Prediction of enteric methane production, yield and intensity of beef cattle using an intercontinental database

Article

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Table S1. Variable summary statistics of Brazilian higher-forage (BRZ-HF; data associated with diets containing ≥ 25% forage), all growing and higher-forage growing cattle entries of the GLOBAL NETWORK beef cattle database.

	BRZ-HF (*n* = 104)				All growing (*n* = 488)				Higher-forage growing (*n* = 373)			
Item*	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
DMI (kg d^{-1})	9.55	5.38	17.5	1.88	9.50	2.47	17.4	2.22	9.16	2.47	17.4	2.27
GEI (MJ d^{-1})	168	92.6	300	32.4	176	44	317	43.6	166	43.8	317	46.3
Diet composition (% of DM)												
CP	14.6	10.0	18.1	2.07	14.1	6.19	19.2	2.27	14.0	6.19	19.2	2.45
EE	2.87	2.12	3.64	0.410	3.43	0.372	7.02	1.36	3.17	0.372	7.02	1.16
Ash	6.31	3.50	9.10	1.89	6.09	3.50	11.4	2.01	6.48	3.50	11.4	2.04
NDF	32.1	17.2	45.9	6.56	35.8	17.2	73.9	11.9	39.2	17.2	73.9	11.5
STA	NA	NA	NA	NA	30.9	5.90	44.4	10.4	25.7	5.90	39.2	8.83
Forage proportion	45.8	27.0	70	12.5	52.2	8.00	100	29.9	65.3	27.0	100	21.1
ADG (kg d^{-1})	1.30	0.295	2.26	0.371	1.27	0.10	3.38	0.418	1.21	0.10	3.38	0.425
BW (kg)	398	228	491	70.7	526	133	768	147	510	133	768	142
Methane emissions												
CH_4 (g d^{-1})	162	91.8	232	29.2	188	40.9	372	67.9	197	40.9	372	71.3
CH_4/DMI (g kg^{-1})	17.4	9.83	29.8	3.92	19.5	8.16	35.1	5.58	21.3	9.93	35.1	5.18
CH_4/ADG (g kg^{-1})♪	4.75	3.31	5.79	0.388	4.98	3.31	6.68	0.522	5.08	3.31	6.68	0.528
Y_m (% of GEI)§	5.5	3.2	9.6	1.2	6.0	2.4	10.3	1.6	6.4	3.0	10.3	1.5

*DM = dry matter, DMI = dry matter intake, GEI = gross energy intake, CP = dietary crude protein, EE = dietary ether extract, Ash = dietary ash, NDF = dietary neutral detergent fiber, STA = dietary starch, ADG = average daily body weight gain, BW = body weight.

‡Min = minimum, Max = maximum, SD = standard deviation.

♪ ln transformed values.

§Methane conversion factor (%): energy of CH_4 as a proportion of GEI; the specific energy of CH_4 is 55.65 MJ kg^{-1}.

Table S2. Brazilian higher-forage data CH_4 emission (g d^{-1} $animal^{-1}$) prediction equations and model performance based on root mean square prediction error (RMSPE; % of mean), RMSPE-observations-standard-deviation-ratio (RSR), mean and slope bias (MB and SB; % of mean square prediction error), and concordance correlation coefficient (CCC).

Model development				Model performance						
Eq.	Category§	Prediction equation*	*n*†	(Sub)set‡	*p*ǂ	RMSPE, %	RSR	MB, %	SB, %	CCC
[48]	DMI_C, Global_C	104 (15) + 5.60 (1.50) × DMI	104	BRZ-HF	75	19.2	1.03	2.45	9.05	0.16
[49]	DMI+NDF_C	126 (26) + 5.58 (1.49) × DMI – 0.707 (0.652) × NDF	104	BRZ-HF	75	19.8	1.06	1.22	14.31	0.14
[50]	DMI+EE_C	150 (28) + 6.31 (1.52) × DMI – 18.2 (9.4) × EE	104	BRZ-HF	104	19.8	1.10	0.43	18.87	0.10
[51]	Diet_C, Animal_C	154 (18) + 6.00 (1.46) × DMI – 8.86 (2.25) × Ash	93	BRZ-HF	75	17.7	1.00	10.60	9.20	0.40
[52]	Animal_no_DMI_C	209 (19) – 1.11 (0.35) × For	104	BRZ-HF	75	21.8	1.21	0.71	32.87	-0.09
[53]	GLOBAL NETWORK Tier 2	[0.055 (0.002) × GEI] / 0.05565	104	BRZ-HF	75	23.6	1.27	0.06	44.28	0.29
[9]	IPCC Tier 2, 2006¶	(0.065 × GEI) / 0.05565	104	BRZ-HF♪	75	33.7	1.81	39.72	33.70	0.21

§ Category acronyms (*e.g.*, DMI_C) are explained in the 'Model development' subsection of the 'Methods and Materials' section. No DMI+STA_C and Animal_no_DMI_C equations available.

* Equations are presented with regression coefficient standard errors in parenthesis; GEI = gross energy intake (MJ d^{-1}), DMI = dry matter intake (kg d^{-1}), NDF = dietary neutral detergent fiber (% of DM), EE = dietary ether extract (% of DM), Ash = dietary Ash (% of DM), For = dietary forage (% of DM).

†*n* = number of observations used to fit model equations.

‡BRZ-HF = Brazilian data associated with a forage content ≥ 25%.

ǂ*p* = numbers of observations used for model evaluation.

¶IPCC = Intergovernmental Panel on Climate Change.

♪ Performance was evaluated, not cross-validated.

Table S3. All-data CH_4 yield (g [kg DMI]$^{-1}$) prediction equations for various categories and model performance across the data (sub)sets based on root mean square prediction error (RMSPE; % of mean), RMSPE-observations-standard-deviation-ratio (RSR), mean and slope bias (MB and SB; % of mean square prediction error), and concordance correlation coefficient (CCC).

Model development				Model performance						
Eq.	Category§	Prediction equation*	*n*†	(Sub)set‡	*p*ǂ	RMSPE, %	RSR	MB, %	SB, %	CCC
[54]	NDF_C	11.7 (0.9) + 0.230 (0.021) × NDF	1021	All-data	743	24.1	0.98	0.15	2.98	0.20
				Higher-forage	633	23.1	1.03	2.22	7.53	0.15
				Lower-forage	110	32.2	1.26	32.81	5.96	-0.03
[55]	STA_C	26.5 (0.9) – 0.192 (0.019) × STA	704	All-data	704	27.0	1.06	2.34	11.29	0.13
				Higher-forage	575	25.5	1.21	10.56	21.74	0.06
				Lower-forage	129	36.5	1.28	38.75	1.27	0.02
[56]	EE_C	23.6 (0.9) – 1.18 (0.23) × EE	754	All-data	743	25.0	1.01	1.52	2.81	0.07
				Higher-forage	633	23.1	1.03	0.00	6.16	0.02
				Lower-forage	110	39.2	1.54	51.38	7.08	0.03
[57]	Diet_no_DMI_C, Animal_no_DMI_C	15.1 (1.3) + 0.111 (0.011) × For – 0.681 (0.223) × EE + 0.178 (0.127) × Ash	743	All-data	743	23.9	0.97	2.89	6.84	0.35
				Higher-forage	633	23.6	1.05	3.21	12.31	0.22
				Lower-forage	110	25.9	1.02	1.16	4.68	-0.02
[58]	Global_no_DMI_C	9.44 (1.26) + 0.121 (0.008) × For + 0.278 (0.076) × CP	1021	All-data	743	23.8	0.96	1.38	7.92	0.37
				Higher-forage	633	23.5	1.05	1.51	13.59	0.23
				Lower-forage	110	25.3	0.99	0.69	0.46	0.06

§ Category acronyms (*e.g.*, NDF_C) are explained in the 'Model development' subsection of the 'Methods and Materials' section.

* Equations are presented with regression coefficient standard errors in parenthesis; NDF = dietary neutral detergent fiber (% of DM), STA = dietary starch (% of DM), EE = dietary ether extract (% of DM, Ash = dietary ash (% of DM), For = dietary forage (% of DM), CP = dietary crude protein (% of DM).

†*n* = number of observations used to fit model equations.

‡All-data = all data collected for analysis, Higher-forage = data associated with a forage content ≥ 25%, Lower-forage = data associated with a forage content ≤ 18%.

ǂ*p* = numbers of observations used for model evaluation.

Table S4. Higher-forage CH_4 yield (g [kg DMI]$^{-1}$) prediction equations for various categories and model performance using the higher-forage subset based on root mean square prediction error (RMSPE; % of mean), RMSPE-observations-standard-deviation-ratio (RSR), mean and slope bias (MB and SB; % of mean square prediction error), and concordance correlation coefficient (CCC).

Model development				Model performance						
Eq.	Category§	Prediction equation*	*n*†	(Sub)set‡	*p*ǂ	RMSPE, %	RSR	MB, %	SB, %	CCC
[59]	NDF_C	17.8 (1.0) + 0.0763 (0.0234) × NDF	882	Higher-forage	633	22.3	1.00	0.23	0.31	0.03
[60]	STA_C	23.2 (0.8) – 0.0512 (0.0206) × STA	575	Higher-forage	575	21.8	1.04	0.79	7.70	-0.04
[61]	EE_C	22.8 (1.0) – 0.767 (0.238) × EE	644	Higher-forage	633	22.9	1.03	0.63	4.44	-0.01
[62]	Diet_no_DMI_C, Animal_no_DMI_C, Global_no_DMI_C	17.3 (0.9) + 0.0565 (0.0115) × For	882	Higher-forage	633	22.0	0.98	0.06	0.46	0.10

§ Category acronyms (*e.g.*, NDF_C) are explained in the 'Model development' subsection of the 'Methods and Materials' section.

* Equations are presented with regression coefficient standard errors in parenthesis; NDF = dietary neutral detergent fiber (% of DM), STA = dietary starch (% of DM), EE = dietary ether extract (% of DM), Ash = dietary ash extract (% of DM), For = dietary forage (% of DM).

†*n* = number of observations used to fit model equations.

‡ Higher-forage = data associated with a forage content ≥ 25%.

ǂ*p* = numbers of observations used for model evaluation.

Table S5. All-data growing cattle data log transformed CH_4 intensity (g [kg ADG]$^{-1}$) prediction equations for various categories and model performance across the data (sub)sets based on root mean square prediction error (RMSPE; % of mean), RMSPE-observations-standard-deviation-ratio (RSR), mean and slope bias (MB and SB; % of mean square prediction error), and concordance correlation coefficient (CCC).

Model development				Model performance						
Eq.	Category§	Prediction equation*	*n*†	(Sub)set‡	*p*ǂ	RMSPE, %	RSR	MB, %	SB, %	CCC
[63]	DMI _C	4.72 (0.15) + 0.0189 (0.0127) × DMI	488	All-data	471	64.6	1.08	10.39	10.20	-0.03
				Higher-forage	356	65.5	1.13	19.20	7.70	-0.03
				Lower-forage	115	44.0	1.11	18.53	0.77	0.00
[64]	DMI+NDF_C	3.48 (0.20) + 0.0363 (0.0116) × DMI + 0.0292 (0.0028) × NDF	488	All-data	471	63.1	1.05	7.38	8.58	0.21
				Higher-forage	356	63.9	1.10	7.72	12.66	0.13
				Lower-forage	115	43.8	1.10	10.18	9.20	-0.04
[65]	DMI+STA_C	5.33 (0.17) + 0.0357 (0.0127) × DMI – 0.0252 (0.0022) × STA	323	All-data	323	56.8	1.08	13.08	5.18	0.15
				Higher-forage	218	57.1	1.23	17.24	17.31	-0.04
				Lower-forage	105	41.1	1.03	4.66	1.59	0.02
[66]	DMI+ EE_C	5.64 (0.26) + 0.0150 (0.0122) × DMI – 0.308 (0.060) × EE	288	All-data	288	62.9	1.42	0.11	52.01	0.16
				Higher-forage	197	55.7	1.31	2.01	41.15	0.15
				Lower-forage	91	83.8	2.18	3.29	77.39	0.12
[67]	Diet_C, Animal_C	4.01 (0.16) + 0.0313 (0.0114) × DMI + 0.0103 (0.0009) × For	488	All-data	471	59.6	0.99	13.94	0.00	0.23
				Higher-forage	356	59.9	1.03	12.56	0.17	0.13
				Lower-forage	115	47.7	1.20	33.34	0.24	0.03
[68]	Animal_no_DMI_C	4.32 (0.11) + 0.0100 (0.0009) × For	488	All-data	471	60.2	1.00	14.39	0.07	0.22
				Higher-forage	356	60.4	1.04	12.72	0.44	0.11
				Lower-forage	115	49.2	1.24	36.00	0.02	0.01
[69]	Global_C	3.79 (0.19) + 0.0102 (0.0009) × For + 0.00106 (0.00031) × BW	471	All-data	471	57.3	0.96	9.04	0.25	0.25
				Higher-forage	356	57.9	1.00	9.26	0.01	0.15
				Lower-forage	115	42.4	1.07	13.17	0.37	0.02

§ Category acronyms (*e.g.*, DMI_C) are explained in the 'Model development' subsection of the 'Methods and Materials' section.

* Equations are presented with regression coefficient standard errors in parenthesis; DMI = dry matter intake (kg d^{-1}), NDF = dietary neutral detergent fiber (% of DM), STA = dietary starch (% of DM), EE = dietary ether extract (% of DM), BW = body weight (kg), For = dietary forage (% of DM).

†*n* = number of observations used to fit model equations.

‡All-data = all growing cattle data, higher-forage = growing cattle data associated with a forage content ≥ 25%, lower-forage = growing cattle data associated with a forage content ≤ 18%.

ǂ*p* = numbers of observations used for model evaluation.

Table S6. Higher-forage growing cattle data log transformed CH_4 intensity (g [kg ADG]$^{-1}$) prediction equations for various categories and model performance using the higher-forage subset based on root mean square prediction error (RMSPE; % of mean), RMSPE-observations-standard-deviation-ratio (RSR), mean and slope bias (MB and SB; % of mean square prediction error), and concordance correlation coefficient (CCC). Model performance was evaluated using back-transformed values of CH_4 intensity.

Model development				Model performance						
Eq.	Category§	Prediction equation*	*n*†	(Sub)set‡	*p*ǂ	RMSPE, %	RSR	MB, %	SB, %	CCC
[70]	DMI _C	4.69 (0.17) + 0.0274 (0.0143) × DMI	373	Higher-forage	356	64.3	1.11	15.15	7.18	-0.03
[71]	DMI+NDF_C	4.15 (0.24) + 0.0290 (0.0141) × DMI + 0.0139 (0.0046) × NDF	373	Higher-forage	356	61.7	1.06	12.78	0.62	0.05
[72]	DMI+STA_C	5.44 (0.18) – $9.74 \cdot 10^{-3}$ ($15.08 \cdot 10^{-3}$) × DMI – $8.31 \cdot 10^{-3}$ ($3.11 \cdot 10^{-3}$) × STA	218	Higher-forage	218	52.8	1.14	12.51	20.50	-0.10
[73]	DMI+EE_C	5.11 (0.30) – 0.00120 (0.01422) × DMI – 0.0747 (0.0748) × EE	197	Higher-forage	197	47.2	1.11	8.94	12.58	-0.07
[74]	Diet_C	4.49 (0.16) + 0.0718 (0.0166) × Ash	362	Higher-forage	345	65.0	1.12	15.90	4.82	-0.01
[75]	Animal_C, Animal_no_DMI_ C	3.75 (0.22) + 0.0739 (0.0164) × Ash + $1.49 \cdot 10^{-3}$ ($0.35 \cdot 10^{-3}$) × BW	345	Higher-forage	345	63.3	1.09	9.63	6.62	0.01
[76]	Global_C	3.61 (0.27) + 0.0149 (0.0044) × NDF + $1.58 \cdot 10^{-3}$ ($0.34 \cdot 10^{-3}$) × BW	356	Higher-forage	356	59.5	1.03	7.96	0.62	0.09

§ Category acronyms (*e.g.*, DMI_C) are explained in the ‘Model development’ subsection of the ‘Methods and Materials’ section.

* Equations are presented with regression coefficient standard errors in parenthesis; DMI = dry matter intake (kg d^{-1}), NDF = dietary neutral detergent fiber (% of DM), STA = dietary starch (% of DM), EE = dietary ether extract (% of DM), For = dietary forage (% of DM), Ash = dietary Ash (% of DM), BW = body weight (kg).

†*n* = number of observations used to fit model equations.

‡ Higher-forage = growing cattle data associated with a forage content ≥ 25%.

ǂ*p* = numbers of observations used for model evaluation.

Figure S1. Observed *vs*. predicted plots for Brazilian higher-forage cattle methane emission (g d^{-1}) prediction equations at different categories, *viz.*, dry matter intake (DMI_C), dry matter intake and neutral detergent fiber (DMI+NDF_C), dry matter intake and ether extract (DMI+EE_C), dietary (Diet_C), animal without DMI (Animal_no_DMI_C), GLOBAL NETWORK Tier 2, and IPCC Tier 2 (2006). The gray and black solid lines represent the fitted regression line for the relationship between observed and predicted values and the identity line ($y = x$), respectively.

Figure S2. Observed *vs*. predicted plots for higher-forage methane yield (g $[\text{kg DMI}]^{-1}$) prediction equations at different categories, *viz*., neutral detergent fiber (NDF_C), starch (STA_C), ether extract (EE_C), dietary composition (Diet_no_DMI_C) and global without DMI (Global_no_DMI_C). The gray and black solid lines represent the fitted regression line for the relationship between observed and predicted values, and the identity line ($y = x$), respectively.

Figure S3. Observed *vs*. predicted plots for all-data cattle methane yield (g $[\text{kg DMI}]^{-1}$) prediction equations at different categories, *viz.*, neutral detergent fiber (NDF_C), starch (STA_C), ether extract (EE_C) and dietary composition (Diet_no_DMI_C). The gray and black solid lines represent the fitted regression line for the relationship between observed and predicted values and the identity line ($y = x$), respectively.

Figure S4. Observed *vs*. predicted plots for all growing cattle data log transformed methane intensity (g $[\text{kg ADG}]^{-1}$) prediction equations at different categories, *viz.*, dry matter intake (DMI_C), dry matter intake and neutral detergent fiber (DMI+NDF_C), dry matter intake and starch (DMI+STA_C), dry matter intake and ether extract (DMI+EE_C), dietary (Diet_C), and animal without DMI (Animal_no_DMI_C) and global (Global_C). The gray and black solid lines represent the fitted regression line for the relationship between observed and predicted values, and the identity line ($y = x$), respectively.

Figure S5. Observed *vs*. predicted plots for higher-forage growing cattle data log transformed methane intensity (g $[\text{kg ADG}]^{-1}$) prediction equations at different categories, *viz.*, dry matter intake (DMI_C), dry matter intake and neutral detergent fiber (DMI+NDF_C), dry matter intake and starch (DMI+STA_C), dry matter intake and ether extract (DMI+EE_C), dietary (Diet_C), animal without DMI (Animal_no_DMI_C), and global (Global_C). The gray and black solid lines represent the fitted regression line for the relationship between observed and predicted values and the identity line ($y = x$), respectively.