



Prediction of enteric methane emission from buffaloes using statistical models



Amlan Kumar Patra*

Department of Animal Nutrition, West Bengal University of Animal and Fishery Sciences, 37 K. B. Sarani, Belgachia, Kolkata 700037, India

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ABSTRACT

Methane (CH₄) production from world buffalo population contributes a substantial share to the global greenhouse gas production by livestock. However, there is no model for predicting enteric CH₄ production in buffaloes, though there are several models developed for prediction of enteric CH₄ from cattle. Thus, the objective of this study was to develop linear and nonlinear statistical models to predict CH₄ production from dietary and animal characteristic variables. A database from 24 publications was constructed, which included 64 mean observations of CH₄ outputs measured on 394 buffaloes. Extant equations developed for cattle were also evaluated for suitability of those CH₄ prediction equations in buffaloes. The simple linear equations that predicted with high precision and accuracy were CH₄ (MJ/day) = 1.29_(±0.576) + 0.788_(±0.099) × dry matter (DM) intake (kg/day) [RMSPE = 19.4%, with 94% of mean square prediction error (MSPE) being random error; R² = 0.81] and CH₄ (MJ/day) = 0.135_(±0.767) + 1.717_(±0.233) × neutral detergent fiber (NDF) intake (kg/day) [RMSPE = 18.3%, with 99.7% of MSPE being random error; R² = 0.79]. Multiple regression equations that predicted CH₄ slightly better than simple prediction equations were CH₄ (MJ/day) = -0.436_(±0.665) + 0.678_(±0.184) × DM intake (kg/day) + 0.697_(±0.347) × NDF intake (kg/day) [RMSPE = 16.1%, with 99.9% of MSPE from random error; R² = 0.85] and CH₄ (MJ/day) = -0.819_(±0.801) + 0.690_(±0.432) × crude protein (CP) intake (kg/day) + 1.527_(±0.215) × NDF intake (kg/day) + 0.930_(±0.413) × non-fibrous carbohydrate (NFC) intake (kg/day) [RMSPE = 16.5%, with 99.7% of MSPE accounting random error; R² = 0.84]. Among the nonlinear equations developed, monomolecular model, CH₄ (MJ/day) = 39.99_(±17.23) × {1 - exp(-0.0276_(±0.0132) × DM intake (kg/day))} [RMSPE = 19.1%, with 99.9% of MSPE accounting random error; R² = 0.80], performed better than other nonlinear models, but the predictability and robustness of the equation did not improve compared with the linear models. Extant equations overestimated the methane production, and had low accuracy and precision. The equations developed in this study would be useful for national inventory preparation to improve an estimation of methane production in buffaloes particularly for tropical feeding situations.

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1. Introduction

Greenhouse gas (GHG) emissions from livestock production system have emerged as great concerns in the recent decades owing to the contribution of a considerable share to the global anthropogenic GHG emissions (Opio et al., 2013). A life cycle analysis of GHG emissions assessed that livestock sectors and animal protein production contribute about 12–18% of total GHG (Steinfeld et al., 2006; Westhoek et al., 2011) accounting 9%, 35–40% and 65% of carbon dioxide, methane and nitrous oxide of global anthropogenic emissions, respectively (Steinfeld et al., 2006). Major share of methane emissions from livestock arises

from enteric fermentation in ruminants (Patra, 2012, 2014). Annually, an estimated 94.9 million tonnes of enteric methane was contributed by different livestock species of the world in 2010 (Patra, 2014). Although enteric methane by cattle largely represented an estimated 74% of total enteric methane, buffalo population was the second most contributor of enteric methane emissions accounting about 11.3% of total enteric methane, followed by sheep (6.4%), goats (4.9%) and other animals (Patra, 2014). Besides, the annual growth rate of enteric methane from buffaloes was 1.57% after goats (2.0%), while growth rate of enteric methane emission from cattle was 0.87% (Patra, 2014). Despite a significant share of enteric methane contributed by buffaloes, methane production from this animal species has not been assessed adequately.

Several statistical and dynamic mechanistic models had been recommended for prediction of methane from cattle and sheep

* Tel.: +91 33 25569234.

E-mail address: patra_amlan@yahoo.com (A.K. Patra).

(Kriss, 1930; Axelsson, 1949; Blaxter and Clapperton, 1965; Mills et al., 2003; Ellis et al., 2007; Kebreab et al., 2008; Ramin and Huhtanen, 2013). Statistical models predict methane production from nutrient intake directly, while dynamic mechanistic models estimate methane emission using mathematical descriptions of rumen fermentation biochemistry (Kebreab et al., 2006; Ellis et al., 2007). These models have been quite useful to predict enteric methane emission from cattle without undertaking extensive and costly experiments. Although numerous statistical models were developed and evaluated from database of dairy and beef cattle, and sheep feeding studies, development of models for predicting enteric methane production in buffaloes has not received attention so far. The models developed for cattle may not have precise predictive ability of methane production for buffaloes. Therefore, the objective of this study were to develop statistical models for prediction of enteric methane production in buffaloes using commonly measured dietary variables, and to validate different existing methane prediction models for cattle using a database of buffaloes.

2. Materials and methods

2.1. Construction of database

A database was compiled from the studies published in journals and conference proceedings for this meta-analytic approach. Criteria for inclusion of studies in the database were that the studies provided an adequate description of the animals, chemical composition and intake of the diet, and in vivo methane production in buffaloes measured using either respiration chamber or sulphur hexafluoride tracer technique. Overall, 24 publications (Barman et al., 2001; Garg et al., 2012; Haque et al., 2004; Kannan and Garg, 2009; Kannan et al., 2010; Khan et al., 1988; Lal et al., 1987; Malik and Singhal, 2009; Mehra et al., 2006; Mohini and Singh, 2001, 2003, 2008; Murarilal et al., 1999; Pattanaik et al., 1996; Prakash et al., 2000; Prusty et al., 2013; Sahoo et al., 1995; Sakthivel, 2012; Santra et al., 1994; Saraswat et al., 2001; Singhal et al., 2006; Tiwari et al., 2000; Turnbull et al., 2000; Varma et al., 2012) that reported data on animal characteristics, composition of diets, methane production, intake and digestibility of nutrients fulfilled the criteria for inclusion in this database. All the studies in these publications were conducted in India as no publication that could fulfill the inclusion criteria was available from other countries to the best of knowledge of the author. This is to mention that most of the buffalo population is centered in South-Asia, and other tropical countries. Thus, dietary and animal characteristics of other buffalo-rearing countries would adequately be similar to this database. There were a total of 64 treatment means obtained from 394 observations from buffaloes. However, treatments ($n=6$) containing feed additives that have antimethogenic properties were removed before statistical analysis.

The investigated dietary and animal factors (independent variables) were body weight (BW), intake (dry matter (DM), individual nutrients, gross energy (GE) and metabolizable energy (ME)) and nutrient composition of diets that were used for regression equation development. Since all variables were not available for all studies in the data set, the number of observations used for regression analyses varied between dietary and response variables depending on the regressor variables available. Data reported in differing units of measure were transformed to the same units. Some records were incomplete or not reported uniformly, which necessitated the calculations from the reported data. Whenever possible, missing chemical composition of the diets was calculated from book values of ingredients (Feedipedia, 2013) or studies included in this dataset with similar ingredients. When a study did not report all possible outcomes and it was not

possible to calculate from the reported data, missing variables were considered as missing data.

2.2. Statistical analysis

2.2.1. Linear model

Statistical analysis procedure used for prediction of methane production from this database has been described elsewhere (Patra, 2010). In brief, all statistical computations were carried out using the PROC MIXED, PROC REG and PROC CORR procedures of the SAS software system. Data were analyzed according to St-Pierre (2001) taking into account the random effect of the study because studies represented random samples of larger population of studies, using PROC MIXED (SAS, 2001) with the following model:

$$Y_{ij} = B_0 + B_1X_{ij} + B_2X_{ij}^2 + s_i + b_iX_{ij} + e_{ij}$$

where:

Y_{ij} = the expected outcome for the dependent variable Y observed at level j of the continuous variable X in the study i .

B_0 = the overall intercept across all studies (fixed effect).

B_1 and B_2 = the overall linear and quadratic regressing coefficient of Y on X , respectively, across all studies (fixed effect).

X_{ij} = the value j of the variable X in study i .

s_i = the random effect of study i .

b_i = the random effect of study i on the regression coefficient of Y on X in study i , and,

e_{ij} = the unexplained residual error.

However, squared term of predictors were not significant ($P > 0.10$) for any equations, and they were removed from the final models. Observed methane production was weighted by the number of animals in each study to take into consideration of unequal variance among studies. The slopes and intercepts by study were included as random effects, and an unstructured variance-covariance matrix (type = un) or a variance component (type = vc) of variance-covariance structure was performed at the random part of the model (St-Pierre, 2001). If random covariance or random slope, they were removed from the model. All significant predictors ($P < 0.10$) of methane outputs and two-way interactions were further used to develop multiple regression equations employing the backward elimination multiple regression procedure following the algorithm reported by Oldick et al. (1999) and Patra (2009). To limit overparameterization of the models, a variance inflation factor less than 100 for every continuous independent variable tested was assumed, as suggested by Oldick et al. (1999). The best-fit equations of multiple regression equations that further improved the relationship obtained from linear regression are presented.

2.2.2. Nonlinear models

Since DM intake as sole independent variable predicted methane emission with highest degree of determination in the linear model, DM intake was used as a determinant for development of non-linear relationships between DM intake and methane outputs, if prediction could be further improved. These were relationships exhibiting diminishing returns (monomolecular), sigmoidal (Gompertz) and exponential behaviours. The PROC NL MIXED of SAS was used to parameterize the non-linear functions with a little modification of the equation used by Schulin-Zeuthen et al. (2007) and the exponential model in the following forms:

$$\text{Monomolecular : } Y = a - (a + b) \times \exp(-c \times x)$$

$$\text{Gompertz : } Y = b \times \exp\left(\frac{(1 - \exp(-c \times x)) \times \ln(a + 2b)}{b}\right) - 2b$$

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