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Critical evaluation of essential oils as rumen modifiers in ruminant nutrition: A review

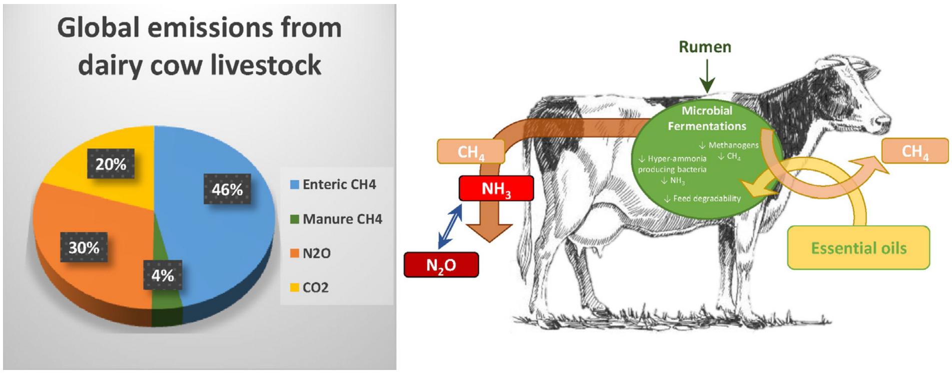
Gabriella Cobellis [a,b,*], Massimo Trabalza-Marinucci [a], Zhongtang Yu [b]

[a] *Dipartimento di Medicina Veterinaria, Università degli Studi di Perugia, Perugia, Italy*
[b] *Department of Animal Sciences, The Ohio State University, Columbus, OH 43210, USA*

HIGHLIGHTS

- Ruminants contributes 16–25% to the global greenhouse gases emissions.
- Decrease methane emission and nitrogen excretion from ruminant livestock industry is urgently needed.
- Essential oils have been shown to be promising feed additives in mitigating methane and ammonia emissions.
- Essential oils have showed inconsistent results about feed degradability and VFA production.
- The mode of action and activities of essential oils on rumen microbiome remain poorly understood.

GRAPHICAL ABSTRACT



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ABSTRACT

Ruminant livestock systems contribute significantly to emission of methane, a potent greenhouse gas as they waste a portion of the ingested energy (2–15%) as methane and a large proportion (75–95%) of the ingested nitrogen as ammonia. Recently, numerous researches have been conducted to evaluate plant secondary metabolites, including essential oils (EO), as natural feed additives in ruminant nutrition and to exploit their potential to improve rumen fermentation efficiency. Essential oils appeared to be very promising compounds as they selectively reduced methane production and protein breakdown in both *in vitro* and *in vivo* studies. However, in some studies, the use of EO as feed additives was accompanied with decreased feed degradability and lowered volatile fatty acid. These adverse effects could be attributed to their broad and often non-specific antimicrobial activities within the rumen. Future research should be directed to identification of the active and useful EO compounds, optimization of EO doses, and use of a whole-farm approach with a focus on animal welfare, performance and economic benefits.

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* Corresponding author at: Dipartimento di Medicina Veterinaria, Università degli Studi di Perugia, via San Costanzo 4, 06126 Perugia, Italy.
E-mail address: cobellis.gabriella@gmail.com (G. Cobellis).

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1. Introduction

1.1. Rumen microbial ecosystem

The rumen microbiome is essential for the ability of ruminants to utilize low-quality feed to produce high-quality protein. This community of microorganisms has been studied more than six decades. The rumen as a unique habitat collectively contains at least 50 genera of bacteria (10^{10}–10^{11} cells/ml), 25 genera of ciliate protozoa (10^4–10^6 cells/ml), six genera of fungi (10^3–10^5 zoospores/ml), some methanogenic archaea (10^9 cells/ml), and bacteriophages (10^8–10^9/ml) (Patra, 2012; Gruninger et al., 2014). Rumen microbial populations can be characterized in different ways according to their morphological (cell shape, flagella, etc.), physiological, and ecological characteristics (Firkins and Yu, 2006), but most of them are obligate anaerobes capable of degrading and/or fermenting structural or storage polysaccharides and proteins of plants. The rumen microbiome is rather stable and the stability is underpinned by three essential properties: resistance, resilience and functional redundancy (Edwards et al., 2008; Weimer, 2015). The diversity structure of rumen microbiome play a key role in ensuring stability of rumen ecosystem and increasing its ability to adapt to a wide range of dietary and management strategies. In fact, ruminal microbiome provides a huge gene pool that can cope with dietary changes by alternating metabolic pathways and stabilize a new equilibrium within the ecosystem (Edwards et al., 2008). From an ecological point of view, ruminal microbiome is highly redundant in functionality because of the narrow substrate range available (primarily polysaccharides, proteins, and lipids). Rumen microbes can be generalists that digest several substrates or specialists specialized to digest only a few specific substrates (Weimer, 2015). Based on their substrates, rumen bacteria can be classified as cellulolytic, proteolytic, lipolytic, or amino acid-fermenting microbes (Firkins and Yu, 2006). They can also be characterized into four different populations based on their localisation in the rumen environment: liquid-associated bacteria (LAB), particle-associated bacteria (PAB), epimural bacteria, and bacteria attached to the surface of protozoa and fungi (McAllister et al., 1994). The microbes in these four locations have different importance and major function and they can be affected differently by the same dietary or additive treatment. The PAB fraction represents about 75% of the total rumen microbial population, and it is responsible for most of the fibrolytic activity (88–91% of the ruminal endoglucanase and xylanase activity), 70% of the amylolytic activity, and 75% of the proteolytic activity in the rumen (Miron et al., 2001). The LAB fraction represents about 20–30% of the total rumen microbial population, and most of them are non-fibrolytic bacteria that only have limited contribution to digestion of insoluble feed particles (Miron et al., 2001). The microbes in these four locations can be affected differently by the same dietary and additive treatment.

Cultivation-based studies provided useful knowledge on the physiology and metabolism of only a small percentage (10–15%) of all the rumen microorganisms (Kim et al., 2011; Morgavi et al., 2013). The use of 16S rRNA gene-based analyses has revealed that the rumen microbiome is very diverse and complex containing hundreds or thousands of species at varying relative abundance (Kim et al., 2011). Much of the knowledge on rumen diversity and composition was derived from sequence analysis of amplicons of rRNA genes (Kim et al., 2011). Contemporary metagenomic techniques allow examination of the detailed diversity, both phylogenetic and functional, of rumen microbiome under different dietary conditions or in response to different feed additives. In this article, previous studies on essential oils (EO) were reviewed, with an emphasis on the mechanistic underpinning of how EO affect rumen microbiome, feed digestion and fermentation, methane emission, and protein degradation.

1.2. Environmental impact of ruminant livestock

Ruminant livestock production has a large environmental impact as it emits methane and excretes nitrogen in large quantities. Ruminants contribute 16–25% to the global greenhouse gases emissions and about 33% to global anthropogenic methane emissions. Methane emission also wastes 2–15% of the ingested energy, varying with the level of feed intake and diet composition (Kumar et al., 2009; Eckard et al., 2011). Methane emission from ruminants derives mainly from enteric fermentation (87% from rumen and 13% from large intestine) but also from their manure (Torrent and Johnson, 1994). Methane produced by enteric fermentation is released to the environment through eructation, normal respiration, and, in small quantities, as flatus.

Livestock manure is also a large source of nitrogen output. Ammonia represents an important component of the manure nitrogen cycle since urease, a microbial enzyme present in large amount in feaces and soil, rapidly converts urea excreted with urine into ammonia. Ammonia, through nitrification process, can be oxidized to form nitrate and nitrous oxide as by-products (de Klein and Eckard, 2008). Both ammonia and nitrate can be readily assimilated by plants, but ammonia is volatile and it can escape to the atmosphere (de Klein and Eckard, 2008). Ammonia loss through volatilization accounts for 30–70% of the ammonia resent in cattle manure (Hristov et al., 2013). Ammonia may return to soil through dry or wet precipitation, contributing to groundwater