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Nitrogen excretion from beef cattle fed a wide range of diets compiled in an intercontinental dataset: a meta-analysis

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Abstract

Manure N from cattle contributes to nitrate leaching, nitrous oxide, and ammonia emissions. Measurement of manure N outputs on commercial beef cattle operations is laborious, expensive, and impractical; therefore, models are needed to predict N excreted in urine and feces. Building robust prediction models requires extensive data from animals under different management systems worldwide. Thus, the study objectives were to 1) collate an international dataset of N excretion in feces and urine based on individual observations from beef cattle; 2) determine the suitability of key variables for predicting fecal, urinary, and total manure N excretion; and 3) develop robust and reliable N excretion prediction models based on individual observation from beef cattle consuming various diets. A meta-analysis based on individual beef data from different experiments was carried out from a raw dataset including 1,004 observations from 33 experiments collected from 5 research institutes in Europe (n = 3), North America (n = 1), and South America (n = 1). A sequential approach was taken in developing models of increasing complexity by incrementally adding significant variables that affected fecal, urinary, or total manure N excretion. Nitrogen excretion was predicted by fitting linear mixed models with experiment as a random effect. Simple models including dry matter intake (**DMI**) were better at predicting fecal N excretion than those using only dietary nutrient composition or body weight (**BW**). Simple models based on N intake performed better for urinary and total manure N excretion than those based on DMI. A model including DMI and dietary component concentrations led to the most robust prediction of fecal and urinary N excretion, generating root mean square prediction errors as a percentage of the observed mean values of 25.0% for feces and 25.6% for urine. Complex total manure N excretion models based on BW and dietary component concentrations led to the lowest prediction errors of about 14.6%. In conclusion, several models to predict N excretion already exist, but the ones developed in this study are based on individual observations encompassing larger variability than the previous developed models. In addition, models that include information on DMI or N intake are required for accurate prediction of fecal, urinary, and total manure N excretion. In the absence of intake data, equations have poor performance as compared with equations based on intake and dietary component concentrations.

Key words: beef cattle, nitrogen excretion, prediction models

Abbreviations: ADG, average daily gain; BIC, Bayesian information criterion; BW; body weight; CCC, concordance correlation coefficient; DMI, dry matter intake; GHG, greenhouse gas; IQR, interquartile range; MB, mean bias; ME, metabolizable energy; NDFI, neutral detergent fiber intake; RSR, RMSPE-observations standard deviation ratio; SP, slope bias; TMR, total mixed ration; VIF, variance inflation factor

Introduction

Ruminants play a key role in the food system because they can convert fiber-rich plants into highly nutritious food for humans. However, there is a growing concern about livestock production because of its negative environmental impact, mainly due to enteric methane (CH_4) emissions but also as a result of N excretion leading to nitrate (NO_3–) leaching and ammonia (NH_3) and nitrous oxide (N_2O) emissions (FAO, 2002). Nitrous oxide is an important greenhouse gas with 265 times greater global warming potential

than CO_2 over a 100-yr period (IPCC, 2007). Volatilization of NH_3 is of particular concern because it contributes to the formation of fine particulate matter that is linked to human respiratory and cardiovascular problems (Fu et al., 1999). In the United States, NH_3 emitted from livestock operations was estimated to contribute on average from 5% to 11% (up to as much as 20%) of the total $PM_{2.5}$ atmospheric concentrations (Hristov, 2011).

The efficiency of feed N conversion into meat protein in cattle varies widely and beef cattle are relatively inefficient, utilizing approximately 20% of dietary N for growth (NRC, 2001). The main driver of N losses from ruminants is excess N intake (Dijkstra et al., 2013b). Variation in dietary N supply affects N excretion in urine and feces, but N in urine is more susceptible to leaching and volatile losses (Hristov et al., 2011). Nitrogen utilization in the rumen is largely dependent on the energy available for microbial protein synthesis, and the large variation in urinary N excretion compared with fecal N excretion presents an opportunity to manipulate diets to reduce N excretion in urine (Dijkstra et al., 2013b).

Predictive equations for estimating N excretion are useful for evaluating potential dietary strategies for N mitigation because measurement of excretion or emissions are costly and difficult to apply on commercial farms. Several models to predict N excretion from beef cattle have been developed (Yan et al., 2007; Waldrip et al., 2013; Dong et al., 2014) using data from various locations around the world. These models used dietary nutrient composition or intake variables and were developed from a limited number of studies based on datasets of treatment means. Models developed using treatment means do not take into account individual animal variability and are less robust than meta-analysis based on individual observations. Therefore, we carried a meta-analysis based on individual beef data from different experiments, and the objectives of the present study were: 1) collate a global dataset of individual observations of fecal and urinary N excretion in beef cattle; 2) determine the suitability of key variables for fecal, urinary, and total manure N excretion; and 3) develop simplified, but robust and reliable, N excretion prediction models based on individual animal data of N excretion from beef cattle consuming different diets.

Materials and Methods

Animal Care and Use Committee approval was not required for this study because the data were obtained from published literature.

Datasets and variable selection
This study is an element of the Global Network project and the Feed and Nutrition Network, which is an activity of the Livestock Research Group of the Global Research Alliance for Agricultural Greenhouse Gases (https://globalresearchalliance.org). The dataset used in the analysis was created using measurements made on individual animals by collaborators from different parts of the world (Canada, Brazil, Ireland, Belgium, and France). The following information was included in the dataset: 1) fecal and urinary N excretion measured by either total feces and urine collection or tracer methods, 2) feed dry matter intake (**DMI;** kg/d), 3) dietary component concentrations (neutral detergent fiber [**NDF**]; acid detergent fiber [**ADF**]; crude protein [**CP**]; starch; ether extract [**EE**]; and % of **DM**), and 4) performance (ADG [g/d] and body

weight [BW; kg]). Daily intake of nutrients (N, NDF, ADF, EE, and starch; g/d) were calculated based on individual DMI and dietary component concentrations within experiments. A total of 1,004 and 688 observations of N excretion in feces and in urine (g/d), respectively, from individual beef cattle (Angus, Belgium blue, Angus × Hereford, and other crossbreeds), were obtained from 33 in vivo experiments from Agriculture and Agri-Food Canada, Lethbridge, Canada (18 experiments, 395 individual data), Universidade Federal de Viçosa, Brazil (7 experiments, 224 individual data), Institute for Agricultural and Fisheries Research, Belgium (2 experiments, 96 individual data), Belfast Institute, Northern Ireland (4 experiments, 68 individual data), and INRAE-UMRH, France (2 experiments, 31 individual data; Supplementary Table S1). In the dataset, Angus beef cattle breed represented 90% of the whole dataset, 14% were finishing animals, 86% were growing animals, and 60% and 40% of the observation were from males and females, respectively. Most diets were fed as total mixed ration or as separate components and included barley silage (14.1.8%, $n = 160$), corn silage (26.6%, $n = 302$), or sugarcane (12.2%, $n = 139$) as the main forage source, or a forage mix (31.3%, $n = 356$). Only 1.4% ($n = 161$) included grass hay as the main forage source and only 4.4% ($n = 50$) included pasture grass. The dataset included diets used to evaluate the effect of source and or level of carbohydrate (12%), CP sources (32.4%), and the lipid effects (1%), or was categorized as control diets (20%). In several experiments, various diets (22%) also included feed additives such as monensin (50% of the data including feed additives), tannins (5%), plant extracts (18%), and other additives (Enzyme, DDGS, and yeast). Measurements of N excretion in feces and urine were conducted using total fecal and urine collection (43%) or marker and spot sampling approaches (57%). Among the tracer used, 39% were indigestible NDF (**iNDF**), 17% ytterbium chloride (YbCl3), 15% Cr-EDTA, 15% acid insoluble ash, and 13% titanium dioxide.

Data preselection for model development
An exploratory analysis was performed to evaluate the data for completeness, consistency in nomenclature of each variable, and the presence of outliers (Pyle, 1999). Measured variables and their summary statistics are given in Table 1. Fecal and urinary N data were analyzed for outliers by using boxplot function in R (version 0.98.1102, R Foundation for Statistical Computing, Vienna, Austria) as well as the interquartile range (**IQR**) method (Zwillinger and Kokoska, 2000). The IQR method aims at identifying outliers by setting up a limit outside of Q1 and Q3. Any values that fall outside of this limit are considered outliers. The factor of 1.5 was used in constructing markers to identify outliers, as shown in equations i–iii:

$$IQR = third\ quartile\ (Q3)\ \times\ first\ quartile\ (Q1), \quad (i)$$

$$Lower\ fence = Q1 - IQR \times 1.5, \quad (ii)$$

$$Upper\ fence = Q3 + IQR \times 1.5. \quad (iii)$$

We also excluded biologically unrealistic observations. These values displayed fecal N excretion of, on average, +215% of N intake, which is biologically unrealistic. In addition,

Table 1. Summary descriptive statistics of the variables used for the development of the models

Variables[1]	n[2]	Mean	SD	Minimum	Maximum
Dietary component concentrations, % DM					
CP	810	14.6	2.99	10.0	23.0
NDF	747	31.8	9.26	11.6	52.1
ADF	520	17.1	7.30	4.0	38.3
EE	376	3.3	0.80	1.4	5.9
Starch	531	31.2	16.13	0.7	67.7
Animal information					
DMI, kg/d	820	8.8	2.31	2.3	14.8
Nitrogen intake, g/d	806	206.0	67.84	44.0	385.7
NDFI, kg/d	752	3.0	1.10	0.5	6.1
ADG, kg/d	500	1.0	0.49	–0.3	2.1
BW, kg	596	569	143.4	180	933
Nitrogen excretion, g/d					
Fecal N	812	64.4	25.85	10.3	137.1
Urinary N	688	89.6	37.91	6.2	188.7
Total manure N	680	151.8	54.46	24.5	321.7

[1]CP, crude protein; NDF, neutral detergent fiber; ADF, acid detergent fiber; EE, ether extract; DMI, dry matter intake; NDFI, neutral detergent fiber intake; ADG, average daily gain; BW, body weight.
[2]Number of observations.

these observations had low DMI (on average 1.69% of BW) that resulted in over 200 g fecal N excretion per day (n = 92), and outliers were above 200 g fecal N excretion per day as shown in the boxplot of fecal N excretion data (Supplementary Table S2). As a result, the dataset used for model development contained 820 observations of fecal N excretion (18% removed from the initial dataset) and 459 observations of urinary N excretion (33% removed) and 459 observations of total manure N excretion.

Statistical analyses
Random-effects model analysis and model development
Linear mixed-effect models were constructed to predict fecal, urinary, and total manure N excretion (g/d) using the final datasets. Random-effect meta-analysis approaches (St-Pierre, 2001) were applied, and N excretion was predicted by fitting a mixed-effect model using the lmer (Bates et al., 2015) procedure of R statistical language. Several models as described later, were developed with different categories of independent variables as fixed effects, and with experiments included as random effects. Variables of interest were first selected based on biological relevance regarding their relationship with N excretion in feces or urine. The potential predictors among the different categories (DMI, dietary component concentrations [CP and NDF], nutrient intakes [N, NDF, ADF, EE, and starch], and performance [BW and ADG]) were individually tested for their effect on fecal, urinary, and total manure N excretion. Those variables that generated a $P < 0.10$ (Supplementary Tables S3–S5) were selected for further assessment.

We started with simple models based on variables that had a significant individual effect on N excretion ($P < 0.10$). Variables where pairwise Pearson's correlations (Supplementary Table S6) for predictors had an absolute value of |r| ≥ 0.5 were not included simultaneously in models to avoid multicollinearity and, with that inaccurate model parameteriza-

tion, decreased statistical power and exclusion of significant predictor variables during model construction (Graham, 2003). For instance, DMI and N intake were correlated (r = 0.78), thus two models were developed using either DMI or N intake. For other correlated variables, such as NDF and ADF (r = 0.87), the model including one or the other variable that led to the lowest Bayesian information criterion (**BIC**), was chosen as the final model and the other one was discarded. Nitrogen excretion prediction models were developed based on the final dataset with up to five different variable categories and using the following information: 1) for simple models; DMI only (DMI_M), N intake only (N intake_M), nutrient intakes (Diet_intake_M), dietary component concentrations (Diet_M), and performance variables (PERF_M) and 2) for complex models; DMI and dietary component concentrations (DMI_diet_M); all significant independent variables among variable categories were used for the full model selection (Full_M). However, simple models for dietary nutrient intakes are not presented for fecal, urinary, or total N excretion as they were all based on N intake.

The mixed-effect model development approach used in this study enabled analysis of fixed effects of independent preselected variables, as well as experiment-specific deviation of the N excretion response, which was considered a random effect. The general mixed-effect model for single and multiple regressions for a response variable was represented as:

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \ldots + \beta_n X_n + R_j + e, \quad (iv)$$

where β_0 denotes the fixed effect of intercept; X_1 to X_n denotes the fixed effects of predictor variables and β_1 to β_n are the corresponding slopes; R_j denotes the random effect of the j experiment (to capture variations such as different regional weather conditions, measurement methods used, research protocols, etc.); and e is the within-experiment error. All variables that had a P-value of <0.1 with regard to

N excretion were further used for model development. The BIC was computed for each model. Models with the lowest BIC were selected to predict each N excretion response at each level of complexity. The BIC was calculated as $n \log (SSE_p/n) + (\log n)\, p$, where p is the number of regression coefficients, n is the sample size, and SSE_p is error sum of squares. A model with a smaller BIC was preferred as this strikes a balance between the goodness of fit and model complexity.

Variance inflation factor analysis was also carried out to assess the independence of predictors in complex models. Influential cases that alter the value of a regression coefficient whenever deleted from an analysis, can affect the validity and robustness of meta-analysis conclusions (Sutton et al., 2000; Viechtbauer and Cheung, 2010). Thus, residuals were visually inspected for patterns and studentized residuals were used to identify observations with high leverage. This arises when an observation influences the regression model to such an extent that the estimated regression function is biased toward that potential observation (St-Pierre, 2007). To account for this, any observations leading to studentized residuals |≥3.0| were removed from the dataset.

Cross-validation and model evaluation

The predictive accuracy of each N excretion model at different levels was evaluated using the k-fold cross-validation method (James et al., 2014). This evaluation data set included a total of 517, 431, and 424 observations for fecal, urinary, and total manure N excretion, respectively, with complete information of each variable used in the models and with folds composed of individual experiments ($n = 33$; Supplementary Figure S7). Each individual fold was treated as an evaluation set, where the prediction of N excretion of each fold was calculated using the model that was fitted from the remaining folds. In this cross-evaluation method, the predictions of all folds were used to conduct model evaluation metrics as described later.

A combination of model evaluation metrics was used to assess model performance. Root mean square of prediction error (**RMSPE**), expressed as a percentage of the observed mean was calculated where a smaller RMSPE indicates better model predictive ability. The mean squared prediction error was decomposed into mean (**MB**) and slope bias (**SB**) deviations to identify systematic biases. The MB and SB were calculated as shown in equations v and vi, respectively, according to Bibby and Toutenburg (1977):

$$MB = (\bar{P} - \bar{O})^2, \tag{v}$$

$$SB = (S_p - r \times S_o)^2, \tag{vi}$$

where $\bar{P}$ and $\bar{O}$ denote the predicted and observed means, S_p denotes the standard deviation of predicted values, S_o denotes the standard deviation of observations, and r denotes the Pearson correlation coefficient.

Furthermore, the concordance correlation coefficient (**CCC**; Lin, 1989) was calculated as follows:

$$CCC = r \times C_b, \tag{vii}$$

where

$$C_b = \left[\frac{\left(v + \frac{1}{v} + u^2\right)}{2} \right]^{-1}, \tag{viii}$$

$$v = \frac{S_o}{S_p}, \tag{ix}$$

$$u = \frac{(\bar{P} - \bar{O})}{(S_o \times S_p)^2}, \tag{x}$$

where $\bar{P}$ and $\bar{O}$, S_o and S_p were defined above, v provides a measure of scale shift, and u provides a measure of location shift. The CCC evaluates the degree of deviation between the best-fit line and the identity line ($y = x$), therefore, the CCC of a model that is closer to 1, indicates better model performance. When using different datasets to compare the performance of models, one can use the ratio of RMSPE and standard deviation of the data (observed values), namely RMSPE-observations standard deviation ratio (**RSR**). This approach considers standardized model performance relative to the variability in observations in different datasets (Moriasi et al., 2007). The RSR was calculated as shown in equation xi,

$$RSR = \frac{RMSPE}{S_o}, \tag{xi}$$

where S_o denotes the standard deviation of observations. Smaller RSR (<1) indicates superior performance given the variability of observations.

Results

Dataset

Summary statistics of the dataset and variables used for model development are presented in Table 1, and summary statistics of variables in the final dataset used for model evaluation are given in Table 2. Mean DMI and N intake in the model development dataset were 8.8 (±2.31) kg/d and 206 (±67.8) g/d, respectively. Mean fecal and urine N excretion were 64.4 (±25.9) and 89.6 (±37.9) g/d, respectively. Diets had on average concentrations of 14.6% CP and 31.8% NDF (DM basis, Table 1) and the BW of cattle averaged 596 (±143.4) kg.

In the final dataset used for model evaluation, DMI and N intake varied between 9.3 and 9.6 kg/d and 218 and 227 g/d, respectively (Table 2). On average, N excretion in feces and urine was 73.7 (±25.1) and 99.5 (±38.2) g/d per animal, respectively, and total manure N excretion was 170.7 (±51.5) g/d.

Mixed-effect models for fecal N excretion

Models to predict N excretion in feces are given in Table 3. Daily N excretion in feces had positive relationships with DMI, N, and NDF intakes (**NDFI**), dietary CP, and NDF, and also with BW. The simple models based on DMI or N intake (equations 1 and 2) had RMSPE of 27.7% and 28.9%; and RSR of 0.81 and 0.85, respectively. The SB and MB for these two models were small (<3.5%). The DMI model tended to underpredict at lower levels of fecal N excretion and overpredict at higher levels of fecal N excretion (Figure 1).

Table 2. Summary descriptive statistics of the variables used for the evaluation of the models

Variables[1]	Fecal N excretion					Urinary N excretion					Total manure N excretion				
	n[2]	Mean	SD	Min[3]	Max[3]	n[2]	Mean	SD	Min[3]	Max[3]	n[2]	Mean	SD	Min[3]	Max[3]
Dietary component concentrations, % DM															
CP	517	14.8	3.08	10.2	23.0	431	14.8	3.22	10.2	23.0	424	14.8	3.21	11.3	23.0
NDF	517	32.4	8.65	11.6	52.1	431	32.9	9.04	11.6	52.1	424	32.8	9.08	11.6	52.1
Performance															
DMI, kg/d	517	9.6	2.10	3.3	14.8	431	9.3	2.03	3.3	13.6	424	9.3	2.03	3.3	13.6
N intake, g/d	517	227	64.7	97.5	386	431	219	64.0	97.5	386	424	218	63.2	97.5	386
NDFI, kg/d	517	3.0	0.99	0.7	5.7										
BW, kg	517	586	134	334	933	431	571	123	334	933	424	570	124	334	933
N excretion, g/d	517	73.7	25.1	14.0	137	431	99.5	38.2	14.0	187.8	424	170.7	51.52	65.3	322

[1]CP, crude protein; NDF, neutral detergent fiber; DMI, dry matter intake; NDFI, neutral detergent fiber intake; ADG, average daily gain; BW, body weight.
[2]n refers to the number of observations used for model evaluation.
[3]Min, minimum; Max, maximum.

Table 3. Prediction equations of fecal N excretion (g/d per animal) according to different categories and performance evaluation

Model development			Model performance[1]					
Equation	Category[2]	Prediction equation	n	RMSPE, %	RSR	MB	SB	CCC
1	DMI_M	$5.03 (\pm3.36) + 6.49 (\pm 0.27) \times DMI$	517	27.7	0.81	3.27	3.46	0.47
2	N intake_M	$13.5 (\pm3.42) + 0.24 (\pm0.01) \times N\ intake$	517	28.9	0.85	2.47	0.01	0.46
3	Diet_M	$24.7 (\pm6.61) + 0.15 (\pm0.02) \times CP + 0.06 (\pm0.01) \times NDF$	517	35.0	1.03	1.61	4.12	0.04
4	PERF_M	$50.8 (\pm6.63) + 0.03 (\pm0.01) \times BW$	517	35.2	1.03	2.05	9.69	−0.04
5	DMI_diet_M	$-37.7 (\pm5.73) + 6.27 (\pm0.29) \times DMI + 0.17 (\pm0.02) \times CP + 0.06 (\pm0.01) \times NDF$	517	25.0	0.73	2.89	5.38	0.59
6	Full_M	$18.8 (\pm7.53) + 0.15 (\pm0.02) \times N\ intake + 8.89 (\pm2.07) \times NDFI$	517	28.1	0.82	3.95	0.08	0.51

[1]n, number of observations used to construct equations. RMSPE, root mean square prediction error expressed as a percentage of observed daily N excretion in feces means; RSR, RMSPE-observations standard deviation ratio; MB, mean bias as a percentage of MSPE; SB, slope bias as a percentage of MSPE; CCC, concordance correlation coefficient.
[2]Simple models: DMI only (DMI_M), N intake only (N intake_M), dietary component concentration variables (Diet_M), and performance variable (PERF_M). Complex models: DMI and dietary component concentrations (DMI_Diet_M), all significant independent variables among variable categories were used for the full model selection (Full_M). DMI, dry matter intake (kg/d); CP, crude protein (g per kg DM); NDF, neutral detergent fiber (g per kg DM); BW, body weight (kg); N intake (g/d); NDFI (kg/d).

The model based on dietary CP and NDF (equation 3) had 35.0% RMSPE, along with 4.1% of SB (Diet_M). The model based on BW (equation 4) had RMSPE of 35.2% as compared with the simple models, along with a larger SB (9.7%; PERF_M).

When both DMI and dietary component concentrations (CP and NDF) were used in the complex models (equation 5; Table 3), the RMSPE (25.0%) and RSR (0.73) were the lowest compared with other models. The Full_M, based on N intake and NDFI (equation 6; Table 3), had similar RMSPE as the DMI_M of 28.1%, along with RSR of 0.82 but greater CCC (0.51). These two complex models tended to underpredict at lower and overpredict at higher levels of fecal N excretion (Figure 2).

Mixed-effect models for urinary N excretion

Models predicting urinary N excretion are given in Table 4. Urinary N excretion had positive relationships with DMI, N intake, dietary CP and NDF concentrations, and BW.

The simple model for urinary N excretion based on DMI had RMSPE of 37.4%, RSR of 0.97, and negligible bias (equation 7; Table 4). However, this model tended to overpredict at lower and underpredict at higher levels of urinary N excretion (Figure 3). The model based on N intake had the best RMSPE of 27.1% and RSR of 0.71, with negligible bias (equation 8; Table 4). Models based on dietary CP and NDF concentrations (equation 9; Table 4) had RMSPE of 31.9% and RSR of 0.83, while the model based on BW (equation 10) had the greatest prediction error of 39.2% and RSR of 1.02. The BW model generated SB of 5.1%, and overpredict at lower and underpredict at higher levels of urinary N excretion (Figure 3).

For the complex models, the lowest RMSPE (25.6%) was for the model that included DMI and dietary CP and NDF concentrations (equation 11; Table 4). The RSR (0.67) was the lowest with DMI_diet_M in the model as compared with all the other models, and negligible bias was reported (<2%) even though it tended to slightly underpredict at lower and overpredict at higher levels of urinary N excretion (Figure 4). The Full_M (equation 12) based on dietary CP concentration and BW generated greater RMSPE (29.4%) and RSR (0.77) compared with a simple model based on N intake or the other complex models.
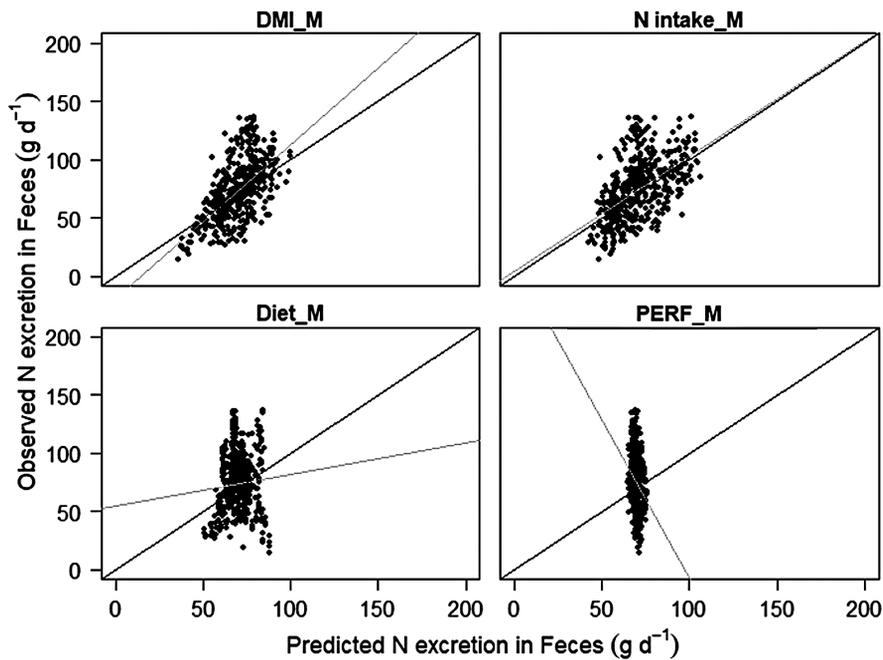
Figure 1. Predicted vs. observed value plots for fecal N excretion (g/d per animal) using simple prediction equations: DMI only (**DMI_M**), N intake only (**N intake_M**), dietary component concentration variables (**Diet_M**), and performance variable (**PERF_M**). The thin and bold solid lines represent the fitted regression line for the relationship between predicted and observed values and the identity line ($y = x$), respectively.
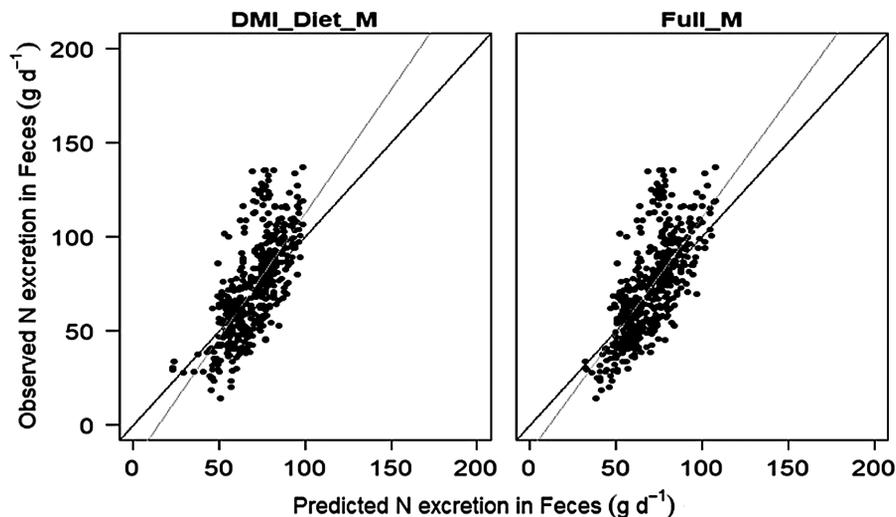
Figure 2. Predicted vs. observed value plots for fecal N excretion (g/d per animal) using complex prediction equations: DMI and dietary component concentrations (**DMI_Diet_M**), all variables having an individual effect on fecal N excretion (**Full_M**). The thin and bold solid lines represent the fitted regression line for the relationship between predicted and observed values and the identity line ($y = x$), respectively.

Mixed-effect models for total manure N excretion

Total manure N excretion had positive relationships with DMI, N intake, dietary CP and NDF concentrations, and BW (Table 5). The model based on DMI had 25.3% RMSPE, with RSR of 0.84 and negligible bias (<2%; equation 13; Table 5), whereas the model based on N intake (equation 14) had a lower RMSPE of 17.1% with negligible bias (<2%) and the lowest RSR (0.57) compared with other simple models. Both DMI and N intake models tended to slightly underpredict with lower levels of total manure N excretion and overpredict at higher levels of total manure N excretion (Figure 5). Other simple models based either on dietary component concentrations or BW (equations 15 and 16) had larger RMSPE of 27.1% and 30.7%, respectively. The RSR was also greater with 0.90 and 1.02 with Diet_M and PERF_M, respectively, and SB of 4.1% for PERF_M.
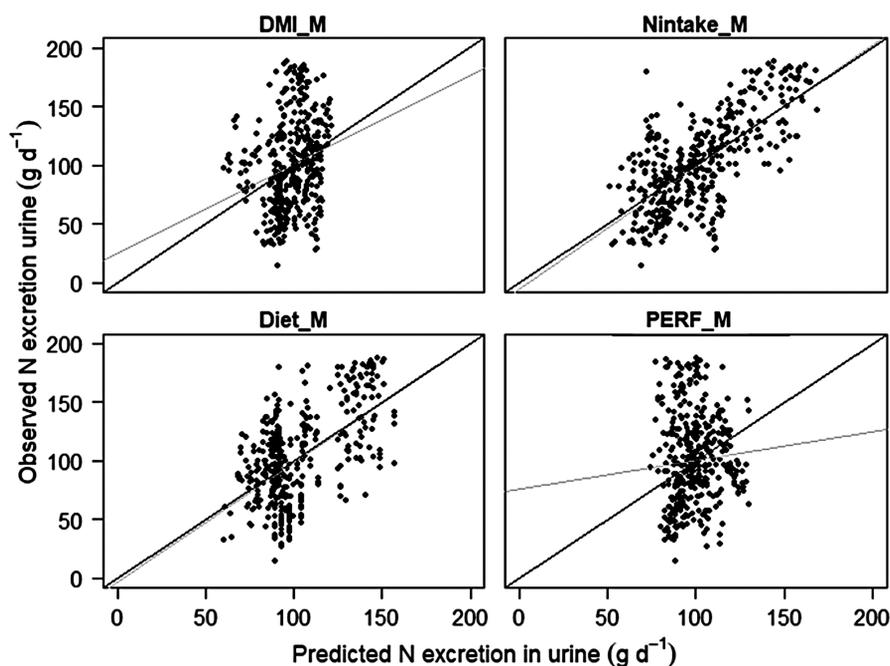
Predictions of total manure N excretion improved with more complex models. Indeed, the models based on DMI, dietary CP, and NDF (equation 17; Table 5) had RMSPE of 15.2%, RSR of 0.50, and Full_M based on BW and dietary CP and NDF (equation 18) had the lowest RMSPE and RSR (14.6% and 0.48, respectively). However, larger SB was observed with the two complex models (>5%) and the model tended to underpredict with lower total manure N excretion and overpredict with higher total manure N excretion (Figure 6).

Table 4. Prediction equations of urinary N excretion (g/d per animal) according to different categories and performance evaluation

Model development			Model performances[1]					
Equation	Category[2]	Prediction equations	*n*	RMSPE, %	RSR	MB	SB	CCC
7	DMI_M	22.4 (±7.21) + 7.56 (± 0.64) × DMI	431	37.4	0.97	0.02	0.58	0.13
8	N intake_M	12.0 (±5.82) + 0.38 (±0.02) × N intake	431	27.1	0.71	0.29	0.16	0.66
9	Diet_M	−25.8 (±11.11) + 0.65 (±0.04) × CP + 0.07 (±0.02) × NDF	431	31.9	0.83	0.44	0.01	0.47
10	PERF_M	36.8 (±11.05) + 0.10 (±0.02) × BW	431	39.2	1.02	0.01	5.07	0.04
11	DMI_diet_M	−96.8 (±11.92) + 6.81 (±0.60) × DMI + 0.69 (±0.04) × CP + 0.09 (±0.02) × NDF	431	25.6	0.67	0.55	1.99	0.69
12	Full_M	−63.0 (±20.34) + 0.67 (±0.07) × CP + 0.10 (±0.02) × BW	431	29.4	0.77	0.28	0.03	0.58

[1]*n*, number of observations used to construct equations. RMSPE, root mean square prediction error expressed as a percentage of observed daily N excretion in feces means; RSR, RMSPE-observations standard deviation ratio; MB, mean bias as a percentage of MSPE; SB, slope bias as a percentage of MSPE; CCC, concordance correlation coefficient.
[2]Simple models: DMI only (DMI_M), N intake only (N intake_M), dietary component concentration variables (Diet_M), and performance variable (PERF_M). Complex models: DMI and dietary component concentrations (DMI_Diet_M), all significant independent variables among variable categories were used for the full model selection (Full_M). DMI, dry matter intake (kg/d); CP, crude protein (g per kg DM); NDF, neutral detergent fiber (g per kg DM); BW, body weight (kg); N intake (g/d).
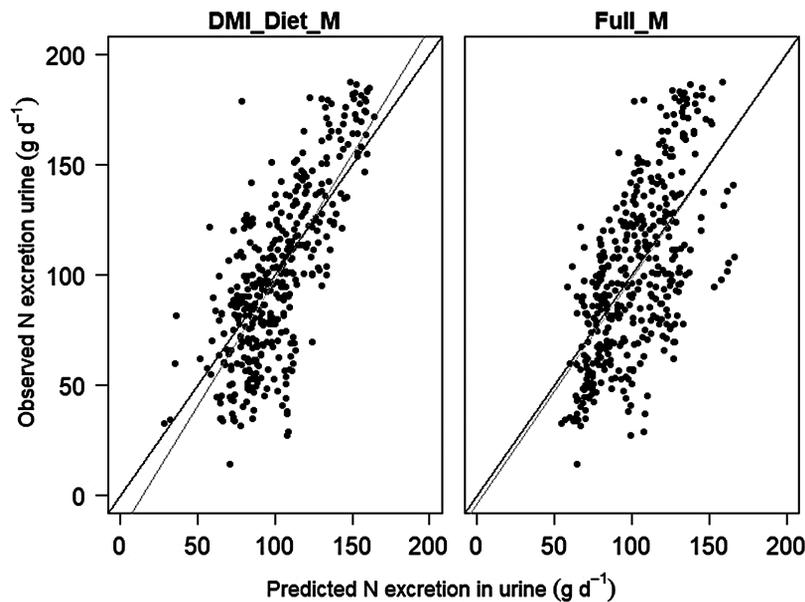

Figure 3 Predicted vs. observed value plots for urinary N excretion (g/d per animal) using simple prediction equations: DMI only (**DMI_M**), N intake only (**N intake_M**), dietary component concentration variables (**Diet_M**), and performance variables (**PERF_M**). The thin and bold solid lines represent the fitted regression line for the relationship between predicted and observed values and the identity line ($y = x$), respectively.

Discussion

The compilation of 33 experiments used for model development contained individual animal observations from mainly Angus beef cattle (90%) across different countries (Brazil, Canada, Belgium, Ireland, and France) and might not be relevant for small landholders in developing countries that use different beef breeds fed different diets. The major ingredients of the diets in the present dataset were corn silage, cereal silage, fresh sugarcane, processed corn or barley grain, and soybean meal. Therefore, the results from this meta-analysis are most applicable to Angus beef cattle fed corn silage, fresh sugar cane, or cereal silage-based diets.

Key predictors in equations

Nitrogen excretion was positively related with DMI and N intake, but N intake models more accurately predicted urinary and total manure N excretion, whereas DMI was more suited for predicting fecal N excretion. Reed et al. (2015) also developed prediction equations based on N intake with observations from steers, heifers, and dry dairy cows. In their meta-analysis, simple equations based on N intake to predict fecal, urinary, and total manure N excretion in steers had 17.6%, 26.5%, and 11.0% prediction errors, respectively. We reported greater prediction errors of 28.9%, 27.1%, and 17.1% for fecal, urinary, and total manure N excretion,

Figure 4. Predicted vs. observed value plots for urinary N excretion (g/d per animal) using complex prediction equations: DMI and dietary component concentrations (**DMI_Diet_M**), all variables having an individual effect on urinary N excretion (**Full_M**). The thin and bold solid lines represent the fitted regression line for the relationship between predicted and observed values and the identity line ($y = x$), respectively.

Table 5. Prediction equations of total manure N excretion (g/d per animal) according to different category and performance evaluation

Model development				Model performances[1]				
Equation	Category[2]	Prediction equations	n	RMSPE, %	RSR	MB	SB	CCC
13	DMI_M	33.3 (±8.90) + 13.60 (±0.78) × DMI	424	25.3	0.84	0.32	1.66	0.42
14	N intake_M	23.1 (±7.18) + 0.63 (±0.02) × N intake	424	17.1	0.57	0.00	1.06	0.8
15	Diet_M	1.98 (±15.21) + 0.80 (±0.05) × CP + 0.12 (±0.03) × NDF	424	27.1	0.90	0.01	0.45	0.35
16	PERF_M	84.6 (±15.22) + 0.14 (±0.02) × BW	424	30.7	1.02	0.14	4.07	0.03
17	DMI_diet_M	−139.4 (±12.92) + 14.0 (±0.67) × DMI + 0.87 (±0.04) × CP + 0.14 (±0.02) × NDF	424	15.2	0.50	0.00	8.87	0.83
18	Full_M	−18.8 (±11.87) + 0.61 (±0.02) × CP + 0.07 (±0.02) × NDF + 0.06 (±0.02) × BW	424	14.6	0.48	0.03	7.93	0.85

[1]n, number of observations used to construct equations. RMSPE, root mean square prediction error expressed as a percentage of observed daily N excretion in feces means; RSR, RMSPE-observations standard deviation ratio; MB, mean bias as a percentage of MSPE; SB, slope bias as a percentage of MSPE; CCC, concordance correlation coefficient.
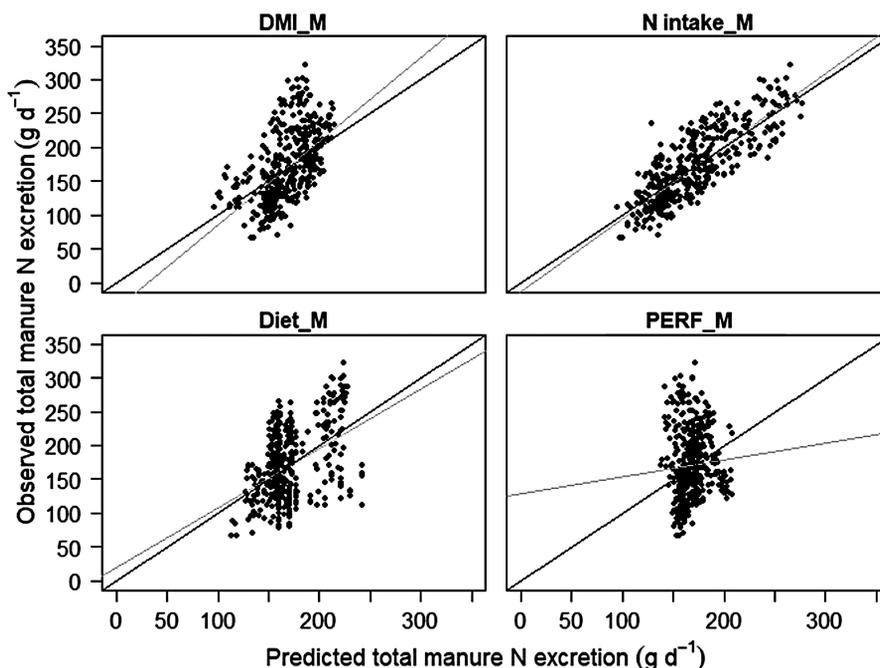[2]Simple models: DMI only (DMI_M), N intake only (N intake_M), dietary component concentration variables (Diet_M), and performance variable (PERF_M). Complex models: DMI and dietary component concentrations (DMI_Diet_M), all significant independent variables among variable categories were used for the full model selection (Full_M). DMI, dry matter intake (kg/d); CP, crude protein (g per kg DM); NDF, neutral detergent fiber (g per kg DM); BW, body weight (kg); N intake (g/d).

respectively, which may be due to more diverse data in terms of animal or diets, used in the current study. Indeed, in Reed et al. (2015), data were from one region and diets were less diverse as compared with our study. Models based on N intake to predict urinary N excretion, developed by Waldrip et al. (2013), had greater prediction error (39%) as compared with this study. Thus, prediction models were more accurate when using a narrow range of observation as observed in Reed et al. (2015), but greater performance was obtained in our study with a large variety of data as compared with Waldrip et al. (2013).

We observed that using N intake was better suited for predicting total manure N excretion than fecal and urinary N excretion as reported in Reed et al. (2015). However, in our study, using N intake rather than DMI improved the prediction of urinary N excretion and total manure N excretion,

whereas DMI was better suited to predicting fecal N excretion. This is mainly because urinary N is more affected by N intake, as any absorbed surplus N that is not used for body N accretion will be excreted in urine (Dijkstra et al., 2013a). A positive relationship between N excretion in urine and N intake has been previously reported for beef cattle (Brake et al., 2010; Waldrip et al., 2013; Dong et al., 2014). Yan et al. (2007) also showed that a reduction in N intake decreased urinary N excretion in beef cattle to a greater extent than in feces.

As expected, dietary CP concentration was positively related to N excretion in fecal, urinary, and total manure N excretion models. Variation in dietary N supply affects particularly urinary N output (Huhtanen et al., 2008). In a meta-analysis, Ohlsson and Kristensen (1998) identified a positive linear relationship between dietary CP concentration

Figure 5. Predicted vs. observed value plots for total N excretion (g/d per animal) using simple prediction equations: DMI only (**DMI_M**), N intake only (**N intake_M**), dietary component concentration variables (**Diet_M**), and performance variable (**PERF_M**). The thin and bold solid lines represent the fitted regression line for the relationship between predicted and observed values and the identity line ($y = x$), respectively.
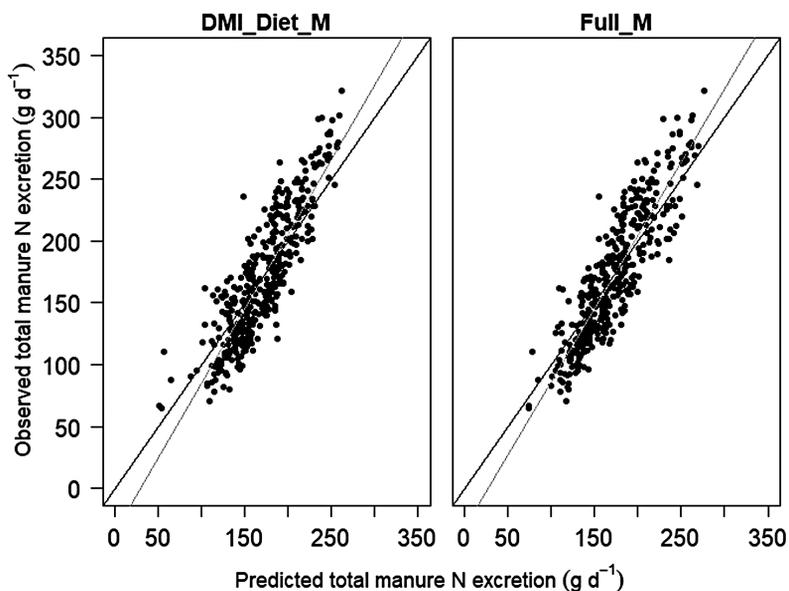
Figure 6. Predicted vs. observed value plots for total N excretion (g/d per animal) using complex prediction equations: DMI and dietary component concentrations (**DMI_Diet_M**), all variables having an individual effect on total manure N excretion (**Full_M**). The thin and bold solid lines represent the fitted regression line for the relationship between predicted and observed values and the identity line ($y = x$), respectively.

and partitioning of excreted N into urine versus feces in dairy cattle, with urinary N representing 25% and 50% of the total excreted N with diets containing 11% and 18% CP, respectively. As expected, dietary factors affect N utilization in ruminants, with the dietary CP concentration being a predominant determinant (Marini et al., 2004). Waldrip et al. (2013) developed fecal and urinary prediction models based on dietary CP concentrations and observed prediction errors of 44% and 73%, respectively, when models were evaluated on an independent dataset. Models

predicting fecal and urinary N excretion based on dietary CP and NDF concentrations (equations 3 and 9) had lower prediction errors than other models, but similar or lower performance than models based on BW. The dietary NDF concentration certainly explained part of the variability in fecal and urinary N excretion that was not accounted when using dietary CP concentration on its own. This also partly explains the prediction performance differences observed between the current study and the one from Waldrip et al. (2013).

Reed et al. (2015) also used CP concentration in their complex models for steers, along with other variables (N intake, BW, and metabolizable energy) depending on the fraction of N excretion predicted. They reported prediction errors of 21.7%, and 9.2% for urinary and total N excretion, respectively. In our study, complex models resulted in greater prediction error than in Reed et al. (2015), which might be due to a more diverse dataset used in our study, for instance, with greater variability in diets or farming systems encountered. Indeed, the model (Full_M, equation 12) based on dietary CP concentration and BW had 29.4% prediction error for urinary N excretion, while the model (Full_M, equation 18) based on CP, NDF concentrations, and BW had a 14.6% prediction error for total manure N excretion. However, the complex equations (equations 11 and 17) based on DMI, CP, and NDF led to lower prediction error with 25.6% and 15.2% for urinary and total manure N excretion, respectively. We also reported greater prediction error for fecal N excretion as compared with Reed et al. (2015), and used different variables with N and NDFI in equation 6 vs. N intake, dietary ME, DM, lignin, ash, and mean BW in Reed et al. (2015). Complex fecal N excretion models were based on N intake and NDFI with a prediction error of 28.1%, while Reed et al. (2015) reported a prediction error of 14.2% with a model based on N intake dietary component concentrations (DM, ash, and lignin), and BW. Prediction error was lower with models based on DMI, CP, and NDF concentrations in our study (equation 5; 25.0%) than models based on DMI only (equation 1; 27.7%), but still greater than those of Reed et al. (2015). However, Reed et al. (2015) used observations from experiments conducted only in the USA and with Holstein, Angus, Hereford, and Angus-Hereford cross steers ($n = 458$), with a mean BW of 317 kg (±86.7). In our study, observations were taken from experimentation conducted in various parts of the world, with mostly Angus or Angus-Hereford cattle weighing on average 569 kg (±143.4). Thus, the different types of diets and cattle used between both meta-analyses could partly explain the differences in results between the two studies. In addition, at this weight of 569 kg, Angus cattle might not be depositing very much protein, which would affect N excretion.

The complex models to predict urinary and total manure N excretion included BW, which was also reported in Reed et al. (2015). However, when used alone in prediction models, BW led to poor prediction performance compared with the other simple equations based on dietary component concentrations. In addition, when BW is used in complex models along with other variables, prediction performance was improved. BW is correlated to DMI and it has been shown that manure production in cattle increases with increasing DMI (Weiss, 2004). Models that include dietary component concentrations have been shown to predict N excretion with greater accuracy compared with models based on BW alone (Castillo et al., 2000; Nennich et al., 2005; Kebreab et al., 2010; Dijkstra et al., 2013a). Simple models based on dietary component concentrations also led to better prediction performance than models based on BW for urinary and total manure N excretion. Thus, predicting N excretion in urine of beef cattle using models based only on BW is not reliable and leads to substantial error. When BW was used along with dietary CP and NDF concentration, the prediction of total manure N excretion was more accurate. Yan et al. (2007) also showed that N excretion was less related to BW than to N intake, but

using BW and dietary N concentration led to better predictions than either one alone.

Overall, using dietary component concentration variables, along with intake (DMI or N intake) explained a larger part of N excretion. This is because N excreted in feces and urine originates from endogenous N, protein synthesis from ruminal microorganisms, and subsequent undigested microbial N, as well from undigested feed protein. All of these factors are affected by intake and dietary component concentration. Huhtanen et al. (2008) reported models based on DMI and N intake improved N excretion prediction compared with models based on DMI only. Using these two variables gives information on intake quantity and quality, which explains a large part of the variability.

Application of N excretion equations

The simplest models for fecal, urinary, and total manure N excretion that used DMI or N intake, led to greater prediction errors (RMSPE and CCC) than complex models in our study. Simple models using only dietary component concentrations, or BW without DMI or N intake had much lower accuracy, indicating that DMI and N intake are the main drivers of N losses in feces, urine, and total manure. Thus, these simple models should be used with great caution as they lead to substantial errors, especially when predicting fecal or urinary N excretion separately. Using the simple model based on N intake to predict total N excretion is preferred as RMSPE is lower and CCC the greater when compared with other fecal and urinary N excretion simple models.

We observed that the accuracy of prediction of N excretion in feces or urine improved in models that included DMI and dietary CP and NDF concentrations. Using BW along with dietary CP and NDF also led to better prediction of urinary and total manure N excretion than simple models. In addition, seasonal BW changes may be observed and are important to take into account for N predictions. All these covariates among others, such as mobilization of body N in more extensive systems, for instance, certainly play a role in mobilization of body N, and using them in prediction models gives more insights into the process of N losses in feces or urine.

Considering the low accuracy of predicting N excretion with simple models, except for the total N excretion prediction model based on N intake, we recommend, for more accurate predictions, the complex model based on DMI to be used for N excretion in feces, urinary, and total manure N excretion, when DMI is measured. Estimation of DMI is still challenging on farms, especially with extensive production systems. In addition, prediction equations based on BW and diet composition for urinary N and manure N excretions performed well and could be used for on-farm predictions too. The above-recommended models provide a simplified tool for beef cattle producers to quantify N excretion, and consequently develop mitigation strategies to reduce N excretion on their operations.

Conclusions

This study compiled a large dataset, based on individual observations from beef cattle fed a wide range of diets from several countries in the world. This individual dataset is the largest used so far to develop fecal, urinary, and total N excretion prediction models. Of the simple models developed, DMI was the primary predictor for fecal N excretion

whereas as expected, N intake was more suited for urine and total manure N excretion. However, predictive performance of these simple models based on DMI or N intake alone was less accurate than complex models. Nonetheless, N intake could be used to predict total N excretion. Prediction accuracy further improved upon adding dietary component concentrations. Therefore, models to predict N excretion based on DMI and dietary CP and NDF concentrations are preferred to predict N excretion in beef cattle. Overall, prediction models developed in this study were less accurate than models developed with observations taken from one location but more accurate than models based on observations gathered from various parts of the world. Thus, these prediction models could assist in quantifying N flow in the environment including into air, surface, and groundwater from different agricultural systems. This information could be used to develop regulatory policies and identify management practices that reduce the impact of large-scale beef feeding operations on the environment.

Supplementary Data

Supplementary data are available at *Journal of Animal Science* online.

Acknowledgments

Conflict of interest statement

The authors have no conflict of interest to declare.

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