# final report

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# Meta-analysis of protein requirements of feedlot cattle

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# Executive summary

This study provides a quantitative evaluation of dietary and other factors that influence the production outputs critical to the profitability and environmental sustainability of cattle production in feedlots. There is a particular focus on the effects of dietary protein and nitrogen intake, evaluated using different methods, on the production performance and on the retention and loss of these dietary components. Initial searches identified more than 20,000 studies. After screening for suitability, studies were extracted into a large database of 77 studies using NDS software (RUM&N Sas, Italy) containing Cornell Net Protein and Carbohydrate Systems (CNCPS 6.55) protein estimation methods, crude protein (CP), estimates of rumen degradable and undegradable protein (RDP and RUP), and metabolisable protein (MP) derived from NRC (2000) level 1. Papers containing detail of nitrogen retention and loss provided a set of 20 studies.

There were three data sets established that addressed: production responses using classical meta-analytical methods; lean muscle yield (LMY) using mixed models regression and; nitrogen retention and loss using classical meta-analytical methods. The data sets contained mutual studies, but the study content differed markedly between the production responses and the nitrogen balance studies and the latter included Latin square studies, whereas the other two data sets did not.

The National Research Council (NRC) (2000) estimates of MP, metabolisable energy (ME, NEm, NEg), and total digestible nutrients (TDN) were provided in NDS and the physically effective neutral detergent fibre (peNDF) from the NDS feedbank was used to calculate the metabolisable protein NRC (2000) estimates. Comparisons between predictions of outcomes derived using dietary CP or NRC (2000) level 1 or CNCPS 6.55 estimated MP and MP amino acids for outcomes were made. These comparisons indicated that the CNCPS 6.55 estimates of MP were generally superior to use of CP to predict outcomes and both of these were superior to estimates of MP based on NRC (2000) level 1 methods. Amino acid models performed consistently well, with the exception of gain to feed, and this raises the potential for amino acid-based models for the prediction of feedlot performance. However, there was strong collinearity between amino acids, suggesting that the particular amino acids identified as being significant may not be definitive. Many models had significant unexplained variance even after evaluation of other explanatory variables including differences in initial bodyweight and differences in dietary inputs such as fibre and ether extract on model fit using meta-regression methods. Interestingly, ether extract entered a large number of models independent of its inclusion in metabolisable energy suggesting that fats may play a role in increasing the efficiency of beef feedlot production as signalling agents.

The LMY models were all very similar in regards to model fit and indicated that the protein and nitrogen estimates were useful in explaining LMY. The LMY models provided the opportunity to evaluate the effect of other factors influencing growth including, sex, breed, hormonal implants, rumen modifiers, and duration of the feeding period. Similarly, the hormonal implant, Synovex H provided a substantial 10 kg advantage in studies in which it was used, while other implants did not always provide significant benefits, despite the point directions being quite large (eg 5 kg). Results from the different models were quite consistent and found that heifers gained approximately 8 kg, cows 3 kg less and bulls 5 kg more than steers. Treatment effects, per se, were only significant for the CP model, indicating that the effects of dietary nitrogen and protein interventions were well

explained by the outcome variables used in the other models, and those models had better statistical fit.

Multivariable models were developed to predict production outcomes and to predict nitrogen retention and loss. The results indicate that feeding additional protein and nitrogen increased retention of nitrogen and that urea and 'other' interventions increased the retention of nitrogen in the body. Only approximately 16% of dietary nitrogen was retained in the body. Nitrogen loss in urine increased with dietary nitrogen and protein intake and faecal loss increased quadratically with increased nitrogen intake. Concentrations of nitrogen in serum and plasma increased linearly with nitrogen intake. Results indicate the potential to increase the efficiency of nitrogen use.

There are indications that optimal dietary protein and nitrogen intake strategies exist as indicated by quadratic terms for protein and nitrogen measures in many of the models developed.

Few studies were present where average daily gain (ADG) exceeded 2.0 kg per day and diets seldom exceeded 13% CP, with many interventions being based solely on non-protein nitrogen. Further, the grain base was substantially corn and corn by-products. These limitations indicate the potential to explore other strategies to increase growth of cattle in feedlots using cereal grains, fats, amino acids, and differing amounts of protein.

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# 1 Background

Substantial numbers of cattle worldwide are finished in feedlot systems. Many studies have individually examined responses to protein or nitrogen additions to the diet. Feeding systems have been developed based on aggregated data. There is a need for a comprehensive examination of the production and nitrogen balance responses to protein interventions in feedlot cattle. In particular, the merit of newer methods of evaluating production responses to protein and nitrogen intervention should be evaluated.

The genesis of modern systems of nutritional evaluation emerged with the development of the Wende system of nutritional analysis and became more quantitative with the emergence of direct and indirect calorimetry. The establishment of nationally supported feed standards including those developed by National Research Council (NRC) in the USA, Agricultural Research Council in the UK and Institut National de la Recherch Agronomique (France) advanced the field. These efforts were complemented by more mechanistic models including those of Baldwin (1995) and the Cornell Net Carbohydrate and Protein System (CNCPS) (Fox et al., 1992). The delivery of more effective models of nutritional response will provide better animal well-being, improve the efficiency of production and reduce environmental waste. Evaluating the effectiveness of models is an important part of the process of improving models.

We hypothesized that the newer systems of evaluation of nitrogen, protein, and amino acids such as CNCPS would provide models that explained more of the variance in production responses than the older models including CP, and NRC (2000). Sources of variation in response to protein or nitrogen were also evaluated using meta-regression and mixed models analysis. Factors that were hypothesized to influence production responses and lean muscle yield (LMY) included: gender, breed, hormonal implants, protein intervention, rumen modifiers, carbohydrate, and lipid components of the diet. Further, we examined the efficiency of retention of nitrogen in the body, losses of nitrogen in faeces and urine and factors that influenced retention or loss of nitrogen.

# 2 Project objectives

1. Conduct a meta-analysis of peer-reviewed published literature to determine:

    a. Optimal levels of dietary protein relevant to the Australian feedlot industry taking into account the effects of Australian carcass endpoints, typical initial body weights, and mature size (gender, implants, breed) on protein requirements if possible.

    b. Effects of protein level and degradability (as expressed as crude protein, RDP/RUP, metabolisable protein, estimated metabolisable amino acid balance or estimated metabolisable amino acid balance over estimated metabolisable energy intake) on carcass gain, retained body nitrogen and nitrogen loss to the environment of feedlot cattle

    c. Effects of protein level and degradability on dry-matter intake and efficiency of hot carcass weight gain of feedlot cattle.

2. The adequacy of published protein systems and the protein deficit/surplus they predict (i.e. CP vs. NRC vs. CNCPS 6.55) to explain nitrogen loss from feedlot cattle. These evaluations will be limited by the number of papers reporting the relevant data for conducting estimations.

# 3 Methodology

## 3.1 Literature search

A comprehensive literature search of English language literature published before and including 2016 was conducted to identify feedlot studies involving treatments with variable nitrogen-based interventions including non-protein nitrogen (NPN), amino acid and protein meals. Literature searches were performed in PubMed (http://www.ncbi.nlm.nih.gov/pubmed; accessed 20 May 2016), Science Direct (http://www.sciencedirect.com/; accessed 5 May 2016), Google Scholar (http://scholar.google.com/; accessed 6 May 2016), and ISI Web of Knowledge (http://wokinfo.com/; accessed 10 May 2016) using the following search or appropriate variation for the specific search engine: (Beef feedlot OR Beef OR Beef cattle) AND (protein OR urea OR non-protein nitrogen OR amino acid) AND (weight gain OR carcass gain OR nitrogen retention OR nitrogen loss OR manure OR urea). Exact search terms for each data base are provided in Appendix Table 1. One minor source http://www.livestocklibrary.com.au/handle/1234/5258 was also searched to obtain articles including those more obscure Australian publications.

## 3.2 Inclusion and exclusion criteria

Studies were included in the meta-analysis if they met the following criteria: they resulted in full manuscripts from peer reviewed English-language journals, they included

the use of a protein or nitrogen supplement against a control, they described a randomisation process, they included replication of treatments, they fed a feedlot diet, they had comprehensive diet definition with specification of individual dietary ingredients and forage analyses, they had detailed cattle responses including weight gain, carcass gain, nitrogen retention or nitrogen loss, they included sufficient data to determine the effect size (ES), they included a measure of effect amenable to ES analysis for continuous data (e.g., standardised mean difference [SMD]), and they included a measure of variance (SE or SD) for each effect estimate or treatment and control comparisons. Study designs were assessed as past studies conducted by our group have identified problems with Latin Square design studies in particular.

## 3.3 Data extraction

The following experimental details were extracted for each study that met the inclusion criteria: author, year, location, journal, trial design, treatment number, treatment description, breed, gender, number of head per treatment and control, number of head per pen of treatment and control, initial body weight, days on feed, implant strategies, grain processing techniques, grain sources, and other potential response modifiers including ionophores and antibiotics. Information on periods of compensatory growth was not available. Production outcome variables extracted included: hot carcass weight (HCW), final body weight (FBW), longissimus muscle area (LMA), fat

thickness (FT), quality grade, average daily gain (ADG), dry matter intake (DMI), gain to feed (G:F), and feed to gain (F:G). Nitrogen outcome variables extracted included: retained body nitrogen (RBN), urinary nitrogen loss (UNL) and faecal nitrogen loss (FNL) and serum and plasma nitrogen (SUN). Dietary parameters were also extracted. The difference between treatment and control was calculated for the following variables: initial body weight, FBW, HCW, G:F, F:G, DMI, ADG, RBN, UNL, FNL, and SUN. Quality grade was not able to be assessed due to the difference in grading systems reported. There were not enough studies that reported F:G to assess. Diet nutrient profiles were obtained by entering diet and feed analysis data from each experiment into an advanced nutrition model (CNCPS 6.55 with NDS platform, RUM&N Sas, Italy) to determine nutrient parameters including crude protein (CP), rumen degradable protein (RDP), rumen undegradable protein (RUP), and individual metabolisable amino acids predicted to be supplied (Van Amburgh et al., 2015). In the cases where nutrient analyses for diet ingredients were not reported, CNCPS 6.55 feed dictionary analyses were used. Results from these were compared to NRC (2000) estimates of metabolisable protein (MP) and to CP.

Dietary values for metabolisable energy (ME), total degradable nutrients (TDN), net energy for maintenance ($NE_m$) and net energy for gain ($NE_g$) were generated using NDS to provide the NRC (2000) values for beef cattle. The effective neutral detergent fibre (eNDF) for NRC (2000) was estimated from the physically effective NDF (peNDF) from the NDS feedbank for diets, in order to estimate efficiency of microbial crude protein production utilising NRC (2000) equations as follows. Microbial MP supplied was estimated assuming a conversion of 64% of microbial CP, and MP from dietary RUP was estimated assuming a digestibility of 80% of the dietary RUP supplied (NRC, 2000). Metabolisable protein supplied from the diet was the sum of microbial MP supplied and MP from dietary RUP supplied. The NRC (1996) level 1 predictions for microbial CP were 0.13 x TDN intake x eNDF adjustment factor, which reduced the microbial CP prediction when diets contained less than 20% predicted NDF.

These estimations of MP produced based on NRC (2000) were used to predict outcomes in meta-regression models.

Nitrogen retention, nitrogen loss, and blood nitrogen were obtained from the data and analysed. These estimates are compared to those derived from NDS.

S*cibus* and Meat and Livestock Australia agreed to evaluate LMY according to recently developed and validated methods used in Australia. Consequently, the following estimates of LMY were made according to methods developed at Murdoch University (Jose et al., pers comm) and the following equations were used. The R-Squared for the regression was 0.71 and root mean square error (RMSE) = 2.79. For steers, bulls and mixed groups the steer equation was used and for heifers, the heifer equation was applied.

*For Steers*

Predicted LMY = 62.1109 + (Leftside HCW x -0.09244) + (LMA x 0.1645) + (RibFat x -0.4936)

*For Heifers*

Predicted LMY = 59.3974 + (Leftside HCW x -0.09244) + (LMA x 0.1645) + (RibFat x -0.4936)

## 3.4 Statistical analysis

The key variables of interest were protein yield in carcass, as represented by FBW, HCW, retained nitrogen and LMY. This study was primarily designed to evaluate dietary factors, including the effects of estimated MP (EMP) amino acids flux (g) or expressed as a proportion of EMP amino acids flux [g divided by estimated ME (Mcal)], on protein yield. The latter is expressed as:

$$\frac{\text{EMP amino acid (g)}}{\text{Estimated ME intake (Mcal)}}$$

Data were extracted from the studies and entered into three final data formats. One data base was evaluated to determine whether the explanatory variables examined predicted 7 outcome variables, specifically FBW, HCW, ADG, DMI, G:F, LMA, and FT using a classical meta-analytical evaluation of responses of the experimental group to the interventions used in the studies, as represented by the differences in dietary inputs provided by the treatment and control groups.

The second data base was similar and examined nitrogen retention studies and the variables: RBN, UNL, FNL, and SUN using classical meta-analytical methods.

A third data base was structured to provide each trial as a single line entry and to examine factors influencing LMY using mixed effects regression analysis. This data base was suited, therefore, to examine the effects of breed, sex, hormonal implants, and dietary feed additives as well as the influence of diet. Factors that were examined included the type of intervention (urea, soyabean meal, ruminally protected protein meal, distillers grains, cottonseed meal, corn gluten feeds or meals, canola meal, fish meal, commercial blends, and other interventions), initial BW of the controls and BW difference between treated and control cattle at the start of the study (kg), duration of the study, breed of cattle, sex of cattle, use of hormonal interventions (including pre-treatment, at treatment onset and re-implantations and timing of treatments), feed additives (monensin, tylosin, lasalocid) and differences between treated and control cattle in their intake of estimated ME (Mcal/d), estimated MP (g), CP (g), soluble protein (g), Protein $A_2$ fraction, Protein $B_1$ (g), Protein $B_2$ (g), RDP at 1x maintenance, RUP at 1x maintenance, acid detergent fibre (ADF; g), acid detergent lignin (ADLG), NDF (g), peNDF (g), NDF from forage (g), sugar (g), starch (g), soluble fibre (g), rumen available fatty acid load (RUFAL; g), ether extract (g), ammonia (g), EMP (estimated MP) Met (g), EMP Lys (g), EMP Arg (g), EMP Thr (g), EMP Leu (g), EMP Ile (g), EMP Val (g), EMP His (g), EMP Phe (g), EMP Trp (g).

All EMP amino acids were separately evaluated and expressed as amino acid mass per estimated MCal ME (g/MCal). An estimate of the non-essential amino acid mass available as MP was derived by subtracting the sum of the amino acids listed above in g from the estimated MP g and the difference between treated and control cattle was evaluated. Further, differences in intake (g per d) of fermentable carbohydrate fractions for NDF, sugar, starch, and soluble fibre between treatment and control cattle were evaluated. The effects of study design (Latin square and Youdan square vs. randomised trials that were not cross-over designs) and grain type were also evaluated. There was sufficient diversity of cattle breeds to test for this effect and the following breed groups were used (1. British crossbred, Angus, or British breeds, 2. British Continental cross, 3. *Bos indicus* cross, and 4. Not identified).

Initial data exploration included production of basic statistics to examine the data for errors and to assess the means and measures of dispersion. Normality of the data was examined for continuous variables which were then centred to allow better interpretation of the coefficients produced in models. Correlations among variables were explored and linear and quadratic relationships were examined using panel plots (Stata Version 14.1, StataCorp College Station, Texas, USA). The quadratic effects of MP amino acids were also tested. During this process, it was noted that there was marked collinearity among most estimates of MP amino acids (r >0.9). Unfortunately, some of the statistical models later developed showed strong evidence of the influence of collinearity in these variables and some models based on MP amino acids were not reported due to the instability of models.

Stata (Stata Version 14.1) was used to analyze differences in the production variables (FBW, HCW, ADG, DMI, G:F, LMA, and FT) and nitrogen balance variables (RBN, UNL, FNL, and SUN) by standardised mean difference (SMD) which is also called effect size (ES) analysis. The difference between treatment and control group means was standardised using the standard deviations of control and treatment groups. The SMD estimates were pooled using the DerSimonian and Laird (1986) random effects models. If the paper reported separate estimates of measure of variance (SE or SD) for each group, these were recorded as such. Many studies reported a common SE or SD and these estimates were used for both control and treatment groups. A random effects weighted mean difference (WMD) between treated and control is provided, with the weighting reflecting the inverse of the variance of the studies included according to no-standard method (Stata Version 14.1).

Random effects models were used for each outcome variable to estimate the effect size, 95% confidence intervals (CI), and statistical significance of SMD. It is recognised that there is a clustering effect that results from multiple comparisons to a single control group, but it is assumed that the variance inflation effect is minor unless there are very large numbers of repeated comparisons. In these data sets that contained a very large number of studies, this effect should be negligible.

Forest plots were produced for all outcome variables using the estimated SMD using random effects models (DerSimonian and Laird, 1986: IntHout et al., 2014). Effects of protein or nitrogen-based interventions on RBN, FNL, and UNL are displayed. Production variables contained too much data to provide legible forest plots. Points to the left of the vertical line in the forest plot represent a reduction in the outcome, whereas points to the right of the line indicate an increase in the outcome variable. Each square represents the mean ES for that study. The upper and lower limit of the line connected to the square represents the upper and lower 95% CI for the ES. The grey vertical line represents the mean difference of zero or no effect and studies that do not include the grey vertical line in the CI are significant.

The weighting of a study is estimated by the inverse of the variance of the ES. Box sizes are proportional to the inverse variance of the estimates (Lean et al., 2009). The size of the square box reflects the relative weighting of the study to the overall ES estimate with larger squares representing greater weight. Boxes draw attention to the studies with the greatest weight.

***Assessment of heterogeneity.*** Variations among the trial level SMD were assessed using a $\chi^2$ ($Q$) test of heterogeneity (Egger and Smith, 2001). Heterogeneity in studies reflects underlying differences in clinical diversity of the herds and interventions used, differences in study design and analytical methods, and statistical variation around responses (Lean et al., 2009). Identifying the presence and

sources of the heterogeneity improves understanding of the responses to the interventions used. We used an α level of 0.10 because of the relatively poor power of the $\chi^2$ test to detect heterogeneity among small numbers of trials (Egger and Smith 2001). Heterogeneity of results among the trials was quantified using the $I^2$ statistic (Higgins and Thompson, 2002), who developed this measure of the impact of heterogeneity on a meta-analysis, from mathematical criteria, that are independent of the number of studies and the treatment effect measure. The $I^2$ statistic is a transformation of the square root of the $\chi^2$ heterogeneity statistic divided by its degrees of freedom and describes the proportion of total variation in study estimates that is due to heterogeneity (Higgins et al., 2003). Negative values of $I^2$ were assigned a value of 0, consequently the value $I^2$ lies between 0 and 1 (Higgins et al., 2003). An $I^2$ value greater than 0.5 indicates substantial heterogeneity. The $\tau^2$ value was also produced, which is an estimate of the between-study variance in a random effects meta-analysis (Higgins and Green, 2011). The square root of this number (i.e., $\tau^2$) is the estimated SD of underlying effects across studies (Higgins and Green, 2011).

***Meta-regression.*** Meta-regression analyses were used to explore the source of heterogeneity of response, using the individual SMD for each trial as the outcome and the associated SE as the measure of variance. Meta-regression was used to test whether there is evidence of different effects in different subgroups of trials or with different covariables (Knapp and Hartung 2003). In order to include more than one covariable in the model, we used the methods of Knapp and Hartung (2003). This method was extended to the case of more than one covariable in the meta-regression, and the use of the smoothed within-trial variance estimates to improve hypothesis testing with regard to the significance levels. A backward stepping regression was performed using all variables identified on univariable analysis. The permutation test approach for assessing the statistical significance of meta-regression methods suggested by Higgins and Thompson (2004), and programmed by Harbord and Higgins (2008) and Harbord and Steichen (2004), was used in our analyses to reduce the risk of type I error.

We recognize that there is a clustering effect that results from multiple comparisons e.g. to a single control group or even trials within study. The results of the Knapp-Hartung test, which do not account for the hierarchical structure of the effects of trial are provided for comparison to robust regression models derived using the same starting variables that account for the nested effect of trials within study (Hedges et al., 2010) and programmed as *robumeta* (StataCorp LP.) and applied by Tanner-Smith and Tipton (2014). Those with a strong interest in statistical methods should consult Hedges et al. (2010) for detail on the theory and testing of the assumptions in regards to robust regression methods. Briefly, in this test the mean effect size from a series of studies is described as follows (Hedges et al., 2010). In this case, the regression model has only an intercept b1 and the weighted mean has the form:

$$b_1 = \frac{\sum_{j=1}^{m} \sum_{i=1}^{k_j} w_{ij} T_{ij}}{\sum_{j=1}^{m} \sum_{i=1}^{k_j} w_{ij}}$$

If all the estimates in the same study are given identical weights, the robust variance estimate (vR) reduces to:

$$v^R = \frac{\sum_{j=1}^{m} w_j^2 (\bar{T}_j - b_1)^2}{\left(\sum_{j=1}^{m} w_j\right)^2}$$

$\bar{T}_j$

where is the unweighted mean of the estimates in the j[th] cluster, b1 is the estimate of the weighted mean, and $w_j$ is the total weight given to estimates in the j[th] cluster. This is a kind of weighted variance which reduces to (m-1)/ m2 times the variance, when the weights within study are identical and (since the correlation coefficient = 1 in this case), robust regression standard error equals 1/ m times the variance of estimated when the weights are equal.

Study design, whether studies were Latin square, Youdan square or randomised designs (factorial or completely randomised without cross-over designs) was tested for significance univariably, but there were no final multivariable models that were significant that included study design.

***Publication bias*.** Presence of publication bias was investigated using funnel plots for all outcome variables but only one example is provided (Appendix Fig. 1). Funnel plots are a simple scatter plot of the intervention effect estimates from individual studies (horizontal axis) plotted against study precision (vertical axis; Light and Pillemer, 1984; Sterne and Harbord, 2004). The name 'funnel plot' arises because precision of the estimated intervention effect increases as the size and precision of a study increases (Sterne and Harbord, 2004). Effect estimates from small studies will scatter more widely at the bottom of the graph and the spread narrows for larger studies (Sterne and Harbord, 2004). In the absence of bias the plot should approximately resemble a symmetrical (inverted) funnel. If there is bias, for example because smaller studies without statistically significant effects remain unpublished, this will lead to an asymmetrical appearance of the funnel plot and a gap will be evident in a bottom corner of the graph. In this situation, the effect calculated in a meta-analysis will tend to overestimate the intervention effect (Sterne and Harbord, 2004). The more pronounced the asymmetry, the more likely it is that the bias will be substantial.

Further exploration of the factors that influenced LMY was conducted using variables that had a *P*<0.2 on univariable analysis. Mixed models analysis was conducted using Stata (Version 14.1) and the mixed methods. Study was included in the model as a random effect to account for variation not described by other factors considered in the model. The intercept, linear, and quadratic terms were tested as fixed effects. The models were not weighted according to the inverse of the study variance because LMY was a synthetic variable, therefore did not have an individual trial estimate of error. The study sizes were relatively consistent with the exception of studies conducted in Calan gates (American Calan Company, New Hampshire) and a decision was made that these did not constitute typical feedlot conditions. Therefore, a weighting based on trial alone would be reasonable. A backward stepping modelling approach was used with the removal of the least significant term at each step and evidence of confounding was evaluated by examination of change in the regression coefficients. The model fit was assessed by evaluating the Akaike's information criteria (AIC) and

comparing this to previous models. Residuals from the random effects model were examined for heteroscedasticity by examination of plots of residuals against fitted values and normality assumptions were tested by evaluating quantiles of the standardised residuals against quantiles of the normal distribution. Assumptions of the normality of distribution of random effects derived from the mixed procedure were tested using graphical assessment of the normality distribution of the best unbiased linear predictors for study.

# 4 Results

## 4.1 Descriptive statistics

Table 1 provides the descriptive statistics for the outcome variables studied. Appendix Table 2 provides descriptive statistics for the explanatory continuous variables. Non-continuous explanatory variables examined included: sex, breed, rumen modifiers, protein treatment intervention, grain type, and hormonal implants used before and during the trials. The number and percentage of each category within these non-continuous variables is provided in Appendix Table 3.

**Table 1.** Descriptive statistics of outcome variables for both production and nitrogen balance including number of observations (No.), mean, standard deviation (SD), minimum, median and maximum.

| Variable | No. | Mean | SD | Minimum | Median | Maximum |
|---|---|---|---|---|---|---|
| ADG, kg/d | 283 | 1.51 | 0.32 | 0.20 | 1.59 | 2.15 |
| Final BW, kg | 246 | 538.1 | 94.5 | 232.0 | 567.0 | 690.0 |
| HCW, kg | 235 | 355.1 | 36.4 | 269.4 | 360.0 | 550.3 |
| G:F, kg/kg | 218 | 0.16 | 0.02 | 0.04 | 0.17 | 0.23 |
| DMI, kg/d | 289 | 9.40 | 1.59 | 4.50 | 9.54 | 12.66 |
| LM area, $cm^2$ | 231 | 84.1 | 8.5 | 32.0 | 84.9 | 101.8 |
| Fat thickness, cm | 236 | 2.87 | 3.86 | 0.61 | 1.29 | 15.50 |
| | | | | | | |
| Nitrogen intake, g/d | 82 | 169.0 | 68.6 | 61.2 | 150.0 | 353.0 |
| Retained body N, g/d | 59 | 40.2 | 18.9 | 8.5 | 37.9 | 87.0 |
| Faecal N loss, g/d | 63 | 48.89 | 15.67 | 29.20 | 45.20 | 101.9 |
| Urinary N, g/d | 48 | 85.45 | 49.69 | 16.70 | 63.3 | 201.0 |

## 4.2 Univariable analyses

The univariable analyses for the production outcomes ADG, FBW, HCW, G:F, DMI, LMA, and FT are provided in Appendix Tables 4-10.

## 4.3 Initial investigations of responses of production variables to treatment

All production outcome variables investigated, with the exception of LMA, had significant differences in response to treatment (Table 2) and there were significant responses to individual treatments (Table 3), however, there was considerable heterogeneity in response (Appendix Table 11).

**Table 2.** Effect size estimates of the effect of nitrogen and protein interventions on production outcomes. The estimates are based on Knapp-Hartung methods and provide the effect size, standard error of the effect size (ES), t-value, *P*-value and 95% CI. The second estimate is provided from the robust regression analysis that accounts for the nested effect of trial within study from Hedges et al., 2010).

| Variable | ES | SE | t-value | *P*-value | 95% CI | | |
|---|---|---|---|---|---|---|---|
| ADG | 0.374 | 0.080 | 4.670 | 0.001 | 0.216 | - | 0.532 |
| Robust estimate | 0.376 | 0.108 | - | 0.001 | 0.160 | - | 0.593 |
| Final BW | 0.260 | 0.072 | 3.590 | 0.001 | 0.117 | - | 0.403 |
| Robust estimate | 0.270 | 0.098 | - | 0.008 | 0.072 | - | 0.468 |
| HCW | 0.213 | 0.060 | 3.520 | 0.001 | 0.093 | - | 0.332 |
| Robust estimate | 0.255 | 0.086 | - | 0.005 | 0.083 | - | 0.427 |
| G:F | 0.319 | 0.085 | 3.750 | 0.001 | 0.151 | - | 0.487 |
| Robust estimate | 0.304 | 0.104 | - | 0.006 | 0.094 | - | 0.514 |
| DMI | 0.169 | 0.063 | 2.680 | 0.008 | 0.045 | - | 0.292 |
| Robust estimate | 0.188 | 0.096 | - | 0.055 | 0.043 | - | 0.380 |
| LM area | -0.074 | 0.052 | -1.420 | 0.157 | -0.178 | - | 0.029 |
| Robust estimate | -0.015 | 0.083 | - | 0.858 | -0.181 | - | 0152 |
| Fat thickness | 0.313 | 0.062 | 5.020 | 0.001 | 0.190 | - | 0.437 |
| Robust estimate | 0.324 | 0.073 | - | 0.001 | 0.177 | - | 0.470 |

**Table 3.** Weighted mean differences and 95% CI between the treatment and control studies in outcomes with the weighting reflecting the inverse of the variance of the studies included according to no-standard method (Stata Version 14).

| Variable | Weighted mean difference | 95% CI | | |
|---|---|---|---|---|
| ADG, kg/d | 0.058 | 0.039 | - | 0.077 |
| Final BW, kg | 5.547 | 3.259 | - | 7.835 |
| HCW, kg | 3.252 | 1.811 | - | 4.692 |
| G:F, kg/kg | 0.004 | 0.002 | - | 0.006 |
| DMI, kg/d | 0.140 | 0.071 | - | 0.208 |
| LM area, $cm^2$ | -0.151 | -0.594 | - | 0.293 |
| Fat thickness, cm | 0.077 | 0.049 | - | 0.106 |

## 4.4 Multivariable high level models

The models in Table 4 are multivariable meta-regression models using the Knapp-Hartung methods for estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$) and using permutation methods (Higgins and Thompson 2004; Harbord and Higgins 2008; Harbord and Steichen 2004) for estimates of *P*-values. These were developed for the different production outcome variables using pre-trial BW differences or the pre-trial control BW and duration of trial as co-variables and differences in energy or estimated MP balance (CNCPS 6.55) between the treatments and controls. These can be compared with models developed on the basis of CP differences (Table 5) or differences in MP estimates based on NRC (2000) level 1 models (Table 6).

The linear regression between the two methods of estimating MP [i.e. CNCPS 6.55 and NRC (2000)] had a strong association ($R^2$ = 0.80; *P* <0.001) and Lin's concordance 0.86 with an z transformed 95% confidence interval of (0.827 to 0.887) (Fig. 1) and a positive intercept of 112 g and slope 0.9.

However, the models developed using the difference in MP (NRC 2000) intake between treatment and control cattle were poorly fitting (low $R^2$ values; Table 6) compared to those developed based on differences in MP (CNCPS 6.55) in Table 4 or CP (Table 5). Only two models, those for FBW and HCW provided a numerically $R^2$ using CP rather than MP (CNCPS 6.55). The MP (CNCPS 6.55) in Table 4 explained a considerable amount of the variation ($R^2$) in the differences in response between the treated and control groups with the exception of G:F and LMA.

It should be noted that for the meta-regression models for differences in production performance between treated and controls, factors such as breed, sex, rumen modification, and hormonal treatments did not enter the models as these were equally applied to the treated and control groups. These effects were tested in some models including FBW and HCW.

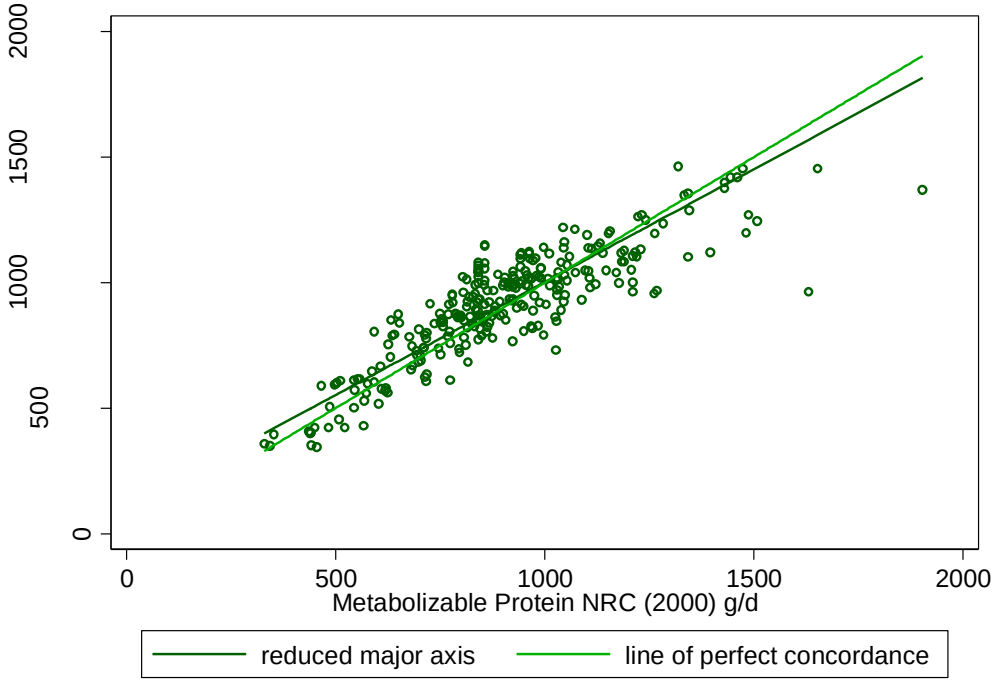


**Fig. 1.** Concordance between Estimated metabolisable protein (MP) as derived using NRC (2000) vs. Cornell (CNCPS) 6.55 derived estimates.

**Table 4.** Outcomes evaluated using multivariable meta-regression models based on differences between treated and control groups for MP estimated in NDS using CNCPS 6.55. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et a., (2010).

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | | | | | | | | |
| Initial BW (Control only), kg | 208 | -0.005 | 0.001 | -0.007 - -0.003 | 68.8 | 36.8 | 0.174 | <0.001 |
| ME, Mcal | | 0.255 | 0.038 | 0.181 - 0.330 | | | | <0.001 |
| MP, g/d | | 0.002 | 0.001 | 0.001 - 0.003 | | | | <0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 - 0.003 | | | | |
| ADG, kg/d (Robust model) | | | | | | | | |
| ME, Mcal | 208 | 0.237 | 0.088 | 0.028 - 0.446 | | | | 0.032 |
| MP, g/d | | 0.003 | 0.001 | 0.001 - 0.019 | | | | <0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Final BW, kg | | | | | | | | |
| Initial BW (Control only), kg | 165 | -0.005 | 0.001 | -0.007 - -0.003 | 91.5 | 17.9 | 0.024 | <0.001 |
| Initial BW, kg | | 0.036 | 0.013 | 0.011 - 0.061 | | | | 0.015 |
| ME, Mcal | | 0.170 | 0.033 | 0.105 - 0.235 | | | | <0.001 |
| MP, g/d | | 0.003 | <0.001 | 0.002 - 0.003 | | | | <0.001 |
| Final BW, kg (Robust model) | | | | | | | | |
| MP, g/d | | 0.003 | <0.001 | 0.001 - 0.005 | | 0 | 0 | 0.005 |
| HCW, kg | | | | | | | | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Initial BW, kg | 172 | -0.003 | 0.001 | -0.005 | - | -0.001 | 86.4 | 10.5 | 0.019 | 0.022 |
| ME, Mcal | | 0.155 | 0.031 | 0.093 | - | 0.217 | | | | <0.001 |
| MP, g/d | | 0.002 | <0.001 | 0.002 | - | 0.003 | | | | <0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | <0.001 |
| HCW, kg (Robust model) | | | | | | | | | | |
| ME, Mcal | | 0.108 | 0.004 | 0.013 | - | 0.202 | | 0 | 0 | 0.031 |
| MP, g/d | | 0.003 | <0.001 | 0.002 | - | 0.005 | | | | 0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.006 |
| G:F, kg/kg | | | | | | | | | | |
| MP, g/d | 157 | 0.001 | 0.001 | <0.001 | - | 0.003 | 25.1 | 64.8 | 0.39 | 0.010 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.027 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 | - | 0.003 | | | | 0.002 |
| G:F, kg/kg (Robust model) | | | | | | | | | | |
| MP, g/d | 157 | 0.001 | 0.001 | -0.002 | - | 0.003 | | 0 | 0 | 0.092 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.001 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 | - | 0.003 | | | | 0.014 |
| DMI, kg/d | | | | | | | | | | |
| ME, Mcal | 212 | 0.264 | 0.031 | 0.202 | - | 0.326 | 66.5 | 19.9 | 0.066 | <0.001 |
| MP, g/d | | 0.003 | <0.001 | 0.002 | - | 0.004 | | | | <0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | <0.001 |
| DMI, kg/d (robust model) | | | | | | | | | | |
| MP, g/d | 212 | 0.004 | <0.001 | 0.002 | - | 0.005 | | 0 | 0 | <0.001 |
| $MP^2$, g/d | | <-0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.018 |
| LM area $cm^2$ | | | | | | | | | | |
| ME, Mcal | 169 | 0.072 | 0.033 | 0.008 | - | 0.137 | NA | 17.2 | 0 | 0.049 |
| MP, g/d | | 0.001 | <0.001 | <0.001 | - | 0.002 | | | | 0.005 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.006 |
| LM area $cm^2$ (Robust model) | No valid model | | | | | | | | | |
| Fat thickness | | | | | | | | | | |
| MP, g/d | 173 | 0.002 | 0.001 | 0.001 | - | 0.003 | 66.9 | 27.0 | 0.035 | <0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.001 |
| Ether extract, g | | 0.001 | 0.001 | <0.001 | - | 0.002 | | | | 0.031 |
| Fat thickness (Robust model) | No valid model | | | | | | | | | |

**Table 5.** Outcomes evaluated using multivariable meta-regression models based on differences between intake of CP for treated and control groups. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. *Adjusted P-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et al., 2010).

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | | | | | | | | |
| Initial BW (Control only), kg | 208 | -0.004 | 0.001 | -0.006 - -0.002 | 65.5 | 36.6 | 0.193 | 0.006 |
| ME, Mcal | | 0.257 | 0.038 | 0.182 - 0.332 | | | | <0.001 |
| CP, g | | 0.002 | <0.001 | 0.002 - 0.003 | | | | <0.001 |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Ether extract, g | | 0.003 | 0.001 | 0.002 - 0.004 | | | | <0.001 |
| ADG, kg/d (Robust model) | | | | | | | | |
| ME, Mcal | 208 | 0.267 | 0.098 | 0.035 - 0.498 | | | | 0.03 |
| CP, g | | 0.003 | <0.001 | 0.002 - 0.004 | | | | <0.001 |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Final BW, kg | | | | | | | | |
| Initial BW, kg | 165 | -0.004 | 0.001 | -0.006 - -0.002 | 99.4 | 13.7 | 0.002 | 0.002* |
| ME, Mcal | | 0.198 | 0.031 | 0.136 - 0.260 | | | | <0.001* |
| CP, g | | 0.002 | <0.001 | 0.002 - 0.003 | | | | <0.001* |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001* |
| Final BW, kg (Robust model) | | | | | | | | |
| Final BW, kg | | | | | | | | |
| CP, g | | 0.003 | <0.001 | 0.002 - 0.004 | | 0 | 0 | 0.004 |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| HCW, kg | | | | | | | | | |
| ME, Mcal | 172 | 0.159 | 0.032 | 0.096 | - 0.221 | 98.7 | 10.0 | 0.002 | <0.001 |
| CP, g | | 0.002 | <0.001 | 0.001 | - 0.003 | | | | <0.001 |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 | - <0.001 | | | | <0.001 |
| Ether extract, g | | 0.001 | <0.001 | <0.001 | - 0.002 | | | | 0.018 |
| HCW, kg (Robust model) | | | | | | | | | |
| ME, Mcal | 172 | 0.142 | 0.045 | 0.037 | - 0.248 | | 0 | 0 | 0.015 |
| CP, g | | 0.002 | <0.001 | 0.002 | - 0.003 | | | | 0.002 |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 | - <0.001 | | | | 0.004 |
| DMI, kg/d | | | | | | | | | |
| ME, Mcal | 212 | 0.287 | 0.033 | 0.221 | - 0.352 | 51.5 | 30.6 | 0.096 | <0.001 |
| CP, g | | 0.002 | <0.001 | 0.001 | - 0.002 | | | | <0.001 |
| $CP^2$, g | | <0.001 | <0.001 | <0.001 | - <0.001 | | | | 0.007 |
| DMI, kg/d (Robust model) | | | | | | | | | |
| ME, Mcal | 212 | 0.306 | 0.125 | 0.005 | - 0.608 | | 0 | 0 | 0.048 |
| CP, g | | 0.001 | <0.001 | <0.001 | - 0.002 | | | | 0.004 |
| G:F, kg/kg | | | | | | | | | |
| CP, g | 157 | 0.002 | 0.001 | 0.001 | - 0.003 | 23.8 | 65.4 | 0.403 | 0.004 |
| $CP^2$, g | | <-0.001 | <0.001 | <0.001 | - 0.001 | | | | 0.001 |
| Ether extract, g | | 0.003 | 0.001 | 0.001 | - 0.004 | | | | <0.001 |
| G:F kg/kg (Robust model) | | | | | | | | | |
| CP, g | 157 | 0.002 | 0.001 | <0.001 | - 0.003 | | 0 | 0 | 0.050 |
| $CP^2$, g | | <-0.001 | <0.001 | <0.001 | - 0.001 | | | | 0.053 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 | - 0.004 | | | | 0.036 |
| LM area $cm^2$ | | | | | | | | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| CP, g | 157 | 0.006 | 0.003 | <-0.001 | - | 0.001 | - | 21.8 | 0 | 0.058 |
| $CP^2$, g | | <-0.001 | <0.001 | <0.001 | - | 0.001 | | | | 0.028 |
| LM area $cm^2$ (Robust model) | No valid model | | | | | | | | | |
| Fat thickness, cm | | | | | | | | | | |
| CP, g | 173 | 0.086 | 0.036 | 0.014 | - | 0.157 | 44.0 | 29.5 | 0.059 | 0.030 |
| $CP^2$, g | | 0.001 | <0.001 | <0.001 | - | 0.001 | | | | 0.005 |
| Ether extract, g | | 0.001 | 0.001 | <0.001 | - | 0.002 | | | | 0.030 |
| Fat thickness, cm (Robust model) | | | | | | | | | | |
| CP, g | 173 | 0.001 | 0.001 | <0.001 | - | 0.001 | | 0 | 0 | 0.053 |
| $CP^2$, g | | 0.001 | 0.001 | <0.001 | - | 0.002 | | | | 0.043 |

**Table 6.** Outcomes evaluated using multivariable meta-regression models based on differences for MP differences between treated and control groups estimated from NRC (2000) level 1. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et al., 2010).

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | No valid model | | | | | | | |
| Final BW, kg | | | | | | | | |
| Initial BW (Control only), kg | 163 | -0.005 | 0.001 | -0.008 - -0.002 | 91.3 | 26.5 | 0.022 | 0.001 |
| Initial BW, kg | | 0.035 | 0.013 | 0.008 - 0.062 | | | | 0.039 |
| ME, Mcal | | 0.194 | 0.036 | 0.123 - 0.265 | | | | <0.001 |
| MP NRC, g/d | | 0.001 | 0.000 | 0.000 - 0.001 | | | | 0.004 |
| Final BW, kg (Robust model) | No valid model | | | | | | | |
| HCW, kg | No valid model | | | | | | | |
| G:F, kg/kg | No valid model | | | | | | | |
| DMI, kg/d | | | | | | | | |
| Initial BW (Control only), kg | 209 | -0.003 | 0.001 | -0.005 - <0.001 | 47.6 | 34.2 | 0.102 | 0.048 |
| ME, Mcal | | 0.300 | 0.035 | 0.232 - 0.369 | | | | <0.001 |
| MP NRC, g/d | | 0.001 | <0.001 | <0.001 - 0.001 | | | | 0.020 |
| DMI, kg/d (Robust model) | No valid model | | | | | | | |
| LM area $cm^2$ | No valid model | | | | | | | |
| Fat thickness, cm | No valid model | | | | | | | |

## 4.5 Multivariable protein fraction models

The models in Table 7 are multivariable models for evaluating the different production outcomes using trial duration, pre-trial BW differences or the pre-trial control BW as co-variables and differences in energy, ether extract and estimated protein fractions in the rumen between the treatments and controls. In general, these models explained slightly less of the variation in outcomes than explained by estimated MP (CNCPS 6.55; Table 4) or CP (Table 5). However, G:F and DMI differences were exceptions to that (Table 7).

**Table 7.** Outcomes evaluated using multivariable meta-regression models based on differences between treated and control groups for ruminal protein fractions[1] estimated in NDS using CNCPS 6.55. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et al., 2010).

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | | | | | | | | |
| Initial BW (Control only), kg | 207 | -0.005 | 0.001 | -0.007 - -0.002 | 65.6 | 38.1 | 0.192 | <0.001 |
| ME, Mcal | | 0.282 | 0.039 | 0.205 - 0.359 | | | | <0.001 |
| Soluble intake protein, g | | 0.001 | <0.001 | <0.001 - 0.001 | | | | 0.725 |
| Soluble intake protein$^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 - 0.003 | | | | <0.001 |
| ADG, kg/d (Robust model) | 207 | | | | | | | |
| ME, Mcal | | 0.266 | 0.092 | 0.046 - 0.486 | | 0 | 0 | 0.025 |
| Soluble intake protein, g | | <0.001 | <0.001 | <0.001 - 0.002 | | | | 0.640 |
| Soluble intake protein$^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | 0.006 |
| Final BW, kg | | | | | | | | |
| Initial BW (Control only), kg | 165 | -0.005 | 0.001 | -0.008 - -0.003 | 87.9 | 24.5 | 0.034 | <0.001 |
| ME, Mcal | | 0.223 | 0.034 | 0.156 - 0.290 | | | | <0.001 |
| Protein $B_1$, g | | 0.002 | <0.001 | 0.001 - 0.002 | | | | <0.001 |
| Final BW, kg (Robust model) | | | | | | | | |
| ME, Mcal | | 0.208 | 0.089 | -0.009 - 0.427 | | | | 0.006 |
| Protein $B_1$, g | | 0.002 | <0.001 | <0.001 - 0.003 | | | | 0.011 |
| HCW, kg | | | | | | | | |
| Initial BW (Control only), kg | 172 | -0.003 | 0.001 | -0.006 - -0.001 | 48 | 21.5 | 0.074 | 0.051 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ME, Mcal | | 0.213 | 0.034 | 0.145 | - | 0.280 | | | <0.001 |
| Protein $B_1$, g | | 0.002 | <0.001 | 0.001 | - | 0.002 | | | <0.001 |
| Protein $A_2$, g | | -0.002 | 0.001 | -0.003 | - | <0.001 | | | 0.131 |
| Protein $A_2^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | 0.007 |
| HCW, kg (Robust model) | | | | | | | | | |
| ME, Mcal | | 0.151 | 0.048 | 0.038 | - | 0.263 | | | 0.015 |
| Protein $B_1$, g | | 0.001 | <0.001 | 0.001 | - | 0.002 | | | 0.048 |
| G:F, kg/kg | | | | | | | | | |
| Soluble intake protein, g | 157 | 0.001 | <0.001 | <0.001 | - | 0.002 | 73.4 | 41.7 | 0.138 | 0.054 |
| Soluble intake protein$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.001 |
| Protein $A_2$, g | | -0.003 | 0.001 | -0.004 | - | -0.002 | | | | <0.001 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 | - | 0.003 | | | | 0.001 |
| G:F, kg/kg (Robust model) | | | | | | | | | |
| Soluble intake protein, g | 157 | 0.001 | <0.001 | <0.001 | - | 0.002 | | 0 | 0 | 0.161 |
| Soluble intake protein$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.029 |
| Protein $A_2$, g | | -0.002 | 0.001 | -0.004 | - | -0.002 | | | | 0.018 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 | - | 0.003 | | | | 0.021 |
| DMI, kg/d | | | | | | | | | |
| ME, Mcal | 212 | 0.310 | 0.029 | 0.253 | - | 0.368 | 100 | 0 | 0 | <0.001 |
| Protein $A_2$, g | | 0.003 | <0.001 | 0.003 | - | 0.004 | | | | <0.001 |
| DMI, kg/d (Robust model) | | | | | | | | | |
| Protein $A_2$, g | | 0.003 | <0.001 | 0.002 | - | 0.004 | | 0 | 0 | <0.001 |
| LM area $cm^2$ | | | | | | | | | |
| ME, Mcal | 169 | 0.096 | 0.033 | 0.030 | - | 0.161 | NA | 18.1 | 0 | 0.004 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Protein $A_2$, g | | 0.001 | <0.001 | <0.001 | - | 0.002 | | | | 0.004 |
| LM area $cm^2$ (Robust model) | | | | | | | | | | |
| ME, Mcal | 169 | 0.102 | 0.004 | -0.003 | - | 0.206 | | 0 | 0 | 0.055 |
| Protein $A_2$, g | | 0.002 | <0.001 | 0.001 | - | 0.003 | | | | 0.006 |
| Fat thickness, cm | | | | | | | | | | |
| Protein $B_1$, g | 173 | 0.001 | <0.001 | 0.001 | - | 0.002 | 41.3 | 29.3 | 0.062 | <0.001 |
| ME, Mcal | | 0.105 | 0.036 | 0.034 | - | 0.176 | | | | 0.004 |
| Fat thickness, cm (Robust model) | | | | | | | | | | |
| Protein $B_1$, g | 173 | 0.001 | <0.001 | 0.001 | - | 0.002 | | 0 | 0 | 0.03 |

[1] Composition and digestion of protein fractions from CNCPS 6.55 is as follows:

A = Ammonia, $NO_3$, amino acids, and peptides, ruminal and intestinal digestion rate is instantaneous (10,000) and 100%, respectively

$B_1$ = Globulins and some albumins, ruminal and intestinal digestion rate is 200-300 %/h and 100%, respectively

$B_2$ = Most albumins and glutelins, ruminal and intestinal digestion rate is 5-15%/h and 100%, respectively

$B_3$ = Prolamins, extension proteins, and denatured proteins, ruminal and intestinal digestion rate is 0.1-1.5%/h and 80%, respectively

C = Maillard products N bound to lignin, ruminal and intestinal digestion rate are both 0%

## 4.6 RDP and RUP models

The models in Table 8 are multivariable models for outcomes using trial duration, pre-trial BW differences or the pre-trial control BW as co-variables and differences in RDP and RUP, ether extract between the treatments and controls. In general, the RUP x1 maintenance models explained less of the variation in outcomes than explained by estimated MP (CNCPS 6.55; Table 4) or CP (Table 5), except for DMI (Table 8). RDP x3 maintenance models explained more variation than the MP (CNCPS 6.55) model for Final BW and HCW (Table 8).

**Table 8.** Outcomes evaluated using multivariable meta-regression models based on differences between treated and control groups in estimated RDP x3 maintenance and RUP x1 maintenance estimated in NDS using CNCPS 6.55. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et al., 2010).

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | | | | | | | | |
| Initial BW (Control only), kg | 207 | -0.005 | 0.001 | -0.008 - -0.003 | 62.6 | 39.5 | 0.211 | <0.001 |
| ME, Mcal | | 0.265 | 0.038 | 0.189 - 0.341 | | | | <0.001 |
| RDP x3 maintenance, g | | 0.002 | <0.001 | 0.001 - 0.002 | | | | 0.001 |
| RDP x3 maintenance$^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Ether extract, g | | 0.003 | <0.001 | 0.002 - 0.004 | | | | <0.001 |
| ADG, kg/d (Robust model) | | | | | | | | |
| Initial BW (Control only), kg | 207 | -0.006 | 0.002 | -0.011 - -0.001 | | 0 | 0 | 0.020 |
| ME, Mcal | | 0.255 | 0.010 | 0.018 - 0.491 | | | | 0.038 |
| RDP x3 maintenance, g | | 0.002 | <0.001 | <0.001 - 0.004 | | | | 0.012 |
| RDP x3 maintenance$^2$, g | | <0.001 | <0.001 | <-0.001 - <-0.001 | | | | 0.022 |
| Ether extract, g | | 0.003 | <0.001 | 0.002 - 0.004 | | | | <0.001 |
| Initial BW (Control only), kg | 207 | -0.004 | 0.001 | -0.007 - -0.002 | 49.2 | 45.2 | 0.287 | 0.005 |
| ME, Mcal | | 0.276 | 0.043 | 0.191 - 0.360 | | | | <0.001 |
| RUP x1 maintenance, g | | 0.002 | 0.001 | 0.001 - 0.003 | | | | 0.024 |
| RUP x1 maintenance$^2$, g | | 0.000 | 0.000 | 0.000 - 0.000 | | | | 0.062 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 - 0.003 | | | | 0.003 |
| ADG, kg/d (Robust model) | No valid model for RUP 1x | | | | | | | |
| Final BW, kg | | | | | | | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 165 | -0.005 | 0.001 | -0.007 | - | -0.003 | 91.9 | 20.7 | 0.023 | <0.001 |
| ME, Mcal | | 0.187 | 0.033 | 0.122 | - | 0.251 | | | | <0.001 |
| RDP x3 maintenance, g | | 0.002 | <0.001 | 0.001 | - | 0.003 | | | | <0.001 |
| RDP x3 maintenance$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.010 |
| Ether extract, g | | 0.001 | <0.001 | 0.001 | - | 0.002 | | | | 0.006 |
| Final BW, kg (Robust model) | 165 | | | | | | | | | |
| RDP x3 maintenance, g | | 0.002 | <0.001 | <0.001 | - | 0.003 | | 0 | 0 | 0.016 |
| HCW, kg | | | | | | | | | | |
| Initial BW (Control only), kg | 171 | -0.003 | 0.001 | -0.005 | - | -0.001 | 94.5 | 14.7 | 0.008 | 0.011 |
| ME, Mcal | | 0.168 | 0.032 | 0.105 | - | 0.231 | | | | <0.001 |
| RDP x3 maintenance, g | | 0.001 | <0.001 | 0.001 | - | 0.002 | | | | <0.001 |
| RDP x3 maintenance$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | <0.001 |
| Ether extract, g | | 0.002 | <0.001 | 0.001 | - | 0.002 | | | | <0.001 |
| HCW, kg (Robust model) | 171 | | | | | | | | | |
| RDP x3 maintenance, g | | 0.002 | <0.001 | <0.001 | - | 0.003 | | 0 | 0 | 0.016 |
| ME, Mcal | 171 | 0.171 | 0.035 | 0.102 | - | 0.240 | 69.9 | 21.6 | 0.044 | <0.001 |
| RUP x1 maintenance, g | | 0.002 | <0.001 | 0.001 | - | 0.003 | | | | <0.001 |
| RUP x1 maintenance$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.004 |
| HCW, kg (Robust model) | 171 | | | | | | | | | |
| RUP x1 maintenance, g | | 0.003 | <0.001 | 0.001 | - | 0.004 | | 0 | 0 | 0.005 |
| RUP x1 maintenance$^2$, g | | <-0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.005 |
| G:F, kg/kg | No valid model | | | | | | | | | |
| DMI, kg/d | | | | | | | | | | |
| ME, Mcal | 211 | 0.276 | 0.033 | 0.212 | - | 0.341 | 48.2 | 32.0 | 0.101 | <0.001 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| RDP x3 maintenance, g | | 0.001 | <0.001 | 0.001 | - | 0.002 | | | | <0.001 |
| Ether extract, g | | 0.001 | <0.001 | <0.001 | - | 0.002 | | | | 0.037 |
| DMI, kg/d (Robust model) | | | | | | | | | | |
| ME, Mcal | 211 | 0.284 | 0.110 | 0.020 | - | 0.548 | | 0 | 0 | 0.038 |
| RDP x3 maintenance, g | | 0.002 | <0.001 | 0.001 | - | 0.003 | | | | 0.001 |
| Ether extract, g | | 0.001 | <0.001 | -<0.001 | - | 0.002 | | | | 0.057 |
| ME, Mcal | 211 | 0.274 | 0.034 | 0.206 | - | 0.342 | 55.7 | 30.0 | 0.086 | <0.001 |
| RUP x1 maintenance, g | | 0.002 | <0.001 | 0.001 | - | 0.003 | | | | <0.001 |
| RUP x1 maintenance$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.001 |
| DMI, kg/d (Robust model) | 211 | | | | | | | | | |
| RUP x1 maintenance, g | | 0.002 | <0.001 | <0.001 | - | 0.004 | | 0 | 0 | <=0.021 |
| RUP x1 maintenance$^2$, g | | <0.001 | <0.001 | <-0.001 | - | <-0.001 | | | | 0.013 |
| LM area cm$^2$ | No valid model | | | | | | | | | |
| Fat thickness | | | | | | | | | | |
| ME, Mcal | 172 | 0.107 | 0.037 | 0.034 | - | 0.179 | 44.6 | 30.6 | 0.059 | 0.004 |
| RUP x1 maintenance, g | | 0.001 | <0.001 | 0.001 | - | 0.002 | | | | <0.001 |
| Fat thickness (Robust model) | | | | | | | | | | |
| RUP x1 maintenance, g | | 0.001 | <0.001 | 0.001 | - | 0.002 | | | | 0.036 |

## 4.7 Multivariable amino acid models

The models in Table 9 are multivariable models for evaluating the different production outcomes using trial duration, pre-trial BW differences or the pre-trial control BW as co-variables and differences in energy and estimated MP amino acids (g/d) between the treatments and controls. Multivariable models (other than quadratic models) were not developed for the differences in amino acid intake expressed as a function of ME intake as there were very few examples of these being more significant than the g of MP amino acid estimates. While these models often explained more of the variation in outcomes than differences in treatments and controls in estimated MP intake (Table 4) or CP (Table 5) in the diet, the models were often unstable due to collinearity among amino acids (Fig. 2). We consider that these models should be interpreted with caution.

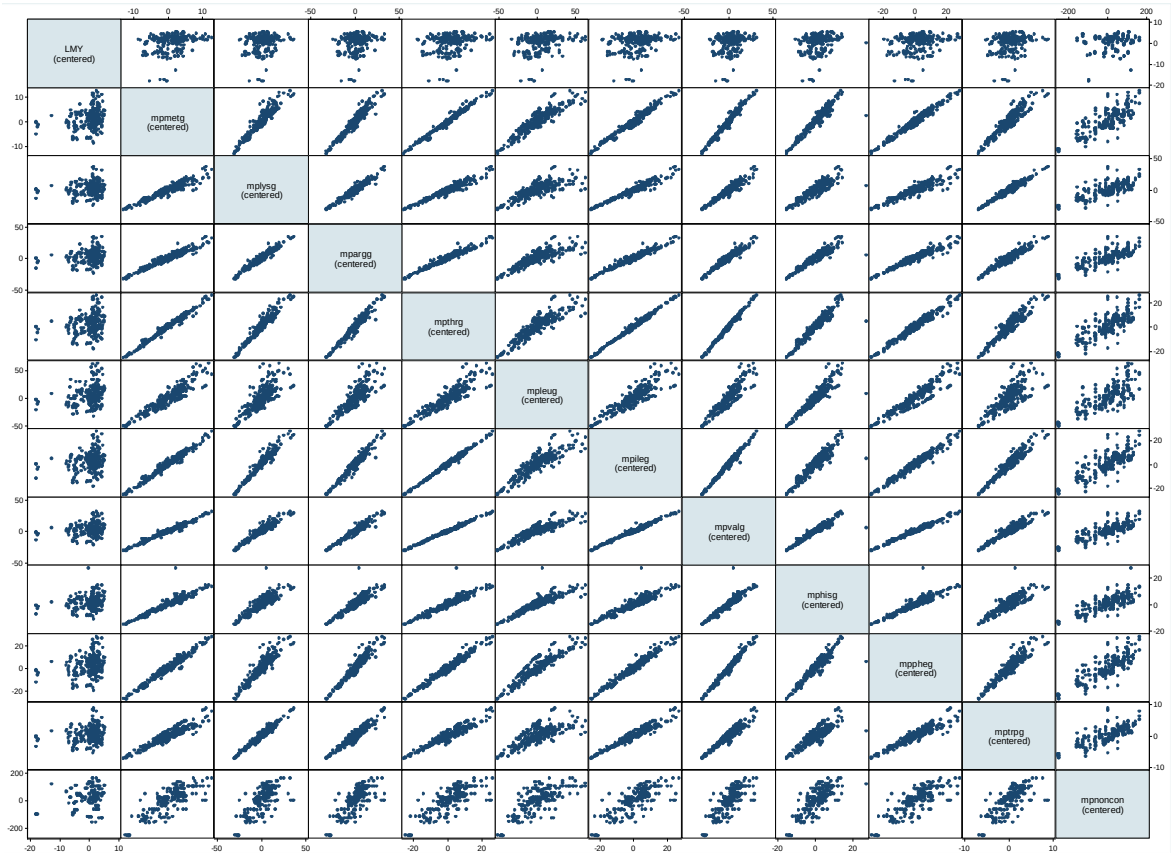


**Fig. 2.** Matrix plot of lean muscle yield (kg) centred against metabolisable protein (MP) amino acid intakes (g/d) centred showing the very marked collinearity among the amino acids.

**Table 9.** Outcomes evaluated using multivariable meta-regression models based on differences between treated and control groups in estimated MP amino acid availability estimated in NDS using CNCPS 6.55. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et al., 2010).

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | | | | | | | | |
| ME, Mcal | 208 | 0.264 | 0.038 | 0.190 - 0.338 | 83.7 | 26.7 | 0.091 | <0.001 |
| MP Thr, g | | -0.091 | 0.033 | -0.156 - -0.026 | | | | 0.070 |
| MP Thr$^2$, g | | -0.008 | 0.002 | -0.011 - -0.005 | | | | <0.001 |
| MP Leu, g | | -0.065 | 0.011 | -0.088 - -0.043 | | | | <0.001 |
| MP Leu$^2$, g | | -0.001 | <0.001 | -0.002 - 0.000 | | | | 0.003 |
| MP Phe, g | | 0.182 | 0.038 | 0.107 - 0.257 | | | | <0.001 |
| MP non-essential AA, g | | 0.008 | 0.002 | 0.003 - 0.013 | | | | 0.007 |
| MP non-essential AA$^2$, g | | <0.001 | <0.001 | <0.001 - <0.001 | | | | <0.001 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 - 0.003 | | | | 0.002 |
| ADG, kg/d (Robust model) | No valid model | | | | | | | |
| Final BW, kg | | | | | | | | |
| Initial BW (Control only), kg | 165 | -0.004 | 0.001 | -0.006 - -0.001 | 100 | 2.1 | 0 | 0.019 |
| ME, Mcal | | 0.175 | 0.031 | 0.113 - 0.236 | | | | <0.001 |
| MP Leu, g | | -0.046 | 0.010 | -0.065 - -0.026 | | | | <0.001 |
| MP Leu$^2$, g | | -0.001 | <0.001 | -0.002 - -0.001 | | | | <0.001 |
| MP Val, g | | -0.115 | 0.040 | -0.194 - -0.036 | | | | 0.053 |
| MP Val$^2$, g | | -0.014 | 0.004 | -0.021 - -0.006 | | | | 0.003 |
| MP Phe, g | | 0.230 | 0.038 | 0.154 - 0.305 | | | | <0.001 |
| MP Phe$^2$, g | | 0.012 | 0.005 | 0.004 - 0.021 | | | | 0.060 |
| MP non-essential AA, g | | 0.004 | 0.002 | -0.001 - 0.009 | | | | 0.523 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| MP non-essential AA$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | 0.002 |
| Final BW, kg (Robust model) | | | | | | | | | |
| MP Leu, g | 165 | -0.047 | 0.017 | -0.083 | - | -0.011 | | | 0.014 |
| MP Leu$^2$, g | | -0.002 | <0.001 | -0.002 | - | -0.001 | | | 0.003 |
| MP Val, g | | -0.030 | 0.063 | -0.102 | - | 0.161 | | | 0.643 |
| MP Val$^2$, g | | -0.016 | 0.004 | -0.027 | - | -0.005 | | | 0.007 |
| MP Phe, g | | 0.140 | 0.079 | -0.029 | - | 0.309 | | | 0.098 |
| MP Phe$^2$, g | | 0.017 | 0.005 | 0.005 | - | 0.028 | | | 0.007 |
| MP non-essential AA, g | | 0.040 | 0.050 | -0.141 | - | 0.060 | | | 0.410 |
| MP non-essential AA$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | 0.046 |
| HCW, kg | | | | | | | | | |
| Initial BW (Control only), kg | 172 | -0.005 | 0.001 | -0.007 | - | -0.002 | 100 | 1.2 | 0 | <0.001 |
| ME, Mcal | | 0.174 | 0.030 | 0.116 | - | 0.233 | | | | <0.001 |
| MP Met, g | | -0.174 | 0.042 | -0.257 | - | -0.091 | | | | <0.001 |
| MP Met$^2$, g | | -0.010 | 0.002 | -0.013 | - | -0.006 | | | | <0.001 |
| MP Phe, g | | 0.120 | 0.021 | 0.080 | - | 0.161 | | | | <0.001 |
| HCW, kg (Robust model) | | | | | | | | | |
| Initial BW (Control only), kg | 172 | -0.005 | 0.002 | -0.010 | - | -0.001 | | 0 | 0 | 0.037 |
| ME, Mcal | | 0.140 | 0.053 | 0.012 | - | 0.267 | | | | 0.036 |
| MP Met, g | | -0.147 | 0.065 | -0.293 | - | -0.002 | | | | 0.048 |
| MP Met$^2$, g | | -0.011 | 0.003 | -0.013 | - | -0.004 | | | | 0.013 |
| MP Phe, g | | 0.111 | 0.005 | 0.041 | - | 0.180 | | | | 0.005 |
| G:F, kg/kg | | | | | | | | | |
| MP Met, g | 157 | -0.030 | 0.055 | -0.139 | - | 0.078 | 44.4 | 53.4 | 0.289 | 0.940 |
| MP Met$^2$, g | | -0.017 | 0.004 | -0.024 | - | -0.010 | | | | <0.001 |
| MP Lys, g | | -0.121 | 0.030 | -0.181 | - | -0.061 | | | | <0.001 |
| MP Trp, g | | 0.762 | 0.169 | 0.429 | - | 1.095 | | | | <0.001 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| G:F, kg/kg (Robust model) | | | | | | | | | |
| MP Met, g | 157 | -0.047 | 0.006 | -0.174 | - | 0.081 | 44.4 | 53.4 | 0.289 | 0.455 |
| MP Met$^2$, g | | -0.017 | 0.003 | -0.026 | - | -0.008 | | | | 0.005 |
| MP Lys, g | | -0.101 | 0.040 | -0.185 | - | -0.016 | | | | 0.022 |
| MP Trp, g | | 0.689 | 0.193 | 0.267 | - | 1.111 | | | | 0.004 |
| DMI, kg/d | | | | | | | | | | |
| ME, Mcal | 212 | 0.289 | 0.030 | 0.229 | - | 0.348 | 100 | 0 | 0 | <0.001 |
| MP Leu, g | | -0.053 | 0.010 | -0.072 | - | -0.034 | | | | <0.001 |
| MP Leu$^2$, g | | -0.001 | 0.000 | -0.001 | - | 0.000 | | | | 0.001 |
| MP Val, g | | 0.149 | 0.048 | 0.054 | - | 0.243 | | | | 0.009 |
| MP Val$^2$, g | | -0.004 | 0.001 | -0.007 | - | -0.001 | | | | 0.010 |
| MP Trp, g | | -0.401 | 0.098 | -0.594 | - | -0.209 | | | | <0.001 |
| MP non-essential AA, g | | 0.008 | 0.002 | 0.004 | - | 0.013 | | | | 0.001 |
| MP non-essential AA$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.009 |
| DMI, kg/d (Robust model) | | | | | | | | | | |
| MP Leu, g | 212 | -0.037 | 0.014 | -0.068 | - | -0.007 | | 0 | 0 | 0.021 |
| MP Leu$^2$, g | | -0.002 | <0.001 | -0.002 | - | -0.001 | | | | 0.007 |
| MP Val, g | | 0.200 | 0.061 | 0.073 | - | 0.327 | | | | 0.004 |
| MP Trp, g | | -0.406 | 0.115 | -0.658 | - | -0.154 | | | | 0.005 |
| MP non-essential AA, g | | 0.003 | 0.003 | -0.004 | - | 0.010 | | | | 0.434 |
| MP non-essential AA$^2$, g | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.038 |
| LM area cm$^2$ | No valid model | | | | | | | | | |
| Fat thickness, cm | | | | | | | | | | |
| MP Leu, g | 173 | -0.009 | 0.016 | -0.040 | - | 0.022 | 78.6 | 22.1 | 0.023 | 0.970 |
| MP Leu$^2$, g | | -0.001 | <0.001 | -0.002 | - | <0.001 | | | | 0.002 |
| MP Phe, g | | 0.122 | 0.058 | 0.007 | - | 0.237 | | | | 0.131 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| MP Phe$^2$, g | | 0.008 | 0.003 | 0.002 | - | 0.014 | | | 0.004 |
| MP Trp, g | | -0.191 | 0.126 | -0.440 | - | 0.059 | | | 0.445 |
| MP Trp$^2$, g | | -0.057 | 0.018 | -0.093 | - | -0.022 | | | 0.001 |
| Fat thickness, cm (Robust model) | | | | | | | | | |
| MP Leu, g | 173 | 0.002 | 0.015 | -0.034 | - | 0.038 | 0 | 0 | 0.908 |
| MP Leu$^2$, g | | -0.002 | 0.001 | -0.002 | - | <-0.001 | | | 0.031 |
| MP Phe, g | | 0.007 | 0.055 | -0.053 | - | 0.197 | | | 0.224 |
| MP Phe$^2$, g | | 0.008 | 0.004 | <-0.001 | - | 0.017 | | | 0.052 |
| MP Trp, g | | -0.059 | 0.123 | -0.325 | - | 0.208 | | | 0.641 |
| MP Trp$^2$, g | | -0.065 | 0.024 | -0.121 | - | -0.009 | | | 0.029 |

## 4.8 Multivariable energy source models

The models in Table 10 are multivariable models for evaluating the different production outcomes using pre-trial BW differences or the pre-trial control BW as co-variables and differences in estimated MP (g/d) between the treatments and controls. In these models, difference in ME intake was not used, rather differences in energy source intake including carbohydrate fractions and ether extract were used to describe energy intake. These models provide insights into diet structure that are potentially important in understanding diet responses, particularly in regard to fibre components. Energy source models in general described the least amount of variation in production outcomes, with the exception of DMI and there were no valid models for some outcomes.

**Table 10.** Outcomes evaluated using multivariable meta-regression models based on differences between treated and control groups in estimated MP and components of the diet contributing to energy intake estimated in NDS using CNCPS 6.55. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. The robust regression model that accounts for the nested effect of trial within study was used to determine the robust model results (Hedges et al., 2010).

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| ADG, kg/d | | | | | | | | | | |
| Initial BW (Control only), kg | 209 | -0.004 | 0.001 | -0.007 | - | -0.001 | 36.8 | 49.5 | 0.350 | 0.010 |
| Initial BW, kg | | 0.050 | 0.017 | 0.017 | - | 0.084 | | | | 0.009 |
| Amylase NDFom, g | | -0.001 | <0.001 | -0.002 | - | -0.001 | | | | <0.001 |
| Physically effective NDF, g | | 0.003 | 0.001 | 0.002 | - | 0.005 | | | | <0.001 |
| Ether extract, g | | 0.005 | 0.001 | 0.004 | - | 0.007 | | | | <0.001 |
| ADG, kg/d (Robust model) | 209 | | | | | | | | | |
| Physically effective NDF, g | | 0.012 | <0.001 | 0.001 | - | 0.024 | | 0 | 0 | 0.039 |
| Ether extract, g | | 0.003 | <0.001 | 0.001 | - | 0.004 | | | | 0.003 |
| Final BW, kg | No valid model | | | | | | | | | |
| HCW, kg | | | | | | | | | | |
| Initial BW, kg | 172 | 0.061 | 0.017 | 0.027 | - | 0.095 | 47.8 | 25.4 | 0.074 | 0.001 |
| Physically effective NDF, g | | 0.001 | <0.001 | <0.001 | - | 0.002 | | | | <0.001 |
| Acid detergent lignin, g | | -0.003 | 0.001 | -0.006 | - | -0.001 | | | | 0.021 |
| Simple sugars, g | | 0.002 | 0.001 | <0.001 | - | 0.003 | | | | 0.028 |
| Ether extract, g | | 0.002 | 0.001 | 0.001 | - | 0.003 | | | | <0.001 |
| HCW, kg (Robust model) | | | | | | | | | | |
| Initial BW, kg | 172 | 0.067 | 0.021 | 0.021 | - | 0.113 | | 0 | 0 | 0.009 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Physically effective NDF, g | | 0.001 | <0.001 | <0.001 | - | 0.002 | | | | 0.030 |
| Ether extract, g | | 0.001 | 0.001 | <0.001 | - | 0.003 | | | | <0.001 |
| G:F, kg/kg | No valid model | | | | | | | | | |
| DMI, kg/d | | | | | | | | | | |
| Initial BW, kg | 212 | 0.047 | 0.013 | 0.022 | - | 0.072 | 69.0 | 22.4 | 0.061 | 0.001 |
| MP, g/d | | 0.003 | 0.001 | 0.002 | - | 0.004 | | | | <0.001 |
| $MP^2$, g/d | | <0.001 | <0.001 | <0.001 | - | <0.001 | | | | 0.049 |
| Amylase NDFom, g | | 0.001 | <0.001 | <0.001 | - | 0.001 | | | | <0.001 |
| Acid detergent lignin, g | | -0.008 | 0.002 | -0.011 | - | -0.004 | | | | <0.001 |
| Simple sugars, g | | 0.002 | 0.001 | 0.001 | - | 0.004 | | | | 0.003 |
| Soluble fibre, g | | -0.001 | <0.001 | -0.001 | - | <0.001 | | | | 0.016 |
| Ether extract, g | | 0.001 | 0.001 | <0.001 | - | 0.003 | | | | 0.028 |
| DMI, kg/d (Robust model) | | | | | | | | | | |
| Simple sugars, g | | 0.003 | 0.001 | 0.001 | - | 0.005 | | 0 | 0 | 0.003 |
| LM area $cm^2$ | No valid model | | | | | | | | | |
| Fat thickness, cm | No valid model | | | | | | | | | |

## 4.9 Predictions of lean muscle yield

There were 230 observations used in the LMY dataset. LMY had a mean±SD of 90.48±4.07 kg and a minimum, median, and maximum of 72.25, 91.76, and 95.91 kg, respectively. There were several approaches used to predict LMY. These approaches differed from the classical meta-analytical approaches because LMY was predicted for each diet and final models included the random effect of study in the unweighted models. The effect of trial nested within study explained 1.1% of the variance and was consequently excluded from the models. The lack of use of a weight for study reflected the fact that LMY is a synthetic variable and consequent lack of estimates of variance. Further, study sizes were of relatively similar size. This provided the advantage of allowing an evaluation of the effects of breed, sex, feeding interventions, diet base (grains and protein interventions), and hormonal implant strategies on LMY. The classical meta-analytical methods of evaluation are effectively balanced for these effects and it is unusual for these effects to come in to the models under those conditions.

The following are the univariable models that predict LMY (Table 11).

**Table 11.** Univariable analyses for lean muscle yield (kg). Includes number of comparisons used (No.), coefficient, standard error (SE), 95% CI, estimates of model fit ($R^2$), *F*-value, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | *F*-value | *P*-value |
|---|---|---|---|---|---|---|---|---|---|
| Pre-study hormonal implant | 231 | -1.105 | 0.822 | -2.725 | - | 0.515 | 0.4 | 1.81 | 0.180 |
| Length of hormonal implant, d | 231 | 1.577 | 0.756 | 0.089 | - | 3.066 | 1.4 | 4.36 | 0.038 |
| Implant no. 2 | 231 | 0.220 | 0.098 | 0.027 | - | 0.412 | 1.7 | 5.05 | 0.026 |
| Monensin dose, mg/kg DM | 231 | 0.123 | 0.018 | 0.088 | - | 0.158 | 17.1 | 48.31 | <0.001 |
| Tylosin dose, mg/kg DM | 231 | 0.150 | 0.051 | 0.049 | - | 0.250 | 3.2 | 8.63 | 0.004 |
| Lasalocid dose, mg/kg DM | 231 | -0.288 | 0.084 | -0.453 | - | -0.123 | 4.5 | 11.83 | 0.001 |
| Treatment length (d) | 231 | 0.033 | 0.008 | 0.018 | - | 0.049 | 7.0 | 18.26 | <0.001 |
| Initial BW, kg | 231 | 0.015 | 0.006 | 0.003 | - | 0.026 | 2.4 | 6.56 | 0.011 |
| ME, Mcal | 231 | 0.417 | 0.072 | 0.274 | - | 0.560 | 12.3 | 33.13 | <0.001 |
| MP, g/d | 231 | 0.005 | 0.001 | 0.002 | - | 0.008 | 4.7 | 12.44 | 0.001 |
| CP, g | 231 | 0.003 | 0.001 | 0.001 | - | 0.005 | 4.1 | 10.82 | 0.001 |
| Soluble intake protein, g | 231 | -0.001 | 0.002 | -0.005 | - | 0.003 | -0.2 | 0.46 | 0.497 |
| Ammonia, g | 231 | 0.002 | 0.002 | -0.002 | - | 0.006 | 0.2 | 1.42 | 0.234 |
| Protein $A_2$, g | 231 | -0.004 | 0.002 | -0.009 | - | 0.000 | 1.4 | 4.23 | 0.041 |
| Protein $B_1$, g | 231 | 0.005 | 0.001 | 0.003 | - | 0.008 | 5.4 | 14.05 | <0.001 |
| Protein $B_2$, g | 231 | 0.007 | 0.003 | 0.001 | - | 0.013 | 1.6 | 4.61 | 0.033 |
| RDP x3 maintenance, g | 230 | 0.006 | 0.002 | 0.003 | - | 0.009 | 5.3 | 13.89 | <0.001 |
| RUP x1 maintenance, g | 230 | 0.004 | 0.001 | 0.001 | - | 0.007 | 2.7 | 6.43 | 0.012 |
| MP Met, g | 231 | 0.251 | 0.065 | 0.122 | - | 0.380 | 5.6 | 14.69 | <0.001 |
| MP Lys, g | 231 | 0.073 | 0.026 | 0.022 | - | 0.123 | 2.9 | 7.96 | 0.005 |
| MP Arg, g | 231 | 0.088 | 0.026 | 0.036 | - | 0.140 | 4.2 | 11.13 | 0.001 |
| MP Thr, g | 231 | 0.119 | 0.033 | 0.055 | - | 0.184 | 5.1 | 13.28 | <0.001 |
| MP Leu, g | 231 | 0.063 | 0.015 | 0.034 | - | 0.092 | 7.0 | 18.26 | <0.001 |
| MP Ile, g | 231 | 0.118 | 0.032 | 0.055 | - | 0.181 | 5.2 | 13.63 | <0.001 |
| MP Val, g | 231 | 0.095 | 0.027 | 0.041 | - | 0.148 | 4.6 | 12.02 | 0.001 |
| MP His, g | 231 | 0.185 | 0.052 | 0.083 | - | 0.288 | 4.8 | 12.69 | <0.001 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| MP Phe, g | 231 | 0.112 | 0.030 | 0.053 | - | 0.170 | 5.4 | 14.13 | <0.001 |
| MP Trp, g | 231 | 0.366 | 0.110 | 0.149 | - | 0.583 | 4.2 | 11.06 | 0.001 |
| MP Non-essential AA, g | 231 | 0.009 | 0.003 | 0.003 | - | 0.014 | 4.4 | 10.62 | 0.001 |
| MP/ME Met, g/Mcal | 231 | -0.906 | 1.996 | -4.840 | - | 3.027 | -0.4 | 0.21 | 0.650 |
| MP/ME Lys, g/Mcal | 231 | -1.151 | 0.743 | -2.614 | - | 0.313 | 0.6 | 2.40 | 0.123 |
| MP/ME Arg, g/Mcal | 231 | -0.900 | 0.777 | -2.432 | - | 0.631 | 0.2 | 1.34 | 0.248 |
| MP/ME Thr, g/Mcal | 231 | -0.715 | 0.969 | -2.624 | - | 1.195 | -0.2 | 0.54 | 0.462 |
| MP/ME Leu, g/Mcal | 231 | 0.297 | 0.447 | -0.584 | - | 1.178 | -0.2 | 0.44 | 0.507 |
| MP/ME Ile, g/Mcal | 231 | -0.612 | 0.971 | -2.525 | - | 1.300 | -0.3 | 0.40 | 0.529 |
| MP/ME Val, g/Mcal | 231 | -0.612 | 0.794 | -2.178 | - | 0.953 | -0.2 | 0.59 | 0.442 |
| MP/ME His, g/Mcal | 231 | -0.691 | 1.474 | -3.596 | - | 2.214 | -0.3 | 0.22 | 0.640 |
| MP/ME Phe, g/Mcal | 231 | -0.248 | 0.921 | -2.062 | - | 1.566 | -0.4 | 0.07 | 0.788 |
| MP/ME Trp, g/Mcal | 231 | -1.646 | 3.339 | -8.225 | - | 4.933 | -0.3 | 0.24 | 0.623 |
| MP/ME Non-essential AA, g/Mcal | 231 | -0.049 | 0.074 | -0.195 | - | 0.097 | -0.2 | 0.44 | 0.508 |
| ADF, g | 231 | -0.001 | 0.001 | -0.003 | - | 0.001 | 0.3 | 1.67 | 0.197 |
| Amylase NDF organic matter basis, g | 231 | -0.001 | 0.001 | -0.002 | - | <0.001 | 0.8 | 2.77 | 0.097 |
| Forage NDF, g | 231 | -0.005 | 0.001 | -0.007 | - | -0.003 | 8.5 | 22.37 | <0.001 |
| Physically effective NDF, g | 231 | -0.004 | 0.001 | -0.006 | - | -0.003 | 8.3 | 21.90 | <0.001 |
| Acid detergent lignin, g | 231 | 0.003 | 0.004 | -0.004 | - | 0.011 | <0.001 | 0.91 | 0.340 |
| Simple sugars, g | 231 | 0.003 | 0.002 | <0.001 | - | 0.006 | 1.1 | 3.58 | 0.060 |
| Starch, g | 231 | 0.001 | <0.001 | <0.001 | - | 0.001 | 2.3 | 6.29 | 0.013 |
| Soluble fibre, g | 231 | 0.004 | 0.001 | 0.002 | - | 0.006 | 5.6 | 14.74 | <0.001 |
| Fermentable simple sugars, g | 231 | 0.004 | 0.002 | <0.001 | - | 0.008 | 1.2 | 3.84 | 0.051 |
| Fermentable starch, g | 231 | 0.001 | 0.000 | <0.001 | - | 0.002 | 4.1 | 10.78 | 0.001 |
| Fermentable soluble fibre, g | 231 | 0.005 | 0.001 | 0.003 | - | 0.007 | 6.3 | 16.54 | <0.001 |
| Fermentable NDF, g | 231 | -0.472 | 0.089 | -0.647 | - | -0.298 | 10.6 | 28.31 | <0.001 |
| Rumen unsaturated fatty acid load, g | 231 | 0.015 | 0.002 | 0.010 | - | 0.019 | 14.3 | 39.24 | <0.001 |
| Ether extract, g | 231 | 0.009 | 0.001 | 0.006 | - | 0.012 | 13.5 | 36.76 | <0.001 |

Mixed models provided models with good fit for the data with sex, implant strategy, treatment duration and initial BW of the controls entering most models (Tables 12 – 17). We found that heifers gained approximately 8 kg, cows 3 kg less and bulls 5 kg more than steers. Treatment effects, *per se*, were only significant for the CP model. Similarly, the hormonal implant, Synovex H provided a substantial 10 kg advantage in studies in which it was used, while other implants did not always provide significant benefits, despite the point directions being quite large (eg 5 kg). The rumen modifiers monensin and tylosin entered a number of the models; lasalocid had too few observations to enter. Interestingly, while the effects of monensin were positive for LMY, the effect of tylosin was negative.

Table 18 provides the AIC and BIC estimates for the models in Tables 12-17, showing best fit for the protein fraction, amino acid, energy components, and MP CNCPS models.

**Table 12.** Random effects mixed model predicting lean muscle yield (kg) based on trial. Predictive variables include sex, implant strategy, treatment type, monensin (mg/kg DM), BW and estimated ME or MP availability as predicted by CNCPS 6.55.

| Lean muscle yield, kg | Coefficient | SE | Z-score | 95% CI | | | *P*-value |
|---|---|---|---|---|---|---|---|
| Sex (reference steers) | | | | | | | |
| Heifers | -7.721 | 3.649 | -2.120 | -14.873 | - | -0.570 | 0.034 |
| Bulls | 5.085 | 2.885 | 1.760 | -0.570 | - | 10.739 | 0.078 |
| Mixed | -2.355 | 0.634 | -3.720 | -3.597 | - | -1.113 | <0.001 |
| Cows | -3.070 | 3.193 | -0.960 | -9.328 | - | 3.188 | 0.336 |
| | | | | | | | |
| Implant (reference no implant) | | | | | | | |
| Revalor-S | 1.149 | 1.328 | 0.870 | -1.454 | - | 3.753 | 0.387 |
| SynovexS | -0.286 | 1.511 | -0.190 | -3.246 | - | 2.675 | 0.850 |
| SynovexH | 10.027 | 4.593 | 2.180 | 1.025 | - | 19.029 | 0.029 |
| Component ES | -2.099 | 1.682 | -1.250 | -5.396 | - | 1.199 | 0.212 |
| Revalor-H | 5.301 | 3.017 | 1.760 | -0.613 | - | 11.214 | 0.079 |
| Ralgro | -1.026 | 1.589 | -0.650 | -4.141 | - | 2.089 | 0.519 |
| Compudose | 5.600 | 2.949 | 1.900 | -0.180 | - | 11.381 | 0.058 |
| Revalor-IS | 0.760 | 2.073 | 0.370 | -3.304 | - | 4.823 | 0.714 |
| SynovexC | 1.516 | 2.976 | 0.510 | -4.316 | - | 7.348 | 0.610 |
| Revalor-XS | 0.059 | 3.014 | 0.020 | -5.849 | - | 5.967 | 0.984 |
| | | | | | | | |
| Monensin dose, mg/kg DM | 0.105 | 0.036 | 2.960 | 0.036 | - | 0.175 | 0.003 |
| Treatment duration, d | 0.069 | 0.014 | 5.090 | 0.042 | - | 0.096 | <0.001 |
| Initial BW, kg | 0.034 | 0.010 | 3.330 | 0.014 | - | 0.054 | 0.001 |
| Estimated ME intake, Mcal/d | 0.154 | 0.035 | 4.420 | 0.086 | - | 0.223 | <0.001 |
| Estimated MP intake, g/d | 0.001 | <0.001 | 3.240 | <0.001 | - | 0.002 | 0.001 |
| Constant | -3.603 | 1.099 | -3.280 | -5.758 | - | -1.449 | 0.001 |
| | | | | | | | |
| Random-effects parameters | Estimate | SE | | 95% CI | | | |
| Study number | | | | | | | |
| Var (constant) | 7.053 | 1.295 | | 4.921 | - | 10.108 | |
| Var (residual) | 0.255 | 0.028 | | 0.206 | - | 0.315 | |

**Table 13.** Random effects mixed model predicting lean muscle yield (kg) based on trial. Predictive variables include sex, implant strategy, treatment type, monensin (mg/kg DM), initial BW and CP.

| Lean muscle yield, kg | Coefficient | SE | Z-score | 95% CI | *P*-value |
|---|---|---|---|---|---|
| Sex (reference steers) | | | | | |
| Heifers | -8.332 | 3.480 | -2.390 | -15.153 - -1.511 | 0.017 |
| Bulls | 4.466 | 2.754 | 1.620 | -0.932 - 9.863 | 0.105 |
| Mixed | 0.437 | 1.243 | 0.350 | -1.999 - 2.872 | 0.725 |
| Cows | -3.309 | 3.055 | -1.080 | -9.296 - 2.679 | 0.279 |
| Implant (reference no implant) | | | | | |
| Revalor-S | 1.024 | 1.266 | 0.810 | -1.458 - 3.505 | 0.419 |
| SynovexS | -1.881 | 1.602 | -1.170 | -5.021 - 1.260 | 0.241 |
| SynovexH | 10.094 | 4.396 | 2.300 | 1.478 - 18.709 | 0.022 |
| Component ES | -3.114 | 1.668 | -1.870 | -6.384 - 0.155 | 0.062 |
| Revalor-H | 5.360 | 2.881 | 1.860 | -0.287 - 11.007 | 0.063 |
| Ralgro | -1.502 | 1.527 | -0.980 | -4.494 - 1.490 | 0.325 |
| Compudose | 5.160 | 2.831 | 1.820 | -0.388 - 10.708 | 0.068 |
| Revalor-IS | 0.136 | 1.993 | 0.070 | -3.769 - 4.041 | 0.946 |
| SynovexC | 0.906 | 2.849 | 0.320 | -4.678 - 6.491 | 0.750 |
| Revalor-XS | -0.315 | 2.874 | -0.110 | -5.949 - 5.318 | 0.913 |
| Protein intervention (reference control for the study) | | | | | |
| Urea | -0.264 | 0.184 | -1.440 | -0.624 - 0.096 | 0.151 |
| Soyabean meal | 0.140 | 0.245 | 0.570 | -0.341 - 0.621 | 0.568 |
| Distillers grain | -0.068 | 0.156 | -0.440 | -0.374 - 0.238 | 0.663 |
| Other | -0.051 | 0.149 | -0.340 | -0.344 - 0.241 | 0.731 |
| Cottonseed meal | -0.101 | 0.294 | -0.340 | -0.678 - 0.476 | 0.733 |
| Grains | 0.126 | 0.306 | 0.410 | -0.474 - 0.727 | 0.680 |
| Corn gluten feed | 0.443 | 0.204 | 2.180 | 0.044 - 0.842 | 0.029 |
| Canola meal | -0.121 | 0.340 | -0.360 | -0.786 - 0.545 | 0.722 |
| Fish meal | 0.443 | 0.612 | 0.720 | -0.756 - 1.643 | 0.469 |
| Commerical blend | -0.262 | 0.413 | -0.630 | -1.071 - 0.547 | 0.526 |
| Monensin dose, mg/kg DM | 0.161 | 0.045 | 3.610 | 0.074 - 0.249 | <0.001 |
| Tylosin dose, mg/kg DM | -0.192 | 0.096 | -2.010 | -0.379 - -0.005 | 0.045 |
| Treatment duration, d | 0.070 | 0.013 | 5.320 | 0.044 - 0.095 | <0.001 |
| Initial BW, kg | 0.029 | 0.010 | 2.980 | 0.010 - 0.049 | 0.003 |
| CP, g | 0.001 | <0.001 | 2.190 | <0.001 - 0.001 | 0.029 |
| ME, Mcal | 0.195 | 0.038 | 5.150 | 0.121 - 0.269 | <0.001 |
| Constant | -12.214 | 2.210 | -5.530 | -16.547 - -7.882 | <0.001 |

| Random-effects parameters | Estimate | SD | 95% CI |
|---|---|---|---|
| Study number | | | |
| Var(constant) | 6.368 | 1.173 | 4.439 - 9.136 |
| Var(residual) | 0.250 | 0.027 | 0.202 - 0.310 |

**Table 14.** Random effects mixed model predicting lean muscle yield (kg) based on trial. Predictive variables include sex, implant strategy, treatment type, monensin (mg/kg DM), initial BW and protein fractions as predicted by CNCPS 6.55.

| Lean muscle yield, kg | Coefficient | SE | Z-score | 95% CI | *P*-value |
|---|---|---|---|---|---|
| Sex (reference steers) | | | | | |
| Heifers | -7.981 | 3.530 | -2.260 | -14.898 - -1.063 | 0.024 |
| Bulls | 4.289 | 2.795 | 1.530 | -1.188 - 9.767 | 0.125 |
| Mixed | 0.428 | 1.254 | 0.340 | -2.030 - 2.886 | 0.733 |
| Cows | -3.414 | 3.092 | -1.100 | -9.474 - 2.647 | 0.270 |
| Implant (reference no implant) | | | | | |
| Revalor-S | 1.062 | 1.286 | 0.830 | -1.458 - 3.581 | 0.409 |
| SynovexS | -1.828 | 1.627 | -1.120 | -5.017 - 1.361 | 0.261 |
| SynovexH | 9.550 | 4.448 | 2.150 | 0.831 - 18.268 | 0.032 |
| Component ES | -3.128 | 1.694 | -1.850 | -6.448 - 0.192 | 0.065 |
| Revalor-H | 5.174 | 2.924 | 1.770 | -0.556 - 10.904 | 0.077 |
| Ralgro | -1.596 | 1.549 | -1.030 | -4.632 - 1.440 | 0.303 |
| Compudose | 4.919 | 2.866 | 1.720 | -0.698 - 10.535 | 0.086 |
| Revalor-IS | 0.311 | 2.018 | 0.150 | -3.645 - 4.266 | 0.878 |
| SynovexC | 0.920 | 2.894 | 0.320 | -4.753 - 6.593 | 0.751 |
| Revalor-XS | -0.124 | 2.916 | -0.040 | -5.839 - 5.591 | 0.966 |
| Monensin dose, mg/kg DM | 0.161 | 0.045 | 3.540 | 0.072 - 0.250 | <0.001 |
| Tylosin dose, mg/kg DM | -0.191 | 0.097 | -1.970 | -0.381 - <0.001 | 0.049 |
| Treatment duration, d | 0.069 | 0.013 | 5.200 | 0.043 - 0.095 | <0.001 |
| Initial BW, kg | 0.030 | 0.010 | 2.980 | 0.010 - 0.050 | 0.003 |
| Protein $A_2$, g | 0.002 | 0.001 | 3.790 | 0.001 - 0.003 | <0.001 |
| ME, Mcal | 0.196 | 0.036 | 5.470 | 0.126 - 0.266 | <0.001 |
| Constant | -12.066 | 2.237 | -5.390 | -16.450 - -7.683 | <0.001 |
| Random-effects parameters | | | | | |
| Study number | | Estimate | SD | 95% CI | |
| Var(constant) | | 6.588 | 1.207 | 4.600 - 9.433 | |
| Var(residual) | | 0.249 | 0.027 | 0.201 - 0.308 | |

**Table 15.** Random effects mixed model predicting lean muscle yield (kg) based on trial. Predictive variables include sex, implant strategy, treatment type, monensin (mg/d), initial BW and RUP as predicted by NRC (2000) level 1.

| Lean muscle yield, kg | Coefficient | SE | Z-score | 95% CI | | | *P*-value |
|---|---|---|---|---|---|---|---|
| Sex (reference steers) | | | | | | | |
| Heifers | -7.854 | 3.507 | -2.240 | -14.728 | - | -0.980 | 0.025 |
| Bulls | 4.752 | 2.777 | 1.710 | -0.690 | - | 10.195 | 0.087 |
| Mixed | 0.106 | 1.242 | 0.090 | -2.327 | - | 2.540 | 0.932 |
| Cows | -3.752 | 3.072 | -1.220 | -9.773 | - | 2.269 | 0.222 |
| Implant (reference no implant) | | | | | | | |
| Revalor-S | 1.090 | 1.277 | 0.850 | -1.413 | - | 3.594 | 0.393 |
| SynovexS | -1.763 | 1.616 | -1.090 | -4.931 | - | 1.405 | 0.275 |
| SynovexH | 9.340 | 4.424 | 2.110 | 0.669 | - | 18.010 | 0.035 |
| Component ES | -2.993 | 1.682 | -1.780 | -6.289 | - | 0.303 | 0.075 |
| Revalor-H | 4.910 | 2.904 | 1.690 | -0.781 | - | 10.601 | 0.091 |
| Ralgro | -1.426 | 1.538 | -0.930 | -4.439 | - | 1.588 | 0.354 |
| Compudose | 5.103 | 2.844 | 1.790 | -0.472 | - | 10.678 | 0.073 |
| Revalor-IS | 0.311 | 2.011 | 0.150 | -3.630 | - | 4.253 | 0.877 |
| SynovexC | 0.915 | 2.875 | 0.320 | -4.721 | - | 6.550 | 0.750 |
| Revalor-XS | -0.028 | 2.901 | -0.010 | -5.713 | - | 5.657 | 0.992 |
| Monensin dose, mg/kg DM | 0.168 | 0.045 | 3.720 | 0.079 | - | 0.256 | <0.001 |
| Tylosin dose, mg/kg DM | -0.207 | 0.096 | -2.150 | -0.396 | - | -0.018 | 0.032 |
| Treatment duration, d | 0.065 | 0.013 | 4.990 | 0.040 | - | 0.091 | <0.001 |
| Initial BW, kg | 0.028 | 0.010 | 2.830 | 0.009 | - | 0.048 | 0.005 |
| RDP x1 maintenance, g | 0.002 | 0.001 | 3.190 | 0.001 | - | 0.003 | 0.001 |
| RUP x1 maintenance$^2$, g | <0.001 | <0.001 | -2.070 | <0.001 | - | <0.001 | 0.038 |
| ME, Mcal | 0.162 | 0.038 | 4.200 | 0.086 | - | 0.237 | <0.001 |
| Constant | -11.632 | 2.222 | -5.230 | -15.988 | - | -7.277 | <0.001 |
| Random-effects parameters | | | | | | | |
| Study number | | Estimate | SD | 95% CI | | | |
| Var(constant) | | 6.494 | 1.191 | 4.533 | - | 9.303 | |
| Var(residual) | | 0.255 | 0.028 | 0.206 | - | 0.316 | |

**Table 16.** Random effects mixed model predicting lean muscle yield (kg) based on trial. Predictive variables include sex, implant strategy, treatment type, monensin (mg/kg DM), initial body weight and estimated metabolisable energy and estimated MP amino acid intake (g/d) as predicted by CNCPS 6.55.

| Lean muscle yield, kg | Coefficient | SE | Z-score | 95% CI | *P*-value |
|---|---|---|---|---|---|
| Sex (reference steers) | | | | | |
| Heifers | -8.496 | 3.634 | -2.340 | -15.619 - -1.373 | 0.019 |
| Bulls | 5.389 | 2.866 | 1.880 | -0.228 - 11.007 | 0.060 |
| Mixed | -1.705 | 0.685 | -2.490 | -3.048 - -0.361 | 0.013 |
| Cows | -2.889 | 3.170 | -0.910 | -9.102 - 3.323 | 0.362 |
| Implant (reference no implant) | | | | | |
| Revalor-S | 1.161 | 1.319 | 0.880 | -1.424 - 3.746 | 0.379 |
| SynovexS | -0.463 | 1.502 | -0.310 | -3.407 - 2.480 | 0.758 |
| SynovexH | 10.881 | 4.573 | 2.380 | 1.918 - 19.844 | 0.017 |
| Component ES | -2.448 | 1.675 | -1.460 | -5.731 - 0.836 | 0.144 |
| Revalor-H | 5.902 | 3.004 | 1.960 | 0.015 - 11.790 | 0.049 |
| Ralgro | -1.198 | 1.580 | -0.760 | -4.294 - 1.898 | 0.448 |
| Compudose | 5.610 | 2.933 | 1.910 | -0.139 - 11.358 | 0.056 |
| Revalor-IS | 0.854 | 2.057 | 0.420 | -3.178 - 4.887 | 0.678 |
| SynovexC | 1.587 | 2.953 | 0.540 | -4.201 - 7.374 | 0.591 |
| Revalor-XS | -0.254 | 2.996 | -0.080 | -6.125 - 5.618 | 0.932 |
| Monensin dose, mg/kg DM | 0.108 | 0.035 | 3.050 | 0.039 - 0.177 | 0.002 |
| Treatment duration, d | 0.073 | 0.014 | 5.380 | 0.046 - 0.100 | <0.001 |
| Initial BW, kg | 0.035 | 0.010 | 3.480 | 0.015 - 0.055 | 0.001 |
| ME intake, Mcal/d | 0.159 | 0.036 | 4.450 | 0.089 - 0.229 | <0.001 |
| MP Thr intake, g/d | 0.135 | 0.051 | 2.660 | 0.036 - 0.235 | 0.008 |
| MP Leu intake, g/d | -0.078 | 0.025 | -3.050 | -0.127 - -0.028 | 0.002 |
| MP Phe intake, g/d | 0.205 | 0.072 | 2.830 | 0.063 - 0.346 | 0.005 |
| MP Trp intake, g/d | -0.654 | 0.229 | -2.860 | -1.102 - -0.206 | 0.004 |
| Constant | -3.653 | 1.092 | -3.350 | -5.793 - -1.512 | 0.001 |
| Random-effects parameters | Estimate | SE | | 95% CI | |
| Study number | | | | | |
| Var (constant) | 6.949 | 1.277 | | 4.847 - 9.962 | |
| Var (residual) | 0.245 | 0.027 | | 0.198 - 0.304 | |

**Table 17.** Random effects mixed model predicting lean muscle yield (kg) based on trial. Predictive variables include sex, implant strategy, monensin (mg/kg DM), initial BW and intake of energy sources (carbohydrates and fats) and estimated MP availability as predicted by CNCPS 6.55.

| Lean muscle yield, kg | Coefficient | SE | Z-score | 95% CI | | | *P*-value |
|---|---|---|---|---|---|---|---|
| Sex (reference steers) | | | | | | | |
| Heifers | -8.717 | 3.634 | -2.400 | -15.840 | - | -1.595 | 0.016 |
| Bulls | 4.838 | 2.871 | 1.690 | -0.789 | - | 10.465 | 0.092 |
| Mixed | 0.162 | 1.277 | 0.130 | -2.341 | - | 2.665 | 0.899 |
| Cows | -3.322 | 3.178 | -1.050 | -9.550 | - | 2.906 | 0.296 |
| Implant (reference no implant) | | | | | | | |
| Revalor-S | 1.109 | 1.320 | 0.840 | -1.478 | - | 3.696 | 0.401 |
| SynovexS | -1.597 | 1.669 | -0.960 | -4.868 | - | 1.674 | 0.339 |
| SynovexH | 10.500 | 4.582 | 2.290 | 1.519 | - | 19.480 | 0.022 |
| Component ES | -3.340 | 1.743 | -1.920 | -6.756 | - | 0.077 | 0.055 |
| Revalor-H | 5.623 | 3.011 | 1.870 | -0.278 | - | 11.524 | 0.062 |
| Ralgro | -1.325 | 1.590 | -0.830 | -4.443 | - | 1.792 | 0.405 |
| Compudose | 4.756 | 2.947 | 1.610 | -1.020 | - | 10.531 | 0.107 |
| Revalor-IS | 0.170 | 2.072 | 0.080 | -3.892 | - | 4.232 | 0.935 |
| SynovexC | 1.090 | 2.972 | 0.370 | -4.735 | - | 6.915 | 0.714 |
| Revalor-XS | -0.276 | 2.995 | -0.090 | -6.146 | - | 5.594 | 0.927 |
| Monensin dose, mg/kg DM | 0.164 | 0.047 | 3.510 | 0.072 | - | 0.255 | <0.001 |
| Tylosin dose, mg/kg DM | -0.196 | 0.100 | -1.970 | -0.391 | - | -0.001 | 0.049 |
| Treatment duration, d | 0.069 | 0.014 | 5.060 | 0.042 | - | 0.095 | <0.001 |
| Initial BW, kg | 0.029 | 0.010 | 2.800 | 0.009 | - | 0.049 | 0.005 |
| NDF, g | 0.001 | <0.001 | 3.030 | <0.001 | - | 0.001 | 0.002 |
| Starch, g | 0.001 | <0.001 | 5.020 | <0.001 | - | 0.001 | <0.001 |
| Soluble intake fibre, g | 0.001 | <0.001 | 3.900 | 0.001 | - | 0.002 | <0.001 |
| MP CNCPS, g/d | 0.001 | <0.001 | 2.450 | <0.001 | - | 0.002 | 0.014 |
| Constant | -12.064 | 2.295 | -5.260 | -16.563 | - | -7.565 | <0.001 |
| Random-effects parameters | | | | | | | |
| Study number | | Estimate | SD | 95% CI | | | |
| Var(constant) | | 6.958 | 1.279 | 4.853 | - | 9.975 | |
| Var(residual) | | 0.242 | 0.026 | 0.196 | - | 0.300 | |

**Table 18.** Comparison of model fits for models in Tables 12-17 based on Akaike's information criterion (AIC) and Bayesian information criterion (BIC).

| Model | No. | Log likelihood (model) | df | AIC | BIC |
|---|---|---|---|---|---|
| MP CNCPS 6.55 | 230 | -308.8 | 22 | 661.7 | 737.3 |
| CP | 230 | -304.2 | 33 | 674.5 | 787.9 |
| Protein fractions | 230 | -304.9 | 23 | 655.8 | 734.8 |
| RDP x3 maintenance | 230 | -306.6 | 32 | 677.2 | 787.2 |
| RUP x1 maintenance | 230 | -306.6 | 24 | 661.2 | 743.7 |
| Amino acid | 230 | -305.2 | 25 | 660.4 | 748.1 |
| Energy components | 230 | -304.1 | 25 | 658.3 | 744.2 |

## 4.10 Nitrogen balance studies

The data used for estimating the effects of feedlot diets on RBN, UNL, FNL, and SUN concentrations were different to those used for production variables. However, similar statistical methods were used.

Appendix Tables 12 – 15 provide the univariable statistics for continuous variables in regard to nitrogen retention and loss examined using classical meta-analysis methods. Other explanatory variables examined but not included in Appendix Tables 12 – 15 were sex, breed, rumen modifiers, protein treatment intervention, grain type, and hormonal implants used before and during the trials. One rumen modifier monensin, produced significant effects on responses and this is reflected in multivariable models.

Table 1 provides the descriptive statistics on the nitrogen variables. Table 19 shows that the weighted mean difference for the different nitrogen variables approaches a balance with intake of nitrogen being accounted for by RBN, FNL and UNL.

For each of the production nitrogen balance variables there were significant effects of the different protein in interventions (Appendix Table 16).

**Table 19.** Weighted mean differences and 95% CI between the treatment and control studies in nitrogen (N) balance outcomes with the weighting reflecting the inverse of the variance of the studies included according to no-standard method (Stata Version 14).

| Variable | Weighted mean difference | 95% CI | | |
|---|---|---|---|---|
| Intake of N, g/d | 43.291 | 35.649 | - | 50.933 |
| Retained body N, g/d | 6.107 | 4.019 | - | 8.195 |
| Urinary N, g/d | 30.669 | 25.413 | - | 35.925 |
| Faecal N, g/d | 4.450 | 2.475 | - | 6.426 |
| Serum and plasma urea N, mg/dL | 3.064 | 2.217 | - | 3.911 |

### 4.10.1 Retained body nitrogen

The only variable that was significant in describing RBN was design code, with Latin Square studies having approximately 1.4 SD, (12 g/d) more RBN than studies using randomised controlled studies. However, Fig. 3 shows that the effects of treatment were significant overall and with urea and other interventions both increasing nitrogen retention.

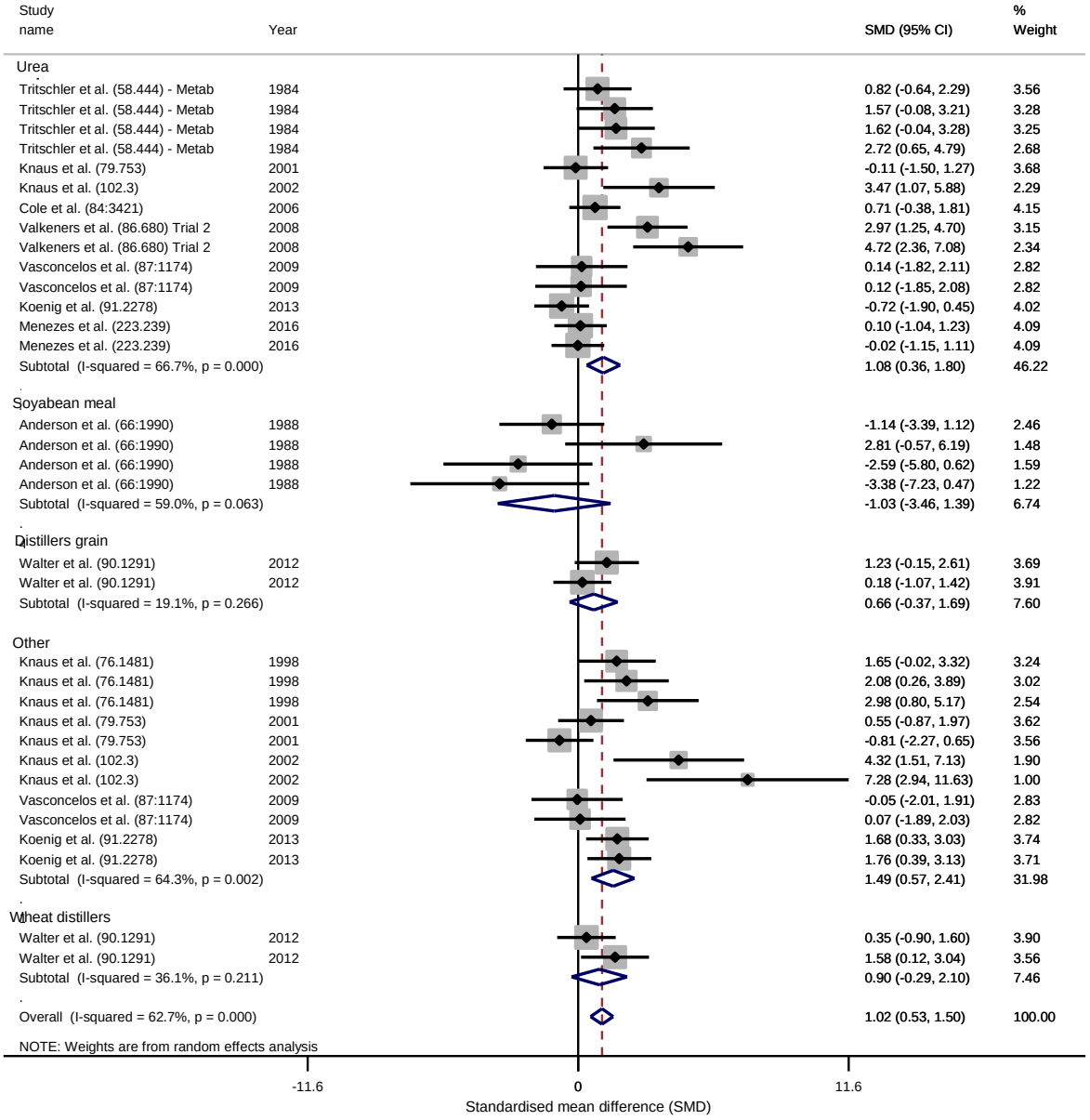


**Fig. 3.** Forest plot of studies which examined the effect of dietary protein and nitrogen interventions on retained body nitrogen. Box sizes of the effect size estimate of each study are proportional to the inverse variance of the estimates. Summary estimates of treatment effects according to dietary treatments (diamond shapes) and all studies (Overall) are reported. There were too few studies to evaluate using robust regression models.

### 4.10.2 Urinary nitrogen loss

Fig. 4 shows the forest plot of the effects of treatment on UNL. The estimate of ES estimated using robust regression models that account for the nested effect of trial within study (Hedges et al., 2010) is 1.72 (95% CI 0.660 to 2.77; *P* =0.006). Models were developed that described UNL (Table 20). A model that included only the difference in CP intake between the treatments and controls was highly significant and explained much of the variance in urinary output with an Adjusted $R^2$ of 0.91. Other models were developed with monensin and estimated MP difference or difference in ADLG intake. Where reliable significant models were identified using the robust regression methods (Hedges et al., 2010), these are displayed in the Table 20. Models were not developed for MP or ME amino acids following investigation of model stability.

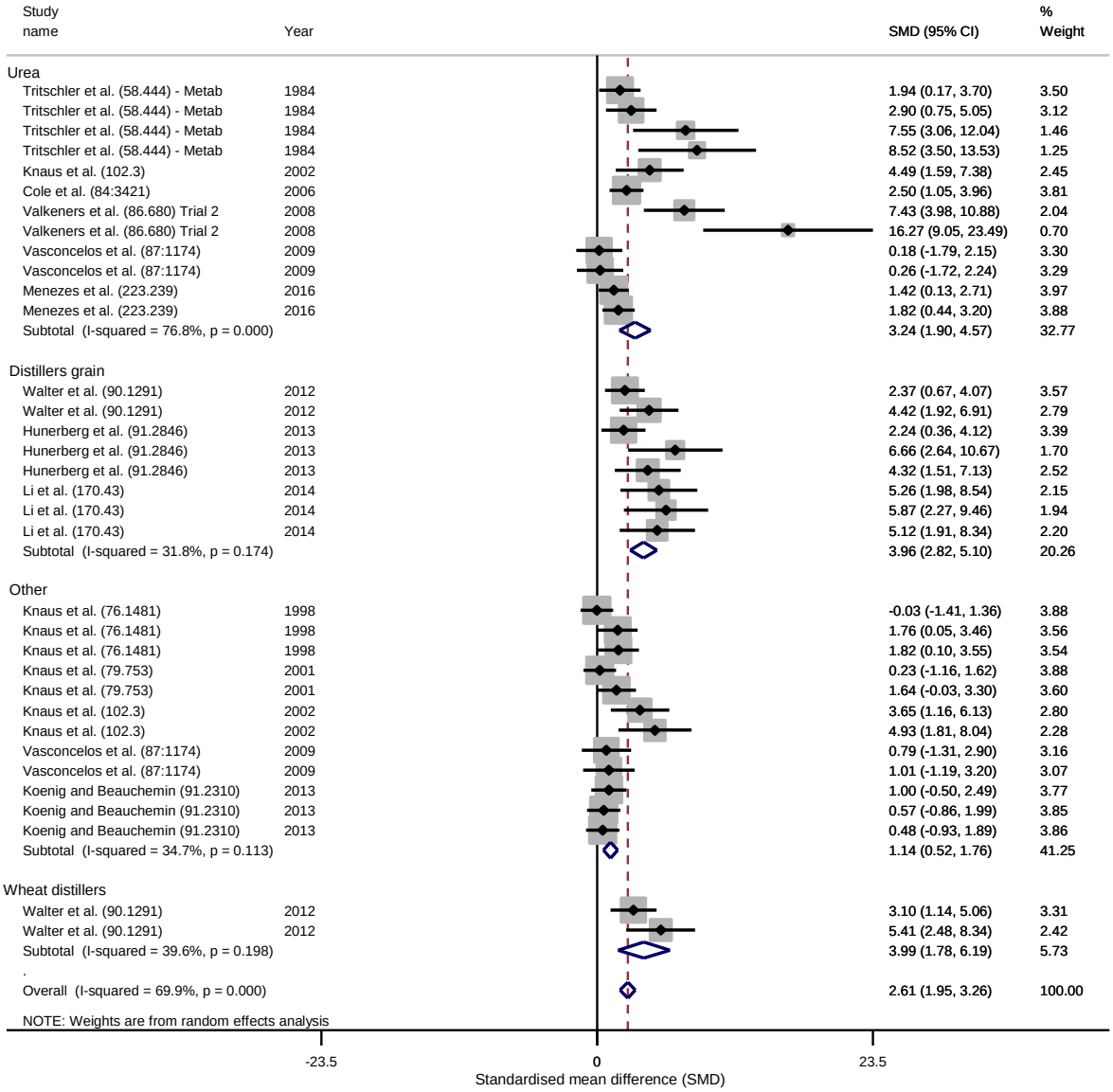


**Fig. 4**. Forest plot of studies which examined the effect of dietary protein and nitrogen interventions on urinary nitrogen loss. Box sizes of the effect size estimate of each study are proportional to the inverse variance of the estimates. Summary estimates of treatment effects according to dietary treatments (diamond shapes) and all studies (Overall) are reported.

**Table 20.** Urinary nitrogen loss (g/d) evaluated using univariable and multivariable meta-regression models based on differences between treated and control groups in intakes of diet fractions and monensin intake. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values. These are compared to robust regression models that account for the nested effect of trial within study (Hedges et al., 2010).

| Variable | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|
| CP, g/d | 0.006 | 0.001 | 0.003 - 0.008 | 0.917 | 0.498 | 0.254 | <0.001 |
| CP, g/d (Robust model) | 0.006 | 0.001 | 0.004 - 0.007 | | 0 | 0 | <0.001 |
| MP, g/d | 0.007 | 0.002 | 0.002 - 0.012 | 0.664 | 0.572 | 1.025 | 0.002 |
| Monensin dose, mg/kg DM | -0.049 | 0.017 | -0.082 - -0.015 | | | | 0.003 |
| MP, g/d (Robust model) | 0.008 | 0.001 | 0.003 - 0.012 | | 0 | 0 | 0.009 |
| Acid detergent lignin, kg/d | 0.058 | 0.016 | 0.027 - 0.090 | 0.772 | 0.517 | 0.695 | <0.001 |
| Monensin dose, mg/kg DM | -0.054 | 0.016 | -0.086 - -0.022 | | | | 0.001 |
| Acid detergent lignin, kg/d (Robust model) | No valid model | | | | | | |

### 4.10.3 Faecal nitrogen loss

Fig. 5 shows the forest plot of the effects of treatment on FNL. The estimate of ES estimated using robust regression models that account for the nested effect of trial within study (Hedges et al., 2010) is 0.522 (95% CI 0.003 to 1.050; *P* =0.040). Only one multivariable model was developed that described FNL and this was based on differences in carbohydrate intakes, specifically of ADF and soluble fibre (Table 21). The robust models developed were not reliable. Univariable models that included only the difference in CP intake or in Protein $A_2$ fraction between the treatments and controls were highly significant and explained much of the variance in FNL with an Adjusted $R^2$ of 60.9 and 76.2, respectively (Appendix Table 14).

**Table 21.** Faecal nitrogen loss (g/d) evaluated using univariable and multivariable meta-regression models based on differences between treated and control groups in intakes of diet fractions. Knapp-Hartung methods were used to derive estimates of the co-efficients, estimates of model fit ($R^2$) and heterogeneity ($I^2$) and variance ($\tau^2$). The permutation methods of Higgins and Thompson (2004), Harbord and Higgins (2008), and Harbord and Steichen (2004) were used for estimates of *P*-values.

| Variable | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | Adjusted *P*-value |
|---|---|---|---|---|---|---|---|---|---|
| ADF, kg/d | 0.008 | 0.003 | 0.003 | - | 0.013 | 0.500 | 0.382 | 0.317 | 0.002 |
| Soluble fibre, kg/d | 0.007 | 0.003 | 0.002 | - | 0.013 | | | | 0.001 |

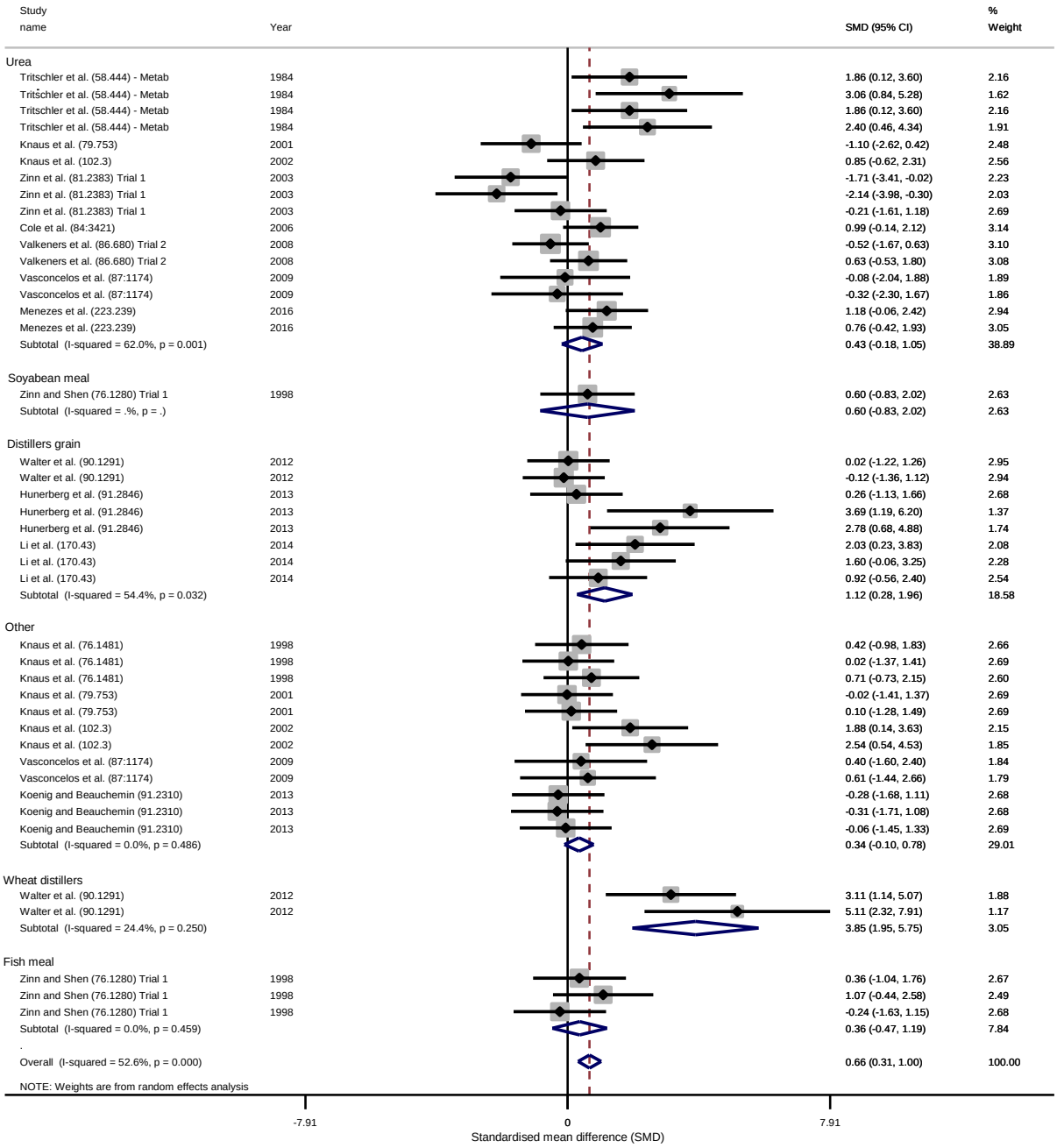


**Fig. 5.** Forest plot of studies which examined the effect of dietary protein and nitrogen interventions on faecal nitrogen loss. Box sizes of the effect size estimate of each study are proportional to the

inverse variance of the estimates. Summary estimates of treatment effects according to dietary treatments (diamond shapes) and all studies (Overall) are reported.

### 4.10.4 Serum and plasma urea nitrogen concentrations

The only significant variable that remained in multivariable models tested was monensin intake (mg/kg DM) that acted to reduce concentrations of serum and plasma nitrogen.

## 4.11 Predictions of nitrogen outputs from nitrogen intake

Further investigation of these data provided evaluations of the relationship between the difference in intake nitrogen between the treated and control cattle and the difference in RBN, UNL, and FNL using mixed models regression with study as a random effect. Figures showing these relationships are provided as Appendix Fig. 2-5. Table 22 shows the coefficients estimated for the relationship between intake N (centred) and RBN (centred), UNL, FNL, and SUN. Only 16% of N was retained in the body. Approximately 60% of N was linearly lost in urine. As the difference in nitrogen supplied increased, the difference in excretion of faecal N increased quadratically (Table 22).

**Table 22.** Random effects mixed model predicting the coefficients and SE, 95% CI, *P*-value, and random effect of study estimated for the relationship between intake N (centred) and Retained body N (centred), Urinary N loss, Faecal N loss, and Serum and plasma urea N.

| | | | | | | | | Study Effect | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Variable | No. | Coefficient | SE | 95% CI | | | *P*-value | Coefficient | SE | 95% CI | | |
| Retained body N, g/d | 43 | 0.160 | 0.034 | 0.093 | - | 0.226 | <0.001 | 55.354 | 24.475 | 23.270 | - | 131.678 |
| Urinary N loss, g/d | 35 | 0.598 | 0.026 | 0.546 | - | 0.650 | <0.001 | <0.001 | <0.001 | <0.001 | - | <0.001 |
| Faecal N loss, g/d | 47 | 0.144 | 0.024 | 0.098 | - | 0.190 | <0.001 | <0.001 | <0.001 | <0.001 | - | <0.001 |
| Faecal N loss$^2$, g/d | | 0.001 | <0.001 | <0.001 | - | 0.002 | 0.002 | | | | | |

# 5 Discussion

This study provides a quantitative evaluation of dietary and other factors that influence the production outputs critical to the profitability and environmental sustainability of cattle production in feedlots. There is a particular focus on the effects of dietary protein and nitrogen intake evaluated using different methods on the production performance and on the retention and loss of these dietary components. The dietary data were extracted rigorously according to previously described methods using feed data from the studies themselves and from the NDS feedbank. Notwithstanding the rigor applied, limitations in the estimates of all dietary components exist including; undescribed variations in the diets fed, feed analyses and estimations. It is anticipated that these errors are likely to be non-differential, that is neither favouring nor supporting the key hypotheses. Under these conditions, errors in estimation are likely to drive hypotheses towards the null and, therefore, findings in the study are likely to be robust, but conservative.

There were three data sets established that addressed: production responses using classical meta-analytical methods; LMY using mixed models regression and; nitrogen retention and loss using

classical meta-analytical methods. The data sets contained mutual studies, but the study content differed markedly between the production responses and the nitrogen balance studies and the latter included Latin Square studies, whereas the other two data sets did not.

## 5.1 Evaluation of models to predict production responses

The effects of treatment on the production responses are evaluated in Table 11, that shows significant responses to the treatments for all production variables tested. There are the results of two statistical models presented. The robust regression models account for the effect of trial within study in models that, therefore, account for much of the variance. Consequently, these models do not allow an exploration of other sources of variance. These are provided in the Knapp-Hartung estimates that allow for investigation of heterogeneity in responses. Investigation of the sources of heterogeneity using meta-regression should identify factors that modify responses to treatment. The robust regression models were very similar in estimates of co-efficients to the Knapp-Hartung and permutation models, but contain fewer variables. In some cases, specifically MP NRC, there were no valid models developed using the robust regression approach.

It is important to note that one of the challenges in interpreting responses to nitrogen and protein interventions is the inherent confounding that results from any single intervention i.e., with rare exceptions such as urea or a heat or formaldehyde protected protein, an intervention does not only supply nitrogen or protein, but changes fermentation of the diet and supplies fats or carbohydrates and other nutrients. Therefore, the evaluation of treatment responses is a relatively crude evaluation of a response to protein or nitrogen and modeling of the responses using the software developed may provide greater insight.

### 5.1.1 Univariable and multivariable evaluation of final body weight, hot carcass weight and average daily gain

While these outcomes have quite similar attributes, the univariable and multivariable models tended to differ. For FBW, the multivariable models all had excellent fit, explaining much of the variance and for the amino acid models, MP CNCPS 6.55 model and CP providing low remaining heterogeneity ($I^2$ <20 with a low $\tau^2$). The amino acid model, in particular, had an $I^2$ of only 2.1 and $\tau^2$ of 0. Models based on MP NRC, protein fractions, and RDP 3x maintenance fitted quite well also. Although there was no valid robust regression model for MP NRC. The similarity in performance of the multivariable models is well reflected in the univariable results, which identified strong associations for differences in intake of some amino acids as well as for ME difference, MP CNCPS 6.55 difference, and CP. The models that had best fit and lowest heterogeneity also had quadratic terms which for FBW included: CP, RDP 3x maintenance and Leu, Val, Phe, and non-essential amino acids. For ADG it included: MP, CP, soluble intake protein, RUP 1x and RDP 3x maintenance, Thr, Leu, and non-essential amino acids. For HCW it included: MP, CP, Protein $A_{2,}$ RUP 1x and RDP 3x maintenance. As noted previously, there is considerable collinearity between amino acids and the identification of particular amino acids as significant should not be considered definitive. Most of the robust models were similar to the permutation and Knapp-Hartung models, but contained fewer variables. The exception to this was the amino acid model for ADG which did not produce any significant predictive variables for the robust model.

For HCW, the univariable outcomes of initial BW difference, ME difference, and difference in ether extract had large associations, but the protein and nitrogen estimates did not. Notwithstanding these results, protein and nitrogen estimates routinely remained in final models. The multivariable models containing amino acid, CP, and RDP x3 maintenance had excellent fit as did MP CNCPS 6.55. These model structures were quite similar and often differed only in the method of protein/ nitrogen estimation. These results were evident in the more parsimonious robust regression models.

The multivariable estimates of ADG fitted less well than those for FBW and HCW. When such outcomes are quite highly correlated, the reasons for this are not clear, but may indicate more inherent variability or error in measurement of ADG considering the problems of estimating and managing body shrink. The heterogeneity remaining as indicated by $I^2$ and $\tau^2$ was higher for ADG than for either FBW or HCW. The robust regression models for ADG contained fewer significant terms than for FBW and HCW.

The other covariables remaining in the FBW, HCW, and ADG models were unsurprising with the exception of ether extract. Initial BW of the controls and difference in BW between the treated and control groups would be expected to influence final outcomes, as would differences in the energy density of the diets used. These variables, though, were often excluded from the robust regression models. However, ether extract entered many of the models, apparently independent of a role in providing energy that should be accounted for in the ME of the diets.

### 5.1.2 Univariable and multivariable evaluation of dry matter intake and gain: feed

The models developed for evaluating differences in DMI between the treated and control groups had relatively modest fits with $R^2$ between 44 to 52, with only MP CNCPS 6.55 ($R^2$ = 67), energy components that included MP CNCPS 6.55 ($R^2$ = 69), amino acid ($R^2$ = 100) and protein fractions ($R^2$ = 100) having good fits. The protein $A_2$ component had a very strong association with DMI, that appeared to be influenced strongly by the energy and protein content of the diet, with few other variables that entered the models. The protein fraction model had an $I^2$ of 0 and a $\tau^2$ of 0 indicating that this and ME differences in diets predicted DMI well and reduced heterogeneity in responses to a low level. This response was the only model for which protein fractions were the best model. However, the fit for the amino acid model was equal with Leu, Val, and non-essential amino acids having linear and quadratic fits and Trp a linear fit. The model that also contained the difference in ME intake between the treatment and control diets also had an $I^2$ of 0 and a $\tau^2$ of 0.

The protein fraction ($R^2$ = 73) model had the best fit for G:F and this variable was notable for the poor fit for the CNCPS 6.55 model. All other models had poor fit for this variable and even the protein model had moderate remaining heterogeneity. Ether extract entered a number of the G:F models.

The robust models were not significant on a number of occasions, but in general were similar in the estimated co-efficients for the remaining terms but contained fewer significant terms than the Knapp-Hartung and permutation models. The MP CNCPS 6.55 and CP models were very similar whether developed by robust methods or by Knapp Hartung and permutation.

### 5.1.3 Univariable and multivariable evaluation of longissimus muscle area and fat thickness

Models evaluating the LMA were poor with very few univariable associations being significant. However, models containing differences between treatments and controls in MP CNCPS 6.55, CP, and protein fraction (protein fraction $A_2$) that contained ME all had low heterogeneity ($I^2$ <20). There were very few models for LMA derived using the robust regression methods.

Fat thickness models provided relatively good fit for difference in amino acid intakes ($R^2$ = 79) and for differences in MP CNCPS 6.55. Interestingly the amino acid model that contained Leu, Phe, and Trp as linear and quadratic effects did not contain the difference in ME between treatment and control diets whereas the other models contained either the difference in ME or ether extract between treatment and control diets. Interestingly, there were robust regression models developed for fat thickness and these included the CP and amino acid models, however, the MP CNCPS 6.55 model was not significant.

The use of ether extract in models containing estimates of ME was not initially intended as the estimated ME of diets comprises, in part, the EE of the diet. The inclusion and subsequent testing of ether extract in the diets reflected the inclusion of these in the RDP and RUP models and an awareness of the univariable significance ($P \leq 0.5$) of ether extract for all variables except LMA. There is an increasing awareness of fats as nutraceutical agents, particularly in regard to reproduction and effects on the neonate (Symonds et al., 2016), but there is little published on the effects of these in stimulating growth in beef cattle, apart from an energetic role. Interestingly, Vasconcelos and Gaylean (2007) note that 71% of clients serviced by feedlot nutritionists in the USA utilise added fats in their diets, with the primary sources being tallow and yellow grease. The treatments used in this study differed significantly in fat content (data not shown) and this factor could influence responses to treatment. Strandvik (2015) notes the roles of fatty acids as active components in membranes, that influence cell signalling, ion channels, receptors, enzymes, and gene expression either directly or through the metabolic products of fats. While the possibility exists that the role of the ether extract in the models reflects unaccounted for energetic benefits, the role of these as metabolic modifiers seems more probable, given that ether extract entered models independently of the ME estimates.

### 5.1.4 Lean muscle yield models

The LMY models were derived using a mixed models regression approach that provided the opportunity to evaluate the effect of other factors influencing growth including, sex, breed, hormonal implants, rumen modifiers, and duration of the feeding period.

The results from the models were quite consistent and found that heifers gained approximately 8 kg less, cows 3 kg less, and bulls 5 kg more than steers. Similarly, Synovex H provided a substantial 10 kg advantage in studies in which it was used, while other implants did not always provide significant benefits, despite the point directions being quite large (eg 5 kg). Considering the established increase in growth rate in response to treatment with growth promotants containing oestradiol and androgens, alone or in combination, with cattle on energy dense diets (Hunter, 2010), and the anabolic effect of these mediated by increased muscle protein synthesis and decreased muscle protein degradation at the cellular level (Dayton and White, 2013) thereby increasing musculature in

all areas of the carcass (Wood et al., 1986), it is unclear why significant increases in LMY were not generally observed. The excess of muscle protein synthesis over degradation in response to treatment with anabolic steroids is the basis of the use of body nitrogen retention as an indicator of anabolic activity (Istasse et al., 1988) and suggests the possibility that more consistent and greater responses to growth promotants might be observed with a greater supply of metabolisable protein at the tissue level.

Treatment effects, *per se*, were only significant for the CP model, indicating that the effects of dietary nitrogen and protein interventions were well explained by the outcome variables used in the other models, and those models had better statistical fit.

The rumen modifiers monensin and tylosin entered a number of the models; lasalocid had too few observations to enter. Interestingly, while the effects of monensin were positive for LMY, the effect of tylosin was negative. The effect of monensin is consistent with the positive effects of monensin that have been previously described for ADG (Duffield et al., 2012), but the negative effects of tylosin differ from the univariable estimate. Tylosin use is primarily directed towards control of liver abscessation, and inherently, control of ruminal acidosis. Studies report weight gains with tylosin use, but almost always in conjunction with monensin use. This finding indicates that tylosin *per se*, may not increase LMY.

As anticipated, effects of treatment duration and initial BW entered all models.

The LMY models were all very similar in regards to the AIC and BIC estimates. The models that provided the poorest fit were RDP 3x maintenance and CP.

## 5.2 A comparison of the results achieved using CNCPS 6.55, crude protein, metabolisable protein estimated using NRC (2000) level 1, protein fractions, and measures of rumen degraded and undegraded dietary protein from NRC (2000)

Importantly, the results indicate that, apart from LMA, models developed using existing nutritional standards predicted outcomes well, with many models exceeding an $R^2$ of 80. The protein models used provided some insights to the success of development of models over time, however, models containing more basic descriptions of feed including CP and RDP/ RUP from the NRC (2000) level 1 performed well in general. The statistical modelling provided clear evidence that the NRC (2000) level 1 estimates of MP were poor predictors of outcomes despite a strong correlation between these and the CNCPS 6.55 estimates of MP. This result may reflect the method used to predict MP NRC. The estimate of peNDF used for feeds was derived from the NDS feedbank rather than the original NRC feedbank, and given that the NRC (2000) level 1 is an empirical model, this decision may have affected the precision of estimation of MP. This concern was tested by including a dichotomous variable for low peNDF (<20%) where the NRC (2000) correction factor is applied for the effect of NDF on microbial protein production and studies with a higher peNDF for which the term is not applied. This variable was not significant in the analyses conducted (data not shown) possibly indicating a more substantive concern with the MP as estimated by NRC (2000).

Gaylean and Tedeschii (2014), using a large database of 285 studies in which microbial CP yield was measured, found that the NRC (1996, 2000) predictions of microbial CP yield, with or without adjustment for peNDF had significant mean and linear bias. Owens and Sapienza (2014) also

assembled 3 substantial data bases, one of which included 155 protein- diet comparisons in growing cattle and evaluated the relationship compared the estimates of microbial CP supply and the UDP, RDP, and MP predicted from TDN, UDP, and RDP tabular estimates for the compiled diets from model 1 of NRC (2000) with microbial crude protein supply, UDP, RDP, and MP measurements within the experiments. They (Owens and Sapienza 2014) found a poor fit for the NRC predictions, especially when the effect of DMI was excluded from the models and noted that implausible predictions of greater MP production than biologically possible were present. Further, Owens and Sapienza (2014) identified that 67% of the diets provided insufficient RDP for maximal microbial protein production. The NRC (2016) notes that estimates of MP production need to reflect availability of nitrogen in the rumen and will not be maximal unless the nitrogen availability is addressed. The NRC (2016) therefore used a correction for less than optimal availability of nitrogen and protein in the rumen and also estimated responses using a fat free TDN. In this data set used for our study only 1.6% of the diets contained more than 12.5% RDP and only 62.8% were >8.5% CP, as estimated at 1 times maintenance. A RDP of 12.5% is consistent with a diet that produces 5 mg/100 ml of ammonia in the rumen, a concentration of ammonia that is associated with optimal microbial production (Satter and Roffler 1975). These observations suggest that our findings of poor predictive value for outcome variables and lack of effect of correction for peNDF may reflect fundamental failings in the NRC (2000) model, rather than use of the more recent estimates of peNDF. The failure to account for the limiting effect of RDP on microbial protein production and estimation of microbial protein production based on TDN and eNDF, without accounting for the effects of fat in TDN are serious model flaws. Specifically, the NRC (1996) Level 1 predictions for microbial CP synthesis made in the computer model use a 0.13 x TDNI x eNDF adj factor that does not account for a reduction in microbial protein synthesis if DIP supply is less than the DIP required for optimal microbial CP synthesis.

The use of CP intake proved superior to CNCPS 6.55 for FBW and HCW but generally explained less of the variance. Use of CP intake was superior to MP estimates derived from NRC (2000) levels 1. The RDP 3x maintenance model performed well for a number of outcomes. The RUP 1x maintenance models performed well in a very little limited number of outcomes. The performance of the MP NRC (2000) estimates may provide a rationale for the limited acceptance of MP NRC (2000) by field nutritionists. However, differences of MP intake between treatments and controls using MP derived from CNCPS 6.55 and the amino acid models provided many promising predictive models suggesting benefits in production outcomes might be achieved by using this approach rather than using CP or NRC (2000) estimates.

The Cornell Net Protein and Carbohydrate Systems (CNCPS) as initially described in a series of four papers (Russell et al., 1992; Sniffen et al., 1992; Fox et al., 1992; O'Connor et al., 1993) predicts nutrient digestion based on the competition between rate of passage and rate of digestion of protein and carbohydrate fractions that are intended to be chemically and digestively uniform using the equation (Kd/(Kd+Kp)) (Sniffen et al., 1992). In CNCPS, bacteria are classified as either structural carbohydrate fermenters or non-structural carbohydrate fermenters. Microbial protein yield for each bacterial type is a function of the growth rate that the available carbohydrate can drive (rate of digestion), the bacterial maintenance rate, and the theoretical maximum growth yield. Bacterial yield is decreased reflecting the energy spilling that results from futile cycles when bacterial growth is limited by substrates such as ammonia and peptides and resulting in a low rumen pH (Russell and Strobel 1993). The yield of non-structural carbohydrate fermenters increases with peptide availability. The majority of diets present in the current study had limited rumenal nitrogen and peptides.

The CNCPS nutritional model has changed considerably over the last two decades. Chemical compositions of about 800 different ingredients in the CNCPS feed library were updated (Higgs et al., 2015). New protein and carbohydrate fractionation schemes and corresponding rates of degradation and passage were developed based on recent research (Van Amburgh et al., 2015). Proteins are categorized into Fraction A1, A2, B1, B2, and C. Soluble CP (soluble in borate-phosphate buffer) is comprised of Ammonia (Fraction A1) in addition to soluble true protein (Fraction A2). As a result of changes in characterisation and rates of degradation and passage, soluble protein now contributes to MP whereas previously most of the soluble protein was converted to rumen ammonia. Furthermore, the rate of ammonia degradation and presumed uptake by rumen bacteria has been reduced. Protein fractions B2 and C are insoluble after boiling in neutral detergent solution while protein fraction C is also insoluble after boiling in acid detergent solution. Protein fraction B2 is slowly degraded while protein fraction C is unavailable. Crude protein which is not soluble in borate-phosphate buffer but is soluble in neutral detergent is estimated to be the B1 fraction which is degraded at an intermediate rate in the rumen. Feed amino acid values and usage efficiencies were also updated based on more recent research.

Further research into production responses with changes in protein intake must be accompanied by laboratory analytical characterization of the protein fractions of feedstuffs and diets since library values provide a guide at best, particularly when they are based on foreign cultivars. As acknowledged in this paper, there is inaccuracy inherent to the use of feed library reference values which would likely be amplified by the application of US values to Australian diets and which could make Australian studies meaningless without corresponding feedstuff analyses.

The amino acid models performed consistently well, with the exception of G:F, LMA and ADG, and this raises the potential for amino acid-based models for the prediction of feedlot performance. However, as noted above, there was strong collinearity of the amino acids, suggesting that the particular amino acids identified in models may not be definitive. Notwithstanding this observation, there was some consistency of amino acids identified in the models with Leu, Phe, and non-essential amino acids entering 50% of the models. This work should be considered in the context that many of the studies used non-protein nitrogen as the treatment intervention and ADG achieved were 1.5 kg/d on average, suggesting that more studies are needed in populations stimulated to achieve greater gains, possibly using higher quality proteins or amino acids. Notwithstanding the latter comments, most of the study diets would have benefited from supply of additional nitrogen, and peptides in the rumen.

There is a difficulty in designing studies to evaluate responses of cattle to proteins. Specifically, the theoretical production response to dietary change to specific amino acids obtained within the MP delivered to the intestine. The difficulty has been to assess the impact of the changes in diet on the supply of MP amino acids in the production context. Simply, the confounding effects of dietary change, that is the removal or dilution of a particular nutrient to increase the MP supply of amino acids necessarily results in other changes in the diet that may influence rumen function, absorption or partition of nutrients. While meta-analytical approaches to evaluating responses are the most powerful available to us, these are limited by the quality and range of the data on which they are based. In this study, the data base was extensive and the range of diets used was quite wide, but the cattle performance, was not high, being only 1.5 kg ADG.

One of the objectives of this series of studies was to identify an optimal nitrogen or protein intake. There is evidence that identifying an optimum is realistic as evidenced by the many analyses that provide quadratic terms in models (Tables 4-10 and Tables 12-17) and in the Appendix Fig. 6 and 7. However, recommending an optimum for any particular model is not a strategy that we generally recommend. The evaluation of LMY identified many modifying factors for most methods used to assess the impact of diet that predict LMY including initial body weights, hormonal treatments, sex, and rumen modifiers (Tables 12-17). In the case of the amino acid models that often had excellent fit the uncertainty regarding the merit of any particular amino acid entering the model, suggests caution in interpretation. Lastly, the goal of good nutritional strategy should be to identify means to perform above the average and there is sufficient residual variance or heterogeneity to provide the opportunity for that. It is also becoming increasingly clear that there are marked differences in the rumen microbiome of cattle that will influence responses of individuals within populations and, potentially among populations (Golder et al., 2014ab). Further, the range of ADG and limitations of diet design with many of the diets being based on urea or corn distillers grains suggests that alternate diets may be identified, which have greater potential for performance. Further research is required as outlined in the recommendations arising from this report to better define the inputs required to model the optimum nitrogen or protein intake with diets of higher protein concentrations that those analysed in this report (ie. greater than 13% CP).

## 5.3 Models evaluating responses to nitrogen and nitrogen balance

The models that were developed using differences in nitrogen intake between the treated and control groups and nitrogen retention or loss in faeces and urine or increases in blood used classical meta-analytical methods. Further investigation was undertaken to examine the results in the context of each diet using mixed models regression methods.

The results indicate that feeding additional protein and nitrogen increased retention of nitrogen and that urea and 'other' interventions increased the retention of nitrogen in the body. However, the model had substantial heterogeneity ($I^2$ = 66) and only study design explained some of this in meta-regression models, as Latin-square studies had higher effect sizes for retained N. The mixed model showed that around 16% of the nitrogen fed was retained in the body and that this was a linear relationship with N intake (Table 22 and Appendix Fig. 2). Koenig et al. (2013) found that N retention was greater earlier in the feeding period, but found little difference among treatments used. The effect of greater N retention earlier in the feeding period is further enhanced in response to treatment with hormonal growth promotants (Hunter et al., 1988).

The difference in nitrogen intake was reflected in increased UNL with the nitrogen and protein interventions individually significantly increasing urinary excretion and as a group. The pooled ES was large (ES = 2.6), but there was substantial heterogeneity ($I^2$ = 70%) that was reduced by meta-regression models containing CP, MP CNCPS 6.55 and monensin, and ADLG and monensin. These models still had substantial remaining heterogeneity ($I^2$ ~ 50%). One of the actions of monensin is to reduce deamination and, thereby, to increase bypass of protein and the lower urinary excretion of N is consistent with this action. Yang and Russell (1993) found a greater than 30% reduction in ruminal ammonia concentrations and increased microbial protein concentration by a similar 30% *in vivo* in response to monensin. These changes were the result of a nearly 10 fold decrease in amino acid fermenting bacteria. McGuffey et al. (2001) concluded that the effects of monensin on inhibition of

deamination were greater than on proteolysis. Poos et al. (1979) found decreased bacterial nitrogen flow to the small intestine of steers fed monensin with diets containing 11.5% CP, indicating that the effects of monensin on protein will be influenced by diet.

The mixed model (Table 22) showed that around 60% of the nitrogen fed was lost in urine and that this was a strong linear relationship. This result was consistent with the estimates from the WMD (Table 20) that estimated approximately 70% loss in urine, 10% loss in faeces, and 14% retention in the body. As the difference in nitrogen supplied increased, the difference in excretion of faecal N increased quadratically (Table 22), indicating that this was perhaps a more sensitive indicator of adequacy of supply in the diet than urinary loss. As expected, the difference in SUN concentrations increased linearly (Table 22).

Overall, the percentage of nitrogen fed that is retained is low and the vast majority is lost in urine as a linear function of intake with faecal excretion increasing quadratically with intake.

# 6 Conclusions/recommendations

The data available are remarkably extensive in providing up to 230 observations that could be used to predict lean muscle yield and approximately 200 observations for other outcomes. There is a high level of internal consistency in the predictive models that have been developed.

The nutritional models used, with the exception of MP NRC provided excellent predictions of performance, particularly MP CNCPS 6.55 and amino acid models, however, protein fractions, CP, and RDP/RUP all yielded good models.

We do not have a high level of confidence in the predictive value of specific amino acids because of the marked collinearity between these. However, the methods used to evaluate these were the most appropriate we could identify and these provided the models with the best statistical fit suggesting a need for much more work in this area. Mixtures of rate limiting amino acids and non-protein nitrogen may provide the potential for greater weight gains and higher nitrogen retention.

However, and importantly, there are relatively few circumstances where average daily gain exceeds 2.0 kg/d in these databases and diets seldom exceed 13% crude protein, with many interventions being based solely on non-protein nitrogen. Consequently, we are reluctant to over-emphasise optimal levels of protein/ nitrogen in the diet as these depend on many factors including, breed, sex, implant strategy, and other factors in the diets as evident in the many analyses provided.

These limitations indicate the potential to explore other strategies to increase growth of cattle in feedlots. Critically, further studies are needed to explore:

- Cattle growing at more than 2 kg/head.day
- Diets based on wheat
- Diets higher in true protein with detailed characterisation of the protein fractions and amino acid profiles, and the carbohydrate fractions
- Diets using NPN and protected amino acids.

The finding in regards to the ether extract content of the diet is important, particularly in regards to the potential for fats to act not just as sources of energy, but to act as metabolic signalling agents.

# 7 Key messages

We identified a large number of studies that evaluated responses of beef feedlot cattle to protein.

Both, production responses to protein and nitrogen balance studies were identified. However, almost all studies were from the USA or Europe.

The computer-based nutrition models available provided good levels of prediction of responses to protein.

The CNCPS 6.55 estimates of MP were generally superior to use of CP to predict outcomes such as average daily gain, hot carcass weight, and feed:gain, and both of these were superior to estimates of MP based on NRC (2000) level 1 methods.

The LMY models were all very similar in regards to model fit and indicated that the protein and nitrogen estimates were useful in explaining LMY. The LMY models provided the opportunity to evaluate the effect of other factors influencing growth including, sex, breed, hormonal implants, rumen modifiers, and duration of the feeding period. Similarly, the hormonal implant, Synovex H provided a substantial 10 kg advantage in studies in which it was used, while other implants did not always provide significant benefits, despite the point directions being quite large (eg 5 kg). Results from the different models were quite consistent and found that heifers gained approximately 8 kg, cows 3 kg less and bulls 5 kg more than steers.

Interestingly, ether extract entered a large number of models independent of its inclusion in metabolisable energy suggesting that fats may play a role in increasing the efficiency of beef feedlot production as signalling agents.

Multivariable models were developed to predict production outcomes and to predict nitrogen retention and loss. The results indicate that feeding additional protein and nitrogen increased retention of nitrogen and that urea and 'other' interventions increased the retention of nitrogen in the body. Only approximately 16% of dietary nitrogen was retained in the body. Nitrogen loss in urine increased with dietary nitrogen and protein intake and faecal loss increased quadratically with increased nitrogen intake. Results indicate the potential to increase the efficiency of nitrogen use.

There are indications that optimal dietary protein and nitrogen intake strategies exist as indicated by quadratic terms for protein and nitrogen measures in many of the models developed.

However, and importantly, there are relatively few circumstances where average daily gain exceeds 2.0 kg/d in these databases and diets seldom exceed 13% crude protein, with many interventions being based solely on non-protein nitrogen. Consequently, we are reluctant to over-emphasise optimal levels of protein/ nitrogen in the diet as these depend on many factors including, breed, sex, implant strategy, and other factors in the diets as evident in the many analyses provided.

These limitations indicate the potential to explore other strategies to increase growth of cattle in feedlots. Critically, further studies are needed to explore:

- Cattle growing at more than 2 kg/head.day
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- Diets higher in true protein with detailed characterisation of the protein fractions and amino acid profiles, and the carbohydrate fractions
- Diets using NPN and protected amino acids.

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# 9 Appendix

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## 9.2 Figures

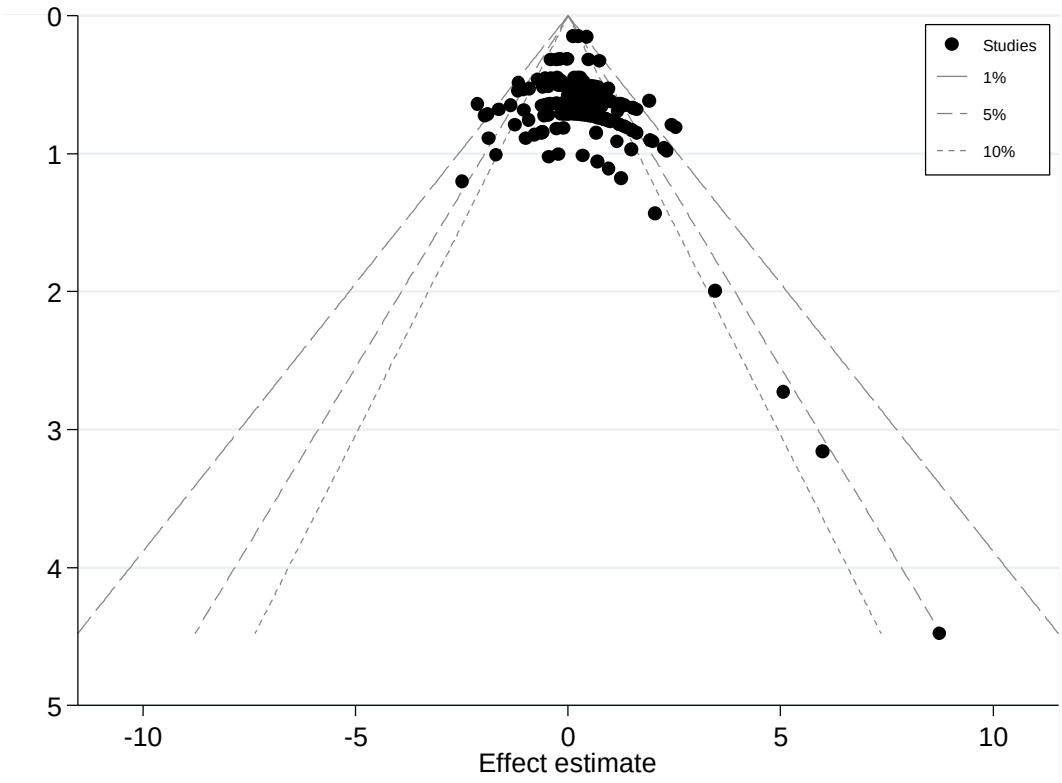


**Fig. 1.** Funnel plot of effects of treatment on the difference in hot carcass weight (kg).

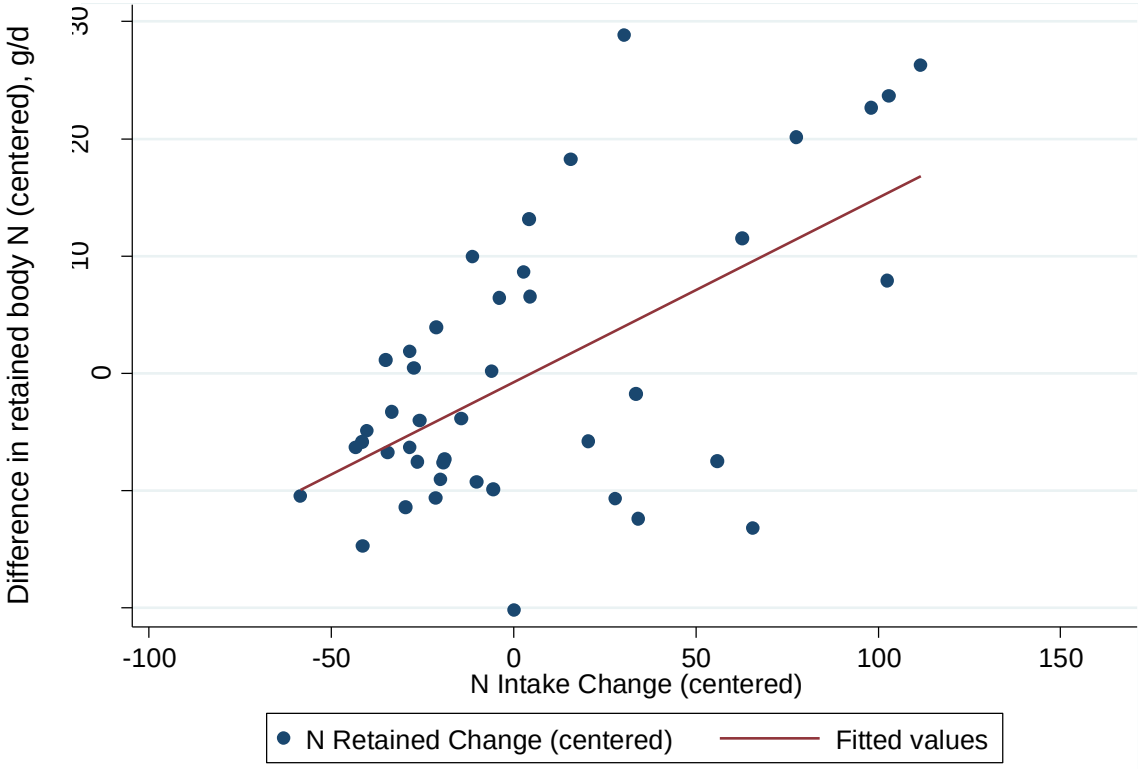


**Fig. 2.** Bivariate fit of retained body nitrogen from all studies by nitrogen intakes

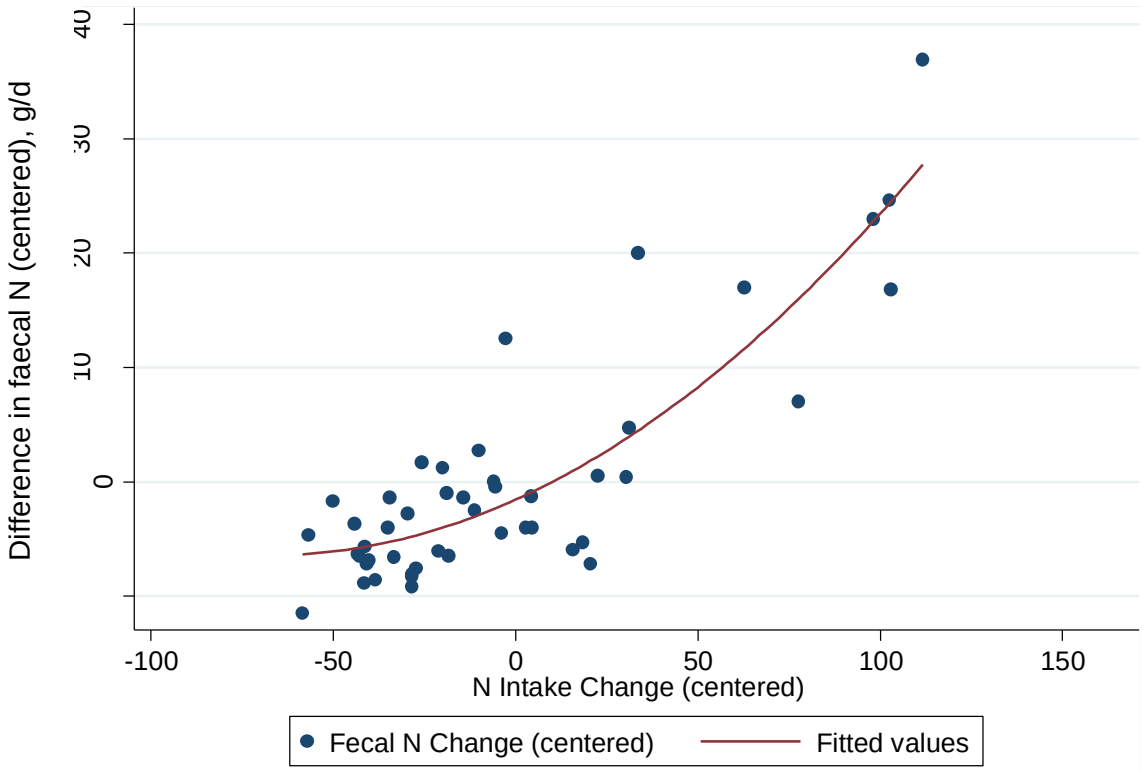


**Fig. 3.** Bivariate fit of faecal nitrogen loss from all studies by nitrogen intakes

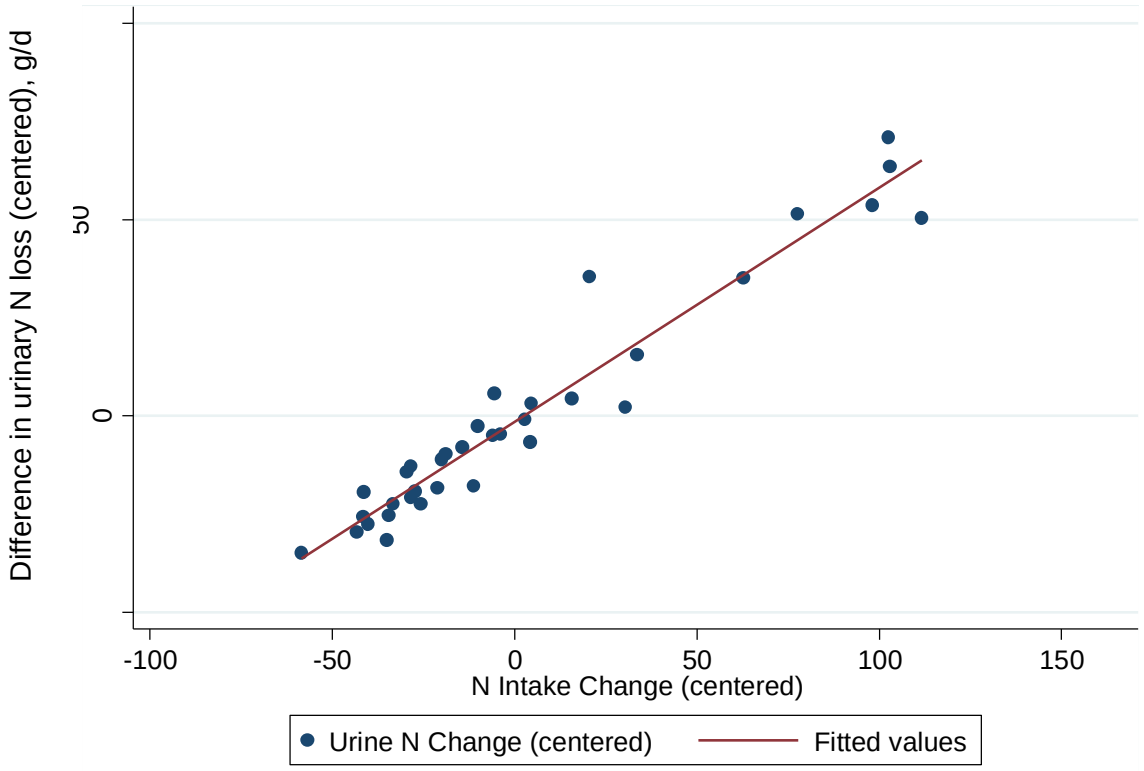


**Fig. 4.** Bivariate fit of urinary nitrogen loss from all studies by nitrogen intakes

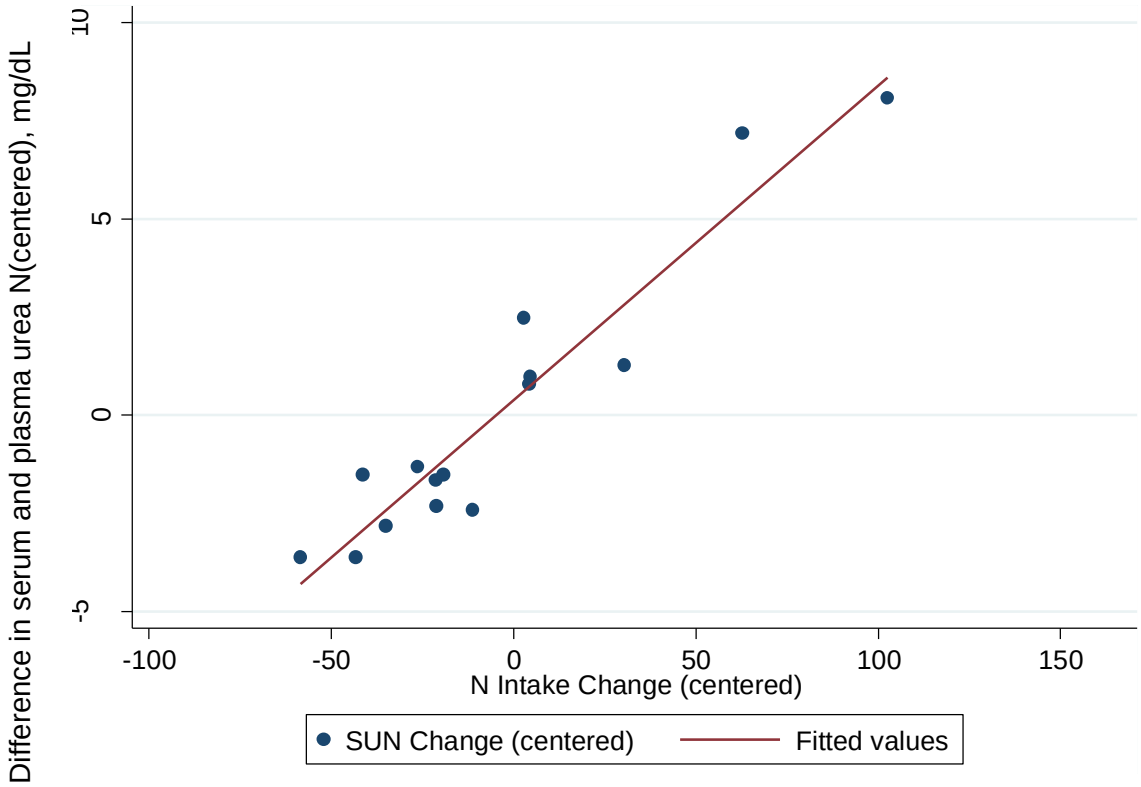


**Fig. 5.** Bivariate fit of serum and plasma urea nitrogen (SUN) from all studies by nitrogen intakes

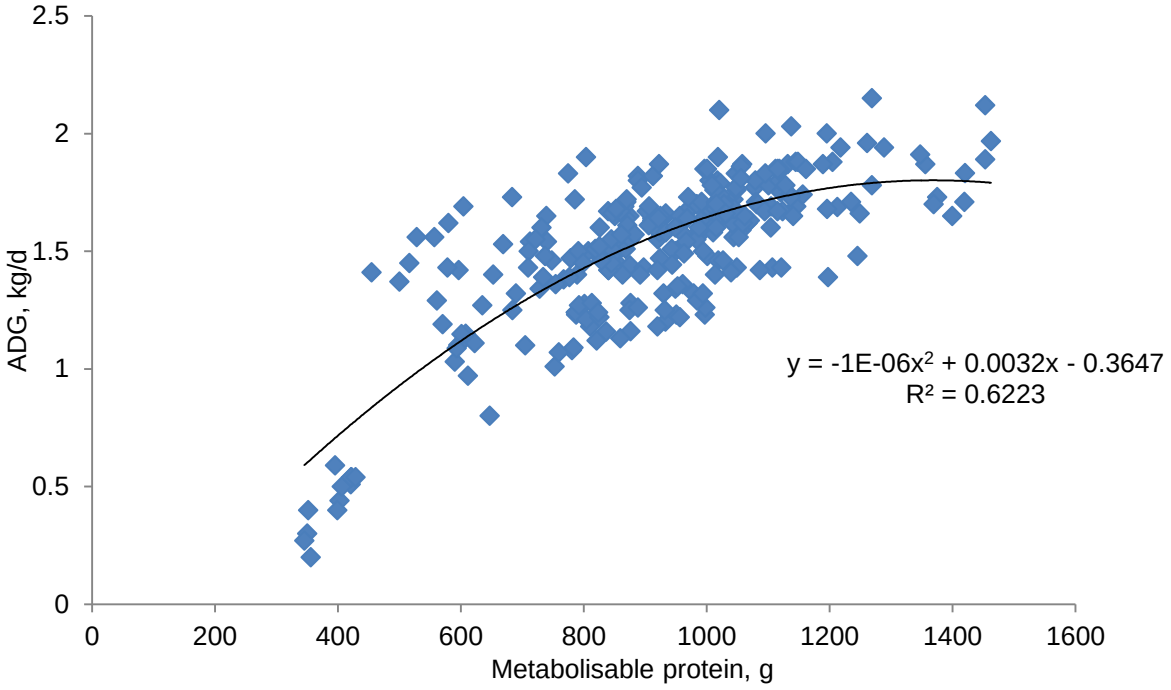


**Fig. 6.** Relationship between metabolisable protein and ADG

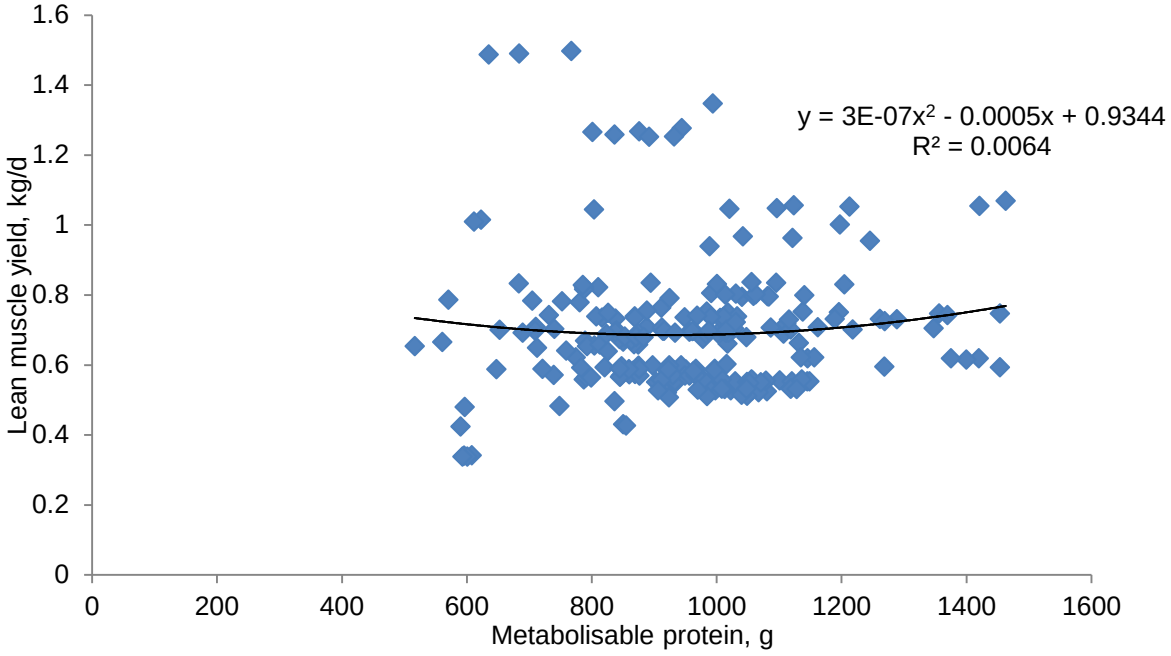


**Fig. 7.** Relationship between metabolisable protein and Lean muscle yield

## 9.3 Tables

**Table 1.** Summary of search engines, search terms, constraints, number of articles that resulted and the number of articles that were downloaded for secondary screening

| Search engine | Search terms | Additional constraints | No. of articles resulting | No. of articles for secondary screening |
|---|---|---|---|---|
| ISI | (Beef feedlot OR Beef OR Beef cattle) AND (protein OR urea OR non-protein OR amino acid) AND (weight gain OR carcass gain OR nitrogen retention OR nitrogen loss OR manure OR urea) | • Foreign languages excluded<br>• Articles, clinical trials or reports only<br>• Refined for veterinary science can agriculture fields | 2,483 | Screened against Google Scholar retained articles to avoid duplication |
| Pubmed | (Beef or Beef Cattle or Beef Feedlot) and (Protein or urea or nitrogen or amino acid or weight or gain or nitrogen retention or nitrogen loss) | First 350 results sorted by relevance | 11,309 | 18 (total) |
| | Beef(w)Cattle<br>Beef(w)Feedlot<br>Protein<br>weight(w)gain and carcass(w)gain and nitrogen(w)retention<br>Nitrogen(w)loss and manure and urea | | 5722 | |
| | Beef(w)Cattle<br>Beef(w)Feedlot<br>Protein<br>urea and non-protein nitrogen and amino acid<br>weight(w)gain and carcass(w)gain and nitrogen(w)retention<br>Nitrogen(w)loss and manure and urea | | 2381 | |
| Google Scholar | Beef Feedlot weight OR and OR gain "protein " | | | 54 |
| | Beef cattle Feedlot protein weight gain carcass grain | | | 51<br>31 |
| | Beef cattle Feedlot non-protein nitrogen urea amino acids carcass weight gain | | | 33 |
| | Beef cattle Feedlot nitrogen OR loss OR manure OR urea "non-protein nitrogen" | | | 26 |
| | Beef cattle Feedlot Nitrogen loss manure urea | | | |
| Science direct | (Beef or Beef Cattle or Beef Feedlot) and (Protein or urea or nitrogen or amino acid or weight or gain or nitrogen retention or nitrogen loss) | | 784 | 31 (total from all 3 searches) |
| | (beef or beef feedlot) and (protein or urea or non-protein nitrogen or amino acid or weight gain or carcass gain or nitrogen retention or nitrogen loss) | | 464<br>506 | |

| | | |
|---|---|---|
| | ALL(Beef or Beef Cattle or Beef Feedlot) and ALL(Protein or urea or non-protein nitrogen or amino acid or weight gain or carcass gain or nitrogen retention or nitrogen loss or manure) | |
| TOTAL | | 430 |

**Table 2.** Descriptive statistics for continuous explanatory variables

| Variable | No. | Mean | SD | Minimum | Maximum |
|---|---|---|---|---|---|
| Initial BW, kg | 297 | 341.9 | 54.4 | 202.7 | 469.0 |
| Treatment length, d | 304 | 129.2 | 38.2 | 28.0 | 267.0 |
| DMI, kg | 304 | 9.3 | 1.6 | 4.5 | 12.7 |
| ME, Mcal | 304 | 24.7 | 4.9 | 8.6 | 34.4 |
| MP, g/d | 304 | 906.0 | 218.2 | 345.4 | 1,462.8 |
| CP, g | 304 | 1,282.1 | 351.3 | 384.5 | 2,430.8 |
| MP NRC, g/d | 282 | 898.0 | 244.0 | 329.3 | 1,903.9 |
| Soluble intake protein, g | 304 | 409.1 | 137.0 | 113.0 | 902.2 |
| Ammonia, g | 304 | 122.6 | 129.9 | 0.0 | 591.5 |
| Protein $A_2$, g | 304 | 286.3 | 124.2 | 105.7 | 902.2 |
| Protein $B_1$, g | 304 | 669.1 | 211.0 | 158.8 | 1,334.8 |
| Protein $B_2$, g | 304 | 121.5 | 80.2 | 16.8 | 585.6 |
| RDP x3 maintenance, g | 303 | 824.3 | 206.8 | 234.1 | 1,363.7 |
| RUP x1 maintenance, g | 303 | 457.3 | 170.3 | 106.9 | 1,136.1 |
| MP Met, g | 304 | 21.0 | 4.9 | 8.1 | 33.8 |
| MP Lys, g | 304 | 55.3 | 12.2 | 24.5 | 92.3 |
| MP Arg, g | 304 | 54.8 | 12.3 | 22.6 | 88.8 |
| MP Thr, g | 304 | 43.0 | 9.8 | 17.5 | 68.9 |
| MP Leu, g | 304 | 78.6 | 21.6 | 27.4 | 142.4 |
| MP Ile, g | 304 | 44.0 | 9.9 | 18.8 | 71.3 |
| MP Val, g | 304 | 50.3 | 11.7 | 20.1 | 81.7 |
| MP His, g | 304 | 24.4 | 6.2 | 9.2 | 51.5 |
| MP Phe, g | 304 | 45.2 | 10.8 | 17.6 | 73.9 |
| MP Trp, g | 304 | 11.9 | 2.8 | 5.0 | 20.8 |
| MP Non-essential AA, g | 304 | 475.2 | 119.9 | 171.0 | 781.4 |
| MP/ME Met, g/Mcal | 304 | 0.9 | 0.1 | 0.5 | 1.3 |
| MP/ME Lys, g/Mcal | 304 | 2.3 | 0.4 | 1.2 | 3.7 |
| MP/ME Arg, g/Mcal | 304 | 2.2 | 0.3 | 1.2 | 3.6 |
| MP/ME Thr, g/Mcal | 304 | 1.8 | 0.3 | 1.0 | 2.7 |
| MP/ME Leu, g/Mcal | 304 | 3.2 | 0.6 | 1.9 | 5.4 |
| MP/ME Ile, g/Mcal | 304 | 1.8 | 0.3 | 1.0 | 2.8 |
| MP/ME Val, g/Mcal | 304 | 2.1 | 0.3 | 1.2 | 3.2 |
| MP/ME His, g/Mcal | 304 | 1.0 | 0.2 | 0.6 | 2.1 |
| MP/ME Phe, g/Mcal | 304 | 1.8 | 0.3 | 1.1 | 2.7 |
| MP/ME Trp, g/Mcal | 304 | 0.5 | 0.1 | 0.3 | 0.8 |
| MP/ME Non-essential AA, g/Mcal | 304 | 19.3 | 3.5 | 11.3 | 32.5 |
| ADF, g | 304 | 906.0 | 350.3 | 326.5 | 2,003.3 |
| Amylase NDF organic matter basis, g | 304 | 1,809.3 | 613.9 | 756.4 | 3,720.8 |
| Forage NDF, g | 304 | 620.1 | 576.8 | 0.0 | 2,663.4 |
| Physically effective NDF, g | 304 | 1,066.1 | 479.5 | 325.5 | 2,804.9 |
| Acid detergent lignin, g | 304 | 212.3 | 74.9 | 93.1 | 424.4 |
| Simple sugars, g | 304 | 348.7 | 176.2 | 47.2 | 1070.2 |
| Starch, g | 304 | 4,597.3 | 1459.0 | 534.2 | 7,757.5 |

| | | | | | |
|---|---|---|---|---|---|
| Soluble fibre, g | 304 | 299.7 | 237.3 | 8.8 | 1,699.2 |
| Fermentable simple sugars, g | 304 | 265.4 | 127.7 | 35.9 | 799.5 |
| Fermentable starch, g | 304 | 3,539.4 | 1089.3 | 405.0 | 6,102.0 |
| Fermentable soluble fibre, g | 304 | 261.6 | 201.0 | 8.8 | 1,478.4 |
| Fermentable NDF, g | 304 | 649.3 | 354.2 | 0.0 | 1,853.2 |
| Rumen unsaturated fatty acid load, g | 304 | 288.0 | 129.3 | 47.7 | 636.9 |
| Ether extract, g | 304 | 457.9 | 191.4 | 84.6 | 951.3 |

**Table 3.** Descriptive statistics for non-continuous explanatory variables

| Variable | No. | Percent |
|---|---|---|
| Sex | | |
| Steers | 265 | 87.2 |
| Heifers | 22 | 7.2 |
| Steers and heifers | 8 | 2.6 |
| Bulls | 6 | 2.0 |
| Cows | 3 | 1.0 |
| Total | 304 | |
| | | |
| Breed | | |
| Britich crossbred, Angus, British Breed | 173 | 56.9 |
| BritishxContinental | 89 | 29.3 |
| *Bos indicus* cross | 24 | 7.9 |
| Not identified | 18 | 5.9 |
| Total | 304 | |
| | | |
| Monensin dose, mg/kg DM | | |
| 0 | 115 | 37.8 |
| 17-25 | 24 | 7.9 |
| 26-35 | 147 | 48.4 |
| 36-37 | 18 | 5.9 |
| Total | 304 | |
| | | |
| Tylosin dose, mg/kg DM | | |
| 0 | 153 | 50.3 |
| 7-10 | 104 | 1.0 |
| 11-22 | 47 | 48.7 |
| Total | 304 | |
| | | |
| Lasalocid dose, mg/kg DM | | |
| 0 | 294 | 96.7 |
| 20 | 6 | 2.0 |
| 40 | 4 | 1.3 |
| Total | 304 | |
| | | |
| Protein treatment intervention | | |
| Control | 77 | 25.3 |
| Other | 58 | 19.1 |
| Distillers grain | 52 | 17.1 |
| Urea | 34 | 11.2 |
| Corn gluten feed | 28 | 9.2 |
| Soyabean meal | 19 | 6.3 |
| Canola meal | 11 | 3.6 |
| Cottonseed meal | 6 | 2.0 |
| Grains | 5 | 1.6 |
| Fish meal | 5 | 1.6 |

| | | |
|---|---|---|
| Protected protein meal | 4 | 1.3 |
| Commerical blend | 4 | 1.3 |
| Wheat distillers | 1 | 0.3 |
| Total | 304 | |
| | | |
| Grain type | | |
| Corn | 247 | 81.3 |
| Barley | 41 | 13.5 |
| Sorghum | 9 | 3.0 |
| Corn and Barley | 7 | 2.3 |
| Total | 304 | |
| | | |
| Hormonal implant | | |
| Revalor-S | 82 | 27.0 |
| No implant | 72 | 23.7 |
| Synovex S | 57 | 18.8 |
| Ralgro | 25 | 8.2 |
| Component ES | 17 | 5.6 |
| Revalor-IS | 14 | 4.6 |
| Compudose | 12 | 4.0 |
| Revalor-H | 8 | 2.6 |
| Synovex H | 6 | 2.0 |
| E2 | 4 | 1.3 |
| Revalor-XS | 4 | 1.3 |
| Synovex C | 3 | 1.0 |
| Total | 304 | |

**Table 4.** Univariable analyses for ADG. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 209 | 0.037 | 0.020 | -0.002 | - | 0.076 | 2.3 | 58.0 | 0.541 | 0.061 |
| Initial BW, kg | 209 | -0.005 | 0.002 | -0.008 | - | -0.001 | 0.4 | 58.4 | 0.552 | 0.004 |
| ME, Mcal | 208 | 0.273 | 0.045 | 0.185 | - | 0.361 | 27.9 | 52.5 | 0.402 | <0.001 |
| MP, g/d | 208 | 0.002 | 0.001 | <0.001 | - | 0.003 | -2.1 | 58.8 | 0.570 | 0.006 |
| CP, g | 209 | 0.001 | <0.001 | <0.001 | - | 0.001 | 0.9 | 58.2 | 0.549 | 0.003 |
| MP NRC, g/d | 206 | 0.001 | <0.001 | <0.001 | - | 0.001 | -1.2 | 57.5 | 0.522 | 0.142 |
| Soluble intake protein, g | 208 | 0.001 | 0.001 | <0.001 | - | 0.002 | 5.5 | 57.6 | 0.522 | 0.071 |
| Ammonia, g | 209 | <0.001 | <0.001 | -0.001 | - | 0.001 | -0.9 | 58.6 | 0.558 | 0.714 |
| Protein $A_2$, g | 209 | 0.001 | 0.001 | -0.001 | - | 0.002 | -2.1 | 58.5 | 0.565 | 0.415 |
| Protein $B_1$, g | 209 | 0.001 | 0.001 | <0.001 | - | 0.002 | 4.5 | 57.9 | 0.529 | 0.007 |
| Protein $B_2$, g | 209 | 0.002 | 0.001 | <0.001 | - | 0.004 | 1.5 | 58.3 | 0.545 | 0.041 |
| RDP x3 maintenance, g | 208 | 0.001 | 0.001 | <0.001 | - | 0.002 | -2.1 | 58.7 | 0.572 | 0.037 |
| RUP x1 maintenance, g | 208 | 0.001 | 0.001 | <0.001 | - | 0.002 | 4.5 | 58.1 | 0.535 | 0.008 |
| MP Met, g | 209 | 0.037 | 0.022 | -0.006 | - | 0.081 | -4.4 | 58.5 | 0.578 | 0.094 |
| MP Lys, g | 209 | 0.010 | 0.008 | -0.005 | - | 0.025 | -4.9 | 58.2 | 0.581 | 0.191 |
| MP Arg, g | 209 | 0.019 | 0.008 | 0.003 | - | 0.035 | -4.3 | 58.6 | 0.577 | 0.023 |
| MP Thr, g | 209 | 0.020 | 0.011 | -0.001 | - | 0.041 | -4.9 | 58.5 | 0.581 | 0.063 |
| MP Leu, g | 209 | 0.011 | 0.005 | <0.001 | - | 0.021 | -1.1 | 58.5 | 0.559 | 0.047 |
| MP Ile, g | 209 | 0.020 | 0.011 | -0.001 | - | 0.041 | -4.6 | 58.5 | 0.579 | 0.061 |
| MP Val, g | 209 | 0.022 | 0.009 | 0.004 | - | 0.041 | -4.4 | 58.6 | 0.578 | 0.019 |
| MP His, g | 209 | 0.048 | 0.018 | 0.013 | - | 0.082 | -1.4 | 58.5 | 0.561 | 0.007 |
| MP Phe, g | 209 | 0.030 | 0.011 | 0.009 | - | 0.051 | -2.1 | 58.5 | 0.566 | 0.005 |
| MP Trp, g | 209 | 0.075 | 0.037 | 0.003 | - | 0.148 | -5.6 | 58.5 | 0.584 | 0.042 |
| MP Non-essential AA, g | 209 | 0.003 | 0.001 | 0.001 | - | 0.005 | -2.0 | 58.5 | 0.565 | 0.005 |
| MP/ME Met, g/Mcal | 209 | -0.135 | 0.580 | -1.278 | - | 1.008 | -0.9 | 57.7 | 0.559 | 0.816 |
| MP/ME Lys, g/Mcal | 209 | -0.077 | 0.199 | -0.470 | - | 0.316 | -0.3 | 57.3 | 0.555 | 0.700 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Arg, g/Mcal | 209 | 0.089 | 0.214 | -0.333 | - | 0.511 | -2.5 | 58.0 | 0.568 | 0.677 |
| MP/ME Thr, g/Mcal | 209 | -0.003 | 0.278 | -0.551 | - | 0.545 | -1.6 | 57.7 | 0.562 | 0.991 |
| MP/ME Leu, g/Mcal | 209 | 0.045 | 0.139 | -0.230 | - | 0.320 | -1.8 | 58.4 | 0.564 | 0.748 |
| MP/ME Ile, g/Mcal | 209 | -0.013 | 0.278 | -0.561 | - | 0.536 | -1.4 | 57.7 | 0.562 | 0.963 |
| MP/ME Val, g/Mcal | 209 | 0.092 | 0.243 | -0.386 | - | 0.571 | -2.5 | 58.0 | 0.567 | 0.704 |
| MP/ME His, g/Mcal | 209 | 0.404 | 0.451 | -0.485 | - | 1.293 | -2.4 | 58.4 | 0.567 | 0.371 |
| MP/ME Phe, g/Mcal | 209 | 0.212 | 0.284 | -0.348 | - | 0.771 | -2.7 | 58.3 | 0.569 | 0.457 |
| MP/ME Trp, g/Mcal | 209 | 0.194 | 0.957 | -1.693 | - | 2.081 | -2.2 | 57.7 | 0.566 | 0.840 |
| MP/ME Non-essential AA, g/Mcal | 209 | 0.018 | 0.024 | -0.030 | - | 0.066 | -2.5 | 58.3 | 0.568 | 0.454 |
| ADF, g | 209 | 0.001 | <0.001 | <0.001 | - | 0.001 | -0.6 | 58.2 | 0.557 | 0.017 |
| Amylase NDF organic matter basis, g | 209 | <0.001 | <0.001 | <0.001 | - | 0.001 | 3.5 | 57.9 | 0.534 | 0.008 |
| Forage NDF, g | 209 | 0.001 | 0.001 | <0.001 | - | 0.001 | -1.5 | 58.5 | 0.562 | 0.229 |
| Physically effective NDF, g | 209 | 0.001 | <0.001 | <0.001 | - | 0.002 | 1.8 | 57.8 | 0.544 | 0.002 |
| Acid detergent lignin, g | 209 | 0.003 | 0.001 | <0.001 | - | 0.005 | -2.2 | 58.6 | 0.566 | 0.046 |
| Simple sugars, g | 209 | 0.002 | 0.001 | <0.001 | - | 0.003 | -2.4 | 58.6 | 0.567 | 0.082 |
| Starch, g | 209 | <0.001 | <0.001 | <0.001 | - | 0.000 | 0.9 | 58.4 | 0.549 | 0.361 |
| Soluble fibre, g | 209 | 0.001 | <0.001 | 0.001 | - | 0.002 | 15.1 | 56.9 | 0.470 | <0.001 |
| Fermentable starch, g | 209 | <0.001 | <0.001 | <0.001 | - | 0.000 | -0.8 | 58.6 | 0.558 | 0.761 |
| Fermentable soluble fibre, g | 209 | 0.002 | <0.001 | 0.001 | - | 0.002 | 15.9 | 56.7 | 0.465 | <0.001 |
| Fermentable NDF, g | 209 | 0.001 | <0.001 | <0.001 | - | 0.002 | 3.9 | 57.7 | 0.532 | 0.009 |
| Ether extract, g | 209 | 0.003 | 0.001 | 0.001 | - | 0.004 | 22.9 | 54.4 | 0.427 | <0.001 |

**Table 5.** Final BW univariable analyses. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 166 | -0.005 | 0.002 | -0.008 | - | -0.002 | 19.4 | 42.9 | 0.227 | <0.001 |
| Initial BW, kg | 166 | 0.048 | 0.016 | 0.017 | - | 0.080 | 19.4 | 43.3 | 0.227 | 0.003 |
| ME, Mcal | 165 | 0.189 | 0.039 | 0.112 | - | 0.266 | 38.0 | 39.3 | 0.175 | <0.001 |
| MP, g/d | 165 | 0.003 | 0.001 | 0.002 | - | 0.004 | 42.0 | 37.9 | 0.164 | <0.001 |
| CP, g | 166 | 0.001 | <0.001 | 0.001 | - | 0.002 | 20.7 | 41.4 | 0.223 | <0.001 |
| MP NRC, g/d | 164 | 0.001 | <0.001 | <0.001 | - | 0.001 | 1.8 | 44.0 | 0.253 | 0.064 |
| Soluble intake protein, g | 165 | 0.001 | 0.001 | <0.001 | - | 0.002 | 0.7 | 45.9 | 0.277 | 0.203 |
| Ammonia, g | 166 | <0.001 | <0.001 | -0.001 | - | 0.001 | -1.9 | 46.3 | 0.286 | 0.685 |
| Protein $A_2$, g | 166 | 0.001 | 0.001 | -0.001 | - | 0.002 | -4.1 | 46.3 | 0.293 | 0.266 |
| Protein $B_1$, g | 166 | 0.001 | <0.001 | 0.001 | - | 0.002 | 17.3 | 42.5 | 0.233 | <0.001 |
| Protein $B_2$, g | 166 | 0.002 | 0.001 | <0.001 | - | 0.003 | 3.3 | 45.5 | 0.272 | 0.105 |
| RDP x3 maintenance, g | 166 | 0.002 | 0.001 | 0.001 | - | 0.003 | 24.1 | 41.2 | 0.213 | <0.001 |
| RUP x1 maintenance, g | 166 | 0.001 | 0.001 | <0.001 | - | 0.002 | 8.4 | 44.5 | 0.258 | 0.017 |
| MP Met, g | 166 | 0.093 | 0.022 | 0.049 | - | 0.137 | 21.5 | 41.4 | 0.221 | <0.001 |
| MP Lys, g | 166 | 0.042 | 0.008 | 0.026 | - | 0.058 | 33.8 | 38.9 | 0.186 | <0.001 |
| MP Arg, g | 166 | 0.050 | 0.008 | 0.034 | - | 0.066 | 53.0 | 34.8 | 0.132 | <0.001 |
| MP Thr, g | 166 | 0.055 | 0.011 | 0.033 | - | 0.077 | 30.4 | 39.4 | 0.196 | <0.001 |
| MP Leu, g | 166 | 0.013 | 0.005 | 0.004 | - | 0.023 | 9.6 | 44.0 | 0.254 | 0.006 |
| MP Ile, g | 166 | 0.054 | 0.011 | 0.033 | - | 0.075 | 32.8 | 38.8 | 0.189 | <0.001 |
| MP Val, g | 166 | 0.047 | 0.009 | 0.029 | - | 0.066 | 31.6 | 39.0 | 0.192 | <0.001 |
| MP His, g | 166 | 0.064 | 0.016 | 0.031 | - | 0.096 | 14.1 | 42.7 | 0.242 | <0.001 |
| MP Phe, g | 166 | 0.050 | 0.010 | 0.031 | - | 0.070 | 34.4 | 38.4 | 0.184 | <0.001 |
| MP Trp, g | 166 | 0.228 | 0.038 | 0.154 | - | 0.303 | 44.2 | 35.5 | 0.157 | <0.001 |
| MP Non-essential AA, g | 166 | 0.004 | 0.001 | 0.002 | - | 0.006 | 26.2 | 40.6 | 0.207 | <0.001 |
| MP/ME Met, g/Mcal | 166 | 1.586 | 0.640 | 0.321 | - | 2.850 | 4.8 | 44.8 | 0.268 | 0.014 |
| MP/ME Lys, g/Mcal | 166 | 0.884 | 0.236 | 0.417 | - | 1.351 | 15.3 | 43.0 | 0.238 | <0.001 |
| MP/ME Arg, g/Mcal | 166 | 1.043 | 0.235 | 0.579 | - | 1.507 | 27.5 | 40.9 | 0.204 | <0.001 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Thr, g/Mcal | 166 | 1.047 | 0.321 | 0.414 | - | 1.681 | 9.7 | 43.8 | 0.254 | 0.001 |
| MP/ME Leu, g/Mcal | 166 | 0.189 | 0.129 | -0.067 | - | 0.444 | -0.4 | 45.8 | 0.282 | 0.146 |
| MP/ME Ile, g/Mcal | 166 | 1.016 | 0.309 | 0.407 | - | 1.625 | 11.3 | 43.5 | 0.249 | 0.001 |
| MP/ME Val, g/Mcal | 166 | 0.873 | 0.267 | 0.347 | - | 1.400 | 9.5 | 43.8 | 0.254 | 0.001 |
| MP/ME His, g/Mcal | 166 | 1.095 | 0.453 | 0.201 | - | 1.989 | 1.6 | 45.2 | 0.277 | 0.017 |
| MP/ME Phe, g/Mcal | 166 | 0.929 | 0.281 | 0.374 | - | 1.484 | 11.5 | 43.3 | 0.249 | 0.001 |
| MP/ME Trp, g/Mcal | 166 | 4.619 | 1.099 | 2.448 | - | 6.789 | 20.2 | 41.5 | 0.224 | <0.001 |
| MP/ME Non-essential AA, g/Mcal | 166 | 0.069 | 0.025 | 0.019 | - | 0.119 | 6.1 | 44.7 | 0.264 | 0.007 |
| ADF, g | 166 | 0.001 | <0.001 | 0.000 | - | 0.001 | 0.2 | 45.6 | 0.28 | 0.090 |
| Amylase NDF organic matter basis, g | 166 | <0.001 | <0.001 | 0.000 | - | 0.001 | -1.6 | 46.1 | 0.285 | 0.145 |
| Forage NDF, g | 166 | 0.001 | 0.001 | -0.001 | - | 0.002 | -4.1 | 46.3 | 0.293 | 0.427 |
| Physically effective NDF, g | 166 | 0.001 | <0.001 | <0.001 | - | 0.001 | -0.6 | 45.6 | 0.283 | 0.029 |
| Acid detergent lignin, g | 166 | 0.003 | 0.001 | <0.001 | - | 0.005 | 3.4 | 45.1 | 0.271 | 0.043 |
| Simple sugars, g | 166 | 0.003 | 0.001 | 0.001 | - | 0.004 | 14.2 | 43.4 | 0.241 | 0.002 |
| Starch, g | 166 | <0.001 | <0.001 | <0.001 | - | <0.001 | -1.2 | 46.3 | 0.284 | 0.675 |
| Soluble fibre, g | 166 | 0.001 | <0.001 | <0.001 | - | 0.001 | 7.2 | 45.3 | 0.261 | 0.020 |
| Fermentable starch, g | 166 | <0.001 | <0.001 | <0.001 | - | <0.001 | -2.9 | 46.4 | 0.289 | 0.757 |
| Fermentable soluble fibre, g | 166 | 0.001 | <0.001 | <0.001 | - | 0.002 | 7.9 | 45.2 | 0.259 | 0.018 |
| Fermentable NDF, g | 166 | 0.001 | <0.001 | <0.001 | - | 0.001 | 0.3 | 45.5 | 0.28 | 0.034 |
| Ether extract, g | 166 | 0.001 | 0.001 | <0.001 | - | 0.002 | 10.1 | 44.7 | 0.253 | 0.046 |

**Table 6.** Univariable analyses for HCW. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 172 | 0.067 | 0.018 | 0.031 | - | 0.103 | 25.4 | 32.9 | 0.106 | <0.001 |
| Initial BW, kg | 172 | -0.004 | 0.001 | -0.006 | - | -0.001 | -8.1 | 36.4 | 0.154 | 0.009 |
| ME, Mcal | 172 | 0.161 | 0.036 | 0.091 | - | 0.231 | 58.6 | 29.7 | 0.059 | <0.001 |
| MP, g/d | 172 | 0.001 | <0.001 | <0.001 | - | 0.002 | -15.8 | 36.7 | 0.165 | 0.006 |
| CP, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.001 | -4.6 | 36.1 | 0.149 | 0.005 |
| MP NRC, g/d | 169 | <0.001 | <0.001 | <0.001 | - | 0.001 | -6.6 | 35.1 | 0.131 | 0.120 |
| Soluble intake protein, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.002 | 2.8 | 36.4 | 0.138 | 0.061 |
| Ammonia, g | 172 | <0.001 | <0.001 | -0.001 | - | <0.001 | -4.7 | 37.3 | 0.149 | 0.280 |
| Protein $A_2$, g | 172 | 0.001 | 0.001 | <0.001 | - | 0.002 | -16.6 | 37.3 | 0.166 | 0.063 |
| Protein $B_1$, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.002 | 3.8 | 35.7 | 0.137 | 0.005 |
| Protein $B_2$, g | 172 | 0.002 | 0.001 | <0.001 | - | 0.003 | -1.5 | 36.7 | 0.144 | 0.055 |
| RDP x3 maintenance, g | 171 | 0.001 | <0.001 | <0.001 | - | 0.001 | -3.9 | 37.3 | 0.151 | 0.045 |
| RUP x1 maintenance, g | 171 | 0.001 | <0.001 | <0.001 | - | 0.002 | 1.8 | 36.3 | 0.143 | 0.009 |
| MP Met, g | 172 | 0.020 | 0.016 | -0.010 | - | 0.051 | -11.0 | 37.5 | 0.158 | 0.192 |
| MP Lys, g | 172 | 0.007 | 0.005 | -0.004 | - | 0.017 | -12.6 | 37.6 | 0.160 | 0.211 |
| MP Arg, g | 172 | 0.013 | 0.006 | 0.002 | - | 0.024 | -14.5 | 37.1 | 0.163 | 0.024 |
| MP Thr, g | 172 | 0.012 | 0.007 | -0.003 | - | 0.027 | -14.3 | 37.5 | 0.162 | 0.107 |
| MP Leu, g | 172 | 0.007 | 0.004 | -0.001 | - | 0.014 | -6.2 | 37.2 | 0.151 | 0.085 |
| MP Ile, g | 172 | 0.012 | 0.007 | -0.003 | - | 0.027 | -12.6 | 37.5 | 0.160 | 0.112 |
| MP Val, g | 172 | 0.014 | 0.007 | 0.001 | - | 0.027 | -15.5 | 37.2 | 0.164 | 0.035 |
| MP His, g | 172 | 0.028 | 0.013 | 0.003 | - | 0.053 | -13.2 | 37.0 | 0.161 | 0.027 |
| MP Phe, g | 172 | 0.019 | 0.008 | 0.004 | - | 0.034 | -10.6 | 36.8 | 0.157 | 0.013 |
| MP Trp, g | 172 | 0.042 | 0.025 | -0.008 | - | 0.092 | -14.3 | 37.5 | 0.162 | 0.096 |
| MP Non-essential AA, g | 172 | 0.002 | 0.001 | 0.001 | - | 0.003 | -13.8 | 36.5 | 0.162 | 0.006 |
| MP/ME Met, g/Mcal | 172 | 0.042 | 0.403 | -0.754 | - | 0.837 | -5.4 | 37.4 | 0.150 | 0.918 |
| MP/ME Lys, g/Mcal | 172 | 0.029 | 0.135 | -0.236 | - | 0.295 | -6.7 | 37.4 | 0.152 | 0.827 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Arg, g/Mcal | 172 | 0.166 | 0.147 | -0.123 | - | 0.456 | -12.8 | 37.6 | 0.16 | 0.259 |
| MP/ME Thr, g/Mcal | 172 | 0.086 | 0.192 | -0.293 | - | 0.466 | -8.7 | 37.5 | 0.155 | 0.654 |
| MP/ME Leu, g/Mcal | 172 | 0.063 | 0.102 | -0.139 | - | 0.265 | -6.9 | 37.6 | 0.152 | 0.540 |
| MP/ME Ile, g/Mcal | 172 | 0.073 | 0.192 | -0.307 | - | 0.452 | -7.7 | 37.5 | 0.153 | 0.707 |
| MP/ME Val, g/Mcal | 172 | 0.146 | 0.171 | -0.192 | - | 0.483 | -11.8 | 37.6 | 0.159 | 0.395 |
| MP/ME His, g/Mcal | 172 | 0.357 | 0.320 | -0.275 | - | 0.990 | -12.4 | 37.6 | 0.160 | 0.266 |
| MP/ME Phe, g/Mcal | 172 | 0.229 | 0.202 | -0.169 | - | 0.627 | -11.3 | 37.6 | 0.158 | 0.257 |
| MP/ME Trp, g/Mcal | 172 | 0.316 | 0.647 | -0.962 | - | 1.594 | -8.8 | 37.5 | 0.155 | 0.626 |
| MP/ME Non-essential AA, g/Mcal | 172 | 0.025 | 0.018 | -0.010 | - | 0.059 | -13.8 | 37.6 | 0.162 | 0.163 |
| ADF, g | 172 | <0.001 | <0.001 | <0.001 | - | 0.001 | -4.8 | 36.9 | 0.149 | 0.084 |
| Amylase NDF organic matter basis, g | 172 | <0.001 | <0.001 | <0.001 | - | 0.001 | -0.2 | 35.8 | 0.142 | 0.008 |
| Forage NDF, g | 172 | <0.001 | <0.001 | -0.001 | - | 0.001 | -2.2 | 37.6 | 0.145 | 0.939 |
| Physically effective NDF, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.001 | 5.6 | 35.1 | 0.134 | 0.004 |
| Acid detergent lignin, g | 172 | 0.001 | 0.001 | -0.001 | - | 0.003 | -8.3 | 37.5 | 0.154 | 0.181 |
| Simple sugars, g | 172 | 0.001 | 0.001 | <0.001 | - | 0.003 | -13.0 | 37.3 | 0.161 | 0.033 |
| Starch, g | 172 | <0.001 | <0.001 | <0.001 | - | <0.001 | -2.8 | 36.9 | 0.146 | 0.067 |
| Soluble fibre, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.001 | 5.5 | 35.8 | 0.134 | 0.011 |
| Fermentable starch, g | 172 | <0.001 | <0.001 | <0.001 | - | <0.001 | -5.4 | 37.5 | 0.150 | 0.315 |
| Fermentable soluble fibre, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.001 | 6.8 | 35.7 | 0.132 | 0.009 |
| Fermentable NDF, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.001 | 6.8 | 35.3 | 0.132 | 0.006 |
| Ether extract, g | 172 | 0.001 | 0.001 | <0.001 | - | 0.002 | 25.5 | 34.4 | 0.106 | 0.006 |

**Table 7.** Univariable analyses for G:F. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 157 | -0.015 | 0.029 | -0.072 | - | 0.042 | -1.3 | 66.8 | 0.527 | 0.616 |
| Initial BW, kg | 157 | -0.001 | 0.002 | -0.005 | - | 0.003 | -23.5 | 66.3 | 0.103 | 0.578 |
| ME, Mcal | 157 | 0.046 | 0.061 | -0.075 | - | 0.166 | 0.3 | 66.6 | 0.519 | 0.453 |
| MP, g/d | 157 | <0.001 | 0.001 | -0.001 | - | 0.001 | -3.1 | 66.4 | 0.537 | 0.623 |
| CP, g | 157 | <0.001 | <0.001 | <0.001 | - | 0.001 | -2.3 | 66.9 | 0.532 | 0.266 |
| MP NRC, g/d | 155 | 0.001 | <0.001 | <0.001 | - | 0.001 | -1.3 | 67.1 | 0.534 | 0.074 |
| Soluble intake protein, g | 157 | 0.002 | 0.001 | 0.001 | - | 0.003 | 12.0 | 66.3 | 0.458 | 0.002 |
| Ammonia, g | 157 | -0.001 | 0.001 | -0.001 | - | 0.000 | -1.0 | 66.3 | 0.526 | 0.311 |
| Protein $A_2$, g | 157 | -0.002 | 0.001 | -0.004 | - | -0.001 | 24.9 | 54.8 | 0.391 | 0.001 |
| Protein $B_1$, g | 157 | 0.001 | 0.001 | 0.000 | - | 0.002 | 7.1 | 64.7 | 0.483 | 0.004 |
| Protein $B_2$, g | 157 | 0.002 | 0.001 | 0.000 | - | 0.004 | -0.1 | 66.8 | 0.521 | 0.071 |
| RDP x3 maintenance, g | 156 | -0.001 | 0.001 | -0.002 | - | 0.000 | 3.1 | 66.8 | 0.505 | 0.121 |
| RUP x1 maintenance, g | 156 | 0.002 | 0.001 | 0.000 | - | 0.003 | 3.5 | 66.3 | 0.503 | 0.005 |
| MP Met, g | 157 | -0.003 | 0.023 | -0.049 | - | 0.044 | -1.3 | 66.5 | 0.527 | 0.912 |
| MP Lys, g | 157 | -0.006 | 0.008 | -0.022 | - | 0.009 | 1.4 | 65.9 | 0.513 | 0.444 |
| MP Arg, g | 157 | 0.001 | 0.009 | -0.016 | - | 0.018 | -2.0 | 66.5 | 0.530 | 0.930 |
| MP Thr, g | 157 | -0.002 | 0.011 | -0.024 | - | 0.021 | -1.2 | 66.3 | 0.526 | 0.882 |
| MP Leu, g | 157 | 0.006 | 0.006 | -0.005 | - | 0.017 | -2.3 | 70.0 | 0.535 | 0.306 |
| MP Ile, g | 157 | 0.001 | 0.011 | -0.021 | - | 0.023 | -1.9 | 66.7 | 0.530 | 0.935 |
| MP Val, g | 157 | 0.002 | 0.010 | -0.018 | - | 0.022 | -2.3 | 66.5 | 0.532 | 0.834 |
| MP His, g | 157 | 0.006 | 0.019 | -0.031 | - | 0.044 | -2.5 | 66.4 | 0.533 | 0.743 |
| MP Phe, g | 157 | 0.012 | 0.012 | -0.011 | - | 0.035 | -2.9 | 67.0 | 0.536 | 0.310 |
| MP Trp, g | 157 | 0.002 | 0.039 | -0.074 | - | 0.079 | -1.9 | 66.7 | 0.53 | 0.949 |
| MP Non-essential AA, g | 157 | 0.001 | 0.001 | -0.001 | - | 0.003 | -3.5 | 66.5 | 0.538 | 0.446 |
| MP/ME Met, g/Mcal | 157 | -0.510 | 0.606 | -1.707 | - | 0.688 | 2.1 | 65.9 | 0.510 | 0.402 |
| MP/ME Lys, g/Mcal | 157 | -0.276 | 0.202 | -0.674 | - | 0.123 | 5.3 | 65.2 | 0.493 | 0.174 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Arg, g/Mcal | 157 | -0.134 | 0.222 | -0.573 | - | 0.305 | 0.9 | 65.9 | 0.516 | 0.547 |
| MP/ME Thr, g/Mcal | 157 | -0.259 | 0.290 | -0.832 | - | 0.314 | 2.5 | 65.8 | 0.507 | 0.374 |
| MP/ME Leu, g/Mcal | 157 | 0.040 | 0.149 | -0.255 | - | 0.335 | -2.1 | 66.9 | 0.531 | 0.790 |
| MP/ME Ile, g/Mcal | 157 | -0.188 | 0.290 | -0.760 | - | 0.384 | 1.1 | 66.2 | 0.515 | 0.518 |
| MP/ME Val, g/Mcal | 157 | -0.151 | 0.258 | -0.661 | - | 0.358 | 0.8 | 66.0 | 0.516 | 0.558 |
| MP/ME His, g/Mcal | 157 | -0.221 | 0.481 | -1.172 | - | 0.730 | 0.1 | 65.8 | 0.520 | 0.646 |
| MP/ME Phe, g/Mcal | 157 | 0.060 | 0.301 | -0.535 | - | 0.655 | -2.2 | 66.8 | 0.532 | 0.842 |
| MP/ME Trp, g/Mcal | 157 | -0.574 | 0.982 | -2.514 | - | 1.365 | 0.6 | 66.4 | 0.517 | 0.559 |
| MP/ME Non-essential AA, g/Mcal | 157 | -0.003 | 0.027 | -0.055 | - | 0.050 | -1.3 | 65.9 | 0.527 | 0.915 |
| ADF, g | 157 | <0.001 | <0.001 | <0.001 | - | 0.001 | -2.6 | 66.9 | 0.534 | 0.398 |
| Amylase NDF organic matter basis, g | 157 | <0.001 | <0.001 | <0.001 | - | <0.001 | -2.3 | 65.2 | 0.532 | 0.638 |
| Forage NDF, g | 157 | <0.001 | <0.001 | -0.001 | - | 0.001 | -1.0 | 66.9 | 0.526 | 0.624 |
| Physically effective NDF, g | 157 | <0.001 | <0.001 | -0.001 | - | 0.001 | 0.7 | 64.6 | 0.517 | 0.411 |
| Acid detergent lignin, g | 157 | 0.002 | 0.001 | -0.001 | - | 0.005 | -1.8 | 66.8 | 0.530 | 0.156 |
| Simple sugars, g | 157 | -0.001 | 0.001 | -0.002 | - | 0.001 | -0.7 | 67.0 | 0.524 | 0.600 |
| Starch, g | 157 | 0.000 | <0.001 | <0.001 | - | <0.001 | -0.9 | 66.9 | 0.525 | 0.031 |
| Soluble fibre, g | 157 | 0.001 | <0.001 | 0.001 | - | 0.002 | 6.8 | 66.9 | 0.485 | 0.001 |
| Fermentable starch, g | 157 | 0.000 | <0.001 | -0.001 | - | 0.000 | -2.8 | 66.6 | 0.535 | 0.071 |
| Fermentable soluble fibre, g | 157 | 0.002 | <0.001 | 0.001 | - | 0.002 | 8.1 | 66.9 | 0.478 | <0.001 |
| Fermentable NDF, g | 157 | 0.000 | <0.001 | -0.001 | - | 0.001 | -1.6 | 65.5 | 0.529 | 0.922 |
| Ether extract, g | 157 | 0.003 | 0.001 | 0.001 | - | 0.004 | 13.7 | 65.7 | 0.449 | <0.001 |

**Table 8.** Univariable analyses for DMI. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 213 | 0.045 | 0.016 | 0.014 | - | 0.075 | 10.8 | 46.3 | 0.176 | 0.004 |
| Initial BW, kg | 213 | -0.002 | 0.001 | -0.005 | - | <0.001 | 4.3 | 47.3 | 0.189 | 0.068 |
| ME, Mcal | 212 | 0.272 | 0.035 | 0.204 | - | 0.341 | 40.0 | 37.8 | 0.118 | <0.001 |
| MP, g/d | 212 | 0.002 | <0.001 | 0.001 | - | 0.002 | 16.5 | 44.1 | 0.164 | <0.001 |
| CP, g | 213 | 0.001 | <0.001 | <0.001 | - | 0.001 | 3.2 | 47.4 | 0.191 | 0.005 |
| MP NRC, g/d | 210 | <0.001 | <0.001 | <0.001 | - | 0.001 | -1.6 | 48.3 | 0.198 | 0.445 |
| Soluble intake protein, g | 212 | <0.001 | <0.001 | -0.001 | - | <0.001 | -2.4 | 48.2 | 0.202 | 0.342 |
| Ammonia, g | 213 | <0.001 | <0.001 | -0.001 | - | 0.001 | -2.0 | 47.4 | 0.201 | 0.951 |
| Protein $A_2$, g | 213 | 0.003 | <0.001 | 0.002 | - | 0.004 | 73.2 | 32.4 | 0.053 | <0.001 |
| Protein $B_1$, g | 213 | 0.000 | <0.001 | -0.001 | - | 0.001 | -2.0 | 48.3 | 0.201 | 0.820 |
| Protein $B_2$, g | 213 | 0.001 | 0.001 | -0.001 | - | 0.003 | 0.5 | 48.1 | 0.196 | 0.265 |
| RDP x3 maintenance, g | 212 | 0.002 | <0.001 | 0.001 | - | 0.002 | 8.2 | 46.3 | 0.180 | <0.001 |
| RUP x1 maintenance, g | 212 | 0.000 | <0.001 | <0.001 | - | 0.001 | -0.8 | 48.4 | 0.197 | 0.418 |
| MP Met, g | 213 | 0.059 | 0.016 | 0.028 | - | 0.091 | 9.3 | 46.0 | 0.179 | <0.001 |
| MP Lys, g | 213 | 0.020 | 0.005 | 0.009 | - | 0.030 | 10.4 | 45.8 | 0.177 | <0.001 |
| MP Arg, g | 213 | 0.024 | 0.006 | 0.012 | - | 0.035 | 13.7 | 45.2 | 0.170 | <0.001 |
| MP Thr, g | 213 | 0.031 | 0.008 | 0.016 | - | 0.046 | 9.7 | 45.6 | 0.178 | <0.001 |
| MP Leu, g | 213 | 0.013 | 0.004 | 0.005 | - | 0.021 | 6.2 | 46.9 | 0.185 | 0.002 |
| MP Ile, g | 213 | 0.029 | 0.008 | 0.014 | - | 0.044 | 8.5 | 46.2 | 0.181 | <0.001 |
| MP Val, g | 213 | 0.029 | 0.007 | 0.015 | - | 0.042 | 10.5 | 45.2 | 0.177 | <0.001 |
| MP His, g | 213 | 0.050 | 0.013 | 0.024 | - | 0.075 | 12.1 | 45.0 | 0.173 | <0.001 |
| MP Phe, g | 213 | 0.029 | 0.008 | 0.014 | - | 0.045 | 8.0 | 46.5 | 0.182 | <0.001 |
| MP Trp, g | 213 | 0.085 | 0.026 | 0.033 | - | 0.137 | 5.3 | 47.0 | 0.187 | 0.002 |
| MP Non-essential AA, g | 213 | 0.003 | 0.001 | 0.002 | - | 0.004 | 17.6 | 43.8 | 0.163 | <0.001 |
| MP/ME Met, g/Mcal | 213 | 0.788 | 0.425 | -0.049 | - | 1.625 | 3.1 | 47.7 | 0.191 | 0.065 |
| MP/ME Lys, g/Mcal | 213 | 0.293 | 0.143 | 0.011 | - | 0.575 | 4.8 | 47.4 | 0.188 | 0.042 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Arg, g/Mcal | 213 | 0.355 | 0.154 | 0.052 | - | 0.658 | 6.6 | 47.2 | 0.184 | 0.022 |
| MP/ME Thr, g/Mcal | 213 | 0.447 | 0.202 | 0.050 | - | 0.845 | 4.0 | 47.4 | 0.189 | 0.028 |
| MP/ME Leu, g/Mcal | 213 | 0.153 | 0.107 | -0.059 | - | 0.364 | 0.9 | 48.1 | 0.197 | 0.157 |
| MP/ME Ile, g/Mcal | 213 | 0.386 | 0.203 | -0.015 | - | 0.786 | 2.8 | 47.8 | 0.192 | 0.059 |
| MP/ME Val, g/Mcal | 213 | 0.412 | 0.178 | 0.061 | - | 0.764 | 4.0 | 47.3 | 0.189 | 0.022 |
| MP/ME His, g/Mcal | 213 | 0.724 | 0.335 | 0.063 | - | 1.385 | 4.6 | 47.0 | 0.188 | 0.032 |
| MP/ME Phe, g/Mcal | 213 | 0.359 | 0.212 | -0.059 | - | 0.777 | 1.4 | 48.0 | 0.195 | 0.092 |
| MP/ME Trp, g/Mcal | 213 | 1.046 | 0.693 | -0.320 | - | 2.412 | 1.2 | 48.1 | 0.195 | 0.133 |
| MP/ME Non-essential AA, g/Mcal | 213 | 0.043 | 0.018 | 0.007 | - | 0.079 | 7.3 | 46.6 | 0.183 | 0.019 |
| ADF, g | 213 | 0.001 | <0.001 | <0.001 | - | 0.001 | 4.2 | 46.4 | 0.189 | 0.004 |
| Amylase NDF organic matter basis, g | 213 | 0.001 | <0.001 | <0.001 | - | 0.001 | 29.8 | 39.6 | 0.139 | <0.001 |
| Forage NDF, g | 213 | 0.001 | <0.001 | <0.001 | - | 0.001 | -1.3 | 48.2 | 0.200 | 0.113 |
| Physically effective NDF, g | 213 | 0.001 | <0.001 | 0.001 | - | 0.002 | 24.4 | 39.9 | 0.149 | <0.001 |
| Acid detergent lignin, g | 213 | 0.002 | 0.001 | <0.001 | - | 0.004 | -0.4 | 48.1 | 0.198 | 0.048 |
| Simple sugars, g | 213 | 0.003 | 0.001 | 0.001 | - | 0.004 | -1.5 | 47.4 | 0.200 | <0.001 |
| Starch, g | 213 | <0.001 | <0.001 | <0.001 | - | <0.001 | -3.9 | 48.4 | 0.205 | 0.204 |
| Soluble fibre, g | 213 | <0.001 | <0.001 | <0.001 | - | 0.001 | 0.4 | 46.6 | 0.197 | 0.640 |
| Fermentable starch, g | 213 | <0.001 | <0.001 | <0.001 | - | <0.001 | -3.9 | 48.1 | 0.205 | 0.576 |
| Fermentable soluble fibre, g | 213 | <0.001 | <0.001 | -0.001 | - | 0.001 | -0.2 | 46.8 | 0.198 | 0.707 |
| Fermentable NDF, g | 213 | 0.001 | <0.001 | 0.001 | - | 0.001 | 19.2 | 42.1 | 0.159 | <0.001 |
| Ether extract, g | 213 | 0.001 | 0.001 | <0.001 | - | 0.002 | 5.9 | 47.2 | 0.186 | 0.052 |

**Table 9.** Univariable analyses for LM area. Includes number of comparisons used (No.), coefficient, SE, 95% CI, heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value. Adjusted $R^2$ values are not available.

| Variable | No. | Coefficient | SE | 95% CI | | | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 169 | -0.007 | 0.016 | -0.038 | - | 0.025 | 23.5 | 0 | 0.680 |
| Initial BW, kg | 169 | -0.002 | 0.001 | -0.004 | - | 0.001 | 22.7 | 0 | 0.168 |
| ME, Mcal | 169 | 0.082 | 0.033 | 0.016 | - | 0.148 | 20.8 | 0 | 0.015 |
| MP, g/d | 169 | <0.001 | <0.001 | <0.001 | - | 0.001 | 23.2 | 0.001 | 0.373 |
| CP, g | 169 | <0.001 | <0.001 | <0.001 | - | <0.001 | 23.6 | 0 | 0.985 |
| MP NRC, g/d | 166 | <0.001 | <0.001 | -0.001 | - | <0.001 | 23.2 | 0 | 0.217 |
| Soluble intake protein, g | 168 | <0.001 | <0.001 | <0.001 | - | 0.001 | 22.0 | 0 | 0.204 |
| Ammonia, g | 169 | <0.001 | <0.001 | -0.001 | - | 0.001 | 23.5 | 0 | 0.698 |
| Protein $A_2$, g | 169 | 0.001 | 0.001 | <0.001 | - | 0.002 | 21.5 | 0.007 | 0.031 |
| Protein $B_1$, g | 169 | <0.001 | <0.001 | -0.001 | - | 0.001 | 23.5 | 0 | 0.657 |
| Protein $B_2$, g | 169 | -0.001 | 0.001 | -0.002 | - | 0.001 | 23.3 | 0 | 0.402 |
| RDP x3 maintenance, g | 168 | <0.001 | <0.001 | <0.001 | - | 0.001 | 24.0 | 0 | 0.690 |
| RUP x1 maintenance, g | 168 | <0.001 | <0.001 | -0.001 | - | 0.000 | 23.9 | 0 | 0.567 |
| MP Met, g | 169 | 0.009 | 0.012 | -0.014 | - | 0.032 | 23.3 | 0 | 0.442 |
| MP Lys, g | 169 | 0.004 | 0.004 | -0.004 | - | 0.011 | 23.2 | 0.003 | 0.347 |
| MP Arg, g | 169 | 0.005 | 0.004 | -0.004 | - | 0.013 | 23.1 | 0.006 | 0.266 |
| MP Thr, g | 169 | 0.005 | 0.006 | -0.006 | - | 0.016 | 23.3 | 0.002 | 0.412 |
| MP Leu, g | 169 | 0.001 | 0.003 | -0.005 | - | 0.007 | 23.6 | 0 | 0.756 |
| MP Ile, g | 169 | 0.004 | 0.006 | -0.007 | - | 0.015 | 23.3 | 0 | 0.441 |
| MP Val, g | 169 | 0.004 | 0.005 | -0.006 | - | 0.014 | 23.4 | 0 | 0.474 |
| MP His, g | 169 | 0.010 | 0.010 | -0.009 | - | 0.029 | 23.1 | 0.002 | 0.312 |
| MP Phe, g | 169 | 0.003 | 0.006 | -0.008 | - | 0.015 | 23.4 | 0 | 0.575 |
| MP Trp, g | 169 | 0.012 | 0.019 | -0.025 | - | 0.049 | 23.4 | 0 | 0.512 |
| MP Non-essential AA, g | 169 | 0.001 | 0.001 | -0.001 | - | 0.002 | 23.3 | 0.001 | 0.385 |
| MP/ME Met, g/Mcal | 169 | 0.122 | 0.301 | -0.472 | - | 0.715 | 23.5 | 0 | 0.687 |
| MP/ME Lys, g/Mcal | 169 | 0.069 | 0.099 | -0.126 | - | 0.263 | 23.4 | 0.001 | 0.487 |
| MP/ME Arg, g/Mcal | 169 | 0.093 | 0.109 | -0.122 | - | 0.308 | 23.3 | 0.004 | 0.396 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| MP/ME Thr, g/Mcal | 169 | 0.071 | 0.142 | -0.208 | - | 0.351 | 23.5 | 0 | 0.614 |
| MP/ME Leu, g/Mcal | 169 | 0.006 | 0.082 | -0.167 | - | 0.155 | 23.6 | 0 | 0.942 |
| MP/ME Ile, g/Mcal | 169 | 0.064 | 0.143 | -0.218 | - | 0.346 | 23.5 | 0 | 0.653 |
| MP/ME Val, g/Mcal | 169 | 0.050 | 0.127 | -0.201 | - | 0.301 | 23.5 | 0 | 0.692 |
| MP/ME His, g/Mcal | 169 | 0.164 | 0.245 | -0.320 | - | 0.648 | 23.4 | 0 | 0.504 |
| MP/ME Phe, g/Mcal | 169 | 0.030 | 0.153 | -0.273 | - | 0.333 | 23.6 | 0 | 0.845 |
| MP/ME Trp, g/Mcal | 169 | 0.169 | 0.471 | -0.761 | - | 1.099 | 23.5 | 0 | 0.721 |
| MP/ME Non-essential AA, g/Mcal | 169 | 0.007 | 0.013 | -0.020 | - | 0.034 | 23.5 | 0 | 0.611 |
| ADF, g | 169 | <0.001 | <0.001 | -0.001 | - | <0.001 | 23.4 | 0 | 0.565 |
| Amylase NDF organic matter basis, g | 169 | <0.001 | <0.001 | 0.000 | - | <0.001 | 23.5 | 0 | 0.630 |
| Forage NDF, g | 169 | <0.001 | <0.001 | -0.001 | - | 0.001 | 23.5 | 0 | 0.734 |
| Physically effective NDF, g | 169 | <0.001 | <0.001 | <0.001 | - | 0.001 | 23.6 | 0 | 0.794 |
| Acid detergent lignin, g | 169 | -0.001 | 0.001 | -0.002 | - | 0.001 | 23.3 | 0 | 0.407 |
| Simple sugars, g | 169 | <0.001 | 0.001 | -0.001 | - | 0.001 | 23.6 | 0 | 0.872 |
| Starch, g | 169 | <0.001 | <0.001 | <0.001 | - | <0.001 | 23.5 | 0 | 0.733 |
| Soluble fibre, g | 169 | <0.001 | <0.001 | <0.001 | - | 0.001 | 22.1 | 0 | 0.070 |
| Fermentable starch, g | 169 | <0.001 | <0.001 | <0.001 | - | <0.001 | 23.6 | 0 | 0.868 |
| Fermentable soluble fibre, g | 169 | 0.001 | <0.001 | <0.001 | - | 0.001 | 22.2 | 0 | 0.078 |
| Fermentable NDF, g | 169 | <0.001 | <0.001 | <0.001 | - | 0.001 | 23.6 | 0 | 0.825 |
| Ether extract, g | 169 | <0.001 | <0.001 | -0.001 | - | 0.001 | 23.5 | 0 | 0.587 |

**Table 10.** Univariable analyses for fat thickness. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 173 | 0.018 | 0.019 | -0.019 | - | 0.055 | 2.1 | 36.9 | 0.103 | 0.326 |
| Initial BW, kg | 173 | 0.001 | 0.001 | -0.001 | - | 0.004 | 0.1 | 36.8 | 0.103 | 0.363 |
| ME, Mcal | 173 | 0.075 | 0.037 | 0.001 | - | 0.149 | 12.7 | 35.7 | 0.092 | 0.046 |
| MP, g/d | 173 | <0.001 | <0.001 | <0.001 | - | 0.002 | -19.4 | 35.8 | 0.126 | 0.007 |
| CP, g | 173 | <0.001 | <0.001 | <0.001 | - | 0.001 | 4.6 | 34.2 | 0.100 | 0.002 |
| MP NRC, g/d | 170 | <0.001 | <0.001 | <0.001 | - | 0.001 | 4.3 | 36.3 | 0.106 | 0.018 |
| Soluble intake protein, g | 172 | <0.001 | <0.001 | -0.001 | - | 0.001 | -1.6 | 36.9 | 0.106 | 0.658 |
| Ammonia, g | 173 | <0.001 | <0.001 | -0.001 | - | 0.001 | -2.9 | 37.2 | 0.108 | 0.983 |
| Protein $A_2$, g | 173 | <0.001 | 0.001 | -0.001 | - | 0.001 | -1.7 | 37.1 | 0.107 | 0.698 |
| Protein $B_1$, g | 173 | 0.001 | <0.001 | 0.001 | - | 0.002 | 16.7 | 32.5 | 0.088 | <0.001 |
| Protein $B_2$, g | 173 | 0.002 | 0.001 | <0.001 | - | 0.003 | 5.2 | 35.7 | 0.100 | 0.037 |
| RDP x3 maintenance, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.001 | -1.27 | 36.7 | 0.108 | 0.120 |
| RUP x1 maintenance, g | 172 | 0.001 | <0.001 | <0.001 | - | 0.002 | 16.51 | 33.7 | 0.089 | 0.001 |
| MP Met, g | 173 | 0.039 | 0.015 | 0.009 | - | 0.069 | -20.5 | 36.1 | 0.127 | 0.011 |
| MP Lys, g | 173 | 0.008 | 0.005 | -0.002 | - | 0.019 | -21.2 | 37.0 | 0.128 | 0.103 |
| MP Arg, g | 173 | 0.013 | 0.006 | 0.001 | - | 0.024 | -22.3 | 36.5 | 0.129 | 0.027 |
| MP Thr, g | 173 | 0.018 | 0.007 | 0.004 | - | 0.033 | -23.4 | 36.3 | 0.130 | 0.015 |
| MP Leu, g | 173 | 0.015 | 0.004 | 0.007 | - | 0.022 | 1.9 | 32.8 | 0.103 | <0.001 |
| MP Ile, g | 173 | 0.019 | 0.007 | 0.005 | - | 0.033 | -22.9 | 36.1 | 0.129 | 0.011 |
| MP Val, g | 173 | 0.019 | 0.007 | 0.006 | - | 0.032 | -22.8 | 35.7 | 0.129 | 0.004 |
| MP His, g | 173 | 0.032 | 0.012 | 0.008 | - | 0.056 | -18.2 | 36.0 | 0.125 | 0.010 |
| MP Phe, g | 173 | 0.028 | 0.008 | 0.013 | - | 0.043 | -17.6 | 34.3 | 0.124 | <0.001 |
| MP Trp, g | 173 | 0.052 | 0.025 | 0.003 | - | 0.101 | -23.7 | 36.7 | 0.130 | 0.039 |
| MP Non-essential AA, g | 173 | 0.002 | 0.001 | 0.001 | - | 0.004 | -15.1 | 34.9 | 0.121 | 0.001 |
| MP/ME Met, g/Mcal | 173 | 0.404 | 0.397 | -0.379 | - | 1.188 | -13.0 | 37.2 | 0.119 | 0.310 |
| MP/ME Lys, g/Mcal | 173 | 0.040 | 0.132 | -0.221 | - | 0.301 | -8.7 | 37.2 | 0.115 | 0.765 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Arg, g/Mcal | 173 | 0.101 | 0.145 | -0.185 | - | 0.387 | -11.7 | 37.2 | 0.118 | 0.487 |
| MP/ME Thr, g/Mcal | 173 | 0.175 | 0.189 | -0.199 | - | 0.549 | -13.5 | 37.2 | 0.120 | 0.357 |
| MP/ME Leu, g/Mcal | 173 | 0.243 | 0.001 | 0.046 | - | 0.441 | -6.4 | 35.8 | 0.112 | 0.016 |
| MP/ME Ile, g/Mcal | 173 | 0.194 | 0.190 | -0.180 | - | 0.569 | -13.9 | 37.2 | 0.120 | 0.307 |
| MP/ME Val, g/Mcal | 173 | 0.211 | 0.169 | -0.122 | - | 0.544 | -14.9 | 37.1 | 0.121 | 0.213 |
| MP/ME His, g/Mcal | 173 | 0.340 | 0.318 | -0.288 | - | 0.968 | -12.3 | 37.1 | 0.118 | 0.287 |
| MP/ME Phe, g/Mcal | 173 | 0.384 | 0.198 | -0.007 | - | 0.775 | -16.4 | 36.6 | 0.123 | 0.054 |
| MP/ME Trp, g/Mcal | 173 | 0.447 | 0.633 | -0.803 | - | 1.697 | -12.6 | 37.2 | 0.119 | 0.481 |
| MP/ME Non-essential AA, g/Mcal | 173 | 0.026 | 0.018 | -0.009 | - | 0.060 | -11.7 | 36.9 | 0.118 | 0.145 |
| ADF, g | 173 | 0.001 | <0.001 | <0.001 | - | 0.001 | 11.4 | 34.8 | 0.093 | 0.010 |
| Amylase NDF organic matter basis, g | 173 | <0.001 | <0.001 | <0.001 | - | 0.001 | 16.3 | 35.3 | 0.088 | 0.031 |
| Forage NDF, g | 173 | 0.001 | <0.001 | <0.001 | - | 0.001 | 9.6 | 36.1 | 0.095 | 0.089 |
| Physically effective NDF, g | 173 | <0.001 | <0.001 | <0.001 | - | 0.001 | 3.7 | 36.5 | 0.102 | 0.171 |
| Acid detergent lignin, g | 173 | 0.002 | 0.001 | <0.001 | - | 0.004 | -5.4 | 36.2 | 0.111 | 0.043 |
| Simple sugars, g | 173 | <0.001 | 0.001 | -0.001 | - | 0.001 | -2.2 | 37.1 | 0.108 | 0.826 |
| Starch, g | 173 | <0.001 | <0.001 | <0.001 | - | <0.001 | -1.9 | 37.1 | 0.107 | 0.662 |
| Soluble fibre, g | 173 | <0.001 | <0.001 | <0.001 | - | 0.001 | 1.6 | 36.5 | 0.104 | 0.130 |
| Fermentable starch, g | 173 | <0.001 | <0.001 | <0.001 | - | <0.001 | -2.1 | 37.1 | 0.108 | 0.462 |
| Fermentable soluble fibre, g | 173 | 0.001 | <0.001 | <0.001 | - | 0.001 | 1.7 | 36.5 | 0.104 | 0.130 |
| Fermentable NDF, g | 173 | 0.001 | <0.001 | <0.001 | - | 0.001 | 24.7 | 34.7 | 0.079 | 0.017 |
| Ether extract, g | 173 | 0.002 | 0.001 | 0.001 | - | 0.003 | 36.6 | 32.6 | 0.067 | 0.001 |

**Table 11.** Standardised mean differences (SMD) and 95% CI for the production outcome variables by nitrogen or protein intervention. Includes degrees of freedom (df), study weight, $I^2$ and $\tau^2$.

| Variable | df | SMD | 95% CI | | | Weight (%) | $I^2$ | $\tau^2$ |
|---|---|---|---|---|---|---|---|---|
| ADG | | | | | | | | |
| Distillers grain | 51 | 0.604 | 0.322 | - | 0.885 | 26.54 | 60.0 | 0.604 |
| Urea | 31 | 0.750 | 0.339 | - | 1.161 | 11.64 | 44.3 | 0.543 |
| Corn gluten feed | 27 | 0.227 | -0.091 | - | 0.545 | 13.21 | 57.9 | 0.259 |
| Soyabean meal | 15 | 1.269 | 0.610 | - | 1.928 | 5.62 | 53.3 | 0.821 |
| Canola meal | 10 | -0.301 | -0.698 | - | 0.097 | 7.17 | 56.3 | 0.225 |
| Cottonseed meal | 5 | 0.119 | -0.403 | - | 0.641 | 3.36 | 16.9 | 0.072 |
| Grains | 4 | -0.719 | -1.644 | - | 0.207 | 3.00 | 71.4 | 0.788 |
| Fish meal | 4 | -1.150 | -1.928 | - | -0.372 | 1.94 | 5.7 | 0.046 |
| Commercial blend | 3 | -0.295 | -1.049 | - | 0.460 | 1.77 | 0 | 0 |
| Protected protein meal | 3 | 0.308 | -0.808 | - | 1.423 | 1.40 | 30.0 | 0.421 |
| Wheat distillers | 0 | 1.346 | -0.235 | - | 2.928 | 0.43 | | |
| Other | 44 | 0.287 | 0.044 | - | 0.530 | 23.93 | 43.4 | 0.282 |
| Overall | 208 | 0.365 | 0.229 | - | 0.500 | 100.00 | 58.4 | 0.478 |
| Final BW | | | | | | | | |
| Distillers grain | 47 | 0.309 | 0.057 | - | 0.562 | 30.09 | 50.9 | 0.383 |
| Urea | 25 | 0.604 | 0.275 | - | 0.933 | 12.45 | 19.7 | 0.139 |
| Corn gluten feed | 13 | -0.002 | -0.300 | - | 0.296 | 10.92 | 51.5 | 0.110 |
| Soyabean meal | 13 | 1.072 | 0.451 | - | 1.694 | 6.45 | 54.0 | 0.716 |
| Canola meal | 4 | 1.041 | 0.234 | - | 1.849 | 2.35 | 26.5 | 0.223 |
| Cottonseed meal | 4 | 0.249 | -0.372 | - | 0.871 | 3.10 | 20.5 | 0.104 |
| Grains | 4 | -0.796 | -1.821 | - | 0.229 | 3.53 | 75.9 | 1.025 |
| Fish meal | 4 | -1.098 | -1.950 | - | -0.246 | 2.09 | 21.1 | 0.200 |
| Commercial blend | 3 | -0.087 | -0.829 | - | 0.654 | 1.99 | 0 | 0 |
| Protected protein meal | 0 | 0.613 | -0.286 | - | 1.512 | 0.88 | | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Wheat distillers | 0 | 1.207 | -0.338 | - | 2.752 | 0.480 | | |
| Other | 37 | 0.118 | -0.077 | - | 0.314 | 25.67 | 10.0 | 0.038 |
| Overall | 165 | 0.259 | 0.131 | - | 0.387 | 100.00 | 46.0 | 0.271 |
| HCW | | | | | | | | |
| Distillers grain | 46 | 0.341 | 0.117 | - | 0.564 | 27.43 | 38.0 | 0.220 |
| Urea | 18 | 0.372 | 0.024 | - | 0.719 | 9.43 | 19.2 | 0.114 |
| Corn gluten feed | 27 | 0.321 | -0.004 | - | 0.646 | 14.90 | 58.8 | 0.272 |
| Soyabean meal | 9 | 1.058 | 0.597 | - | 1.518 | 4.41 | 0 | 0 |
| Canola meal | 8 | -0.14 | -0.380 | - | 0.099 | 8.87 | 0 | 0 |
| Cottonseed meal | 5 | 0.135 | -0.492 | - | 0.761 | 3.60 | 39.2 | 0.234 |
| Grains | 3 | -1.074 | -2.391 | - | 0.243 | 2.37 | 78.8 | 1.418 |
| Fish meal | 1 | -1.366 | -3.150 | - | 0.417 | 0.57 | 37.7 | 0.653 |
| Commercial blend | 3 | -0.414 | -1.174 | - | 0.346 | 1.67 | 0 | 0 |
| Other | 42 | 0.131 | -0.041 | - | 0.304 | 26.75 | 0 | 0 |
| Overall | 171 | 0.217 | 0.105 | - | 0.329 | 100.00 | 37.2 | 0.173 |
| G:F | | | | | | | | |
| Distillers grain | 47 | 0.774 | 0.492 | - | 1.057 | 29.47 | 57.2 | 0.526 |
| Urea | 20 | 0.239 | -0.182 | - | 0.661 | 12.24 | 47.8 | 0.447 |
| Corn gluten feed | 19 | -0.413 | -0.704 | - | -0.122 | 13.42 | 49.7 | 0.145 |
| Soyabean meal | 6 | 0.855 | -0.011 | - | 1.722 | 4.22 | 64.6 | 0.869 |
| Canola meal | 7 | -0.608 | -0.895 | - | -0.32 | 6.94 | 21.0 | 0.036 |
| Cottonseed meal | 3 | -0.017 | -0.536 | - | 0.503 | 2.94 | 0 | 0 |
| Grains | 2 | -1.016 | -3.778 | - | 1.746 | 1.88 | 92.4 | 5.496 |
| Fish meal | 1 | -2.273 | -18.669 | - | 14.122 | 0.16 | 92.7 | 129.896 |
| Commercial blend | 0 | 1.938 | 0.376 | - | 3.499 | 0.53 | | |
| Wheat distillers | 0 | 0.074 | -1.312 | - | 1.461 | 0.60 | | |
| Other | 41 | 0.323 | 0.133 | - | 0.514 | 27.60 | 9.6 | 0.038 |
| Overall | 156 | 0.328 | 0.170 | - | 0.486 | 100.00 | 66.7 | 0.585 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| DMI | | | | | | | | |
| Distillers grain | 51 | 0.113 | -0.092 | - | 0.318 | 27.03 | 32.0 | 0.172 |
| Urea | 33 | 0.507 | 0.081 | - | 0.933 | 11.37 | 49.9 | 0.694 |
| Corn gluten feed | 27 | 0.762 | 0.476 | - | 1.048 | 12.71 | 44.9 | 0.163 |
| Soyabean meal | 15 | 0.595 | 0.109 | - | 1.080 | 5.89 | 32.3 | 0.287 |
| Canola meal | 10 | 0.280 | -0.007 | - | 0.566 | 7.37 | 23.9 | 0.053 |
| Cottonseed meal | 5 | 0.043 | -0.575 | - | 0.662 | 3.22 | 37.9 | 0.221 |
| Grains | 4 | -0.401 | -0.958 | - | 0.156 | 3.11 | 29.5 | 0.119 |
| Fish meal | 4 | -2.263 | -3.180 | - | -1.346 | 1.30 | 0 | 0 |
| Commercial blend | 3 | -0.932 | -1.732 | - | -0.133 | 1.52 | 0 | 0 |
| Protected protein meal | 3 | 0.374 | -0.341 | - | 1.089 | 1.49 | 0 | 0 |
| Wheat distillers | 0 | 0.556 | -0.866 | - | 1.977 | 0.45 | | |
| Other | 46 | -0.082 | -0.253 | - | 0.089 | 24.54 | 0 | 0 |
| Overall | 212 | 0.171 | 0.051 | - | 0.291 | 100.00 | 48.2 | 0.314 |
| | | | | | | | | |
| LM area | | | | | | | | |
| Distillers grain | 46 | -0.201 | -0.369 | - | -0.034 | 29.29 | 0 | 0 |
| Urea | 22 | -0.049 | -0.403 | - | 0.305 | 10.10 | 24.3 | 0.175 |
| Corn gluten feed | 24 | 0.360 | 0.08 | - | 0.640 | 11.32 | 0 | 0 |
| Soyabean meal | 9 | 0.266 | -0.474 | - | 1.007 | 4.34 | 56.5 | 0.728 |
| Canola meal | 8 | -0.077 | -0.315 | - | 0.161 | 10.30 | 0 | 0 |
| Cottonseed meal | 5 | -0.152 | -1.017 | - | 0.712 | 3.58 | 66.1 | 0.750 |
| Grains | 3 | -0.440 | -1.734 | - | 0.854 | 2.59 | 79.9 | 1.386 |
| Fish meal | 1 | -0.149 | -1.293 | - | 0.994 | 0.75 | 0 | 0 |
| Commercial blend | 3 | -0.074 | -0.818 | - | 0.671 | 1.70 | 0 | 0 |
| Other | 38 | -0.120 | -0.333 | - | 0.094 | 26.04 | 28.4 | 0.128 |
| Overall | 168 | -0.066 | -0.173 | - | 0.040 | 100.00 | 23.1 | 0.108 |
| | | | | | | | | |
| Fat thickness | | | | | | | | |
| Distillers grain | 46 | 0.721 | 0.456 | - | 0.985 | 27.49 | 51.7 | 0.414 |
| Urea | 22 | 0.357 | 0.018 | - | 0.696 | 10.50 | 16.5 | 0.110 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Corn gluten feed | 24 | 0.162 | -0.191 | - | 0.515 | 11.49 | 28.4 | 0.213 |
| Soyabean meal | 9 | 0.679 | -0.010 | - | 1.369 | 4.64 | 51.2 | 0.594 |
| Canola meal | 8 | -0.055 | -0.294 | - | 0.184 | 8.86 | 0 | 0 |
| Cottonseed meal | 5 | -0.265 | -0.726 | - | 0.196 | 3.97 | 0 | 0 |
| Grains | 3 | -0.120 | -0.922 | - | 0.682 | 2.86 | 54.1 | 0.362 |
| Fish meal | 1 | -0.721 | -1.914 | - | 0.473 | 0.78 | 0 | 0 |
| Commercial blend | 3 | -0.071 | -0.813 | - | 0.670 | 1.88 | 0 | 0 |
| Other | 42 | 0.257 | 0.073 | - | 0.441 | 27.52 | 8.1 | 0.031 |
| Overall | 172 | 0.331 | 0.211 | - | 0.452 | 100.00 | 36.9 | 0.219 |

**Table 12.** Retained body N univariable analyses. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 33 | 0.185 | 0.181 | -0.185 | - | 0.555 | -17.0 | 63.8 | 1.401 | 0.316 |
| Initial BW, kg | 33 | <0.001 | 0.004 | -0.009 | - | 0.009 | -8.5 | 63.4 | 1.299 | 0.985 |
| ME, Mcal | 33 | -0.035 | 0.259 | -0.564 | - | 0.493 | -9.9 | 63.9 | 1.315 | 0.892 |
| MP, g/d | 33 | -0.001 | 0.002 | -0.005 | - | 0.004 | -9.3 | 63.9 | 1.308 | 0.824 |
| CP, g | 33 | <0.001 | 0.001 | -0.003 | - | 0.003 | -9.6 | 63.9 | 1.311 | 0.766 |
| Soluble intake protein, g | 33 | <0.001 | 0.003 | -0.008 | - | 0.007 | -7.1 | 62.6 | 1.282 | 0.901 |
| Ammonia, g | 33 | <0.001 | 0.003 | -0.006 | - | 0.006 | -7.9 | 62.8 | 1.291 | 0.944 |
| Protein $A_2$, g | 33 | <0.001 | 0.007 | -0.014 | - | 0.015 | -7.2 | 63.6 | 1.284 | 0.958 |
| Protein $B_1$, g | 33 | 0.001 | 0.002 | -0.003 | - | 0.006 | -4.7 | 63.4 | 1.253 | 0.539 |
| Protein $B_2$, g | 33 | <0.001 | 0.003 | -0.007 | - | 0.007 | -9.7 | 63.8 | 1.313 | 0.977 |
| RDP x3 maintenance, g | 33 | <0.001 | 0.001 | -0.003 | - | 0.003 | -9.5 | 63.8 | 1.311 | 0.963 |
| RUP x1 maintenance, g | 33 | 0.001 | 0.002 | -0.004 | - | 0.006 | -8.4 | 63.6 | 1.298 | 0.714 |
| MP Met, g | 33 | -0.073 | 0.100 | -0.278 | - | 0.132 | -6.7 | 63.5 | 1.277 | 0.474 |
| MP Lys, g | 33 | -0.016 | 0.038 | -0.094 | - | 0.062 | -7.2 | 63.6 | 1.283 | 0.675 |
| MP Arg, g | 33 | -0.013 | 0.035 | -0.085 | - | 0.059 | -8.7 | 63.8 | 1.301 | 0.718 |
| MP Thr, g | 33 | -0.027 | 0.048 | -0.126 | - | 0.072 | -7.4 | 63.6 | 1.286 | 0.585 |
| MP Leu, g | 33 | -0.009 | 0.024 | -0.057 | - | 0.039 | -8.4 | 63.7 | 1.298 | 0.712 |
| MP Ile, g | 33 | -0.025 | 0.043 | -0.113 | - | 0.062 | -8.5 | 63.7 | 1.299 | 0.559 |
| MP Val, g | 33 | -0.017 | 0.042 | -0.102 | - | 0.068 | -7.6 | 63.7 | 1.288 | 0.682 |
| MP His, g | 33 | -0.013 | 0.083 | -0.182 | - | 0.157 | -8.5 | 63.8 | 1.299 | 0.881 |
| MP Phe, g | 33 | -0.013 | 0.044 | -0.102 | - | 0.076 | -8.6 | 63.8 | 1.300 | 0.769 |
| MP Trp, g | 33 | -0.056 | 0.164 | -0.390 | - | 0.278 | -8.6 | 63.8 | 1.300 | 0.735 |
| MP Non-essential AA, g | 33 | 0.000 | 0.002 | -0.005 | - | 0.005 | -10.6 | 63.9 | 1.324 | 0.997 |
| MP/ME Met, g/Mcal | 33 | -0.565 | 2.052 | -4.749 | - | 3.619 | -8.7 | 63.8 | 1.301 | 0.785 |
| MP/ME Lys, g/Mcal | 33 | 0.150 | 0.778 | -1.437 | - | 1.737 | -9.7 | 63.9 | 1.313 | 0.848 |
| MP/ME Arg, g/Mcal | 33 | 0.078 | 0.679 | -1.307 | - | 1.462 | -9.4 | 63.9 | 1.310 | 0.910 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Thr, g/Mcal | 33 | -0.046 | 0.990 | -2.066 | - | 1.973 | -9.4 | 63.8 | 1.309 | 0.963 |
| MP/ME Leu, g/Mcal | 33 | 0.007 | 0.497 | -1.006 | - | 1.020 | -9.7 | 63.9 | 1.314 | 0.989 |
| MP/ME Ile, g/Mcal | 33 | -0.115 | 0.890 | -1.931 | - | 1.701 | -9.5 | 63.9 | 1.310 | 0.898 |
| MP/ME Val, g/Mcal | 33 | 0.076 | 0.837 | -1.632 | - | 1.784 | -9.7 | 63.9 | 1.313 | 0.928 |
| MP/ME His, g/Mcal | 33 | 0.580 | 1.658 | -2.802 | - | 3.962 | -10.5 | 63.9 | 1.322 | 0.729 |
| MP/ME Phe, g/Mcal | 33 | 0.145 | 0.870 | -1.629 | - | 1.918 | -9.8 | 63.9 | 1.314 | 0.869 |
| MP/ME Trp, g/Mcal | 33 | 0.624 | 3.285 | -6.075 | - | 7.323 | -9.4 | 63.9 | 1.309 | 0.851 |
| MP/ME Non-essential AA, g/Mcal | 33 | -0.058 | 0.107 | -0.275 | - | 0.159 | -6.1 | 63.5 | 1.270 | 0.590 |
| ADF, g | 33 | -0.002 | 0.004 | -0.010 | - | 0.005 | -8.8 | 63.8 | 1.303 | 0.556 |
| Amylase NDF organic matter basis, g | 33 | -0.001 | 0.001 | -0.003 | - | 0.002 | -8.6 | 63.7 | 1.300 | 0.565 |
| Forage NDF, g | 33 | -0.013 | 0.008 | -0.030 | - | 0.003 | 27.5 | 58.9 | 0.868 | 0.111 |
| Physically effective NDF, g | 33 | -0.004 | 0.005 | -0.013 | - | 0.005 | -5.8 | 63.2 | 1.267 | 0.392 |
| Acid detergent lignin, g | 33 | -0.008 | 0.015 | -0.040 | - | 0.023 | -8.8 | 63.8 | 1.302 | 0.583 |
| Simple sugars, g | 33 | -0.003 | 0.008 | -0.019 | - | 0.013 | -11.7 | 63.8 | 1.337 | 0.699 |
| Starch, g | 33 | <0.001 | 0.001 | -0.001 | - | 0.001 | -9.7 | 63.9 | 1.314 | 0.973 |
| Soluble fibre, g | 33 | 0.001 | 0.005 | -0.009 | - | 0.011 | -6.8 | 63.6 | 1.278 | 0.807 |
| Fermentable starch, g | 33 | 0.000 | 0.001 | -0.001 | - | 0.001 | -9.8 | 63.9 | 1.314 | 0.986 |
| Fermentable soluble fibre, g | 33 | 0.001 | 0.006 | -0.011 | - | 0.012 | -7.9 | 63.7 | 1.292 | 0.903 |
| Fermentable NDF, g | 33 | -0.001 | 0.003 | -0.006 | - | 0.004 | -8.4 | 63.6 | 1.297 | 0.622 |
| Ether extract, g | 33 | -0.002 | 0.004 | -0.009 | - | 0.006 | -8.7 | 63.7 | 1.301 | 0.639 |
| Trial design | 33 | 1.406 | 0.518 | 0.350 | - | 2.462 | 22.2 | 57.9 | 0.931 | 0.011 |
| Hormonal implant yes or no | 33 | 0.452 | 0.607 | -0.786 | - | 1.691 | -8.3 | 63.5 | 1.297 | 0.462 |
| Monensin dose, mg/kg DM | 33 | -0.015 | 0.014 | -0.044 | - | 0.013 | -1.3 | 63.1 | 1.213 | 0.286 |
| Tylosin dose, mg/kg DM | 33 | -0.061 | 0.059 | -0.182 | - | 0.060 | -3.5 | 63.3 | 1.239 | 0.314 |

**Table 13.** Urinary N loss univariable analyses. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | | | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 31 | -0.194 | 0.450 | -1.115 | - | 0.726 | -9.4 | 71.3 | 3.332 | 0.669 |
| Initial BW, kg | 31 | -0.003 | 0.005 | -0.012 | - | 0.007 | -6.0 | 70.8 | 3.227 | 0.573 |
| ME, Mcal | 34 | -0.339 | 0.330 | -1.011 | - | 0.332 | 7.6 | 69.2 | 2.816 | 0.311 |
| MP, g/d | 34 | 0.007 | 0.003 | 0.001 | - | 0.012 | 50.0 | 62.7 | 1.524 | 0.018 |
| CP, g | 34 | 0.006 | 0.001 | 0.003 | - | 0.008 | 91.7 | 49.8 | 0.254 | <0.001 |
| Soluble intake protein, g | 34 | 0.002 | 0.005 | -0.009 | - | 0.012 | -9.2 | 70.8 | 3.328 | 0.754 |
| Ammonia, g | 34 | -0.003 | 0.005 | -0.013 | - | 0.007 | 0.7 | 69.8 | 3.027 | 0.525 |
| Protein $A_2$, g | 34 | 0.034 | 0.011 | 0.012 | - | 0.055 | 57.2 | 61.0 | 1.306 | 0.004 |
| Protein $B_1$, g | 34 | 0.009 | 0.004 | 0.002 | - | 0.017 | 47.2 | 62.7 | 1.611 | 0.019 |
| Protein $B_2$, g | 34 | 0.007 | 0.002 | 0.003 | - | 0.012 | 69.6 | 58.7 | 0.926 | 0.002 |
| RDP x3 maintenance, g | 34 | 0.005 | 0.002 | 0.002 | - | 0.009 | 62.0 | 59.6 | 1.159 | 0.003 |
| RUP x1 maintenance, g | 34 | 0.008 | 0.002 | 0.004 | - | 0.013 | 79.9 | 56.6 | 0.6141 | 0.001 |
| MP Met, g | 34 | 0.227 | 0.125 | -0.027 | - | 0.481 | 28.3 | 66.1 | 2.186 | 0.078 |
| MP Lys, g | 34 | 0.052 | 0.047 | -0.044 | - | 0.149 | 8.1 | 68.9 | 2.802 | 0.276 |
| MP Arg, g | 34 | 0.086 | 0.045 | -0.005 | - | 0.178 | 29.8 | 65.9 | 2.141 | 0.063 |
| MP Thr, g | 34 | 0.112 | 0.061 | -0.012 | - | 0.235 | 28.8 | 66.0 | 2.17 | 0.075 |
| MP Leu, g | 34 | 0.071 | 0.031 | 0.008 | - | 0.135 | 45.4 | 63.2 | 1.664 | 0.029 |
| MP Ile, g | 34 | 0.105 | 0.054 | -0.005 | - | 0.215 | 30.4 | 66.0 | 2.123 | 0.060 |
| MP Val, g | 34 | 0.108 | 0.051 | 0.006 | - | 0.211 | 39.1 | 64.5 | 1.857 | 0.040 |
| MP His, g | 34 | 0.251 | 0.101 | 0.045 | - | 0.456 | 50.4 | 62.6 | 1.511 | 0.018 |
| MP Phe, g | 34 | 0.130 | 0.052 | 0.023 | - | 0.237 | 48.3 | 63.0 | 1.576 | 0.018 |
| MP Trp, g | 34 | 0.381 | 0.194 | -0.014 | - | 0.777 | 28.8 | 66.3 | 2.169 | 0.058 |
| MP Non-essential AA, g | 34 | -0.003 | 0.003 | -0.010 | - | 0.003 | -1.7 | 70.6 | 3.100 | 0.325 |
| MP/ME Met, g/Mcal | 34 | 6.102 | 2.500 | 1.010 | - | 11.194 | 50.9 | 62.2 | 1.498 | 0.020 |
| MP/ME Lys, g/Mcal | 34 | 1.751 | 0.997 | -0.279 | - | 3.782 | 28.3 | 65.7 | 2.186 | 0.088 |
| MP/ME Arg, g/Mcal | 34 | 2.085 | 0.863 | 0.326 | - | 3.843 | 46.8 | 62.9 | 1.622 | 0.022 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Thr, g/Mcal | 34 | 3.076 | 1.210 | 0.611 | - | 5.541 | 54.3 | 61.7 | 1.393 | 0.016 |
| MP/ME Leu, g/Mcal | 34 | 1.701 | 0.604 | 0.470 | - | 2.932 | 65.5 | 59.7 | 1.051 | 0.008 |
| MP/ME Ile, g/Mcal | 34 | 2.825 | 1.083 | 0.618 | - | 5.032 | 53.6 | 61.8 | 1.415 | 0.014 |
| MP/ME Val, g/Mcal | 34 | 2.861 | 0.975 | 0.876 | - | 4.846 | 67.7 | 59.4 | 0.986 | 0.006 |
| MP/ME His, g/Mcal | 34 | 6.025 | 1.873 | 2.211 | - | 9.840 | 75.8 | 58.0 | 0.737 | 0.003 |
| MP/ME Phe, g/Mcal | 34 | 3.181 | 0.987 | 1.171 | - | 5.191 | 73.4 | 58.2 | 0.813 | 0.003 |
| MP/ME Trp, g/Mcal | 34 | 10.344 | 3.860 | 2.482 | - | 18.207 | 53.2 | 61.9 | 1.427 | 0.012 |
| MP/ME Non-essential AA, g/Mcal | 34 | -0.228 | 0.134 | -0.500 | - | 0.045 | 20.0 | 67.5 | 2.439 | 0.098 |
| ADF, g | 34 | 0.006 | 0.005 | -0.005 | - | 0.016 | 8.4 | 68.3 | 2.794 | 0.295 |
| Amylase NDF organic matter basis, g | 34 | 0.002 | 0.002 | -0.002 | - | 0.005 | 4.4 | 68.6 | 2.916 | 0.409 |
| Forage NDF, g | 34 | -0.007 | 0.003 | -0.014 | - | -0.001 | 33.3 | 65.9 | 2.034 | 0.038 |
| Physically effective NDF, g | 34 | -0.005 | 0.002 | -0.010 | - | -0.001 | 42.1 | 64.2 | 1.765 | 0.020 |
| Acid detergent lignin, g | 34 | 0.046 | 0.019 | 0.009 | - | 0.084 | 49.3 | 62.2 | 1.546 | 0.018 |
| Simple sugars, g | 34 | 0.022 | 0.015 | -0.008 | - | 0.052 | 9.4 | 68.8 | 2.762 | 0.141 |
| Starch, g | 34 | -0.001 | 0.001 | -0.002 | - | 0.000 | 47.4 | 63.1 | 1.604 | 0.025 |
| Soluble fibre, g | 34 | 0.005 | 0.007 | -0.009 | - | 0.020 | -4.0 | 70.4 | 3.172 | 0.440 |
| Fermentable starch, g | 34 | -0.001 | 0.001 | -0.003 | - | 0.000 | 49.7 | 62.6 | 1.532 | 0.020 |
| Fermentable soluble fibre, g | 34 | 0.007 | 0.008 | -0.009 | - | 0.023 | -2.9 | 70.2 | 3.136 | 0.388 |
| Fermentable NDF, g | 34 | 0.005 | 0.004 | -0.002 | - | 0.013 | 18.5 | 67.2 | 2.484 | 0.140 |
| Ether extract, g | 34 | 0.004 | 0.005 | -0.007 | - | 0.014 | 3.4 | 68.7 | 2.947 | 0.455 |
| Trial design | 34 | 1.935 | 0.934 | 0.032 | - | 3.838 | 9.4 | 69.7 | 2.761 | 0.046 |
| Hormonal implant yes or no | 34 | -0.532 | 0.876 | -2.315 | - | 1.252 | -6.3 | 70.7 | 3.24 | 0.548 |
| Monensin dose, mg/kg DM | 34 | -0.052 | 0.020 | -0.092 | - | -0.012 | 20.5 | 67.1 | 2.423 | 0.013 |
| Tylosin dose, mg/kg DM | 34 | -0.134 | 0.086 | -0.308 | - | 0.041 | 1.0 | 70.4 | 3.019 | 0.129 |

**Table 14.** Faecal N loss univariable analyses. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 39 | 0.040 | 0.208 | -0.383 - 0.462 | -10.4 | 51.1 | 0.573 | 0.850 |
| Initial BW, kg | 39 | 0.001 | 0.002 | -0.003 - 0.005 | -9.0 | 50.9 | 0.566 | 0.507 |
| ME, Mcal | 42 | 0.028 | 0.168 | -0.312 - 0.368 | -5.8 | 53.4 | 0.670 | 0.869 |
| MP, g/d | 42 | 0.003 | 0.001 | 0.001 - 0.006 | 28.7 | 46.3 | 0.451 | 0.009 |
| CP, g | 42 | 0.003 | 0.001 | 0.001 - 0.004 | 60.9 | 34.8 | 0.248 | <0.001 |
| Soluble intake protein, g | 42 | <0.001 | 0.002 | -0.004 - 0.003 | -8.2 | 53.7 | 0.685 | 0.841 |
| Ammonia, g | 42 | -0.002 | 0.002 | -0.005 - 0.001 | -0.3 | 52.3 | 0.635 | 0.182 |
| Protein $A_2$, g | 42 | 0.022 | 0.005 | 0.013 - 0.031 | 76.2 | 27.5 | 0.151 | <0.001 |
| Protein $B_1$, g | 42 | 0.004 | 0.002 | 0.001 - 0.008 | 31.6 | 46.1 | 0.433 | 0.009 |
| Protein $B_2$, g | 42 | 0.004 | 0.001 | 0.002 - 0.006 | 45.3 | 41.4 | 0.346 | 0.001 |
| RDP x3 maintenance, g | 42 | 0.003 | 0.001 | 0.001 - 0.005 | 23.5 | 45.66 | 0.484 | 0.003 |
| RUP x1 maintenance, g | 42 | 0.005 | 0.001 | 0.002 - 0.007 | 44.9 | 39.49 | 0.349 | 0.000 |
| MP Met, g | 42 | 0.101 | 0.056 | -0.012 - 0.214 | 10.2 | 50.6 | 0.568 | 0.079 |
| MP Lys, g | 42 | 0.033 | 0.021 | -0.009 - 0.074 | 11.9 | 50.7 | 0.558 | 0.120 |
| MP Arg, g | 42 | 0.046 | 0.020 | 0.006 - 0.085 | 24.8 | 47.9 | 0.476 | 0.025 |
| MP Thr, g | 42 | 0.053 | 0.026 | 0.000 - 0.106 | 15.5 | 49.6 | 0.535 | 0.051 |
| MP Leu, g | 42 | 0.027 | 0.014 | -0.001 - 0.056 | 7.9 | 50.6 | 0.583 | 0.061 |
| MP Ile, g | 42 | 0.052 | 0.024 | 0.004 - 0.100 | 18.6 | 48.9 | 0.515 | 0.034 |
| MP Val, g | 42 | 0.051 | 0.022 | 0.007 - 0.096 | 21.4 | 48.3 | 0.497 | 0.024 |
| MP His, g | 42 | 0.114 | 0.045 | 0.023 - 0.205 | 24.5 | 47.5 | 0.478 | 0.016 |
| MP Phe, g | 42 | 0.061 | 0.023 | 0.014 - 0.108 | 26.7 | 46.9 | 0.464 | 0.012 |
| MP Trp, g | 42 | 0.212 | 0.085 | 0.040 - 0.383 | 28.0 | 47.1 | 0.456 | 0.017 |
| MP Non-essential AA, g | 42 | -0.001 | 0.002 | -0.005 - 0.002 | -8.7 | 53.4 | 0.688 | 0.351 |
| MP/ME Met, g/Mcal | 42 | 1.964 | 1.175 | -0.411 - 4.338 | 6.1 | 51.1 | 0.594 | 0.102 |
| MP/ME Lys, g/Mcal | 42 | 0.699 | 0.430 | -0.171 - 1.569 | 10.7 | 50.7 | 0.565 | 0.112 |
| MP/ME Arg, g/Mcal | 42 | 0.878 | 0.395 | 0.080 - 1.677 | 20.0 | 48.6 | 0.506 | 0.032 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| MP/ME Thr, g/Mcal | 42 | 1.056 | 0.550 | -0.056 | - | 2.169 | 11.7 | 50.1 | 0.559 | 0.062 |
| MP/ME Leu, g/Mcal | 42 | 0.539 | 0.295 | -0.058 | - | 1.136 | 5.3 | 51.0 | 0.599 | 0.076 |
| MP/ME Ile, g/Mcal | 42 | 1.041 | 0.500 | 0.031 | - | 2.052 | 14.5 | 49.5 | 0.541 | 0.044 |
| MP/ME Val, g/Mcal | 42 | 1.018 | 0.456 | 0.097 | - | 1.939 | 17.1 | 48.9 | 0.525 | 0.031 |
| MP/ME His, g/Mcal | 42 | 2.213 | 0.917 | 0.359 | - | 4.067 | 20.6 | 48.1 | 0.502 | 0.021 |
| MP/ME Phe, g/Mcal | 42 | 1.198 | 0.479 | 0.229 | - | 2.166 | 21.8 | 47.7 | 0.495 | 0.017 |
| MP/ME Trp, g/Mcal | 42 | 4.314 | 1.765 | 0.747 | - | 7.880 | 24.0 | 47.6 | 0.481 | 0.019 |
| MP/ME Non-essential AA, g/Mcal | 42 | -0.005 | 0.003 | -0.011 | - | 0.000 | 14.5 | 49.7 | 0.542 | 0.042 |
| ADF, g | 42 | 0.008 | 0.003 | 0.003 | - | 0.014 | 23.0 | 45.9 | 0.488 | 0.004 |
| Amylase NDF organic matter basis, g | 42 | 0.002 | 0.001 | 0.000 | - | 0.003 | -7.7 | 52.5 | 0.681 | 0.102 |
| Forage NDF, g | 42 | -0.002 | 0.002 | -0.005 | - | 0.001 | 3.8 | 52.1 | 0.609 | 0.229 |
| Physically effective NDF, g | 42 | -0.002 | 0.001 | -0.004 | - | 0.000 | 5.5 | 51.3 | 0.598 | 0.097 |
| Acid detergent lignin, g | 42 | 0.026 | 0.010 | 0.006 | - | 0.046 | 14.4 | 48.4 | 0.542 | 0.011 |
| Simple sugars, g | 42 | 0.017 | 0.006 | 0.004 | - | 0.029 | 31.5 | 45.9 | 0.433 | 0.009 |
| Starch, g | 42 | -0.001 | 0.000 | -0.001 | - | 0.000 | -0.1 | 51.3 | 0.634 | 0.050 |
| Soluble fibre, g | 42 | 0.007 | 0.003 | 0.001 | - | 0.013 | 31.2 | 47.3 | 0.436 | 0.027 |
| Fermentable starch, g | 42 | -0.001 | 0.000 | -0.001 | - | 0.000 | 1.3 | 51.0 | 0.625 | 0.039 |
| Fermentable soluble fibre, g | 42 | 0.008 | 0.003 | 0.001 | - | 0.015 | 30.5 | 47.3 | 0.440 | 0.026 |
| Fermentable NDF, g | 42 | 0.004 | 0.002 | <0.001 | - | 0.008 | -0.3 | 50.9 | 0.635 | 0.031 |
| Ether extract, g | 42 | <0.001 | 0.002 | -0.005 | - | 0.005 | -8.6 | 53.7 | 0.687 | 0.998 |
| Hormonal implant yes or no | 42 | 0.492 | 0.382 | -0.280 | - | 1.264 | 11.9 | 51.1 | 0.558 | 0.205 |
| Monensin dose, mg/kg DM | 42 | -0.010 | 0.010 | -0.030 | - | 0.011 | 3.1 | 52.3 | 0.613 | 0.346 |

**Table 15.** Serum and plasma urea N univariable analyses. Includes number of comparisons used (No.), coefficient, SE, 95% CI, estimates of model fit ($R^2$), heterogeneity as assessed by $I^2$ and $\tau^2$, and *P*-value.

| Variable | No. | Coefficient | SE | 95% CI | Adjusted $R^2$ | $I^2$ | $\tau^2$ | *P*-value |
|---|---|---|---|---|---|---|---|---|
| Initial BW (Control only), kg | 12 | 0.558 | 0.501 | -0.558 - 1.674 | 17.4 | 49.0 | 0.743 | 0.292 |
| Initial BW, kg | 12 | -0.001 | 0.005 | -0.011 - 0.010 | 22.7 | 57.0 | 1.104 | 0.902 |
| ME, Mcal | 15 | -0.440 | 0.430 | -1.370 - 0.489 | 0.2 | 55.3 | 1.085 | 0.325 |
| MP, g/d | 15 | 0.008 | 0.003 | 0.002 - 0.014 | 69.4 | 27.7 | 0.333 | 0.013 |
| CP, g | 15 | 0.005 | 0.001 | 0.002 - 0.007 | 100.0 | 0 | 0 | 0.001 |
| Soluble intake protein, g | 15 | 0.001 | 0.004 | -0.007 - 0.010 | -13.2 | 57.5 | 1.231 | 0.730 |
| Ammonia, g | 15 | -0.001 | 0.003 | -0.009 - 0.006 | -10.8 | 56.5 | 1.204 | 0.665 |
| Protein $A_2$, g | 15 | 0.021 | 0.008 | 0.005 - 0.038 | 62.3 | 30.6 | 0.410 | 0.016 |
| Protein $B_1$, g | 15 | 0.006 | 0.002 | 0.001 - 0.011 | 58.0 | 30.7 | 0.457 | 0.016 |
| Protein $B_2$, g | 15 | 0.004 | 0.002 | -0.001 - 0.009 | 23.1 | 48.7 | 0.836 | 0.117 |
| RDP x3 maintenance, g | 15 | 0.009 | 0.002 | 0.005 - 0.014 | 100.0 | 0 | 0 | 0.001 |
| RUP x1 maintenance, g | 15 | 0.006 | 0.003 | 0.000 - 0.011 | 38.8 | 42.0 | 0.665 | 0.051 |
| MP Met, g | 15 | 0.408 | 0.148 | 0.087 - 0.728 | 79.1 | 28.8 | 0.228 | 0.017 |
| MP Lys, g | 15 | 0.049 | 0.042 | -0.041 - 0.140 | 19.0 | 48.5 | 0.881 | 0.260 |
| MP Arg, g | 15 | 0.106 | 0.044 | 0.011 - 0.200 | 64.1 | 33.8 | 0.390 | 0.031 |
| MP Thr, g | 15 | 0.159 | 0.065 | 0.019 - 0.299 | 68.3 | 33.0 | 0.345 | 0.029 |
| MP Leu, g | 15 | 0.129 | 0.029 | 0.066 - 0.193 | 100.0 | 0 | 0 | 0.001 |
| MP Ile, g | 15 | 0.168 | 0.055 | 0.049 - 0.287 | 85.0 | 24.0 | 0.163 | 0.009 |
| MP Val, g | 15 | 0.146 | 0.053 | 0.031 - 0.261 | 75.6 | 29.1 | 0.265 | 0.017 |
| MP His, g | 15 | 0.304 | 0.094 | 0.101 - 0.507 | 88.1 | 21.0 | 0.130 | 0.006 |
| MP Phe, g | 15 | 0.184 | 0.048 | 0.080 - 0.288 | 98.7 | 9.4 | 0.015 | 0.002 |
| MP Trp, g | 15 | 0.451 | 0.196 | 0.029 - 0.874 | 61.8 | 35.3 | 0.415 | 0.038 |
| MP Non-essential AA, g | 15 | -0.018 | 0.006 | -0.030 - -0.005 | 82.8 | 25.3 | 0.187 | 0.011 |
| MP/ME Met, g/Mcal | 15 | 14.078 | 3.064 | 7.458 - 20.697 | 100.0 | 0 | 0 | 0.001 |
| MP/ME Lys, g/Mcal | 15 | 1.881 | 0.914 | -0.095 - 3.856 | 52.4 | 38.9 | 0.517 | 0.060 |
| MP/ME Arg, g/Mcal | 15 | 3.029 | 0.822 | 1.252 - 4.805 | 90.5 | 12.0 | 0.104 | 0.003 |
| MP/ME Thr, g/Mcal | 15 | 4.958 | 1.206 | 2.354 - 7.563 | 100.0 | 2.4 | 0 | 0.001 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| MP/ME Leu, g/Mcal | 15 | 2.601 | 0.593 | 1.320 | - | 3.881 | 100.0 | 0 | 0 | 0.001 |
| MP/ME Ile, g/Mcal | 15 | 4.997 | 1.098 | 2.624 | - | 7.370 | 100.0 | 0 | 0 | 0.001 |
| MP/ME Val, g/Mcal | 15 | 3.792 | 0.998 | 1.636 | - | 5.949 | 93.7 | 9.5 | 0.069 | 0.002 |
| MP/ME His, g/Mcal | 15 | 6.470 | 1.784 | 2.617 | - | 10.323 | 91.5 | 13.4 | 0.092 | 0.003 |
| MP/ME Phe, g/Mcal | 15 | 4.297 | 0.966 | 2.210 | - | 6.385 | 100.0 | 0 | 0 | 0.001 |
| MP/ME Trp, g/Mcal | 15 | 14.192 | 3.609 | 6.396 | - | 21.988 | 100.0 | 7.2 | 0 | 0.002 |
| MP/ME Non-essential AA, g/Mcal | 15 | -0.158 | 0.111 | -0.397 | - | 0.082 | 22.1 | 47.7 | 0.846 | 0.178 |
| ADF, g | 15 | 0.007 | 0.008 | -0.011 | - | 0.025 | -3.5 | 56.2 | 1.125 | 0.438 |
| Amylase NDF organic matter basis, g | 15 | 0.001 | 0.005 | -0.010 | - | 0.013 | -10.8 | 57.6 | 1.204 | 0.795 |
| Forage NDF, g | 15 | -0.013 | 0.004 | -0.022 | - | -0.003 | 68.4 | 27.9 | 0.344 | 0.011 |
| Physically effective NDF, g | 15 | -0.005 | 0.002 | -0.009 | - | -0.001 | 50.1 | 37.2 | 0.542 | 0.028 |
| Acid detergent lignin, g | 15 | 0.037 | 0.028 | -0.023 | - | 0.098 | 9.3 | 52.8 | 0.986 | 0.205 |
| Simple sugars, g | 15 | 0.024 | 0.009 | 0.005 | - | 0.044 | 54.9 | 32.3 | 0.490 | 0.019 |
| Starch, g | 15 | -0.001 | 0.001 | -0.003 | - | 0.000 | 62.1 | 31.7 | 0.412 | 0.016 |
| Soluble fibre, g | 15 | 0.013 | 0.004 | 0.004 | - | 0.022 | 72.5 | 20.8 | 0.299 | 0.006 |
| Fermentable starch, g | 15 | -0.002 | 0.001 | -0.003 | - | 0.000 | 57.9 | 34.0 | 0.458 | 0.021 |
| Fermentable soluble fibre, g | 15 | 0.015 | 0.005 | 0.005 | - | 0.025 | 73.7 | 20.9 | 0.286 | 0.006 |
| Fermentable NDF, g | 15 | 0.019 | 0.006 | 0.006 | - | 0.032 | 71.5 | 24.5 | 0.310 | 0.008 |
| Ether extract, g | 15 | 0.006 | 0.006 | -0.007 | - | 0.018 | 2.3 | 54.5 | 1.062 | 0.343 |
| Trial design | 15 | -0.933 | 0.879 | -2.832 | - | 0.965 | 14.0 | 49.5 | 0.935 | 0.308 |
| Hormonal implant yes or no | 15 | -1.977 | 0.991 | -4.118 | - | 0.165 | 32.7 | 45.1 | 0.732 | 0.068 |
| Monensin dose, mg/kg DM | 15 | -0.075 | 0.015 | -0.107 | - | -0.042 | 100.0 | 0 | 0 | <0.001 |

**Table 16.** Standardised mean differences (SMD), 95% CI for nitrogen balance outcomes by nitrogen or protein intervention. Including degrees of freedom (df), study weight, heterogeneity as assessed by heterogeneity statistic, $I^2$, and $\tau^2$.

| Variable | df | SMD | 95% CI | | Weight (%) | $I^2$ | $\tau^2$ |
|---|---|---|---|---|---|---|---|
| N intake | | | | | | | |
| Urea | 12 | 3.806 | 2.187 | 5.424 | 36.23 | 81.4 | 6.082 |
| Distillers grain | 7 | 3.202 | 2.333 | 4.070 | 25.57 | 12.1 | 0.192 |
| Wheat distillers | 1 | 4.091 | 1.387 | 6.796 | 6.43 | 56.7 | 2.243 |
| Other | 11 | 2.167 | 0.768 | 3.566 | 31.77 | 75.3 | 3.464 |
| Overall | 34 | 3.188 | 2.366 | 4.009 | 100.00 | 75.6 | 3.858 |
| Retained body N | | | | | | | |
| Urea | 13 | 1.079 | 0.361 | 1.796 | 46.22 | 66.7 | 1.186 |
| Soyabean meal | 3 | -1.033 | -3.46 | 1.394 | 6.74 | 59 | 3.567 |
| Distillers grain | 1 | 0.658 | -0.37 | 1.685 | 7.60 | 19.1 | 0.106 |
| Wheat distillers | 1 | 0.904 | -0.293 | 2.102 | 7.46 | 36.1 | 0.272 |
| Other | 10 | 1.493 | 0.574 | 2.412 | 31.98 | 64.3 | 1.459 |
| Overall | 32 | 1.017 | 0.533 | 1.501 | 100.00 | 62.7 | 1.156 |
| Faecal N loss | | | | | | | |
| Urea | 15 | 0.435 | -0.180 | 1.049 | 38.89 | 62 | 0.937 |
| Distillers grain | 7 | 1.121 | 0.284 | 1.957 | 18.58 | 54.4 | 0.766 |
| Wheat distillers | 2 | 3.853 | 1.954 | 5.752 | 3.05 | 0 | 0 |
| Fish meal | 1 | 0.361 | -0.466 | 1.188 | 7.84 | 24.4 | 0.490 |
| Soyabean meal | 0 | 0.595 | -0.831 | 2.021 | 2.63 | | |
| Other | 11 | 0.343 | -0.097 | 0.783 | 29.01 | 0 | 0 |
| Overall | 41 | 0.657 | 0.309 | 1.005 | 100.00 | 52.6 | 0.670 |
| Urinary N loss | | | | | | | |
| Urea | 11 | 3.236 | 1.898 | 4.573 | 32.77 | 76.8 | 3.705 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Distillers grain | 7 | 3.960 | 2.821 | - | 5.099 | 20.26 | 31.8 | 0.826 |
| Wheat distillers | 1 | 3.988 | 1.783 | - | 6.193 | 5.73 | 39.6 | 1.058 |
| Other | 11 | 1.141 | 0.524 | - | 1.758 | 41.25 | 34.7 | 0.399 |
| Overall | 33 | 2.608 | 1.954 | - | 3.262 | 100.00 | 69.9 | 2.367 |
| | | | | | | | | |
| Serum and plasma urea N | | | | | | | | |
| Urea | 2 | 2.349 | -0.006 | - | 4.704 | 20.49 | 78.2 | 3.278 |
| Distillers grain | 2 | 3.964 | 2.439 | - | 5.489 | 14.30 | 0 | 0 |
| Other | 8 | 1.965 | 1.180 | - | 2.750 | 65.22 | 44.2 | 0.625 |
| Overall | 14 | 2.315 | 1.588 | - | 3.043 | 100.00 | 54.3 | 1.066 |