nutritional strategies to manipulate circulating IGF-1 concentration of weaner cattle in northern Australian beef cattle herds.

Given the strong evidence that supports a direct effect of IGF-1 on protein accretion in ruminants and the influence of nutrient status on IGF-1 concentration, it is not surprising that the steers monitored in this experiment had low LWG and low serum IGF-1 concentration. A decrease in circulating IGF-1 in response to nutrient restriction would reduce tissue accretion and allow limited nutrient supply to be directed to maintenance rather than production. If IGF-1 is involved in the regulation of post-weaning LWG, and there was a positive correlation between change in IGF-1 concentration and liveweight change between weaning and 91 days after weaning, any strategies that can increase the circulating IGF-1 concentration, inhibit the effect of binding proteins or decrease degradation rates may result in increases in LWG of steers over the dry season after weaning. Hormone growth promotants (Revalor-S) have increased serum IGF-1 concentration, feed:gain and ADG of steers fed a concentrate based diet (Pampusch et al., 2003). Treatment with bST similarly increased circulating IGF-1 in ruminants, with the response dependent on the nutritional status of the implanted animals (Elsasser et al., 1989, Rausch et al., 2002). Increased protein supply (Liu et al., 1997) and increased energy intake(Houseknecht et al., 1988, Hayden et al., 1993) also increase the circulating IGF-1 concentration in ruminants, so any supplementation or management strategies that can increase protein supply to, or energy intake of, weaners will increase circulating IGF-1 and LWG.

8.6 Summary

1. Variation exists in post-weaning LWG of *Bos indicus* steers grazing dry season pastures under commercial conditions. However, within this mob after approximately 12 months of grazing together there was only 12 kg difference in liveweight between steers that had different LWG over three months post-weaning, which is unlikely to be of biological or economic significance.

2. **Differences in liveweight 91 days after weaning are essentially maintained over 12 months. Any management strategies implemented that aim to increase the tail of the weaner mob, would need to consider the costs and benefits associated with implementation in relation to a modest 12 kg increase in liveweight over a 12 month period measured in the present experiment.**

3. There are no differences in LWG of weaner steers that had different LWG post-weaning, when fed either higher or lower CP forages in pens (steers fed higher protein diets in pens had higher LWG than steers fed lower protein diets, regardless of post-weaning LWG), suggesting that the differences in liveweight observed after weaning are not genetic in origin but are a function of differences which emerge during the weaning process.

4. There are no differences between weaners selected post-weaning on LWG in rumen ammonia-N concentration, which was higher for steers fed a higher protein compared to a lower protein diet. This indicates that differences in post-weaning LWG are not related to rumen function, in support of earlier work (Turnbull et al., 2008).

5. Insulin-like growth factor-1 concentration was positively correlated with liveweight at all stages of the experiment. Strategies to increase the IGF-1 concentration in weaned cattle grazing low protein pastures during the dry season should promote LWG.

6. Measurements of the metabolites examined in the current experiment provide little or no information on the variation in LWG evident in northern Australian beef cattle after weaning.

7. Variation in LWG in cattle after weaning is probably related to the stress response and recovery associated with weaning and marking, or possibly grazing behaviour and supplement intake of young steers, rather than any genetic or disease factors.

8. A more detailed examination of the response of animals to weaning and marking in the period immediately after these events is warranted to develop strategies to better manage animals during that time. It is likely that implementation of management strategies around weaning will improve the liveweight of weaners during the immediate post-weaning period and at approximately 12 months after weaning.

9 A toolkit for monitoring liveweight gain

In planning the current project there was interest in assessing whether the findings of this project might be able to inform the development of an analytical toolkit and associated data requirements that might allow any individual property owner/manager to better understand the liveweight performance of beef cattle on their property(s) and identify major drivers of liveweight and weight gain. The practical application of such a toolkit would then be expected to allow individual properties to identify strategies for improving liveweight performance in their post-weaning cattle.

While the current study has produced a substantive body of data and information describing LWG performance in northern beef herds it has not identified specific management strategies that are suitable for incorporation into a toolkit.

There is considered to be value in developing best practice guidelines for use of weigh scales for collection of weight data during routine management of cattle on extensive properties. It is acknowledged that many producers already routinely collect weight data but development of best practice guidelines may help ensure optimal data quality and ability to use results to compare assess and compare performance over time. Factors that may be considered in best practice guidelines for weighing of young cattle include:

- Selection, installation and maintenance of weighing systems including such factors as fixed platform vs mobile platform, siting of scales to ensure load cells are level, removing dirt or other material from load cells before weighing and at intervals through the use period;
- Ensuring scales are weighing accurately by calibration of scales at regular intervals (weighing a known standard weight) and occasionally running a repeatability study by weighing a sample of animals 2-3 times in one day;
- Incorporation of weighing into routine cattle management practices;
- Weighing a random sample of cattle vs weighing all cattle (pros and cons, how to select a random sample);
- Standardised management of animals prior to weighing (time from yarding to weighing, curfews);
- Standardised management of cattle during weighing to ensure cattle are moved quietly, standing squarely and no leaning on the crush and that the scales return to zero between animals;
- Electronic collection of animal ID and liveweight and management of data (data transfer, storage, backup, linking multiple weights by mob or animal ID);

- Analysis of weight data to produce summary statistics (average weight, standard deviation, confidence intervals, percentiles, average daily gain for multiple measurements on the same mobs/animals);
- Interpretation of findings and how to use the information;
- Recent and future technical advances such as automatic walk-through weighing platforms that might allow more frequent collection of weight measures and animal identification data.

10 Overall discussion

The first component of the project involved analysis of historical datasets collected from the Beef CRC and two northern beef properties.

Animal age at weaning explained more of the total variance in weaning weight than any other factor that was modelled, accounting for 18 to 40% of the total variance in weaning weight in models that did not contain any fixed effects (null or intercept only models). The next most important factor varied between the three datasets but tended to be associated with property (CRC dataset included multiple properties) or season. Sire explained between 3 and 9% of the residual variance in multivariable models that included all significant fixed effects that were available in the datasets.

Similar findings were obtained from models using post-weaning ADG as the outcome. The most important fixed effects tended to be those associated with property or season, and sire explained between 2 and 21% of residual variance in multivariable models.

The second and main component of the Liveweight Gain project involved multiple years of data collection from animals on 11 participating properties from the Ord Victoria Plain region (on the WA side of the border with NT) to the Barkly, encompassing a range of land systems. The participating properties were not randomly selected but are considered representative of northern beef properties. Only one property was lost before completing the final measurement on enrolled animals.

The successful completion of data collection from enrolled cattle over multiple years reflected the commitment of the participating properties and their staff, and the involvement of a large number of field staff and researchers from the Northern Territory Department of Primary Industries and Fisheries and from other organisations. A total of 2,256 animals were enrolled in the study and successful data collection occurred on 2,443 animals (97%) at Obs1, and 2,175 (86%) at Obs3. One property withdrew from the study prior to the last observation and of the remaining 10 properties, successful data collection occurred on 1,815 animals (81%) at Obs4. The progressive loss of animals from follow up over time was expected in the planning of the study and the efforts of all people involved is acknowledged in minimising the rate of loss from follow up.

The report provides summary measures of LWG that are considered representative of northern beef properties.

A major finding was that very little of the variation in LWG was explained by the multivariable models.

Enrolment year had the biggest impact on dry season growth, reflecting the importance of seasonal rainfall in influencing dry season weight gain. Year of enrolment was directly related to climate extremes in that the study period incorporated both severe dry periods that covered the initial enrolment years (2008-2009) and extremely wet periods that covered the later enrolment year (2010). A strong association between seasonal climate measures and liveweight performance was expected and has been described previously (McCown, 1981a, McCown, 1981b, McCown et al., 1981, Winter et al., 1990, Low and Wood, 1979).

Weaning weight and hip height at weaning also appeared to be associated with dry season ADG. The largest dry season weight gains were observed in animals that were taller at weaning and animals that were lighter at weaning. Others have noted previously that dry season weight gains may be better in lighter weaners compared to heavier weaners (Ridley and Schatz, 2006, Jones and Coates, 1992).

Animals that were taller at weaning had a higher wet season rate of growth compared to animals that were shorter at weaning. In addition there was a tendency for a significant interaction between hip height at weaning and weaning weight, meaning that in taller animals there was a beneficial impact of being heavier than average. The highest wet season growth was observed in those animals that were taller than average at weaning and that were heavier than average at weaning.

When annual growth rate for the year post-weaning was considered, the explanatory factor with the biggest impact was year of enrolment. Since year of enrolment had little impact on wet season growth, then its impact on annual growth is presumed to result from the impact on dry season growth. This reflects the potential for increased variability in dry season growth depending on season and if there are favourable conditions then the improvement in dry season growth has the potential to have a major impact on annual growth rates as well. This is consistent with McCown (1981) who stated that the dry season is the primary determinant of net annual weight gain in northern Australian cattle.

There was an impact of flight speed with animals with faster flight speed measurements (indicating more flighty behaviour) having reduced annual growth rates compared to those animals with slower flight speeds. The effect was small and not necessarily biologically important but may suggest that selecting for temperament may have a beneficial impact on growth. This association has been previously described for feedlot performance (Burrow and Dillon, 1997, Fell et al., 1999) and in grazing animals (Tulloh, 1961, Fordyce et al., 1985, Cafe et al., 2011).

It is important to note that while annual growth rate was higher in those animals that were lighter at weaning, the increased growth rate in lighter weaners was not enough to overcome the weight advantage conferred on those animals that were heavier at weaning. When looking at final liveweight as an outcome (Obs4_LWT), the heaviest animals were those that were heavier at weaning even though they had lower dry season and annual growth rates than their cohorts that were lighter at weaning. Burrow *et al. (1991)* have stated that selection of animals for increased liveweight at any age is associated with increased liveweight at any other age.

There was a wide variation in average weaning weights between properties (overall average 187 kg, range from 133 kg to 224 kg). These results are consistent with previously reported summary estimates of weaning weight for northern regions (Bortolussi et al., 2005b).

Liveweight measurements were found to be repeatable when the same animals were weighed on two occasions on the same day, giving confidence in the ability of the project to collect valid weight measures. There were differences in repeatability by weighing system (fixed weigh systems performed better than portable platforms) as expected.

A variety of measures were collected on animals associated with management of animals at the time of castration and dehorning. There were no meaningful associations between measures associated with dehorning or castration and growth rate (ADG_DS, ADG_WS or ADG_AN). These findings support the conclusion that these procedures have little long term adverse effect on animal performance and provide confidence in the way that commercial operators are handling cattle and applying routine procedures under commercial conditions.

Animals were inspected at each observation for the presence of flies and ticks and skin lesions associated with fly activity. There were no adverse effects of flies or ticks on LWG measures in this study, perhaps because burdens observed in this study were mostly below levels likely to result in adverse effects. Previous authors have reported potential for adverse effects of cattle ticks (Turner and Short, 1971b, Holroyd and Dunster, 1978, Jonsson, 2006) on liveweight gain in cattle, though *Bos indicus* cattle generally are expected to have a high level of resistance to ticks and are less likely to be adversely affected (Utech et al., 1978, Jonsson, 2006). Similarly there have been reports of adverse effects of buffalo fly on liveweight in cattle (Peter et al., 2005, Jonsson and Mayer, 1999, Schatz, 2011), though there is similar breed associated variation in susceptibility to fly irritation as is reported for tick resistance (Doube, 1984, Fordyce et al., 1996) and adverse effects may require a combination of heavy burdens with other factors such as susceptible cattle and feed constraints in order to be apparent.

Hormonal growth promotants were used on almost all properties but there was very little consistency between properties in how they were used (Section 4.3.23). Animals received either one or more implants and implants were administered to animals at varying times (as calves, branding, weaning or at later musters). HGP administration was generally associated with a significant improvement in ADG and administration of HGP to calves appeared to produce a higher ADG_WS and ADG_AN compared with administration at weaning.

In an unexpected finding, one property was identified as having a high rate of loss of HGP implants (56% of animals were found to have lost their implants) (Section 4.3.24). Losses were associated mostly with infection and abscessation at the implant site. With the exception of this one property other properties experienced loss rate ranging from 2 to 12%. Loss of implants was associated with a reduced weight gain and represents a significant cost. Implant loss appears preventable through training and use of best practice technique. This finding reinforces the value of training and optimal technique when administering HGP implants (Cowley, 2011a).

DNA methods were developed in a nested study to identify sires for cattle enrolled in the project using tail hair samples collected from enrolled cattle and sires used on those properties. Analyses were conducted separately within each property since sire was confounded with property. Animals in these models were all from the same property and all born in the same year, in effect controlling for two of the large contributory explanatory factors that had been important in the sire models from the historical datasets. Models using weaning weight and annual ADG (ADG_AN) as outcomes indicated that sire accounted for between 0 and 30% of unexplained variance (Section 4.3.25).

The results are consistent with the expectation that northern producers can expect a response to genetic selection even though the environmental stressors of the relatively harsh northern Australian regions may constrain liveweight responses to selection when compared to more favourable environmental conditions in the southern regions of the country (Frisch, 1981, Frisch and Vercoe, 1984, Fordyce et al., 1996). While not surprising, it is reassuring to note that even in the harsh two season environment of the far north (dry season where animals grow relatively little and often struggle to maintain their weight and wet where they have to produce almost all of their annual achievable growth), there is every reason to expect that there will be measurable responses to sire selection.

Faecal NIRS (F.NIRS) testing was used to assess diet preferences and diet quality for animals selected from the highest and lowest performances on annual ADG (Section 5). Four outcomes were assessed from F.NIRS testing: faecal nitrogen (FEC_N%), total crude protein (CP%), dry matter digestibility (DMD%) and dietary non-grass proportion (DNG%).

There was little evidence for any association between results from F.NIRS testing and ADG measures.

The findings suggested a lack of association between measures of diet quality or preference (based on faecal sample measurements) and annual ADG performance. Seasonal variation in pasture quality is a major driver of weight gain (Dixon and Coates, 2010, Dixon et al., 2011), but this may not necessarily relate to variation in diet selection between high and low growing animals.

A small sample of animals had blood samples collected for disease testing and for liver function testing. There were no associations between presence of seropositive results for diseases (Bovine Ephemeral Fever, Anaplasmosis or Bovine Virus Diarrhoea Virus) and LWG measures. There was also no association between liver function tests and LWG measures. These findings suggest that the cohort of young animals enrolled in this study were healthy and not adversely affected by these conditions during the measurement period of the study.

While BEF is considered to be an important disease of Australian cattle (Uren, 1993) it may be that adverse effects are more likely in older heavier animals and less likely in younger animals (Nandi and Negi, 1999) and McGown (2010) failed to find a beneficial effect of vaccination against BEF on weight gains in steers.

Bovine Anaplasmosis testing was limited to those properties that were located within the known positive area or the control zone (7 of 11 properties). All properties returned some positive test results indicating exposure and four of the seven returned 80% or high seropositive results. There was no association between anaplasmosis and ADG_AN category or other growth measures. While tick fever (Babesiosis and Anaplasmosis) have the potential to cause clinical disease in Australian cattle, the high *Bos indicus* content in northern cattle and associated tick resistance may mean that clinical effects are less apparent (Bock et al., 1999b, Bock et al., 1999a).

Bovine virus diarrhoea (BVDV) prevalence was tested at Obs1 and Obs4. There was a noticeable increase in the percentage of animals that tested positive at Obs4 relative to Obs1 for some properties, reflecting the increased opportunity for exposure on properties where BVD virus was circulating. In contrast some other properties continued to have very low percentages of positive animals suggesting that there was little or no active infection on those properties.

Faecal egg burdens (FEC) and faecal oocyst burdens (FOC) were measured on a sample of more than 500 animals from the 11 properties. Between 0 and 80% of animals in any one property and at any one observation, had epg counts that were 200 or higher (classified as potentially meaningful burdens). While there appeared to be variation between properties with respect to epg, there

appeared to be a general trend for higher epg at observations that were possibly associated with the wet season (Obs 2 and 4).

There was no statistical association ($p>0.05$) between measures of worm or coccidial burden and LWG measures. This finding is consistent with earlier reports suggesting that clinical disease due to helminth parasites in northern Australia may be dependent on a combination of wet conditions and heavy stocking rates in susceptible cattle (Radunz, 1992, Winks et al., 1983). However, it should be noted that internal parasites do have the potential to be an issue when seasonal and pasture conditions are conducive and producers should continue to monitor young cattle in particular for evidence consistent with clinical parasite burdens.

A subset of worm eggs were submitted for larval culture to identify worm types to one of four categories: *Oesophagostomum* spp, *Cooperia, Haemonchus,* and *Trichostrongylus*.

Almost all animals had *Haemonchus* burdens at all measuring occasions and there was a higher percentage of animals where *Haemonchus* appeared to be the dominant worm genera (of the identified genera). There were relatively few isolations of *Oesophagostomum* spp (roundworms) or *Cooperia* spp and no identifications of *Trichostrongylus* spp.

The pen trial represented an experimental trial that was nested within the broader project to investigate animal factors that might explain divergence in post-weaning growth.

Male calves were assigned to high ADG and low ADG groups based on their performance over 91 days post-weaning (Phase 1). They were then assigned to one of two diets in Phase 2 (low protein or high protein hay), over 13 weeks. On completion of Phase 2, animals were then transferred to a single pasture and grazed over the following six months (October to April).

Phase 1 classification had no effect on animal growth in Phase 2. During Phase 3, there were small differences in ADG that were considered to be not practically important but that reflected both the Phase 1 and Phase 2 results.

Results suggested that animal-level effects due to genetics or differences in intake, maintenance energy requirements or efficiency of use of energy were not likely to be major factors contributing to divergent post-weaning weight gains. The fact that differences appeared during paddock grazing (Phase 1) and did not persist when fed under controlled conditions (Phase 2), may be related to variation in grazing behaviour, diet selection and associated energy expenditure (i.e. some animals

may expend less energy grazing to achieve the same nutrient intake as other animals in the mob). There may also be individual animal variation in response to experiences associated with weaning.

Measurements of various metabolites provided little or no additional information on possible explanations for any variation in weight and growth, suggesting that variation in animal metabolism was not likely to be contributing to differences in weight or growth.

There were a number of constraints that affected the analyses.

There was strong clustering of weight and growth measurements at the property level, as evidenced by high intra-class correlation coefficients (ICC). These findings suggest that unmeasured factors operating at the property level have a large influence on liveweight and growth. Some factors such as sire identity were unable to be incorporated into statistical models using combined data from all properties because of confounding and this meant that the influence of these factors in final models is incorporated into the unmeasured property-level effects. Other factors such as variation in season were not very well captured because the study only involved a small number of years that appeared to be unusually dry (first cohort) or unusually wet (second cohort), meaning that while the effects of season were able to be incorporated into statistical models indirectly as year of enrolment, the effects may not be typical and were also confounded partially with cohort.

The study involved observations on commercial properties under routine management. This meant that it was not possible to impose standardised protocols on all properties to ensure for example that explanatory factors were managed in the same way on all properties. In some cases this provided analytical challenges because of variation between properties in how some procedures were implemented or measured.

It was not possible to collect data on animal birth dates for animals born under extensive commercial conditions. This was a problem because as indicated above, age at weaning is the biggest driver of weaning weight. The approach taken in multivariable analyses was to incorporate a fixed effect for weaning weight in statistical models with ADG as the outcome, therefore adjusting analyses for the effect of starting weight. While this does allow indirect adjustment for the effects of animal age, it may also have the potential on occasion to interfere with assessment of the effects of other fixed effects of interest (animal, mob and property level factors), particularly if these other factors of interest were possibly confounded with animal age.

11 Conclusions and recommendations

This study has produced summary statistics on post-weaning performance in northern Australian cattle.

The study has also explored possible associations between weight and growth outcomes and a large number of possible explanatory factors operating at animal, paddock/mob and property levels.

A small number of recommendations have been developed below from the findings and experiences of the current study.

The current study incorporated activities looking at repeatability and accuracy of weighing systems and management of animals around the time of weighing in response to concerns over variability in weighing platforms and management of cattle as they were yarded and handled around weighing.

Advances in technology and the increasing availability and uptake of NLIS readers and associated hardware and software for crush-side collection of animal identity, weight and other performance measures provide opportunities for increasing data collection. There is a need for best practice information on how best to implement regular liveweight weighing into routine animal management procedures in order to maximise the accuracy and precision and value of measurements for producers.

Recommendation 1: *That industry consider developing a best practice guideline describing the selection and implementation of liveweight weighing systems on beef producing properties to ensure collection of accurate and precise liveweight data to aid producers in understanding and improving cattle performance.*

The findings of the current study suggest that management procedures such as dehorning and castration have little effect on annual measures of weight gain in surviving animals. There is similarly relatively little evidence of important population-level adverse effects of parasites, diseases or factors such as poisonous plants that may affect liver function on liveweight or growth measures in generally healthy cattle. It is important to note that individual producers should still monitor their cattle for these conditions and be prepared to intervene if there is any evidence suggesting that these conditions may be affecting their cattle. However, the findings of the current study suggest that these conditions need not be included in future research into factors affecting liveweight in generally healthy animals.

The major drivers of LWG variation in the 12 months post-weaning identified in this study were weaning weight and weaning height, seasonal conditions and their presumed effects on diet quality and quantity, and property level effects that may incorporate effects associated with animal characteristics (breed for example), soil and pasture quality, season, and management decisions. The current study was only able to effectively measure some of these factors and because of confounding with property was not able to effectively include all of the measured factors into multivariable analyses. There are a number of important lessons to be gained from the current study that should be considered for future field research.

Designing a study that can effectively assess effects of property-level variability in liveweight performance measures, and seasonal variation in rainfall and pasture, is a major challenge because of the requirement to collect similar data from a larger number of properties, covering a large geographic area and over a relatively long period of time. The fact that animals may only be yarded perhaps two times per year means that collection of measurement data on animal factors is limited.

These issues mean that it is difficult and expensive to collect as much data as might be required to allow effective measurement of outcomes of interest and to allow assessment of possible risk factors.

An alternative may be to simplify the data collection process to a core dataset that has direct and ongoing value to producers and to develop cost-effective data collection mechanisms that can be implemented by producers as part of their ongoing routine animal management procedures. Coupling this with NLIS-associated technology so that animal records can be effectively linked to a lifetime unique identification provides increased power for all producers to collect and use animal-level data for management purposes.

The value to producers lies in more effective information for optimal management with the effectiveness of additional or improved information based on economic measures such as benefit to cost. The broader benefit from collating standardised information across multiple properties is in defining and benchmarking performance, identifying problems or knowledge gaps and contributing to strategic research to further improve welfare and productivity.

There are likely to be challenges in dealing with centralised data warehousing and development of analytical and reporting routines to ensure timely return of additional value to participating producers.

***Recommendation 2**: That consideration be given to developing a relatively low cost, sustainable system built around collection of cattle liveweight data and incorporating a limited set of other animal performance measures that can be linked to animal or mob identification data and integrated into routine property management procedures.*

There are a number of focused topic areas identified in the current study that are considered worthy of further research.

There is a long term liveweight advantage for those animals that are heavier and taller at weaning. There may is value in further investigating the differential effects of weight and height growth in young animals on post-weaning growth. It would be important to be able to accurately determine animal age in these studies to adjust for age when comparing effects of weight vs height at different ages.

The current study was not able to demonstrate value of F.NIRS measurements for addressing these questions but this may have been in part due to the limited number of samples that were able to be collected. It may be possible to perform a more intensive study (more frequent sampling) on a limited number of properties in order to further investigate this issue.

The current study had limited capability to investigate sire contributions to variation in liveweight and weight gain. The potential for producers to improve productivity through genetic selection remains of great interest and this is reflected in recent and ongoing work in this area (Barwick et al., 2009a, Barwick et al., 2009b, Johnston et al., 2009, Wolcott et al., 2011). A large-scale project along the lines of some of the work done through the Beef CRC but with more focus on northern Australian production systems would be effective in delivering information but would require similarly large-scale investment (Burrow and Bindon, 2005, McKiernan et al., 2005). Smaller, focused projects may be possible involving use of selected sires in single mating groups on one or more properties, or through generation of cohorts of weaners from known sires and then assigning subsets of these animals to be grown out on different properties. These projects would be able to provide reasonable estimates of possible weight gain differences between sire groups as an indication of achievable gains under commercial conditions.

Finally, while the current study did not find any adverse effects of parasite burdens on LWG measures, a number of individual animals were identified with relatively high faecal egg counts. It is possible that internal parasites may be having an adverse effect on young cattle either on some properties or in some seasons and further information on parasite burdens in young northern cattle would be useful for producers.

***Recommendation 3**: That consideration be given to further specific R&D on the following areas:*

- *Factors influencing liveweight and hip height at weaning.*
- *Further studies on the use of faecal NIRS or other methods that might allow exploration of grazing behaviour, diet selection and net energy measures associated with grazing (energy costs vs energy gains at the animal level associated with different grazing behaviours), and associated impacts on liveweight performance.*
- *Further studies on potential for performance response to genetic selection.*

12 Success in achieving objectives

Performance is reviewed against each of the six project objectives.

1. Analyse data from Beef CRC herds and stud herds from two major pastoral companies in northern Australia and determined the amount of liveweight gain variation in growing animals that can be attributed to genetic and environmental influences.

This objective has been achieved. Datasets were sourced from the Beef CRC and from two northern beef properties and subjected to statistical analyses to generate descriptive summaries of liveweight gain performance. Multivariable analyses were applied to each dataset to estimate the proportion of variance in liveweight and growth measures that could be attributed to genetic and other influences.

2. Estimate the proportion of variance in liveweight gain explained by a specific set of determinants under study, within and between selected study mobs in the Northern Territory.

This objective has been achieved.

A total of 11 northern properties were enrolled in the project and longitudinal data collection processes implemented on these properties to follow animals during the 12 months post-weaning. Liveweight measurements taken during routine handling of enrolled animals were used to generate the major outcomes of interest: liveweight measurements at three time periods: Obs1 - at weaning and time of enrolment; Obs3 – around the end of the dry, and; Obs4 – around the end of the wet. The liveweight measures were then used to produce estimates of average daily gain (ADG) for three periods: dry season growth (ADG_DS), wet season growth (ADG_WS), and annual growth (ADG_AN).

A large amount of additional information and data was collected on factors at animal, paddock and property levels that were considered capable of influencing animal liveweight.

Summary statistics were generated for LWG measures including variance estimates and assessment of potential drivers of LWG. Statistical modelling was not able to explain very much of the variance in LWG measures.

3. Identify the influence of other difficult-to-measure causal factors such as foraging behaviour and feed efficiency, from a series of smaller scale nested experiments.

This objective has been achieved.

We found that foraging behaviour and feed efficiency were not related to variation in LWG within mobs

4. Report the potential impacts of studies of high and low growth animal identified in Objective 2 in pen studies at the Katherine Research Property.

This objective has been achieved as part of the reporting of the pen trial performed at the Katherine Research Station to explore factors associated with divergent post-weaning liveweight gain.

5. Develop a practical analytical toolkit and determined data requirements for investigating and identifying the drivers of live weight growth performance in individual herds.

This objective was not achieved as there was a lack of impact on variation in LWG from the many factors measured and accounted for. As such, a decision tool would not assist producers at this stage.

6. Develop strategies that can be identified using an analytical toolkit to reduce the number of poor performing animals and increase average herd performance.

This objective was not achieved as described for the previous objective.

The combination of individual animal identification through NLIS and use of data recording systems in association with routine management procedures will allow producers to collect and use information on individual animal performance for optimising animal and herd performance. It is suggested that producers can use liveweight data to identify potential problem areas (poor performing animals, mobs, seasons etc) and then combine this with other information or discussions

with other sources (technical officers, consultants etc) to identify strategies to improve performance.

13 Acknowledgements

The Liveweight Gain project has involved collaborative efforts from many people including property and technical staff, commercial collaborators and scientists. Acknowledgement is extended to all those individuals who have assisted through the course of the project.

The efforts of the 11 participating properties in providing access to cattle over a prolonged period of time and in assisting with data collection procedures and providing additional information, is greatly appreciated. This project would not have been possible without the generous contribution from management and staff on the participating properties.

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14 Publications and public addresses arising from the project

Animal Production Science, 2012, 52, 647-652

E. Martinez, K, Turnbull, S. Quigley, S. Streeter, A. Swain, A. Klieve, D. Ouwerkerk, D. Poppi. "Liquid-phase denaturant gradient gel electrophoresis profiles of rumen bacteria from Brahman cross steers selected into two groups on the basis of post-weaning liveweight gain on low crude protein pasture".

North Australian Beef Research Update Conference 2011

C. Duggan, S. Streeter. "Shooting blanks or failure to compete? Low calf output in multi-sire extensive NT herds".

T. Farmer, T. Cowley, S. Streeter, N. Perkins, S. Quigley, D. Poppi. "Live weight gain of weaner steers selected on growth rate after weaning and fed Cavalcade (*Centrosema pascuorum*) or Mekong grass (*Brachiaria brizantha*) hay".

E. Martinez, K. Turnbull, S. Quigley, S. Streeter, A. Swain, A. Klieve, D. Ouwerkerk, D. Poppi. "Relationship between rumen bacterial populations and post-weaning live weight gain in steers selected on different growth rates in the Northern Territory".

S. Streeter, M. Hearnden. "Repeatability of liveweight measurement for two common weighing systems".

S. Streeter, J. Ward, N. Perkins. "Steers ranked on dry season weight gain re-rank on wet season growth".

T. Cowley. ""Hormone free": Variable HGP retention rates in Northern Territory cattle".

Feedback magazine April 2008

S. Streeter. "Raising the poor do-ers".

Kidman Springs Field Day 2012

N. Perkins & S. Streeter. "Factors affecting liveweight gain in north Australian beef herds".

Barkly herd Management Forum 2011

T. Cowley. “HGP loss”

Kidman Springs Field Day 2010

T. Cowley. “The importance of hygiene and correct implantation techniques in HGP use”.

Sturt Plateau Field Day 2009

S. Streeter. “Investigating factors affecting liveweight gain in extensive NT herds”.

Barkly Herd Management Forum 2009

S. Streeter. “Putting together pieces of the weight gain pie”.

Kidman Springs Field Day 2008

S. Streeter. “Identifying casual factors affecting liveweight gain in Northern territory cattle herds”.

15 Appendices

15.1 Land system descriptions for experimental sites

Table 75: Land system descriptions for experimental sites

Land system	Description of land system	Description of major soil type	Description of major vegetation	Reference
Argyle	Several medium and small areas of gently undulating "black soil" plains	Brown and grey cracking clays	Mitchell grass plains - A*strebla pectinata, elymoides, squarrosa* (barley, weeping and bull Mitchell grasses), *Dichanthium fecundum* (curly bluegrass), *Aristida latifolia* (feather-top wiregrass), *Chrysopogon fallax* (ribbon grass), *Iseilema* spp. (flinders grasses), Sorghum timorense (annual sorghum)	Stewart et al. (1970)
Atlas_II6	Flat to very gently undulating plains with a thin scattering of gravel on the surface; widely spaced narrow drainage-ways; some shallow depressions and some low rises with gilgais. Similar to Creswell land system (Christian et al., 1954)	Self-mulching grey clays	Based on Creswell vegetation description: Dominated by *Eulalia fulva* (silky brown top), *Dichanthium fecundum* (curly bluegrass). Other grasses include *Astrebla squarrosa* (bull Mitchell grass), *Astrebla elymoides* (weeping Mitchell grass), *Aristida latifolia* (feather-top wiregrass), *Chrysopogon fallax* (ribbon grass), *Dichanthium superciliatum* (tassel bluegrass), *Sehima nervosum* (white grass) and *Bothriochloa* spp. (blue grasses)	Northcote et al. (1960-68)
Austral	A number of small areas of gently undulating Mitchell grass plains	Heavy grey pedocals and heavy brown pedocals	Dominated by *Astrebla pectinata* (barley Mitchell grass) with fairly widely spaced *Acacia georginae* (Gidgee). Less common tussock grasses include *Astrebla squarrosa* (bull Mitchell grass), *Astrebla elymoides* (weeping Mitchell grass), *Aristida latifolia* (feather-top wiregrass) and *Chrysopogon fallax* (golden beard grass).	Christian et al. (1954)
Banjo	Gently undulating to almost level plains; predominantly loamy red earths with gravelly red and yellow earths and lithosols; mixed eucalypt woodland over perennial grasses.	loamy red earths / Shallow gravelly red and yellow lithosols	Mixed perennial grasses - *Sorghum plumosum* (perennial sorghum), *Chrysopogon fallax* (ribbon grass), *Triodia pungens* (soft spinifex), *Themeda triandra* (kangaroo grass)	Day et al. (1985)
Barkly1	Very gently undulating to nearly flat Mitchell grass plains (minimal amount of chert pebbles on surface)	Heavy grey pedocals	Dominated by *Astrebla pectinata* (barley Mitchell grass) . Less common tussock grasses include *Astrebla squarrosa* (bull Mitchell grass), *Astrebla elymoides* (weeping Mitchell grass), *Aristida latifolia* (feather-top wiregrass) and *Chrysopogon fallax* (golden beard grass). Additional grasses include *Panicum decompositum* (native millet), *Aristida inaequiglumis* (curly wiregrass), *Spathia neurosa* (spathe grass). Annual grasses include *Iseilema spp.* (flinders grass), B*rachyachne convergens* (native couch), *Polymeria* spp., *Flaveria australasica* (speedy weed)	Christian et al. (1954)

Barkly2	Very gently undulating to nearly flat Mitchell grass plains (moderate amount of chert pebbles on surface)	Heavy grey pedocals	Dominated by *Astrebla pectinata* (barley Mitchell grass). Less common tussock grasses include *Astrebla squarrosa* (bull Mitchell grass), *Astrebla elymoides* (weeping Mitchell grass), *Aristida latifolia* (feather-top wiregrass) and *Chrysopogon fallax* (golden beard grass).	Christian et al. (1954)
Beetaloo	Gently undulating country with various lateritic soils, mostly with Lancewood Forest, in the north-west corner of the Barkly Report area	Lateritic red earths and lateritic podzolic soils	*Acacia shirleyi* (Lancewood) forest. Scattered plants of *Aristida pruinosa* (gulf wiregrass) and *Heteropogon contortus* (black spear grass), *Enneapogon* sp. (oatgrasses), *Eriachne* sp. (wanderrie grasses).	Christian et al. (1954)
Birrimbah	Gently undulating plains, predominantly broad gravelly rises and slopes; shallow gravelly red earths, lithosols and earthy sands; eucalypt woodlands over perennial grasses.	shallow gravelly red earths lithosols and earthy sands	Mixed perennial grasses (moderately dense) - *Triodia bitextura* (feather-top spinifex), *Sorghum plumosum* (perennial sorghum), *Sehima nervosum* (white grass), *Themeda triandra* (kangaroo grass)	Day et al. (1985)
Cliffdale	Gently undulating to hilly terrain on basalt, dolerite, agglomerate and other volcanic and sometimes non-volcanic rocks	Lithosols with rock outcrop, euchrozems, red and black earths and red clays	Sparse to mid dense - *Chrysopogon fallax* (ribbon grass), *Sehima nervosum* (white grass), *Heteropogon contortus* (black spear grass), *Themeda triandra* (kangaroo grass), *Sorghum plumosum* (perennial sorghum), *Aristida hygrometrica* (kerosene grass), *Dichanthium fecundum* (curly blue grass), *Eulalia fulva* (silky brown top), *Eriachne obtusa* (wanderrie grass).	Aldrick and Wilson (1992)
Creswell	Discontinuous areas of very gently undulating to nearly flat black-soil grasslands	Northern heavy grey pedocals	Dominated by *Eulalia fulva* (silky brown top), *Dichanthium fecundum* (curly bluegrass). Other grasses include *Astrebla squarrosa* (bull Mitchell grass), *Astrebla elymoides* (weeping Mitchell grass), *Aristida latifolia* (feather-top wiregrass), *Chrysopogon fallax* (ribbon grass), *Dichanthium superciliatum* (tassel bluegrass), *Sehima nervosum* (white grass) and *Bothriochloa* spp. (blue grasses)	Christian et al. (1954)
Drylake	Very gently undulating, lightly timbered plains with 'fluffy' soils locally known as 'dry bog'	Heavy grey pedocals	*Eucalyptus microtheca* (Coolibah) with *Chenopodium auricomum* (bluebush) in hollows. Grass layer includes *Eulalia fulva* (silky brown top), *Dichanthium fecundum* (curly bluegrass), *Aristida latifolia* (feather-top wiregrass), *Panicum decompositum* (native millet), *Astrebla elymoides* (weeping Mitchell grass), *Chrysopogon fallax* (ribbon grass)	Christian et al. (1954)
Elliot	Deep sandy, gently undulating, scrubby or sparsely timbered country with poorly developed dune formations in some parts.	Lateritic red sands	Dominant shrubs are *Jacksonia odontoclada* and *Acacia* spp. (Including *A. lysiphloia* (turpentine) *A. hilliana* (Hill's table top wattle) and *A. monticola* (red wattle). Ground layer dominated by *Triodia* spp. (spinifex), *Sorghum plumosum* (perennial sorghum), *Aristida pruinosa* (gulf wiregrass) and *Cymbopogon bombycinus* (lemon-scented grass), *Eragrostis xerophila* (Knottybutt neverfail)	Christian et al. (1954)

Favenc	Steep hills on mainly argillaceous sediments	Lithosols and brown earths	Very sparse - (80%) *Triodia bitextura* (spinifex), *Chrysopogon fallax* (ribbon grass), *Eriachne obtusa* (wanderrie grass), *Aristida hygrometrica* (kerosene grass). Mid dense (20%) - *Chrysopogon fallax* (ribbon grass), *Sorghum plumosum* (perennial sorghum), *Sehima nervosum* (white grass), *Heteropogon contortus* (black spear grass), *Themeda triandra* (kangaroo grass), *Eulalia fulva* (silky brown top)	Aldrick and Wilson (1992)
Franklin	Many small areas of mesas and dissection scarps capped with lateritic material, scattered throughout the southern half of the Vic-Ord Report area	Gravelly skeletal soils	*Triodia pungens* (soft spinifex) dominated / Tippera tall grass - *Themeda triandra* (kangaroo grass), *Sorghum plumosum* (perennial sorghum), *Sehima nervosum* (white grass), *Chrysopogon fallax* (ribbon grass)	Stewart et al. (1970)
Joanundah	Several small areas of very gently undulating black-soil plains with Coolibah trees	Heavy grey pedocals	Dominated by *Eulalia fulva* (silky brown top), *Dichanthium fecundum* (curly bluegrass) with some *Eucalyptus microtheca* (Coolibah) in parts. Other grasses include *Astrebla squarrosa* (bull Mitchell grass), *Astrebla elymoides* (weeping Mitchell grass), *Aristida latifolia* (feather-top wiregrass), *Chrysopogon fallax* (ribbon grass), *Dichanthium superciliatum* (tassel bluegrass), *Sehima nervosum* (white grass) and *Bothriochloa* spp. (blue grasses)	Christian et al. (1954)
Larrimah	Flood plains not associated with present streams; olive brown, brown and grey clays; mainly eucalypt woodlands and mixed shrublands.	olive brown, brown cracking clays and self-mulching grey clays	Mixed perennial grasses (dense) - *Aristida latifolia* (feather-top wiregrass), *Chrysopogon fallax* (ribbon grass), *Sorghum plumosum* (perennial sorghum), *Dichanthium sericum* (QLD bluegrass)	Day et al. (1985)
Legune	Nearly flat grasslands behind the littoral fringe at the mouth of the Keep and Victoria Rivers	Grey cracking clays	Saline short grasses - Dominated by *Xerochloa imberbis* (northern rice grass) and/or *Sporobolus virginicus* (marine couch). Patches of Blue grass tall grass plains -*Dichanthium spp.* (blue grasses), *Sorghum plumosum* (perennial sorghum), *Eulalia fulva* (silky brown top), *Ophiuros exaltatus* (cane grass), *Astrebla squarrosa* (bull Mitchell grass)	Stewart et al. (1970)
McArthur	Broad or narrow fluvial corridors conducting regional drainage across various land systems towards the coast	Grey and brown clays, red and yellow earths and siliceous sands	Dense - *Chrysopogon fallax* (ribbon grass), *Iseilema* spp. (flinders grasses), *Eulalia fulva* (silky brown top), *Sorghum plumosum* (perennial sorghum), *Aristida latifolia* (feather-top wiregrass), *Brachyachne convergens* (native couch) and *Panicum* spp. (millet sp.). Smaller areas of sparse *Heteropogon contortus* (black spear grass), *Aristida latifolia* (feather-top wiregrass), *Pseudoraphis spinescens* (spiny mud grass), *Aristida hygrometrica* (kerosene grass), *Cynodon dactylon* (perennial couch grass)	Aldrick and Wilson (1992)
Merring	Undulating low gravelly crests and slopes with isolated ridges containing some elements of Woggaman and Claravale land systems, extremely variable soils in drainage depressions	shallow gravelly lithosols, red earths and earthy sands	Mixed perennial grasses (moderately dense) - *Triodia bitextura* (feather-top spinifex), *Sorghum plumosum* (perennial sorghum), *Sehima nervosum* (white grass), *Themeda triandra* (kangaroo grass)	Day et al. (1985)

Pinkerton	Rugged stony country on sedimentary rocks in the northern part of the area	Rocky skeletal soils	Upland tall grasses - Dominated by *Sorghum timorense* and *Triodia bitextura* (spinifex)	Stewart et al. (1970)
Sylvester	Many small areas of bluebush swamp	Heavy grey pedocals	*Chenopodium auricomum* (Northern Bluebush) dominates with sparse *Astrebla elymoides* (weeping Mitchell grass), *Astrebla squarrosa* (bull Mitchell grass), *Aristida latifolia* (feather-top wiregrass), *Dichanthium* spp. (bluegrasses), *Eriachne nervosa* (plains wanderrie) and *Eulalia fulva* (silky brown top). *Cullen cinereum* (Annual verbine) and *Iseilema* spp. (flinders grasses) common when water recedes	Christian et al. (Christian et al., 1954)
Wavehill	Gently undulating basalt "black soil" country, occurring in one large area near Wave Hill and many small areas scattered throughout the southern half of the area	Brown and grey cracking clays	Mitchell grass plains - A*strebla pectinata, elymoides, squarrosa* (barley, weeping and bull Mitchell grasses), *Dichanthium fecundum* (curly bluegrass), *Aristida latifolia* (feather-top wiregrass), *Chrysopogon fallax* (ribbon grass), *Iseilema* spp. (flinders grasses), Sorghum timorense (annual sorghum)	Stewart et al. (1970)
Property=6 Improved DS			Floodplain area with predominantly *Hymenachne* spp and *Oryza meridionalis* (wild rice grass), with some *Andropogon gayanus* (gamba grass), *Urochloa mutica* (para grass), *U. humidicola* (tully grass) and *Pseudoraphis spinescens* (spiny mud grass)	B. Beumer, pers comm.
Property=6 Improved WS			Predominantly *Urochloa humidicola*	B. Beumer, pers comm.

15.2 Identification of outlier data

A systematic protocol was generated for reviewing data and identifying suspected outlier values that may have represented data entry errors or animals that were not typical of the target population.

Summary statistics were generated for each continuous outcome (such as ADG_DS, ADG_WS, ADG_AN) and the mean and standard deviation (sd) then used to determine 99% confidence limits using the Z-distribution. These are the lower and upper bounds that should contain 99% of observations, leaving 0.5% beyond each bound ie 0.5% greater than the upper bound and 0.5% less than the lower bound.

- Lower 99% CL = mean – 2.57583*sd
- Upper 99% CL = mean + 2.57583*sd

Box plots and histograms were also generated for each of the outcomes of interest to visually assess the distribution pattern.

The 99% confidence limits are the cut-off values that should separate the upper 0.5% and the lower 0.5% of values based on the normal distribution. Given the total number of observations that were used to generate the summary statistics, it was possible to compare the theoretical expectation of the number of values that might be outside the 99% cut points (0.5% above the upper cut point and 0.5% below the lower cut point) and then compare this to the actual number of observations that were above or below the cut points.

An example of a situation where problematic values were identified using this approach is provided below. There was a was a group of 33 recorded values that were lower than the lower bound of the 99% confidence limit for ADG_DS.

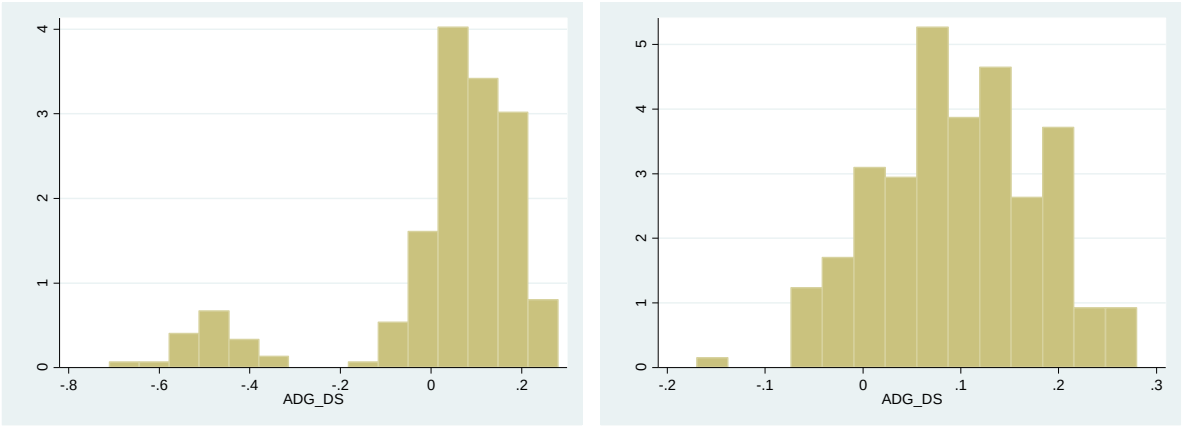


Figure 16: Histogram of ADG_DS for one property only. The plot on the left shows all values and includes measures that were lower than the expected lower 99% confidence limit (using standard deviation and z-score). The right plot shows the same data once these 33 values have been removed.

Many of these outliers in ADG_DS were from one property and there was concern that one of the constituent weights (Obs1_LWT or Obs3_LWT) may have experienced a problem in the way that weighings were managed for a part of the day on one weighing occasion. Examples of problems include someone inadvertently standing on the scales while weighing, not ensuring cattle had all feet placed on the scales, or a physical obstruction or some other problem interfering with measurement in some way. Inspection of data for Obs1_time (the time of day when obs1_LWT was made) did not show any evidence of a run of errors during one period of time – the outlier values were scattered through much of the day. This suggested that there may have been a flaw or problem in the approach to weighing on that day, that was only present on some occasions.

The approach developed for identifying and removing outliers was to generate upper and lower margins on the overall combined dataset using the 99% confidence limit approach. All values outside these margins were then removed – and replaced as missing values. This ensured that a simple and consistent, rules-based approach was used. Applying the approach to the entire dataset (over 1,000 data points) and not to each individual property dataset also meant that the cut off values were derived from a larger dataset more representative of an entire population.

Where ADG values were replaced with missing values, the assumption was that one or both of the contributing body weight measures was incorrect since the dates of weighing were well defined. Where ADG records were removed because they were outliers, one or both of the underlying body weight measures was assumed to be incorrect. It was difficult to determine which of these weight measures might have been wrong (an incorrect increase in one weight or an incorrect decrease in the other). As a

result, the approach taken was to remove both contributing body weights on each occasion where an ADG record was removed.

Exploratory analyses were also conducted of the various explanatory variables and there were on occasion a small number of data points that were outside the upper or lower 99% CL. On most occasions the percentage of outliers was small and consistent with statistical expectations of 0.5% of observations above the upper cut point or below the lower cut point.

Table 76: Count of records where weight measures were recoded as missing data based on assessment as outliers

prop_n	ADG_DS	ADG_WS	ADG_AN	Obs1_LWT	Obs3_LWT	Obs4_LWT
1	13		5	18	13	5
2		1			1	1
3	1	2	1	1	3	3
4	2			2	2	
5	2	4		2	4	4
6		1	1	1	1	1
7	25	8	15	32	30	17
8			1	1		1
9	6	2		6	6	2
10	2			2	2	
11	0	5	1	1	2	5
Total	51	23	24	66	64	39

Table 77: Count of the number of records where hip height, hip growth and flight speed were recoded as missing data based on assessment as outliers

prop_n	HipGrow_DS	HipGrow_WS	HipGrow_AN	Obs2 HH	Obs3 HH	Obs4 HH	Flight speed
1							3
2	4			4	4		5
3		1			1	1	1
4	4			4	4		
5	4	7	19	23	11	19	
6							1
7	4	4	1	5	8	5	1
8	4	2	1	4	6	3	
9	1			1	1		12
10							1
11	1			1	1		1
Total	22	14	21	42	36	28	25

15.3 Repeatability of body weight measures

Experiences during the pilot phase of the project and discussion with property management as animals were enrolled in the study indicated that there were two different weighing systems that would be used (portable weigh platform and fixed scales that were set in place at some yards). While a standardised process was followed when weighing that included consideration of curfews and calibration of scales using known weights, there were concerns over how repeatable weight measurements might be and whether there might be differences in performance between portable platform measurements and weigh box measurements.

A nested study was implemented where a sample of animals on a subset of properties were weighed twice within a short time period (Streeter and Hearnden, 2011). Animals were weighed and then immediately run round and back through the scales for a second measurement. The two measurements were then assessed for levels of agreement, using methods described by Bland and Altman (Bland and Altman, 1999). Scatter plots were generated that plotted the average bodyweight (average of the two measurements) on the x-axis versus the difference in body weight (difference between the two measurements for each animal) on the y-axis. 95% limits of agreement were then estimated using methods described by Bland and Altman (1999). In addition 95% limits of agreement were also estimated in turn for each of the upper and lower limits of agreement, as a measure of the precision of the estimated limits of agreement. These approaches were applied to the complete dataset (184 records from four properties) and then separately to the two weighing systems (94 records for weigh box and 90 records for the portable platform).

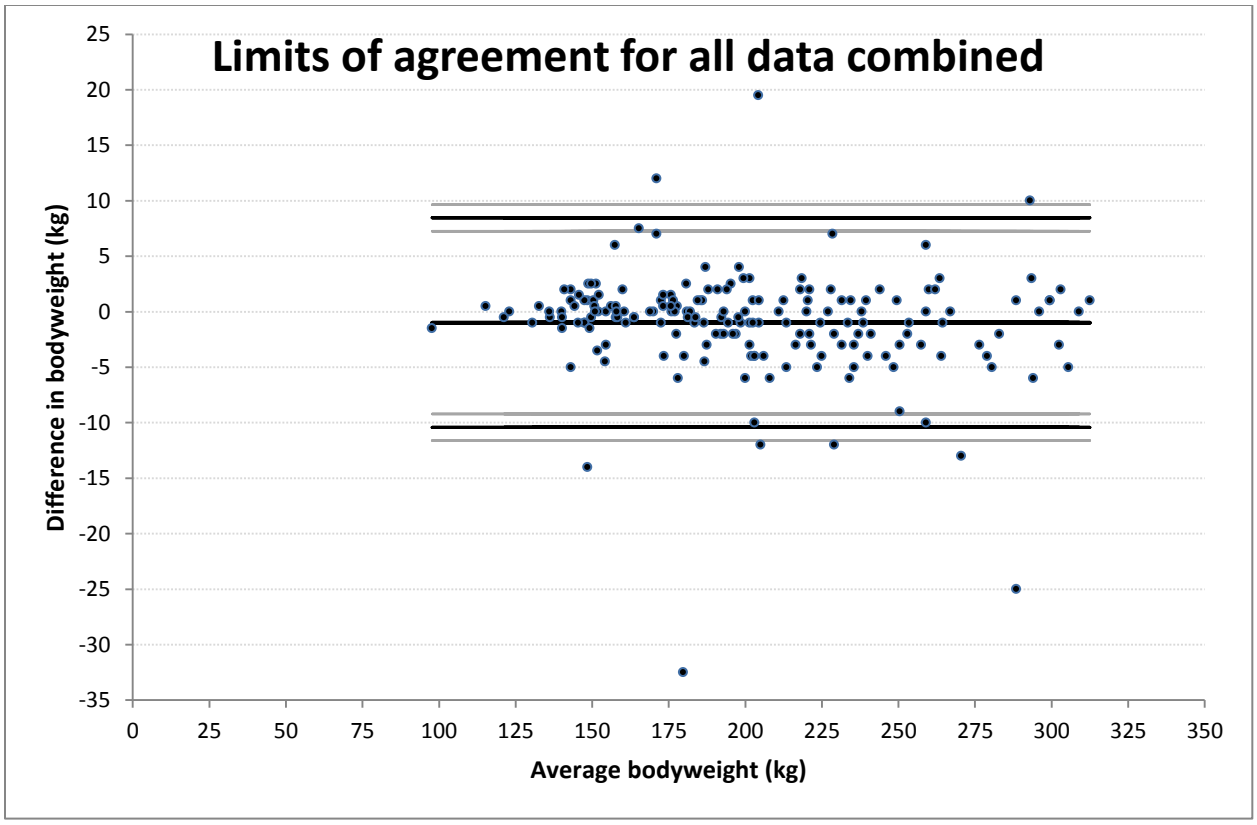


Figure 17: 95% Limits of agreement between two successive measurements of bodyweight in 184 animals, using data from two different weighing systems.

The dots represent individual measures (difference between two bodyweight measurements on the same animal).

The mean difference between the two bodyweight measurements is represented by the central thick line (y=-0.98 kg). This is a measure of bias or overall agreement. The fact that the mean difference is close to zero is a measure of the agreement between the two successive measures.

The standard deviation of the difference can be easily calculated and if the differences are normally distributed then we can assume that 95% of the difference values might lie between the interval between 1.96*SD either side of the mean difference. These thresholds are represented by the two darker lines above and below the central dark line. These are termed the 95% limits of agreement. These limits define the range within which most difference will lie. The limits lie within an interval of about +/- 10kg from the mean difference. There are a small number of individual data points that lie

outside these limits and these points represent individual animals where the two body weight measures differed by larger amounts.

The two pale lines that are above and below each of the upper and lower lines of agreement, represent a measure of the precision of the limits of agreement. Each of these pairs of lines defines a 95% confidence interval around the line of agreement and is intended to provide an additional indication of the uncertainty surround these estimates.

It is important to note that decisions about what might constitute an acceptable level of agreement, is something that cannot be answered by a statistical analysis. The above plot is a descriptive output and requires interpretation based on what is deemed to be acceptable using an understanding of biology. The plot indicates that 95% of the measures lie within plus or minus 10kg of the mean difference.

The next two plots provide the same output separately for each of the two weighing systems.

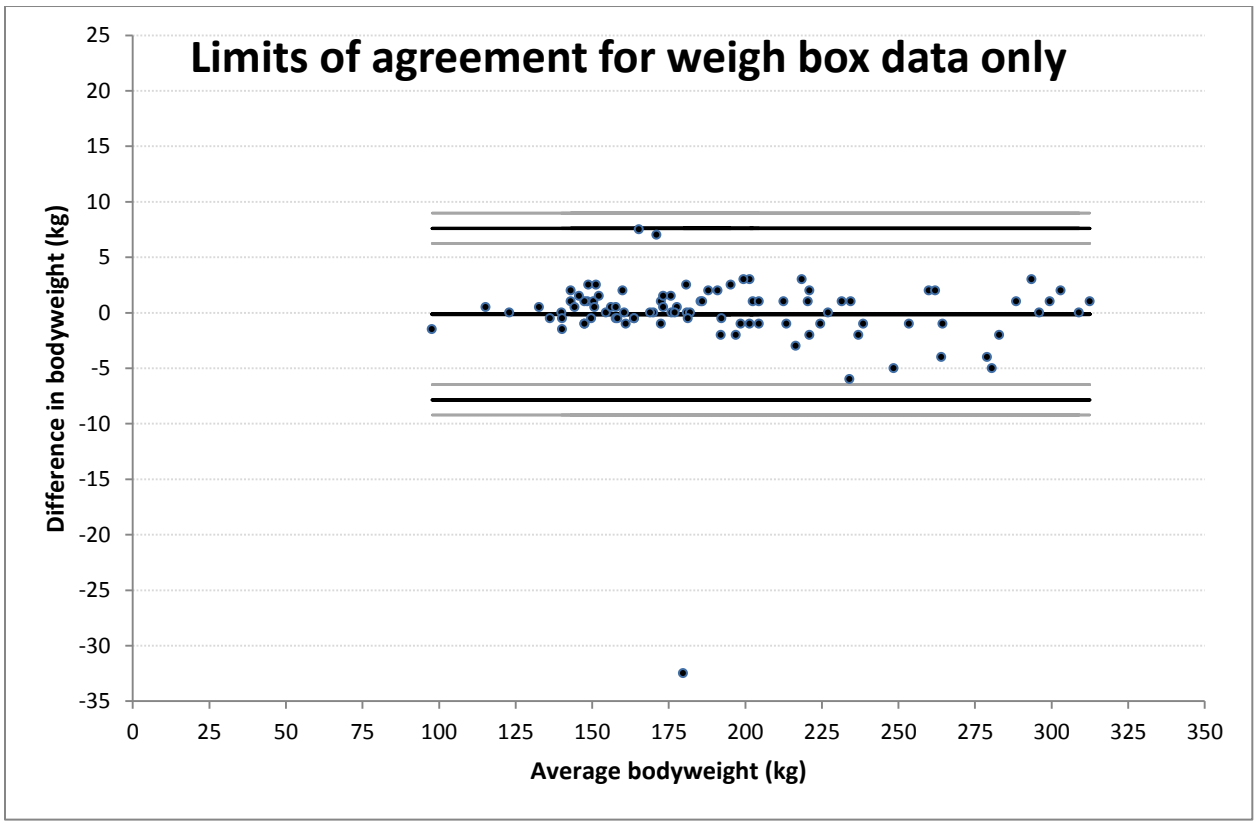


Figure 18: 95% Limits of agreement between two successive measurements of bodyweight in 184 animals, using data from fixed weigh boxes only.

Notice that the fixed weigh boxes provide a tighter level of agreement, with the mean difference now being -0.11kg (closer to zero) and the 95% limits of agreement lying between plus or minus 7.5kg.

In contrast the plot for the portable platform data (below) shows less repeatability. The mean difference is -1.9kg and the 95% limits of agreement range from -12.6kg to 8.8kg.

These results were in line with expectations in that the fixed weigh boxes performed more effectively than portable platforms as mechanisms for generating repeatable weight measures. Both systems had individual animals with low repeatability as indicated by large differences between successive measures. The portably platform had a wider limit of agreement and more measures that were close to the margins of agreement or outside the margins.

The findings provided reassurance for the project that weight measures were broadly repeatable while also confirming that studies where weight measures are important, should attempt to use fixed scale systems rather than portable platforms to ensure higher levels of repeatability.

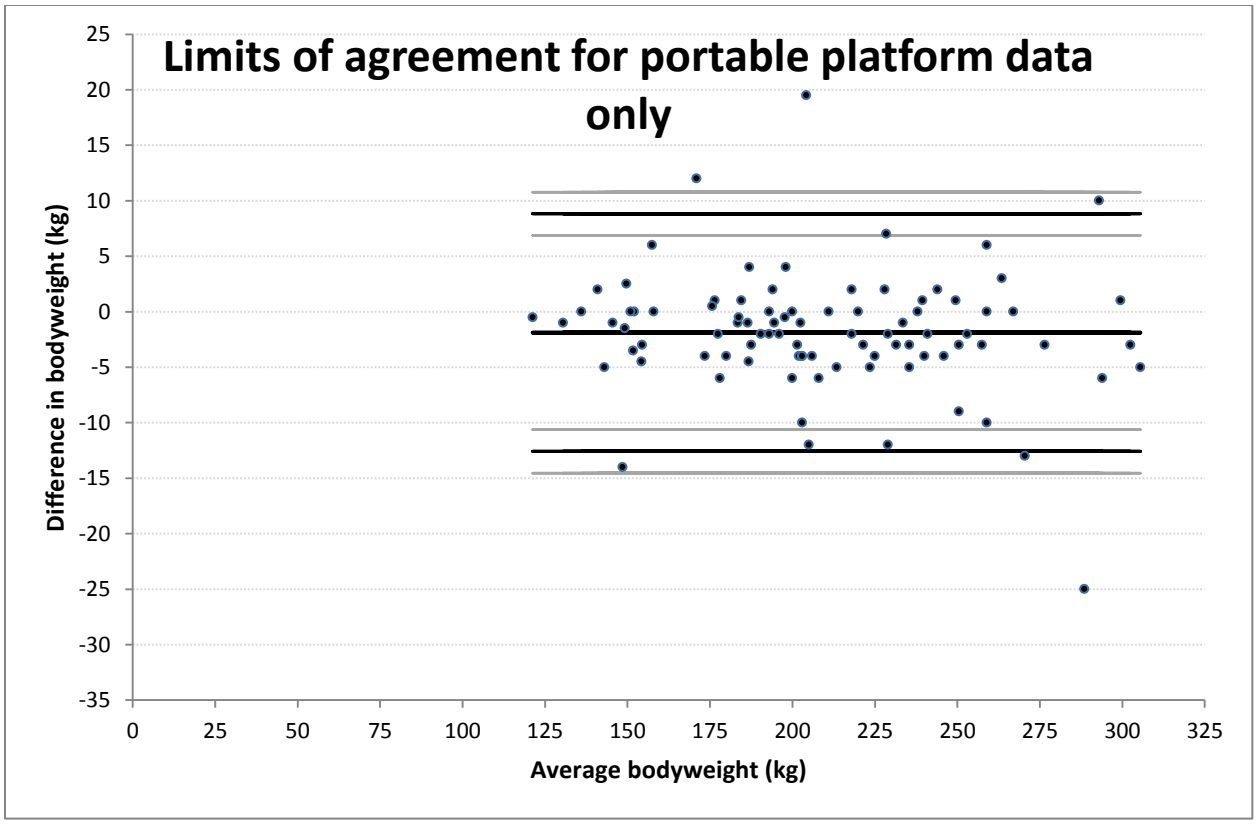


Figure 19: Limits of agreement between two successive measurements of bodyweight in 184 animals, using data from portable platforms only.

15.4 Impact of day and time on LWT

Table 78: Results of comparisons of Obs1_LWT by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

		Quartiles of time of day			
		1	2	3	4
Prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
1	n	33	34	30	67
	min & max time	7:00am			4:37pm
	mean Obs1_LWT	221.55	223.62	217.63	222.74
	standard error	9.14	9.01	9.59	6.42
	Comparisons of means	NS			
2	n	64	48	42	98
	min & max time	7:18am			3:21pm
	mean Obs1_LWT	223.25	226.26	223.68	190.93
	standard error	5.11	5.91	6.31	4.13
	Comparisons of means	a	a	a	b
3	n	0	0	52	169
	min & max time			12:05pm	6:35pm
	mean Obs1_LWT			131.73	133.63
	standard error			2.76	1.53
	Comparisons of means			NS	
4	n	105	28	56	94
	min & max time	7:08am			5:36pm
	mean Obs1_LWT	160.08	171.5	156.7	158.2
	standard error	2.86	5.53	3.91	3.02

	Comparisons of means	ab	b	a	a
5	n	82	93	53	4
	min & max time	7:26am			2:02pm
	mean Obs1_LWT	216.6	211.7	206.1	207.3
	standard error	3.96	3.82	4.93	17.94
	Comparisons of means	NS			
7	n	16	60	24	118
	min & max time	8:55am			5:44pm
	mean Obs1_LWT	179.47	182.85	184.46	179.12
	standard error	6.54	3.37	5.34	2.41
	Comparisons of means	all NS			
10	n	14	62	60	101
	min & max time	8:51am			5:23pm
	mean Obs1_LWT	229.64	223.15	209.5	217.17
	standard error	7.96	3.78	3.84	2.96
	Comparisons of means	a	a	b	ab

Table 79: Results of comparisons of Obs1_hip height by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

		Quartiles of time of day			
		1	2	3	4
Prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
7	n	18	60	32	131
	mean Obs1_hip	112.3	114.6	113.4	114.2

	standard error	1.18	0.64	0.88	0.44
	Comparisons of means	all NS			
10	n	15	60	60	99
	mean Obs1_hip	119.6	119.1	118.9	120.1
	standard error	1.21	0.6	0.6	0.47
	Comparisons of means	NS			

Table 80: Results of comparisons of Obs2_LWT by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

		Quartiles of time of day			
		1	2	3	4
Prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
1	n	23	35	26	124
	min & max time	7:03am			6:23pm
	mean Obs2_LWT	196.02	215.73	211.65	213.81
	standard error	9.95	8.07	9.36	4.29
	Comparisons of means	all NS			
2	n	43	54	24	125
	min & max time	8:30am			5:54pm
	mean Obs2_LWT	206.58	205.5	204.92	221.49
	standard error	6.6	5.89	8.83	3.87
	Comparisons of means	ab	a	ab	b
3	n	157	61	0	0
	min & max time	5:00am	12:00pm		
	mean Obs2_LWT	137.94	147.8		
	standard error	1.93	3.1		
	Comparisons of means	a	b		
4	n	50	28	70	84
	min & max time	7:26am			5:41pm
	mean Obs2_LWT	164.81	163.38	168.8	161.33
	standard error	4.22	5.63	3.56	3.25
	Comparisons of means	all NS			

5	n	82	52	37	59
	min & max time	7:20am			5:35pm
	mean Obs2_LWT	196.34	197.89	203.73	202.18
	standard error	3.8	4.78	5.66	4.48
	Comparisons of means	All NS			
11	n	19	61	43	39
	min & max time	9:27am			3:05pm
	mean Obs2_LWT	184.18	174.82	183.23	178.4
	standard error	8.84	4.94	5.88	6.18
	Comparisons of means	all NS			

Table 81: Results of comparisons of Obs2_hip height by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
1	n	25	35	26	124
	mean Obs2_hip height	111.1	113.9	113.3	114.4
	standard error	1.42	1.2	1.39	0.64
	Comparisons of means	NS			
2	n	40	53	24	123
	mean Obs2_hip height	117.7	117.9	120.8	121.5
	standard error	1.02	0.89	1.32	0.58
	Comparisons of means	a	a	ab	b
3	n	155	62	0	0
	mean Obs2_hip height	105.6	107.5		
	standard error	0.36	0.56		
	Comparisons of means	a	b		
4	n	49	28	72	88
	mean Obs2_hip height	110.4	110.9	111.9	111.3
	standard error	0.79	1.04	0.65	0.59
	Comparisons of means	NS			
5	n	72	51	35	54
	mean Obs2_hip height	117.8	117.6	117.4	117.03
	standard error	0.65	0.77	0.93	0.75
	Comparisons of means	NS			
11	n	19	59	41	39
	mean Obs2_hip	112.5	111.6	112.7	112.2

standard error	1.22	0.69	0.83	0.85
Comparisons of means	NS			

Table 82: Results of comparisons of Obs3_LWT by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

		Quartiles of time of day			
		1	2	3	4
Prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
2	n	62	56	22	65
	min & max time	7:22am			4:41pm
	mean Obs3_LWT	213.5	217.8	215.6	222.9
	standard error	5.62	5.91	9.43	5.49
	Comparisons of means	all NS			
3	n	15	60	47	84
	min & max time	9:39am			4:16pm
	mean Obs3_LWT	166	147.3	146.8	146.7
	standard error	5.29	2.64	2.99	2.23
	Comparisons of means	a	b	b	b
4	n	47	22	57	51
	min & max time	7:51am			5:03pm
	mean Obs3_LWT	166.7	163.7	162.1	158.5
	standard error	3.62	5.3	3.29	3.48
	Comparisons of means	all NS			
5	n	35	56	78	54
	min & max time	8:47am			2:01pm
	mean Obs3_LWT	204.1	194.7	207.9	211.8
	standard error	5.55	4.39	3.72	4.47
	Comparisons of means	ab	a	b	b

7	n	59	87	50	0
	min & max time	8:22am		1:00pm	
	mean Obs3_LWT	199.7	190.64	185.01	
	standard error	3.16	2.6	3.42	
	Comparisons of means	a	b	b	
8	n	85	93	0	0
	min & max time	7:42am	11:40am		
	mean Obs3_LWT	199.2	204.6		
	standard error	4.59	4.38		
	Comparisons of means	all NS			
10	n	186	21	0	0
	min & max time	7:52am	10:21am		
	mean Obs3_LWT	232.06	230.33		
	standard error	2.13	6.33		
	Comparisons of means	all NS			

Table 83: Results of comparisons of Obs3_hip height by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
2	n	60	54	21	66
	mean Obs3_hip height	123.2	123.8	122.9	123.7
	standard error	0.81	0.86	1.37	0.77
	Comparisons of means	NS			
3	n	14	62	47	88
	mean Obs3_hip height	115.4	111.8	111.2	110.9
	standard error	1.3	0.6	0.69	0.51
	Comparisons of means	a	b	b	b
4	n	47	21	56	51
	mean Obs3_hip height	113.9	114.9	114.3	114.3
	standard error	0.75	1.12	0.69	0.72
	Comparisons of means	NS			
5	n	33	59	74	49
	mean Obs3_hip height	123.4	121.9	123.8	125.8
	standard error	0.86	0.65	0.58	0.71
	Comparisons of means	ab	a	b	c
7	n	68	94	55	0
	mean Obs3_hip	119.5	119.3	118	
	standard error	0.56	0.48	0.63	
	Comparisons of means	NS			
8	n	84	89	0	0
	mean Obs3_hip	118.4	120		

	standard error	0.59	0.57		
	Comparisons of means	a	b		
10	n	186	22	0	0
	mean Obs3_hip	124.4	125.1		
	standard error	0.31	0.91		
	Comparisons of means	NS			

Table 84: Results of comparisons of Obs4_LWT by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

		Quartiles of time of day			
		1	2	3	4
Prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
2	n	140	57	30	0
	min & max time	6:45am		1:00pm	
	mean Obs4_LWT	274.3	282.1	288.4	
	standard error	3.87	6.07	8.37	
	Comparisons of means	all NS			
3	n	49	50	29	66
	min & max time	8:03am			2:02pm
	mean Obs4_LWT	208.7	199.8	213.7	208.5
	standard error	4	3.96	5.2	3.45
	Comparisons of means	ab	a	b	ab
6	n	19	46	72	42
	min & max time	9:20am			3:41pm
	mean Obs4_LWT	306.9	301.5	302.2	293.4
	standard error	7.8	5.04	4.03	5.27
	Comparisons of means	all NS			
7	n	59	41	33	88
	min & max time	7:11am			4:18pm
	mean Obs4_LWT	286.44	276.05	270.64	245.3
	standard error	4.24	5.1	5.68	3.48
	Comparisons of means	a	ab	b	c

8	n	0	0	76	110
	min & max time			12:17pm	4:09pm
	mean Obs4_LWT			305.5	298.3
	standard error			5.24	4.43
	Comparisons of means			all NS	
11	n	36	109	22	42
	min & max time	8:47am			3:11pm
	mean Obs4_LWT	252.6	266	259.7	259.2
	standard error	7.6	4.37	9.73	7.04
	Comparisons of means	all NS			

Table 85: Results of comparisons of Obs4_hip height by categories of time of day. Within each property each mean was compared to each other mean (NS=not significant, different letters in the same row represent significant differences with p<0.05).

prop_n	Variable	<10am	10 to 12	12 to 2	>2pm
2	n	140	57	29	0
	mean Obs4_hip height	128.5	129.2	129.8	
	standard error	0.48	0.75	1.06	
	Comparisons of means	NS			
3	n	50	49	31	68
	mean Obs4_hip height	120.2	119.2	120.2	120
	standard error	0.69	0.7	0.88	0.6
	Comparisons of means	NS			
6	n	20	45	72	42
	mean Obs3_hip	128.5	128.1	128.9	127.6
	standard error	0.99	0.66	0.52	0.68
	Comparisons of means	NS			
7	n	59	40	36	89
	mean Obs3_hip	129.1	127.9	128.8	127.5
	standard error	0.59	0.71	0.75	0.48
	Comparisons of means	a	ab	ab	b
8	n	0	0	72	108
	mean Obs3_hip			129.9	129
	standard error			0.5	0.41
	Comparisons of means			NS	
11	n	35	112	22	43
	mean Obs3_hip	119.7	122.6	122.6	123.1

standard error	0.86	0.48	1.09	0.78
Comparisons of means	a	b	b	b

Inspection of the results in the above tables does not support a clear pattern of gradually diminishing average LWT over the course of a day. There are individual instances where the mean LWT in the last time period of the day was the lowest. However, there are as many other instances where the last LWT was the same or even higher than the first LWT.

On one occasion (property 1, Obs1) animals that were held over to be processed the following day were provided with access to feed and water overnight. When an overall daily average LWT was estimated the average LWT on the second day was higher than the average LWT on the first day (216.5 vs 194.8 kg, p=0.005).

On another occasions where the same situation occurred (property 5, Obs2), there was no difference in overall daily LWT means (201.3 on first day, 196.7 kg on the second day, p=0.3).

There was no significant difference between LWT for those animals in different time quartiles through the course of a single day (p>0.05). In general the mean LWT in later time quartiles (later in the day) was slightly smaller than mean LWT in the first time quartile (early morning), the effect was not significant. This is consistent with the expectation that most of the shrinkage associated with curfew will already have been completed through the overnight feed curfew and while some additional shrinkage might be expected through the course of the day of processing the impact on body weight was non-significant.

15.5 Association between hip height and ADG measures

The following matrix shows scatter plots of ADG_DS on the y-axis and weaning hip height (Obs1_hip) for each property. The last plot shows all properties combined. The red lines are smoothed fitted lines which mainly illustrate relatively little association between hip height at weaning and dry season weight gain.

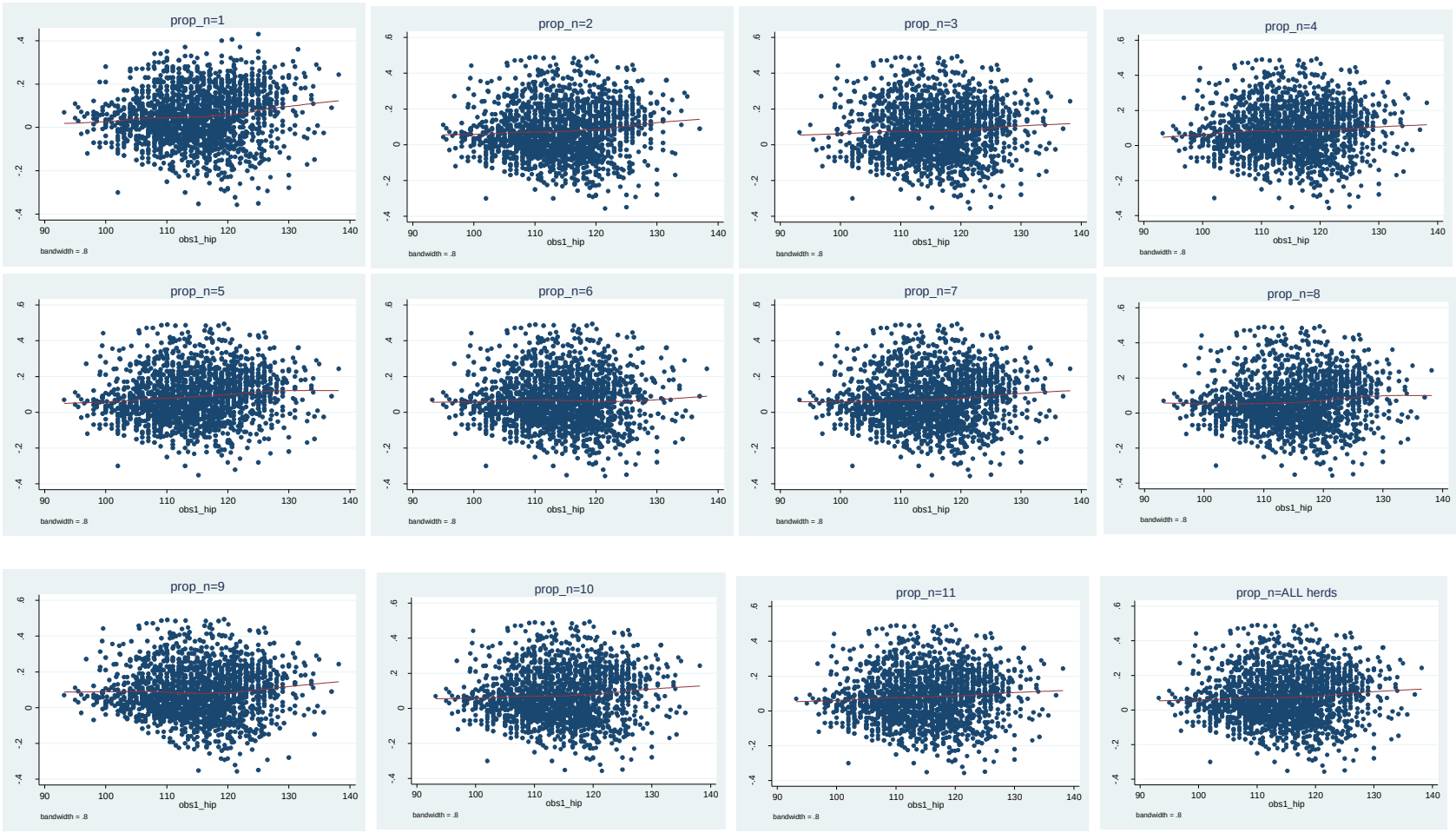


Figure 20: Scatter plots of ADG_DS as outcome and Obs1_hip for each property. The last plot shows all properties combined.

15.6 Differential growth – height and weight (LWT)

There was interest in exploring whether there were differences in growth patterns between smaller vs larger weaners and also between skeletal growth (hip height) vs LWT.

To investigate this further, new variables were generated to allow LWT and hip height to be expressed as quartiles (q1= lowest 25%, q2=25-50%, q3=50-75%, and q4 = highest 25%).By combining these two sets of quartiles (LWT and hip height), animals could be assigned to different combinations such as short and light vs tall and heavy.

Because individual properties tended to vary widely about when they weaned their cattle, Obs1_LWT and height were different between different properties. Quartiles were therefore generated within each property, and then these were combined into a single variable that allowed quartiles to be expressed across the entire dataset.

Table 86: Counts of measurements for all herds combined provided that they had Obs1 and Obs3 measures recorded for weight and hip height, arranged by quartiles of Obs1_LWT and quartiles of Obs1_hip. Note that quartiles were generated separately within each property and then data combined.

Quartiles of	Quartiles of Obs1 hip				
Obs1_LWT	1	2	3	4	Total

1	302	91	14	6	413
2	113	178	102	36	429
3	34	111	170	104	419
4	6	42	104	254	406
Total	455	422	390	400	1,667

The first quartile (Q=1) represents the smallest measure (lowest LWT or shortest height).

There were very few animals that were in one extreme quartile for one measure (say Obs1_LWT_q=1) and the other extreme for the other measure (Obs1_hip_q=4).

Table 87: Descriptive means for each property based on quartiles for Obs1 Hip. Quartiles estimated separately within each property. Properties 1 to 5

prop_n	Obs1_hip quartiles	Obs1_hip mean (cm)	Obs3_hip mean (cm)	Obs4_hip mean (cm)	Obs1_LWT mean (kg)	Obs3_LWT mean (kg)	Obs4_LWT mean (kg)	ADG_DS mean (kg/d)	ADG_WS mean (kg/d)	ADG_AN mean (kg/d)
1	1	104.2	NA	129.8	152.1	195	334.9	0.264	0.48	0.41
1	2	111.3	NA	134.5	193.8	242.6	380.2	0.311	0.48	0.42
1	3	116.7	NA	136	236.8	284.7	407.6	0.31	0.42	0.38
1	4	122.3	NA	139	270.1	312.5	425.7	0.27	0.39	0.35
2	1	111.7	116.3	123.3	163.7	170	233.3	0.06	0.29	0.21
2	2	118.3	122.5	127.3	205.4	211.5	267.4	0.05	0.27	0.19
2	3	122.2	125.5	130.3	227	233.7	295.4	0.05	0.29	0.2
2	4	128.5	130.3	135	251.9	260.1	320.4	0.07	0.28	0.2
3	1	100.7	107.1	115.2	117	131.3	186.2	0.05	0.42	0.17
3	2	104.9	110.2	119	128.1	146.7	204.5	0.07	0.45	0.19
3	3	107.9	113	121.1	137.8	150.2	209.2	0.05	0.46	0.17
3	4	111.9	116.4	124.6	154.1	167.5	230.5	0.05	0.49	0.19
4	1	104.3	107.9	NA	132.6	139	NA	-0.02	NA	NA
4	2	109.6	111.4	NA	152.2	150.8	NA	-0.03	NA	NA
4	3	113.6	116.2	NA	173.2	168.4	NA	-0.07	NA	NA
4	4	118.4	119.6	NA	193.4	187.4	NA	-0.04	NA	NA

5	**1**	110.3	117.6	127.7	178.9	175.2	254.8	-0.03	0.53	0.26
5	**2**	116	122.7	131.1	208.7	201.3	279.4	-0.06	0.53	0.25
5	**3**	119.5	125.7	131.2	228.9	209.7	305.1	-0.06	0.57	0.27
5	**4**	124.3	129.5	130.3	249.3	238.2	325.1	-0.08	0.57	0.26

Table 88: Descriptive means for each property based on quartiles for Obs1_Hip. Quartiles estimated separately within each property. Properties 6 to 11

prop_n	Obs1_hip quartiles	Obs1_hip mean (cm)	Obs3_hip mean (cm)	Obs4_hip mean (cm)	Obs1_LWT mean (kg)	Obs3_LWT mean (kg)	Obs4_LWT mean (kg)	ADG_DS mean (kg/d)	ADG_WS mean (kg/d)	ADG_AN mean (kg/d)
6	1	116.89	119.44	123.63	189.37	220.02	269.83	0.191	0.295	0.244
6	2	122.7	124.72	128.47	222.89	253.25	301.17	0.184	0.287	0.236
6	3	125.48	126.18	129.59	238.35	264.63	309.43	0.161	0.261	0.214
6	4	128.95	130.08	132.75	253.99	278.24	329.31	0.154	0.302	0.231
7	1	108.33	113.93	123.57	157.8	169.86	2541.89	0.112	0.441	0.29
7	2	113.11	118.5	128.02	175.18	186.96	254.46	0.106	0.395	0.277
7	3	116.1	120.64	129.81	189.12	199.47	280.47	0.097	0.511	0.328
7	4	119.95	124	132.32	202.57	211.73	287.39	0.077	0.463	0.299
8	1	106.11	114.27	125.64	139.64	169.29	268	0.192	0.47	0.35
8	2	110.51	117.68	128.6	157.7	186.6	290	0.194	0.49	0.36
8	3	114.08	119.75	129.95	172.6	200.2	299	0.185	0.49	0.35
8	4	121.18	126.39	134.26	219.74	256.1	354	0.215	0.5	0.37
9	1	102.19	105.71	NA	133.14	126.25	214.3	-0.062	0.47	0.243
9	2	107.12	108.93	NA	149.32	141.46	234.7	-0.073	0.51	0.251
9	3	110.24	111.65	NA	161.92	147.35	256.64	-0.094	0.52	0.258

9	**4**	119.24	119.09	NA	211.23	195.94	294.95	-0.124	0.53	0.233
10	**1**	113.64	119.43	125.84	189.49	204.8	319.7	0.095	0.57	0.34
10	**2**	118.62	124.05	130.14	215.5	228.5	334.7	0.079	0.56	0.33
10	**3**	121.41	125.74	131.65	226.5	240.2	339.3	0.077	0.56	0.34
10	**4**	125.38	128.68	134.41	243.4	256	347	0.076	0.53	0.32
11	**1**	106.13	111	116.96	141.4	144.9	223.8	0.031	0.388	0.244
11	**2**	111.93	116.24	121.86	172.5	175.9	250.4	0.037	0.373	0.238
11	**3**	115.14	118.91	124.08	190.4	193.9	279.1	0.029	0.423	0.264
11	**4**	119.22	122.24	126.02	212.9	210	298.3	-0.034	0.439	0.265

Table 89: Descriptive means of 100-day hip height growth for each quartile of Obs1_HIP. Quartiles were estimated separately within each property. Properties 1 to 5

prop_n	Obs1_hip quartiles	Obs1_hip mean (cm)	Obs1_LWT mean (kg)	hipgrow100 Obs2 to 3 (cm/100d)	hipgrow100 Obs3 to 4 (cm/100d)	hip grow100 Obs2 to 4 (cm/100d)	LWT to hip ratio
1	**1**	104.2	152.1	NA	NA	6.03	1.47
1	**2**	111.3	193.8	NA	NA	5.45	1.75

1	**3**	116.7	236.8	NA	NA	4.53	2
1	**4**	122.3	270.1	NA	NA	3.94	2.15
2	**1**	111.7	163.7	5.26	3.22	3.76	1.47
2	**2**	118.3	205.4	4.52	2.22	2.94	1.75
2	**3**	122.2	227	3.88	2.36	2.65	1.89
2	**4**	128.5	251.9	2.79	2.39	2.18	1.98
3	**1**	100.7	117	2.48	6.2	3.8	1.22
3	**2**	104.9	128.1	2.15	6.7	3.7	1.31
3	**3**	107.9	137.8	1.98	6.3	3.4	1.35
3	**4**	111.9	154.1	1.88	6.4	3.3	1.45
4	**1**	104.3	132.6	4.64	NA	NA	1.29
4	**2**	109.6	152.2	3.44	NA	NA	1.43
4	**3**	113.6	173.2	4.42	NA	NA	1.54
4	**4**	118.4	193.4	3.15	NA	NA	1.65
5	**1**	110.3	178.9	6.15	6.54	6.38	1.52
5	**2**	116	208.7	5.8	6.28	5.8	1.68
5	**3**	119.5	228.9	5.33	4.33	4.45	1.79
5	**4**	124.3	249.3	4.4	2.9	2.87	1.88

Table 90: Descriptive means of 100-day hip height growth for each quartile of Obs1_HIP. Quartiles were estimated separately within each property. Properties 6 to 11.

prop_n	Obs1_hip quartiles	Obs1_hip mean (cm)	Obs1_LWT mean (kg)	hipgrow100 Obs2 to 3 (cm/100d)	hipgrow100 Obs3 to 4 (cm/100d)	hip grow100 Obs2 to 4 (cm/100d)	LWT to hip ratio
6	1	116.89	189.37	2.31	2.69	2.04	1.62
6	2	122.7	222.89	1.72	2.43	1.74	1.82
6	3	125.48	238.35	1.19	2.12	1.38	1.9
6	4	128.95	253.99	1.37	1.62	1.33	1.97
7	1	108.33	157.8	5.05	5.77	5.51	1.45
7	2	113.11	175.18	4.93	5.75	5.42	1.55
7	3	116.1	189.12	4.14	5.5	4.97	1.63
7	4	119.95	202.57	3.89	5.01	4.62	1.69

8	**1**	106.11	139.64	5.95	5.45	5.56	1.32
8	**2**	110.51	157.7	5.14	5.04	5.09	1.43
8	**3**	114.08	172.6	4	4.94	4.45	1.51
8	**4**	121.18	219.74	3.95	3.98	3.83	1.81
9	**1**	102.19	133.14	3.14	NA	NA	1.3
9	**2**	107.12	149.32	2.54	NA	NA	1.39
9	**3**	110.24	161.92	2.21	NA	NA	1.47
9	**4**	119.24	211.23	1.74	NA	NA	1.77
10	**1**	113.64	189.49	3.39	3.28	3.36	1.67
10	**2**	118.62	215.5	3.16	3	3.21	1.82
10	**3**	121.41	226.5	2.77	3.59	3.15	1.87
10	**4**	125.38	243.4	2.44	3.65	2.65	1.94
11	**1**	106.13	141.4	4.19	3	3.4	1.33
11	**2**	111.93	172.5	4.12	3.12	3.18	1.54
11	**3**	115.14	190.4	3.67	2.66	2.87	1.65
11	**4**	119.22	212.9	3.43	2.12	2.36	1.79

In an attempt to generate sufficient numbers for valid comparisons, a number of comparisons were done by combining the lower two quartiles and upper two quartiles for each measure. Quartiles 1 & 2 combined represent those animals that are lower than average for either LWT or height. This approach allowed assessment of the following four combinations:

- Obs1_LWT_q=1&2 + Obs1_hip_q=1 &2
    - these animals are lighter than average and shorter than average (light/short)
- Obs1_LWT_q=1&2 plus Obs1_hip=3&4
    - lighter than average and taller than average (light/tall)
- Obs1_LWT_q=3&4 plus Obs1_hip=3&4
    - heavier than average & taller than average (heavy/tall)
- Obs1_LWT_q=3&4 plus Obs1_hip_q=1&2
    - heavier than average & shorter than average (heavy/short)

Table 91: Predicted dry season average daily gain (ADG_DS; kg/hd/d) arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with ADG_DS as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval, DS=dry season.

Weaning weight	Weaning hip height		Predicted ADG_DS kg/hd/d	se	95% CI Lower	95% CI Upper
< median	< median	light/short	0.055	0.018	0.019	0.092
< median	> median	light/tall	0.057	0.019	0.019	0.095
> median	< median	heavy/short	0.010	0.019	-0.027	0.048
> median	> median	heavy/tall	0.018	0.018	-0.018	0.055

The interaction between Obs1_hip and Obs1_LWT was not significant (p=0.6) and the main effect of Obs1_hip was not significant (p=0.8) indicating that dry season weight gain was not dependent on hip height at weaning.

In contrast there was an association with weaning weight with lighter animals at weaning having a larger rate of dry season weight gain than heavier animals at weaning.

Table 92: Predicted wet season average daily gain (ADG_WS; kg/hd/d) arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with ADG_WS as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval, WS=wet season.

Weaning weight	Weaning hip height		Predicted ADG_WS kg/hd/d	se	95% CI Lower	95% CI Upper
< median	< median	light/short	0.428	0.040	0.350	0.506
< median	> median	light/tall	0.441	0.041	0.361	0.520
> median	< median	heavy/short	0.423	0.041	0.344	0.502
> median	> median	heavy/tall	0.456	0.040	0.378	0.534

The interaction between Obs1_hip and Obs1_LWT was not significant (p=0.2) and the main effect of Obs1_hip was not significant (p=0.3) indicating that wet season weight gain was not dependent on hip height at weaning. There was also no significant effect of weaning weight (p=0.7). These findings suggest that wet season growth is largely independent of animal characteristics at time of weaning.

Table 93: Predicted annual average daily gain (ADG_AN; kg/hd/d) arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with ADG_AN as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval, AN=annual season.

Weaning weight	Weaning hip height		Predicted ADG_AN kg/hd/d	se	95% CI Lower	95% CI Upper
< median	< median	light/short	0.254	0.014	0.225	0.282
< median	> median	light/tall	0.268	0.015	0.238	0.298

> median	< median	heavy/short	0.228	0.015	0.199	0.258
> median	> median	heavy/tall	0.249	0.015	0.220	0.277

The interaction between Obs1_hip and Obs1_LWT was not significant (p=0.5) but the main effects of Obs1_hip (p=0.03) and Obs1_LWT (p<0.001) were both significant. Animals that were taller at weaning had a higher annual weight gain than animals that were shorter at weaning. Animals that were lighter at weaning had a higher annual weight gain than animals that were heavier at weaning.

The best performance in terms of weight gain over the 12 months post-weaning was in those animals that were tallest and lightest at weaning. The worst performance was in those animals that were shortest and heaviest at weaning.

Table 94: Predicted dry season growth in hip height (cm per 100 days) arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with gry season hip growth as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval, DS=dry season.

Weaning weight	Weaning hip height		Predicted DS hip height growth cm per 100 days	se	95% CI Lower	95% CI Upper
< median	< median	light/short	3.673	0.431	2.828	4.519
< median	> median	light/tall	2.665	0.454	1.775	3.555
> median	< median	heavy/short	4.114	0.445	3.241	4.987
> median	> median	heavy/tall	3.012	0.431	2.166	3.858

Animals that were shorter at weaning, had faster rates of growth in hip height over the dry season compared to those animals that were taller at weaning. Animals that were heavier at weaning had faster rates of growth in hip height over the dry season compared to those animals that were lighter at weaning. The interaction between Obs1_hip and Obs1_LWT was not significant (p=0.7).

Table 95: Predicted wet season growth in hip height (cm per 100 days) arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with wet season hip growth as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval, WS=wet season.

Weaning weight	Weaning hip height		Predicted WS hip height growth cm per 100 days	se	95% CI Lower	95% CI Upper
< median	< median	light/short	4.66	0.61	3.46	5.87
< median	> median	light/tall	3.88	0.63	2.64	5.11
> median	< median	heavy/short	4.14	0.63	2.91	5.38
> median	> median	heavy/tall	3.93	0.62	2.72	5.13

Animals that were shorter at weaning, had faster rates of growth in hip height over the wet season compared to those animals that were taller at weaning.

The interaction between Obs1_hip and Obs1_LWT was significant (p=0.035).

Animals that were lighter and shorter at weaning had faster rates of growth in hip height over the wet season compared to those animals that were heavier and shorter at weaning (p=0.005). In contrast there was no effect of weight class in animals that were taller at weaning (p=0.8).

Table 96: Predicted annual growth in hip height (cm per 100 days) arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with annual hip growth as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval, AN=annual season.

Weaning weight	Weaning hip height		Predicted AN hip height growth cm per 100 days	se	95% CI Lower	95% CI Upper
< median	< median	light/short	4.01	0.49	3.06	4.96
< median	> median	light/tall	3.04	0.49	2.07	4.00
> median	< median	heavy/short	3.81	0.49	2.84	4.77
> median	> median	heavy/tall	3.12	0.49	2.17	4.07

Animals that were shorter at weaning, had faster rates of growth in hip height over the dry season compared to those animals that were taller at weaning.

There was no significant effect of Obs1_LWT on annual hip growth (p=0.08) and no significant interaction between Obs1_LWT and Obs1_Hip height on annual hip growth (p=0.09).

Caution is required in interpreting these findings, particularly since animals enrolled in this study had unknown birth dates and it is likely that variation in animal age at weaning was a major contributor to the variation in both liveweight and hip height at weaning.

A similar modelling approach was then used with Obs4_LWT as the outcome, representing liveweight at a point about 12 months post-weaning.

Table 97: Predicted Obs4_LWT arranged by categories of Obs1 hip height (less than or equal to the median, greater than the median) and weaning weight (less than or equal to the median, and greater than the median). Results from a multivariable model with Obs4_LWT as the outcome and fixed effects including Obs1 hip height (0<=median, 1>median), Obs1_LWT (0<= median, 1>median), interaction between Obs1 hip height and Obs1_LWT categories, year of enrolment and a random effect coding for property. se=standard error, CI=confidence interval.

Weaning weight	Weaning hip height	Predicted Obs4_LWT kg	se	95% CI Lower	95% CI Upper

< median	< median	light/short	247.2	11.8	224.1	270.4
< median	> median	light/tall	267.9	12.0	244.4	291.5
> median	< median	heavy/short	282.2	12.0	258.8	305.7
> median	> median	heavy/tall	301.1	11.8	278.0	324.3

The interaction between Obs1_hip height and Obs1_LWT was not significant (p=0.6).

The heaviest animals at the final observation point (Obs4_LWT) were those that were tallest and heaviest at weaning, and the lightest animals were those that were lightest and shortest at weaning.

15.7 Flight speed

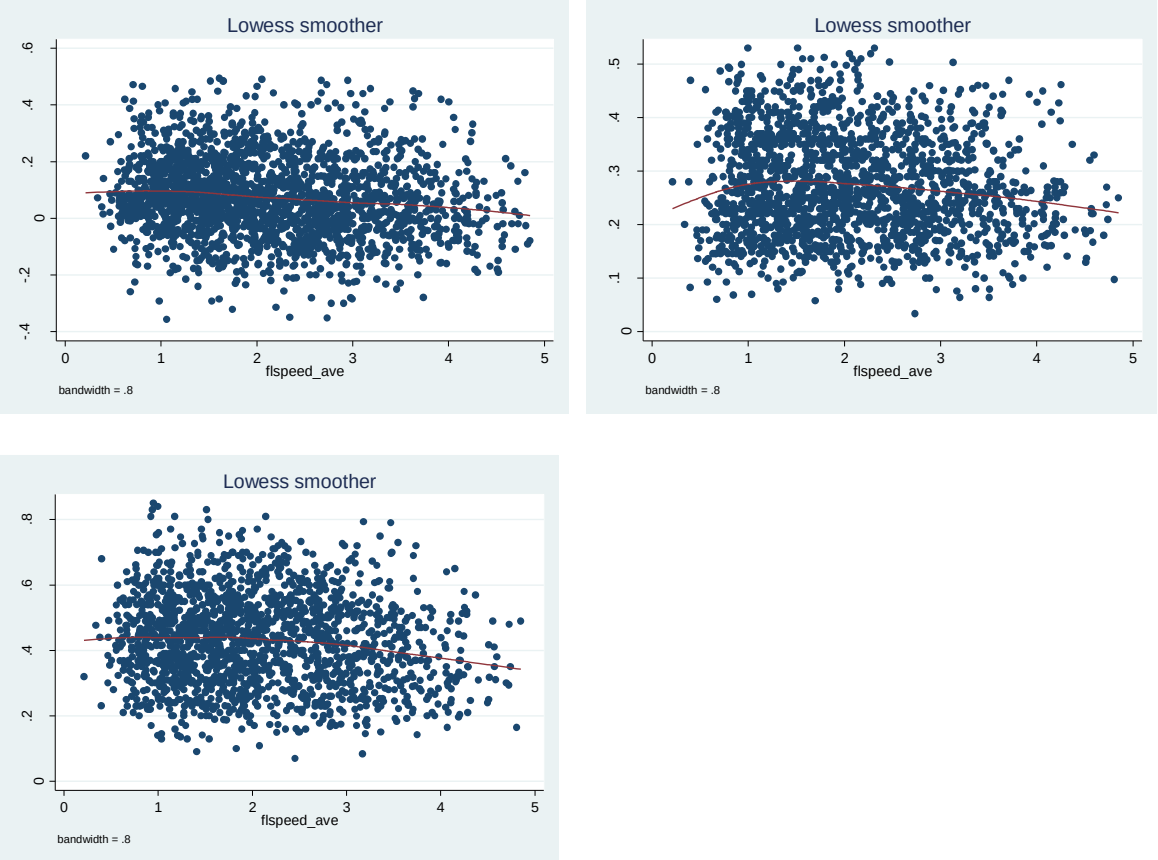


Figure 21: Scatter plots of average flight speed for all animals and ADG_DS, ADG_WS and ADG_AN

Regressions were performed to test association between flight speed and ADG measures. Each analysis incorporated the ADG measure as the outcome and a continuous predictor for average flight speed. All models included a fixed effect for herd-group and a random effect for property.

Table 98: P-values and r-squared values generated from regression analyses in all herds to compare ADG outcomes against flight speed. Each model incorporated a random effect coding for property.

				95% CI		
Outcome	**Coefficient**	**se**	**p-value**	**low**	**up**	**r-sq**
ADG_DS	0.003	0.002	0.240	-0.002	0.007	2.3%

ADG_WS	-0.008	0.003	0.010	-0.014	-0.002	1.1%
ADG_AN	-0.006	0.002	0.002	-0.009	-0.002	3.00%

There was no statistical association between flight speed and dry season ADG but there was a small negative association between flight speed and wet season and annual growth. These findings indicate that animals that are more flighty may have a slightly lower annual growth performance. The low r-squared values indicate that flight speed accounts for a very small proportion of the variability in ADG estimates.

15.8 Body condition score (BCS)

There was a strong association between liveweight and body condition score at any one measuring point, as shown in the following figure.

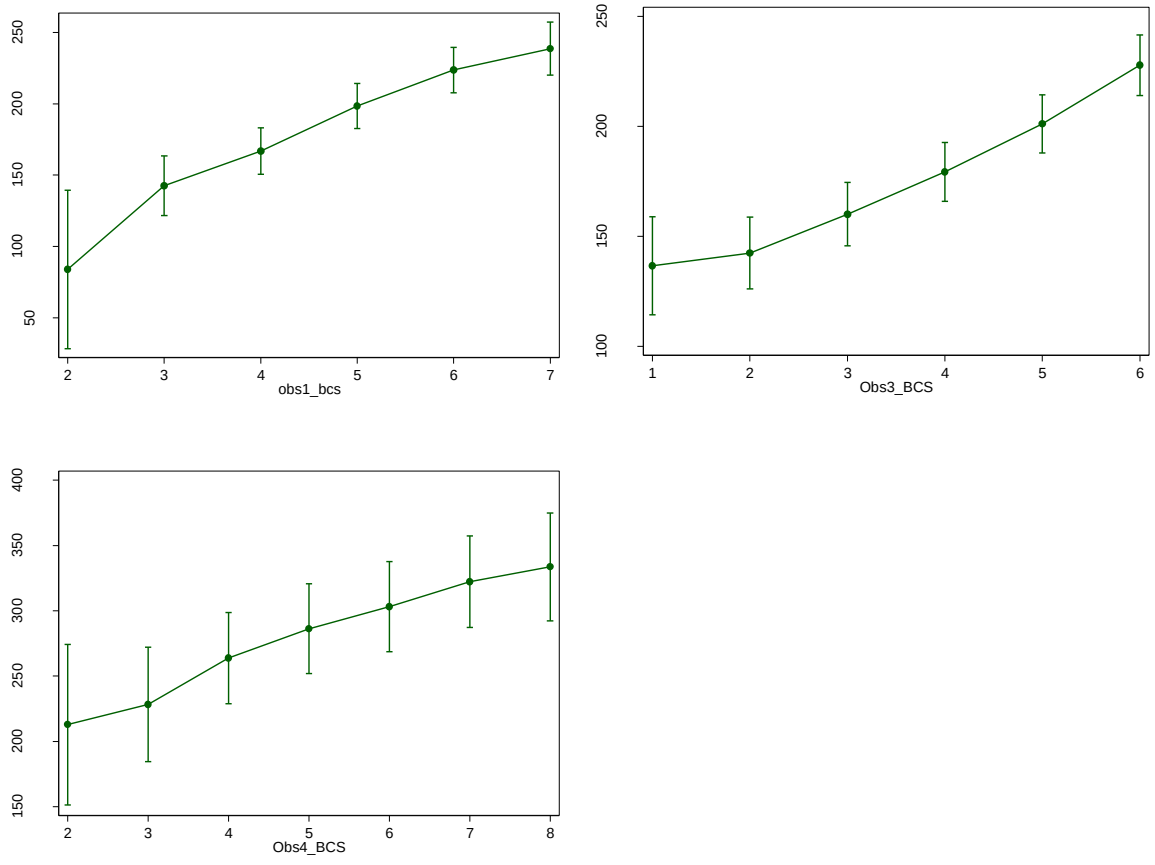


Figure 22: Predicted mean liveweight by body condition score at each of Obs1, Obs3 and Obs4. Drawn from multivariable models with liveweight as the outcome and BCS as the predictor. All models incorporated a fixed effect coding for year and a random effect coding for property.

Table 99: Counts of animals arranged by different BCS measuring occasions

	Obs3_BCS					
Obs1_BCS	**2**	**3**	**4**	**5**	**6**	**Total**
2	1	0	1	0	0	2
3	2	1	10	9	1	23
4	1	14	49	75	5	144
5	1	7	110	512	77	707
6	1	0	12	239	119	371
7	0	0	0	19	15	34
Total	6	22	182	854	217	1,281

	Obs4_BCS							
Obs1_BCS	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**Total**
2	0	1	0	1	0	0	0	2
3	1	0	7	11	2	0	0	21
4	2	5	21	76	25	5	0	134
5	2	5	78	342	180	48	6	661
6	0	0	10	117	114	53	4	298

7	0	0	1	7	10	10	1	29
Total	5	11	117	554	331	116	11	1,145

	Obs4_BCS							
Obs3_BCS	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**Total**
1	0	0	0	0	1	0	0	1
2	1	1	1	4	1	0	0	8
3	2	4	17	15	6	0	0	44
4	1	6	55	180	76	5	0	323
5	0	2	89	452	295	76	9	923
6	1	0	5	77	90	35	2	210
Total	5	13	167	728	469	116	11	1,509

The above tables allow inspection of distribution of animals between BCS scores and also the movement of animals from one score to another in subsequent measuring occasions. There appears to be generally a small amount of movement between scores.

Between Obs1 and Obs3, there was more downward movement than upward movement and the mean difference (Obs3 – Obs1) was -0.2 score units.

In contrast from Obs1 to Obs4, there was a general upward trend in BCS and the mean difference was 0.23 score units. This reflects the wet season growth.

Table 100: Model output from regression models using ADG measures as outcomes and fitting BCS category as a predictor. All models included a fixed effect for year of enrolment and a random effect for property.

Outcome	ADG_DS			95% CI	
Variable	**Level**	**Mean**	**se**	**low**	**up**
Obs1_BCS	2	0.065	0.09	-0.12	0.25
	3	0.1	0.03	0.04	0.16
	4	0.1	0.02	0.05	0.15
	5	0.07	0.02	0.02	0.11
	6	0.04	0.02	-0.003	0.09
	7	0.02	0.03	-0.04	0.07

Overall effect of Obs1_BCS significant: p<0.001

Outcome	ADG_WS			95% CI	
Variable	**Level**	**Mean**	**se**	**low**	**up**
Obs1_BCS	2	0.47	0.09	0.29	0.65
	3	0.46	0.05	0.36	0.56
	4	0.41	0.05	0.32	0.5
	5	0.42	0.04	0.33	0.51
	6	0.42	0.04	0.33	0.51
	7	0.43	0.05	0.33	0.53

Overall effect of Obs1_BCS not significant: p=0.41

Outcome	ADG_AN			95% CI	
Variable	**Level**	**Mean**	**se**	**low**	**up**
Obs1_BCS	2	0.19	0.05	0.08	0.29
	3	0.27	0.02	0.22	0.31
	4	0.27	0.02	0.24	0.3

5	0.26	0.02	0.23	0.29
6	0.25	0.02	0.22	0.29
7	0.25	0.02	0.21	0.29

Overall effect of Obs1_BCS not significant: p=0.2

There was a significant association between Obs1_BCS and ADG_DS. Animals in the highest BCS score levels had lower ADG values during the dry season.

In contrast there was no association between Obs1_BCS and ADG_WS or ADG_AN. There was also no association between Obs3_BCS and ADG_WS.

15.9 Dehorning method

The two main forms of dehorning are amputation and cautery disbudding with amputation being more commonly applied in northern beef areas of Australia.

While there are a number of specific techniques that may be classified as amputation, the three main tools used in northern Australia include dehorning knives, scoop dehorners and cup dehorners. A dehorning knife is curved in shape and has a blunted tip and is the preferred instrument for use on younger calves up to about 2-3 months of age(La Fontaine and Dde Witte, 2002, Laing, 2009). There are different types of scoop dehorners though they all operate on the same general principle. The dehorner is placed over the horn and the handles pushed/pulled apart to 'scoop' out the horn and surrounding tissue. Scoop dehorners are generally used on slightly older animals (2-6 months of age)(La Fontaine and Dde Witte, 2002). Cup dehorners are large instruments that are opened and placed over the horn and then closed to remove the horn base in a scissor action. Cup dehorners may be used on animals up to 12 months of age. Other tools are available such as the parrot beak dehorner, saws or surgical wire, all of which are generally used for tipping of older animals rather than attempting to remove all of the horn material and adjacent tissue to prevent regrowth.

Cautery disbudding involves the destruction of the horn bud with the use of a hot iron. The iron is heated either in a furnace or by an electrical element and is placed on the horn bud of the animal. The hot iron is held in place until all the horn and surrounding tissue is destroyed. The cauterising effect minimises blood loss and may reduce risk of wound infection. Cautery should only be used on young claves (up to about 2 months of age)(Irwin and Walker, 1998).

Management of cattle in northern Australia often means that animals are only mustered during the dry season. Under these conditions properties may conduct one or two rounds of mustering each year (April to June, and August to November depending on the season).

It is common under northern conditions for branding, castration and dehorning to all take place at the same time as weaning, and for these procedures to be applied to a wide range of size and age of animals. It was expected that there would be a range of different methods being applied given that animals may range widely in size at the time of dehorning.

Table 101: Description of dehorning tools

Dehorning tool	Diagram
Dehorning knife	
Cup	
Scoop	
Parrot beak	
Hot Iron	

The following table presents summary counts of animals that were dehorned on each property and the tool used

Table 102: Summary count of animals on each property for which records of dehorning were available.

prop_n	Cup	Dehorn knife	Hot iron	Knife	Parrot beak	Scoop	no record	Total
1	115	60	0	0	0	0	56	231
2	77	169	0	0	0	0	8	254
3	0	0	168	0	0	4	52	224
4	26	180	0	0	19	0	64	289
5	38	0	0	211	0	0	1	250
6	0	0	0	0	0	0	186	186
7	0	0	0	0	0	0	250	250
8	0	0	0	0	0	0	207	207
9	48	0	0	105	2	0	0	155
10	0	0	0	0	0	0	239	239
11	0	0	0	25	0	91	125	241
Total	304	409	168	341	21	95	1,188	2,526

Most animals in the column labelled “no record” were considered likely to be polled though this may not have been the case on all properties.

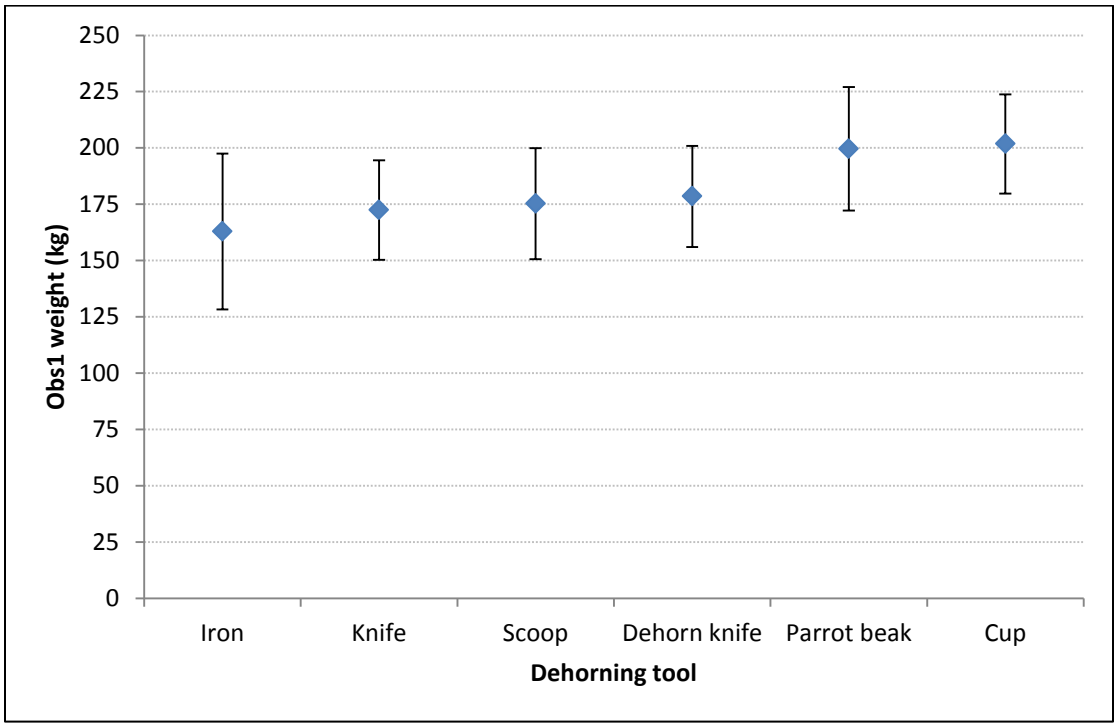


Figure 23: Mean Obs1_LWT (weaning weight) displayed by dehorning tool for those animals that were dehorned. Bars represent 95% confidence interval.

There was a significant association between weaning weight and tool type. Animals dehorned with a hot iron had the lowest weaning weight and were significantly lighter than animals dehorned with cup dehorners ($p=0.02$) but not different to any other tool. In contrast animals dehorned with cup dehorners were significantly heavier than those dehorned with other tools ($p<0.05$) with the exception of Parrot beak dehorners ($p=0.8$).

A series of regression equations were explored to look for possible associations between dehorning tool and ADG measures. Findings were confounded by the apparent association between weaning weight and dehorning tool and associations between weaning weight and subsequent measures of growth rate. Additional work is required to determine whether different types of dehorning tool have the potential to affect weight gain when applied to animals of similar weaning weight and under similar management conditions.

15.10 Dehorning wound size

Wound size (cm^2) of the dehorning wound was recorded for some cattle.

For cattle dehorned by hot iron the recorded wound size was assumed to be the same as the area of the hot iron itself and all entries were therefore recorded as a constant value (14.372 cm^2). These values were not based on a measurement of the actual wound but were based on a measurement of the iron dimensions. As a result, wound size measures for irons were removed from the dataset for analytical purposes.

Figure 24: Scatter plot of Obs1_LWT and dehorning wound size. R-squared=0.2

There was a significant and positive association between Obs1_LWT and dehorning wound size, and the association appeared linear. Larger animals had a larger wound size.

Regressions were run to assess for any evidence of an association between wound size and ADG outcomes. Models incorporated Obs1_LWT to adjust for the effect of body weight and also a random effect for property. Three models were run with outcomes representing dry, wet and annual ADG. Each model incorporated all available data (from all eleven properties).

There was no evidence for any association between wound size and any ADG measure ($p>0.05$).

Because there may be some concerns over the inclusion of two explanatory factors that were correlated (Obs1_LWT and wound size), models were re-run with these two variables both centred. Similar results were obtained (no effect of wound size on any ADG measure).

A regression model was also run to determine if there was an association between tool category and wound size. Iron was excluded from this analysis because the wound size measurement for iron was not based on a measurement. The model incorporated Obs1_LWT as a covariate and a random effect for property.

Mean wound size (cm^2) for each tool is reported below. There was significant variation between tool categories. The dehorning knife produced a wound that was significantly smaller than all other tools (adjusted for weaning weight and property level effects).

Table 103: Summary statistics for wound size recorded for each tool type. Pair-wise comparisons were then performed to compare mean wound size by tool type. Significant comparisons are listed (p<0.05).

Tool	Wound size	sem	95% CI Low	95%CI Up
Cup	59.41	7.07	45.54	73.27
Dehorn knife	43.04	7.15	29.03	57.05
Knife	60.78	7.08	46.89	74.66
Parrot beak	50.78	8.08	34.94	66.63
Scoop	59.37	7.55	44.59	74.16
Significant differences				
Dehorn knife vs Cup				
Dehorn knife vs Knife				
Dehorn knife vs Parrot beak				
Dehorn knife vs Scoop				
Cup vs Parrot beak				
Knife vs Parrot beak				

15.11 Exposure of frontal sinus

Animals that were subjected to dehorning were inspected immediately following dehorning and the wound classified as exposing the sinus or not (recorded as a binary variable: yes, no).

Table 104: Count of cattle with exposed sinus recorded at time of dehorning, presented by tool category. The final three rows present the mean percentage of animals with an exposed sinus and the 95% confidence interval.

exposed	Cup	Dehorn knife	Knife	Iron	Parrot beak	Scoop	Total
No	79	263	92	155	15	1	605
Yes	225	146	246	13	6	94	730
Total	304	409	338	168	21	95	1335
% exposed	74.0	35.7	72.8	7.7	28.6	98.9	54.7
95% CI Low	68.9	31.2	67.8	4.6	13.8	94.3	52.0
95% CI Up	78.6	40.5	77.3	12.8	50.0	99.8	57.4

There was interest in assessing whether there was an association between risk of sinus exposure and weaning weight. A series of t-tests were done within each tool-category to compare the Obs1_LWT between the two levels of sinus_exposed. For all tools except the dehorning knife, there was no difference in Obs1_LWT between animals that had an exposed sinus and those that did not.

There was a significant association between sinus exposure and Obs1_LWT for dehorning knife only ($p<0.05$). There were a total of 396 animals that were dehorned with the dehorning knife and that had Obs1_LWT and sinus exposure recorded (251 had no sinus exposure and 145 had an exposed sinus). Animals with an exposed sinus were significantly heavier at dehorning (200.7 kg), compared with animals that did not have an exposed sinus (171.5 kg). These findings suggest that heavier animals that are dehorned with a dehorning knife have a higher risk of sinus exposure.

There was no statistical association between exposure of the sinus and any ADG outcome (DS, WS or AN; $p>0.05$).

15.12 Bleeding after dehorning

Table 105: Mean ADG_DS generated from a regression model with ADG_DS as the outcome and fixed effects factors coding for bleeding score and Obs1_LWT. The model also included a random effect for property.

Bleed score	ADG_DS	sem	95%CI Low	95%CI Up
0	0.033	0.050	-0.066	0.131
2	0.031	0.050	-0.067	0.129
3	0.030	0.050	-0.068	0.129

There were no differences between bleed scores with respect to ADG_DS ($p>0.05$).

Table 106: Mean ADG_WS generated from a regression model with ADG_DS as the outcome and fixed effects factors coding for bleeding score and Obs1_LWT. The model also included a random effect for property.

Bleed score	ADG_WS	sem	95%CI Low	95%CI Up
0	0.445	0.038	0.371	0.519
2	0.428	0.038	0.354	0.502
3	0.431	0.038	0.357	0.505

There was a significant difference in ADG_WS between bleed score 0 and 2 ($p=0.04$) while other comparisons were not different ($p>0.05$).

Table 107: Mean ADG_AN generated from a regression model with ADG_DS as the outcome and fixed effects factors coding for bleeding score and Obs1_LWT. The model also included a random effect for property.

Bleed score	ADG_AN	sem	95%CI Low	95%CI Up
0	0.257	0.031	0.196	0.318
2	0.250	0.031	0.189	0.311
3	0.246	0.031	0.185	0.307

There was a significant difference in ADG_AN between bleed score 0 and 3 (p=0.04) while other comparisons were not different (p>0.05).

These findings suggest that there could be an association between increased bleeding and reduced growth, but caution is urged in interpreting these findings. Bleeding is correlated to other factors such as wound size and body weight and may be linked to tool type and other factors that were not measured. The effect of bleeding is considered likely to be largest in the shortest time frame since animals that recover from a bleeding episode are likely to have regenerated red blood cells quite quickly. The fact that there was no statistical association between bleeding and dry season growth is suggestive that there may not be a real association. However, increased bleeding may also be an indication of risk of other events such as infection which may in turn have a longer lasting adverse effect. Further work is necessary to understand the details of this possible association.

15.13 Dehorn wound healing

Healing of dehorning wounds was assessed at a separate observation about 2-3 weeks after dehorning. Wounds were assessed individually while the animal was restrained in the crush and wounds were palpated as necessary to complete the assessment including applying gentle pressure to detect a discharge.

Table 108: Description of categories of horn healing

Horn heal score	Description
0	No dehorning (polled or missed)
1	Well healed. Clean and dry.
2	Well healed. Discharge odourless and clear (or fresh blood)
3	Partially healed. Small amount discharge
4	Partially healed. Large amount of discharge. Offensive odour.
5	Swelling, inflamed. Offensive odour. Possible presence of fly larvae.

Table 109: Count of observations for dehorn wound healing by property

	Property								
Heal score	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**11**	**Total**
1	90	57	148	105	100	0	81	2	583
2	49	104	16	80	65	0	17	45	376
3	33	82	6	10	67	5	35	58	296
Total	172	243	170	195	232	5	133	105	1,255

Table 110: Mean wound size (cm^2) for each level of healing score

Heal score	Wound size	sem	95%CI Low	95%CI Up
1	49.9	7.2	35.8	64.0
2	57.4	7.2	43.3	71.5
3	62.8	7.2	48.6	76.9

There was a significant association between dehorning wound size and wound healing score. Each healing score level was significantly different to each other level ($P<0.05$). Wounds with higher healing scores had a larger area than wounds with lower healing scores.

15.14 Castration tool

Table 111: Summary count of observations on castration tool by property

Castration	Property							
tool	**1**	**2**	**3**	**4**	**5**	**9**	**11**	**Total**
band	0	0	221	0	0	0	0	221
pocket knife	0	0	0	0	250	0	0	250

scalpel	229	251	0	277	0	153	123	1,033
Total	229	251	221	277	250	153	123	1,504

15.15 Castration sterilisation

Table 112: Summary count of observations on castration sterilisation by property

Castration	Property						
sterilisation	**1**	**2**	**3**	**4**	**9**	**11**	**Total**
antiseptic	138	0	221	277	153	27	816
nothing	87	251	0	0	0	96	434
Total	225	251	221	277	153	123	1,250

15.16 Castration type (high vs low)

The approach to castration was classified as high or low based on where the spermatic cord was severed.

Table 113: Summary count of observations on castration type (high/low) by property

Castration	Property							
high or low	**1**	**2**	**3**	**4**	**5**	**9**	**11**	**Total**
high	150	164	211	249	231	153	117	1,275
low	75	70	10	28	5	0	2	190
Total	225	234	221	277	236	153	119	1,465

There was a significant association between castration type (high vs low) and weaning weight. Animals that were classified as being castrated high, had a significantly smaller weaning weight ($p<0.001$).

Table 114: Mean weaning weight (Obs1_LWT) by castration type (high vs low)

Castration	Weaning		95% CI	
high/low	weight	sem	Low	Up
High	177.1	12.0	153.7	200.6
Low	193.4	12.3	169.4	217.5

Regression models were performed to look for associations between castration type and ADG measures. Each model had fixed effects coding for Obs1_LWT and castration type, and a random effect coding for property. There was an apparent association between castration type and ADG_DS.

Animals recorded as having a high castration, had a lower ADG_DS than animals recorded as having a low castration (p=0.001).

Table 115: Mean ADG_DS by castration type (high vs low)

Castration			95% CI	
high/low	ADG_DS	sem	Low	Up
High	0.028	0.049	-0.069	0.124
Low	0.054	0.050	-0.043	0.152

There was no association between castration type and either ADG_WS or ADG_AN.

15.17 Bleeding at castration

Bleeding at castration was recorded visually soon after animals were released from restraint. Animals were scored on a 4-point scale (0=no bleed, 1=drip, 2=steady stream, 3=rapid spurt).

Scores were aggregated into a two-level scale (0=no bleed or drip, 1=stream or spurt).

Table 116: Summary counts of observations on castration bleeding score by property

Castration bleeding	property 1	2	4	5	9	11	Total
none or drip	158	241	233	241	147	114	1,134
stream or spurt	56	10	43	9	7	9	134
Total	214	251	276	250	154	123	1,268

Table 117: Mean weaning weight by castration bleeding score

Castration bleeding	Weaning weight	sem	95% CI Low	Up
none or drip	184.9	11.6	162.0	207.7
stream or spurt	205.4	12.1	181.6	229.1

Animals with a worse bleeding score at castration were significantly heavier than animals with a better bleeding score ($p<0.001$).

There was no statistical association between castration bleeding score and any ADG measure.

Animals that were castrated low were 2.6 times more likely to have a higher bleeding score compared to animals that were castrated high (relative risk=2.6, 95% CI from 1.9 to 3.7, chi-squared p-value <0.001).

There was no association between castration bleed score and environmental temperature or humidity measured around the time of castration.

15.18 Scrotal healing score

Animals were assessed at a separate observation period about 2-3 weeks after castration. Animals were inspected individually while restrained in a crush and the genital area palpated if necessary.

Table 118: Description of scrotal healing score

Castration heal score	Description
0	No castration performed
1	Well healed, clean & dry
2	Well healed, minor swelling
3	Partially healed, small amount discharge when palpated, moderate swelling
4	Partially healed, large amount of discharge, offensive odour, moderate swelling
5	Severe swelling, variable discharge

Table 119: Summary count of scrotal healing score by property

Castration healing score	property 1	2	3	4	5	9	11	Total
1	38	63	35	35	125	68	6	370
2	53	40	76	104	39	23	36	371
3	62	104	83	74	38	31	38	430
4	70	39	24	27	25	10	30	225
Total	223	246	218	240	227	132	110	1,396

There was no association between scrotal healing score and castration bleeding score.

There was also no association between scrotal healing score and any measure of ADG.

There was an association between healing score and weaning weight.

Table 120: Mean weaning weight for each level of scrotal healing score

Castration healing score	Weaning weight	sem	95% CI Low	95% CI Up
1	170.3	12.7	145.4	195.2
2	179.9	12.7	155.0	204.8
3	181.0	12.7	156.1	205.8
4	189.9	12.8	164.8	215.0

Animals in healing score 1 were lighter than all other levels ($p<0.05$) and animals in healing score 4 were heavier than all other levels ($p<0.05$). There was no difference in weight between scores 2 and 3.

15.19 Observation 2 liveweight

Observation 2 (Obs2) was intended to allow assessment of animals at about 3 weeks (range from two to four weeks) after Observation 1, largely to assess various parameters related to wound healing for wounds associated with dehorning and castration. Observation 2 measurements only occurred on those properties where animals were being subjected to these husbandry measures at the time of the first Observation.

Animals were weighed at Obs2 but since these measurements were only 2-4 weeks after Obs1 and only occurred on eight of the eleven enrolled properties, these measurements were not used in the main statistical analyses.

Summary statistics are presented here for those properties where Obs2 took place and summary statistics for Obs1 are also displayed to allow comparison.

Table 121: Summary statistics for Obs1 LWT and Obs2 LWT limited to those properties where Obs2 took place, showing property number, number of animals enrolled, n=number of animals measured at each Obs, SD=standard deviation, min=minimum, max=maximum.

	Property number							
Obs1 LWT	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**11**
n enrolled	**231**	**254**	**224**	**250**	**289**	**207**	**155**	**241**
month	May-09	Aug-09	Apr-09	May-09	Jul-09	May-10	Jun-08	Jun-10
dates	27 & 28	01	09	31/5 & 1/6	29 & 30	31/5 & 1/6	6th	7/6 & 4/8
n	208	252	221	283	248	205	148	239
mean (kg)	214.39	211.33	133.19	159.9	212.96	171.49	161.1	177.02
SD	51.2	43.833	19.9	29.38	35.86	39.01	39.71	35.68
min	91	104	88	87.5	131	84	101	60.5
max	303	338	190	246	307	348	334	269
	Property number							
Obs2 LWT	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**11**

month	Jun-09	Aug-09	May-09	Jun-09	Aug-09	Jun-10	Jun-10	Jul-10
days from Obs1	19	22	22	29	23	15	21	24
n	219	246	218	232	230	202	134	214
mean (kg)	210.99	213.76	140.69	164.5797	199.38	172.81	157.70	182.23
SD	47.50	43.72	24.54	29.78	34.34	41.09	37.40	37.78
min	92.5	105	62	96.5	117	85	104	75
max	304	356	206	253	278	348	301	272

When all the data were averaged the overall mean weight change from Obs1 to Obs2 was 0.09 kg, indicating that there was almost no change. Within individual properties the mean LWT change from Obs1 to Obs2 ranged from a loss of 13.6kg to an increase of 7.5kg and five of the eight properties displayed an increase in LWT while the other three displayed a decrease in mean LWT.

Obs1 and Obs2 took place in the dry season (May to August). Not all animals on each property were subjected to husbandry procedures at Obs1.

Table 122: Summary statistics for Obs2 LWT arranged into groups within each property based on whether or not individual animals were dehorned at Obs1.

	Property number						
Not dehorned	**1**	**2**	**3**	**4**	**5**	**8**	**11**
n	50	5	50	47	1	202	108
Mean LWT (kg)	200.97	251.60	139.28	162.97	228.00	172.81	203.85
SD	53.29	33.72	26.33	31.12	.	41.09	33.66
Min	92.5	219	62	113	228	85	92.5
Max	300	305	198	253	228	348	272
	Property number						

Dehorned	1	2	3	4	5	9	11
n	169	241	168	185	229	134	106
Mean LWT (kg)	213.95	212.97	141.11	164.99	199.25	157.70	160.21
SD	45.40	43.61	24.04	29.50	34.37	37.40	27.76
Min	116	105	72	96.5	117	104	75
Max	304	356	206	246	278	301	215

As indicated earlier it is possible that the choice of dehorning tool may have been influenced by liveweight and therefore it is difficult to compare the effect of dehorning on animal LWT measures. The mean LWT values show that on some properties animals that were dehorned at Obs1 had a higher mean LWT at Obs2 compared to animals that were not dehorned at Obs1. There are also some properties where this effect is reversed.

15.20 Observation 2 missingness as an indicator of mortality

Under routine commercial operations on extensive beef properties it is common to use missingness as an indication of animal mortality since cattle are often mustered infrequently and it is difficult to regularly inspect animals on pasture because of the large land areas and low stocking density on many northern beef properties. Mortalities are often defined by absence of individual animals from a number of consecutive musters of both the paddock(s) they are expected to be in and adjacent paddocks. There is variability in the number of consecutive musters that an animal may be recorded as missing before it is classified as dead but many producers appear to rely on two to five consecutive musters or up to three consecutive years.

The current study followed enrolled animals in the first round muster of one year and followed them for about 12 months post-weaning. Data on individual animals was inspected to look for missingness as an indicator of mortality. The record of individual animals enrolled in the study was used as the starting list of animals. Records of individuals yarded at each of the successive observation points were used to identify those animals that had been enrolled at Obs1 and then were recorded as missing for all subsequent observations. Data from property 4 was not used for this assessment because this property withdrew from the study prior to Obs4.

Table 123: Count of animals enrolled in the study by property and count of animals recorded as missing at all subsequent observations. Missingness is expressed as a percentage of the starting count and with 95% confidence interval (CI).

	Missing	No. enrolled	Missing	95% CI	
Property	(n)	(n)	(%)	Lower	Upper
1	3	231	1.30	0.44	3.75
2	6	254	2.36	1.09	5.06
3	2	224	0.89	0.25	3.20
5	2	289	0.69	0.19	2.49
6	2	186	1.08	0.30	3.84
7	8	250	3.20	1.63	6.19
8	2	207	0.97	0.27	3.45
9	5	155	3.23	1.39	7.33
10	11	239	4.60	2.59	8.05
11	3	241	1.24	0.42	3.60
Total	44	2276	1.93	1.44	2.59

These records provide a measure of missingness over a period of about 12 months and this measure does provide an indication of mortality. Caution is required in interpreting this measure because the period was considered to be shorter than periods used under routine commercial conditions for classifying missing animals as likely to be dead. Some animals might therefore be alive and identified subsequently in following musters of the same or adjacent paddocks.

15.21 Tick scores

The original methodology for assessing tick burdens involved counting the ticks on one side of the body while an animal was restrained in the crush and assigning the result to a six-level score:

- 0=no ticks;
- 1= 1 to less than 10 ticks;
- 2=11-30 ticks;
- 3=31-80 ticks;
- 4=81-150 ticks;
- 5= more than 150 ticks

Preliminary review of the score data indicated that there were very few animals with scores greater than 2 and it was not possible to use the full scoring system in any statistical analyses because there were insufficient observations to generate means and allow comparisons between score levels. As a result the score was refined to a 3-level score (0=no ticks, 1=<10 ticks and 2=>10 ticks).

Summary statistics are presented below for ADG measures at each observation, arranged by tick score.

Table 124: Summary statistics for ADG measures by tick score level from data collected at Observation 2.

Obs2 Tick score		ADG_DS	ADG_WS	ADG_AN
0	Count of properties	7	7	7
	Count of animals	1273	996	1022
	Mean ADG (kg/hd/day)	0.059	0.430	0.283
	Standard error	0.004	0.004	0.003
1	Count of properties	3	3	3
	Count of animals	27	24	24
	Mean ADG (kg/hd/day)	0.016	0.443	0.257
	Standard error	0.027	0.024	0.016

2	Count of properties	1	1	1
	Count of animals	14	13	16
	Mean ADG (kg/hd/day)	0.224	0.518	0.377
	Standard error	0.020	0.032	0.019
3	Count of properties	1	1	1
	Count of animals	3	3	5
	Mean ADG (kg/hd/day)	0.223	0.453	0.334
	Standard error	0.047	0.007	0.022

Table 125: Summary statistics for ADG measures by tick score level from data collected at Observation 3.

Obs3 Tick score		ADG_DS	ADG_WS	ADG_AN
0	Count of properties	10	10	10
	Count of animals	1404	1131	1135
	Mean ADG (kg/hd/day)	0.044	0.445	0.260
	Standard error	0.003	0.004	0.003
1	Count of properties	7	7	7
	Count of animals	522	385	387
	Mean ADG (kg/hd/day)	0.070	0.379	0.251
	Standard error	0.006	0.006	0.004
2	Count of properties	6	6	6
	Count of animals	43	34	34
	Mean ADG (kg/hd/day)	0.028	0.411	0.252
	Standard error	0.020	0.026	0.015
3	Count of properties	0	0	0
	Count of animals			
	Mean ADG (kg/hd/day)			
	Standard error			

Table 126: Summary statistics for ADG measures by tick score level from data collected at Observation 4.

Obs4 Tick score		ADG_DS	ADG_WS	ADG_AN
0	Count of properties	9	9	9
	Count of animals	1356	1357	1396
	Mean ADG (kg/hd/day)	0.107	0.445	0.285

	Standard error	0.004	0.004	0.003
1	Count of properties	5	5	5
	Count of animals	208	209	214
	Mean ADG (kg/hd/day)	0.046	0.350	0.230
	Standard error	0.007	0.009	0.005
2	Count of properties	3	3	3
	Count of animals	71	70	75
	Mean ADG (kg/hd/day)	0.047	0.298	0.205
	Standard error	0.015	0.011	0.007
3	Count of properties	2	2	2
	Count of animals	15	15	17
	Mean ADG (kg/hd/day)	0.008	0.271	0.186
	Standard error	0.031	0.023	0.017

15.22 Fly counts

Buffalo fly were counted and recorded at three periods (Obs2, Obs3 and Obs4). Fly counts were recoded into a 3 category score: 0=no fly, 1=1 to 30 and 2=31 to 80, 3= 81+.

Table 127: Summary of fly score by property for Obs2

Obs2	**Property**							
Fly score	**1**	**2**	**4**	**5**	**8**	**9**	**11**	**Total**
none	128	246	137	128	202	101	80	1,022
up to 30	89	1	105	103	0	31	131	460
31 to 80	5	0	0	1	0	1	3	10
>80	1	0	0	0	0	0	0	1

Total	223	247	242	232	202	133	214	1,493

Table 128: Summary counts for each level of fly score by property for Obs3

Obs3	Property										
Fly score	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
none	213	210	65	106	135	2	0	142	2	17	892
up to 30	25	3	111	122	46	161	83	0	137	187	875
31 to 80	0	0	0	0	0	56	60	0	58	24	198
>80	0	0	0	0	0	7	37	0	13	3	60
Total	238	213	176	228	181	226	180	142	210	231	2,025

Table 129: Summary counts for each level of fly score by property for Obs4

Obs4	Property									
Fly score	**1**	**2**	**3**	**5**	**6**	**7**	**8**	**10**	**11**	**Total**
none	213	93	1	0	1	0	1	0	1	310
up to 30	0	134	120	63	45	121	85	54	148	770
31 to 80	0	0	49	71	88	68	52	34	42	404
>80	0	0	27	81	47	50	49	18	23	295
Total	213	227	197	215	181	239	187	106	214	1,779

There were so few flies in the upper categories at Obs2 that comparisons for these categories were unreliable.

Regression analyses were run with each ADG measure as an outcome and with fixed effects coding for fly score and Obs1_LWT. A random effect was added to code for property.

There was no association between fly score for the lower categories and any ADG measure.

There were significant associations between Obs3 fly scores and ADG measures but generally these were not consistent with an adverse effect of flies. As shown below, increasing fly score (more flies) was associated with an increase in ADG_DS, though the effect was only significant for the middle two levels of fly score compared with the highest fly score.

Table 130: Mean ADG_DS for each level of fly score at Obs3

Obs3	ADG_DS		95% CI	
fly score	mean	sem	Low	Up
none	0.053	0.032	-0.010	0.115
up to 30	0.042	0.032	-0.021	0.104
31 to 80	0.048	0.032	-0.015	0.112
>80	0.079	0.034	0.013	0.145

A similar effect was seen with ADG_WS. Animals with no observed flies (score=0) had a significantly lower ADG_WS than all other levels of fly score while there was no difference between any level of fly score other than the zero level.

Table 131: Mean ADG_WS for each level of fly score at Obs3

Obs3	ADG_WS		95% CI	
fly score	mean	sem	Low	Up
none	0.425	0.033	0.359	0.490
up to 30	0.451	0.033	0.385	0.516
31 to 80	0.456	0.034	0.388	0.524
>80	0.468	0.037	0.395	0.541

A similar effect was seen for annual ADG (ADG_AN). The highest ADG was seen in animals with the heaviest fly counts. The two highest fly score levels were not different and the two lowest fly score levels were not different. Annual ADG in animals without any flies were significantly lower than animals in the top two categories ($p<0.05$). Annual ADG in animals with up to 30 flies was significantly lower than animals in the highest fly category ($p<0.05$). Other comparisons were not different ($p>0.05$).

Table 132: Mean ADG_AN for fly score at Obs3

Obs3	ADG_AN	95% CI

fly score	mean	sem	Low	Up
none	0.257	0.018	0.221	0.294
up to 30	0.266	0.018	0.229	0.302
31 to 80	0.274	0.019	0.237	0.312
>80	0.295	0.021	0.254	0.336

There was no association between fly score at Obs4 and any measure of ADG. It is interesting to note that the highest ADG_AN was seen in the heaviest fly score category (though there was no statistical difference between any level).

Table 133: Mean ADG_AN by fly score for Obs4 fly counts.

Obs4	ADG_AN		95% CI	
fly score	mean	sem	Low	Up
none	0.269	0.026	0.219	0.319
up to 30	0.276	0.025	0.228	0.324
31 to 80	0.285	0.025	0.236	0.333
>80	0.285	0.025	0.236	0.334

15.23 Lesions attributed to Buffalo fly

A visual assessment was made of skin lesions attributed to flies. Lesions were scored by size and whether they were acute or chronic in appearance.

Table 134: Scoring system for fly lesions

Lesion score	
Acute vs chronic	Size score

			no
1	acute	0	lesion
2	chronic	1	<2cm^2
		2	2-5cm^2
		3	5-10cm^2
		4	>10cm^2

There were insufficient observations at Obs2 to warrant analysis.

In an attempt to simplify analyses, first comparisons were done to compare all acute lesions to all chronic lesions using separate analyses for each ADG outcome. There was no evidence of any effect of acute vs chronic lesions and all lesions were then assessed based on size alone.

There were so few animals with lesions scoring 4 for size that these animals were recoded as score=3 for analysis.

Table 135: Summary count of observations by fly lesion size at Obs3

Obs3	**Property**										
Fly lesion	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
no lesion	195	61	114	227	184	145	16	129	96	225	1,392
<2cm^2	2	93	35	1	0	63	41	7	73	3	318
2-5cm^2	6	32	13	0	0	18	78	5	24	2	178
>5cm^2	3	21	6	0	0	1	44	1	16	1	93
Total	206	207	168	228	184	227	179	142	209	231	1,981

Table 136: Summary count of observations by fly lesion size at Obs 4.

Obs4	**Property**

Fly lesion	1	2	3	5	6	7	8	10	11	Total
no lesion	212	171	158	41	181	237	53	93	175	1,321
<2cm^2	0	22	30	18	0	0	63	5	25	163
2-5cm^2	0	19	9	63	0	2	57	7	6	163
>5cm^2	1	15	0	93	0	0	11	1	8	129
Total	213	227	197	215	181	239	184	106	214	1,776

There was no association between lesion size and ADG measures.

15.24 HGP

Table 137: Description of HGP use by property

Property	HGP timing	Product	Comment
1	Weaning	Compudose 400	
2	Not used		
3	Not used		
4	2nd round muster	Compudose 400	Animals that missed muster did not receive implant
5	Not used		
6	Calf only	Compudose 400	
7	Weaning	Compudose 400	
8	1. Calf+ 2. Weaning	1. Revalor 400 + Compudose 200 2. Revalor 400	Calf+ animals reimplanted at 2nd round muster
9	Not used		

10	1. Calf only 2. Calf+	1. Product unknown 2. Compudose G	Animals that missed muster missed being reimplanted, and last 19 of mustered animals missed reimplant
11	1. Calf only 2. Weaning	1. Compudose 400 2. Compudose 400	

Table 138: Summary count of animal records of HGP use by property

	Property											
hgp_timing	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
calf only	0	0	0	0	0	184	0	0	0	46	115	345
calf+	0	0	0	0	0	0	0	22	0	188	0	210
branding	231	0	0	0	0	0	0	0	0	0	0	231
2nd round muster	0	0	0	179	0	0	0	0	0	0	0	179
weaning	0	0	0	0	0	0	223	185	0	0	124	532
Not used	0	254	224	5	250	2	27	0	155	5	2	890
Unknown	0	0	0	105	0	0	0	0	0	0	0	105
Total	231	254	224	289	250	186	250	207	155	239	241	2,526

The fact that not every property had all categories and that some properties only had one category meant that it was not possible to combine data from multiple properties into one analysis. Other property level effects (pasture, season, management, genetics, etc) may also be confounded with HGP, meaning that it was difficult to compare data for different usages of HGP when data may be completely confounded with property.

As a result analyses were done within individual properties to try and tease out some inferences concerning HGP.

Obs1_LWT was added to models to try and account for weaning weight when assessing effect of HGP.

- Prop_n=7: never vs weaning
  - ADG_DS: Animals receiving HGP at weaning had a lower ADG_DS than animals that did not receive HGP
    - weaning: mean=0.093, sem=0.006
    - never: mean=0.14, sem=0.019
    - significantly different p=0.02
  - ADG_WS: Animals receiving HGP had a higher ADG_WS.
    - weaning: mean= 0.46, sem=0.012
    - never: mean=0.35, sem=0.04
    - p-value=0.018
  - ADG_AN: Animals receiving HGP had higher ADG but the effect was not significant.
    - weaning: mean=0.31, sem=0.007
    - never: mean=0.27, sem=0.023
    - p-value=0.083

- Prop_n=11: calf only vs weaning
  - ADG_DS: Animals receiving HGP as calf only had a higher ADG_DS than animals that received it at weaning only.
    - calf only: mean=0.039, sem=0.007
    - weaning: mean=0.015, sem=0.007
    - p-value=0.001
  - ADG_WS: no effect of HGP
    - calf only: mean=0.41, sem=0.012
    - weaning: mean=0.404, sem=0.013
    - p-value=0.9
  - HGP14: no effect of HGP
    - calf only: mean=0.25, sem=0.008
    - weaning: mean=0.26, sem=0.008
    - p-value=0.3

- prop_n=10: calf only vs calf +
  - ADG_DS: no difference
    - calf only: mean=0.076, sem=0.016
    - calf+: mean=0.083, sem=0.005
    - p-value=0.7
  - ADG_WS: no effect.
    - calf only: mean=0.57, sem=0.044
    - calf+: mean=0.55, sem=0.008

        - p-value=0.7
    - ADG_AN: There were significant differences
        - calf only: mean=0.36, sem=0.012
        - calf+: mean=0.33, sem=0.006
        - never used: mean=0.26, sem=0.03 (5 animals)
        - p-value
            - calf only vs calf+: p=0.048
            - calf only vs never: p=0.004
            - calf+ vs never: p=0.025
- prop_n=8: calf + vs weaning
    - ADG_DS: Animals implanted as a calf had a higher ADG than those implanted at weaning
        - calf+: mean=0.28, sem=0.021
        - weaning mean=0.19, sem=0.006
        - p-value<0.001
    - ADG_WS: no difference
        - calf+: mean=0.47, sem=0.022
        - weaning mean=0.48, sem=0.006
        - p-value=0.7
    - ADG_AN: calf+ had higher ADG
        - calf+: mean=0.39, sem=0.017
        - weaning mean=0.35, sem=0.005
        - p-value=0.044

15.24.1 Impact of loss of HGP implants

One property had implanted HGP and then had experienced significant loss of implants from cattle over the wet period. Losses were attributed mainly to infection at the implantation site. In observations at Obs4, a total of 126 of 227 animals (56%) had lost their implants.

Observations on losses of implants at other properties suggested that losses did occur but at much lower rates. The experiences at this individual property provided a further opportunity to assess the impact of HGP implants.

    - ADG_DS: Animals that retained their implants had a higher ADG
        - implants retained: mean=0.31, sem=0.012
        - implants lost: mean=0.27, sem=0.01
        - p-value=0.019
    - ADG_WS: no difference
        - implants retained: mean=0.45 , sem=0.01

        - implants lost: mean=0.43, sem=0.009
        - p-value=0.3
    - ADG_AN: Animals that retained their implants had a higher ADG
        - implants retained: mean=0.40, sem=0.007
        - implants lost: mean=0.38, sem=0.006
        - p-value=0.023

15.24.2 Recommendations concerning implanting technique

Correct implanting technique is important when using HGPs (Cowley, 2011b, Partridge, 2010). If the implant is lost as a result of poor technique then this will result in a direct loss of the cost of implant and administration, and the opportunity cost of the potential weight gain associated with the HGP that is not realised.

It is important to provide training in good techniques and to combine this with some form of quality assurance (inspection) to ensure compliance with protocols and allow identification and correction of any problems.

Good implanting technique is based on the following practices:

- Insert the HGP in the middle third of the back of the ear (see below). This is important to allow adequate blood flow across the implant which is required for efficient hormone absorption.
- While holding the point of the ear, slide the needle between the skin and cartilage, being careful to avoid major blood vessels
- Withdraw the gun slightly while squeezing the trigger to allow room for the implant to be inserted
- Leave about 1cm of skin between the HGP and the wound entry
- Pinch the injection site closed and check a HGP has been inserted.

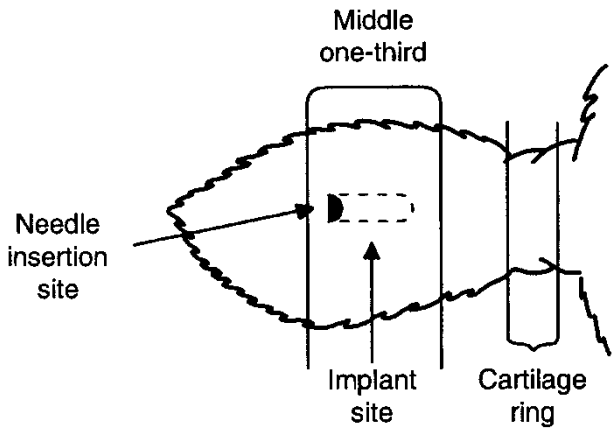


Figure 25: Correct placement of HGPs. From (Cowley, 2011b)

It is also important to combine good hygiene with correct insertion technique to ensure minimal risk of complications. An infection at the implant site can lead to an abscess and then expelling of the HGP. Alternatively, it could lead to scarring which impacts blood flow to the implant and so effects absorption.

Good hygiene involves the following:

- Ensure the needle is sharp (rough edges catch and spread dirt and animal matter)
- Disinfect the needle of the applicator in between each animal (simply dip into a hibitane solution)
- Regularly clean the applicator with an antiseptic solution
- Take great care to avoid contamination of HGPs or applicators and if contaminated, clean applicators/implants by rinsing thoroughly in a strong antiseptic solution before implanting.
- Keep the crush area as clean as possible to minimise the risk of dirt contamination during implantation.

15.25 Determining half-sib groups of calves[d]

15.25.1 Introduction

Studying the relative impact of additive genetic variance on quantitative traits requires accurate parentage inference. As the impact of males to genetic gain is substantially greater than for females in polygamous species, accurate sire assignment is an essential component for such studies. Misidentification of sires has been shown to result in increased genetic correlations among direct effects and decreased correlation between maternal effects (Senneke et al., 2004).

The current study was presented with progeny that were enrolled in the study having been derived from unknown sires. As a result there was interest in sire assignment using microsatellite genotyping of bulls and calves, with parentage assigned by exclusion. Exclusion parentage assignment is the gold standard method (Jones et al., 2010). It is based on Mendelian inheritance, in which a parent and offspring share one allele at every tested locus. Failure to share an allele at even one locus is sufficient to exclude that individual as a parent. In its strictest application, genotyping errors are not taken into account. With a sufficient number of polymorphic microsatellite loci, it is possible to exclude all but one parent for an offspring. Of course, adequate sampling of parents is required, with poor sampling coverage resulting in offspring without an assigned parent.

There have been significant recent advances and interest in determining kinship and pedigree relationships based on microsatellite genotyping data (reviewed in (Blouin, 2003)) and used for quantitative genetic studies for example in bighorn sheep (Coltman et al., 2005). In the absence of parental genotypes, alternative methods have been developed to identify full-sib or half-sib groupings. For the analysis of additive genetic variance, such a grouping of half-sib calves would provide information on sire effects, even without knowing the identity of that sire. However, the reconstruction of half-sib groupings is hindered by the variable number of alleles that can be shared by two half-sibs. For example, at a biallelic locus, a sire will pass one allele at random to each of his offspring and so two of his offspring will share either zero or one allele. If the sire is heterozygous at the locus, then any two randomly selected half sibs will not share either of the sire's alleles at that locus 50% of the time. The sharing of alleles is, of course, complicated by alleles inherited from the dam, particularly if alleles are shared between the sire and the dam.

[d] Report prepared by Dr Jennifer Seddon, Senior Lecturer in Animal Genetics, School of Veterinary Science, The University of Queensland, Gatton QLD 4343

Among the programs that perform half---sib group reconstruction (HSGR) are COLONY2 (Wang, 2004, Wang and Santure, 2009) and KINGROUP (Konovalov et al., 2004). COLONY2 assesses partitions of half sib families using a simulated annealing approach to maximise the likelihood value of the partition. It creates partitions using all individuals simultaneously (Jones et al., 2010). KINGROUP uses a pairwise likelihood approach by testing if a hypothesised pedigree relationship is significantly more likely than an alternative specified relationship (as originally implemented in KINSHIP) (Queller and Goodnight, 1989) and then maximises the overall likelihood of the partition of half-sib groupings.

An accurate HSGR method would reduce time and monetary costs in sampling and genotyping sires, and allow studies to be conducted where sire information was unobtainable. Here, HSGR was evaluated for accuracy in recovering half-sib groups by using half-sib groups known to share a sire by exclusion parentage assignment. Five breeding paddocks of extensively managed cattle from the Northern Territory had calves and sires genotyped. The maximum likelihood methods implemented in COLONY2 and KINGROUP were employed to cluster calves into half-sib groups without using the sire genotypes. If accurately reconstructed, half-sib groups were expected to share a sire assigned by exclusion and also the progeny of one sire were expected to form a single reconstructed cluster.

15.25.2 Methods

Tail hair samples were collected by Northern Territory Department of Resources from bulls and calves from five populations: one breeding paddock on each of three properties (property=1, 3 & 9) and two breeding paddocks from an additional property (property=2, groups 1 and 2). It was assumed that the majority of bulls were mustered and sampled. Because this is an extensively managed system, it is possible that non-mustered bulls sired calves in the paddock.

DNA was extracted and microsatellite genotypes were obtained by the Animal Genetics Laboratory, School of Veterinary Science, The University of Queensland, using the 15 microsatellite loci panel employed for commercial parentage analysis. Sire assignment for calves was undertaken by exclusion and required a match of one allele at every locus, with no mismatches (eg for genotyping error) accepted for sire assignment. Genetic diversity parameters were calculated using Microsatellite Toolkit for Excel (animalgenomics.ucd.ie/sdepark/ms---toolkit/) and allelic richness, the number of alleles corrected for sample size, in FSAT version 2.9.3.2 (Goudet, 2001).

Two programs were used to determine half-sib groups. COLONY version 2.0 (Wang, 2004, Wang and Santure, 2009) was used with a full likelihood analysis, a medium length run and allele frequencies estimated from the data, and assuming a polygamous male mating system and no sibship priors. No genotyping error rate was incorporated into the analyses, although COLONY2 is able to do so, because the results were

compared against parentage based on exclusion with complete allele matching ie without mismatches. KINGROUP version 2.08(Konovalov et al., 2004) (http://code.google.com/p/kingroup/) was used according to the manual, with a descending ratio algorithm to test a primary hypothesis of half sibling (Rp=0.5 and Rm=0, where Rp is the paternal relatedness coefficient and Rm is the maternal relatedness coefficient) against a complex null hypothesis that ranged from unrelated (Rp=0, Rm=0) to parent-offspring (Rp=1.0, Rm=0). Although the half-sibling hypothesis forms part of the null hypothesis, it was excluded during analysis.

15.25.3 Results

The five tested populations had between 18 and 109 sires and 123 and 230 progeny. There was overall high diversity among all the tested populations, with expected heterozygosity in excess of

70% among sires and 71% among progeny. The greatest expected heterozygosity was found in the calves of property=1 and least in the sires of property=9, although the differences were relatively small. Allelic richness, which is the average number of alleles per locus corrected for sample size, showed greater diversity among calves than among bulls, although similar values were found within calves and within sires. There were four pairs of samples with identical multilocus genotypes across all 15 loci, two matches among progeny in property=1 and one each among progeny in property=2 (group 1) and property=9.

Table 139: Genetic diversity of sire and progeny populations

Property	Sires N	Hexp	Hobs	AR	Calves N	Hexp	Hobs	AR
1	62	0.753	0.8	6.97	230	0.769	0.7781	9.18
2 (group 1	23	0.7302	0.7478	6.29	127	0.7151	0.7228	9.03
2 (group 2)	18	0.7016	0.7444	5.8	123	0.7143	0.7305	8.92
3	74	0.7166	0.7126	6.86	224	0.7359	0.7405	9.28
9	109	0.6961	0.6869	6.1	155	0.7233	0.7246	9.41

N, sample size; Hexp, unbiased expected heterozygosity; Hobs, observed heterozygosity; AR, allelic richness (average number of alleles per locus corrected for sample size).

The level of paternity assignment by exclusion varied substantially among populations from 40% of calves assigned a sire to 90% (Table 141). Hence, there are varying, but often substantial, numbers of calves for which a sire could not be assigned by exclusion. Similarly, the number of sires with calves varied from only 38% to 83%.

Table 140: Parentage identification by exclusion

Property	Number of sires	Number of sires with calves	Percentage of sires with calves	Number of calves	No of calves matched to sire	Percent calves matched to sire
1	62	40	65%	230	121	53%
2 (group 1	23	18	78%	127	91	72%
2 (group 2)	18	15	83%	123	111	90%
3	74	54	73%	224	177	79%
9	109	41	38%	155	62	40%

The accuracy of the results of the two tested half-sib reconstruction programs was evaluated in two ways. Firstly, calves were grouped by their sire assigned by exclusion and groups containing more than one calf were considered as half-sib sire groups. It was expected that each half-sib exclusion sire group would consist of calves from a single HSGR cluster. This analysis showed only 24% to 53% of the half-sib exclusion sire

groups had a single HSGR COLONY2 cluster and this accurately placed 28% to 51% of calves in a correct half-sib grouping. Note that calves without sire assignment and those which were the only offspring of a sire were discarded prior to the analysis. For KINGROUP, values were lower with only 6% to 26% of the half-sib exclusion sire groups having a single HSGR KINGROUP cluster and this accurately placed only 4% to 29% of calves in an accurate half-sib grouping.

Table 141: Results of half-sib sire group cluster (HSGR) analysis using COLONY2

Property	Number of exclusion based sire groups[a]	No of calves[b]	No sire groups with one COLONY2 cluster[c]	Accuracy[d]	Number of calves in accurate sire groups	% calves in accurate sire groups
1	25	106	6	24%	35	33%
2 (group 1	17	90	9	53%	46	51%
2 (group 2)	14	109	6	43%	52	48%
3	34	157	11	32%	46	29%
9	15	36	4	27%	8	28%

[a] Number of half-sib groups based on exclusion-base sire

[b] Number of calves in half-sib exclusion sire group

[c] Number of half-sib sire groups with only one COLONY2 cluster for all members

[d] Accuracy is the number of exclusion based half-sib sire groups with only one COLONY2 cluster for all members as a percentage of all testable half-sib exclusion sire groups.

Table 142: Results of half-sib sire group cluster (HSGR) analysis using KINGROUP

Property	Number of exclusion based sire groups[a]	No of calves[b]	No sire groups with one KINGROUP cluster[c]	Accuracy[d]	Number of calves in accurate sire groups	% calves in accurate sire groups
1	25	106	4	16%	13	12%
2 (group 1	17	90	1	6%	4	4%
2 (group 2)	14	109	1	7%	7	6%

3	34	157	9	26%	46	29%
9	15	36	2	13%	4	11%

[a] Number of half-sib groups based on exclusion-base sire

[b] Number of calves in half-sib exclusion sire group

[c] Number of half-sib sire groups with only one KINGROUP cluster for all members

[d] Accuracy is the number of exclusion based half-sib sire groups with only one KINGROUP cluster for all members as a percentage of all testable half-sib exclusion sire groups.

Secondly, for each population, progeny were grouped into HSGR clusters of half-sibs and the number of exclusion-based sires for calves in each cluster recorded. For a proportion of the clusters, no progeny had an exclusion sire assigned and these were discarded. These could not be used to test the validity of the program as they may represent correct half-sib groups for a non-genotyped sire but this could not be verified. Accuracy of the half-sib reconstruction program was evaluated by the proportion of clusters for which all members of the cluster had the one exclusion-assigned sire. Under this assumption, accuracy of COLONY2 was low, varying from 3% to 58% of HSGR clusters. The greatest accuracy was found in the population with the highest number of calves with an assigned sire (property=2, group 2), and the lowest in the population with the least number of calves with an assigned sire (property=9). The highest accuracy of 58% of accurate clusters (property=2, group2) accounted for 59% of calves placed within an accurate half-sib cluster. For KINGROUP, the number of clusters formed for each population was similar to that calculated by COLONY2. However, the number of clusters with only one exclusion-assigned sire for all members of a cluster was extremely low (from 1 to 5 clusters) and this gave low accuracy (from 3% to 19%) and accounted for low numbers of calves in an accurate cluster (from 0.5% to 19%).

Table 143: Accuracy of HSGR clusters based on sire groups per cluster, using COLONY2

Property	No of HSGR clusters	No of HSGR clusters with no assigned sire	No of calves	No of HSGR clusters with one assigned sire	Accuracy	No of calves in accurate sire groups	% calves in accurate sire groups
1	57	9	25	7	15%	40	42%
2 (group 1	30	5	19	9	36%	41	38%
2 (group 2)	21	2	12	11	58%	66	59%
3	49	2	8	10	21%	55	25%
9	41	10	29	1	3%	4	3%

Table 144: Accuracy of HSGR clusters based on sire groups per cluster, using KINGROUP

Property	No of HSGR clusters	No of HSGR clusters with no assigned sire	No of calves	No of HSGR clusters with one assigned sire	Accuracy	No of calves in accurate sire groups	% calves in accurate sire groups
1	46	6	21	1	3%	1	0.50%
2 (group 1	30	4	10	5	19%	15	19%
2 (group 2)	21	1	1	3	15%	9	8%
3	40	2	2	1	3%	1	0.60%
9	39	7	20	1	3%	1	3%

Accuracy is the number of HSGR clusters for which there is only one assigned sire and for which that sire is assigned to all members of the cluster, calculated as a percentage of the number of HSGR clusters less the number of HSGR clusters without any exclusion based assigned sires.

The percentage of calves in accurate sire groups is calculated as the number of calves in an accurate HSGR cluster divided by (the total number of calves less the number of calves in an HSGR cluster with no assigned sire).

Table 145: Examples of accurate and inaccurate HSGR clusters

Explanation	Progeny ID	Cluster No	Exclusion assigned sire	Method	Location
Accurate clustering					
	155414	1	155307	COLONY2	prop=2 (group2)
	155435	1	155307		
	155441	1	155307		
	144543	1	155307		
	155495	1	155307		
	155507	1	155307		
	155518	1	155307		
	155520	1	155307		
Inaccurate clustering. Same COLONY2 cluster but different assigned sire					
	155422	8	155298	COLOONY2	prop=2 (group2)
	155447	8	155294		
	155467	8	155295		
Inaccurate clustering. Same KINGROUP cluster but different exclusion assigned sires					
	122550	15	122509	KINGROUP	prop=9
	122612	15	122459		
	122569	15	122456		
	122528	15	none		
	122585	15	none		
	122595	15	none		
	122642	15	none		
Inaccurate clustering. Same exclusion assigned sire but different HSGR clusters					
	149088	18	148975	COLONY2	prop=3

149006	18	148975
149155	18	148975
149195	18	148975

15.25.4 Discussion

The identification of half-siblings is difficult because there is no requisite sharing of parental alleles. However, a known or reconstructed parental genotype can be used to identify possible offspring, which, by definition, form a group of postulated half-siblings. Half-sib reconstruction methods utilise an optimality criterion to select among the possible half-sib groupings. The ability of such methods to accurately recover true half-sibling groups will be influenced by the number of progeny per parent and by the polymorphism of the microsatellite markers used.

In this study, the number of calves with assigned sires by exclusion was variable, and for some populations was as low as 40%. This likely represents inadequate sampling of the sires on these properties, either because of incomplete mustering of the bulls or because calves were sired by unknown bulls. The latter is suggested for property=9 by the high level (62%) of sampled bulls that have no calves. The alternative explanation of genotype error, which would result in exclusion of sires because of incomplete matching of alleles, is unlikely to vary among populations, and hence is an unlikely explanation for non-assigned sires. A low level of sampled sires does not greatly affect the exclusion method, as calves without sampled sires are simply not assigned a sire from amongst the pool of candidate sires (Jones et al., 2010). However, this impacted on the ability of this study to test the accuracy of half-sib reconstruction methods as it limited the amount of data for 'known' half-sib groups, particularly for property=9.

Overall, there was a generally poor performance of the half-sib reconstruction methods tested here in recovering clusters. Exclusion was used to assign sires to calves and groups of calves that had the same sire, that is groups of half-siblings, were designated as 'true' half-sibling groups. These would be expected to have members from a single reconstructed cluster, but only 6% to 53% did, depending on the population and method. Conversely, clusters of half-siblings that were reconstructed by the analysis methods would be expected to have all cluster members with the same sire assigned by exclusion, but only 3% to 58% did. Accuracy values were, in general, higher for COLONY than KINGROUP. A similar improved performance of COLONY over KINGROUP was identified in full-sibling reconstruction in bumblebees (Lepais et al., 2010). This may result from the higher power associated with simultaneous partitioning of all individuals in COLONY than the pairwise approach of KINGROUP (Jones et al., 2010).

Half-sib reconstruction methods have been successfully used with few, large groupings. In this study, for all accuracy measures except the number of KINGROUP clusters per sire group, the greatest accuracy was found for property=2 (groups 1 and 2). Interestingly, these were the two populations with the highest percentage of sires with exclusion assigned calves and which showed a bias to higher numbers of calves per sire. A study of three salmon populations with 263 to 403 individuals per population used two HSGR methods (Herbinger et al., 2006). Using randomisation trials to determine significance supported the accuracy of large kin groups (for example containing 14 to 48 individuals per cluster) but there was a discrepancy among reconstruction methods in the reconstruction of small family units and these small clusters were found to be non-significant (Herbinger et al., 2006). Sibship inference is expected to be increasingly inaccurate with a decreasing sample size, at least in part because allele frequencies are less representative when determined from a small sample size (Wang, 2004), and thus the likelihood values of the putative relationship are affected. A need for a large number of progeny for improved performance of half-sibling reconstruction methods raises concern for their use in mammals, where progeny numbers from a parent can be small even in polygamous mating systems.

A further issue in the accuracy of sibship reconstruction is the overlap in relatedness coefficients among relationship categories (Wang, 2004). Theoretical relatedness coefficients can be calculated for putative relationships, for example 0.25 for half-siblings. However, observed relatedness values for known half-sibling pairs will be distributed around this value, with the variance in the distribution, and hence power to discriminate among the relationship categories, influenced by the number and polymorphism of the marker loci (Blouin, 2003). However, unaccounted for relationships may further complicate the comparison of likelihoods for the relationship classes. In this study, an assumption that parents (both cows and bulls) are unrelated may be unwarranted, resulting in a pair of non-half-sib calves in reality being first cousins (relatedness coefficient of 0.125) although we are testing a null hypothesis of unrelated (relatedness coefficient of 0). A similar situation arises not only with domestic herd animals, but may be likely to arise with endangered animals, which tend to have small population sizes and associated high degrees of inbreeding.

While the level of accuracy of the HSGR methods tested in this study may be acceptable in some instances, these methods are insufficient for use in quantitative trait analyses in mammalian populations or with population sizes similar to those in this study Under such conditions, HSGR methods cannot be considered as a replacement for exclusion based parentage methods.

15.26 Effect of sire identity on variance in weight/growth

An attempt was made to identify sires for those animals that were enrolled in the study. Preliminary results from DNA analyses indicated variable levels of matching between properties. On some properties there were relatively few matches (fewer than 50% of enrolled animals were able to be matched to a sire) and the most

likely explanation was that there had been other sires in the paddock at mating time that were not available to have hairs collected. In contrast there were other properties where over 70% of animals were matched. A decision was made to test a sample of animals from each property (about 30 to 50 animals) against the sires that had been sampled for that property. If more than 50% of animals were able to be matched to a sire, then all remaining animal samples were tested. If fewer than 50% of animals were able to be matched to a sire then sire identification was abandoned for that property.

A total of 7 of the 11 properties met the above criteria and data from these properties were used for sire analyses.

Table 146: Summary count of number of records with sire able to be identified by property

	Property						
Summary	**1**	**2**	**3**	**5**	**6**	**7**	**11**
# calves matched	121	201	176	135	131	159	166
Total records	231	254	254	289	186	250	241
% records with sire ID'd	52%	79%	69%	47%	70%	64%	69%
# sires ID'd	41	33	54	48	29	43	30
Freq of calves per sire							
1	15	2	20	19	7	10	6
2	7	2	13	9	4	7	4
3	6	1	3	8	2	8	2
4	4	7	5	5	4	4	1
5	3	3	4	2	5	4	3
>5	5	18	9	5	7	10	14
mean	3	6.1	3.3	2.8	4.5	3.7	5.3
median	2	6	2	2	4	3	5

records with sireID & ADG

ADG_DS	107	189	162	123	127	125	158
ADG_WS	110	176	150	108	126	136	144
ADG_AN	106	181	154	115	126	141	148

The bottom three rows in the table provide a summary count of the number of records for each property that contain valid data for sireID and for each of the ADG values. These counts represent those data that can be used for estimating variance since they omit records that have sireID and no ADG.

A series of random effect models were used for these properties to estimate the contribution of sire to variance in ADG. Separate models were run for each ADG measure. Each model had no fixed effects and had a random effect entered for sireID. Variance estimates at sire and residual level were used to estimate the proportion of variance at the sire level.

Modelling was then repeated with Obs1_LWT added as a predictor.

Finally models were repeated with point weight estimates (Obs1_LWT, Obs3_LWT and Obs4_LWT) as the outcomes instead of ADG estimates.

Predicted random effects were then generated for each sire and a predicted ADG_AN for each sire. These estimates were used to calculate the effect of best and worst sires over a 400 day interval approximating ADG_AN.

Table 147: Percentage of variance in ADG_DS that was explained by sire. Derived from separate models run within each property. Each model included no fixed effects and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**26.1**	73.9	0.0034821	0.009873	0.013355
2	**2.0**	98.0	0.0002871	0.014349	0.014636
3	**16.3**	83.7	0.0002592	0.001331	0.00159

5	**4.7**	95.3	0.0004589	0.009304	0.009763
6	**10.0**	90.0	0.000756	0.006792	0.007548
7	**17.3**	82.7	0.0013089	0.006271	0.00758
11	**17.0**	83.0	0.0009663	0.004714	0.005681

Table 148: Percentage of variance in ADG_DS that was explained by sire. Derived from separate models run within each property. Each model included a fixed effect coding for Obs1_LWT and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**27.0**	73.0	0.0036061	0.009771	0.013377
2	**1.4**	98.6	0.0002012	0.01404	0.014241
3	**12.2**	87.8	0.0001747	0.001253	0.001427
5	**3.7**	96.3	0.0003263	0.008449	0.008775
6	**13.9**	86.1	0.0009259	0.00575	0.006676
7	**15.1**	84.9	0.0010244	0.005778	0.006802
11	**12.1**	87.9	0.0006259	0.004529	0.005155

Adding Obs1_LWT to models as a fixed effect has reduced the % variance at the sire level by a small amount in most models and increased it in a couple.

Table 149: Percentage of variance in ADG_WS that was explained by sire. Derived from separate models run within each property. Each model included no fixed effects and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**13.5**	86.5	0.0013183	0.008472	0.00979
2	**0.3**	99.7	0.0000151	0.004871	0.004886
3	**20.3**	79.7	0.0021388	0.008384	0.010523
5	**6.9**	93.1	0.0001777	0.002397	0.002575
6	**16.5**	83.5	0.0009426	0.004787	0.00573
7	**5.1**	94.9	0.0015069	0.027953	0.02946
11	**17.5**	82.5	0.0026394	0.012432	0.015072

Table 150: Percentage of variance in ADG_WS that was explained by sire. Derived from separate models run within each property. Each model included a fixed effect coding for Obs1_LWT and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**10.3**	89.7	0.0007619	0.006655	0.007417
2	**0.0**	100.0	1.56E-10	0.004844	0.004844
3	**22.3**	77.7	0.0021537	0.007512	0.009665
5	**0.0**	100.0	5.81E-16	0.014622	0.014622
6	**17.3**	82.7	0.0009983	0.004766	0.005765
7	**0.3**	99.7	0.0000894	0.026563	0.026653
11	**14.9**	85.1	0.0020774	0.011824	0.013901

Adding Obs1_LWT to models as a fixed effect has reduced the % variance at the sire level by a small amount in most models and increased it in some properties.

Table 151: Percentage of variance in ADG_AN explained by sire. Derived from separate models run within each property. Each model included no fixed effects and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**11.1**	88.9	0.0004744	0.003781	0.004255
2	**6.8**	93.2	0.0002173	0.00298	0.003197
3	**14.5**	85.5	0.0002701	0.001594	0.001864
5	**18.4**	81.6	0.0005372	0.002381	0.002918
6	**8.4**	91.6	0.0003165	0.003456	0.003773
7	**0.0**	100.0	6.85E-18	0.011142	0.011142
11	**6.9**	93.1	0.0003955	0.005309	0.005704

Table 152: Percentage of variance in ADG_AN explained by sire. Each model included a fixed effect coding for Obs1_LWT and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**7.5**	92.5	0.0002789	0.003461	0.00374
2	**6.7**	93.3	0.0002144	0.002998	0.003212
3	**14.3**	85.7	0.0002689	0.001606	0.001875
5	**18.0**	82.0	0.0005318	0.00243	0.002962
6	**13.0**	87.0	0.0004507	0.003028	0.003479
7	**0.0**	100.0	3.2E-23	0.010467	0.010467
11	**5.5**	94.5	0.0003092	0.005263	0.005572

Adding Obs1_LWT to models as a fixed effect has reduced the % variance at the sire level by a small amount in most models and increased it in some properties.

Table 153: Predicted ADG for best and worst sires using data from one property and for ADG_AN.

Sire	Fitted_ADG_AN	total LWT diff (400d)
Single worst	0.215979	
Single best	0.250887	
Diff	0.034908	14.0
Worst 10%	0.218019	
Best 10%	0.245604	
Diff	0.027585	11.0

Taking the predicted ADG_AN value for the single best and worst sires (incorporating both fixed and random effects) and the best and worst 10% of sires, and applying that predicted ADG over a 400 day growth period, produces an estimate of the overall weight difference in kg between progeny of these sires.

Table 154: Percentage of variance in Obs1_LWT that was explained by sire. Derived from separate models run within each property. Each model included no fixed effects and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**29.5**	70.5	840.3646	2004.425	2844.79
2	**3.0**	97.0	48.94328	1602.67	1651.613
3	**0.0**	100.0	1.12E-13	352.4853	352.4853
5	**8.4**	91.6	113.3927	1235.67	1349.063
6	**5.5**	94.5	74.29051	1283.106	1357.397
7	**11.4**	88.6	73.98781	576.5379	650.5257
11	**7.8**	92.2	95.88958	1127.003	1222.893

Table 155: Percentage of variance in Obs3_LWT that was explained by sire. Derived from separate models run within each property. Each model included no fixed effects and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**23.3**	76.7	757.8659	2494.357	3252.223
2	**2.2**	97.8	37.51879	1638.094	1675.613
3	**0.0**	100.0	1.85E-13	347.6225	347.6225
5	**8.9**	91.1	109.4006	1117.233	1226.634
6	**9.7**	90.3	115.053	1072.73	1187.783
7	**0.0**	100.0	9.34E-22	545.9197	545.9197
11	**2.6**	97.4	29.14185	1072.891	1102.033

Table 156: Percentage of variance in Obs4_LWT that was explained by sire. Derived from separate models run within each property. Each model included no fixed effects and a random effect coding for sire

Property	% Variance explained by		Variance estimates		
	Sire	Unexplained	Sire	Residual	Total
1	**20.7**	79.3	543.7083	2086.139	2629.847
2	**0.9**	99.1	18.50746	1951.749	1970.256
3	**2.9**	97.1	19.19915	644.6371	663.8363
5	**8.9**	91.1	145.2547	1482.308	1627.563
6	**11.8**	88.2	156.7235	1172.595	1329.319
7	**0.0**	100.0	0.00561	1272.047	1272.053
11	**14.1**	85.9	307.8668	1880.074	2187.941

Three historical datasets were analysed prior to this study being completed: one from the beef CRC and two from beef properties in northern Australia (CE=commercial enterprise and RS=research property). The following table provides summary statistics from the three datasets to provide some comparison with the datasets from the longitudinal study.

Table 157: Summary data from three retrospective datasets.

	CRC data			Prop_RS		Prop_CE	
Summary	**Wean wt**	**400d LWT**	**ADG**	**Wean wt**	**ADG**	**Wean wt**	**ADG**
# calves matched	5427	1551	1553	2219	1439	1373	1196
Total records	5625	1607	1609	2219	1439	1373	1196
% with sire ID'd	96%	97%	97%	100%	100%	100%	100%
# sires ID'd	213	191	191	147	135	74	73
Freq of calves per sire							
1	3	4	4	23	21	11	10
2	1	9	9	20	18	6	7
3	0	20	20	16	14	1	1
4	0	18	18	13	13	3	3
5	4	27	27	5	7	3	4
>5	205	113	113	70	62	50	48
mean	25.5	8.1	8.1	15.1	10.7	18.6	16.4
median	21	7	7	5	5	12	11
Mean age	201	398		196		192	
Min	52	316		81		60	
Max	334	490		285		399	
Days post weaning							

mean	471	190	339
min	316	99	103
max	500	336	593

Analyses conducted on the historical industry datasets has been described in an earlier section of this report. There are important distinctions when comparing the findings to those reported from the longitudinal study. The first is that there were many more animal records and also more sires with multiple progeny. In addition the industry datasets included measurements of additional factors that could be fitted as fixed effects in the analyses, accounting for more of the variance and in all likelihood producing more accurate estimates of the contribution of sires to variance in weight and growth outcomes. The following table provides summaries of the variance contribution from sire in a form that allows more direct comparison with the other outputs in this section. The results are taken directly from tables already described in the earlier section.

Table 158: Estimates of the % variance explained by sire in CRC, DDRF and Commercial Enterprise (CE) property datasets

Property	% of Total variance explained by model	% of Total variance at sire level	% of unexplained variance at sire level
CRC Wean wt			
Intercept only	**0.0%**	42.1%	42.1%
Full model*	**70.2%**	4.4%	14.9%
* weanage, sex, breed, season, birthyr, herd			
CRC Body weight at ~400days			

Intercept only	**0.0%**	38.9%	38.9%
Full model*	78.6%	3.2%	15.0%
* wean wt, sex, breed, hgp, birth yr, year, herd			
CRC ADG Wean to 500d pw			
Intercept only	**0.0%**	44.2%	44.2%
Full model*	62.0%	5.0%	13.3%
* weant wt, sex, breed, hgp, birth yr, herd			
DDRF Wean wt			
Intercept only	**0.0%**	41.4%	41.4%
Full model*	67.4%	2.6%	7.9%
* wean age, sex, birth yr, wean season			
DDRF ADG wean to 400d			
Intercept only	**0.0%**	47.2%	47.2%
Full model*	69.8%	1.5%	5.1%
* weanwt, sex, birth yr, season			
CE Wean wt			
Intercept only	**0.0%**	30.9%	30.9%
Full model*	61.1%	9.3%	23.8%
* wean age, sex, birth yr, wean season			
CE ADG wean to 500d			
Intercept only	**0.0%**	61.5%	61.5%
Full model*	46.4%	21.4%	39.9%
* sex, birth yr, season			

15.27 Liver function tests

Liver function tests were classified by the analysing laboratory as being normal, lower than normal or higher than normal. There were occasional individual animals that had results for one or more parameters that were either lower than normal or higher than normal. None of the animals were identified on visual inspection as being abnormal in appearance of behaviour and there was no suspicion that individual animals might have been suffering from some disease or that they may have had abnormal liver function.

There are probably two broad explanations for variability in these test results. In a population of animals it is expected that some animals will have variable results for any one test, without necessarily having liver pathology (the range of normal values). This is considered likely to be the major explanation for occasional values that may be higher or lower than a pre-defined normal range. It is not clear what the parameters were to define the normal range in this case and if the normal range were based on a 90% or 95% confidence limit (or some similar sort of approach) then we can expect 5 or 10% of normal animals to have values outside the normal range. The other potentially likely explanation is that at any given point in time, some animals may be suffering from a temporary or chronic insult to normal liver function such that test results might be abnormal. Such results may be secondary to infection, parasites or poisons. There was little evidence that there was any major difference between the two ADG classes (high vs low) in probability of having an abnormal test result.

Table 159: Count of number of samples from each of four properties and from each of two ADG_AN categories (high and low) and results for live function tests. Results were classified by the analysing laboratory as lower than normal (<Normal), normal or higher than normal (>Normal).

			High ADG_AN			Low ADG_AN			
			Test classification			Test classification			
Property	N	Parameter	<Normal	Normal	>Normal	N	<Normal	Normal	>Normal
1	9	Total bilirubin	0	9	0	8	0	8	0
2	5	Total bilirubin	0	5	0	5	0	5	0
3	4	Total bilirubin	0	4	0	5	0	4	1
5	6	Total bilirubin	0	6	0	4	0	4	0
1	9	Aspartate aminotransferase	0	9	0	8	0	8	0
2	5	Aspartate aminotransferase	1	4	0	5	2	3	0
3	4	Aspartate aminotransferase	1	3	0	5	0	5	0
5	6	Aspartate aminotransferase	2	4	0	4	2	2	0
1	9	Alkaline phosphatase	0	7	2	8	0	7	1
2	5	Alkaline phosphatase	0	5	0	5	0	5	0
3	4	Alkaline phosphatase	0	4	0	5	0	5	0
5	6	Alkaline phosphatase	0	6	0	4	0	4	0
1	9	Gamma glutamyltransferase	0	9	0	8	1	7	0
2	5	Gamma glutamyltransferase	0	4	1	5	0	5	0
3	4	Gamma glutamyltransferase	0	4	0	5	1	4	0
5	6	Gamma glutamyltransferase	0	6	0	4	0	4	0
1	9	Total protein	0	8	0	8	0	7	1

2	5	Total protein	0	3	2	5	0	4	1
3	4	Total protein	0	4	0	5	0	3	2
5	6	Total protein	0	6	0	4	0	3	1
1	9	Albumin	0	1	7	8	0	1	7
2	5	Albumin	0	0	5	5	0	2	3
3	4	Albumin	0	3	1	5	0	2	3
5	6	Albumin	0	0	6	4	0	0	4
1	9	Globulin	0	8	0	8	0	8	0
2	5	Globulin	0	5	0	5	0	4	1
3	4	Globulin	0	4	0	5	0	4	1
5	6	Globulin	0	6	0	4	0	4	0

A series of t-tests were used to compare values between each of the two classes of ADG_AN (low vs high) and box plots were used to show the range of values for individual animals in each of the classes of ADG_AN.

There was a difference in globulin concentration between ADG_AN=low and ADG_AN=high. Animals in the low class for ADG_AN had a higher globulin concentration (mean= 41.05, se=1.42) compared to animals in the high class for ADG_AN (mean=37.63, se=0.86; p=0.041). It is not clear why this apparent difference might have been present.

There were no differences between ADG_AN=low and ADG_AN=high for any of the other outcomes that were tested (p>0.05).

15.28 Use of faecal NIRS to study diet selection

The following tables provide summary statistics for all 11 properties based on the top and bottom 40 records for different outcomes and the average across all available records for each outcome.

15.28.1 Descriptive summaries

Table 160: Summary statistics for ADG_DS for all 11 properties. N=total animals enrolled from each property, n=number of animals in each property with valid measurements for the outcome in this table, sd=standard deviation.

			ADG_DS_ALL		ADG_DS_Top40		ADG_DS_Bottom 40		Ratio	
prop_n	N	n	mean	sd	mean	sd	mean	sd	top to mean	top to bottom
1	231	202	0.290	0.108	0.439	0.031	0.133	0.053	1.5	3.3
2	254	236	0.056	0.118	0.226	0.050	-0.122	0.062	4.0	3.9
3	224	207	0.053	0.039	0.106	0.019	-0.003	0.023	2.0	35.8
4	289	177	-0.042	0.079	0.061	0.047	-0.147	0.040	3.5	2.4
5	250	225	-0.057	0.106	0.097	0.076	-0.210	0.057	3.7	2.5
6	186	182	0.174	0.084	0.279	0.039	0.057	0.050	1.6	4.9
7	250	201	0.097	0.081	0.209	0.027	-0.017	0.037	2.1	14.5
8	207	177	0.196	0.078	0.298	0.037	0.092	0.042	1.5	3.2
9	155	133	-0.086	0.072	-0.006	0.029	-0.169	0.053	1.9	2.0
10	239	207	0.082	0.077	0.174	0.036	-0.032	0.073	2.1	7.5
11	241	228	0.019	0.076	0.127	0.044	-0.094	0.047	6.6	3.4
Total	2526	2175	0.073	0.137						

Table 161: Summary statistics for ADG_AN for all 11 properties. N=total animals enrolled from each property, n=number of animals in each property with valid measurements for the outcome in this table, sd=standard deviation.

			ADG_AN_ALL		ADG_AN_Top40		ADG_AN_Bottom		Ratio	

							40			
prop_n	N	n	mean	sd	mean	sd	mean	sd	top to mean	top to bottom
1	231	192	0.389	0.066	0.470	0.022	0.293	0.047	1.2	1.6
2	254	226	0.200	0.056	0.285	0.025	0.120	0.031	1.4	2.4
3	224	194	0.180	0.045	0.243	0.019	0.120	0.021	1.3	2.0
4	289									
5	250	215	0.260	0.055	0.342	0.029	0.179	0.023	1.3	1.9
6	186	178	0.232	0.060	0.312	0.029	0.152	0.028	1.3	2.1
7	250	223	0.301	0.105	0.456	0.042	0.152	0.037	1.5	3.0
8	207	185	0.355	0.059	0.427	0.025	0.273	0.045	1.2	1.6
9	155	86	0.247	0.056	0.293	0.030	0.200	0.038	1.2	1.5
10	239	107	0.331	0.060	0.389	0.034	0.270	0.035	1.2	1.4
11	241	212	0.253	0.075	0.370	0.045	0.155	0.027	1.5	2.4
Total	2526	1818	0.272	0.093						

Table 162: Summary statistics for ADG_WS for all 11 properties. N=total animals enrolled from each property, n=number of animals in each property with valid measurements for the outcome in this table, sd=standard deviation.

			ADG_WS_ALL		ADG_WS_Top40		ADG_WS_Bottom 40		Ratio	
prop_n	N	n	mean	sd	mean	sd	mean	sd	top to mean	top to bottom
1	231	201	0.443	0.100	0.584	0.050	0.301	0.044	1.3	1.9
2	254	220	0.283	0.071	0.383	0.046	0.181	0.031	1.4	2.1
3	224	191	0.456	0.103	0.599	0.051	0.318	0.043	1.3	1.9
4	289									
5	250	202	0.545	0.113	0.699	0.041	0.383	0.065	1.3	1.8

6	186	178	0.286	0.075	0.386	0.038	0.191	0.039	1.4	2.0
7	250	214	0.455	0.170	0.708	0.066	0.220	0.047	1.6	3.2
8	207	173	0.484	0.075	0.581	0.059	0.397	0.038	1.2	1.5
9	155	82	0.506	0.097	0.582	0.061	0.430	0.062	1.2	1.4
10	239	88	0.554	0.076	0.619	0.038	0.488	0.052	1.1	1.3
11	241	206	0.405	0.118	0.594	0.078	0.259	0.044	1.5	2.3
Total	2526	1755	0.430	0.139						

Table 163: Summary statistics for Obs1_LWT for all 11 properties. N=total animals enrolled from each property, n=number of animals in each property with valid measurements for the outcome in this table, sd=standard deviation.

			Obs1_LWT all samples		Obs1_LWT Top40		Obs1_LWT Bottom40		Ratio	
prop_n	N	n	mean	sd	mean	sd	mean	sd	top to mean	top to bottom
1	231	208	214.4	51.2	285.6	10.7	143.3	16.0	1.3	2.0
2	254	252	211.3	43.8	280.6	23.5	144.0	16.9	1.3	1.9
3	224	221	133.2	19.9	162.8	11.6	105.0	7.6	1.2	1.6
4	289	283	159.9	29.4	208.1	12.5	116.5	8.2	1.3	1.8
5	250	248	213.0	35.9	267.4	14.9	158.8	11.6	1.3	1.7
6	186	184	224.5	35.4	268.9	13.2	173.6	17.4	1.2	1.5
7	250	218	180.8	26.1	217.4	15.1	143.7	13.0	1.2	1.5
8	207	205	171.5	39.0	234.3	35.1	130.1	12.1	1.4	1.8
9	155	148	161.1	39.7	211.8	40.1	124.9	9.5	1.3	1.7
10	239	237	217.5	30.1	261.3	15.5	172.1	11.6	1.2	1.5
11	241	239	177.0	35.7	229.2	14.4	121.8	19.0	1.3	1.9
Total	2526	2443	187.9	45.6						

Table 164: Summary statistics for Obs3_LWT for all 11 properties. N=total animals enrolled from each property, n=number of animals in each property with valid measurements for the outcome in this table, sd=standard deviation.

			Obs_LWT All samples		Obs3_LWT Top40		Obs3_LWT Bottom40		Ratio	
prop_n	N	n	mean	sd	mean	sd	mean	sd	top to mean	top to bottom
1	231	207	260.0	53.1	330.9	14.5	182.2	17.4	1.3	1.8
2	254	237	218.3	44.0	285.5	24.1	152.9	17.8	1.3	1.9
3	224	207	148.3	20.9	178.3	11.7	118.9	9.7	1.2	1.5
4	289	177	162.5	24.8	196.5	15.6	131.5	9.3	1.2	1.5
5	250	223	204.9	33.2	253.2	16.4	157.6	13.8	1.2	1.6
6	186	182	252.5	32.8	295.2	13.5	207.1	17.9	1.2	1.4
7	250	196	191.9	24.7	227.0	15.4	159.1	10.6	1.2	1.4
8	207	178	202.0	42.3	265.4	38.2	160.3	14.1	1.3	1.7
9	155	134	150.7	35.5	192.4	36.5	120.6	8.8	1.3	1.6
10	239	207	231.9	28.9	273.4	14.3	191.7	12.2	1.2	1.4
11	241	227	179.9	33.3	227.1	11.7	129.2	17.5	1.3	1.8
Total	2526	2175	202.0	50.1						

Table 165: Summary statistics for Obs4_LWT for all 11 properties. N=total animals enrolled from each property, n=number of animals in each property with valid measurements for the outcome in this table, sd=standard deviation.

			Obs4_LWT All samples		Obs4_LWT Top40		Obs4_LWT Bottom40		Ratio	
prop_n	N	n	mean	sd	mean	sd	mean	sd	top to mean	top to bottom
1	231	196	386.5	48.0	451.4	21.7	317.6	21.2	1.2	1.4
2	254	227	278.1	45.9	347.4	26.0	212.5	17.7	1.2	1.6
3	224	194	207.1	28.2	245.8	16.3	168.5	13.6	1.2	1.5

4	289									
5	250	211	286.5	38.6	343.4	15.9	231.1	14.7	1.2	1.5
6	186	179	300.5	34.1	345.7	14.6	255.5	18.4	1.2	1.4
7	250	221	265.8	36.8	318.8	18.3	212.7	15.2	1.2	1.5
8	207	186	301.3	45.7	368.2	39.8	249.1	17.6	1.2	1.5
9	155	85	244.9	41.7	277.9	36.4	213.0	15.7	1.1	1.3
10	239	107	334.7	23.3	357.4	14.7	311.8	13.6	1.1	1.1
11	241	209	261.6	45.6	328.4	23.4	197.6	22.5	1.3	1.7
Total	2526	1815	286.2	61.3						

There were concerns that even where there was no association between faecal NIRS outcomes and the category for annual growth rate (ADG_AN), there potentially might be associations with other weight or growth outcomes such as individual observation weights or ADG_DS and ADG_WS.

The faecal samples sent for analysis had all been selected based on the individual animal rankings within each property for ADG_AN.

The rankings for ADG_AN were not necessarily the same as the rankings within any one property for other weight-based outcomes such as Obs1_LWT or ADG_DS etc.

In a separate process and using the entire dataset, a series of variables were created to code for quartiles of various weight outcomes within each property. These are defined for one property below for illustrative purposes.

For property=3:

- Obs3_LWT_rank for property=3
    - 1= quartile 1 for Obs3_LWT (lowest 25%), assessed only against all Obs3_LWT measurements in property=3
    - 2=quartile 2 for Obs3_LWT (the second 25%)
    - 3=quartile 3

    - 4=quartile 4 (highest 25%)
- Obs4_LWT _rank for property=3
    - 1 to 4 as above
- ADG_DS_rank for property=3
    - 1 to 4 as above
- ADG_WS_rank for property=3
    - 1 to 4 as above

Then a matching process based on individual animal ID code was used to determine the ranking for each of these weight measurements for all animals in the NIRS dataset.

It was expected that, while animals in the NIRS dataset had been selected only from the lowest and highest values for ADG_AN, the selected animals would probably contain some animals from each quartile for each of the other weight measurements. Although not shown, the sample sizes in each of the upper and lower quartiles for other outcomes generally ranged from between 10 to 25 observations for each.

15.28.2 Faecal Nitrogen %

Mean Faecal N% estimates were generated for each level of ADG ranking (high and low) for ADG_AN, ADG_DS, ADG_WS and compared using t-tests. Results for comparisons performed on ADG_AN were presented in Section 5.3 of the main report. Results for other ADG outcomes (ADG_DS and ADG_WS) are presented here.

Table 166:Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP and ADG_DS rank. Data from property=1 and Obs3.

Faecal N%		ADG_DS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	1.49	0.04	1.42	1.55
		4	1.32	0.05	1.21	1.42
	HGP=YES	1	1.3	0.04	1.21	1.38
		4	1.27	0.04	1.19	1.35
	HGP=NO	ave over both	1.42	0.03	1.36	1.47
	HGP=YES	ave over both	1.29	0.03	1.23	1.35
	ave over both	rank=1	1.39	0.03	1.34	1.45
	ave over both	rank=4	1.29	0.03	1.23	1.36

Comparisons	**Other factor**	**p-value**
ADG_DS=1 vs ADG_DS=4	Averaged over both levels of HGP	0.01
HGP=no vs HGP=yes	Averaged over both levels of ADG_DS	0.001
Interaction (HGP*ADG_DS)		0.1

There was no effect of the interaction term, indicating that the effect of HGP was not modified by the effect of ADG_DS_rank (and vice versa).

There were significant main effects.

Animals retaining HGP had significantly lower faecal N% (1.29) compared with animals that did not retain HGP (1.42, p=0.001).

Animals in the lowest quartile for ADG_DS had a higher faecal N% (1.39) compared with animals in the highest quartile for ADG_DS (1.29, p=0.01).

Table 167: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Faecal Nitrogen (%). Data from property=2, 3, 4, 5 & 7 and Obs=2 & 3. Within each observation and property, t-tests were used to compare mean Faecal Nitrogen % between ADG_DS rank, and p-values are reported in the last column.

Faecal N%		ADG_DS			
Property	Obs	rank	Mean	se	p-value
2	2	1	1.32	0.03	
		4	1.32	0.02	0.9
	3	1	1.06	0.02	
		4	1.03	0.02	0.3
3	2	1	1.19	0.08	
		4	1.11	0.03	0.4
	3	1	1.7	0.03	
		4	1.7	0.03	0.5
4	2	1	1.14	0.02	
		4	1.12	0.02	0.5
	3	1	1.26	0.02	
		4	1.27	0.02	0.7
5	2	1	1.41	0.09	
		4	1.28	0.04	0.2
	3	1	1.16	0.03	
		4	1.14	0.04	0.8
7	2	1	1.001	0.03	
		4	1.04	0.04	0.4
	3	1	2.11	0.09	
		4	2.14	0.09	0.8

Table 168: Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs3.

Faecal N%		ADG_WS			95% CI	
Property	Obs=3	rank	Mean	se	lower	upper
1	HGP=NO	1	1.41	0.03	1.34	1.47
		4	1.38	0.04	1.3	1.45
	HGP=YES	1	1.28	0.04	1.2	1.35
		4	1.37	0.04	1.29	1.46
	HGP=NO	ave over both	1.39	0.02	1.34	1.44
	HGP=YES	ave over both	1.32	0.03	1.26	1.37
	ave over both	rank=1	1.35	0.02	1.3	1.4
	ave over both	rank=4	1.37	0.03	1.32	1.43

Comparisons	Other factor	p-value
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.6
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.013
Interaction (HGP*ADG_WS)		0.11

There was no effect of the interaction term, indicating that the effect of HGP was not modified by the effect of ADG_WS_rank (and vice versa).

There were significant main effects.

Animals retaining HGP had significantly lower faecal N% (1.32) compared with animals that did not retain HGP (1.39, p=0.013).

There was no difference between quartiles for ADG_WS_rank. Animals in the lowest quartile for ADG_WS had similar faecal N% (1.35) compared with animals in the highest quartile for ADG_DS (1.37, p=0.6).

Table 169: Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs4.

Faecal N%		ADG_WS			95% CI	
Property	Obs=4	rank	Mean	se	lower	upper
1	HGP=NO	1	1.01	0.03	0.94	1.07
		4	1.17	0.04	1.09	1.25
	HGP=YES	1	1	0.04	0.91	1.09
		4	1.12	0.05	1.01	1.22
	HGP=NO	ave over both	1.07	0.03	1.02	1.12
	HGP=YES	ave over both	1.04	0.03	0.98	1.11
	ave over both	rank=1	1.01	0.03	0.95	1.06
	ave over both	rank=4	1.15	0.03	1.08	1.22

Comparisons	Other factor	p-value
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.004
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.9
Interaction (HGP*ADG_WS)		0.6

There was no effect of the interaction term, indicating that the effect of HGP was not modified by the effect of ADG_WS_rank (and vice versa).

There were significant main effects.

Animals retaining HGP were not different to animals that did not retain HGP (p=0.9).

There was a difference between quartiles for ADG_WS_rank. Animals in the lowest quartile for ADG_WS had a lower faecal N% (1.01) compared with animals in the highest quartile for ADG_DS (1.15, p=0.004).

Table 170: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Faecal Nitrogen (%). Data from property=2, 3, 5 & 7 and Obs=3 & 4. Within each observation and property, t-tests were used to compare mean Faecal Nitrogen % between ADG_WS rank, and p-values are reported in the last column.

Faecal N%		ADG_WS			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	3	1	1.05	0.02	
		4	1.05	0.02	0.8
	4	1	1.44	0.07	
		4	1.4	0.04	0.3
3	3	1	1.73	0.03	
		4	1.64	0.04	0.07
	4	1	1.24	0.03	
		4	1.18	0.03	0.14
5	3	1	1.15	0.03	
		4	1.13	0.02	0.7
	4	1	1.61	0.05	
		4	1.56	0.05	0.5
7	3	1	2.13	0.06	
		4	2.14	0.08	0.9
	4	1	2.12	0.06	
		4	2.14	0.06	0.7

Table 171: Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP and Obs3_LWT. Data from property=1 and Obs3.

Faecal N%		Obs3_LWT			95% CI	
Property	Obs=3	rank	Mean	se	lower	upper
1	HGP=NO	1	1.45	0.04	1.37	1.53
		4	1.41	0.05	1.32	1.5
	HGP=YES	1	1.36	0.05	1.26	1.45
		4	1.29	0.04	1.2	1.37
	HGP=NO	ave over both	1.43	0.03	1.37	1.49
	HGP=YES	ave over both	1.32	0.03	1.26	1.38
	ave over both	rank=1	1.41	0.03	1.34	1.47
	ave over both	rank=4	1.35	0.03	1.29	1.41

Comparisons	Other factor	p-value
Obs3_LWT=1 vs Obs3_LWT=4	Averaged over both levels of HGP	0.12
HGP=no vs HGP=yes	Averaged over both levels of Obs3_LWT	0.5
Interaction (HGP*Obs3_LWT)		0.8

There was no effect of the interaction term, indicating that the effect of HGP was not modified by the effect of Obs3_wt_rank (and vice versa).

There were no significant main effects.

Table 172: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Faecal Nitrogen (%). Data from property=2, 3, 4, 5 & 7 and Obs=3. Within each observation and property, t-tests were used to compare mean

Faecal Nitrogen % between Obs3_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Faecal N%		Obs3_LWT			
Property	Obs	rank	Mean	se	p-value
2	3	1	2.13	0.06	
		4	2.14	0.08	0.9
3	3	1	1.72	0.04	
		4	1.66	0.05	0.04
4	3	1	1.29	0.03	
		4	1.25	0.02	0.35
5	3	1	1.13	0.03	
		4	1.11	0.03	0.6
7	3	1	2.09	0.08	
		4	2.01	0.12	0.5

Table 173: Summary statistics for Faecal Nitrogen% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing FecN% between groups based on HGP and Obs4_LWT. Data from property=1 and Obs4.

Faecal N%		Obs4_LWT			95% CI	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	1.1	0.05	0.99	1.2
		4	1.12	0.07	0.98	1.25
	HGP=YES	1	1.07	0.05	0.97	1.18
		4	1.12	0.05	1.01	1.22
	HGP=NO	ave over both	1.11	0.04	1.03	1.19
	HGP=YES	ave over both	1.09	0.04	1.02	1.17
	ave over both	rank=1	1.09	0.04	1.01	1.16
	ave over both	rank=4	1.12	0.04	1.03	1.2

Comparisons	**Other factor**	**p-value**
Obs4_LWT=1 vs Obs4_LWT=4	Averaged over both levels of HGP	0.8
HGP=no vs HGP=yes	Averaged over both levels of Obs4_LWT	0.7
Interaction (HGP*Obs4_LWT)		0.8

Table 174: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Faecal Nitrogen (%). Data from property=2, 3, 5 & 7 and Obs=4. Within each observation and property, t-tests were used to compare mean Faecal Nitrogen % between Obs4_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Faecal N%		Obs4_LWT			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	4	1	2.12	0.06	
		4	2.14	0.06	0.7

3	4	1	1.25	0.03	
		4	1.19	0.03	0.14
5	4	1	1.72	0.07	
		4	1.46	0.04	0.0016
7	4	1	2.16	0.07	
		4	2.11	0.06	0.6

15.28.3 Dietary Crude Protein %

A series of comparisons were performed to determine whether the highest vs lowest quartile for various weight measurements was associated with a difference in mean diet CP%.

Comparing lowest and highest quartiles of ADG_DS:

- Property = 1
    - no effect of ADG_DS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_DS_rank.

- Property= 2
    - Animals in the lowest rank for ADG_DS at Obs2 (quartile=1) had a lower diet CP% (mean=4.12, se=0.12) compared with animals in the highest quartile (quartile=4; mean=4.62, sem=0.12, p=0.005)
- There were no other significant differences between lowest and highest quartiles of ADG_DS_rank at either Obs2 or 3 for properties 2, 3, 4, 5 & 7.

Comparing lowest and highest quartiles of ADG_WS:

- Property = 1, Obs3
    - no effect of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property = 1, Obs4
    - no effect of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property= 2, 3, 4, 5, 7 & Obs3 & Obs4
    - No effect of ADG_WS_rank on diet CP%.

Comparing lowest and highest quartiles of Obs3_wt:

- Property = 1, Obs3
    - no effect of Obs3wt_rank and no effect of HGP retention status or of the interaction between HGP retention and Obs3wt_rank.
- Property= 2, Obs3
    - Animals in the lowest quartile for Obs3_wt (quartile =1) had a lower mean diet CP% (mean=3.6, se=0.08) compared with animals in the highest quartile (q=4; mean=3.9, se=0.09, p=0.02).
- Property= 3, 4, 5, 7 & Obs3
    - No effect of Obs3_wt_rank on diet CP%.

Comparing lowest and highest quartiles of Obs4_wt:

- Property = 1, Obs4
    - There was a significant interaction between Obs4wt_rank and HGP retention status.
        - For those animals in Obs4wt_rank=1, there was no difference between HGP groups in mean diet CP% (p=0.08).
        - For those animals in Obs4wt_rank=4, HGP=no animals had a higher diet CP% (mean=6.6, se=0.38) compared with HGP=yes animals (4.88, se=0.29, p=0.001).

  - For those animals in HGP=NO, animals with Obs4wt_rank=1 had a lower mean diet CP% (5.53, se=0.29) compared with animals with Obs4wt_rank=4 (mean=6.6, se=0.38, p=0.03).
  - For those animals in HGP=YES, animals with Obs4wt_rank=1 had a higher mean diet CP% (6.29, se=0.3) compared with animals with Obs4wt_rank=4 (mean=4.88, se=0.29, p=0.002).
- Property= 5, Obs4
  - Animals in the lowest quartile for Obs4_wt (quartile =1) had a higher mean diet CP% (mean=6.89, se=0.23) compared with animals in the highest quartile (q=4; mean=6.33, se=0.13, p=0.034).
- Property= 2, 3, 4, 7 & Obs4
  - No effect of Obs4_wt_rank on diet CP%.

Table 175: Summary statistics for Dietary Crude Protein (CP%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing CP% between groups based on HGP and ADG_DS rank. Data from property=1 and Obs3.

Diet CP%		ADG_DS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	8.37	0.26	7.86	8.87
		4	7.61	0.39	6.84	8.37
	HGP=YES	1	7.99	0.32	7.37	8.62
		4	7.78	0.31	7.18	8.38
	HGP=NO	ave over both	8.05	0.22	7.62	8.49
	HGP=YES	ave over both	7.9	0.23	7.46	8.35
	ave over both	rank=1	8.18	0.2	7.78	8.58
	ave over both	rank=4	7.69	0.25	7.2	8.18

Comparisons	**Other factor**	**p-value**
ADG_DS=1 vs ADG_DS=4	Averaged over both levels of HGP	0.11
HGP=no vs HGP=yes	Averaged over both levels of ADG_DS	0.37
Interaction (HGP*ADG_DS)		0.4

Table 176: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dietary Crude Protein %. Data from property=2, 3, 4, 5 & 7 and Obs= 2 & 3. Within each observation and property, t-tests were used to compare mean CP% between ADG_DS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Diet CP% Property	Obs	ADG_DS rank	Mean	se	p-value
2	2	1	4.12	0.12	
		4	4.62	0.12	0.005
	3	1	3.73	0.11	
		4	3.9	0.09	0.23
3	2	1	5.33	0.35	
		4	5.27	0.18	0.9
	3	1	10.44	0.27	
		4	10.79	0.16	0.31
4	2	1	6.13	0.17	
		4	6.37	0.17	0.33
	3	1	6.97	0.12	
		4	7.08	0.11	0.5
5	2	1	6.73	0.4	
		4	6.39	0.15	0.4
	3	1	4.57	0.19	
		4	4.75	0.14	0.43
7	2	1	4.59	0.17	
		4	4.95	0.21	0.2
	3	1	10.43	0.34	
		4	11.19	0.34	0.12

Table 177: Summary statistics for Dietary Crude Protein (CP%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing CP% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs3.

Diet CP%		ADG_WS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	8	0.19	7.8	8.55
		4	8.42	0.3	7.84	9
	HGP=YES	1	7.7	0.3	7.11	8.28
		4	8.26	0.34	7.61	8.92
	HGP=NO	ave over both	8.18	0.19	7.8	8.55
	HGP=YES	ave over both	7.94	0.22	7.5	8.37
	ave over both	rank=1	7.87	0.19	7.49	8.24
	ave over both	rank=4	8.35	0.22	7.92	8.79

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.28
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.44
Interaction (HGP*ADG_WS)		0.8

Table 178: Summary statistics for Dietary Crude Protein (CP%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing CP% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs4.

Diet CP%		ADG_WS			95% CI	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	5.61	0.21	5.2	6.01

	4	6.16	0.28	5.62	6.7
HGP=YES	1	5.41	0.29	4.85	5.97
	4	5.8	0.35	5.11	6.49
HGP=NO	ave over both	5.81	0.17	5.49	6.14
HGP=YES	ave over both	5.55	0.22	5.12	5.99
ave over both	rank=1	5.54	0.17	5.21	5.87
ave over both	rank=4	6.03	0.22	5.6	6.46

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.12
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.58
Interaction (HGP*ADG_WS)		0.8

Table 179: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dietary Crude Protein %. Data from property=2, 3, 5 & 7 and Obs= 3 & 4. Within each observation and property, t-tests were used to compare mean CP% between ADG_WS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Diet CP%		ADG_WS			
Property	Obs	rank	Mean	se	p-value
2	3	1	3.69	0.07	
		4	3.88	0.11	0.15
	4	1	5.16	0.27	
		4	5.1	0.11	0.8
3	3	1	10.64	0.25	
		4	10.33	0.26	0.4
	4	1	5.27	0.17	
		4	5	0.18	0.3
5	3	1	4.51	0.16	
		4	4.65	0.15	0.5
	4	1	6.86	0.14	
		4	6.57	0.17	0.2
7	3	1	10.52	0.2	
		4	11.11	0.4	0.2
	4	1	8.36	0.3	
		4	8.84	0.29	0.25

Table 180: Summary statistics for Dietary Crude Protein (CP%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing CP% between groups based on HGP and Obs3_LWT rank. Data from property=1 and Obs3.

Diet CP%		Obs3_LWT			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	8.48	0.31	7.87	9.08
		4	7.97	0.35	7.28	8.66
	HGP=YES	1	8.05	0.35	7.36	8.73
		4	7.65	0.32	7.02	8.28
	HGP=NO	ave over both	8.23	0.23	7.77	8.69
	HGP=YES	ave over both	7.85	0.24	7.38	8.32
	ave over both	rank=1	8.27	0.23	7.81	8.72
	ave over both	rank=4	7.81	0.24	7.35	8.28

Comparisons	**Other factor**	**p-value**
Obs3_LWT=1 vs Obs3_LWT=4	Averaged over both levels of HGP	0.29
HGP=no vs HGP=yes	Averaged over both levels of Obs3_LWT	0.36
Interaction (HGP*Obs3_LWT)		0.87

Table 181: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dietary Crude Protein %. Data from property=2, 3, 4, 5 & 7 and Obs= 3. Within each observation and property, t-tests were used to compare mean CP % between Obs3_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Diet CP%		Obs3_LWT			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**

2	3	1	3.6	0.08	
		4	3.9	0.09	0.02
3	3	1	10.63	0.33	
		4	10.27	0.27	0.4
4	3	1	7.16	0.14	
		4	7	0.17	0.5
5	3	1	4.66	0.18	
		4	4.44	0.19	0.4
7	3	1	10.84	0.3	
		4	9.91	0.41	0.09

Table 182: Summary statistics for Dietary Crude Protein (CP%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing CP% between groups based on HGP and Obs4_LWT rank. Data from property=1 and Obs4.

Diet CP%		Obs4_LWT			95% CI	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	5.53	0.29	4.96	6.1
		4	6.6	0.38	5.86	7.34
	HGP=YES	1	6.29	0.3	5.7	6.89
		4	4.88	0.29	4.31	5.44
	HGP=NO	ave over both	6.01	0.23	5.55	6.47
	HGP=YES	ave over both	5.65	0.21	5.24	6.07
	ave over both	rank=1	5.95	0.21	5.53	6.36
	ave over both	rank=4	5.66	0.23	5.2	6.11

Comparisons	**Other factor**	**p-value**
Obs4_LWT=1 vs Obs4_LWT=4	Averaged over both levels of HGP	0.031
HGP=no vs HGP=yes	Averaged over both levels of Obs4_LWT	0.08
Interaction (HGP*Obs4_LWT)		<0.001

Table 183: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dietary Crude Protein %. Data from property=2, 3, 5 & 7 and Obs= 4. Within each observation and property, t-tests were used to compare mean CP% between Obs4_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Diet CP%		Obs4_LWT			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	4	1	5.39	0.19	

		4	4.91	0.21	0.12
3	4	1	5.24	0.169	
		4	5.03	0.17	0.36
5	4	1	6.89	0.23	
		4	6.33	0.13	0.034
7	4	1	8.64	0.38	
		4	8.89	0.33	0.6

15.28.4 Dry Matter Digestibility (DMD%)

Comparing lowest and highest quartiles of ADG_DS:

- Property = 1
    - no effect of ADG_DS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_DS_rank.
- Property= 7 & Obs2
    - Animals in the lowest rank for ADG_DS at Obs2 (quartile=1) had a higher in vivo DMD (mean=53.34, se=0.25) compared with animals in the highest quartile (quartile=4; mean=51.81, sem=0.44, p=0.0035)

- There were no other significant differences between lowest and highest quartiles of ADG_DS_rank at either Obs2 or 3 for properties 2, 3, 4, 5 & 7.

Comparing lowest and highest quartiles of ADG_WS:

- Property = 1, Obs3
  - no effect of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property = 1, Obs4
  - no effect of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property= 2, 3, 4, 5, 7 & Obs3 & Obs4
  - No effect of ADG_WS_rank on in vivo DMD

Comparing lowest and highest quartiles of Obs3_wt:

- Property = 1, Obs3
  - no effect of Obs3wt_rank and no effect of HGP retention status or of the interaction between HGP retention and Obs3wt_rank.
- Property= 2, 3, 4, 5, 7 & Obs3
  - No effect of Obs3_wt_rank on in vivo DMD

Comparing lowest and highest quartiles of Obs4_wt:

- Property = 1, Obs4
  - no effect of Obs4wt_rank and no effect of HGP retention status or of the interaction between HGP retention and Obs4wt_rank.
- Property= 2, Obs4
  - Animals in the lowest quartile for Obs4_wt (quartile =1) had a higher mean in vivo DMD (mean=51.16, se=0.36) compared with animals in the highest quartile (q=4; mean=49.88, se=0.37, p=0.023).
- Property=5, Obs4
  - Animals in the lowest quartile for Obs4_wt (quartile =1) had a higher mean in vivo DMD (mean=55.03, se=0.44) compared with animals in the highest quartile (q=4; mean=54, se=0.22, p=0.035).
- Property= 3, 4, 7 & Obs4
  - No effect of Obs4_wt_rank on in vivo DMD.

Table 184: Summary statistics for Dry Matter Digestibility (DMD%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD% between groups based on HGP and ADG_DS rank. Data from property=1 and Obs3.

In Vivo DMD		ADG_DS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	58.48	0.41	57.68	59.29
		4	57.73	0.61	56.53	58.94
	HGP=YES	1	58.49	0.5	57.51	59.48
		4	57.45	0.48	56.51	58.4
	HGP=NO	ave over both	58.17	0.35	57.49	58.86
	HGP=YES	ave over both	58.06	0.36	57.37	58.76
	ave over both	rank=1	58.49	0.32	57.86	59.12
	ave over both	rank=4	57.59	0.39	56.83	58.36

Comparisons	**Other factor**	**p-value**
ADG_DS=1 vs ADG_DS=4	Averaged over both levels of HGP	0.3
HGP=no vs HGP=yes	Averaged over both levels of ADG_DS	0.9
Interaction (HGP*ADG_DS)		0.8

Table 185: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dry Matter Digestibility (DMD%). Data from property=2, 3, 4, 5 & 7 and Obs= 2 & 3. Within each observation and property, t-tests were used to compare mean DMD% between ADG_DS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

In Vivo DMD		ADG_DS			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	2	1	56.43	0.26	
		4	56.95	0.18	0.09
	3	1	55.86	0.27	
		4	56.45	0.26	0.12

3	2	1	50.03	0.47	
		4	49.65	0.36	0.5
	3	1	59.06	0.34	
		4	59.23	0.42	0.8
4	2	1	48.71	0.28	
		4	48.87	0.29	0.7
	3	1	58.94	0.28	
		4	49.03	0.21	0.8
5	2	1	53.69	0.73	
		4	536.34	0.34	0.6
	3	1	54.38	0.56	
		4	55.47	0.5	0.15
7	2	1	53.34	0.25	
		4	51.81	0.44	0.0035
	3	1	59.31	0.45	
		4	59.78	0.51	0.5

Table 186: Summary statistics for Dry Matter Digestibility (DMD%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs3.

In Vivo DMD		ADG_WS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	58.52	0.43	57.68	59.37

		4	58.24	0.52	57.23	59.25
	HGP=YES	1	57.91	0.52	56.9	58.93
		4	58.39	0.58	57.25	59.54
	HGP=NO	ave over both	58.4	0.33	57.75	59.05
	HGP=YES	ave over both	58.12	0.39	57.36	58.87
	ave over both	rank=1	58.26	0.33	57.61	58.91
	ave over both	rank=4	58.31	0.39	57.55	59.06

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.7
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.4
Interaction (HGP*ADG_WS)		0.5

Table 187: Summary statistics for Dry Matter Digestibility (DMD%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs4.

In Vivo DMD		**ADG_WS**			**95% CI**	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	52.43	0.38	51.68	53.18
		4	52.28	0.51	51.28	53.28
	HGP=YES	1	52.01	0.53	50.97	53.05
		4	51.42	0.65	50.15	52.69
	HGP=NO	ave over both	52.38	0.31	51.78	52.98
	HGP=YES	ave over both	51.79	0.41	50.98	52.6
	ave over both	rank=1	52.28	0.31	51.67	52.89
	ave over both	rank=4	51.97	0.4	51.19	52.76

Comparisons	**Other factor**	**p-value**

ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.8
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.5
Interaction (HGP*ADG_WS)		0.7

Table 188:Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dry Matter Digestibility (DMD%). Data from property=2, 3, 5 & 7 and Obs= 3 & 4. Within each observation and property, t-tests were used to compare mean DMD% between ADG_WS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

In Vivo DMD		ADG_WS			
Property	Obs	rank	Mean	se	p-value
2	3	1	56.75	0.24	
		4	56.13	0.3	0.11
	4	1	50.65	0.38	
		4	50.03	0.28	0.2
3	3	1	59.16	0.28	
		4	59.01	0.57	0.8
	4	1	53.85	0.33	
		4	53.9	0.25	0.9
5	3	1	55.46	0.46	
		4	54.64	0.3	0.16
	4	1	54.56	0.3	

		4	54.22	0.31	0.4
7	3	1	59.17	0.25	
		4	59.95	0.46	0.13
	4	1	55.99	0.31	
		4	56.62	0.28	0.14

Table 189: Summary statistics for Dry Matter Digestibility (DMD%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD% between groups based on HGP and Obs3_LWT rank. Data from property=1 and Obs3.

In Vivo DMD		Obs3_LWT			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	58.09	0.53	57.04	59.14
		4	59.1	0.61	57.91	60.29
	HGP=YES	1	57.19	0.61	56	58.38
		4	58.96	0.56	57.87	60.05
	HGP=NO	ave over both	58.58	0.4	57.79	59.37
	HGP=YES	ave over both	58.06	0.41	57.25	58.57
	ave over both	rank=1	57.65	0.4	56.86	58.44
	ave over both	rank=4	59.03	0.41	58.22	59.84

Comparisons	**Other factor**	**p-value**
Obs3_LWT=1 vs Obs3_LWT=4	Averaged over both levels of HGP	0.2
HGP=no vs HGP=yes	Averaged over both levels of Obs3_LWT	0.3
Interaction (HGP*Obs3_LWT)		0.5

Table 190:Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dry Matter Digestibility (DMD%). Data from property=2, 3, 4, 5 & 7 and Obs=3. Within each observation and property, t-tests were used to compare mean DMD% between Obs3_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

In Vivo DMD		Obs3_LWT			
Property	Obs	rank	Mean	se	p-value
2	3	1	56.64	0.28	
		4	56.26	0.28	0.35
3	3	1	59.24	0.62	
		4	58.68	0.57	0.5
4	3	1	49.34	0.28	
		4	48.82	0.33	0.24
5	3	1	55.42	0.51	
		4	54.8	0.51	0.4
7	3	1	59.64	0.47	
		4	58.45	0.41	0.12

Table 191: Summary statistics for Dry Matter Digestibility (DMD%; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD% between groups based on HGP and Obs4_LWT rank. Data from property=1 and Obs4.

In Vivo DMD		Obs4_LWT			95% CI	
Property	Obs=4	rank	Mean	se	lower	upper
1	HGP=NO	1	52.96	0.59	51.81	54.11
		4	52.31	0.77	50.81	53.82
	HGP=YES	1	51.71	0.61	50.51	52.91
		4	52.56	0.59	51.41	53.71

HGP=NO	ave over both	52.67	0.48	51.74	53.59
HGP=YES	ave over both	52.1	0.43	51.26	52.93
ave over both	rank=1	52.28	0.43	51.43	53.11
ave over both	rank=4	52.45	0.47	51.52	53.37

Comparisons	**Other factor**	**p-value**
Obs4_LWT=1 vs Obs4_LWT=4	Averaged over both levels of HGP	0.5
HGP=no vs HGP=yes	Averaged over both levels of Obs4_LWT	0.15
Interaction (HGP*Obs4_LWT)		0.3

Table 192:Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Dry Matter Digestibility (DMD%). Data from property=2, 3, 5 & 7 and Obs=4. Within each observation and property, t-tests were used to compare mean DMD% between Obs4_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

In Vivo DMD		Obs4_LWT			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	4	1	51.16	0.36	
		4	49.88	0.37	0.023
3	4	1	53.91	0.36	
		4	53.5	0.45	0.5
5	4	1	55.03	0.44	
		4	54	0.22	0.035
7	4	1	56.11	0.31	
		4	56.54	0.35	0.4

15.28.5 Ratio of DMD(%) : CP (%)

Comparing lowest and highest quartiles of ADG_DS:

- Property = 1
  - no effect on the mean DMD:CP ratio of ADG_DS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_DS_rank.
- Property= 2 & Obs2
  - Animals in the lowest rank for ADG_DS at Obs2 (quartile=1) had a higher DMD:CP ratio (mean=87.67, se=2.6) compared with animals in the highest quartile (quartile=4; mean=78.3, sem=1.97, p=0.006)
- There were no other significant differences between lowest and highest quartiles of ADG_DS_rank at either Obs2 or 3 for properties 3, 4, 5 or at Obs3 for property=2.

Comparing lowest and highest quartiles of ADG_WS:

- Property = 1, Obs3
  - no effect on the mean DMD:CP ratio of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property = 1, Obs4
  - no effect on the mean DMD:CP ratio of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property= 2, 3, 5, 7 & Obs3 & Obs4
  - No effect of ADG_WS_rank on DMD:CP ratio

Comparing lowest and highest quartiles of Obs3_wt:

- Property = 1, Obs3
  - no effect on the mean DMD:CP ratio of Obs3wt_rank and no effect of HGP retention status or of the interaction between HGP retention and Obs3wt_rank.
- Property= 2, 3, 4, 5, 7 & Obs3
  - No effect of Obs3_wt_rank on DMD:CP ratio

Comparing lowest and highest quartiles of Obs4_wt:

- Property = 1, Obs4
  - There was a significant effect of the interaction between HGP retention and Obs4wt_rank on the DMD:CP ratio.
    - The mean DMD:CP ratio for animals in the highest quartile of Obs4LWT and that had retained their HGP implant (70.36, se=3.29) was higher than the mean DMD:CP ratio

in the three other combinations (quartile 1 of Obs4 LWT & lost HGP implant; quartile 4 of Obs4 LWT & lost HGP implant; quartile 1 of Obs4 LWT & retained HGP implant; $p<0.05$).

- Property= 2, 3, 4, 5, 7 & Obs3
    - No effect of Obs4_wt_rank on DMD:CP ratio

Table 193: Summary statistics for DMD:CP ratio: mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD:CP ratio between groups based on HGP and ADG_DS rank. Data from property=1 and Obs3.

In Vivo DMD		ADG_DS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	58.48	0.41	57.68	59.29
		4	57.73	0.61	56.53	58.94
	HGP=YES	1	58.49	0.5	57.51	59.48
		4	57.45	0.48	56.51	58.4
	HGP=NO	ave over both	58.17	0.35	57.49	58.86
	HGP=YES	ave over both	58.06	0.36	57.37	58.76
	ave over both	rank=1	58.49	0.32	57.86	59.12
	ave over both	rank=4	57.59	0.39	56.83	58.36

Comparisons	**Other factor**	**p-value**
ADG_DS=1 vs ADG_DS=4	Averaged over both levels of HGP	0.3
HGP=no vs HGP=yes	Averaged over both levels of ADG_DS	0.9
Interaction (HGP*ADG_DS)		0.8

Table 194: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for DMD:CP ratio. Data from property=2, 3, 4, 5 & 7 and Obs= 2 & 3. Within each observation and property, t-tests were used to compare mean DMD:CP ratio between ADG_DS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

DMD:CP ratio		ADG_DS			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	2	1	87.67	2.6	
		4	78.30	1.97	0.006
	3	1	95.15	2.49	
		4	91.62	1.9	0.3

3	2	1	62.06	2.61	
		4	60.14	1.81	0.56
	3	1	59.06	0.34	
		4	59.23	0.42	0.75
4	2	1	50.75	1.24	
		4	48.83	1.13	0.26
	3	1	44.19	0.69	
		4	43.52	0.58	0.46
5	2	1	51.57	2.31	
		4	52.62	1.05	0.65
	3	1	76.31	2.92	
		4	74.35	2.47	0.61
7	2	1	74.49	2.78	
		4	67.24	2.55	0.07
	3	1	36.11	1.17	
		4	33.76	0.85	0.11

Table 195: Summary statistics for DMD:CP ratio; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD:CP ratio between groups based on HGP and ADG_WS rank. Data from property=1 and Obs3.

DMD:CP ratio		ADG_WS			95% CI	
Property	Obs=3	rank	Mean	se	lower	upper
	HGP=N					
1	O	1	46.46	1.21	44.08	48.83

		4	44.22	1.45	41.38	47.06
	HGP=YES	1	47.38	1.45	44.54	50.22
		4	44.74	1.63	41.53	47.94
	HGP=NO	ave over both	45.51	0.93	43.69	47.33
	HGP=YES	ave over both	46.26	1.08	44.13	48.38
	ave over both	rank=1	46.85	0.93	45.03	48.67
	ave over both	rank=4	44.44	1.08	42.31	46.56

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.6
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.2
Interaction (HGP*ADG_WS)		0.9

Table 196: Summary statistics for DMD:CP ratio; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD:CP ratio between groups based on HGP and ADG_WS rank. Data from property=1 and Obs4.

DMD:CP ratio		**ADG_WS**			**95% CI**	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	59.79	2.57	54.75	64.83
		4	54.64	3.42	47.93	61.34
	HGP=YES	1	63.57	3.56	56.59	70.54
		4	57.28	4.36	48.74	65.82
	HGP=N	ave over both	57.86	2.06	53.83	61.89

O					
HGP=YES	ave over both	61.21	2.76	55.80	66.62
ave over both	rank=1	61.14	2.08	57.05	65.22
ave over both	rank=4	55.58	2.69	50.30	60.86

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.4
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.2
Interaction (HGP*ADG_WS)		0.9

Table 197: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for DMD:CP ratio. Data from property=2, 3, 5 & 7 and Obs= 3 & 4. Within each observation and property, t-tests were used to compare mean DMD:CP ratio between ADG_WS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

In Vivo DMD		**ADG_WS**			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	3	1	96.85	1.8	
		4	92.02	2.25	0.1
	4	1	64.9	3.34	
		4	61.91	1.25	0.41
3	3	1	35.22	0.82	
		4	35.98	0.59	0.47
	4	1	65.74	2.32	
		4	69.11	2.41	0.32
5	3	1	79.84	3.17	

		4	75.28	2.48	0.28
	4	1	50.257	0.99	
		4	52.16	1.08	0.21
7	3	1	35.46	0.58	
		4	34.65	0.99	0.48
	4	1	43.05	1.33	
		4	41.19	1.36	0.33

Table 198: Summary statistics for DMD:CP ratio; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD:CP ratio between groups based on HGP and Obs3_LWT rank. Data from property=1 and Obs3.

DMD:CP ratio		Obs3_LWT			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	43.96	1.35	41.31	46.61
		4	46.79	1.54	43.77	49.82
	HGP=YES	1	44.65	1.54	41.63	47.68
		4	48.60	1.41	45.84	51.36
	HGP=NO	ave over both	45.34	1.02	43.34	47.35
	HGP=YES	ave over both	46.58	1.05	44.53	48.63
	ave over both	rank=1	44.30	1.02	42.29	46.30
	ave over both	rank=4	47.67	1.05	45.62	49.73

Comparisons	**Other factor**	**p-value**
Obs3_LWT=1 vs Obs3_LWT=4	Averaged over both levels of HGP	0.7
HGP=no vs HGP=yes	Averaged over both levels of Obs3_LWT	0.2
Interaction (HGP*Obs3_LWT)		0.7

Table 199:Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for DMD:CP ratio. Data from property=2, 3, 4, 5 & 7 and Obs=3. Within each observation and property, t-tests were used to compare mean DMD:CP ratio between Obs3_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

DMD:CP ratio		Obs3_LWT			
Property	Obs	rank	Mean	se	p-value
2	3	1	99.34	2.08	
		4	91.23	1.86	0.006
3	3	1	35.24	0.84	
		4	35.95	0.64	0.51
4	3	1	43.35	0.77	
		4	44.02	0.92	0.6
5	3	1	76.35	3.37	
		4	79.72	3.43	0.5
7	3	1	34.87	0.96	
		4	37.32	1.32	0.15

Table 200: Summary statistics for DMD:CP ratio; mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing DMD:CP ratio between groups based on HGP and Obs4_LWT rank. Data from property=1 and Obs4.

DMD:CP ratio		Obs4_LWT			95% CI	
Property	Obs=4	rank	Mean	se	lower	upper
1	HGP=NO	1	60.72	3.29	54.28	67.17
		4	51.55	4.31	43.11	59.99
	HGP=YES	1	52.41	3.43	45.68	59.14

		4	70.36	3.29	63.91	76.80
	HGP=NO	ave over both	56.57	2.65	51.38	61.77
	HGP=YES	ave over both	60.53	2.40	55.83	65.23
	ave over both	rank=1	56.17	2.40	51.47	60.87
	ave over both	rank=4	61.85	2.65	56.65	67.05

Comparisons	**Other factor**	**p-value**
Obs4_LWT=1 vs Obs4_LWT=4	Averaged over both levels of HGP	0.09
HGP=no vs HGP=yes	Averaged over both levels of Obs4_LWT	0.1
Interaction (HGP*Obs4_LWT)		0.001

Table 201: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for DMD:CP ratio. Data from property=2, 3, 5 & 7 and Obs=4. Within each observation and property, t-tests were used to compare mean DMD:CP ratio between Obs4_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

DMD:CP ratio		Obs4_LWT			
Property	Obs	rank	Mean	se	p-value
2	4	1	60.48	1.97	
		4	66.23	2.78	0.13
3	4	1	65.73	2.27	
		4	68.17	2.34	0.45
5	4	1	50.67	1.49	
		4	53.7	0.92	0.08
7	4	1	41.86	1.51	
		4	40.78	1.51	0.62

15.28.6 Non-Grass %

Comparing lowest and highest quartiles of ADG_DS:

- Property = 1
  - no effect of ADG_DS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_DS_rank.
- Property= 4 & Obs3
  - Animals in the lowest rank for ADG_DS at Obs2 (quartile=1) had a lower non-grass % (mean=17.09, se=1.07) compared with animals in the highest quartile (quartile=4; mean=20.86, sem=1.38, p=0.036)
- There were no other significant differences between lowest and highest quartiles of ADG_DS_rank at either Obs2 or 3 for properties 2, 3, 4, 5 & 7.

Comparing lowest and highest quartiles of ADG_WS:

- Property = 1, Obs3
  - no effect of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.

- Property = 1, Obs4
    - no effect of ADG_WS_rank and no effect of HGP retention status or of the interaction between HGP retention and ADG_WS_rank.
- Property= 2, 3, 4, 5, 7 & Obs3 & Obs4
    - No effect of ADG_WS_rank on non-grass%.

Comparing lowest and highest quartiles of Obs3_wt:

- Property = 1, Obs3
    - no effect of Obs3wt_rank and no effect of HGP retention status or of the interaction between HGP retention and obs3WT_rank.
- Property= 2, 3, 4, 5, 7 & Obs3
    - No effect of Obs3_wt_rank on non-grass %

Comparing lowest and highest quartiles of Obs4_wt:

- Property = 1, Obs4
    - no effect of Obs4wt_rank and no effect of HGP retention status or of the interaction between HGP retention and Obs4wt_rank.
- Property= 2, 3, 4, 5, 7 & Obs4
    - No effect of Obs4_wt_rank on non-grass %

Table 202:Summary statistics for Non-Grass% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing N-G% between groups based on HGP and ADG_DS rank. Data from property=1 and Obs3.

Non-grass%		ADG_DS			95% CI	
Property	Obs=3	rank	Mean	se	lower	upper
1	HGP=NO	1	28.03	1.38	25.32	30.75
		4	26.43	2.08	22.36	30.5
	HGP=YES	1	27.76	1.7	24.43	31.08
		4	27.4	1.63	24.2	30.59
	HGP=NO	ave over both	27.37	1.18	25.06	29.69
	HGP=YES	ave over both	27.61	1.2	25.25	29.96

ave over both	rank=1	27.9	1.09	25.76	30.04	
ave over both	rank=4	26.9	1.33	24.3	29.5	

Comparisons	**Other factor**	**p-value**
ADG_DS=1 vs ADG_DS=4	Averaged over both levels of HGP	0.5
HGP=no vs HGP=yes	Averaged over both levels of ADG_DS	0.9
Interaction (HGP*ADG_DS)		0.7

Table 203: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Non-Grass%. Data from property=2, 3, 4, 5 & 7 and Obs= 2 & 3. Within each observation and property, t-tests were used to compare mean N-G% between ADG_DS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Non-grass%		ADG_DS			
Property	Obs	rank	Mean	se	p-value
2	2	1	9.33	0.44	
		4	9.41	0.54	0.9
	3	1	9.07	0.47	
		4	9.73	0.44	0.3
3	2	1	9.78	1.04	
		4	11.92	0.79	0.1
	3	1	9.78	1.04	
		4	11.39	0.79	0.2
4	2	1	17.59	1.01	
		4	20.86	1.38	0.06
	3	1	17.09	1.07	
		4	20.86	1.38	0.036
5	2	1	19.26	1.44	
		4	19.88	1.08	0.7
	3	1	18.91	1.35	
		4	19.88	1.08	0.6
7	2	1	15.64	1.03	
		4	19.36	1.97	0.09
	3	1	15.99	1.22	
		4	20.58	2.21	0.08

Table 204: Summary statistics for Non-Grass% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing N-G% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs3.

Non-grass%		ADG_WS			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	25.73	1.39	23	28.46
		4	26.81	1.67	23.54	30.08
	HGP=YES	1	27.37	1.67	24.11	30.64
		4	30.81	1.88	27.12	34.49
	HGP=NO	ave over both	26.19	1.07	24.09	28.28
	HGP=YES	ave over both	28.83	1.25	26.38	31.27
	ave over both	rank=1	26.43	1.07	24.33	28.52
	ave over both	rank=4	28.5	1.25	26.06	30.95

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.6
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.5
Interaction (HGP*ADG_WS)		0.5

Table 205: Summary statistics for Non-Grass% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing N-G% between groups based on HGP and ADG_WS rank. Data from property=1 and Obs4.

Non-grass%		ADG_WS			95% CI	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	24.54	1.36	21.87	27.21
		4	26.09	1.81	22.54	29.65
	HGP=YES	1	28.29	1.89	24.59	31.98
		4	30.65	2.31	26.12	35.18
	HGP=NO	ave over both	25.12	1.09	22.98	27.26

HGP=YES	ave over both	29.17	1.46	26.3	32.04
ave over both	rank=1	25.88	1.11	23.71	28.04
ave over both	rank=4	27.72	1.43	24.92	30.52

Comparisons	**Other factor**	**p-value**
ADG_WS=1 vs ADG_WS=4	Averaged over both levels of HGP	0.5
HGP=no vs HGP=yes	Averaged over both levels of ADG_WS	0.1
Interaction (HGP*ADG_WS)		0.8

Table 206: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Non-Grass%. Data from property=2, 3, 5 & 7 and Obs= 3 & 4. Within each observation and property, t-tests were used to compare mean N-G% between ADG_WS ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Non-grass%		**ADG_WS**			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	3	1	10.08	0.61	
		4	8.66	0.47	0.08
	4	1	10.46	0.68	
		4	8.62	0.66	0.06
3	3	1	10.8	1.25	
		4	12.06	1.28	0.5
	4	1	10.8	1.25	
		4	12.15	1.36	0.5
5	3	1	18.48	1.03	
		4	18.23	1.1	0.9
	4	1	18.48	1.03	
		4	18.23	1.1	0.9
7	3	1	14.86	1.6	

	4	16.31	1.36	0.5
4	1	12.97	1.07	
	4	16.26	1.31	0.06

Table 207: Summary statistics for Non-Grass% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing N-G% between groups based on HGP and Obs3_LWT rank. Data from property=1 and Obs3.

Non-grass%		Obs3_LWT			95% CI	
Property	**Obs=3**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	27.89	1.75	24.46	31.32
		4	23.8	1.99	19.9	27.71
	HGP=YES	1	31.19	1.99	27.28	35.1
		4	27.13	1.82	23.56	30.69
	HGP=NO	ave over both	25.89	1.32	23.3	28.49
	HGP=YES	ave over both	29.2	1.35	26.55	31.85
	ave over both	rank=1	29.5	1.32	26.91	32.09
	ave over both	rank=4	25.43	1.35	22.78	28.08

Comparisons	**Other factor**	**p-value**
Obs3_LWT=1 vs Obs3_LWT=4	Averaged over both levels of HGP	0.13
HGP=no vs HGP=yes	Averaged over both levels of Obs3_LWT	0.2
Interaction (HGP*Obs3_LWT)		0.9

Table 208: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Non-Grass%. Data from property=2, 3, 4, 5 & 7 and Obs=3. Within each observation and property, t-tests were used to compare mean N-G% between Obs3_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

Non-grass%		Obs3_LWT			
Property	**Obs**	**rank**	**Mean**	**se**	**p-value**
2	3	1	11	0.69	
		4	10.06	0.4	0.23
3	3	1	12.13	1.23	
		4	12.12	1.41	0.9

4	3	1	20.08	1.55	
		4	16.99	1.66	0.2
5	3	1	18.96	1.17	
		4	17.73	1.12	0.45
7	3	1	16.75	1.14	
		4	15.6	4.77	0.75

Table 209: Summary statistics for Non-Grass% (mean, se=standard error, 95% CI=confidence intervals) and results of pairwise t-tests comparing N-G% between groups based on HGP and Obs4_LWT rank. Data from property=1 and Obs4.

Non-grass%		Obs4_LWT			95% CI	
Property	**Obs=4**	**rank**	**Mean**	**se**	**lower**	**upper**
1	HGP=NO	1	28.3.	2.05	24.28	32.32
		4	25.23	2.69	19.97	30.5
	HGP=YES	1	27.85	2.14	23.65	32.05
		4	24.01	2.05	19.99	28.04
	HGP=NO	ave over both	26.91	1.66	23.67	30.16
	HGP=YES	ave over both	26.12	1.5	23.18	29.05
	ave over both	rank=1	28.05	1.5	25.12	30.99
	ave over both	rank=4	24.57	1.66	21.32	27.81

Comparisons	**Other factor**	**p-value**
Obs4_LWT=1 vs Obs4_LWT=4	Averaged over both levels of HGP	0.4
HGP=no vs HGP=yes	Averaged over both levels of Obs4_LWT	0.9
Interaction (HGP*Obs4_LWT)		0.9

Table 210: Summary statistics (mean, se=standard error, 95% CI=confidence intervals) for Non-Grass%. Data from property=2, 3, 5 & 7 and Obs=4. Within each observation and property, t-tests were used to compare mean N-G% between Obs4_LWT ranks (1=first quartile and 4=4th quartile), and p-values are reported in the last column.

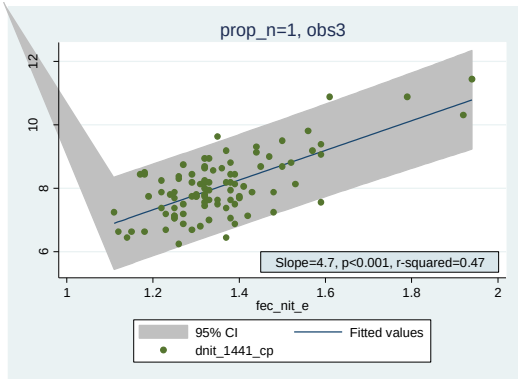
Non-grass%	**Obs4_LWT**

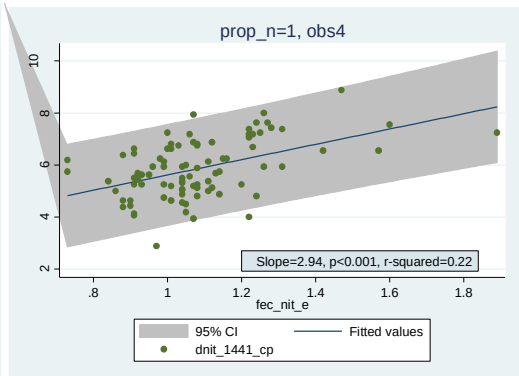
Property	Obs	rank	Mean	se	p-value
2	4	1	10.5	0.92	
		4	9.71	0.56	0.44
3	4	1	11.38	1.25	
		4	12.17	1.31	0.66
5	4	1	19.22	1.42	
		4	18.33	1.25	0.64
7	4	1	14.78	1.1	
		4	15.9	1.8	0.6

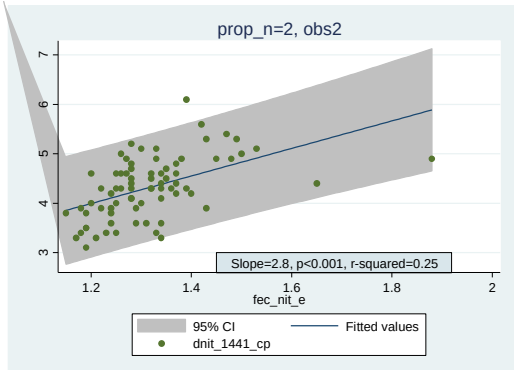
15.28.7 Plots of Faecal Nitrogen % vs Dietary Crude Protein %

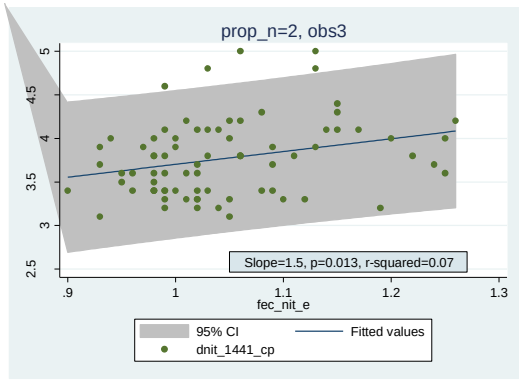
The expectation from the underlying modeling is that a simple regression with dietary CP% (DNIT1441_Diet CP%) as the outcome and with faecal N% (FECN_Fec N%) as the explanatory variable, should produce a reasonably good correlation with a slope coefficient around 6.5 (Dixon, personal communication 2011).

These were checked by performing separate regressions for each combination of property and observation. Outputs are presented as plots showing the individual points as dots, a fitted regression line and a shaded region representing the 95% prediction limits.









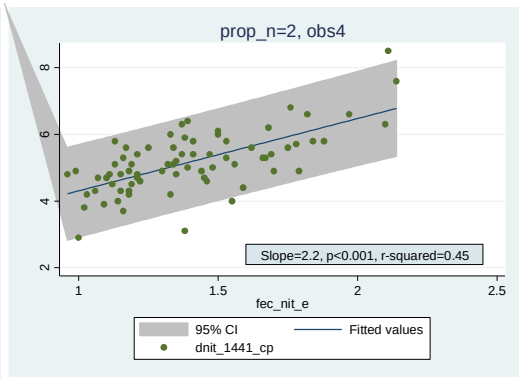
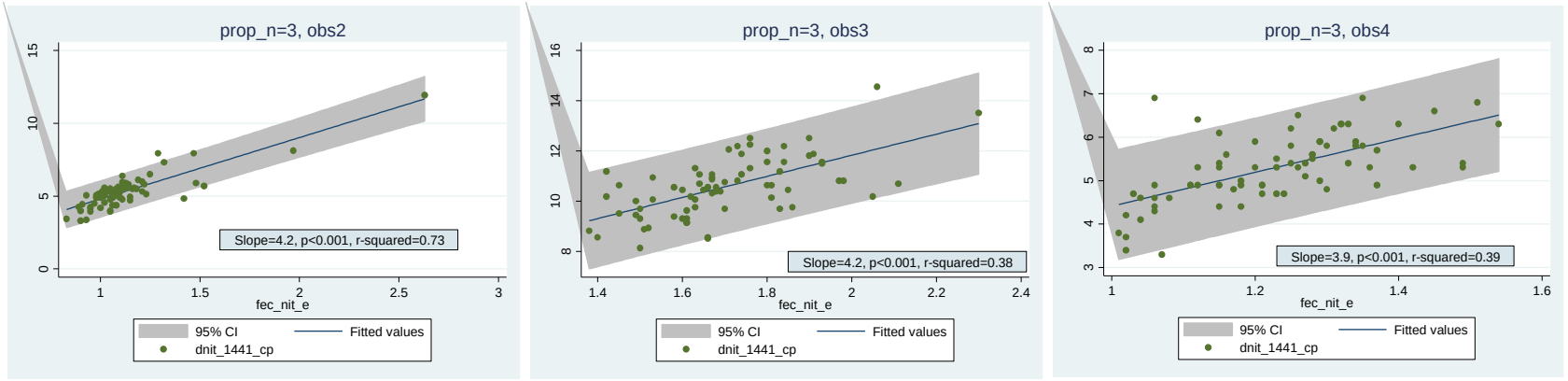


Figure 26: Dietary CP% by faecal nitrogen for prop_n=1 and 2 with separate plots for each observation. Each plot displays the slope & p-value & r-squared value from a simple regression.



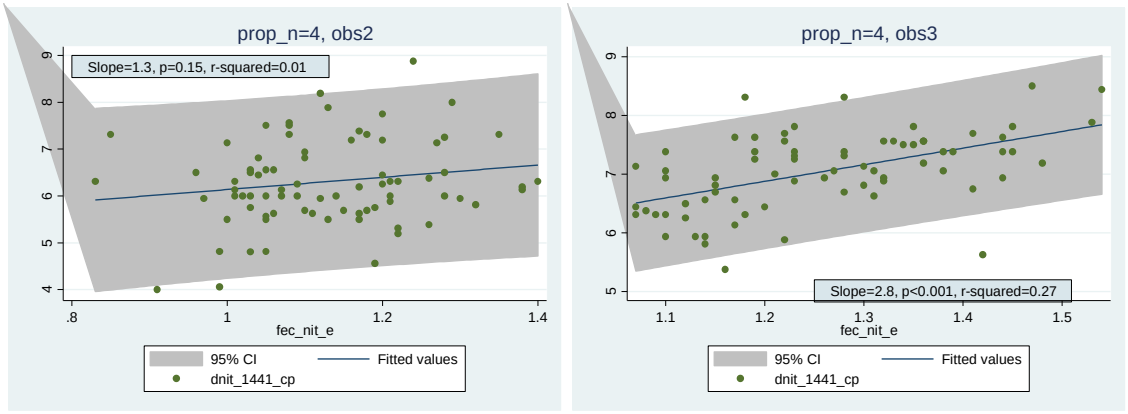


Figure 27: Dietary CP% by faecal nitrogen for prop_n=3 & 4 and separate plots for each observation Each plot displays the slope & p-value & r-squared value from a simple regression.

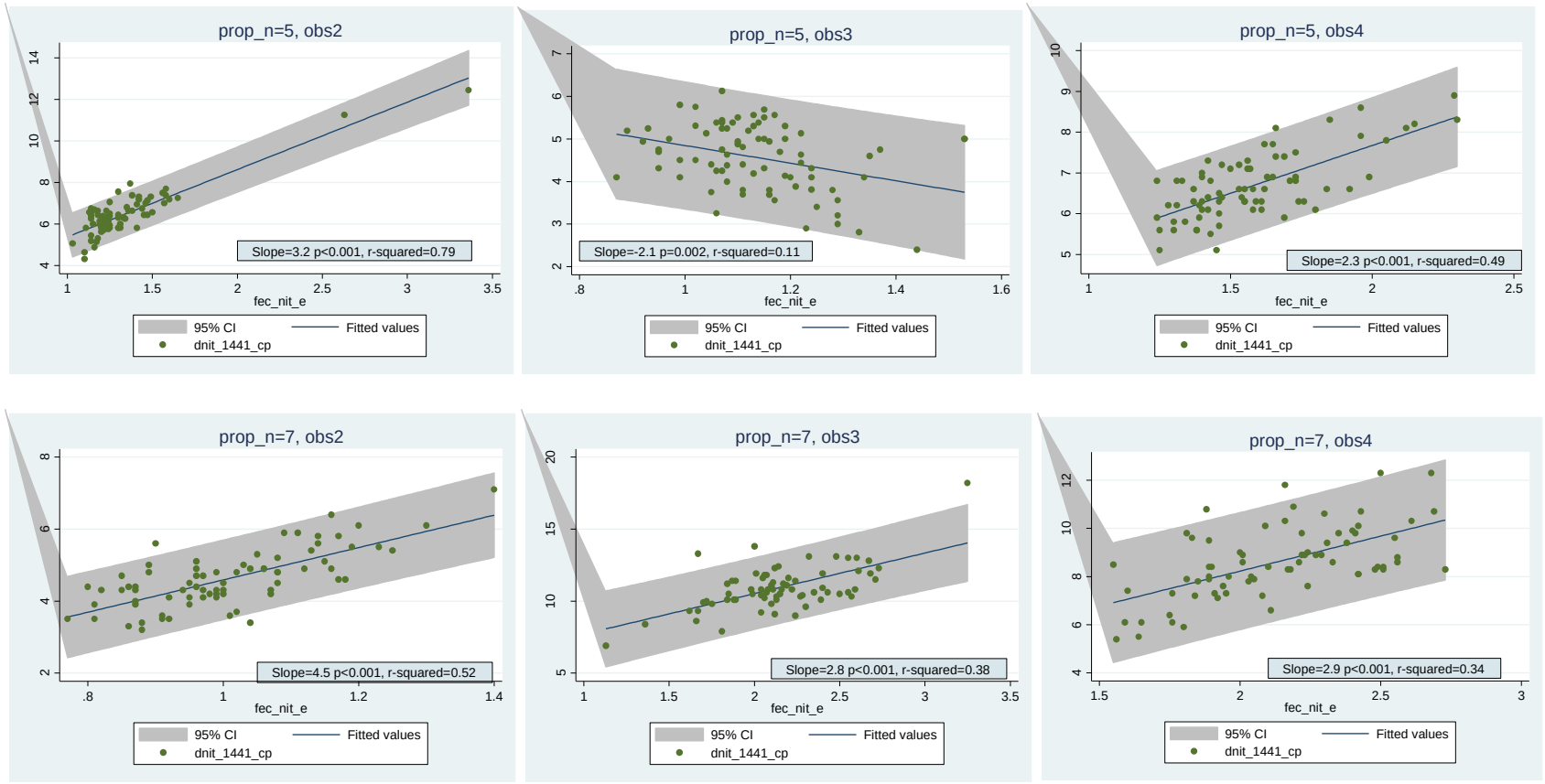


Figure 28: Dietary CP% by faecal nitrogen for each observation in prop_n=5 & 7. Each plot displays the slope & p-value & r-squared value from a simple regression.

The plots in in the Figures above show that the relationship between faecal nitrogen (fec_nit_e) and dietary crude protein (dnit_1441_cp) was generally positive though the slope coefficients were consistently lower than the expected value of 6.5.

The regression fit varied between observations and properties, perhaps reflecting changes in climate, rainfall, soil and other factors that might influence vegetation (presence, species & growth).

On one occasion (prop_n=5, obs=3) the slope was negative.

15.29 Cattle tick zones in the Northern Territory

The Northern Territory has four cattle tick zones[e]

- The Parkhurst Infected Zone – Parkhurst strain cattle ticks are known to be present here.
- The Infected Zone – cattle ticks are known to be present here.
- The Control Zone – this is a buffer zone separating the infected zone from the free zone. Cattle ticks may occur on some properties in this zone.
- The Free Zone – no cattle ticks are known to be present here.

[e] http://www.nt.gov.au/d/Content/File/p/Anim_Dis/718.pdf

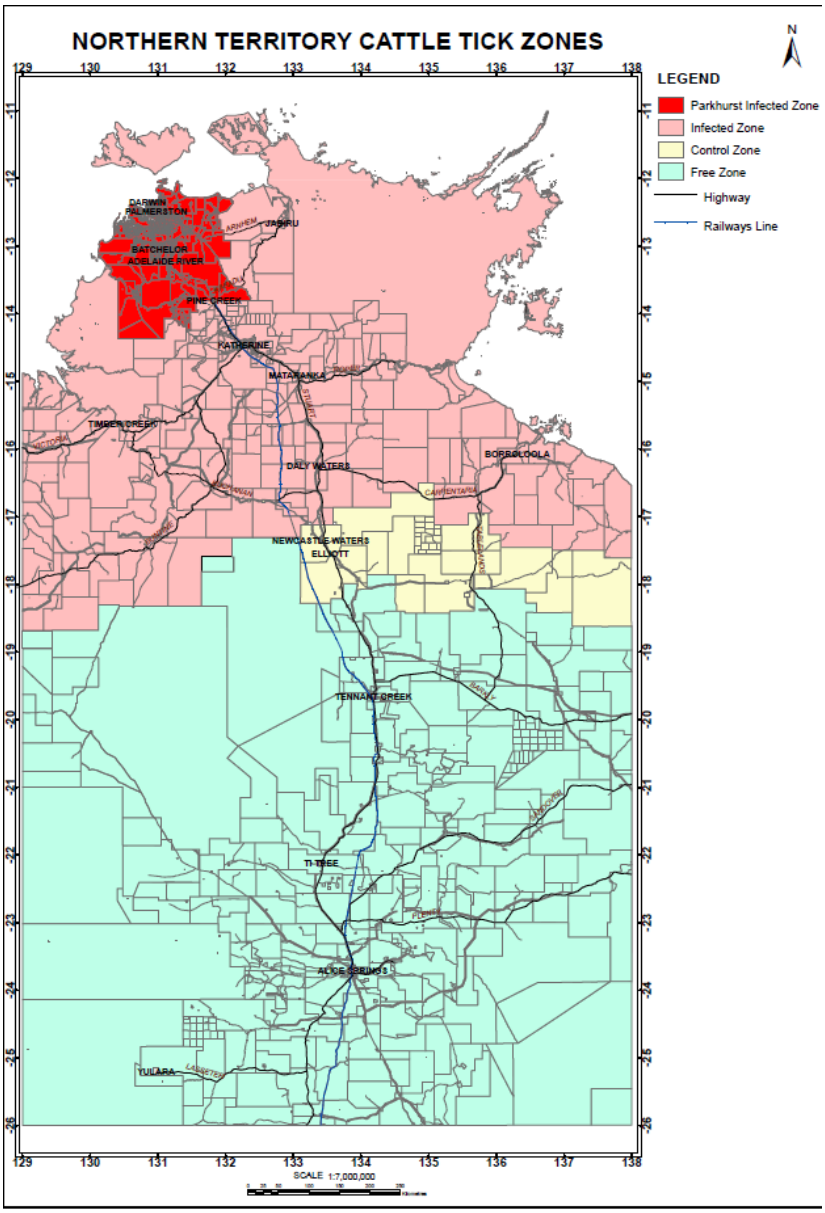


Figure 29: Map depicting NT cattle tick zones.

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