The use of direct-fed microbials for mitigation of ruminant methane emissions: a review

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Concerns about the environmental effect and the economic burden of methane (CH₄) emissions from ruminants are driving the search for ways to mitigate rumen methanogenesis. The use of direct-fed microbials (DFM) is one possible option to decrease CH₄ emission from ruminants. Direct-fed microbials are already used in ruminants mainly to increase productivity and to improve health, and are readily accepted by producers and consumers alike. However, studies on the use of DFM as rumen CH₄ mitigants are scarce. A few studies using Saccharomyces cerevisiae have shown a CH₄-decreasing effect but, to date, there has not been a systematic exploration of DFM as modulators of rumen methanogenesis. In this review, we explored biochemical pathways competing with methanogenesis that, potentially, could be modulated by the use of DFM. Pathways involving the redirection of H₂ away from methanogenesis and pathways producing less H₂ during feed fermentation are the preferred options. Propionate formation is an example of the latter option that in addition to decrease CH₄ formation increases the retention of energy from the diet. Homoacetogenesis is a pathway using H₂ to produce acetate, however up to now no acetogen has been shown to efficiently compete with methanogens in the rumen. Nitrate and sulphate reduction are pathways competing with methanogenesis, but the availability of these substances in the rumen is limited. Although there were studies using nitrate and sulphate as chemical additives, use of DFM for improving these processes and decrease the accumulation of toxic metabolites needs to be explored more. There are some other pathways such as methanotrophy and capnophily or modes of action such as inhibition of methanogens that theoretically could be provided by DFM and affect methanogenesis. We conclude that DFM is a promising alternative for rumen methane mitigation that should be further explored for their practical usage.

Keywords: direct-fed microbials, biochemical pathways, methane, rumen

Implications

Methane produced in the rumen contributes significantly to the global emission of greenhouse gases. Among the different strategies researched to reduce rumen methanogenesis, the use of direct-fed microbials (DFM) has received little attention so far. From a practical perspective, the DFM concept is well known to farmers as it is already utilised to increase animal productivity and to improve their health. This review explores the possibilities to modify some rumen biochemical pathways to decrease methanogenesis by using DFM.

Introduction

Methane (CH₄) is an important greenhouse gas (GHG) that has a global warming potential 25 times higher than that of carbon dioxide (CO₂; Intergovernmental Panel on Climate Change, 2007). Ruminants are the single largest source of CH₄ emission from agriculture, globally contributing about 40% of the emissions produced by human-related activities (Steinfeld et al., 2006). Enteric CH₄ is produced in the rumen and to a lesser extent in the large intestine of ruminants. The rumen is the primary location for microbial fermentation of plant material in ruminants and it contains a microbial population made up of bacteria, archaea (methanogens), protozoa, fungi and phage. These rumen microorganisms function via complex interactions, which are essential to sustain their population and activity. The ingested feed is digested and fermented by bacteria, protozoa and fungi into short chain fatty acids (VFA), which are then used by the host as its energy source. Molecular hydrogen (H₂) is an important by-product of this fermentation and is used by rumen methanogens to reduce CO₂ into CH₄.

Concerns about the environment and energy economics (about 5% to 9% of dietary gross energy loss) of rumen CH₄...
emission compel researchers to look for ways to decrease rumen methanogenesis (Martin et al., 2010; Buddle et al., 2011). Among the different strategies studied, one promising method is the manipulation of biochemical pathways existing in the rumen to produce less CH₄. Use of direct-fed microbials (DFM) for this manipulation is one possible option. Direct-fed microbials have been defined as a ‘source of live, naturally occurring microorganisms’ (Krehbiel et al., 2003) and, they have been successfully used in ruminant production to increase productivity, to prevent digestive disorders like acidosis and to decrease pathogenic load in young animals (Adamset al., 2008; McAllisteret al., 2011; Lettat et al., 2012b). They are an accepted alternative to the use of antibiotics and chemical substances that may induce a risk of antibiotic resistance and residues in animal products. However, to date there is little evidence to suggest the efficacy of DFM to control the production of CH₄ in ruminants.

The majority of rumen methanogens use H₂ to reduce CO₂ to CH₄. Some rumen methanogens can utilise formate or methyl group containing compounds such as methanol and methylamine (Janssen and Kirs, 2008). Carbon dioxide constitutes up to 65% of total gas in the rumen (Elliset al., 1991) and it is not a limiting substrate of rumen methanogenesis. Therefore, H₂ is a key compound for controlling CH₄ production. The major biochemical pathways explored in this review to decrease CH₄ emissions from ruminants by using DFM are the redirection of H₂ away from methanogenesis and decreased production of H₂ during feed fermentation. Other potential pathways are also briefly explored in this review. The different pathways that could be modulated to decrease rumen methanogenesis by providing DFM are shown in Figure 1. Biohydrogenation of
unsaturated fatty acids is another $H_2$-utilising pathway present in the rumen. However, biohydrogenation accounts only for 1% to 2% of the $H_2$ consumed (Nagaraja et al., 1997). As such, this pathway is not discussed in this review.

**Yeast (Saccharomyces cerevisiae)**

*Saccharomyces cerevisiae* is the most commonly used DFM in ruminant production and not surprisingly is the DFM that has been more extensively studied for its effect on rumen methanogenesis. However, results from both *in vitro* (Table 1) and *in vivo* (Table 2) studies are inconsistent. These variations can be partly explained by the differences in experimental conditions (yeast strains and formats (live culture or freeze-dried preparation), dose, animal species, physiological state of animals and diets) but also because up to now no strain has been selected based on effects on methanogenesis. The effects and modes of action of yeast on rumen fermentation have been extensively studied (Newbold et al., 1996; Chaucheyras-Durand et al., 2008). Chaucheyras-Durand et al. (2008) in their review identified three main effects of yeast on rumen development: improvement of rumen maturity by favouring microbial establishment, stabilising rumen pH and increasing fibre degradation. Live yeast also showed beneficial effects on the growth and $H_2$-utilisation of acetogenic bacteria *in vitro* (Chaucheyras-Durand et al., 1995). Being an aerobic organism, the above mentioned effects may be due to the ability of yeast to remove the trace amounts of oxygen present in the rumen and/or due to the micronutrients present in the yeast itself (McAllister et al., 2011).

**Propionate-forming bacteria**

The major VFA produced in the rumen are acetic, propionic and butyric acids and their proportion mainly depends on the diet offered to the animal. Ruminants fed a concentrate-based diet produce proportionally more propionate than those fed a high forage diet, which produces more acetate. Propionate formation consumes reducing equivalents, pyruvate is reduced to acetyl-CoA, which eventually reacts with oxaloacetate to form succinyl-CoA. Succinyl-CoA is the major pathway in the rumen and along this pathway propionate is produced through two pathways: succinate pathway and acrylate pathway (Figure 1). Succinate pathway is the major pathway in the rumen and along this pathway intermediate products such as malate, fumarate and succinate are formed. Moreover, this pathway involves a mixture of bacteria such as lactate producers (e.g. *Streptococcus bovis*), lactate utilisers (e.g. *Selenomonas ruminantium*), fumarate reducers (e.g. *Wolinella succinogenes*), succinate producers (*Fibrobacter succinogenes*) and succinate utilisers (e.g. *S. ruminantium*).

The acrylate pathway is also an important propionate-producing pathway in the rumen. Lactate-utilising *Megasphaera
elsdenii is the major rumen bacteria involved in this pathway (Russell and Wallace, 1997), which requires the presence of lactate. In the absence of lactate, M. elsdenii utilise glucose and produce acetate and butyrate but not propionate (Hino et al., 1994). Lactate-producing bacteria such as Streptococcus bovis play therefore a regulatory role in this pathway. There are other bacterial spp. in the rumen that can utilise lactate (e.g. S. ruminantium and Propionibacterium spp.) but in vitro (Counotte et al., 1981) and in vivo (Klieve et al., 2003) studies have shown that M. elsdenii is the key species performing this function. It has been shown that in cows supplemented with a M. elsdenii DFM, the pattern of rumen fermentation was altered in favour of propionate with potential benefits on energy balance and animal productivity (Henning et al., 2010; Aikman et al., 2011). Hino et al. (1994) have also shown that combining lactate-producing bacteria with M. elsdenii is effective for increasing propionate production. Some strains of the rumen bacterium Prevotella ruminicola can also form propionate via the acrylate pathway, but the amount of propionate formed by these strains is not significant in the rumen (Wallnofer and Baldwin, 1967).

Propionate formation is the main rumen biochemical pathway explored and exploited by bacterial DFM in ruminant production (Seo et al., 2010). Propionibacterium spp. and/or Lactobacillus spp. were used to increase animal productivity (Ghorbani et al., 2002; Adams et al., 2008), M. elsdenii, Propionibacterium spp. and/or Lactobacillus spp. were used to prevent rumen acidosis in concentrate-fed animals (Aikman et al., 2011; Lettata et al., 2012b) and Lactobacillus spp. were used to decrease pathogenic load in young animals (McAllister et al., 2011) but CH4 production was not measured in any of these studies. Decrease in CH4 emission was recently observed in lactating dairy cows receiving a mixed Propionibacterium jensenii – Lactobacillus spp. DFM (Lettata et al., 2012a) showing the potential of this approach to mitigate rumen CH4 emission.

Nitrate/nitrite-reducing bacteria

Nitrate can act as an alternative H2 sink to CO2 in the rumen. The predominant pathway of nitrate metabolism in the rumen has been assumed to be dissimilatory nitrate reduction in which nitrate is reduced to ammonia in two-step processes: nitrate to nitrite and nitrite to ammonia. The potential use of nitrate to decrease rumen methanogenesis has been hindered by the toxicity of the intermediate product nitrite. Rumen microbes rapidly reduce the nitrate into nitrite, but the rate of reduction of nitrite into ammonia is slower, which can cause nitrite accumulation in the rumen (Iwamoto et al., 1999). When nitrite is absorbed from the rumen into the blood it converts blood haemoglobin into methaemoglobin and if its concentration is high it causes the condition called methaemoglobinemia. Methaemoglobinemia decreases the blood’s capacity to transport oxygen to tissues, resulting in depressed performances and, in severe cases, death of the animal (Morris et al., 1958). Many studies on nitrate supplementation were focused on avoiding this nitrite toxicity. As a result, several

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<th>Yeast preparation</th>
<th>Animal species</th>
<th>Diet</th>
<th>Effect on CH4 production</th>
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<tr>
<td>Strain CNCM 1-1096 (1.38 × 10^7 CFU/kg LBW)</td>
<td>Sheep (defaunated and refaunated)</td>
<td>Timothy grass hay (44.5%), barley (44.5%), and soya bean meal (11%)</td>
<td>No effect</td>
</tr>
<tr>
<td>Strain CNCM 1-1077 (4.67 × 10^5 CFU/kg LBW)</td>
<td>Lactating dairy cows</td>
<td>Barley silage (75%), barley (19%) and supplement (6%)</td>
<td>No effect</td>
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<tr>
<td>Two commercial products Procreatin-7 and Levucell sc (CNCM 1-1077) (1.92 × 10^8 and 5.77 × 10^7 CFU/kg LBW)</td>
<td>Dairy steers</td>
<td>Barley silage (60%), alfalfa hay (30%) and concentrate (10 %)</td>
<td>3% decrease per kg DM intake with Procreatin-7</td>
</tr>
<tr>
<td>Two commercial products Lactobacillus sc and a novel strain (1.32 × 10^7 CFU/kg LBW)</td>
<td>Dry dairy cows (non-lactating cow)</td>
<td>Barley silage (50%), steam-rolled barley (19.5%) and pelleted supplement (30.5%)</td>
<td>7% decrease per kg DM and gross energy intake with novel strain</td>
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<td>DFM = direct-fed microbial; LBW = live body weight; DM = dry matter.</td>
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Doses are given as colony forming units (CFU) per kg LBW. Commercial producers: CNCM 1-1096 and CNCM 1-1077 – Institut Pasteur, France; Procreatin-7, Saf Agri, Levucell sc – Lallemand Inc.
solutions were proposed to avoid this problem (Alaboudi and Jones, 1985; Takahashi and Young, 1991; van Zijl, 2010). Among them, the use of nitrite-reducing bacteria as DFM was tested (Anderson and Rasmussen, 1998).

Bacteria with the ability to reduce nitrate, nitrite or both compounds are already present in the rumen. The major nitrate-reducing bacteria *W. succinogenes* and *S. ruminantium* are both present at a concentration of 10⁶ cells/ml of rumen fluid (Asanuma et al., 2002; Yoshii et al., 2003). However, to compete with methanogens present at about 10² cells/ml (Jeyanathan et al., 2011) it may be advantageous to increase the number and/or the activity of nitrate- and/or nitrite-reducing bacteria in the rumen if nitrate is going to be a strategy to decrease methanogenesis. Bacteria that have the ability to reduce nitrate or nitrite are more active when nitrate is included in the diet. Iwamoto et al. (2002) showed that addition of nitrate increased the number of nitrate-reducing bacteria such as *W. succinogenes* and *Veillonella parvula* *in vitro*. But, this increase may not be sufficient to compete with methanogenesis. Therefore, providing nitrate- and/or nitrite-reducing bacteria as DFM along with nitrate may improve the nitrate reduction process and avoid nitrite toxicity.

Denitrification is another nitrate/nitrite-reduction pathway in which nitrate or nitrite are reduced via gaseous nitrogen oxides (NO and NO₂) to N₂. Denitrification is prominent in the soil ecosystem (McKenney et al., 1982; Raciti et al., 2011). The presence of more organic carbon in the soil is thought to be the reason for this high denitrification activity (Tiedje et al., 1982). Although the rumen has considerable organic carbon and has the possibility of inoculation of denitrifiers from soil through feed, denitrification process has not been reported in the rumen. Short turnover time of the rumen contents may be the reason for this observation (Ao, 2008). However, traces of NO₂ were observed when rumen liquor from cattle was incubated with nitrate *in vitro* (Kaspar and Tiedje, 1981). This NO₂ was thought to be the by-product of dissimilatory nitrate reduction by rumen bacteria. Kaspar (1982) tested five *Propionibacterium* species for their ability to reduce nitrate and found all five species reduced nitrate to NO₂, but not to N₂. Reduction of nitrate to NO₂ by *Propionibacterium* spp. was considered to be a detoxification mechanism rather than a part of an energy transformation reaction. As *Propionibacterium* spp. are present in the rumen NO₂ production occurs in the rumen and NO₂ is present in rumen gases, although in trace amounts.

There have been only few published studies on the use of nitrate/nitrite-reducing bacteria as DFM to decrease rumen methanogenesis. In an *in vitro* trial, Anderson and Rasmussen (1998) inoculated the nitrate-reducing rumen bacterium *Denitrobacterium detoxificans* strain NPOH1 along with added nitrate (10 μmol/ml) and observed up to 95% decrease in the CH₄ production without nitrite accumulation. In the absence of *D. detoxificans* the decrease in CH₄ production was only 25% and nitrite accumulation was observed. In another *in vitro* study addition of nitrate-reducing bacteria *W. succinogenes*, *S. ruminantium* or *V. parvula* to mixed methanogens in the presence of nitrate (5 mM) drastically decreased methanogenesis (>70% decrease). The highest decrease was observed with *W. succinogenes*, with low nitrite accumulated in the culture media compared with the other two nitrate-reducing bacteria (Iwamoto et al., 2002). Nitrite-reducing *Escherichia coli* strains decreased nitrite accumulation *in vitro* as well as *in vivo* when added with nitrate (Larson et al., 2005b and 2005c). *Propionibacterium acidipropionici*, which has the ability to reduce nitrite into N₂O (Rehberger and Hibberd, 2000) is commercially available to avoid nitrite toxicity in cows fed high nitrate forages. For the bacterial species mentioned above, however, there is still scarce *in vivo* data on their ability to decrease CH₄ production and/or avoid nitrite toxicity particularly when nitrate is used as feed additive.

In addition to the bacteria mentioned above, other isolates have also shown the ability to decrease CH₄ emission in the presence of nitrate *in vitro*. Asanuma et al. (2003) isolated a *Clostridium* sp. from dog faeces with high nitrite-reducing activity and Sakthivel et al. (2012) isolated a bacterium from a buffalo rumen. Both bacteria alleviate nitrite toxicity, the buffalo isolate in particular nearly inhibited methanogenesis when combined with 10 mM nitrate without a negative effect on feed digestibility. In contrast, nitrate alone, although it decreased CH₄ production by 69%, decreased feed digestibility by 14%. These two bacteria need to be fully characterised and, more importantly, their effect on the decrease in CH₄ emission has to be confirmed *in vivo*.

Nitrate as feed additive can decrease rumen methanogenesis in different ruminant species and production conditions (van Zijl, 2011; Hulshof et al., 2012). It is noted that nitrate could replace urea used as a nitrogen source for rumen microbial protein synthesis in diets with low N. In an *in vivo* study Li et al. (2012) replaced 1.5% urea by 3% calcium nitrate with a decreasing effect on CH₄ emission. However, the possible negative impact of long term supplementation of nitrate on animal health and on the environment has to be explored more. As mentioned earlier, DFM can be used to avoid these negative effects (Perdok et al., 2011).

**Sulphate-reducing bacteria**

Competitive and co-operative relationships between methanogens and sulphate-reducing bacteria (SRB) have been described in anaerobic environments including in the rumen. In anaerobic environments, in which sulphate is not limiting, SRB compete with methanogens for common substrates (e.g. H₂, formate and acetate). As the energetic of sulphate reduction is slightly more favourable than methanogenesis (−152 kJ v. −131 kJ/mol; Gibson et al., 1993), encouraging competition between these two groups theoretically decreases methanogenesis. The co-operative relationship between methanogens and SRB is another example of interspecies H₂ transfer. In sulphate-depleted environments they grow in syntrophy with methanogens by producing H₂. Limited sulphate availability in the rumen likely makes SRB as net producers of H₂ (Bryant et al., 1977).

The population of SRB in the rumen is low (10³ to 10⁶ cells/ml) and mainly from the genus *Desulfovibrio* and *Desulfitomaculum*.
was enhanced (Cummingset al., 1995). As such, sulphate into the rumen. In an experiment with steers fed methanogens is largely determined by the introduction of SRB in the rumen. The ability of SRB to compete with sulphur reduction may be facilitated by introducing SRB when sulphate is used as an additive to decrease methanogenesis. However, there were only few studies on effect of sulphate supplementation in rumen methanogenesis (Morvan et al., 1996; van Zijderveld et al., 2010). The toxic end product (H₂S) resulting from the sulphate reduction is the major reason for the lack of studies on this option.

Using sulphate alone as an additive cannot be an alternative for reducing rumen methanogenesis due to the sulphide toxicity. However, SRB are versatile organisms and published information indicates that they may possess some characteristics favouring rumen CH₄ mitigation. For instance, a decrease in CH₄ emission was observed in an *in vitro* study using the newly identified SRB, *Fusobacterium* sp., as a DFM with a high sulphate diet. The CH₄ production at 72 h was decreased from 2.66 to 1.64 mmol/g dry matter (DM) without H₂S accumulation (Paul et al., 2011). Fibre digestion and number of cellulolytic bacteria were also increased. Absence of sulphide accumulation in this study may be due to its rapid utilisation by other microbes such as cellulolytic bacteria for synthesis of sulphur-containing amino acids (Bryant, 1973) or *Fusobacterium* sp. itself might be able to oxidise sulphide into sulphate as described in the termite gut (Droge et al., 2005). The full characterisation of the isolated *Fusobacterium* sp. as well as additional studies are needed to gain a better understanding of this effect.

Major interactions were observed between nitrate and sulphate metabolism in microorganisms that are present in diverse anaerobic ecosystems (Garcia-de-Lomas et al., 2007; Hubert and Voordouw, 2007; van Zijderveld et al., 2010). Importantly, many SRB appear to have dual roles, that is, they reduce inorganic and organic sulphur, and the majority of them can reduce nitrite to ammonia. Their ability to reduce nitrite was explored to avoid the potential toxicity of nitrite ammonification in nitrate-reducing-sulphide-oxidising bacteria (NR-SOB) (Garcia-de-Lomas et al., 2007; Hubert and Voordouw, 2007). These bacteria reduce nitrate to nitrite and oxidise sulphide to sulphate when further reducing nitrite to ammonia. The low concentration of H₂S certainly limits the abundance of this group of bacteria in the rumen. However, physiological similarities between *W. succinogenes* and NR-SOB *Sulphurospirillum deleyianum*, suggest that this function is present in the rumen (Simon, 2002). Indeed, *W. succinogenes* can grow using sulphide as an electron donor and fumarate as an electron acceptor (Macy et al., 1978). The possibility of preventing nitrite toxicity by provision of sulphate further suggests that some nitrate reducing bacteria present in the rumen may possess the characteristic of NR-SOB (Ao, 2008).

**Homoeacetogens**

Homoeacetogens are present in diverse environments including rumen, and have the ability to produce acetate via heterotrophic and autotrophic growth. They grow heterotrophically by utilising sugars and autotrophically by utilising formate, CO and H₂/CO₂. Promoting the autotrophic growth of homoeacetogens (*Wood-Ljungdahl pathway*) is thought to be a competitive pathway to methanogenesis as the same substrates are used. Acetate is a beneficial nutrient for the host and for other microbes within the rumen community.

The population of homoeacetogens in the rumen highly varies (undetectable to 10⁷ cells/ml) depending on diet, age of the animal and time of sampling (Leedle and Greening, 1988; Fonty et al., 2007). They are among the first species to colonise the rumen but their numbers decrease when methanogens appear at 30 h after birth (Morvan et al., 1994). In a study using lambs placed in a sterile isolator 17 h after birth, the acetogen population was increased up to 5 × 10⁸ cells/ml at 150 days before methanogens inoculation (Gagen et al., 2012). A similar observation was reported previously by Fonty et al. (2007) in their study with methanogen-free lambs. A negative correlation between numbers of homoeacetogenic bacteria and methanogens has been described in the rumen of adult ruminants (Doré et al., 1995). Notwithstanding, using acetogens as a DFM to decrease rumen methanogenesis has some limitations. Methanogens have a lower threshold for H₂ than acetogens and the energy yield from methanogenesis is greater than that from acetogenesis (Thauer et al., 1977). As such, at the low H₂ concentrations prevailing in the rumen, methanogens out-compete acetogens. In addition, acetogens can grow heterotrophically by utilising sugars and other substrates (e.g. alcohols, organic acids; Ragsdale and Pierce, 2008).

Several attempts to increase the reductive acetogenesis process in the rumen by supplying DFM containing homoeacetogens of rumen and non-rumen origin were unsuccessful. Lopez et al. (1999) tested six acetogenic bacteria for their effect on rumen CH₄ emission *in vitro* and found that only two of them slightly decreased methanogenesis. *Peptostreptococcus productus*, an acetogen isolated from an anaerobic sludge digester promoted acetogenesis *in vitro* only when methanogenesis was selectively inhibited (Nollet et al., 1997 and 1998). The same acetogen administered in association with spent *Lactobacillus plantarum* culture media failed to sustain the antimethanogenic effect for long term in sheep (Nollet et al., 1998). In another *in vitro* study, a combination of an acetogen (isolated from a lamb) and yeast stimulated acetogenesis significantly in the presence of
methanogens (Chaucheyras et al., 1995). Further confirmations of above observations by in vitro or in vivo studies were not reported so far.

Homooacetogens have been shown to sustain a functional rumen in methanogen-free lambs (Fonty et al., 2007) and studies have already shown that by inhibiting methanogenesis, the acetogenesis can be stimulated (Boccazzi and Patterson, 1996; Nollet et al., 1997). However, acetogens were less efficient in H2 capture from fermentation (28% to 46%) than methanogens (>90%; Fonty et al., 2007; Gagen et al., 2012) and this may affect the overall fermentation process in the rumen. Identifying homooacetogens that are competitive to methanogens in the rumen is required. Recently, in an attempt to isolate rumen acetogenic bacteria able to grow on low threshold concentrations of H2, an isolate was successfully obtained using H2-limited continuous cultures (Boccazzi and Patterson, 2011). Such acetogens could compete with methanogens in the rumen. Homooacetogenesis is competitive to methanogenesis in the gut microbial ecosystem of humans, rodents, macropods, and wood-digesting termites (Breznak and Switzer, 1986). The Tammar wallaby (Macropus eugenii) is a foregut fermenter but it is a low CH4 emitter. The homooacetogen population in Tammar wallaby forestomach is different compared with that found in ruminants (Gagen et al., 2010), which can be one of the reasons for lower CH4 emission. The acetogens in the Tammer Wallaby may be more effective hydrogenotrophs than those in the rumen and possibly better competing with methanogens. If this is true, these animals may act as a source of novel acetogens to be used as DFM. The success of such option mainly depends on the ability of those acetogens to be active under rumen conditions.

**Methyloptrophs**

Methyloptrophs are microorganisms able to utilise one-carbon organic compounds such as methanol and methylamine as carbon sources and thus competing for substrates with methanogens. Some methyloptrophs, the methanotrophs are also capable to use CH4 avoiding its release into the atmosphere. Understanding the pathways involved in the metabolism of these compounds may provide a novel biological control agent in mitigating rumen CH4 emission.

Up to now, there is little evidence to suggest that methanotrophy is important in the rumen. Only one study reported possible, albeit low 0.2% to 0.5%, methanotrophy in rumen fluid (Kajikawa et al., 2003). In another study bacterial clones closely related to *Nitrosomonas* spp. were identified from a clone library constructed from samples of bacterial communities attached to the rumen epithelium (Mitsumori et al., 2002). Members of the genus *Nitrosomonas* are ammonia-oxidising bacteria, which have the ability to oxidise CH4 under some conditions (Hyman and Wood, 1983; Jiang and Bakken, 1999). Close to the rumen wall there is always ammonia as urea coming from blood, which is rapidly degraded by ureolytic bacteria attached to the rumen wall (Cheng and Wallace, 1979). Therefore, there is a possibility that *Nitrosomonas* spp. in the rumen wall may be involved in CH4 oxidation. However, their presence in the rumen epithelium was not always observed suggesting that they are minor or occasional members (Sadet-Bourgeteau et al., 2010; Li et al., 2011).

Several clone libraries of rumen samples reported significant numbers of bacteria belonging to the phylum *Verrucomicrobia* (Romero-Perez et al., 2011; Godoy-Vitorino et al., 2012). Although their role in the rumen is not well understood, some members of the *Verrucomicrobia* have been found to oxidise CH4 as the sole source of carbon and energy in non-rumen environments (Hou et al., 2008). Information on whether *Verrucomicrobia* are capable of this function in the rumen is still missing. Also, Kliewe et al. (2012) identified clones related to CH4-oxidising archaea in the rumen of cows. Methane-oxidising archaea have been described as having an important role in aquatic ecosystems (Hallam et al., 2003; Knittel et al., 2005). Although the rumen conditions with a nutrient-rich environment and a high turnover rate does not favour the activity of methane-oxidising archaea, their importance remains to be assessed.

Other than methanotrophs, methyloptrophs that can utilise methanol and/or methylamine could also be helpful in reducing methanogenesis. Methanol and methylamine are substrates, in some cases the unique substrate, for some rumen methanogens. For example, methanogens belonging to the genus *Methanospirillum* absolutely require methanol (Miller and Wolin, 1985) while genus *Methanomicrococcus* require methanol or methylamine (Sprenger et al., 2000) for their growth. The *Methanosarcina* spp. can also utilise methanol and methylamine as substrates, although they are not their obligatory requirements (Jarvis et al., 2000). Recent reports on a human methanogen isolate and on termite gut enrichment cultures suggested that methanol may be an obligatory requirement for rumen cluster C group (Dridi et al., 2012; Paul et al., 2012).

Among the methyloptrophic methanogens, *Methanospirillum* spp. are common inhabitants of the rumen and found to be an important group in forage-fed cow, sheep and red deer (Jeyanathan et al., 2011). Although they are categorised as a minor group based on the meta-analysis of partial 16S rRNA sequences by Janssen and Kirs (2008), recent studies showed that they are ubiquitous members of the rumen in different ruminant species, fed different diets and at various geographical locations (Franzolin et al., 2012; St-Pierre and Wright, 2012). *Methanomicrococcus* and *Methanosarcina* were also retrieved from several rumen clone libraries (Whitford et al., 2001; Sundset et al., 2009), but not in significant numbers. Instead, the rumen cluster C group is one of the major methanogen groups (Janssen and Kirs, 2008) sometimes contributing up to 80% of the total clones analysed (Wright et al., 2006). If their substrate requirement is similar to the human and termite representatives, methanol could be an important substrate for rumen methanogenesis. Methanol is formed by enzymatic cleavage of pectin methyl esters by anaerobic pectinolytic bacteria in the rumen. Utilisation of
these substrates (methanol and/or methylamine) by organisms other than methanogens theoretically could decrease methanogenesis. However, the affinity of these substrates to methanogens and other organisms has to be considered. Methanol can also be utilised by homoacetogens (Lopez et al., 1999). Other than acetogens, there are no other methylotrophic bacteria reported in the rumen. Understanding methylotrophy especially methanotrophy in other environments such as soil may help to identify potential DFM, which could decrease rumen methanogenesis.

### Capnophiles

Capnophiles are microorganisms that require high levels of CO₂ for their growth. The rumen is an anaerobic environment where CO₂ is the major gas. The presence of capnophiles in the rumen is therefore expected but their use as scavengers of CO₂ to mitigate methanogenesis is questionable as this gas is not a limiting substrate for rumen methanogens. Dehority (1971) suggested two types of CO₂ requirement among rumen bacteria: biosynthesis type in which CO₂ is required for cell growth (e.g. S. bovis) and the second type includes bacteria that are forming succinate in addition to biosynthesis (e.g. Actinobacillus succinogenes, Mannheimia succiniciproducens, succinivibrio dextrinosolvens). During succinate production, CO₂ is attached to the three-carbon phosphoenolpyruvate, an end product in glycolysis, to generate the four-carbon compound, oxaloacetate. Oxaloacetate accepts two pairs of electrons, when reduced into succinate. As such, both CO₂ and H₂ are used during this succinate formation and may have an impact on rumen methanogenesis. Succinate is also an important intermediate product during the propionate production.

The Tammer wallaby produces only one-fifth of the amount of CH₄ produced by ruminants per unit of digestible energy intake (Kempton et al., 1976). A physiological difference such as shorter retention time of feed in the foregut partially explains intake (Kempton et al., 1976). A physiological difference such as shorter retention time of feed in the foregut partially explains this. The presence of a novel group of aceticogenic bacteria may be the reason for this lower CH₄ emission (Gagen et al., 2010). Presence of capnophiles may also be contributing to this observation. In a clone library constructed from foregut samples of Tammer wallaby, a large proportion of novel capnophiles (9% of all sequences recovered in the 16S rRNA clone library) was observed (Pope et al., 2011). These clones were assigned to a group within the family Succinivibrionaceae. A member from this group was isolated and the genome sequence of this isolate proved that it is a capnophile dependent on CO₂ to support its metabolism via succinate biosynthesis (Pope et al., 2011). A clear understanding of their pathway in the rumen and other similar environment is needed to assess their potential as rumen CH₄ mitigants.

### Other possible bacterial DFM

Bacterial cellulolytic populations in the rumen are the major contributors to fibre degradation. Some like Ruminococcus spp. primarily produce acetate, which leads to more H₂ production. However, the major cellulolytic bacterium, F. succinogenes, primarily produces succinate that leads to propionate production with less H₂ formation. Using bacteria which produce less H₂ as DFM may help to decrease methanogenesis without impairing fibre degradation especially in forage-fed animals. Less H₂ production was observed in gnotobiotically reared lambs inoculated with F. succinogenes as the only cellulolytic microbe compared to lambs inoculated with Ruminococcus species. Also, the rumen contents from F. succinogenes-containing-lambs produced less CH₄ in vitro (Chaucheyras-Durand et al., 2010). However, cellulolytic organisms such as F. succinogenes are already present in the rumen in high numbers and studies using fibrolytic bacteria as DFM did not demonstrate any improvement in cellulose digestion (Dehority and Triabasso, 1998; Krause et al., 2001).

Some bacteria have demonstrated inhibitory activity against methanogens. For example, some lactic acid-producing bacteria produce bacteriocins that can act against methanogens (Nollet et al., 1998; Lee et al., 2002b; Asa et al., 2010). Nisin, a bacteriocin produced by Lactococcus lactis subsp. lactis is widely utilised in the food industry for controlling pathogenic bacteria. In vitro experiments have shown that nisin suppresses methanogenesis as much as 20% without negative impact on VFA production (Callaway et al., 1997; Sar et al., 2005a). However, nisin is susceptible to rumen proteases (Lee et al., 2002a) limiting its utilisation in vivo. The spent media of L. plantarum decreased methanogenesis by 18% in vitro (Nollet et al., 1998) while compounds produced by another L. plantarum strain decreased methanogenesis by 90% (Asa et al., 2010). Bovicin HCS, a bacteriocin produced by S. bovis HCS, inhibited CH₄ production by 53% in vitro (Lee et al., 2002b). In contrast, there is less information on the effect of these bacteriocins in vivo. Nollet et al. (1998) tested the effect of spent L. Plantarum media with an acetogen DFM on sheep and found only a short-term effect (80% decrease after 3 days of treatment). Although there is a possibility to use bacteriocins as additives to decrease rumen methanogenesis, the administration of DFM-producing bacteriocins in vivo may not be possible. The requirement of large population densities to induce bacteriocin production could make this option physiologically unsuitable and, certainly, economically not possible.

Formate is an important substrate used by rumen methanogens (Hungate et al., 1970). It is known that SRB and nitrate-reducing bacteria can utilise formate as H₂ donors. Nitrate-reducing bacteria probably out-compete the methanogens in formate utilisation because of their high affinity (Asanuma et al., 2002). But limited availability of nitrate and sulphate prevents them to utilise formate. Rumen bacteria such as F. succinogenes and Anaerovibrio lipolytica also can consume formate (Asanuma et al., 1998). These bacteria are already present in the rumen in high numbers. As such, their ability to utilise formate may be less efficient than that of methanogens. Identifying and isolating formate-utilising bacteria, which can compete with methanogens may be one possibility to decrease CH₄ emission from ruminants.
Concluding remarks

Many of the bacterial strains, mentioned in this review as potential DFM for reducing rumen methanogenesis, are isolates that can be or are actually grown industrially. However, relatively few of them have been tested for their anti-methanogenic activity. In addition to these already available microorganisms, the rumen as well as other environments are rich sources of potential DFM as the vast majority of microorganisms have not been yet cultured. Developments in genomics will help to identify microbes that could have the ability to decrease methanogenesis in the rumen.

The most promising species/strains studied so far have more than one feature considered to be beneficial in reducing methanogenesis. For example, some of the lactic acid bacteria produce antimethanogenic substances (e.g. L. lactis), nitrate and sulphate-reducing bacteria can utilise formate as substrate and some of the propionate-producing bacteria can reduce nitrate (W. succinogenes). This metabolic multiplicity seems important and should be sought when selecting candidates to be used as DFM. For the same reason, combination of different groups of bacteria could increase the efficacy of antimethanogenic DFM. If the DFM has particular nutrient requirements, incorporating them in the preparation as prebiotics might also help them to function efficiently in the rumen.

There are also technological aspects that should be considered for the development of DFM. All the bacteria presently used as DFM in ruminant production are facultative anaerobes that were mainly isolated from dairy products. Industrial preparation of anaerobic bacteria is technically difficult and costly as compared with standard production in the presence of oxygen. This constrain limits, for the time being, the type of DFM that can be developed for in-farm use. In addition, keeping obligate anaerobic bacteria viable for long periods after production is a challenge. Development of encapsulation methods for strictly anaerobic bacteria may help to overcome this problem. Technical advancements for the preparation of anaerobic bacteria are necessary to increase the scope of antimethanogenic DFM.

For newly developed DFM, in vivo trials are particularly important as DFM might both influence the rumen environment and induce shifts in the microbiota that will not occur in vitro. Such microbial changes have to be assessed to avoid any negative impacts on animals, the environment as well as consumers. Another aspect to consider is the persistency of the antimethanogenic effect that should be assessed in long-term animal trials. As for other mitigation strategies using feed additives and supplements, DFM have to be administered daily to be efficacious.

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