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# Enteric methane output and weight accumulation of Nguni and Bonsmara cows raised under different grazing conditions

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## Abstract

Several experts throughout the world have focused a lot of their research on the rise in methane concentrations in the atmosphere and its causes. Cattle are the livestock species that contribute the most to methane emissions, according to research conducted over the previous three decades. A greenhouse gas called enteric methane (CH<sub>4</sub>) is created by microbial fermentation in the rumen and is released into the atmosphere through a variety of excretory processes. To reduce methane emissions, research on the ways that various breeds of cattle are reared on different grazing regimes should be prioritized. The goal of the current study was to measure the weight gain and intestinal methane emission of Nguni and Bonsmara cows grown under various grazing conditions. Eighty-four cows belonging to the 2 grazing systems were randomly selected and grouped according to three age groups: A (young adult cow,  $n = 7$ , 24–48 months), B (adult,  $n = 7$ , 60–80 months), and C (old adult,  $n = 7$ , 90–120 months) are three different age groups for adult cows. Methane production was higher per head in older animals, with C producing the most, followed by B and A ( $C > B > A$ ;  $P 0.0001$ ). In Bonsmara, body condition, body weight (BW), dry matter intake (DMI), and daily methane were all higher ( $P 0.05$ ). Nguni had more methane per pound of weight ( $P 0.05$ ), although methane per kilogram of body mass ( $P > 0.05$ ) was similar across breeds. In the commercial system, body condition, BW, and DMI were higher ( $P 0.05$ ). On the other hand, communal grazing resulted in increased daily methane production, methane per DMI, and methane produced per BW. These findings support the notion that breed genetics, grazing system, and age all have an impact on methane levels and performance. So, all these aspects must be taken into account in breeding strategies for traits like methane production that are challenging to assess.

**Keywords** Cattle breed, Commercial farming, Enteric methane, Grazing systems, Weight gain

## Introduction

The need for animal protein is always rising, and environmental concerns are posing new problems for livestock production systems all over the world (O'Mara 2011).

Livestock farmers have been under intense pressure to increase the number of their animals in order to meet the rising demand for meat and protein as a solution to this problem (UN 2012; Berman 2011). Ruminants have the ability to use fibre that non-ruminants cannot directly utilize (Kumar et al. 2015). The production of greenhouse gases (GHG), especially ruminal methane, is a drawback of this procedure (Mapfumo et al. 2018). The microorganisms in the rumen that produce methane are called methanogens (Jiyana et al. 2021). Methane gas is one of the by-products of their usage of hydrogen to reduce carbon dioxide (CO<sub>2</sub>) and provide energy for growth. Suppose this hydrogen is not utilized, it can prevent rumen

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metabolism (Palangi et al. 2022a). Methane production is influenced by the quantity and calibre of feed ingested by the animals (Singh 2010). The main source of methane gas has been found to be ruminants (NRC 2002). Enteric methane is the type of gas produced directly by these animals' digestive systems. Enteric methane's contribution to the accumulation of GHG and its capacity to squander feed energy are both global issues, according to (Wright et al. 2004). Five to 10% of the world's GHG emissions are caused by the agriculture system (Jonker et al. 2020). Sixty per cent of cattle contributions come from enteric fermentation (Banakar et al. 2018). Compared to other domestic ruminants, beef cattle are identified as the primary source of enteric methane generation (Alexandratos 2009). According to (Palangi et al. 2022b), domestic ruminants create about 65% of their methane from beef cattle, 22% from dairy cattle, and just 13% from sheep and goats. According to Grainger and Beauchemin (2011), varied grazing patterns should be considered when evaluating strategies for identifying and reducing the resulting methane emissions from different beef breeds. In these huge livestock production systems, calculating methane emissions and mitigating them requires multidisciplinary approaches including different breeds of cattle at varying ages. Different grazing systems may contribute to breed-specific variances in methane emissions. An attractive possibility for rumen biomarkers of methane emissions is the metagenomic study (Ross et al. 2013; Roehe et al. 2016; Wallace et al. 2017). This makes it possible to choose and breed cattle of low methane-emitting breeds or individuals within a breed, which may ultimately result in a reduction of emissions in different grazing regimes. The microbiota of the rumen ecosystem, which produces ruminant livestock, includes fungi, bacteria, ciliated protozoa, phages, and archaea and is diverse and essential (Morgavi et al. 2013). Although the composition of the rumen microbiota inside an individual is consistent (Jami and Mizrahi 2012; Hernandez-Sanabria et al. 2013), breeds may have different rumen microbiotas that are also influenced by environmental influences from different grazing patterns. Several studies have indicated that the host's genetic makeup has an impact on the gut bacteria (Tims et al. 2011; Turnbaugh et al. 2011; Li et al. 2019). Since their mechanisms for producing methane are intertwined, the breed effect on the rumen microbial ecology and methanogens cannot be ignored. The age factor in connection to methane emission from various cow breeds should also be taken into account at the same time. A number of variables, including genetics, breed, nutrition, and grazing practices throughout diverse geographic ranges, affect the amount of ruminal methane that is emitted. These elements may have an impact on CH<sub>4</sub> emission directly, indirectly, or

jointly. This is because rumen microbes adjust and react to environmental changes, which produce physiological changes in the host (Basarab et al. 2013; Carberry et al. 2014; Henderson et al. 2015; Zhao et al. 2015; Roehe et al. 2016). Age-related physiological responses, microbial communities, and methane production from the animal host (ruminant) have received little study attention in relation to the aforementioned components. Assume that the rumen microbiota adjusts or responds to the host's age. In that situation, it means that the interactions and composition that control the synthesis of methane and the metabolism of energy may change with age. According to (Jami et al. 2013), nutrition and the host's age from birth to 2 years affected the bacterial community in the rumen. The current study attempted to elaborate on the effect of age, breed, and grazing system on methane emission from Nguni and Bonsmara cows because the author did not correlate this with intestinal methane generation.

## Materials and methods

### Ethical clearance

Ethical clearance to conduct the study was reviewed and approved by the University of Fort Hare Research Ethics Committee with certificate number MUC041SKAY01.

### Study site

The study was conducted in Alice which falls under Amathole District Municipality and Bathurst Research Station which is demarcated in Sarah Baartman District Municipality. Both study sites are situated in the Eastern Cape province, South Africa. Alice is geographically located at 32° 8' E longitude and 26° 85' S latitude and is 500 m above sea level. Its annual rainfall is 480 mm, and the average temperature is 18.7 °C [Eastern Cape Socio-Economic Consultative Council (ECSECC) 2012]. Alice belongs to Bisho Thornveld, and its vegetation is largely characterized by several grass species such as *Digitaria eriantha*, *Aristida Congesta*, *Cynodon dactylon*, *Eragrostis* spp., *Sporobolus fimbriatus*, *Themeda triandra*, and *Sporobolus africanus* grass species. *Maytenus polyacantha*, *Scutia myrtina*, and *Acacia karroo* are the dominant tree species (Mucina et al. 2006). Bathurst Research Station belong to the Kowie Thicket biome and is located at 33° 30' S latitude and 26° 49' E longitude, at 708 m above sea level. The station's annual rainfall is 624 mm, while its temperature ranges between 13–29 in summer and 1–12 °C in winter. Tall-grown thickets characterize the vegetation of the area. Succulent aloes and euphorbias dominate it with a thick understory consisting of woody lianas (*Capparis*, *Rhoicissus*, *Aloe*, *Secamone*), shrubby succulents (*Crassulacae*, *Asphodelaceae*), and thorny shrubs. However, moister south-facing slopes support thorny thickets dominated by low-grown evergreen trees (*Euclea*, *Pappea*, *Cussonia*, *Ptaeroxylon*, *Hippobromus*, *Schotia*)

and shrubs (*Putterlickia*, *Gymnosporia*, *Carissa*, *Azima*) with less pronounced participation of succulent shrubs and trees; due to low radiation intensity, the herbaceous layer is poorly developed.

### Experimental design

Two cattle breeds (Nguni, and Bonsmara) raised under commercial and traditional or communal grazing systems were selected to participate in the trial. The animals were grouped into 3 different age groups using a  $2 \times 3$  factorial experimental design. A total number of 84 healthy cows aged 24–120 months were selected randomly and grouped by age as follows: A (young adult cows,  $n = 7$ , 24–48 months old), B (adult cows,  $n = 7$ , 60–80 months old), and C (old adult cows,  $n = 7$ , 90–120 months) per breed in either grazing systems. Communal grazing systems refer to an area of grazing land which is directly owned in undivided shares by all members of a community while in a commercial set-up, an individual farmer privately owns the land and has an organized grazing routine. All the selected cows had similar parity and physiological status and had unlimited ability to graze in the field. Data was collected on methane production and several performance parameters such as bodyweight by a weighing scale and condition for 12 days. During this period, body condition scores were assessed based on the 5-point scale (1=very thin or emaciated to 5=obese). According to (Aumont et al. 1994 and Enicias and Lardy 2002), assessment of body condition involved visual appraisal, palpation of the spinal process, lumbar vertebrae area between the back of the ribs, and the front of the pelvic bones of each individual cow. One assessor conducted this throughout the study period for consistency. Methane emission was measured for all activities, including feeding, ruminating, and resting, either standing or lying every day. Pasture samples were also taken from the study sites for proximate nutrient composition analysis.

### Forage nutrient composition

Random and blended samples of plant species were collected using a 1-m by 1-m quadrant in a belt transect measuring 100 by 25 m in the communal grazing areas and from each paddock of the commercial grazing system. The weight of plant samples was obtained by weighing before drying. Plant samples were oven dried at 60 °C for 48 h and re-weighed to establish the plant sample's dry matter content. Samples were then ground and sieved through a 2-mm sieve before proximate analyses of neutral detergent fibre (NDF), acid detergent fibre (ADF), and acid detergent lignin (ADL) as described by Mertens (2002). Total digestible nutrients (TDN) were determined conventionally from the calculation ( $TDN = 0.479 NDF + 0.704 NFC + 1.594 EE + 0.714 CP$ ) where  $NFC = OM - (NDF + EE + CP)$ .

### Laser methane detector

A hand-held LMD (Crowcon, Tokyo Gas Engineering Co. Ltd. 2006) was used to measure the enteric methane production when the animals were resting (either standing or lying down). LMD measures the concentration of  $CH_4$  between the equipment and the target point. It is based on infrared absorption spectroscopy and measures  $CH_4$  values as a plume. The equipment works effectively between 0 and 40 °C temperature range, 20–90% humidity range, with a reaction time of 0.1 s. The LMD can detect  $CH_4$  concentrations between 1 and 50,000 ppm within up to 150 m.

### Measuring methane

Point measurements (expressed in ppm/m) were taken continuously for 4 min by 60 s intervals at a distance of 3 m away from each animal, following the method by (Jones et al. 2011 and Jonker et al. 2020). Due to the data's cyclic nature (respiratory tidal cycle), a point measurement over each exhalation-inhalation cycle was taken. The peaks of each cycle determined the enteric methane output of each individual cow. Before commencing measurements for each day, the LMD was offset to adjust it to the ambient  $CH_4$  in the atmosphere. Off-setting the LMD was done to account for the  $CH_4$  in the environment before the machine records the gas concentrations from the point source (Chagunda and Yan 2011). Gas column density for  $CH_4$  was measured by directing the auxiliary LMD targeting the (visible HeNe laser) collimated laser beam on the cow's nostril to estimate the gas concentration 3 m away from each cow (Chagunda et al. 2009; Jones et al. 2011; McGinn et al. 2011). The 3-m distance aimed to minimize any disturbances from the observer to each cow's state of rest, feeding, or ruminating and subsequently converted the ppm/m into ppm (Chagunda et al. 2009; Chagunda 2013).

### Calculating methane produced

The point measurements from each cow were used to estimate the amount of  $CH_4$  produced, either resting or standing per day. The amount of methane produced was expressed as a proportion of the tidal volume (Tenney 1982). Calculations derived from the tidal volume were then converted into grams per day using the density of  $CH_4$  following the formulae developed by (Chagunda et al. 2009). The following formula was used:

$$M_{DG} = 0.00066715 \times M_{TV} \times TV_r$$

where  $M_{DG}$  is the daily enteric methane expressed in grams after including the specific density conversion factor,  $M_{TV}$  is the methane from breath point measurements in millilitres during various activities, and  $TV_r$  represents the tidal volume of air when the animals were feeding,

ruminating, or resting (either standing or lying down). Data from live weight was used to estimate CH<sub>4</sub> per 100 kg of live weight and dry matter intake (DMI), where percentages of live body weight estimated to equal to DMI used were derived from studies (Du Toit et al. 2013). Values of DMI were then used to make calculations of the subsequent CH<sub>4</sub> output per kilogram DMI.

### Statistical analysis

Data collected were analysed using the Statistical Analysis Software (version 9.4) with days of sampling as repeated factors, while grazing system, breed, age group, and their interactions were fixed factors, and each individual cow was considered an experimental unit. The grazing system was the only factor for forage nutrient composition. The mean separation was done using Tukey's least significant difference (LSD) method. Variables with a  $P < 0.05$  were accepted to be significant.

The following model below was adopted for the analysis.

$$y_{ijkh} = \mu + \tau_i + \delta_j + t_k + (\tau * \delta)_{ij} + (\tau * t)_{ik} + (\delta * t)_{jk} + \varepsilon_{ijkh}$$

where

$y_{ijkh}$  = response variable, i.e. methane production;  $\mu$  = the overall mean;  $\tau_i$  = the effect of grazing system where ( $i = 2$ ; communal and commercial grazing systems);  $\delta_j$  = the effect of breed where ( $j = 3$ ; Nguni and Bonsmara breeds); and  $t_k$  = the effect of age category where ( $k = 3$ ; A, B, and C where category A contains cows between 2 and 4 years, B contains cows between 4 and 6 years, and C contains cows between 7 and 9 years). The effect of interactions  $(\tau * \delta)_{ij}$ ,  $(\tau * t)_{ik}$ , and  $(\delta * t)_{jk}$  was between grazing systems and breed, grazing system and age category, and breed and age category  $\tau * \delta$ ,  $\tau * t$ ,  $\delta * t$ .  $\varepsilon_{ijkh}$  = random error

## Results

### Proximate composition of pastures from grazing areas

Proximate nutrient composition of the pasture samples collected during the current study is described in Table 1. Apart from higher content ( $P < 0.05$ ) of acid detergent fibre and ash from the two grazing systems, none of the variables showed any significant differences with regard to the nutritional composition of the collected pasture samples.

### Effect of single factors on methane production and performance

The results for the methane production, DMI, and performance variables according to different age groups of the two cattle breeds are shown in Table 2. Older animals

**Table 1** Proximate composition of pastures from grazing systems

Fractions/compositions	Commercial	Communal	SEM	P-value
Dry matter (%)	92.55	92.10	0.226	0.1753
Ash (%)	8.94	8.27	0.210	0.0321
Ether extract (%)	1.41	1.42	0.064	0.9193
Crude protein (%)	12.12	12.36	0.313	0.5867
Neutral detergent fibre (%)	61.21	60.60	0.417	0.3119
Acid detergent fibre (%)	30.63	28.27	0.494	0.0021
Total digestible nutrient (%)	52.76	53.22	0.159	0.0503
Non-fibre carbohydrate (%)	17.82	18.62	0.363	0.1313

produced significantly higher methane per head ( $C > B > A$ ;  $P < 0.0001$ ) irrespective of the breed or grazing system.

Nevertheless, methane production did not differ across age groups when determined using DMI and body weight ( $P > 0.05$ ; Table 2). DMI and bodyweight were considerably different from one another and higher in older animals. All age groups' physical condition was the same ( $P > 0.05$ ; Table 2). Independent of other variables, Bonsmara beef cows had higher body condition, body weight, DMI, and daily methane per head ( $P < 0.05$ ; Table 3). The output of methane per unit of body weight was higher in Nguni cows; however, methane per unit of dry matter did not differ between breeds ( $P > 0.05$ ; Table 3). In the commercial grazing regime, physical condition, body weight, and DMI were higher ( $P < 0.05$ ; Table 4). On the other hand, daily methane production as well as methane production per DMI and body weight was all higher in the communal grazing system ( $P < 0.05$ ; Table 4).

### Effect of interaction of factors on methane production

For some variables and some parameters, the interaction of factors had a substantial impact (Table 5). Body weight, DMI, and methane production in Bonsmara in either grazing system showed a significant and greater ( $P < 0.05$ ) breed-breed interaction. In a communal context, it had no effect on the production of methane per DMI, per body weight, or between breeds ( $P > 0.05$ ). In age group C for both grazing systems, the interaction between grazing system and age was significant and higher ( $P < 0.05$ ) for body condition, body weight, and DMI. The generation of methane, methane per DMI, and methane per body weight in all ages were not impacted ( $P > 0.05$ ).

In age group C for either breed, the interaction between breed and age was greater ( $P < 0.05$ ) and more significant for bodyweight, DMI, and methane production. For both

**Table 2** Means ( $\pm$  SEM) of methane production and weight accumulation as affected by age

Variables	Age group			P-value
	A (n = 7)	B (n = 7)	C (n = 7)	
Body weight (kg)	3.13 <sup>a</sup> $\pm$ 0.022	3.14 <sup>a</sup> $\pm$ 0.022	3.16 <sup>a</sup> $\pm$ 0.022	0.5895
DMI (kg/day)	282.60 <sup>c</sup> $\pm$ 2.912	409.52 <sup>b</sup> $\pm$ 2.963	496.05 <sup>a</sup> $\pm$ 2.947	< 0.0001
CH <sub>4</sub> (g/day/head)	7.65 <sup>c</sup> $\pm$ 0.079	11.06 <sup>b</sup> $\pm$ 0.080	13.41 <sup>a</sup> $\pm$ 0.080	< 0.0001
CH <sub>4</sub> (g/kg DMI)	176.32 <sup>c</sup> $\pm$ 4.057	267.71 <sup>b</sup> $\pm$ 4.127	294.27 <sup>a</sup> $\pm$ 4.106	< 0.0001
CH <sub>4</sub> (g/100 kg body weight)	24.61 <sup>a</sup> $\pm$ 0.654	24.96 <sup>a</sup> $\pm$ 0.665	22.30 <sup>b</sup> $\pm$ 0.662	0.1035
Body weight (kg)	66.12 <sup>a</sup> $\pm$ 1.711	67.24 <sup>a</sup> $\pm$ 1.741	59.97 <sup>b</sup> $\pm$ 1.732	0.0901

Different letters "a, b and c" represent significant differences ( $P \leq 0.05$ ) between age groups

**Table 3** Means ( $\pm$  SEM) of methane production and other performance parameters as affected by breed

Performance and methane production	Breed		P-value
	Bonsmara	Nguni	
Body condition score (BCS)	3.23 <sup>a</sup> $\pm$ 0.018	3.05 <sup>b</sup> $\pm$ 0.018	< 0.0001
Body weight (kg)	424.09 <sup>a</sup> $\pm$ 2.387	368.02 <sup>b</sup> $\pm$ 2.415	< 0.0001
DMI (kg/day)	11.47 <sup>a</sup> $\pm$ 0.065	9.95 <sup>b</sup> $\pm$ 0.065	< 0.0001
CH <sub>4</sub> (g/day/head)	254.32 <sup>a</sup> $\pm$ 3.326	237.88 <sup>b</sup> $\pm$ 3.364	0.0005
CH <sub>4</sub> (g/kg DMI)	23.10 <sup>a</sup> $\pm$ 0.536	24.81 <sup>a</sup> $\pm$ 0.542	0.0873
CH <sub>4</sub> (g/100 kg body weight)	62.16 <sup>b</sup> $\pm$ 1.403	66.73 <sup>a</sup> $\pm$ 1.419	0.0223

Different letters "a and b" represent significant differences ( $P \leq 0.05$ ) between breeds

**Table 4** Means ( $\pm$  SEM) of methane production and other performance parameters as affected by grazing system

Parameter	Grazing		P-value
	Commercial	Communal	
BCS	3.22 <sup>a</sup> $\pm$ 0.018	3.06 <sup>b</sup> $\pm$ 0.018	< 0.0001
Body weight (kg)	410.34 <sup>a</sup> $\pm$ 2.397	381.77 <sup>b</sup> $\pm$ 2.405	< 0.0001
DMI (kg/day)	11.49 <sup>a</sup> $\pm$ 0.065	9.93 <sup>b</sup> $\pm$ 0.065	< 0.0001
CH <sub>4</sub> (g/day/head)	240.30 <sup>b</sup> $\pm$ 3.339	251.90 <sup>a</sup> $\pm$ 3.350	< 0.0144
CH <sub>4</sub> (g/kg DMI)	21.49 <sup>b</sup> $\pm$ 0.538	26.42 <sup>a</sup> $\pm$ 0.540	< 0.0001
CH <sub>4</sub> (g/100 kg body weight)	60.16 <sup>b</sup> $\pm$ 1.408	68.72 <sup>a</sup> $\pm$ 1.413	< 0.0001

Different letters "a and b" represent significant differences ( $P \leq 0.05$ ) between grazing systems

breeds, it had no effect on body condition, methane per DMI, or methane per body weight at any age ( $P > 0.05$ ).

## Discussion

The methane values found in the current study are in the same ballpark as those found in earlier investigations on cattle. In general, the study's measurements of methane production are higher than those made public by (Bird-Gardiner et al. 2015). Yet, they are consistent with the South African commercial beef cattle report

by (Du Toit et al. 2014). Ruminants' retention time, body weight, and DMI have all been linked to studies on the impact of age on methane emission (Molano and Clark 2008; Swainson et al. 2010; Jiao et al. 2017). In the current study, breed and grazing system were just as important as age in determining the animals' bodily condition. Younger animals created more methane, while older animals were heavier and produced more methane per DMI and body weight. Our results support those of recent studies (Bird-Gardiner et al. 2015; Liu et al. 2017), which found that methane output rises with age. The association between ruminal inefficiencies and ageing and physiological status, which are known to effect changes in the rumen microbiota and methanogens in particular, can be blamed for this (Kumar et al. 2015; Pitta et al. 2016; Wang et al. 2016; Dill-Mcfarland et al. 2017).

The quantitative examination of overall methanogen and bacterial population numbers demonstrates that the methanogen population increases with age, which lends weight to the aforementioned claim. The role of rumen-dwelling methanogens in the production of methane in ruminants has always attracted scientific attention, but other microbes and particular bacteria have not been well studied in relation to age-driven physiological changes and the status of the animal in relation to methane production. Yet, studies have described the coexistence of archaea, bacteria, fungi, and ciliates that relate to the hosts' physiological status in various ways (Fouts et al. 2012; Lee et al. 2012; Kittekmann et al. 2013; Li et al. 2015).

The current study demonstrates that the Bonsmara breed produced more methane than the Nguni breed and had superior physical condition, greater body weight, and DMI. Nguni nonetheless generated more methane per unit of body weight. This suggests a considerable breed influence on ruminal methane that has been previously documented (Bird-Gardiner et al. 2015; Roehe et al. 2016; Noel et al. 2019). (De Mulder et al. 2018)'s findings, which did not identify a breed influence on

**Table 5** Means ( $\pm$  SEM) of methane production and other performance parameters as affected by the interaction

		BCS	Bodyweight (kg)	DMI (kg/day)	CH <sub>4</sub> (g/day/head)	CH <sub>4</sub> (g/kg DMI)	CH <sub>4</sub> (g/100 kg BW)
Communal	Bonsmara	3.13 <sup>a</sup> $\pm$ 0.025	404.85 <sup>a</sup> $\pm$ 3.362	10.53 <sup>a</sup> $\pm$ 0.091	255.15 <sup>a</sup> $\pm$ 468	25.14 <sup>a</sup> $\pm$ 0.755	65.36 <sup>a</sup> $\pm$ 1.976
	Nguni	3.00 <sup>b</sup> $\pm$ 0.025	358.69 <sup>b</sup> $\pm$ 3.440	9.33 <sup>b</sup> $\pm$ 0.093	248.64 <sup>a</sup> $\pm$ 4.792	27.71 <sup>a</sup> $\pm$ 0.772	72.09 <sup>a</sup> $\pm$ 2.021
Commercial	Bonsmara	3.34 <sup>a</sup> $\pm$ 0.025	443.34 <sup>a</sup> $\pm$ 3.390	12.41 <sup>a</sup> $\pm$ 0.092	253.49 <sup>a</sup> $\pm$ 4.723	21.06 <sup>a</sup> $\pm$ 0.761	58.96 <sup>a</sup> $\pm$ 1.992
	Nguni	3.10 <sup>b</sup> $\pm$ 0.025	377.35 <sup>b</sup> $\pm$ 3.390	10.57 <sup>b</sup> $\pm$ 0.092	227.11 <sup>b</sup> $\pm$ 4.723	21.92 <sup>a</sup> $\pm$ 0.761	61.37 <sup>a</sup> $\pm$ -1.992
Grazing $\times$ age							
Communal	A	3.08 <sup>a</sup> $\pm$ 0.031	264.12 <sup>c</sup> $\pm$ 4.118	6.87 <sup>c</sup> $\pm$ 0.111	181.79 <sup>c</sup> $\pm$ 5.737	28.17 <sup>a</sup> $\pm$ 0.924	73.31 <sup>a</sup> $\pm$ 2.420
	B	3.10 <sup>a</sup> $\pm$ 0.031	403.15 <sup>b</sup> $\pm$ 4.209	10.48 <sup>b</sup> $\pm$ 0.114	270.79 <sup>b</sup> $\pm$ 5.864	26.48 <sup>a</sup> $\pm$ 0.945	68.84 <sup>a</sup> $\pm$ 2.473
	C	3.01 <sup>a</sup> $\pm$ 0.031	478.04 <sup>a</sup> $\pm$ 4.169	12.43 <sup>a</sup> $\pm$ 0.113	303.11 <sup>a</sup> $\pm$ 5.808	24.62 <sup>a</sup> $\pm$ 0.936	64.02 <sup>a</sup> $\pm$ 2.449
Commercial	A	3.18 <sup>ab</sup> $\pm$ 0.031	301.08 <sup>c</sup> $\pm$ 4.1178	8.43 <sup>c</sup> $\pm$ 0.111	170.86 <sup>b</sup> $\pm$ 5.737	21.05 <sup>a</sup> $\pm$ 0.924	58.94 <sup>a</sup> $\pm$ 2.420
	B	3.17 <sup>b</sup> $\pm$ 0.031	415.89 <sup>b</sup> $\pm$ 4.169	11.64 <sup>b</sup> $\pm$ 0.113	264.63 <sup>a</sup> $\pm$ 5.808	23.44 <sup>a</sup> $\pm$ 0.936	65.64 <sup>a</sup> $\pm$ 2.449
	C	3.30 <sup>a</sup> $\pm$ 0.031	514.06 <sup>a</sup> $\pm$ 4.169	14.39 <sup>a</sup> $\pm$ 0.113	285.42 <sup>a</sup> $\pm$ 5.808	19.97 <sup>a</sup> $\pm$ 0.936	55.91 <sup>a</sup> $\pm$ 2.449
Breed $\times$ age							
Bonsmara	A	3.18 <sup>cb</sup> $\pm$ 0.031	301.06 <sup>c</sup> $\pm$ 4.118	8.15 <sup>c</sup> $\pm$ 0.111	175.46 <sup>c</sup> $\pm$ 5.737	23.12 <sup>a</sup> $\pm$ 0.924	62.16 <sup>ab</sup> $\pm$ 2.420
	B	3.19 <sup>b</sup> $\pm$ 0.031	427.74 <sup>b</sup> $\pm$ 4.118	11.56 <sup>b</sup> $\pm$ 0.111	279.14 <sup>b</sup> $\pm$ 5.737	24.93 <sup>a</sup> $\pm$ 0.924	67.14 <sup>a</sup> $\pm$ 2.420
	C	3.32 <sup>a</sup> $\pm$ 0.031	543.47 <sup>a</sup> $\pm$ 4.169	14.70 <sup>a</sup> $\pm$ 0.112	308.37 <sup>a</sup> $\pm$ 5.808	21.25 <sup>a</sup> $\pm$ 0.936	57.18 <sup>b</sup> $\pm$ 2.449
Nguni	A	3.07 <sup>a</sup> $\pm$ 0.031	264.14 <sup>c</sup> $\pm$ 4.118	7.15 <sup>c</sup> $\pm$ 0.111	177.19 <sup>c</sup> $\pm$ 5.737	26.10 <sup>a</sup> $\pm$ 0.924	70.08 <sup>a</sup> $\pm$ 2.420
	B	3.09 <sup>a</sup> $\pm$ 0.032	391.30 <sup>b</sup> $\pm$ 4.2601	10.57 <sup>b</sup> $\pm$ 0.115	256.28 <sup>b</sup> $\pm$ 5.935	24.99 <sup>a</sup> $\pm$ 0.956	67.35 <sup>a</sup> $\pm$ 2.503
	C	2.99 <sup>a</sup> $\pm$ 0.031	448.63 <sup>a</sup> $\pm$ 4.1685	12.12 <sup>a</sup> $\pm$ 0.112	280.16 <sup>a</sup> $\pm$ 5.808	23.34 <sup>a</sup> $\pm$ 0.936	62.75 <sup>a</sup> $\pm$ 2.449
Interactions				<i>P</i> -value			
Grazing $\times$ breed		0.0996	0.0036	0.0004	0.0359	0.2606	0.2783
Grazing $\times$ age		0.0376	0.0046	0.0019	0.6094	0.0874	0.0721
Breed $\times$ age		0.1414	< 0.0001	< 0.0001	0.0219	0.2796	0.2716

Different letters "a, b, c, and d" represent significant interaction effects ( $P \leq 0.05$ ) between breeds, age groups and grazing systems

methane output and only weakly attributed the variation in methane production to feed-related parameters, are in conflict with this. This study's findings on the breed impact conflict with those of (Mapfumo et al. 2018), who found no interbreed variance in methane generation and attributed this to cattle breeds' similar foraging traits and evolutionary tactics (Scholtz et al. 2013). Why Nguni produced more methane on a BW basis than Bonsmara is unclear. Even yet, the outcome of the present investigation might be explained by host genetic components, within-breed variance, or even peculiarities in the experimental animals. The influence of the microbial profile and its correlation with breed type differences may result in host genetics having an impact on methane emissions. The biological factors such as pH of ruminal digesta controlled by saliva bicarbonates, VFAs absorption rate, and proton passage rate out of the rumen that relates to the mechanisms that underlie breed genetics influence on host-microbial profile are partly genetically determined (Aschenbach et al. 2011; Appuhamy et al. 2014). The rumen's microbial population and methane generation are also impacted by changes in the digesta's passage rate, contraction severity, and physical structure. Smaller rumen sizes have been linked to lower methane emissions because of shorter digesta retention times, according to (Goopy et al. 2014).

Digesta retention duration in ruminants is heritable, claim (Smuts et al. 1995). (Wang and Kasper 2014) came to the conclusion that the microbiome and its host have a very complex interaction. Therefore, it can be concluded that there were fewer methane emissions as a result of the interaction between Nguni cows (the host) and their ruminal microbiota. For efficient breeding and selection, more research should be done to identify the precise mechanism causing the low methane emission in Nguni beef breeds. Animals in the community grazing system created more methane on a daily basis regardless of breed or age, but animals in the commercial grazing system had superior body condition, higher body weight, and DMI. Comparable grazing methods in South Africa produced similar outcomes elsewhere (Du Toit et al. 2013). The nutritional composition of the natural pastures from both grazing systems in this study was similar, with the exception of ash and acid detergent fibre fractions, which were slightly higher in the commercial grazing system (Table 1). Thus, these variations in methane generation may be brought on by variations in the fatty acid composition of the pastures in each grazing setting. An analysis of 29 studies using meta-analysis provides strong evidence in favour of this claim (Patra 2013).

Variations in feed consumption, outflow rates, and digesta retention time, which are influenced by both

inter- and intra-breed variances, can also cause variations in enteric methane output (Hammond et al. 2014; Vendl et al. 2016). Moreover, communal foraging practices might expose animals that are allowed to roam free and without control to a variety of food species. Variations in the species composition lead to greater heterogeneity in forage quality and quantity, which determines unevenly shifting trends in forage availability every day (Pinka 2006; Estevez et al. 2007). Higher methane levels in communal systems may be caused by this. According to a previous study, good pasture management using paddocks and pasture resting resulted in good-quality feed, which in this study was associated with reduced methane values in commercial systems (Zhao et al. 2015). This is consistent with data from (DeRamus et al. 2003) who discovered a 22% decline in beef cattle grazing on forages from commercial grazing system when compared with communal/continuous or emergent grazing system. According to the literature, well-managed pastures create more propionate during their fermentation, which reduces the amount of hydrogen that is available for methanogenesis (Beauchemin and McGinn 2005; Janssen 2010; Cottle et al. 2011).

There were not many significant factor interactions. They have a similar explanation. For instance, given a similar grazing habitat, the relationship between breed and grazing system reveals that Bonsmara produce more methane. This is explained by the breed or host genetics mentioned above. Moreover, there was a substantial and higher level of interaction between breed and age for BW, DMI, and methane production in age group C for both breeds. This is also linked to the age-related microbial change that was previously mentioned. Although it had an impact on body condition, DMI, and BW, the relationship between grazing and age did not significantly affect methane generation.

## Conclusion

Age was shown to be the primary determining factor in the study's findings that communally maintained cattle create more enteric methane than those kept in commercial farming settings. This could be explained by the conditions on the grazing range for elderly animals, ruminal inefficiencies, and the fact that ruminal methanogen populations rise with age. The Nguni breed produced low methane per head but higher methane on a BW basis compared to Bonsmara, indicating that breed or host genetics and age greatly impact methane emissions. This could be as a result of breed type or host genetic variations influencing the features of rumen fermentation as well as the dynamics of the microbial composition.

## Authors' contributions

MS revised the manuscript and made a substantial contribution to the manuscript. KD conceived, planned, and produced the first draft of this manuscript. JI.F made suggestions and reviewed and supervised the write-up. CM made suggestions and supervised the write-up. KD made suggestions and supervised the write-up. The authors read and approved the final manuscript.

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## Availability of data and materials

Data will be provided upon request.

## Declarations

### Ethics approval and consent to participate

Ethical clearance was obtained from the University of Fort Hare Research Ethics Committee with certificate number MUC041SKAY01 that approved the use of animals for study purposes.

### Consent for publication

The authors affirm that the content of this manuscript has not been published or submitted to any journal elsewhere, and acknowledgement has been made where the work of others has been used.

### Competing interests

The authors declare that they have no competing interests.

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## References

- Alexandratos, N. 2009. *World food and agriculture to 2030/2050: highlights and views from mid-2009. paper for the expert meeting on how to feed the world in 2050*, 24–26. Rome: FAO.
- Appuhamy, J.A.D.R.N., C. Wagner-Riddle, D.P. Casper, J. France, and E. Kebreab. 2014. Quantifying body water kinetics and fecal and urinary water output from lactating Holstein dairy cows. *Journal of Dairy Science* 97: 6177–6195.
- Aschenbach, J.R., G.B. Penner, F. Stumpff, and G. Gäbel. 2011. Ruminant nutrition symposium: role of fermentation acid absorption in the regulation of ruminal pH12. *Journal of Animal Science* 89: 1092–1107 (Narnia).
- Aumont, G., F. Poisot, G. Saminadin, H. Borel, and G. Alexandre. 1994. Body condition score and adipose cell size determination for in vivo assessment of body composition and post-mortem predictors of carcass components of Creole goats. *Small Ruminant Research* 15: 77–85.
- Banakar, P.S., N. Anand Kumar, G.C. Shashank, and L. Neeti. 2018. Physical effective fibre in ruminant nutrition: a review. *Journal of Pharmacognosy and Phytochemistry* 7: 303–308.
- Basarab, J., K. Beauchemin, V. Baron, K.H. Omski, L.L. Guan, S.P. Miller, and J.J. Crowley. 2013. Reducing GHG emissions through genetic improvement for feed efficiency: Effects on economically important traits and enteric methane production. *Animal* 7: 303–315.
- Beauchemin, K., and S. McGinn. 2005. Methane emissions from feedlot cattle fed barley or corn diets. *Journal of Animal Science* 83: 653–661.
- Berman, A. 2011. Invited review: Are adaptations present to support dairy cattle productivity in warm climates? *Journal of Dairy Science* 94: 2147–2158.
- Bird-Gardiner, T., K. Donoghue, P. Arthur, R. Herd, and R. Hegarty. 2015. Divergent selection for methane yield in beef cattle. In *Proc. Association for the Advancement of Animal Breeding and Genetics* 21: 122–125.
- Carberry, C., S. Waters, and D. Kenny. 2014. Rumen methanogenic genotypes differ in abundance according to host residual feed intake phenotype and diet type. *Applied and Environmental Microbiology* 80: 586–594.

- Chagunda, M.G.G. 2013. Opportunities and challenges in the use of the laser methane detector to monitor enteric methane emissions from ruminants. *Animal* 7: 394–400.
- Chagunda, M.G.G., D. Ross, and D.J. Roberts. 2009. On the use of a laser methane detector in dairy cows. *Computers and Electronics in Agriculture* 68: 157–160.
- Chagunda, M., T. Yan, and T. 2011. Do methane measurements from a laser detector and an indirect open-circuit respiration calorimetric chamber agree sufficiently closely? *Animal Feed Science and Technology* 165: 8–14.
- Cottle, D.J., J.V. Nolan, and S.G. Wiedemann. 2011. Ruminant enteric methane mitigation: a review. *Animal Production Science* 51: 491–514.
- De Mulder, T., N. Peiren, L. Vandaele, T. Ruttink, S. De Campeneere, T. Van de Wiele, and K. Goossens. 2018. Impact of breed on the rumen microbial community composition and methane emission of holstein friesian and belgian blue heifers. *Livestock Science* 207: 38–44 (Elsevier).
- DeRamus, H.A., T.C. Clement, D.D. Giampola, and P.C. Dickson. 2003. Methane emissions of beef cattle on forages. *Journal of Environment Quality* 32 (1): 269.
- Dill-McFarland, K.A., J.D. Breaker, and G. Suen. 2017. Microbial succession in the gastrointestinal tract of dairy cows from 2 weeks to first lactation. *Scientific Reports* 7: 40864 (Nature Publishing Group).
- Du Toit, C.J., H. Meissner, and W. Van Nieke. 2013. Direct methane and nitrous oxide emissions of South African dairy and beef cattle. *South African Journal of Animal Science* 43: 320–339.
- Du Toit, C., H. Meissner, and W. Van Niekerk. 2014. Direct methane and nitrous oxide emissions of South African dairy and beef cattle. *South African Journal of Animal Science* 43: 320 (South African Society for Animal Science).
- Eastern Cape Socio-Economic Consultative Council (ECSECC) (2012). Eastern Cape Development Indicators—2012. [http://www.ecsecc.org/files/library/documents/EasternCape\\_withDMs.pdf](http://www.ecsecc.org/files/library/documents/EasternCape_withDMs.pdf). Accessed 27 Oct 2020
- Enicias, A.M. and G. Lardy. 2002. Body condition scoring: Managing your herd through body condition scoring <https://library.ndsu.edu/ir/bitstream/handle/10365/5343/as1026.pdf?sequence1&isAllowed=y>. Accessed 29 Nov 2020
- Estevez, I., I.-L. Andersen, and E. Nævdal. 2007. Group size, density and social dynamics in farm animals. *Applied Animal Behaviour Science* 103: 185–204.
- Fouts, D.E., S. Szpakowski, J. Purushe, M. Torralba, R.C. Waterman, M.D. MacNeil, L.J. Alexander, and K.E. Nelson. 2012. Next generation sequencing to define prokaryotic and fungal diversity in the bovine rumen. *PLoS ONE* 7: e48289.
- Goopy, J.P., A. Donaldson, R. Hegarty, P.E. Vercoe, F. Haynes, M. Barnett, and V.H. Oddy. 2014. Low-methane yield sheep have smaller rumens and shorter rumen retention time. *British Journal of Nutrition* 111: 578–585 (Cambridge University Press).
- Grainger, C., and K. Beauchemin. 2011. Can enteric methane emissions from ruminants be lowered without lowering their production? *Animal Feed Science and Technology* 166: 308–320.
- Hammond, K., D. Pacheco, J. Burk, J. Koolaard, S. Muetzel, and G. Waghorn. 2014. The effects of fresh forages and feed intake level on digesta kinetics and enteric methane emissions from sheep. *Animal Feed Science and Technology* 193: 32–43.
- Henderson, G., F. Cox, S. Ganesh, A. Jonker, W. Young, G.R. Collaborators, L. Abecia, E. Angarita, P. Aravena, G. Arenas, and C. Ariza. 2015. Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. *Science Report* 5: 14567.
- Hernandez-Sanabria, E., L.A. Goonewardene, Z. Wang, M. Zhou, S.S. Moore, and L.L. Guan. 2013. Influence of sire breed on the interplay among rumen microbial populations inhabiting the rumen liquid of the progeny in beef cattle. *PLoS ONE* 8: 1–29.
- Jami, E., A. Israel, A. Kotser, I. Mizrahi. 2013. Exploring the bovine rumen bacterial community from birth to adulthood. *ISME J* 7, 1069
- Jami, E., and I. Mizrahi. 2012. Composition and similarity of bovine rumen microbiota across individual animals. *PLoS ONE* 7: e33306.
- Janssen, P.H. 2010. Influence of hydrogen on rumen methane formation and fermentation balances through microbial growth kinetics and fermentation thermodynamics. *Animal Feed Science and Technology* 160: 1–22 (Elsevier).
- Jiao, P.X., L.Y. Wei, N.D. Walker, F.Z. Liu, L.Y. Chen, K.A. Beauchemin, and W.Z. Yang. 2017. Comparison of non-encapsulated and encapsulated active dried yeast on ruminal pH and fermentation, and site and extent of feed digestion in beef heifers fed high-grain diets. *Animal Feed Science and Technology* 228: 13–22 (Elsevier).
- Jiyana, S.T., M.M. Ratsaka, K.J. Leeuw, and K.R. Mbatha. 2021. Effects of dietary fibre level on rumen pH, total microbial count and methanogenic archaea in Bonsmara and Nguni steers. *South African Journal of Animal Science* 51 (1): 75–80.
- Jones, F.M., F.A. Phillips, T. Naylor, and N.B. Mercer. 2011. Methane emissions from grazing Angus beef cows selected for divergent residual feed intake. *Animal Feed Science and Technology* 166–167: 302–307.
- Jonker, A., M.G.G. Chagunda, M. Grobler, G.C. Waghorn, and J.D. van Wynaarde. 2020. Hand held laser methane detector to determine methane plume concentrations from ruminants. In *Guidelines for estimating methane emissions from individual ruminants using: GreenFeed, 'sniffers', hand-held laser detector and portable accumulation chambers*, 41–47. Ministry for Primary Industries (New Zealand Agricultural Greenhouse Gas Research Centre): Publisher.
- Kittlmann, S., H. Seedorf, W.A. Walters, J.C. Clemente, R. Knight, J.I. Gordon, and P.H. Janssen. 2013. Simultaneous amplicon sequencing to explore co-occurrence patterns of bacterial, archaeal and eukaryotic microorganisms in rumen microbial communities. *PLoS ONE* 8: e47879.
- Kumar, S., N. Indugu, B. Vecchiarelli, and D.W. Pitta. 2015. Associative patterns among anaerobic fungi, methanogenic archaea, and bacterial communities in response to changes in diet and age in the rumen of dairy cows. *Frontiers in Microbiology* 6: 781 (Frontiers).
- Lee, H., J. Jung, Y. Oh, S. Lee, E. Madsen, and C. Jeon. 2012. Comparative survey of rumen microbial communities and metabolites across one caprine and three bovine groups, using bar-coded pyrosequencing and <sup>1</sup>H nuclear magnetic resonance spectroscopy. *Applied Environmental Microbiology* 78: 5983–5993.
- Li, Z., A.-D.G. Wright, H. Liu, Z. Fan, F. Yang, Z. Zhang, and G. Li. 2015. Response of the rumen microbiota of sika deer (*Cervus nippon*) fed different concentrations of tannin rich plants. *PLoS ONE* 10: e0123481.
- Li, F., T.C.A. Hitch, Y. Chen, C.J. Creevey, and L.L. Guan. 2019. Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. *Microbiome* 7: 6 (BioMed Central).
- Liu, C., Q. Meng, Y. Chen, M. Xu, M. Shen, R. Gao, and S. Gan. 2017. Role of age-related shifts in rumen bacteria and methanogens in methane production in cattle. *Frontiers in Microbiology* 8: 1563 (Frontiers Media S.A.).
- McGinn, S.M., D. Turner, N. Tomkins, E. Charmley, G. Bishop-Hurley, and D. Chen. 2011. Methane emissions from grazing cattle using point-source dispersion. *Journal of Environment Quality* 40: 22.
- Mapfumo, L., V. Muchenje, M.M. Scholtz, S.M. Grobler and J.F. Mupangwa. 2018. Enteric methane output from selected herds of beef cattle raised under extensive arid rangelands. *Pastoralism: Research, Policy and Practice SHORT*, 8 (1)
- Molano, G., and H. Clark. 2008. The effect of level of intake and forage quality on methane production by sheep. *Australian Journal of Experimental Agriculture* 48: 219.
- Morgavi, D.P., W.J. Kelly, P.H. Janssen, and G.T. Attwood. 2013. Rumen microbial (meta)genomics and its application to ruminant production. *Animal* 7: 184–201.
- Mucina, L., D. Hoare, M. Lötter, P. du Preez, M. Rutherford, C. Scott-Shaw, G. Bredenkamp, L. Powrie, L. Scott, K.G. Camp, and S. Cilliers. 2006. Grassland biome, Savanna biome and Albany Thicket biome. *The vegetation of South Africa, Lesotho and Swaziland South African National Biodiversity* 19: 347–558.
- Noel, S.J., D.W. Olijhoek, F. Mclean, P. Løvendahl, P. Lund, and O. Højberg. 2019. Rumen and fecal microbial community structure of Holstein and Jersey dairy cows as affected by breed, diet, and residual feed intake. *Animals* 9: 498.
- O'Mara, F.P. 2011. The significance of livestock as a contributor to global greenhouse gas emissions today and in the near future. *Animal Feed Science and Technology* 166–167: 7–15.
- Palangi, V., and M. Lackner. 2022b. Management of enteric methane emissions in ruminants using feed additives: a review. *Animals* 12 (24): 3452 Regards.
- Palangi, V., A. Taghizadeh, S. Abachi, and M. Lackner. 2022a. Strategies to mitigate enteric methane emissions in ruminants: a review. *Sustainability* 14 (20): 13229.



- Patra, A.K. 2013. The effect of dietary fats on methane emissions, and its other effects on digestibility, rumen fermentation and lactation performance in cattle: a meta-analysis. *Livestock Science* 155: 244–254.
- Pitta, D.W., N. Indugu, S. Kumar, B. Vecchiarelli, R. Sinha, and L.D. Baker. 2016. Metagenomic assessment of the functional potential of the rumen microbiome in Holstein dairy cows. *Anaerobe* 38: 50–60.
- Roehe, R., R.J. Dewhurst, C.-A. Duthie, J.A. Rooke, N. McKain, D.W. Ross, J.J. Hyslop, A. Waterhouse, T.C. Freeman, M. Watson, and R.J. Wallace. 2016. Bovine host genetic variation influences rumen microbial methane production with best selection criterion for low methane emitting and efficiently feed converting hosts based on metagenomic gene abundance. *PLoS Genetics* 12: e1005846.
- Ross, E.M., P.J. Moate, L.C. Marett, B.G. Cocks, and B.J. Hayes. 2013. Metagenomic predictions: From microbiome to complex health and environmental phenotypes in humans and cattle. *PLoS ONE* 8: e73056.
- Scholtz, M.M., A. Maiwashe, F.W.C. Neso, A. Theunissen, W.J. Olivier, M.C. Mokobate, and J. Hendriks. 2013. Livestock breeding for sustainability to mitigate global warming, with the emphasis on developing countries. *South African Journal of Animal Science* 43 (3): 269–281.
- Singh, B. 2010. Some nutritional strategies for mitigation of methane emissions. In: International conference on “Physiological capacity building in livestock under changing climate scenario”. Physiology and Climatology division, Indian Veterinary Research Institute, Izatnagar, 243122, Uttar Pradesh, India, November 11–13, pp 142–158.
- Smuts, M., H. Meissner, and P. Cronje. 1995. Retention time of digesta in the rumen: its repeatability and relationship with wool production of Merino rams. *Journal of Animal Science* 73: 206–210.
- Špinková, M. 2006. How important is natural behaviour in animal farming systems? *Applied Animal Behaviour Science* 100: 117–128.
- Swainson, N.M., S.O. Hoskin, H. Clark, and N. Lopez-Villalobos. 2010. The effect of age on methane emissions from young, weaned red deer (*Cervus elaphus*) stags grazing perennial-ryegrass (*Lolium perenne*)-based pasture. *New Zealand Journal of Agricultural Research* 50: 407–416.
- Tenney, S. 1982. Respiration in mammals. In *Duke's physiology of domestic animals*, 9th ed., ed. M.J. Swenson, 175–202. London: Cornell University Press Ltd.
- Tims, S., E.G. Zoetendal, W.M. de Vos, and M. Kleerebezem. 2011. Host genotype and the effect on microbial communities. In *Metagenomics of the human body*, (15–41. New York: Springer).
- Turnbaugh, P., M. Hamady, T. Yatsunenko, and B. Cantarel. 2011. A core gut microbiome in obese and lean twins. *Nature* 457: 480–484
- UN, 2012. World population prospects the 2010 revisions - Population Division - United Nations, (New York-USA)
- Vendl, C., S. Frei, M. Dittmann, S. Furrer, S. Ortmann, A. Lawrenz, B. Lange, A. Munn, M. Kreuzer, and M. Clauss. 2016. Methane production by two non-ruminant foregut-fermenting herbivores: the collared peccary (*Pecari tajacu*) and the pygmy hippopotamus (*Hexaprotodon liberiensis*). *Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology* 191: 107–114.
- Wallace, R.J., T.J. Snelling, C.A. McCartney, I. Tapio, and F. Strozzi. 2017. Application of meta-omics techniques to understand greenhouse gas emissions originating from ruminal metabolism. *Genetics Selection Evolution* 49: 9.
- Wang, Y., and L.H. Kasper. 2014. The role of microbiome in central nervous system disorders. *Brain, Behavior, and Immunity* 38: 1–12.
- Wang, L., Q. Xu, F. Kong, Y. Yang, D. Wu, S. Mishra, and Y. Li. 2016. Exploring the goat rumen microbiome from seven days to two years. *PLoS ONE* 11 (5): e0154354.
- Wright, A.D.G., A.J. Williams, B. Winder, C.T. Christophersen, S.L. Rodgers, and K.D. Smith. 2004. Molecular diversity of rumen methanogens from sheep in Western Australia. *Applied and Environmental Microbiology* 70 (3): 1263–1270.
- Zhao, Y., A. Aubry, and N. O'Connell. 2015. Effects of breed, sex, and concentrate supplementation on digestibility, enteric methane emissions, and nitrogen utilization efficiency in growing lambs offered fresh grass. *Journal of Animal Science* 93: 5764–5773.

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