

Evaluation of BR-Goats and Sheep models for predicting dry matter intake in Pelibuey lambs

Evaluación de modelos BR-Caprinos y Ovinos para predecir consumo de materia seca en corderos Pelibuey

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ABSTRACT. This study evaluated four equations for predicting dry matter intake (DMI) in confined Pelibuey lambs under tropical conditions. The original dataset comprised 30 lambs (13.1 ± 2.8 kg body weight; 60 d of age); after applying the studentized residual criterion, 28 animals remained in the analysis. Performance was evaluated using regression analysis, root mean squared error of prediction (RMSEP), concordance correlation coefficient (CCC), modeling efficiency (MEF), and error decomposition. Equation 1 had the lowest RMSEP (82.03 g/d) and highest MEF (0.71), although its intercept differed from zero. Equation 2 was the only model whose intercept and slope did not differ from zero and unity, respectively. Equations 3 and 4 showed proportional bias. These results indicate that model performance depends on the evaluation criterion and that additional independent evaluations are required before these equations can be routinely applied.

Keywords: External validation, hair sheep, precision feeding, tropical conditions, nutritional models.

RESUMEN. Este estudio evaluó cuatro ecuaciones para predecir el consumo de materia seca (CMS) en corderos Pelibuey confinados bajo condiciones tropicales. El conjunto original incluyó 30 corderos (13.1 ± 2.8 kg de peso vivo; 60 d de edad); después de aplicar el criterio de residuos studentizados, 28 animales permanecieron en el análisis. El desempeño se evaluó mediante regresión, raíz del error cuadrático medio de predicción (RECMF), coeficiente de correlación de concordancia (CCC), eficiencia del modelo (MEF) y descomposición del error. La Ecuación 1 presentó la menor RECMF (82.03 g/d) y la mayor MEF (0.71), aunque su intercepto difirió de cero. La Ecuación 2 fue la única cuyo intercepto y pendiente no difirieron de cero y uno, respectivamente. Las Ecuaciones 3 y 4 mostraron sesgo proporcional. Los resultados indican que el desempeño depende del criterio utilizado y que se requieren evaluaciones independientes antes de su aplicación rutinaria.

Palabras clave: Validación externa, ovinos de pelo, alimentación de precisión, condiciones tropicales, modelos nutricionales.

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INTRODUCTION

Accurate prediction of dry matter intake (DMI) is essential for formulating diets, managing feeding programs, and assessing animal performance. However, the performance of prediction equations may decline when they are applied to populations or production conditions that differ from those used for their development. Genotype, diet, management, physiological status, and environmental conditions can influence voluntary feed intake and, consequently, model performance (Bateki and Dickhoefer 2019; Gurgel *et al.* 2021; Azevêdo *et al.* 2024). Therefore, equations should be independently evaluated before being applied outside their original development domain.

Several nutritional systems provide equations for predicting DMI in small ruminants, including the National Research Council (NRC 2007), Small Ruminant Nutrition System (Cannas *et al.* 2004), Agricultural and Food Research Council (AFRC 1993), Institut National de la Recherche Agronomique (INRA 2007), and Commonwealth Scientific and Industrial Research Organisation (CSIRO 2007). Many equations incorporated into these international systems were developed predominantly from wool sheep or temperate production conditions. More recently, the BR-Goats and Sheep system compiled and proposed equations based on data obtained from goats and sheep raised under Brazilian conditions (Azevêdo *et al.* 2024), representing an important advance for small-ruminant nutrition in tropical regions.

Nevertheless, the transferability of the equations evaluated by Azevêdo *et al.* (2024) to Pelibuey lambs raised under tropical confinement has not been independently assessed. Such evaluation is necessary because predictive performance within the development population does not ensure equivalent performance in a different genotype or production environment. Therefore, this study aimed to evaluate the adequacy of four DMI prediction equations using an independent dataset of confined Pelibuey lambs raised under tropical conditions.

MATERIALS AND METHODS

Animals, management, and experimental design

An independent dataset comprising observations from 30 Pelibuey lambs was used. At the beginning of the experiment, the lambs had a mean body weight (BW) of 13.1 ± 2.8 kg and a mean age of 60 days. Animals were assigned to three dietary treatments, with 10 lambs per treatment, and housed for 49 days in individual elevated pens equipped with a roof, feeder, and drinker.

The evaluated diets were Starter (I), Weaning and Growing (DyD), and a 50:50 mixture of Starter and Weaning and Growing feeds (I + DyD) (Hernández-de los Santos *et al.* 2022). Lambs were fed *ad libitum* twice daily. Feed allowance was adjusted weekly to maintain refusals at approximately 10% of the amount offered. Body weight was recorded at the beginning of the experiment and every 14 days thereafter using a digital scale. The BW entered into the prediction equations was calculated as the arithmetic mean of the initial and final BW. Total weight gain was calculated as final BW minus initial BW, and average daily gain (ADG) was calculated by dividing total weight gain by the 49 days experimental period.

The amounts of feed offered and refused were recorded for each animal. Bothlik the 49-d experimental period by averaging daily values. Feed offered and refusals were converted to a DM basis using their respective laboratory-determined DM concentrations. Individual observed DMI was then calculated as the mean daily difference between the amounts of DM offered and refused.

Externally studentized residuals were examined to identify potentially atypical observations. Two animals were excluded because their absolute externally studentized residuals exceeded the predefined threshold of 2.5. The same analytical dataset was used to evaluate all equations. Consequently, although the original dataset comprised 30 lambs, the final analytical dataset included 28 animals.

Ethical statement and study location

The original experiment was conducted from August to September 2019 at the Centro de Integración Ovina del Sureste (CIOS), located in Centro Municipality, Tabasco, Mexico (17°47'13.0" N, 92°57'49.3" W; 10 m above sea level). The region has a humid tropical climate, with minimum and maximum temperatures of approximately 18 and 36 °C, respectively, and a mean annual rainfall of 2,299 mm (Hernández-de los Santos *et al.* 2022).

Formal approval by an institutional animal ethics committee was not required at the time the experiment was conducted in 2019. Nevertheless, all procedures involving animals were conducted in accordance with the animal-care and research guidelines in effect at the Universidad Juárez Autónoma de Tabasco. The experiment formed part of institutional research project PFI: UJAT-DACA-2015-IA-02.

Chemical analyses

Feed samples were dried at 60 °C for 48 h to determine dry matter (DM) and ground using a mill fitted with a 1-mm screen prior to chemical analysis. Nitrogen content was determined using the Kjeldahl method (AOAC 1980). Organic matter (OM) was determined by incineration in a muffle furnace at 600 °C for 6 h, while neutral detergent fiber (NDF) and acid detergent fiber (ADF) were analyzed according to Van Soest *et al.* (1991). The chemical composition of the experimental diets is presented in Table 1.

Table 1. Proximate composition of the experimental diets.

Treatment	DM	Protein	NDF	ADF	Ash	OM
I	93.30	20.89	37.25	6.69	7.62	92.38
DyD	90.83	16.84	29.85	5.96	7.30	92.70
I+DyD	91.88	19.47	35.82	6.10	7.54	92.46

DM = dry matter; NDF = neutral detergent fiber; ADF = acid detergent fiber; OM = organic matter.

Statistical analysis and model evaluation

Descriptive statistics were calculated using the PROC SUMMARY procedure of SAS 9.0.2 (SAS Institute Inc., Cary, NC, USA). The following equations were evaluated:

$$\text{Equation 1: } DMI \text{ (kg/d)} = 0.311 + 0.0197 \times BW + 0.682 \times ADG_{kg}$$

(Cabral *et al.* 2008)

Equation 2: $DMI (g/d) = 156.17 + 28.29 \times BW + 0.87 \times ADG_g$

(Vieira *et al.* 2013)

Equation 3: $DMI (g/d) = 50.5773 + 1.4423 \times ADG_g + 28.4406 \times BW$

(Oliveira *et al.* 2020)

Equation 4: $DMI (g/d) = -145.68 + 77.3709 \times BW^{0.75} + 1.3985 \times ADG_g$

(BR-Goats and Sheep; Azevêdo *et al.* 2024)

where BW is body weight (kg), calculated as the arithmetic mean of the initial and final body weights; $BW^{0.75}$ is metabolic body weight ($kg^{0.75}$); ADG_{kg} is average daily gain expressed in kg/d; and ADG_g is average daily gain expressed in g/d. Predictions generated by Equation 1 were converted from kg/d to g/d before model evaluation.

Model adequacy was evaluated by regressing observed DMI (Y) on predicted DMI (X):

$$Y_i = \beta_0 + \beta_1 X_i + \varepsilon_i$$

where Y_i is the observed DMI, X_i is the corresponding predicted DMI, β_0 is the regression intercept, β_1 is the regression slope, and ε_i is the residual error. Constant and proportional biases were assessed by testing the null hypotheses $H_0: \beta_0 = 0$ and $H_0: \beta_1 = 1$, respectively. Failure to reject both null hypotheses was interpreted as no statistical evidence of constant or proportional bias.

Predictive performance was evaluated using the coefficient of determination (r^2), mean squared error of prediction (MSEP), root mean squared error of prediction (RMSEP), RMSEP expressed as a percentage of mean observed DMI, concordance correlation coefficient (CCC), bias correction factor (Cb), Pearson correlation coefficient (ρ), modeling efficiency (MEF), and coefficient of model determination (CD). The MSEP was decomposed into mean bias, systematic bias, and random error according to Tedeschi (2006). Mean bias represents the difference between the mean observed and predicted values, systematic bias represents deviation of the fitted regression slope from unity, and random error represents variation not explained by the fitted relationship.

The CCC was used to quantify agreement between observed and predicted values and was decomposed into ρ , representing precision, and Cb, representing departure from the line of identity (Lin 1989; Tedeschi 2006). Values closer to 1 indicate greater agreement, although the metrics were interpreted jointly rather than according to arbitrary classification thresholds. An MEF value of 1 indicates perfect prediction, a value of 0 indicates that the model performs similarly to the mean observed value, and negative values indicate poorer performance than the observed mean. A CD value close to 1 indicates adequate representation of the observed variability; values greater or lower than 1 indicate under- or overestimation of that variability, respectively. Statistical significance was declared at $P < 0.05$. Model evaluation statistics were calculated using the Model Evaluation System described by Tedeschi (2006).

RESULTS AND DISCUSSION

Table 2 summarizes the final dataset used to evaluate the four DMI prediction equations. The 28 Pelibuey lambs included in the analysis had a mean BW of 17.68 ± 4.85 kg, ranging from 5.80 to 25.50 kg, and a mean metabolic BW of 8.55 ± 1.86 kg^{0.75}. Mean observed DMI was 762.60 ± 155.00 g days, with values ranging from 472.69 to 1,050.50 g days. Average daily gain was 0.22 ± 0.06 kg days, equivalent to 222.38 ± 60.30 g days.

Table 2. Descriptive statistics of body weight, dry matter intake (DMI), and average daily gain (ADG) in confined Pelibuey lambs.

Variable	Description	Mean	SD	Minimum	Maximum	CV
ADG ¹	Average daily gain (kg days)	0.22	0.06	0.06	0.36	27.12
ADG ²	Average daily gain (g days)	222.38	60.30	63.50	356.10	27.12
BW	Body weight (kg)	17.68	4.85	5.80	25.50	27.46
BW ^{0.75}	Metabolic BW (kg)	8.55	1.86	3.74	11.35	21.73
DMI	Dry matter intake (g days)	762.60	155.00	472.69	1050.50	20.32

BW = body weight (kg); BW^{0.75} = metabolic BW (kg); ADG¹: average daily gain (kg days); ADG²: average daily gain (g days); SD = standard deviation and CV = coefficient of variation.

The intercept differed from zero for Equations 1 and 4 ($P = 0.018$ and 0.013 , respectively), indicating constant bias, but not for Equations 2 and 3 ($P = 0.615$ and 0.087 , respectively). The slope did not differ from unity for Equations 1 and 2 ($P = 0.058$ and 0.07 , respectively), whereas as slopes lower than unity were detected for Equations 3 and 4 ($P < 0.001$), indicating proportional bias (Table 3). Therefore, Equation 2 was the only model for which the intercept and slope did not differ from zero and unity, respectively. Predictive performance varied according to the evaluation criterion. Equation 1 had the lowest RMSEP (82.03 g día; 10.76% of mean observed DMI) and highest MEF (0.71), followed by Equation 4, with an RMSEP of 100.63 g days and an MEF of 0.56. Equation 3 had the highest RMSEP (132.41 g día; 17.36% of mean observed DMI), lowest MEF (0.24), and lowest CCC (0.76). The CCC values for Equations 1, 2, and 4 were 0.83, 0.79, and 0.84, respectively (Figure 1). Mean bias accounted for most of the MSE of Equations 2, 3, and 4, representing 62.27%, 70.91%, and 40.97%, respectively. In contrast, random error was the largest component of the MSE of Equation 1, accounting for 56.76%, followed by mean bias (34.71%) and systematic bias (8.52%). These results indicate differences among equations in overall prediction error, agreement, calibration, and representation of observed variability.

The present study showed that the predictive performance of the four DMI equations was model- and criterion-dependent when evaluated in confined Pelibuey lambs under tropical conditions. Equation 1 had the lowest RMSEP and highest MEF, indicating the lowest overall prediction error among the evaluated equations. However, its intercept differed from zero, providing evidence of constant bias. Equation 2 was the only model for which the intercept and slope did not differ from zero and unity, respectively, although its RMSEP and MEF were less favorable than those of Equation 1. Equations 3 and 4 had slopes lower than unity, indicating proportional bias. These findings demonstrate that model adequacy cannot be determined from a single statistic because

overall prediction error, concordance, calibration, and modeling efficiency describe different aspects of predictive performance (Tedeschi 2006).

Table 3. Predictive performance of dry matter intake equations evaluated in confined Pelibuey lambs (n = 28).

Variable	Observed	Equation 1	Equation 2	Equation 3	Equation 4
Mean	762.60	810.93	849.76	874.10	827.01
SD	154.99	117.26	164.15	188.46	190.04
Minimum	472.69	584.80	525.05	474.92	432.58
Maximum	1050.50	1000.49	1116.29	1171.58	1116.04
r ²		0.83	0.82	0.86	0.84
q		0.91	0.91	0.93	0.92
CCC		0.83	0.79	0.76	0.84
Cb		0.90	0.86	0.81	0.91
MEF		0.71	0.47	0.24	0.56
CD		1.48	0.68	0.49	0.59
Regression analysis					
Intercept (β_0)					
Estimate		-216.99	34.20	95.00	145.00
SE		86.22	67.16	53.46	54.52
P-value ($\beta_0 = 0$)		0.018	0.615	0.087	0.013
Slope (β_1)					
Estimate		1.21	0.85	0.76	0.75
SE		0.105	0.07	0.06	0.06
P-value ($\beta_1 = 1$)		0.058	0.07	0.001	0.001
MSEP source, % MSEP					
Mean bias		34.71	62.27	70.91	40.97
Systematic bias		8.52	4.34	10.90	22.05
Random error		56.76	33.39	18.18	36.98
Root MSEP					
Estimate		82.03	110.46	132.41	100.63
% of the mean		10.76	14.48	17.36	13.19

Observed = evaluation dataset; CCC = concordance correlation coefficient; q = Pearson correlation coefficient, representing precision; Cb = bias correction factor, representing accuracy; MEF = modeling efficiency; CD = coefficient of model determination; SD = standard deviation; MSEP = mean squared error of prediction; RMSEP = root mean squared error of prediction; SE = standard error. The *P*-values for the intercept and slope correspond to the null hypotheses $H_0: \beta_0 = 0$ and $H_0: \beta_1 = 1$, respectively.

Azevêdo *et al.* (2024) evaluated the same four equations using an independent dataset derived from experiments conducted in Brazil. In that evaluation, Equation 1, originally proposed by Cabral *et al.* (2008), showed evidence of both constant and proportional bias because the hypotheses that the intercept was zero and the slope was unity were rejected. In contrast, Equations 2, 3, and 4 showed no evidence of constant or proportional bias under the conditions evaluated by Azevêdo *et al.* (2024). The present results differed: Equation 1 showed constant but not proportional bias;

Equation 2 showed no statistical evidence of either type of bias; Equation 3 showed proportional but not constant bias; and Equation 4 showed both constant and proportional bias. These differences indicate that an equation showing adequate calibration in one evaluation population may not retain the same calibration when transferred to another genotype, body-weight range, diet, or management condition.

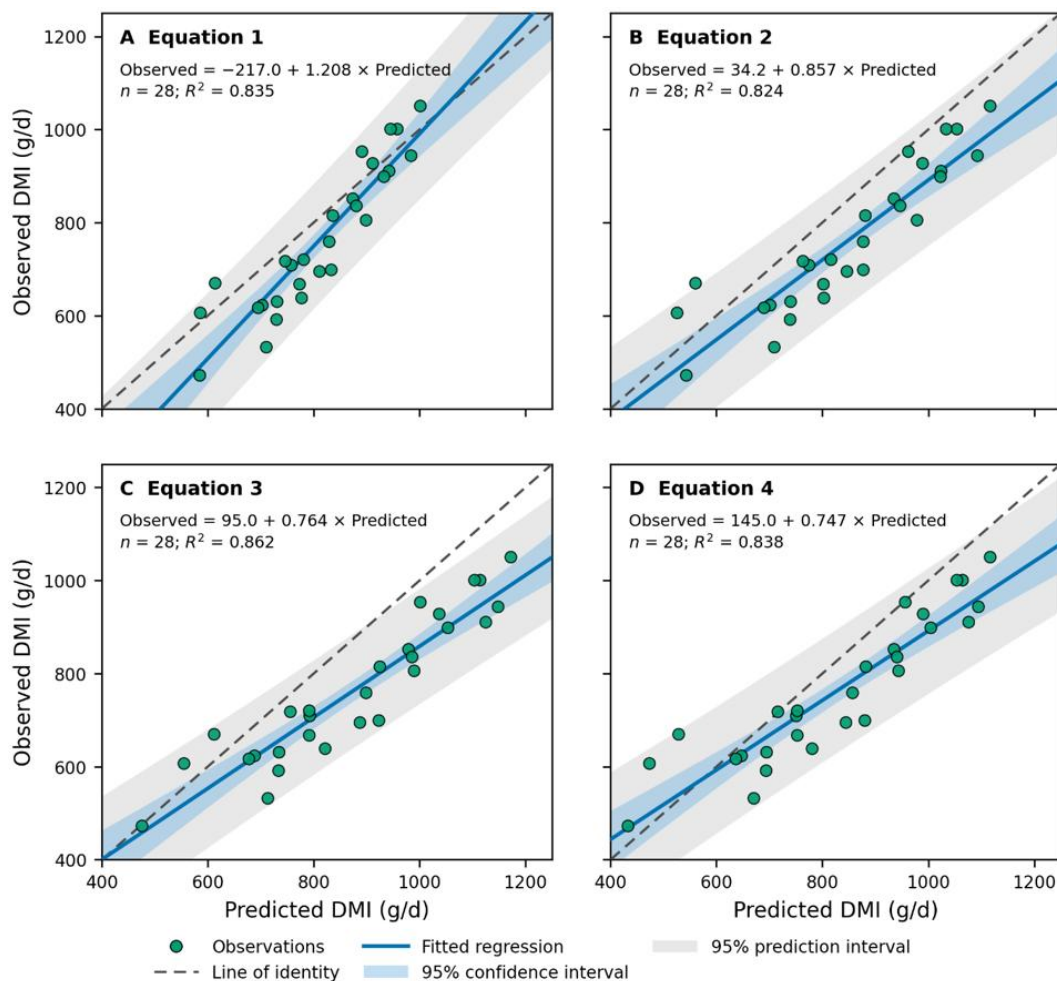


Figure 1. Relationship between observed and predicted dry matter intake (DMI) for four equations evaluated in confined Pelibuey lambs. Green circles represent individual observations ($n = 28$). The gray dashed line represents the line of identity ($y = x$), and the solid blue line represents the fitted regression of observed on predicted DMI. Blue shading indicates the 95% confidence interval of the fitted regression, whereas gray shading indicates the 95% prediction interval.

The regression results also differed between studies. Azevêdo *et al.* (2024) found evidence of constant and proportional bias for Equation 1, whereas Equations 2, 3, and 4 showed no significant departures from a zero intercept or unit slope. In the present evaluation, Equation 1 showed constant but not proportional bias, Equation 2 showed no statistical evidence of either type of bias, Equation 3 showed proportional but not constant bias, and Equation 4 showed both constant and proportional bias. These differences demonstrate that calibration may change when an equation is transferred to animals differing in genotype, body-weight range, diet, or management conditions.

In the evaluation conducted by Azevêdo *et al.* (2024), mean observed DMI was 1,047.36 g/d, and Equations 3 and 4 showed the most favorable performance among the models examined. Equation 4 had a slightly lower RMSEP than Equation 3 (166.77 vs. 168.26 g/d) and a marginally higher r^2 (0.487 vs. 0.475). However, this ranking was not reproduced in the present study. In Pelibuey lambs, Equation 1 had the lowest RMSEP and highest MEF, whereas Equation 3 had the highest RMSEP, lowest MEF, and lowest CCC. Therefore, the favorable performance of Equations 3 and 4 reported by Azevêdo *et al.* (2024) should be interpreted as specific to their evaluation dataset rather than as evidence of general superiority.

All four equations showed strong linear associations between observed and predicted DMI, as indicated by r^2 values ranging from 0.82 to 0.86 and Pearson correlation coefficients ranging from 0.91 to 0.93. Nevertheless, a strong correlation does not necessarily indicate accurate prediction or agreement with the line of identity. The CCC ranged from 0.76 to 0.84, while Cb ranged from 0.81 to 0.91, demonstrating differences in agreement and accuracy among equations. These metrics should be interpreted jointly with RMSEP, MEF, regression parameters, and MSE decomposition because each describes a different aspect of model performance (Tedeschi 2006).

The decomposition of MSE provided additional information about the origin of prediction errors. Random error was the largest component for Equation 1, accounting for 56.76% of MSE, whereas mean bias predominated for Equations 2, 3, and 4, accounting for 62.27, 70.91, and 40.97% of MSE, respectively. The predominance of mean bias indicates differences between the average observed and predicted DMI. For Equation 2, this numerical contribution should not be interpreted as contradicting the nonsignificant intercept test. MSE decomposition quantifies the contribution of each error source, whereas the intercept test evaluates whether the estimated deviation differs statistically from zero, which is influenced by sample size and residual variability.

Equation 4, developed within the BR-Goats and Sheep system, included metabolic BW and ADG but did not provide the most favorable performance in the present dataset. Its RMSEP was lower than those of Equations 2 and 3 but higher than that of Equation 1, and both its intercept and slope differed from their expected values. Thus, incorporating biologically relevant predictors does not ensure adequate transferability to every evaluation population. The results complement those of Gurgel *et al.* (2021), who reported limitations in the application of available DMI equations to meat sheep managed on tropical pastures. Although their production conditions differed from the confinement system evaluated here, both studies demonstrate the importance of assessing prediction equations within the population and management conditions in which they are intended to be used.

Among the evaluated equations, Equation 1 showed the most favorable overall error-based performance, based on its lower RMSEP and higher MEF, but it exhibited constant bias. Equation 2 was the only model without statistical evidence of constant or proportional bias, although its RMSEP and MEF were less favorable than those of Equation 1. Consequently, no equation was superior according to every evaluation criterion. The original dataset comprised 30 lambs, but the final analysis included 28 animals after application of the predefined residual criterion. Although this independent dataset allows an initial external assessment, its limited size, narrow population, and restricted experimental conditions require cautious interpretation. Further evaluations using

larger independent populations, broader body-weight ranges, and different feeding systems are necessary before routine application of these equations in tropical hair sheep and precision-feeding programs.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

STATEMENT ON THE USE OF GENERATIVE ARTIFICIAL INTELLIGENCE TOOLS

During the revision of this manuscript, the authors used ChatGPT (OpenAI) for English-language editing and to improve the clarity, conciseness, and organization of the text. All AI-assisted content was reviewed and verified by the authors, who assume full responsibility for the accuracy and integrity of the manuscript.

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