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Global beef cattle methane emissions: yield prediction by cluster and meta-analyses

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Abstract. Methane yield values (MY; g methane/kg dry-matter intake) in beef cattle reported in the global literature (expanded MitiGate database of methane-mitigation studies) were analysed by cluster and meta-analyses. The Ward and k means cluster analyses included accounting for the categorical effects of methane measurement method, cattle breed type, country or region of study, age and sex of cattle, and proportion of grain in the diet and the standardised continuous variables of number of animals, liveweight and MY. After removal of data from outlier studies, meta-analyses were conducted on subsets of data to produce prediction equations for MY. Removing outliers with absolute studentised residual values of >1, followed by meta-analysis of data accounting for categorical effects, is recommended as a method for predicting MY. The large differences among some countries in MY values were significant but difficult to interpret. On the basis of the datasets available, a single, global MY or percentage of gross energy in feed converted to methane (Y_m) value is not appropriate for use in Intergovernmental Panel on Climate Change (IPCC) greenhouse accounting methods around the world. Therefore, ideally country-specific MY values should be used in each country's accounts (i.e. an IPCC Tier 2 or 3 approach) from data generated within that country.

Additional keywords: greenhouse accounting, methane yield, outliers.

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Introduction

Robust estimates of daily methane production (MP, g) and methane yield (MY, MP/kg daily dry-matter intake (DMI)) are needed for the calculation of methane emissions for national greenhouse gas (GHG) inventory reporting (UNFCCC 2015). Veneman *et al*. (2016) recently described their online database (MitiGate) of MY metadata collated from international sheep and cattle methane-mitigation studies. They suggested that the database could be continually updated with new MP and MY data by research workers. MitiGate currently contains data from

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412 sheep, beef and dairy cattle publications. The eight largest published beef MY datasets with all data needed for meta-analyses are from Herd *et al*. (2014), Richmond *et al*. (2015), Rooke *et al*. (2014), McGinn *et al*. (2009), Eugène *et al*. (2011), Fitzsimons *et al*. (2013), Boadi *et al*. (2004) and Velazco *et al*. (2014). Most of these datasets were missing from the MitiGate database at the time of our study, but were included in the meta-analysis presented in the current paper.

Escobar-Bahamondes *et al*. (2017) recently evaluated MP prediction equations from five studies (Ellis *et al*. 2007, 2009; Yan *et al*. 2009; Ricci *et al*. 2013; Moraes *et al*. 2014). Only Ricci *et al*. (2013) and Yan *et al*. (2009) are included in MitiGate and they are not beef cattle studies. Escobar-Bahamondes *et al*. (2017) noted that the data from Ellis *et al*. (2009); Yan *et al*. (2009) and Ricci *et al*. (2013) that they used were not available in the published literature.

No guidance is given on the MitiGate website for the choice of data to analyse. Within some subsets of data, the results of particular studies can become outliers and should, therefore, be excluded. There are different approaches available to determine outliers. Ungerfeld *et al*. (2007) identified outliers by removing data one by one, using an absolute studentised residual value over 2 standard deviations, or a leverage value over $2k/n$ (where k = number of independent variables and n = number of studies) or Cook's distance over 90%. Boval *et al*. (2015) removed outliers that were greater than an absolute value of 3 of normalised residuals. Escobar-Bahamondes *et al*. (2016) identified and excluded outliers by using Mahalanobis distance calculated from various dietary components, liveweight (LW), DMI and MP.

Diaz *et al*. (2013) used a cluster analysis approach to allow the formation of groups of results of similar studies before conducting a meta-analysis of genetic parameters. The *k*-means approach to clustering is an iterative fitting process to form a user-specified number of clusters. The *k*-means method first selects a set of n points called cluster seeds, as a first estimate of the means of the clusters. Each observation is assigned to the nearest seed to form a set of temporary clusters. The seeds are then replaced by the cluster means, the points are reassigned, and the process continues until no further changes occur in the clusters. The *k*-means approach is a special case of a general approach called the expectation maximisation algorithm (JMP 2015). With smaller data tables (<200 studies), the results can be highly sensitive to the order of the observations in the data table. *k*-means clustering supports only numeric values (treats values as continuous) and ignores categorical (nominal and ordinal) variables.

Recently Charmley *et al*. (2016) conducted a meta-analysis of MP and DMI data from Australian, forage-fed, beef-cattle methane-chamber studies to develop a universal MP prediction equation for use in Australian GHG accounting. If one relationship could be recommended for all forage-fed beef cattle in Australia, then could a global equation with country or region and dietary correction effects (if needed) be developed? The Global Rumen Census project reported that global solutions to reduce methane emissions from ruminant animals should be feasible, because the microbes causing the emissions are similar around the world (Henderson *et al*. 2015).

Our study has expanded the MitiGate database and conducted cluster analyses and meta-analyses of MY. The aim was to explore the potential and associated uncertainty with using a global MY equation for use in Tier 1 IPCC default GHG accounting methods around the world when there is a lack of country-specific data.

Materials and methods

Data

The metadata and MY values for only control treatments from beef experiments in the MitiGate database (Veneman *et al*. 2016) were downloaded into an Excel spreadsheet and data were screened and corrected for transcription errors, such as control cattle being recorded as treated groups from some papers and *vice versa*. Data were added from non-included, available papers to expand the currently available database. Rows of data were then excluded from further analyses, if any metadata (i.e. effects in the fitted models) were not recorded in the study (see Tables S1 and S2, available as Supplementary material for this paper). Some studies provided multiple (control) MY values. Cluster analyses are best conducted with only a small number of levels of each categorical variable, so measurement methods, breeds, diets and countries were each amalgamated into three to five groupings or levels, as described below.

Cluster-analysis methods

Dummy variables were coded for categorical effects, as follows:

d_measure: chamber 0, sulfur hexafluoride tracer (SF6) 1, Greenfeed emission monitoring units (GEM) 2, (measure = MP measurement method used);

d_breed: British 0, European 1, Tropical 2, Crossbred 3, Unknown 4 (breed = cattle type);

d_country: Australia 0, Americas 1, Europe 2, Other 3 (country = continent);

d_sex: calves, 0, steers/bulls 1, heifers 2, cows 3 (sex = age and sex);

d_diet: no grain (roughage) 0, 1–50% grain 1, 50–75% grain 2, >75% grain 3 (diet = % grain).

Quantitative variables (number of animals, LW and MY) were standardised to a scale of 0–1 for all records, by using the formula $z = (X - \text{minimum}) / (\text{maximum} - \text{minimum})$.

The data were also analysed using two-way Ward's hierarchical cluster analyses (JMP 2015) with all dummy and standardised variables. Also the Ward's analysis was conducted for individual countries with no d_country dummy variable. The data were also analysed using *k*-means cluster analyses and principal components with two or three clusters with and without the inclusion of the categorical variables. *k* means tend to produce equal-sized clusters, while the expectation–maximisation algorithm benefits from the normal distribution present in the dataset. However, when the normal mixture *k*-means option was run, with outliers that do not fall into any of the normal clusters automatically excluded to a fourth cluster, the three clusters overlapped more. Different clusters of studies were generated each time the data were re-analysed due to the random selection of initial cluster centres. The cluster number allocated to each study was calculated from the formula $((z\_N - \text{cluster mean}) / \text{cluster standard deviation})^2$.

Meta-analysis

The studies had their least-square means (LSMs) of MY and standard errors of these LSMs (s.e.m.), or reported variance parameters such as standard deviation, residual mean square or standard error of differences (that could be used to calculate the s.e.m.), collated in a dataset. Where an estimate of MY s.e.m. was not given in a study, the relative s.e. (rse) was set equal to s.e./mean, then for a ratio of means (MY = mean MP : mean DMI), rse (of MY) was calculated as square root $[rse(MP)^2 + rse(DMI)^2]$, where MY s.e.m. was equal to MY × MY rse. Results from bulls and heifers in the study of Herd *et al*. (2014) could be separated by having access to the raw data. When MP results were reported in litres of methane, a conversion factor of 0.716 (specific gravity at standard temperature and pressure) was used to calculate grams of methane.

The meta-analyses were conducted using a least-square residual maximum-likelihood (REML) model in the statistical package JMP, following the methods of Sauvant *et al*. (2008). In brief, the LSM observations were weighted by the inverse of the squares of their standard errors, i.e. the reciprocals of the s.e.m. However, when such weights are used, the resulting measures of model errors (such as, for example, standard error, standard error of predictions) are no longer expressed in the original scale of the data. To maintain the expressions of dispersion in the original scale of the measurements, the approach of St-Pierre (2001) of dividing each weight by the mean of all weights, and using the resulting values as weighting factors in the analysis, was used. Under this procedure, the average weight used is algebraically equal to 1.0, thus resulting in expressions of dispersion that are in the same scale as the original data. The study effect was considered random because it represents, in essence, the sum of many effects on the dependent variable, MY. Statistical theory indicates that these effects would be close to Gaussian (normal), thus being much better estimated if treated as random effects (Sauvant *et al.* 2008). The root mean-square errors (RMSE) of the REML models serve to aggregate the residuals (observed–predicted) into a single measure of the precision of the model prediction. The weighting factors were calculated on the basis of the studies allocated to each of the clusters included in any analysis, so they varied when different clusters or combinations of clusters were analysed.

The categorical effects included in the REML models were subsets of those used in the cluster analyses and are shown in prediction Eqns 1–4 in the Results section. The data were too sparse to enable model solutions to be found when interaction effects among diet, breed or country were included in any models. Adding more categorical effects, such as, for example, conserved versus fresh forage, would also likely have resulted in solution singularity problems.

Results

Cluster analyses

Ward's hiercharchial clusters (2-way) for all studies are shown in Fig. 1.

In order of importance, the categorical effects that best separate clusters of studies are those that result in the greatest distance between clusters, namely breed, measurement method, sex, diet and country (Table 1). Studies that join closer to the left of the cluster diagram are less disparate in MY values. Studies that join in the last clustering (1 cluster) were the most disparate (Beauchemin and McGinn 2005; Herd *et al.* 2014). Groups of studies to be collated for a meta-analysis could be those that cluster together earlier or those studies in the same path of the constellation plots. As there were numerous paths in these plots, the hierarchial clustering method was rejected as a data-filtering method. The *k*-means clustering technique was used instead to generate two large clusters and a third small cluster, and meta-analyses were conducted on these two large clusters separately or with all data combined.

The Ward's hiercharchial and *k*-means cluster means from the various analyses are shown in Table 2. *k*-mean cluster values (1, 2 and 3) were assigned to each study from the *k*-means cluster without categorical variables analysis.

Clusters are shown in Fig. 2 and these clusters were meta-analysed separately or with all clusters included. On average, studies in the third cluster (3) were slightly smaller studies with lighter cattle with lower MY values than were studies in the second cluster (2). Cluster 1 was solely the male and female results in the large study of Herd *et al*. (2014) and was the last cluster (7) in the Ward's hiercharchial analysis.

All-clusters model

The REML model for all included data (51 papers, 138 MY estimates), with studies fit as a random effect, had a prediction Eqn 1 for MY, as follows:

$$\begin{aligned}\text{MY (g/kgDMI)} = {} & 20.34 + \\ & \text{d\_measure}\ (0 = 1.98, 1 = -3.86, 2 = 1.88) + \\ & \text{d\_breed}\ (0 = -0.56, 1 = 4.65, 2 = -3.80, \\ & \quad 3 = -1.76, 4 = 1.48) + \\ & \text{d\_diet}\ (0 = 5.70, 1 = 2.69, 2 = -1.81, 3 = -6.58) + \\ & \text{country}\ (\text{Australia} = -4.53, \text{Brazil} = -3.84, \\ & \quad \text{Canada} = -5.74, \text{France} = 5.69, \text{India} = 0.52, \\ & \quad \text{Ireland} = 8.97, \text{NZ} = 0.94, \text{Switzerland} = -3.91, \\ & \quad \text{UK} = 1.90). \end{aligned} \quad (1)$$

Table 1. Number of clusters, distance, variable and joiner with all studies included

The history of the cluster from each data point in its own cluster to all points in one cluster is shown in Fig. 1. The order of the clusters at each join is unimportant, essentially being an accident of how the data were sorted. Dummy and normalised variables are described in Materials and methods

Number of clusters	Distance	Variable	Joiner
7	8.775	d_diet	d-country
6	9.440	d_measure	z_LW
5	10.580	d_measure	z_MY
4	11.818	d_sex	d_diet
3	11.822	d_measure	z_N
2	16.973	d_breed	d_sex
1	23.992	d_measure	d_breed

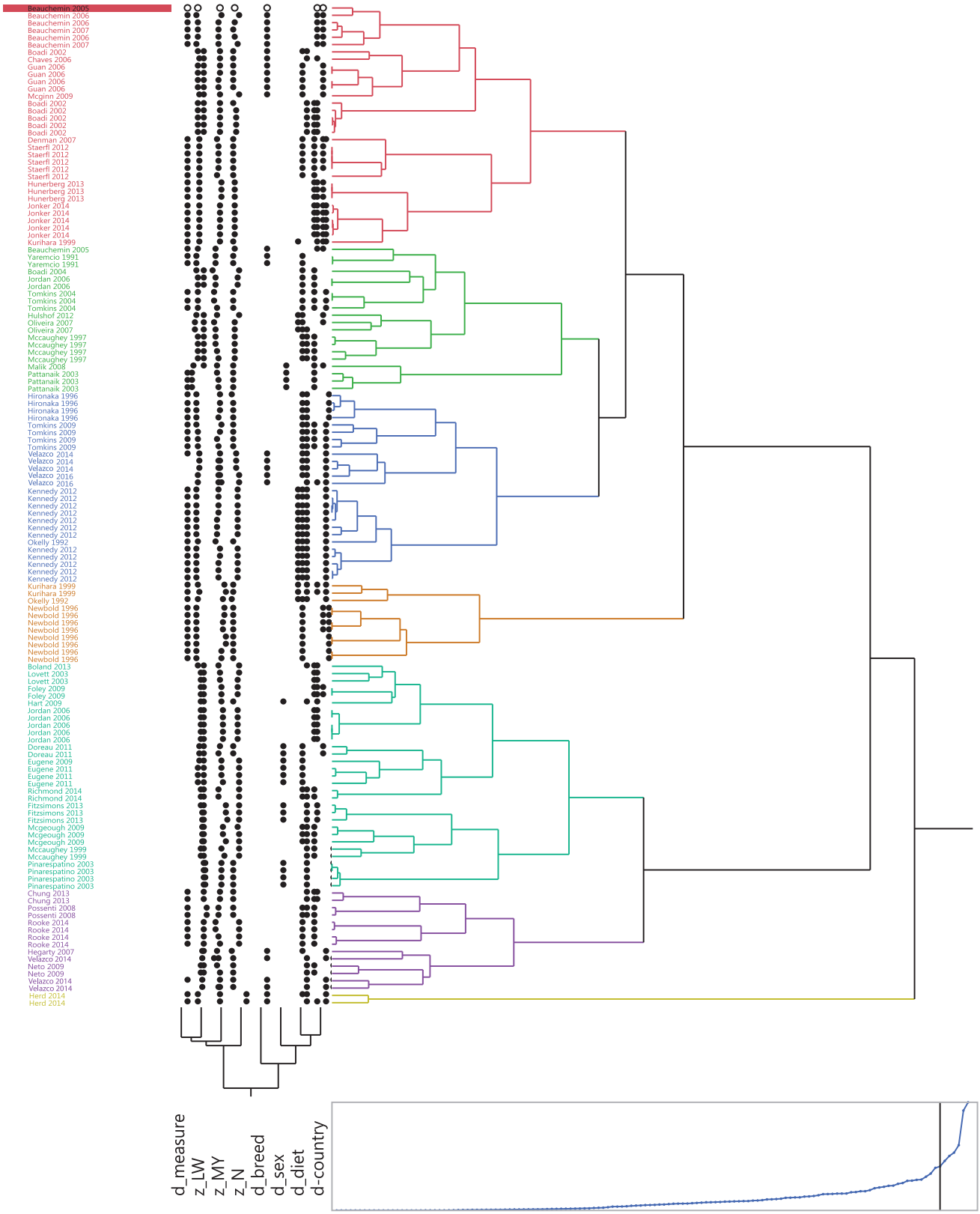

Fig. 1. Hierarchial clustering dendrogram of methane-yield (MY) studies. Seven clusters are shown in different colours. The studies at the top (Beauchemin and McGinn 2005) and bottom (Herd *et al.* 2014) are the most disparate in MY and are the last joined. The dendrogram shows which cluster each study is in and when it entered the cluster. The scree plot beneath the dendrogram has a point for each cluster join. The ordinate is the distance that was bridged to join the clusters at each step. Where the distance jumps up suddenly are an appropriate number of clusters.

Equation 1 had $R^2 = 0.65$ and RMSE = 3.95. No effects or LSM differences were significant ($P < 0.05$), including the random effect of studies. The LSM of MY values for all data are shown in Table 3. The LSM for an effect is equal to its effect size in the model plus the overall intercept (20.34) in predictive Eqn 1.

The MY values from beef cattle studies conducted in Brazil, Switzerland, Australia and Canada had (non-significantly; $P > 0.05$) lower LSM, while the LSM values from studies in Ireland, France, the United Kingdom, New Zealand, and India were (not significantly; $P > 0.05$) higher. Data screening removed all beef MY studies from USA, Denmark and Japan (Table S2). Studies with beef cattle conducted in Ireland had the highest MY value (29.31 g/kg DMI), while studies with cattle in Canada had the lowest (14.60 g/kg DMI). Interactions of country with diet or breed fixed effects could not be included in the models due to the sparsity of data.

When d_country (amalgamation of countries into continents) was fitted as an effect instead of country, then the d_diet and d_country effects became significant ($P < 0.05$) but the goodness of fit of the model (as measured by R^2 and RMSE) slightly decreased. Higher-roughage diets (d_diet = 0, 1) had significantly ($P < 0.05$) higher MY values than did higher-grain diets and European studies had significantly ($P < 0.05$) higher MY values than did those from North and South America (Canada and Brazil).

Cluster 2 (larger studies, heavier cattle) model

The REML model for Cluster 2 studies, with studies fit as a random effect, had a prediction Eqn 2 for MY, as follows:

$$\begin{aligned}\text{MY (g/kg DMI)} = 27.74 + \\ \text{d\_measure}(0 = -1.79, 1 = 3.62, 2 = -1.83) + \\ \text{d\_breed}\ (0 = -3.79, 1 = -2.08, 2 = 3.09, \\ 3 = -3.67, 4 = 6.45) + \\ \text{d\_diet}\ (0 = 0.74, 1 = 0.31, 2 = 0.12, 3 = -1.17) + \\ \text{d\_country}\ (\text{Australia} = 1.59, \text{Americas} = -0.20, \\ \text{Europe} = -1.39).\end{aligned} \quad (2)$$

Equation 2 had $R^2 = 0.90$ and RMSE = 1.20. No effects were significant ($P < 0.05$) with LSMs shown in Table 4.

Cluster 3 (smaller studies, lighter cattle) model

The REML model for Cluster 3 results, with studies fit as a random effect, had a prediction Eqn 3 for MY, as follows:

$$\begin{aligned}\text{MY (g/kg DMI)} = 17.63 + \\ \text{d\_breed}\ (0 = 1.66, 1 = 0.48, 2 = -2.77, 3 = -1.69, 4 = 2.33) \\ \text{d\_measure}\ (0 = 1.14, 1 = -0.57, 2 = -0.57) + \\ \text{d\_diet}\ (0 = 5.25, 1 = 2.48, 2 = -4.27, 3 = -3.47) + \\ \text{d\_country}\ (\text{Australia} = -2.43, \text{Americas} = -4.21, \\ \text{Europe} = 0.17, \text{Other} = 6.46).\end{aligned} \quad (3)$$

Equation 3 had $R^2 = 0.53$ and RMSE = 4.91. The LSMs were not significantly different (Table 5).

Table 2. Cluster means for Ward's hierarchial clusters, *k* means with and without categorical variables included in the analysis, and *k* means normal mixture option with outliers placed in cluster 0

Dummy and normalised variables are described in Materials and methods

Cluster	No.	d_measure	d_breed	d_sex	d_diet	d_country	z_N	z_LW	z_MY
				Ward's hierarchial clusters					
1	33	0.716	4.476	2.558	1.648	1.928	0.026	0.426	0.490
2	20	0.824	5.274	2.020	2.477	2.286	0.025	0.290	0.252
3	26	0.683	4.853	2.149	0.832	1.244	0.034	0.323	0.452
4	11	0.504	6.649	2.247	1.920	2.378	0.012	0.324	0.791
5	31	1.087	4.879	2.697	1.797	2.797	0.057	0.598	0.659
6	14	0.795	4.939	2.709	1.687	1.981	0.044	0.764	0.397
7	2	0.504	2.146	2.465	0.832	1.109	0.996	0.366	0.518
				k *means with and without categorical variables included in the analysis*					
1	76	0.763	1.684	1.829	0.697	1.158	0.038	0.529	0.568
2	2	0	0	1.5	0	0	0.996	0.366	0.518
3	59	0.186	2.814	0.932	1.034	1.085	0.031	0.353	0.415
Eigenvalues		2.027	1.630	1.154	1.007	0.839	0.620	0.421	0.302
1	2						0.996	0.366	0.518
2	60						0.040	0.551	0.650
3	75						0.031	0.373	0.382
Eigenvalues							1.189	0.999	0.812
				k *means normal mixture option with outliers placed in cluster 0*					
1	47	1.000	1.894	1.639	0.959	1.596	0.042	0.528	0.545
2	36	0.166	2.722	1.416	0.250	0.388	0.029	0.353	0.477
3	26	0.0002	2.385	1.308	1.192	1.692	0.017	0.369	0.539
0	28	Outliers							
Eigenvalues		2.027	1.630	1.154	1.007	0.839	0.620	0.421	0.302

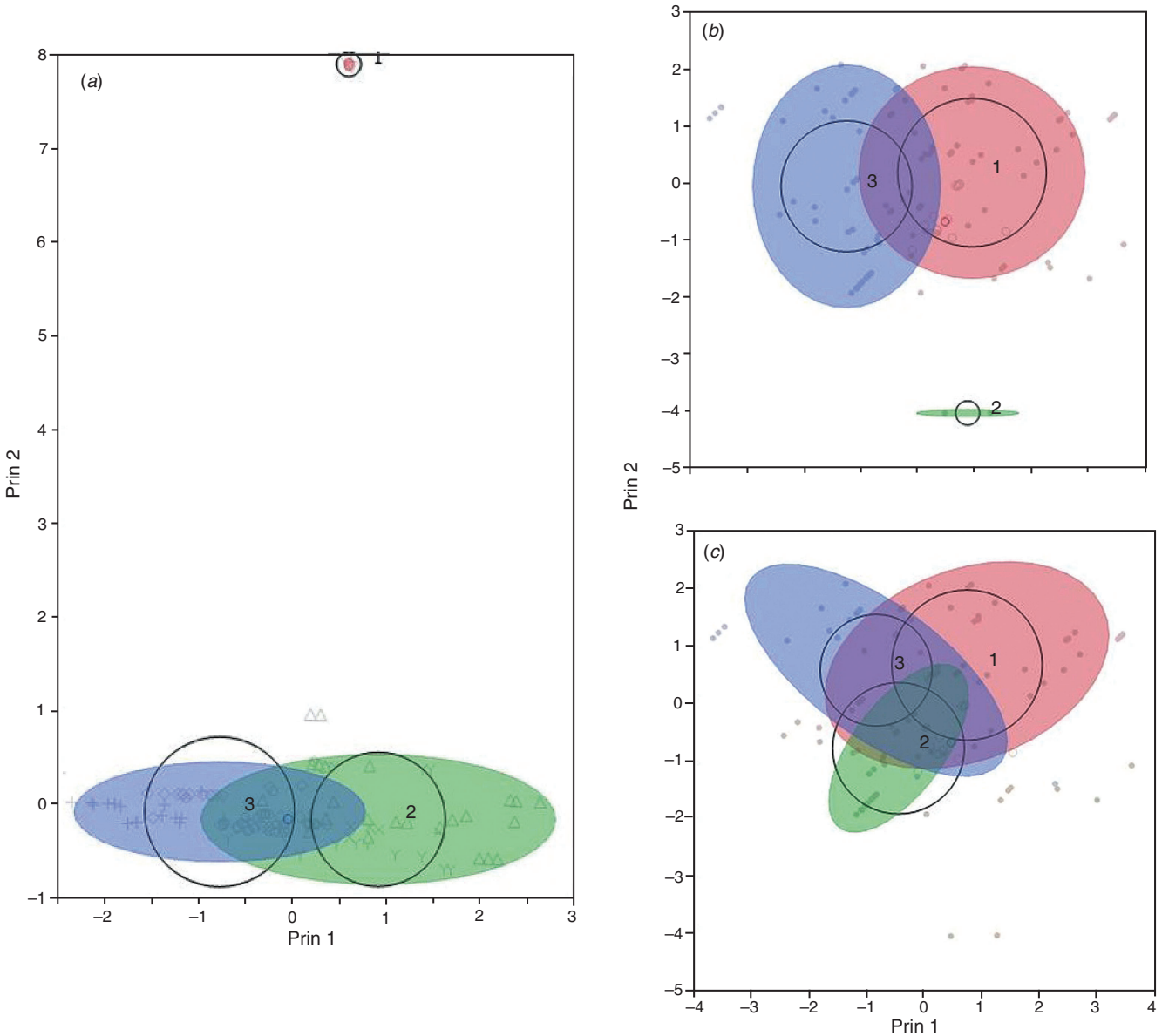

Fig. 2. Biplot of principal components from *k*-means three-cluster analysis; (*a*) without categorical variables, (*b*) with categorical variables, (*c*) normal mixture option with outliers removed. The clusters of studies from option *a* were meta-analysed separately or together.

There were no consistent trends for the effects of measurement method, breed, diet or continent when comparing the LSM results or prediction equations from Clusters 2 and 3. Cluster 1, which consisted only of data from Herd *et al*. (2014) had a LSM value for MY of 22.96 g/kg DMI.

Outliers

The mean studentised residual value from the all-in model was 0.089 ± 1.267, with quartiles of –0.110, and a value range from –9.380 to 9.319. There were only three rows of data from 138 rows with absolute studentised residual (ASR) values for MY greater than or equal to 1.96 from the all-in analysis. These MY values were from trials reported by Beauchemin and McGinn (2005) and Boadi *et al*. (2004). When the threshold for outlier exclusion was reduced to an ASR value of 1.0 (which includes 66% of the normal distribution), seven data rows were excluded. With an ASR value of 0.9, nine data rows were excluded and, with an ASR value of 0.8, 13 data rows were excluded.

All-clusters model excluding outliers

Data with seven outlier rows removed (ASR threshold value = 1.0) were chosen for further analyses. The excluded rows of data were from Beauchemin and McGinn (2005), Boadi *et al*. (2004), Boland *et al*. (2013), McCaughey *et al*. (1999) and Velazco *et al*. (2016). The REML model, with studies fit as a random effect, had a prediction Eqn 4 for MY, as follows:

Table 3. Methane yield (g methane/kg dry-matter intake) least-square means for all included data

Measurement method: 0, chamber; 1, sulfur hexafluoride tracer (SF6); 2, Greenfeed emission monitoring units. Breed: 0, British; 1, European; 2, Tropical; 3, Crossbred; 4, unknown. Diet: 0, no grain (roughage); 1, 1–50% grain; 2, 50–75% grain; 3, >75% grain

Fixed categorical effect	Level				
	0	1	2	3	4
Measurement method	22.32	16.48	22.23		
Breed	19.78	24.99	16.54	18.58	21.82
Diet	26.04	23.04	18.53	13.76	
Country					
Ireland	29.31				
France	26.03				
United Kingdom	22.24				
New Zealand	21.28				
India	20.86				
Brazil	16.50				
Switzerland	16.44				
Australia	15.82				
Canada	14.60				

Table 4. Methane yield (g methane/kg dry matter intake) least-squares means for cluster 2 data

Measurement method: 0, chamber; 1, sulfur hexafluoride tracer (SF6); 2, Greenfeed emission monitoring units. Breed: 0, British; 1, European; 2, Tropical; 3, Crossbred; 4, unknown. Diet: 0, no grain (roughage); 1, 1–50% grain; 2, 50–75% grain; 3, >75% grain

Fixed categorical effect	Level				
	0	1	2	3	4
Measurement method	25.95	31.37	25.91		
Breed	23.96	25.66	30.83	24.08	34.19
Diet	28.48	28.05	27.87	26.58	
Continent					
Australia	29.34				
Americas	27.54				
Europe	26.35				

$$\begin{aligned}\text{MY (g/kg DMI)} = 21.85 + \\ \text{d\_measure}\ (0 = 0.77, 1 = -2.55, 2 = 1.77) + \\ \text{d\_breed}\ (0 = -0.61, 1 = 3.41, 2 = -1.75, \\ 3 = -2.29, 4 = 1.25) + \\ \text{d\_diet}\ (0 = 3.76, 1 = 2.01, 2 = 1.49, 3 = -7.26) + \\ \text{country}\ (\text{Australia} = -3.37, \text{Brazil} = -4.84, \\ \text{Canada} = -1.77, \text{France} = 4.19, \text{India} = -2.55, \\ \text{Ireland} = 8.67, \text{NZ} = 1.84, \text{Switzerland} = -3.66, \text{UK} = 1.48).\end{aligned} \quad (4)$$

Equation 4 had R^2 = 0.90, RMSE = 1.20, which was, as expected, a much improved fit compared with the all-clusters model with no outliers removed. Significant differences in MY LSM are shown in Table 6.

Table 5. Methane yield (g methane/kg dry-matter intake) least-square means for Cluster 3 data

Measurement method: 0, chamber; 1, sulfur hexafluoride tracer (SF6); 2, Greenfeed emission monitoring units. Breed: 0, British; 1, European; 2, Tropical; 3, Crossbred; 4, unknown. Diet: 0, no grain (roughage); 1, 1–50% grain; 2, 50–75% grain; 3, >75% grain

Fixed categorical effect	Level				
	0	1	2	3	4
Measurement method	18.77	17.07	17.06		
Breed	19.29	18.11	14.86	15.94	19.96
Diet	22.89	20.12	13.36	14.17	
Continent					
Other	24.10				
Europe	17.80				
Australia	15.20				
Americas	13.42				

Table 6. Methane yield (g methane/kg dry-matter intake) least-square means for all data with seven outliers excluded

Measurement method: 0, chamber; 1, sulfur hexafluoride tracer (SF6); 2, Greenfeed emission monitoring units. Breed: 0, British; 1, European; 2, Tropical; 3, Crossbred; 4, unknown. Diet: 0, no grain (roughage); 1, 1–50% grain; 2, 50–75% grain; 3, >75% grain. For measurement method, breed and diet, least-square means within a row followed by the same letter are not significantly different (at $P = 0.05$). For Country, least-square means within a column followed by the same letter are not significantly different (at $P = 0.05$)

Fixed categorical effect	Level				
	0	1	2	3	4
Measurement method	22.62a	19.30ab	23.62b		
Breed	21.24a	25.26a	20.10a	19.56a	23.10a
Diet	25.61a	23.86a	23.33a	14.59b	
Country					
Ireland	30.52a				
France	26.04ab				
New Zealand	23.69ab				
United Kingdom	23.33b				
Canada	20.08b				
India	19.30b				
Australia	18.48b				
Switzerland	18.19b				
Brazil	17.01b				

One example of using predictive Eqn 4, which can be compared with the prediction equation of Charmley *et al.* (2016), is for British cattle breeds, measured in chambers, on a roughage diet in Australia. In this case, the MY value solves to 21.85 + 0.77 – 0.61 + 3.76 – 3.37 = 22.40 ± 1.20 g methane/kg DMI.

The changes in predicted MY value with changes in measurement method, breed, diet or country are given by the size of the fixed-effect categorical values. For example, MY measured with a GreenFeed Emissions Monitoring system (d_measure = 2) rather than a chamber (d_measure = 0) was predicted to be 1.77 – 0.77 = 1.0 g methane/kg DMI higher. However, this does not suggest or prove that one measurement

method gives more accurate values for the true MY than does another, but the effect-level difference allows a correction to be made for methane-measurement method.

Discussion

Country and other effects

Overall differences among countries were not significant, but some individual countries were significantly different from each other in the MY value. The country effect is an unknown mixture of the inherent MY value of animals from each country, independent of the other fitted effects, and the skills and expertise of the technicians and scientists deploying specific equipment used in measuring animals in each country. These effects could be interpreted more clearly only if representative samples of animals from different countries were transported to a common centre for measurement or scientists from different countries measured exactly the same animals using the same methods. None of these situations is likely to happen due to their cost and impracticality. Data were too sparse to study the interactions of country with any other effects causing singularities in any model. There is no evidence in the literature for significant interactions between country and breed or country and diet type for MY.

Henderson *et al*. (2015) suggested that rumen methanogens in cattle around the world have similar genetics, which could suggest that MY may be similar everywhere. No strong associations were found between the most abundant rumen bacteria and archaea (~3% of microbes that are mostly autotrophic methanogens). However, Wallace *et al*. (2015) reported that the abundance of archaeal genes in ruminal digesta correlated strongly with differing methane emissions from individual animals. Lower emissions were accompanied by higher *Succinovibrionaceae* abundance and changes in acetate and hydrogen production leading to less methanogenesis. Large numbers of predicted protein sequences, nearly all unknown, differed between high- and low-methane-emitting cattle.

Different species of rumen biota, while a major factor affecting rumen methanogenesis, are not the only factor (Eckard *et al.* 2010; Cottle *et al.* 2011). Other factors include level and variation of DMI, type of carbohydrate in the diet, feed digestibility and processing, addition of additives such as lipids or ionophores to the diet, as well as manipulations of the ruminal microflora. Efficiency of feed use depends on the type of animal, the type or quality and quantity of feed and environmental conditions (Cottle and Pitchford 2014). Country variation in MY value may be due to effects not included in the model, such as, for example, conserved versus fresh forage, and proportion of legume. However, adding additional effects to a model when data are sparse often has the problem that model solutions are not obtained.

National accounts based on IPCC (2006) use the percentage of gross energy (GE) in feed converted to methane (Y_m) to calculate methane production. The values of Y_m and MY respectively predict the percentage of feed energy and feed dry weight converted to methane energy and dry weight. It is proposed that it is problematic to have a universal MY or Y_m value for use in all countries for national accounting, given the significance and size of some of the fixed effects found in this meta-analysis, including specific countries. However, prediction Eqn 4 could be used, for example, for different countries and diets to provide a MY (or Y_m) value to be used in the national accounts of various countries.

The IPCC Tier 1 guidelines for national GHG inventories (IPCC 2006) use the same methane-conversion factor (Y_m) of 6.5% for grazing beef cattle and 3% for feedlot cattle in all major beef regions. Methane production of beef cattle in IPCC-based national inventories, using Tier 1, 2 or 3 approaches, is calculated using IPCC (2006) eqn 10.21, as follows:

$$EF = 365 \times GEI \times Y_m/100/55.65,$$

where

EF = emission factor, kg methane/head.year (MP = EF/365),
GEI = gross energy intake, MJ/head/day,
Y_m = percentage of gross energy in feed converted to methane,
55.65 (MJ/kg methane) = the energy content of methane.

IPCC (2006) recommends that either Tier 2 or Tier 3 approaches are used for beef cattle. This is where regional, national and global estimates of enteric methane generation rely on small-scale determinations of GEI, Y_m and the influence of feed and animal properties on GEI and Y_m. The GEI values depend on the assumed DMI level and diet quality for different classes of animals. Default feed intakes (kg/day) and energy intakes (MJ/day) for beef-stock classes and regions are listed in IPPC Volume 4 Appendix B, based on the report of Gibbs and Johnson (1994). These different intake levels lead to the different default Tier 1 values for EF (or MP) listed for the various regions (IPCC 2006). These values for North America, western Europe, eastern Europe, Oceania, Latin America, Asia, Africa, Middle East and Indian subcontinent are 14.5, 15.6, 15.9, 16.4, 15.3, 12.9, 8.5 and 7.4 g methane/day respectively.

From our review of the national inventories of the major beef-producing nations, the value of Y_m for grazing cattle has not been modified from the Tier 1 value of 6.5%; for example, the USA inventory (US EPA 2017) still uses the Y_m value of 6.5% recommended by Johnson (2002). The value of MY (g methane/kg DMI) = GE content of DM × Y_m / 100 / 55.65. As the GE content of pasture and grain is typically 18.45 MJ/kg DM (Cottle *et al*. 2011), the Tier 1 MY value = 21.5, assuming Y_m = 6.5% for pasture, and MY = 9.9 for grain, assuming Y_m = 3%, for all countries. Thus, universal values for Y_m, and hence MY, appear to be used to estimate beef MP in most national inventories.

Other methane meta-analyses

Most published methane related meta-analyses have been focussed on mitigation strategies rather than estimating MY values in control, non-mitigated animals. Examples of meta-analyses focussed on mitigation strategies include Ungerfeld *et al*. (2007), Beauchemin *et al*. (2008), Eugène *et al*. (2008), Grainger and Beauchemin (2011), Jayanegara *et al*. (2011), Patra (2013), Hristov *et al*. (2013*a*) and the more recent papers by Veneman *et al*. (2016) and Escobar-Bahamondes *et al*. (2017).

Ramin and Huhtanen (2013) estimated beef cattle MY as 21.9 g/kg DMI from their meta-analysis of five beef papers (Kirkpatrick *et al.* 1997; Kurihara *et al.* 1999; Beauchemin and McGinn 2005, 2006; Beauchemin *et al.* 2007). Our predicted MY value from the data that excluded outliers,

which interestingly included some of the papers analysed by Ramin and Huhtanen (2013), was 22.4 g/kg DMI for British cattle breeds, measured in chambers, on a roughage diet in Australia. This estimate from many more studies is very similar to their estimate from Canadian, Australian and Irish studies. Ramin and Huhtanen (2013) may have fit too many dietary fixed effects (organic matter digestibility, neutral detergent fibre, non-fibre carbohydrates and ether extract) to their MY models for the relative small number of beef studies they analysed.

Ricci *et al*. (2013) reported a meta-analysis of 38 beef studies where MP, DMI, type of enterprise, diet type, physiological stage, MP measurement technique, intake restriction and methane-mitigation treatment were used as classificatory factors. A series of equations for different physiological stages and diet types based on DMI or GE intake explained 96% of the variation in observed MP outputs. Hristov *et al*. (2013*a*, 2013*b*) also demonstrated a simple relationship between MP and DMI (MP (g/day) = 19.14 × DMI + 2.54) in a meta-analysis of dairy data. Similarly, Dijkstra *et al*. (2011) reported that MY for dairy cows in The Netherlands was 23.1 g MP/kg DMI, suggesting a linear relationship between MP and DMI, with an intercept of zero.

Most national inventories predict MP from its linear, not curvilinear, relationship with predicted DMI. This has the implicit assumption that the MY value is constant for all DMI values if there is no intercept in the MP/DMI equation (e.g. Bannink *et al*. 2011; Charmley *et al*. 2016). If there is an intercept in the MP/DMI equation (e.g. Hristov *et al*. 2013*a*, 2013*b*), then the MY–DMI relationship is slightly curvilinear. Appuhamy *et al*. (2016) found that MP in dairy cows could be predicted successfully if DMI could be estimated accurately. However, they found that the best methane-prediction model for North American lactating dairy-cow studies (modified from Nielsen *et al*. 2013) was different than the best model for European, Australian and New Zealand studies (Yan *et al*. 2000).

Charmley *et al*. (2016) analysed a total of 1034 individual animal records of MP to re-assess the relationship between MP and DMI. Data were restricted to trials conducted in the past 10 years using respiration chambers, with cattle fed forage-based diets (forage >70%). Results from diets considered to inhibit methanogenesis were omitted from the dataset. Records were from beef cattle fed temperate forages (680 records) and beef cattle fed tropical forages (133 records). Relationships were very similar for both forages and a single relationship for MP on a DMI basis was proposed for the purposes of Australian national inventory. This relationship was as follows: MP (g/day) = 20.7 (±0.28) × DMI (kg/day; $R^2 = 0.92$, $P < 0.001$), i.e. MY = 20.7. The prediction of MY value for Australian beef cattle on non-grain diets measured in chambers in Eqn 4, derived from an analysis of global MY data, was 21.85 + 0.77 + d_breed (0, 1, 2, average of 0.35) + 3.76 – 3.37 = 23.4. This is 2.7 g/kg DMI higher than the MY value of Charmley *et al*. (2016).

Charmley *et al*. (2016) noted that MP and DMI variances increase as MP and DMI levels increase while their coefficient of variance remain steady. They also analysed Australian MY data (i.e. the data formed by the ratio MP : DMI) directly. This reduced variance heterogeneity, but not completely. It also simplified the fixed-effects model to one without DMI, as Charmley *et al*. (2016) noted a perceived difficulty of dealing with DMI on both sides of the model equation for MP. However, they still argued that analysing MP in terms of DMI was conceptually the simplest.

For the classes of beef cattle used, Charmley *et al*. (2016) found that MY ranged from 19.6 ± 0.49 to 21.5 ± 0.45 g/kg DMI, which is close but lower than our Australian predicted values, as noted above, and previously published values. Charmley *et al*. (2016) noted that Irish beef data suggested a higher MY value of ~25 g/kg DMI (Yan *et al*. 2009), while our Eqn 4 fixed-effect value for Ireland was 8.7, compared with –3.4 for Australia. Thus, our prediction of the difference between Australia and Ireland in MY value from our higher number of studies was a larger difference of 12.04 g/kg DMI. Their analysis included Australian trials with growing beef cattle fed diets containing 0–70% concentrate. This discrepancy between Irish and Australian data may be attributed to the predominance of extensively fermented grass silages in many of the Irish studies. Dairy research from the United Kingdom (Hammond *et al*. 2014) supports Irish research (Yan *et al*. 2000), showing that MY is higher for ensiled forages than fresh pasture. We included relative amount of grain in the diet (d_diet) as a fixed categorical effect, but other dietary effects, such as fresh versus ensiled pasture, were not included for reasons given previously.

Use of the MitiGate database

The MitiGate database potentially provides a very useful global resource for collation of results from ruminant methane studies. However, control versus mitigation-treatment data from MitiGate need to be accurately transcribed from the original publications. Some control (non-mitigated) MY values were listed as the mitigated treatment values and *vice versa*, so data need to be checked. Some large beef methane-study results have not been uploaded yet. About 50% of the 326 beef cattle methane-related papers in MitiGate reported methane production in units of either grams or litres of methane per kilogram DMI. The other publications (in decreasing frequency) used a variety of methane units, including %GEI, L/day, g/day, g/kg organic matter intake, mol/mol glucose equivalent, MJ/day, MJ/100 MJ GE, MJ/kg BW, MJ/MJ GE, KJ/$BW^{0.75}$, mcal/100 mcal, mcal/day, mL/min, mmol/L, %gas, g/h, g/kg LW.day, g/MJ ME, kcal/day and L/kg $BW^{0.75}$. Some publication authors have used different methane units in their own different studies. Some of these units are not easy to convert to g MP/kg DMI and consistency would be helpful when collating MP or MY results. We suggest g MP/kg DMI as an emerging standard and, thus, the preferred MY unit. MitiGate does not include DMI data, so it is not possible to calculate MP from the MitiGate MY values.

The meta-analyses of selected subsets from the MitiGate database in regard to mitigation effects are based on the metaphor method using R as described by Viechtbauer (2010), which is based on the ratio of the mean MY value of control and treated animals. If particular mitigation options are being compared the user could download all data for those options, with no guidance given on outlier study removal. The metaphor method, while valid, differs from the methods of Sauvant *et al*. (2008), which are the basis of many published meta-analyses in ruminant nutrition.

The current classification of methane-mitigation options in MitiGate does not include management options, such as faster

growth to sale weight of stock or younger age structures, which are probably the most cost-effective mitigation options available (Eckard *et al.* 2010; Cottle *et al.* 2011; Cottle and Eckard 2014; Mazzetto *et al.* 2015). It could, therefore, be useful to add these management options in MitiGate by adding studies that have MY values for control versus modified management systems.

Conclusions

Our main aim was to explore the potential and associated uncertainty with using a standard MY estimate for use in Tier 1 IPCC default GHG accounting methods around the world. We conclude that the differences in MY values from beef-cattle studies with different methane-measurement methods, breeds and diets in different countries are such that a universal MY value cannot be recommended at this stage. A more accurate approach would be to use a predictive equation, such as our Eqn 4, derived from country-specific data to provide Y_m or MY values in national accounting methods that also take account of different breeds and diets. Such equations can be regularly updated in meta-analyses as more data become available.

Conflicts of interest

The authors declare no conflicts of interest.

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