Review Article

METHANE EMISSION FROM RUMINANTS AND ITS MITIGATING MEASURES USING PROBIOTIC– A REVIEW

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Abstract: Methane emitted from ruminants is one of the major greenhouse gases that have a high global warming potential. Methane is produced as a by-product of anaerobic fermentation in thereticulo-rumen of ruminants in a large part, due to the activity of methanogenic *archaea*. Many strategies were studied, one among is the use of probioticto manipulate the biochemical pathways existing in the rumen to produce less methane. The *Saccharomycescerevisiae* is the most commonly used direct fed microbial in ruminant production and which is more extensively studied for its effect on rumen methanogenesis. In this process to minimize the methane emission from ruminants through probiotic, the literature pertaining to the study was reviewed and is discussed below
Keywords: Ruminants, Methane, Probiotic, *Saccharomyces cerevisiae.*

INTRODUCTION

Methane emitted from ruminants is one of the majorgreenhouse gases that has a global warming potential 25 times higher than that of carbon dioxide (IPCC, 2007) and represents an energy loss for the host animal of 2 to 12 per cent of dietary energy (Johnson and Johnson, 1995). Although hydrogen (H_2) is one of the major end products of fermentation by protozoa, fungi and pure monocultures of some bacteria, it does not accumulate in the rumen, because it is immediately used by other bacteria which are present in the mixed microbial ecosystem (Moss *et al*., 2000).Methane is produced as a by-product of anaerobic fermentation in thereticulo-rumen of ruminants in a large part, due to the activity of methanogenic *archaea*. Due to the complexity of the rumen microbial ecosystem, other microorganisms also regulate and alter methane production (Morgavi *et al.,* 2010). Globally, ruminants produce approximately 80 million tons of methane annually which accounts for nearly 28 per cent of anthropomorphic greenhouse gas emission (Beauchemin *et al*., 2008). Methane emissions from livestock are estimated at about 2.2 billion tons of carbon dioxide equivalent, accounting to 35 per cent of the total anthropogenic methane emissions (FAO, 2013). Methane emitted from ruminants is generated in the rumen by hydrogenotrophic

methanogens that utilize hydrogen to reduce CO_2 and is a significant electron sink in the rumen ecosystem (Klieve and Hegart, 1999).

REDUCTION OF METHANE EMISSION FROM RUMINANTS

Enormous research is currently underway in the field of nutrition to reduce methane emission from cattle. Mitigation strategies such as use of ionophores (monensin), propionate enhancers, malic acid, stimulation of acetogens by supplementing reductive acetogens isolated from rumen, methane oxidizers, defaunation, probiotic, prebiotic and immunization have been studied for their role in methane reduction with specific advantages and disadvantages (Moss *et al*., 2000).

METHANE MITIGATION USING PROBIOTIC

Among the different strategies studied, one promising method is the manipulation of biochemical pathways existing in the rumen to produce less methane. Use of direct-fed microbials (DFM) or probiotic is one of the possible options to manipulate it. 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 methanein ruminants (Jeyanathan *et al*., 2014).

The major biochemical pathways to decrease methane emission by using DFM are the redirection of hydrogen ions away from methanogenesis and decreased production of hydrogen during feed fermentation. Lactic acid utilizing bacteria like *Megasphaeraelsdenii, Propionibacterium spp.* and yeast like *S. cerevisiae* have major effects on methanogenesis by decreasing methane (Seo *et al*., 2010). Apart from these, other rumen isolated organisms like propionate forming bacteria (*Streptococcus bovis, Fibrobactersuccinogenes*), nitrate/nitrite reducing bacteria (*Wolinellasuccinogenes* and *Selenomonasruminantium, Propionibacterium spp.*), sulphate reducing bacteria (*Desulfovibrio spp., Desulfotomaculum spp.* And *Fusobacterium spp.*), homoacetogens (*Peptostreptococcusproductus*), methylotrophs (*Nitrosomonas spp., Methanomicrococcus spp. and Methanosarcino spp.*) and capnophiles (*Actinobacillussuccinogenes, Manheimiasucciniproducens and Succinivibriodextrinosolvens*) are also used in many *in vitro* and some *in vivo* studies for methane inhibition (Jeyanathan *et al*., 2014).

Methane mitigation using *S. cerevisiae*

The *S. cerevisiae* is the most commonly used direct fed microbial in ruminant production and which is more extensively studied for its effect on rumen methanogenesis. The *S. cerevisiae*

supplements can beneficially modify rumen microbial activities, fermentative and digestive functions in the rumen (Denev *et al*., 2007).

S. cerevisiae action on total gas production

When hay plus concentrate was incubated with twin strain of *S. cerevisiae* live cells (strain 8417 and 1026 -5 x 10^9 live organisms / g) at a dose of 20, 40 and 60 mg/60 ml, there was an increased total gas production in a dose dependent manner *in vitro* (Lila *et al*., 2006). Tang *et al*. (2008) also inferred that the rate of gas production and total gas production was linearly increased for cereal straws by addition of *S. cerevisiae*. The study by Malik and Singh (2009) demonstrated that the highest total gas production was in group supplemented with *S. cerevisiae* 225 followed by *S. cerevisiae*50, 189 and 186 *in vitro* at a dose rate of 10^9 CFU / conical flask. Elghandour *et al*. (2014) reported that both low and high doses of *S. Cerevisiae* improved the asymptotic gas production *in vitro* during the period before the first 24 hours. After 24 hours and up to 72 hours of incubation, the highest dose (12 mg – 1 x 10^{10} cells / g) of *S. cerevisiae* had increased *in vitro* gas production, the lowest dose had the lowest *in vitro* gas production compared to other doses.

Besharati (2015) observed that *in vitro* gas production value of biscuit waste was improved with addition of yeast (*S. cerevisiae*). Moreover Salem *et al.* (2015) reported that the addition of*S. Cerevisiae* linearly increased the gas production during the first 12 hour of incubation. When Wang *et al*. (2016) incubated rice straw with different yeast species, maximum gas production for *S. cerevisiae* was 16 per cent higher than *Candida utilis* and also found that the dose effects of yeast addition on *in vitro* gas production parameters were dependent on yeast species.

Contrastingly, Gong *et al*. (2013) studied that the yeast cultures contained 1.8 x 10^{10} cells / g, which when added at the rates of 0.2 mg and 0.4 mg / ml of the fermented inoculums decreased total gas production in intestinal contents of pigs.

S. cerevisiae action on methane gas production

Yeast cultures reduce methane production in three ways: i) by reducing protozoa numbers ii) by increasing butyrate or propionate production and iii) by promoting acetogenesis (Newbold *et al.,* 1998). The commonly using direct fed microbials *S. cerevisiae*in ruminants has been more extensively studied for its effect on rumen methanogenesis. *S. cerevisiae* might stimulate the growth of acetogenic bacteria capable of using metabolic hydrogen (H_2) in the rumen, thus diverting H_2 from methanogenesis. The effects of *S. cerevisiae* on methane production in short term incubations with rumen fluid have been variable. Live yeast also

showed beneficial effects on the growth and H_2 utilization of acetogenic bacteria *in vitro* (Chaucheyras- Durand *et al*., 1995).

Lynch and Martin (2002) co incubated alfalfa hay and coastal bermuda grass hay separately with either a *S. cerevisiae* culture (0.35 and 0.73 g / L - 1.16 x 10^4 CFU / g) or *S. cerevisiae* live cells (0.35 and 0.73 g / L – 1.39 x 10^7 CFU / g) for 24-48 hours and observed a reduction in methane output only with 0.35 g / L *S. cerevisiae* live cells with alfalfa hay and concluded that *in vitro* system decreased methane production by 20 per cent after 48 hours of incubation. Similarly, Mwenya *et al*. (2004) also reported that sheep fed 70:30 forage: concentrate diet produced 10 per cent less methane when received daily 4 g of a yeast culture *Trichosporomsericeum* containing 1.2–2.3× 10^7 CFU / g. Malik and Singh (2009) also found that the methane production (14.60, 14.17, 12.60, 13.53, 12.87, 14.23, 14.00 and 13.2 ml / 100 g of organic matter digested) was lower in groups supplemented with *S. Cerevisiae* at a dose of 10^9 CFU compared to control (15.63 ml / 100 g of organic matter digested).

Similar results were also observed by Chung *et al*. (2011) who reported that *S. Cerevisiae* supplementation (1.32 x 10^7 CFU / kg live body weight) decreased methane by 7 per cent per kg dry matter and gross energy intake. Moreover, Gong *et al*. (2013) suggested that live yeast cells at the dose rate of 0.2 mg and 0.4 mg (1.8 x 10^{10} CFU / g) per ml of the fermented inoculums suppressed *in vitro* methane production, when inoculated into the large intestinal contents of pigs and Salem *et al*. (2015) also reported that *S. cerevisiae* supplementation decreased methane production at 24 hours in horses. Consistent with the earlier findings, *O'Brien et al*. (2014) reported that *in vitro* perennial rye grass incubation along with *S. cerevisiae* caused a dose-dependent decline in methane / dry matter intake. Interestingly, Ruiz *et al*. (2016) evaluated the effect of *Candida norvegensis* viable yeast culture on *in vitro* ruminal fermentation of oat straw and concluded that production of methane was decreased at 8 hours of incubation.

However, Oeztuerk *et al*. (2016) also confirmed that hydrolyzed whole yeast significantly increased methane concentration by *in vitro* when compared with control. The addition of *S. cerevisiae* to cereal straws at a dose of 0.25 x 10^7, 0.50 x 10^7 and 0.75 x 10^7 CFU *in vitro* caused overall increase in methane production. Highest methane production was observed at a dose of 0.50 x 10^7 CFU, which was 33 per cent higher than the control (Wang *et al*., 2016). Contrastingly, Lila *et al*. (2004) also reported no effect of twin-strains of *S. cerevisiae* (0.33– 1.32 g / L – 5 x 10^9 live cells / g) on *in vitro* methane output when co-incubated with sudan grass hay and concentrate (1.5 : 1) and McGinn *et al*. (2004) also concluded that *S. cerevisiae*

$(1.5 \times 10^{10}$ CFU / g - 4.0 g / day and strain CNCM I-1077- 2×10^{10} CFU / g - 1.0 g / day) had no effect on methane emission in cattle. Elghandour *et al*. (2014) and Yang *et al*. (2015) inferred that there was no effect on methane production, when fibrous feeds were incubated with *S. cerevisiae* at various doses.

These variations can be partly explained by the differences in experimental conditions viz., yeast strains, formats - live culture or freeze-dried preparation, dose, animal species, physiological state of animals and diets (Patra, 2012).

CONCLUSION

The review clearly shows that the yeast *S. cerevisiae* is having influence on total gas production and methane production in ruminants. However the usable extent and variations are continued concerns. It may depend on the strain of yeast and mainly on the diets used. Some more research is warranted to use it extensively in field against methane mitigation in ruminant.

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