J. Dairy Sci. 99:1–8
http://dx.doi.org/10.3168/jds.2015-9638

Prediction of intake in growing dairy heifers under tropical conditions

A. S. Oliveira[1] and V. B. Ferreira
Instituto de Ciências Agrárias e Ambientais, Universidade Federal de Mato Grosso - Campus Sinop, Sinop, Mato Grosso, Brazil, 78557-267

ABSTRACT

A meta-analysis was conducted to develop models of the prediction of dry matter intake (DMI) in growing dairy heifers [postweaning to 390 kg of body weight (BW)] under tropical conditions. The adequacy of the models was assessed in a comparison with the 4 US models currently used to predict DMI [Quigley; National Research Council; and 2 Hoffman models]. The data set was created using 95 treatment means from 28 studies published in journals. The data set (studies) was randomly divided into 2 data subsets for the statistical analyses. The first data subset was used to develop the prediction equations for DMI (17 studies; 58 treatment means), and the second data subset was used to assess the adequacy of the predictive models (11 studies; 37 treatment means). The models were developed using nonlinear and linear mixed analyses. Breed (*Bos taurus* vs. *Bos taurus* × *Bos indicus*), BW (240.2 ± 62.2 kg), and average daily gain (ADG, 0.83 ± 0.28 kg/d) were the independent variables. No significant effects of the breed or the interactions between the breed and metabolic BW ($BW^{0.75}$) or breed and ADG were detected. Thus, nonlinear [$DMI = 0.1175 \times BW^{0.75} - 3.4984 \times e^{(-2.4690 \times ADG)}$] and linear models [$DMI = 8.7147 - 0.2402 \times BW^{0.75} + 0.0027 \times (BW^{0.75})^2 + 3.6050 \times ADG - 1.4168 \times ADG^2$] were proposed for both breeds. The nonlinear model explained 81% of the variation in the DMI, over-predicted the DMI by 0.21 kg/d and predicted the DMI with a higher accuracy and precision than the linear model [root mean square error of prediction (RMSEP) = 8.82 vs. 10.71% of the observed DMI, respectively]. The Quigley model explained only 54% of the variation in the DMI and was the fourth most accurate and precise model (RMSEP = 11.21% of the observed DMI). The National Research Council model explained 69% of the variation in the DMI but under-predicted the DMI by 0.53 kg/d, with an RMSEP of 12.72% of the observed DMI and presence of systematic constant bias. The Hoffman exponential model I (BW as the input) adequately predicted the DMI with an accuracy that was similar to the proposed nonlinear model. The equation of the Hoffman exponential model I explained 75% of the variation in the DMI and over-predicted the DMI by 0.07 kg/d, which was the second most accurate and precise equation (RMSEP = 9.35% of the observed DMI). However, the Hoffman exponential model II (BW and diet NDF as the inputs) did not adequately predict the DMI, because it explained only 54% of the variation in the DMI, under-predicted the DMI by 0.72 kg/d, and had a high RMSEP (17.96% of the observed DMI). The use of nonlinear models increase the accuracy and the precision of the prediction of DMI compared with the linear models. Only the models proposed in the present study, the Hoffman exponential model I (BW as the input), and the Quigley model were adequate for the prediction of the DMI of growing dairy heifers under tropical conditions.

Key words: feed intake, meta-analysis, modeling

INTRODUCTION

The accurate prediction of feed intake by cattle is essential to optimize the use of nutrients and the productive, economic, and environmental performance of dairy cattle systems (Souza et al., 2014). However, the accurate estimation of the DMI remains a challenge. Because of the difficulty in the use of complex predictive DMI models with the accuracy and the simplicity necessary for the formulation and evaluation of diets, and despite the complexity of the mechanisms that regulate feed intake, several current predictive US models (Quigley et al., 1986; NRC, 2001; Hoffman et al., 2008) use empirical approaches to predict the DMI of dairy heifers with animal (i.e., BW and ADG) or diet variables as inputs (i.e., NE_M, TDN, and NDF).

However, the application of empirical models is population-dependent, and the use of such models is limited to specific diets, animal breeds, and conditions of management and environment. Although US models are those used most commonly in Brazil to predict the DMI of dairy heifers, these models may lack the accuracy and the precision to predict the DMI under tropi-

---

Received March 27, 2015.
Accepted October 25, 2015.
[1] Corresponding author: andresoli@ufmt.br

cal conditions because of the differences between the Brazilian and US dairy cattle systems, environmental conditions, genetic background of the heifers, and the typical species and nutritional composition of the forages. Therefore, we hypothesized that empirical models developed for tropical conditions would be more accurate and precise than the currently used US models.

Thus, our objectives were (1) to develop models (linear and nonlinear) to predict the DMI in dairy heifers under tropical conditions with BW and ADG as inputs, and (2) to evaluate and compare the adequacy of the proposed models with the current US models (Quigley et al., 1986; NRC, 2001; Hoffman et al., 2008) using an independent data set.

MATERIALS AND METHODS

Data Set

The data set used in the current study was developed from 28 studies (95 treatment means; 596 heifers postweaning) published in journals from 1999 to 2014. All journals cited are not included in the list of predatory journals compiled by Beall (2015). The criteria adopted for inclusion in the data set were: (1) the experiment was conducted under tropical conditions; (2) the heifers were under different feeding management systems and levels of production; (3) the animals did not receive milk or milk replacer; (4) the estimation of pasture intake was based only on external and internal markers to determine the fecal output of DM; and (4) the descriptions of the animals (e.g., BW, ADG, and breed) and the experimental diets (e.g., ingredients and chemical composition) were adequate. All studies used individual animal measurements. We did not find pen-based intake studies.

Specifically, the data set was composed of the breeds *Bos taurus* × *Bos indicus* (78%) and *Bos taurus* (22%), which were fed either TMR (82%) or pasture-based diets (18%). The forages used for the TMR-fed heifers included sugarcane (*Saccharum officinarum*; 32.9%), corn (*Zea mays*) silage (19.7%), Bermudagrass hay (*Cynodon* spp.; 15.8%), elephant grass (*Pennisetum purpureum*, Schum.) silage (13.2%), sorghum silage (5.3%), a mixture of corn silage and sugarcane or elephant grass silage (10.6%), and a mixture of spineless cactus (*Opuntia ficus-indica* Mill.) and elephant grass silage (2.5%). The forages grazed by the pasture-fed heifers included brachiaria grass (*Brachiaria* spp.; 82.3%), mixture of pastures based on African stargrass (*Cynodon nlemfuensis*), ratana (*Ischaemum indicum*), and candelario (*Pennisetum purpureum*; 11.8%), and ryegrass (*Lolium multiflorum*, Lam.) plus oats (*Avena strygosa*, Schreb.; 5.9%).

The BW of the heifers was based only on measurements from nonfasting animals. Thus, in the studies that reported only fasting BW, the BW was estimated by dividing the fasting BW by 0.96 (NRC, 2000). The data set was classified by breed (*Bos taurus* × *Bos indicus* crossbreed and *Bos taurus*). For statistical analyses, the data set was randomly divided into 2 data subsets, with the first data subset (17 studies; 58 treatment means; Table 1 and Appendix 1) used to develop the models to predict the DMI and the second data subset (11 studies; 37 treatment means; Table 1 and Appendix 2) used to assess the adequacy of the newly developed DMI prediction models in a comparison with the 4 currently available models (Table 2). The complete data set is available in an Excel (Microsoft Corp., Redmond, WA) file in Supplementary Tables S1 and S2 (http://dx.doi.org/10.3168/jds.2015-9638).

Model Development

The linear and nonlinear models used to predict the DMI were adjusted with the inclusion of the metabolic BW (**$\mathbf{BW^{0.75}}$**), ADG, and breed (*Bos taurus* vs. *Bos taurus* × *Bos indicus*) as fixed effects and the study as a random effect. Because the data set was developed using observations from several studies in which different feeding systems, environmental conditions, and experimental methodologies were used, it was necessary to quantify the variance associated with the study and to predict the fixed effects adjusted for the study effect. Therefore, each study in the data set was treated as a random sample from the larger population of studies (St-Pierre, 2001; Sauvant et al., 2008).

All the parameter coefficients for the linear model were estimated using the linear mixed procedure (St-Pierre, 2001). The nonlinear mixed (i.e., NLMIXED) procedure (Littell et al., 2006) was used to fit the nonlinear models for the prediction of the DMI. The Gauss-Newton method was used for the convergence. The critical level of probability for a type I error was set at $\alpha = 0.05$. If the interactions breed × $BW^{0.75}$ and breed × ADG were not significant ($P > 0.05$), they were excluded from the models.

Model Evaluation

The adequacy of the 2 DMI predictive proposed models and of the current US models (Table 1) were assessed for precision and accuracy using the following approaches: graphic analysis, linear regression of the observed and the predicted values, coefficient of determination, mean square error of prediction (**MSEP**), root MSEP (**RMSEP**), and concordance correlation coefficient (**CCC**) analysis using the Model Evaluation