METHANE EMISSIONS ESTIMATED BASED ON MILK FATTY ACIDS OF JERSEY AND FLECKVIEH X JERSEY COWS IN A PASTURE-BASED SYSTEM

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SUMMARY

Methane emissions by dairy cows have become a major environmental issue as it has been suggested as a major contributor to global warming. In this paper, the methane emissions of 40 Jersey and 62 Fleckvieh x Jersey (FxJ) cows were predicted using specific milk fatty acids (FAs). Cows were on kikuyu pasture supplemented during pasture shortages with a replacement mixture consisting of lucerne hay, oat hay and soybean meal. All cows received the same concentrate mixture twice a day after milking at 7 kg per cow per day. Milk samples (153 Jersey and 283 FxJ), were collected every 35 days over the lactation period, starting from 10 days after calving as per standard milk recording procedures. At least three and maximum seven milk samples per cow were collected over the lactation period. FAs were determined by gas chromatography. From this, methane emissions per unit of dry matter intake using two prediction equations were predicted. Predicted methane emissions varied between breeds although differences were small ($P>0.05$). Using Methane equation 2 and 3, predicted methane emissions for Jersey and FxJ cows were 26.2±1.07 and 25.8±0.94 and 24.6±0.99 and 24.4±1.08 g/kg feed DM, respectively. Methane emissions in both breeds showed curvilinear ($P<0.05$) trends over the lactation period. Over all cows, lactation stage and breeds, the coefficient of variation in predicted methane emissions for Jersey and FxJ cows was approximately 20%, possibly indicating genetic variation among cows. This variation could be used towards reducing methane production in dairy cows.

INTRODUCTION

Methane (CH_4) emissions by dairy cows are a major environmental issue as it has been suggested to be a major contributor to global warming. Dairy cows, being ruminants, contribute directly to greenhouse gas (GHG) emissions as CH_4, a major GHG, is produced through the fermentation processes in the rumen. Methane is released into the atmosphere by natural processes of eructation and breathing. Knapp *et al.* (2014) pointed out that to mitigate enteric CH_4 emissions per unit of energy-corrected milk, herd productivity, not individual animal productivity is important to environmental sustainability. This concept was demonstrated by Capper *et al.* (2009) in comparing US dairy production systems in 1944 and 2007 showing that while the carbon footprint of modern dairy cows increased from 13.5 to 27.8 CO_2 equivalents kg/cow, the CO_2 equivalent production decreased from 3.66 to 1.35 kg/kg milk. This resulted mainly from an improved genetic merit for milk production in dairy cows, better diet formulation, improved herd health and housing. The overall improvement in production resulted in 64% fewer dairy cows to produce the required milk output. Van de Haar & St Pierre (2006) and Chagunda *et al.* (2009) showed that more energy efficient dairy cows produce less methane and nitrogen per unit product. Selecting for dairy cows for more efficient feed use would bring together higher production and reduced resource requirements (Bell *et al.* 2012). However, by breeding for cows to produce less methane without forfeiting production would have a greater improvement on the industry’s environmental foot-print. To enable this, a robust indicator trait that can be used together with production traits is required. Dijkstra *et al.* (2011) developed an indicator for methane production of dairy cows based on milk FAs. However, correlations between methane production and individual milk FAs are not consistent among studies (Visker *et al.*, 2014). Early work by Tyrrell *et al.* (1991) did not show breed differences between Holstein and Jersey cows for maintenance and production requirements per unit of metabolic body weight. Münger & Kreuzer (2006) also found no differences between Jerseys, Holsteins and Simmental in CH_4 per DM intake in a 3-three comparison with direct measurements of CH_4 and milk production, although Simmentals produced more CH_4/energy corrected milk because of a higher body size. The aim of this paper is to compare the predicted methane emissions of Jersey and FxJ cows in a pasture-based feeding system.

MATERIAL AND METHODS

Location and Animals. This paper was based on an on-going breed comparison study at the Elsenburg Research Farm of the Western Cape Department of Agriculture. Jersey and F bulls were used on two comparable groups of Jersey cows regarding breeding value for milk yield, to create a FxJ crossbred herd with a purebred Jersey herd as control. Cows were mostly on kikuyu pasture (*Pennisetum clandestinum*) being supplemented with a concentrate mixture twice a day after milking at 7 kg per cow per day regardless of milk yield and lactation stage. Fresh drinking water was freely available at all times. Milk samples, 153 from Jersey and 283 from FxJ, were collected over the lactation period starting from 10 days after calving every 35 days as per usual milk recording procedures. At least three and maximum seven milk samples per cow were collected over the lactation period. FAs were determined by gas chromatography. As the original aim of the study was the comparison of the production performance of the two breeds, cows were, at times, specifically during pasture shortages, supplemented with a pasture replacement mixture consisting of lucerne hay, oat hay and soybean meal. Results on the production performance of Jersey and FxJ cows have been reported by Goni *et al.* (2014).

Milk sampling and fatty acid analyses. Milk samples for FA analyses were collected and recorded every five weeks according to standard milk recording procedures. At each recording event, milk samples were collected from cows of both breeds from 10 days after calving (DIM) to about 175 DIM (milk tests 1 to 5) and thereafter from 240 DIM (milk tests 7 to 8). Milk samples were collected at the evening and next morning's milking session and combined. Milk samples for FA analyses were kept frozen at -20°C until laboratory analysis and FA composition of milk samples was obtained by gas chromatography at IBMB, CPUT, Bellville, Cape Town. Thirty six FA were detected and concentration levels determined. Breed differences for FAs were reported by Sasanti *et al.* (2012). For the present study methane emissions were predicted using the methane prediction formulae 2 and 3 as suggested by Visker *et al.* (2014):

CH_4 (g/kg feed DM) = 28.60 - 1.13 x C4:0 + 0.36 x C18:0 - 2.57 x C18:1*trans*10+11 - 9.29 x C18:1*cis* 11 for Methane 2.

CH_4 (g/kg feed DM) = 27.13 – 3.04 x C4:0 + 2.71 x C6:0 – 1.63 x C18:1*trans10+11* for Methane 3.

Statistical analyses. Predicted methane emissions (prediction models 2 and 3) were compared between breeds by analysis of variance using samples of all cows within breed as replicates using the GLM procedure (SAS Institute Inc.).

RESULTS AND DISCUSSION

The fat content in J milk was higher ($P<0.05$) than in FxJ milk, i.e. 4.09±0.85 and 3.87±0.74% (Table 1). Goni *et al.* (2014) found that although the fat percentage of the milk of FxJ cows was lower ($P<0.05$) than J cows, the fat yield of FxJ cows was higher ($P<0.05$) than that of J cows because of a higher milk yield. The differences between breeds in methane production as predicted by methane prediction equations 2 and 3 were, however, small. Methane emissions found by Visker *et al*. (2014) using the same equations, were lower than the results in the present study, being 21.34±1.23 and 20.87±0.82 for methane prediction models 2 and 3, respectively. Similarly, as found by Visker *et al*. (2014), the present study also showed that for both Jersey and FxJ cows the methane production was lower for the Methane3 prediction model in comparison to Methane2. The coefficient of variation was high (*ca*. 20%) for both prediction models possibly indicating differences among cows within breeds. This variation could possibly be used to identify more efficient cows in terms of methane production.

Table 1. The mean milk fat content (%) and methane production based on fatty acids in the milk of Jersey (J) and Fleckvieh x Jersey (FxJ) cows in a pasture-based feeding system

Parameters	Fat %		Methane2		Methane3	
Breeds	J	FxJ	J	FxJ	J	FxJ
Mean (g/kg feed DM)	4.09^{a}	3.87^{b}	26.2	25.8	24.6	24.4
Standard deviation	0.85	0.74	1.07	0.94	0.99	1.08
Minimum	2.60	1.59	20.5	21.8	21.1	14.7
Maximum	7.80	6.49	28.5	28.4	26.3	28.7

^{a,b}Values with different superscripts within column between breeds differ at $P<0.05$

The effect of lactation stage as indicated by milk test on methane production is shown in Figure 1. Methane production for both methane prediction equations showed curvilinear trends towards the end of the lactation similar as the fat percentage for both breeds.

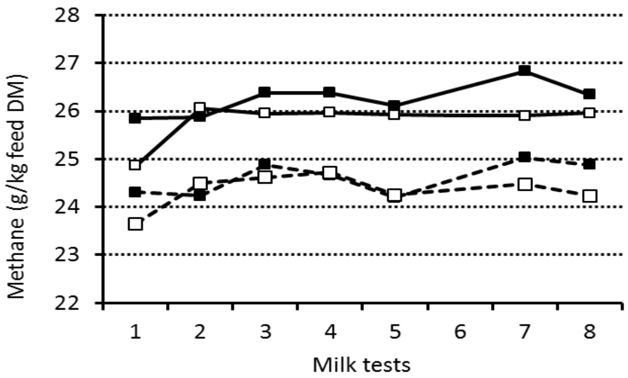

Figure 1. Methane production as affected by milk test for Jersey (■) and Fleckvieh x Jersey (□) cows using two prediction models (solid lines = Methane 2 and dash lines = Methane 3)

Although Garnsworthy *et al*. (2012) recorded methane emission rate during milking in automatic milking stations as CH_4/day, in contrast to the current study using predicted methane emissions as CH_4/kg DM, their study showed that between-cow variation in methane emission rate was greater than within-cow variation. These differences between cows were ascribed to variations in body weight, milk yield, parity and week of lactation. Using daily methane emissions averaged on a weekly basis, Garnsworthy *et al*. (2012) showed an increase over the first 10 weeks of the lactation consistent with expected increases in feed intake because of milk yield increases. Lassen *et al*. (2013) demonstrated genetic variations with a heritability estimate of 0.21 using methane emission rates determined in automatic milking stations. High variation among cows increases the level of replication required to obtain reliable estimates of methane emissions and to assess the effect of mitigation strategies (Garnsworthy *et al*. 2012). Because milk is routinely collected for milk recording, FA profiles could easily be obtained using gas chromatography or infrared profiles (Visker *et al*. 2014). Regression equations developed by Visker *et al*. (2014) are probably not appropriate for the current study as diets differed. Chilliard *et al*. (2009) showed that CH_4 output was positively and strongly correlated to milk FA 6:0 to 16:0 based on the use of acetate produced in the rumen during fiber digestion. It was suggested that milk FA profile can be considered to be a potential indicator of *in vivo* CH_4 output, but studies using other dietary supplements reported contrasting results. Therefore, it appears that suitable equations should be developed for specific feeding programmes. For the present study it was, however, possible to show differences between cows within breeds.

CONCLUSION

This study showed that predicted methane emissions by using regression equations varied between cows within breed, while only small differences between Jersey and FxJ cows were observed. Within breed differences indicate possible genetic variation among cows which may be exploited towards reducing methane production in dairy cows.

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