



Review Article

Rumen microbiota succession throughout the perinatal period and its association with postpartum production traits in dairy cows: A review

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ABSTRACT

The transition period for dairy cows usually refers to the 3 weeks pre-calving to the 3 weeks post-calving. During this period, dairy cows undergo metabolic and physiological adaptations because of their susceptibility to metabolic and infectious diseases. Poor feeding management under these circumstances may adversely affect the health and subsequent production performance of the cows. Owing to long-term adaptation and evolution, the rumen has become a unique ecosystem inhabited by a complex microbial community closely associated with its natural host. Dietary components are metabolized by the rumen microbiota, and volatile fatty acids and microbial protein products can be used as precursor substances for synthesizing meat and milk components. The successful transition of perinatal dairy cows includes changes in diet, physiology, and the rumen microbiota. Rumen microbial profiles have been confirmed to be heritable and repairable; however, adverse circumstances affect rumen microbial composition, host digestion and metabolism, as well as postpartum production traits of dairy cows for a certain period. Preliminary evidence indicates a close relationship between the rumen microbiota and animal performance. Therefore, changes in rumen microbes during the transition period and the intrinsic links between the microbiota and host postpartum phenotypic traits need to be better understood to optimize production performance in ruminants.

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1. Introduction

Research studies have previously focused on the lactation period of dairy cows because this stage provides direct economic benefits to dairy farms. However, the perinatal period is equally important because it is closely related to postpartum health and subsequent

production performance and lifespan of cows. The biological features of perinatal dairy cows have been extensively studied for over two decades, and the related biology has been described as “the final frontier” (Drackley, 1999). Cows commonly experience a decrease in dry matter intake (DMI) before calving (Mann et al., 2015), which is more prominent in primiparous cows (Neave et al., 2017). The imbalance between energy intake and postpartum nutrient outflow mobilizes body tissues to meet lactation needs. Body tissue mobilization partially alleviates the negative energy balance (NEB) of dairy cows but may also induce a series of problems. For instance, glycerol and free fatty acids released from body tissues accumulate in the liver, thus increasing the hepatic metabolic burden (Contreras et al., 2018). The NEB decreases the sensitivity of the immune system of dairy cows, leading to immunosuppression (Gu et al., 2023; Trevisi and Minuti, 2018). Pro- or anti-inflammatory cytokines secreted from adipose tissue may induce local or systemic inflammatory responses (Haussler et al.,

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2022; Nishimura et al., 2009). In addition, lipid and protein mobilization produces large amounts of reactive oxygen species (Sordillo and Raphael, 2013), and an imbalance in these substances may cause oxidative stress (Abuelo et al., 2019). Given these distinct physiological characteristics, the probability of disease occurrence in the perinatal period is higher than that at any other period in the lactation cycle of dairy cows (LeBlanc et al., 2006); for example, for ketosis and mastitis, the probability is highest within 3 weeks postpartum (Macrae et al., 2019; Redfern et al., 2021). These circumstances pose significant challenges to the health of perinatal cows.

The rumen is an important microecosystem that allows ruminants to digest different types of feed, especially plant-derived feed resources, via microbial fermentation. Over thousands of years, hosts have established an interdependent symbiotic relationship with their microbiota. The health and microbiota structure of the rumen of dairy cows are essential for efficient milk production. Rumen microbes are closely related to various production traits, as most milk precursors are derived from fermented products (Golder et al., 2023; Huang et al., 2021; Xue et al., 2020). The type of diet affects the rumen fermentation pattern, and the accepted feeding strategy is to switch to a relatively low-fiber, high-energy diet postpartum to maximize production performance. This approach may affect the structure of microbial communities in the rumen. For instance, the relative abundance of some cellulolytic bacteria decreases over the transition period (Bach et al., 2019; Pitta et al., 2014; Wang et al., 2012), while the abundance of some carbohydrate- and lactic acid-utilizing bacteria increases with increasing proportion of dietary concentrates (Zhu et al., 2018, 2017). This adaptive change promotes the utilization of different dietary nutrients. Some changes may adversely affect perinatal dairy cows under special circumstances. For example, the proportion of Christensenellaceae and *Streptococcus bovis* increases in postpartum rumen fluid, whereas that of *Selenomonas ruminantium* decreases under severe NEB conditions (Xiang et al., 2022). Christensenellaceae is inversely correlated with propionate concentrations (Zhang et al., 2022); whereas *S. bovis* and *S. ruminantium* are lactic acid producers and consumers, respectively (Russell and Hino, 1985; Wang et al., 2012). This imbalance may disrupt the metabolism of propionate and lactic acid and, together with the ineffective management of perinatal dairy cows, may aggravate the NEB and increase the probability of postpartum diseases. Furthermore, the rumen microbiota is closely related to host physiology, and most volatile fatty acids (VFA) are incorporated into the rumen wall, where they serve as an important source of energy for ruminants (Russell, 2002). The effective succession of the rumen microbiota during the transition period is closely related to the postpartum production of phenotypic traits and affects host health. Therefore, investigating the growth and functional characteristics of the rumen microbiota and the mechanisms underlying the interactions and competition of the constituent microorganisms will help to promote nutrient utilization in the rumen, reduce greenhouse gas emissions, and improve food quality and safety. In this paper, we review the rumen microbial succession throughout the perinatal period and the relationship between microbes and postpartum production traits to understand the temporal changes in rumen microbes and their potential regulatory role in postpartum production phenotypic traits.

2. Significant role of rumen bacteria in host metabolism

In contrast to non-ruminants, ruminants have a unique ability to utilize the nutrients present in plant fibers. Degraded plant cellulose and hemicellulose produce VFA, which account for 60% to 70% of the metabolizable energy of the host (McCartney et al., 2013).

Rumen microbiology has led to research on modern livestock production. Owing to long-term adaptation and evolution, the rumen has become a complex microbial ecosystem, and rumen microbes and hosts have established a dynamic balance of mutual restriction and interdependence, which is important for maintaining the health, production efficiency, and food safety of ruminants (Fig. 1). Bacteria, protozoa, and fungi exist in close proximity in the rumen. Among these, bacteria account for most of the microbes in the rumen (Pitta et al., 2014). Rumen protozoa and fungi are also important components of rumen microecology and participate in rumen metabolism and various nutrient degradation processes; however, we consider them to be outside the scope of the present study. Bacteroidetes, Firmicutes, and Proteobacteria are relatively abundant in the rumen (Creevey et al., 2014; Snelling and Wallace, 2017; Xue et al., 2020). *Fibrobacter succinogenes*, *Ruminococcus flavefaciens*, *Ruminococcus albus*, and *Butyrivibrio fibrisolvens* are the main cellulolytic bacteria (Krause et al., 2003); *Prevotella*, *B. fibrisolvens*, and *R. flavefaciens* are the predominant hemicellulose digesters (Morais and Mizrahi, 2019). These bacteria are present in almost all ruminants and can thus be considered to be the core rumen bacterial microbiota. Structural carbohydrates are an essential energy source for ruminants, and several cellulolytic and hemicellulolytic bacteria, such as *B. fibrisolvens*, *Prevotella*, and *F. succinogenes*, also digest these sources of nutrients (Puniya et al., 2015). This indicates that some rumen bacteria are functionally diverse. *S. bovis*, *Ruminobacter amylophilus*, *Succinimonas amylytica*, and *S. ruminantium* are important starch-utilizing bacteria in the rumen (Puniya et al., 2015). Among these, *S. bovis* plays an increased digestive role in relatively high-starch diets, and lactate is the primary end-product of its metabolism. *S. ruminantium* is a lactic-utilizing microbe that converts lactic acid into propionic acid (Russell and Hino, 1985; Wang et al., 2012). This type of microbe thus helps to avoid lactate accumulation in the rumen.

Low-abundance microorganisms in the rumen belonging to the domain Archaea have attracted extensive attention because some of them are methanogenic (Table 1). Methane adversely affects the global climate, and methanogenesis is an energy-inefficient utilization pattern. Various strategies for mitigating methane emissions from livestock production processes have been implemented to date, which have achieved promising results (Dalby et al., 2020; Yang et al., 2016). Regardless of those adverse effects, methanogens are present in the rumen of all ruminants and are considered core microbes (Henderson et al., 2015). Rumen microbial communities grow in cooperative, mutually-restricted, and dynamically-balanced ecosystems. Hence, there is a need to understand the changes in the rumen microbiota during the transition period to provide a basis for optimizing feeding management and postpartum production traits.

3. Rumen microbiota changes during the transition period

The biological characteristics of peripartum dairy cows have been thoroughly investigated over the past decades (Drackley, 1999, 2006; McFadden, 2020). Perinatal dairy cows are susceptible to metabolic disorders and immunological challenges from the prepartum to the postpartum period. NEB occurs and reaches a nadir during the first 3 weeks post-calving. These factors significantly influence animal health, productivity, and profitability (Mulligan and Doherty, 2008; Trevisi and Minuti, 2018). The rumen is a highly specialized bioreactor inhabited by various microbes that work cooperatively or independently to digest different nutrient components and convert them into available ingredients. Furthermore, fermented products, such as VFA, can be absorbed and transported to the circulatory system to maintain basic metabolism, muscle development, or milk component synthesis

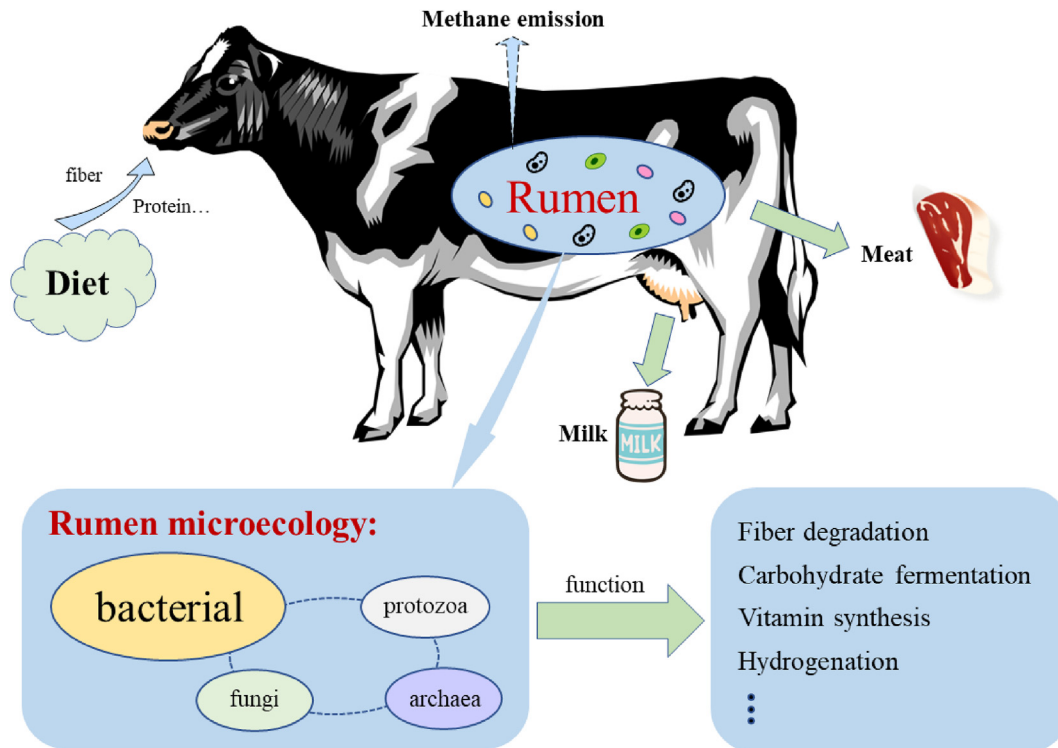


Fig. 1. The role of rumen microbes in the metabolism of host.

Table 1
The rumen microbes and major functions in the rumen.

Phylum	Family	Genus	Function and products	
Bacteroidetes	Prevotellaceae	<i>Prevotella</i>	Function: Protein, carbohydrate degradation Products: Succinate, lactate, acetate, propionate and formate	
		<i>Prevotellaceae_NK3B31</i>		
		<i>Prevotellaceae_UCG-004</i>		
		<i>Prevotellaceae_Ga6A1</i>		
		<i>Prevotellaceae_YAB2003</i>		
		<i>Prevotellaceae_UCG-003</i>		
		<i>Prevotellaceae_UCG-001</i>		
		<i>CF231</i>		
		<i>YRC22</i>	Not well been defined yet	
		Firmicutes	Rikenellaceae	<i>Rikenellaceae_RC9</i>
Ruminococcaceae	<i>Ruminococcus</i>		Function: Cellulose, hemicellulose degradation Products: Succinate, acetate and formate	
	<i>Clostridium IV</i>			
	<i>Saccharofermentans</i>			
	<i>Flavonifractor</i>			
	<i>Ruminococcaceae family</i>			
	<i>Unclassified_Ruminococcaceae</i>			
	Selenomonadaceae		<i>Selenomonas ruminantium organisms</i>	Function: Carbohydrate fermentation, lactate utilization Products: Propionate
	Veillonellaceae		<i>Megasphaera elsdenii</i>	Function: Carbohydrate fermentation, lactate utilization Products: Propionate
	Lactobacillaceae		<i>Lactobacillus</i>	Function: Carbohydrate fermentation Products: Lactate, volatile fatty acids
	Streptococcaceae	<i>Streptococcus</i>	Function: Carbohydrate fermentation Products: Lactate	
Proteobacteria	Christensenellaceae	<i>Christensenellaceae_R-7group</i>	Function: Structural carbohydrates digestion Products: Acetate and butyrate	
		Lachnospiraceae	<i>Butyrivibrio</i>	Function: Protein, carbohydrates digestion Products: Lactate, butyrate and short-chain fatty acid
		<i>Coprococcus</i>		
		<i>Moryella</i>		
		<i>Lachnospiraceae_UCG-009</i>		
		<i>Unclassified_Lachnospiraceae</i>		
		Clostridiaceae	<i>Clostridium</i>	Function: Cellulose and hemicellulose degradation Products: Organic acids, carbon dioxide, and hydrogen gas
		Succinivibrionaceae	<i>Succinivibrio</i>	Function: Starch, pectin degradation Products: Succinate and propionate
		<i>Succinimonas</i>		
		<i>Ruminobacter</i>		
Archaea	Methanobacteriaceae	<i>Unclassified_Succinivibrionaceae</i>		
		<i>Methanosphaera</i>	Function: Methanol, CO ₂ and H ₂ utilization Products: Methane	
		<i>Methanobrevibacter</i>		

(Reynolds et al., 1988). Rumen microbes are commonly heritable, and host factors can affect their community structure and function (Abbas et al., 2020; Difford et al., 2018; Sasson et al., 2017). Given the unique physiology of perinatal dairy cows, changes in the rumen microbiota may affect rumen digestion, metabolism, and postpartum production performance. The successful transition from pregnancy to postpartum is critical to achieving high milk production performance.

3.1. Rumen microbiota from prepartum to postpartum

During the perinatal period, adaptation of rumen microbiota to different nutritional management strategies can facilitate the switch from pregnancy to lactation. Rumen health is partly related to changes in rumen microbial community structure and abundance (Khafipour et al., 2016), which undergo significant changes between the prepartum and postpartum period; moreover, this phenomenon is relatively dynamic (Huang et al., 2021; Pitta et al., 2014; Zhu et al., 2018). In a rumen fluid sampling study in cows fed corn silage and corn-based diet, rumen microbial community diversity (indicated by Shannon and Chao 2 diversity indices) was found not to significantly differ across the perinatal period (–3 weeks to 3 weeks) (Wang et al., 2012). Similarly, rumen microbial alpha diversity (Shannon and Simpson indices) did not change during the perinatal period of another study (Derakhshani et al., 2016). However, some studies on cows fed corn silage, grass silage and spring barley base diet indicated that the Chao 1 richness index and the number of rumen microbiota species decreased from prepartum (–3 weeks) to postpartum (4 weeks) (Lima et al., 2015; Zhu et al., 2018). Another study revealed that the Shannon diversity index was consistent with the findings of Zhu et al. (2017, 2018) on the seventh day before calving, whereas the diversity of rumen microbes returned to prenatal levels at 3 weeks postpartum (Bach et al., 2019). Although the results of microbial diversity in these studies were varied, the overall evidence indicates a complex change in the rumen microbiota during the transition period.

The predominant rumen microbes are Bacteroidetes, Firmicutes, and Proteobacteria, and their relative abundance varied in different studies (Jami and Mizrahi, 2012; Pitta et al., 2014; Wang et al., 2012; Zhu et al., 2018). A previous study revealed that Bacteroidetes significantly decreased from the prenatal to the postpartum period, mainly manifested as a decrease in RF16, unclassified Bacteroidales, less dominant Bacteroidaceae, and BS11 (Zhu et al., 2018). In contrast, Prevotellaceae exhibited different changes and significant increases in postpartum rumen fluid samples (Huang et al., 2021; Zhu et al., 2018), which is consistent with other research on peripartum cows or cows fed a relatively higher concentrate diet during the early lactation stage (Bach et al., 2019; Henderson et al., 2015). Prevotellaceae is the most abundant rumen bacterial species and plays an important role in the degradation of polysaccharides and proteins and the fermentation of starch (Deusch et al., 2017; Stevenson and Weimer, 2007). Peripartum dairy cows undergo a diet shift from a forage-based diet to a concentrate-based diet; thus, the increased abundance of Prevotellaceae may be beneficial for cows that need to digest relatively higher levels of protein and starch in their postpartum diets. Prevotellaceae is involved in the degradation of protein and starch (Deusch et al., 2017) and has a positive correlation with propionate production (Henderson et al., 2015); thus, the important characteristic of high-producing dairy cows may be a relatively higher abundance of Prevotellaceae in the rumen. This has also been confirmed other studies, which revealed that rumen *Prevotella* species are more enriched in dairy cows with high amounts of milk or milk protein production (Sofyan et al., 2019; Xue et al., 2020). Thus, Prevotellaceae can be considered

one of the core rumen microbes and is closely associated with the lactation performance of dairy cows.

Firmicutes is another predominant phylum in the rumen bacterial assemblage and is mainly composed of Lachnospiraceae, Ruminococcaceae, and Christenellaceae (Pinnell et al., 2022; Zhu et al., 2018). Of these, Lachnospiraceae abundance does not change from the prenatal to postpartum periods, whereas Ruminococcaceae abundance decreases in the postpartum rumen fluid of dairy cows (Pitta et al., 2014; Wang et al., 2012; Zhu et al., 2018). Ruminococcaceae is associated with fiber digestion (Liu et al., 2016; Shen et al., 2017), and the observed decrease in the abundance of this family may stem from a shift in dietary structure over the perinatal period. Zhu et al. (2018) found that the abundance of some cellulolytic bacteria, such as *Ruminococcus*, *Butyrivibrio*, and *Fibrobacter*, did not significantly change from prepartum to postpartum. However, this finding is inconsistent with that of Lima et al. (2015) who found a decrease in the abundance of these bacteria during the postpartum period. This observation may be due to the difference in the dietary ingredients, nutritional value, and energy content of these feeds, which may affect the relative abundance of those bacteria. However, it is difficult to compare results between studies given the lack of adequate dietary information. Christenellaceae are well-characterized acetate and butyrate producers involved in structural carbohydrate digestion (Morotomi et al., 2012). Their relative abundance is enriched in the prepartum (Bach et al., 2019; Derakhshani et al., 2016; Zhu et al., 2018) and around the calving (Huang et al., 2021) stages of the ruminal ecosystem, which may have negative outcomes for dairy cows, especially for postpartum cows experiencing a state of severe NEB.

Proteobacteria is another dominant bacterial phylum in the rumen microbiota which, together with Bacteroidetes and Firmicutes, plays a non-negligible role in the utilization of soluble carbohydrates (Pitta et al., 2016). Typically, Proteobacteria becomes one of the dominant phyla when ruminants are fed a starch-based diet (Kang et al., 2013; Pang et al., 2022; Wang et al., 2020), and Proteobacteria (including class Gammaproteobacteria and Succinivibrionaceae) abundance significantly increases throughout the perinatal period (Zhu et al., 2018, 2017). This increase in Proteobacteria could enhance the adaptability of cows to postpartum diets, as bacteria in this phylum are commonly involved in starch digestion. However, some studies found that the relative abundance of Proteobacteria exhibits irregular changes during the perinatal period (Pitta et al., 2014; Wang et al., 2012). The discrepancies in these results may be due to the differences in the sampling, detection, and analytic methods used, and to differences in the diet; additional research is needed to clarify these inconsistencies.

No difference exists in the diversity index of rumen Archaea from the prepartum to the postpartum periods; however, the abundance of some Archaea changes significantly during the perinatal period (Kumar et al., 2015). *Methanobrevibacter* is the most abundant Archaea genus in the rumen (>95%), and its relative abundance is reduced in both multiparous (Bach et al., 2019) and primiparous cattle (Kumar et al., 2015) from the pregnancy to lactation periods. *Methanobrevibacter* is the main methane-producing bacterium (Cersosimo et al., 2016; Xue et al., 2020; Zhou et al., 2009), and relatively high-grain rations typically result in a relatively lower production of methane than a high proportion of forage diet (Aguerre et al., 2011); thus, the postpartum diet of dairy cows may have a negative relationship with rumen methanogens. However, some studies reported that *Methanobrevibacter* abundance did not change in primiparous (Zhu et al., 2017) and multiparous (Kumar et al., 2015) cows during the transition period, and a downward trend was observed as lactation proceeded, with a return to the postpartum level before drying (Cersosimo et al.,

2016). Overall, dramatic shifts were observed in rumen microbiota composition and abundance during the transition period, characterized by a decrease in some fiber-utilizing bacteria and their partial replacement by soluble carbohydrate-utilizing bacteria (Fig. 2). However, some studies have reported different results, largely due to differences in the diet structure of peripartum dairy cows. Future work should focus more on this aspect to deepen our understanding of the functional changes in the rumen microbiota community during the perinatal period. More specifically, studies should focus on heritable microbes because they are more strongly related to host traits than non-heritable microbes (Sasson et al., 2017; Wallace et al., 2019; Zang et al., 2022). Thus, understanding functional changes in heritable microbes may provide new options for phenotypic improvement.

3.2. Ketosis and rumen microbiota

Energy homeostasis is also essential for maintaining animal health and meeting energy requirements. During the perinatal period, especially around calving, animals experience NEB due to insufficient dietary intake and lactation onset. Appropriate body tissue mobilization is necessary for early lactating cows to meet their milk secretion requirements. However, the intense mobilization of body tissues may have detrimental effects on reproductivity, lactation performance, and welfare (Contreras et al., 2017; Mann, 2022). Long-term NEB induces metabolic disorders. Ketosis is regarded as one of the most devastating diseases during the freshening period of dairy cows and causes economic loss. The disease is characterized by ketone bodies accumulating in various body fluids, including beta-hydroxybutyrate acid (BHBA), acetoacetate, and acetone (Cainzos et al., 2022; Deniz et al., 2020). Ketosis affects the metabolite profiles of the rumen, mainly manifested as high concentrations of butyric acid, sucrose, BHBA, and valerate, and low concentrations of glucose and propionate (Eom et al., 2021). However, high concentrations of butyrate and valerate may pose challenges, as approximately 30% of butyrate and 20% of valerate can be converted into BHBA and subsequently taken up by the rumen epithelial wall and transported throughout the body via the circulatory system (Doreau et al., 2001). Ketosis affects rumen function; thus, changes in the rumen microbiota may be closely associated with the occurrence of ketosis in the perinatal period.

Previous research revealed that the rumen microbial community diversity did not differ among cows in normal (100 DIM), transition, and ketosis conditions; however, changes were observed in the abundance of some rumen microbes. For instance, the relative abundance of *S. bovis* increased, while that of *M. elsdenii* and *S. ruminantium* was reduced in transition and ketosis cows (Wang et al., 2012). The decrease in *M. elsdenii* and *S. ruminantium* may exacerbate the NEB of transition or ketosis in dairy cows because they can utilize carbohydrates or lactic acid as substrates to synthesize propionate (Henning et al., 2010; Russell and Hino, 1985; Stevenson and Weimer, 2007). Moreover, rumen microbial richness decreased in cows with subclinical ketosis (Xiang et al., 2022), which is inconsistent with the research of Wang et al. (2012). Further analysis indicated that the abundance of several rumen microbes, such as *Bacteroidota*, *Christensenellaceae_R-7*, *Ruminococcus*, and *Thermomonas*, increased, whereas rumen *Prevotella* abundance decreased in dairy cows with subclinical ketosis. *Christensenellaceae_R-7* and *Thermomonas* had a positive correlation with blood BHBA content, while *Prevotella* had a negative correlation with BHBA (Xiang et al., 2022). *Christensenellaceae* produces acetate and butyrate by utilizing structural carbohydrates (Lima et al., 2015; Morotomi et al., 2012) and has a positive and negative correlation with BHBA and propionate concentrations, respectively (Zhang et al., 2022), and is possibly involved in the production of ketone bodies. In contrast, *Prevotella* species are significantly positively correlated with rumen propionate concentrations (Zhu et al., 2018). A case study predicted the relationship among rumen microbes, milk BHBA, and acetone; milk ketone bodies were strongly associated with rumen *Prevotellaceae* and *Ruminococcaceae* (Gebreyesus et al., 2020), both of which have a negative relationship with BHBA (Scharen et al., 2018) and NEB (Derakhshani et al., 2016). Thus, milk BHBA and acetone concentrations can be used to predict the rumen microbial composition of dairy cows. Few research studies have revealed that ketosis affects rumen microbial composition and reduces the relative abundance of propionic acid-producing microbes in the rumen because propionate is an important gluconeogenesis substrate. This negative effect may aggravate the problem of insufficient glucose supply in dairy cows experiencing NEB over the transition period (Fig. 2). However, more parallel and longitudinal studies are needed to confirm these alterations. These studies should include cows with

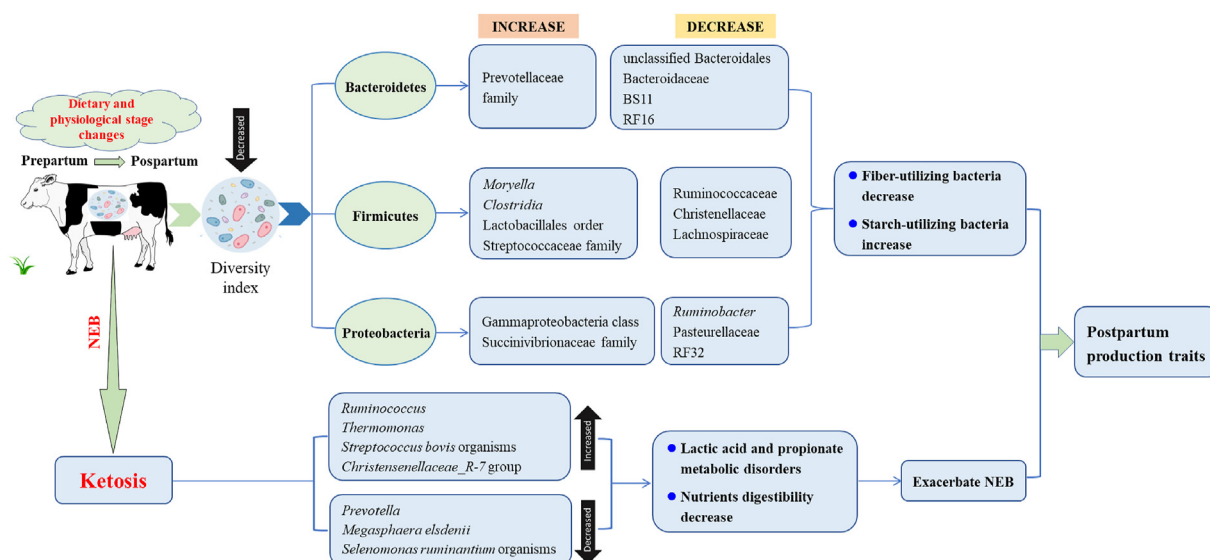


Fig. 2. The change of rumen microbes from prepartum to postpartum in dairy cows. NEB = negative energy balance.

subclinical and clinical ketosis or cows with different body mobilization conditions.

4. Relationship between rumen microbiota and postpartum production traits

In modern dairy production systems, transition dairy cows face multiple challenges, including dietary changes, immunosuppression, and the shift from pregnancy to lactation. These factors affect cow health, productivity, and product quality. Despite dietary effects on the diversity of rumen microbiota, host factors also affect the number, community structure, and function of rumen microbes, and heritable and non-heritable rumen microbes contribute differently to production traits (Zang et al., 2022). Previous studies on the gut–microbiota–brain axis pathway revealed that microbes are important for regulating host metabolism (Rainard, 2017; Saint-Georges-Chaumet and Edeas, 2016). This may be a crucial factor for optimizing milk or meat production. In some cases, rumen microbiota is ranked as a better indicator for predicting animal performance than other factors (Gleason and White, 2018). Therefore, the interrelationships between the rumen microbiota and production traits should be further investigated to optimize the performance of ruminants.

Recent advancements in research have led to greater attention being paid to understanding the contribution of rumen microbiota to production traits. An exploratory study on lactating dairy cows revealed that some production phenotypes are closely related to rumen microbes. For example, the Firmicutes to Bacteroidetes ratio had a positive association with milk fat percentage, in that Lachnospiraceae and *Moryella* (Firmicutes) were negatively correlated with milk fat yield, while *Prevotella* (Bacteroidetes) had a positive correlation with milk fat yield (Jami et al., 2014). *Prevotella* is a predominant member of the rumen microbiota, and contrastingly shows a negative correlation with milk fat percentage (Chiquette et al., 2008; Indugu et al., 2017). This discrepancy may be attributable to the dilution effect of milk volume on fat percentage, as some previous studies have revealed a positive correlation between *Prevotella* and milk production volume (Indugu et al., 2017; Xue et al., 2020; Zhu et al., 2021). In addition, the genetic diversity of *Prevotella* may result in a wider spread of the responses of individual populations to dietary components, which also may contribute to different correlations with milk fat percentage (Bekele et al., 2010). Jami et al. (2014) discovered that some rumen microbes were correlated with milk production; the order Coriobacteriales, family Coriobacteriaceae, and genera *Adlercreutzia* and *Desulfovibrio* were positively correlated and the family Clostridiales, and Family XIII and *F16* were negatively correlated with milk yield. Research on dairy farms with different production levels (high and low milk yields) revealed that *Prevotella* and Succinivibrionaceae positively contributed to high milk yields, and Succinivibrionaceae were abundant in both primiparous and multiparous cows in high-yield dairy farms (Indugu et al., 2017). Succinivibrionaceae exhibits a positive correlation with gross feed efficiency (Shabat et al., 2016) and can convert succinate to propionate and regulate milk production (Liu et al., 2013). This may be one of the reasons for its association with high productivity. In another study on high and low milk production, *Prevotella_1*, *Eubacterium coprostanoligenes*, and *Treponema_2* were positively correlated with milk yield, whereas Lachnospiraceae_NK3A20, *Coprococcus_1*, *Oribacterium*, *Mogibacterium*, and Prevotellaceae had a negative association with milk production (Tong et al., 2018). These studies presented associations between some rumen bacteria and production traits in lactating dairy cows; however, the findings (except those regarding *Prevotella* species) have proven difficult to replicate, and the precise function of some microbes that

relate to production traits remains unknown. Furthermore, previous research has reported that production traits can only be partially explained by the rumen microbiota (Xue et al., 2020); thus, further detailed characterization is needed to confirm the reliability of these associations in lactating cows.

The successful transition of perinatal dairy cows is vital because failure in management can affect their production, reproductive performance, and welfare in the subsequent lactation cycle. The rumen microbial community undergoes significant changes during the perinatal period, leading to uncertain effects on the productivity of postpartum cows. Preliminary research evaluated the relevance of the postpartum rumen microbiota for milk production and discovered that Prevotellaceae 2 and R4-41B have a strong positive and negative correlation with weekly milk production in multiparous postpartum dairy cows, respectively. In primiparous postpartum dairy cows, Erysipelotrichaceae and Deltaproteobacteria had strong positive and negative correlations, respectively, with average weekly milk production (Lima et al., 2015). Subsequent analysis showed that an unclassified genus of Coriobacteriaceae (Actinobacteria) was the only genus positively correlated with milk production, whereas Catabacteriaceae, unclassified BS11, and the genus *Oscillospira* (Firmicutes) had negative associations with milk production. Furthermore, *Clostridium*, unclassified Lachnospiraceae, and Erysipelotrichaceae were positively correlated with milk protein percentage (Derakhshani et al., 2016). One study evaluated the possible relevance of the rumen microbiota for phenotype traits prior to the dry period using Spearman's correlation and revealed that *Prevotella* abundance and milk yield were positively correlated, whereas *Methanobrevibacter*, *Ruminococcus*, and *Streptococcus* had a negative correlation with milk production (Chuang et al., 2020). The relative abundance of *Prevotella* increases postpartum (Bach et al., 2019; Pitta et al., 2014; Zhu et al., 2018). The genus can participate in polysaccharide and protein degradation and starch fermentation (Deusch et al., 2017; Stevenson and Weimer, 2007), which supports the positive correlation between *Prevotella* and high milk production. *Methanobrevibacter* is the main methanogen in the rumen. The production of methane is inefficient and a source of energy loss in ruminants and can adversely affect the environment (Cersosimo et al., 2016; Løvendahl et al., 2018). The abundance of rumen *Methanobrevibacter* was different between high- and low-producing dairy cows, a relationship confirmed in many other experimental animal studies (Xue et al., 2020, 2022). Currently, evidence of the relationship between rumen microbiota and postpartum production traits is lacking, and certain knowledge gaps exist in our understanding of the structural and functional changes in heritable and non-heritable rumen microbes throughout the perinatal period. Future work is needed to investigate these correlations. The parity and body condition of prenatal dairy cows should be considered because of differences in body mobilization during the transition period. These factors may also affect the rumen microbial community, postpartum performance, and milk composition. Additional research is required to fully explore the contributions of the rumen microbial community to postpartum production traits under different feeding conditions, including grazing and intensive farming or overfeeding conditions. Furthermore, genetic × environmental × microbial interactions should be considered in future research to better explain the variance in postpartum production performance.

5. Role of nutraceuticals in regulating rumen microbiota during the transition period

The adoption of a prepartum high-fiber diet following by a postpartum high-concentrate diet is a prevalent feeding approach in contemporary dairy production systems. Therefore, rumen microbes must adapt to this change to further optimize rumen

function and generate raw materials for the synthesis of milk components (Lima et al., 2015; Minuti et al., 2015; Reynolds et al., 1988). Rumen functions are affected by many factors, and their internal environment can be modified. Effective nutritional management can improve the rumen microbial community, increasing nutrient availability.

5.1. Live yeast culture and its products

Live yeast cultures and fermented products have been widely used in livestock production. Live yeast and yeast-based products can improve dairy cow milk quality and production efficiency (Carpinelli et al., 2021; Hansen et al., 2017; Pinloche et al., 2013). The feeding of 5 g/day live yeast to cows can activate rumen fiber-degrading bacteria (*Fibrobacter* and *Ruminococcus*) and lactate-utilizing bacteria (*Megasphaera* and *Selenomonas*) (Pinloche et al., 2013). Similar results for rumen *Fibrobacter* have been observed in mid-to-late lactating dairy cows fed with 10 g/day of active yeast product (Uyeno et al., 2017). The presence of live yeast has an impact on the structure and abundance of the rumen microbiota in perinatal dairy cows. Most of them, including Bacteroidales, Lachnospiraceae, and *Flexilinea*, increase in the rumen before calving; only *Streptococcus* increases postpartum (Bach et al., 2019). Another study revealed that supplementing perinatal cows with yeast culture product (14 g/day) could also promote the growth of rumen cellulolytic and lactate-utilizing bacterial populations, such as *F. succinogenes* and *M. elsdenii* (Carpinelli et al., 2021), indicating that live yeast and yeast-based products could regulate rumen function by improving the rumen microbial community. Yeast culture and its products contain various factors that stimulate the growth of rumen bacteria, especially lactic acid utilization factors (Chaucheyras-Durand et al., 2008). Shabat et al. (2016) discovered a strong correlation between lactic acid-utilizing bacteria and feed efficiency. This type of bacteria may re-direct rumen lactate to propionate synthesis, thereby helping to stabilize rumen pH (Shabat et al., 2016), which may help to prevent the occurrence of ruminal ketosis and acidosis. Thus, the increase of fiber-degrading and lactate-utilizing bacterial abundance is important for improving fiber digestibility and stabilizing the ruminal environment. However, further efforts are warranted to clarify the long-term postpartum effects and the potential mechanisms by which yeast culture exerts these effects.

5.2. Methyl donor substance

Methyl donors, such as choline, methionine, and their analogs, can improve livestock production performance, immunometabolism, and liver function (Davidson et al., 2008; Wang et al., 2022; Zhou et al., 2016). Understanding the effects of methyl donor substances on the rumen fluid microbiota and revealing its potential connection to lactation performance would be of enormous interest. A recent study using multi-omics integrated analysis revealed that mid-lactation dairy cows fed 20 g/day rumen-protected methionine had an increased abundance of rumen *Saccharofermentan*, *Acetobacter*, and *unclassified_f_Lachnospiraceae*. These bacteria contribute to improved milk fat content (Gu et al., 2021). Similarly, a recent study on lactating yaks revealed that rumen Proteobacteria and *Prevotella_1* abundance increased following supplementation with rumen-protected methionine (50.0 g/day), and *Prevotella_1* had a positive association with DMI and rumen NH₃-N concentration (Zhao et al., 2021). An in vitro study showed that supplementation with 20 mg of calcium salt of the hydroxy analog of methionine increased *Prevotella_1*, *Streptococcus*, and *Desulfovibrio* abundance in the rumen, and those rumen microorganisms had a positive association with dry matter digestibility and

microbial protein concentration (Li et al., 2023). These findings indicate that methionine and its analogs can affect rumen microbial communities, fermentation parameters, and production phenotypes. In perinatal dairy cows, rumen-protected methionine supplementation also alters the rumen bacterial community; the abundance of several bacteria such as *Succinivibrio dextrinosolvens*, *F. succinogenes*, and *S. amylolytica* was enriched prepartum, whereas the abundance of *F. succinogenes* and *S. ruminantium* was decreased in postpartum rumen fluid samples (Abdelmegeid et al., 2018). This condition may originate from the relatively higher DMI in the postpartum methionine-treated group (19.6 kg/day vs. 13.9 kg/day), as higher feed intake and a diet with a high dietary concentrate proportion increase the liquid dilution rate (Stokes et al., 1985), which can partially explain the lower abundance of these bacteria. Further research is required to provide converging evidence and explain this discrepancy. Choline, a methyl donor in dairy cows, is involved in transmethylation reactions involving folate and vitamin B₁₂, such as methionine and carnitine synthesis and DNA methylation. Research on pregnant ewes revealed that supplementation with rumen-protective choline chloride did not affect rumen fermentation under NEB conditions (Guo et al., 2020). However, the contribution of choline supplementation to the rumen microbial community in perinatal dairy cows cannot currently be well assessed due to a lack of studies. Future research should consider this association as a potential area of concern.

5.3. Essential oils

Plant extracts have various biological functions in animal husbandry, such as antimicrobial activity, growth promotion, and antioxidation. Their application in livestock production has attracted great interest (Durmic and Blache, 2012; Nehme et al., 2021). Essential oils, which are natural plant extracts, have been shown to reduce methane emission by interacting with rumen microbial cell membranes (Busquet et al., 2005, 2006). The impact of essential oils on rumen fermentation function has been thoroughly reviewed (Calsamiglia et al., 2007). In vitro studies have shown that supplementation with different concentrations of essential oils (0.25, 0.5, or 1.0 g/L) such as clove, eucalyptus, garlic, oregano, and peppermint oils can reduce the abundance of methanogenic archaeal bacteria (average decrease of 41.5%). They may also decrease the abundance of some cellulolytic bacteria, such as *R. flavefaciens*, *R. albus*, and *F. succinogenes*, which can adversely affect DM apparent digestibility (average decrease of 6.1%), especially at high doses (Patra and Yu, 2012). Low-dose essential oils do not appear to negatively influence rumen function and nutrient digestibility. Instead, they promote the growth of some microbes, such as *R. flavefaciens*, *R. albus*, and *S. ruminantium* (Cobellis et al., 2016; Kim et al., 2019; Zhou et al., 2019). Consequently, further in vivo or in vitro studies are needed to assess the appropriate dose for essential oils when applied in production practices. A blend of essential oils (containing thymol, guaiacol, eugenol, vanillin, salicylaldehyde, and limonene) had no noticeable effects on the structure of the rumen microbial community in perinatal cows (Scharen et al., 2017), which aligns with the results of several other studies on lactating dairy cattle (Benchaar et al., 2007; Giannenas et al., 2011). Additional horizontal studies are required to evaluate these effects due to the paucity of adequate data for perinatal dairy cows.

6. Conclusions and perspectives

The perinatal period has gained attention as it presents challenges and opportunities for dairy cows. Effective management during this period is crucial for productivity, farm profitability,

animal health, and animal welfare. In this review, we focused on the succession of rumen microbiota throughout the perinatal period and its relationship with postpartum production traits. The successful transition of the rumen microbial community is critical for dairy cows, as microbes affect rumen digestive metabolism and are also closely related to various postpartum performance traits. The prepartum and postpartum diets of dairy cows significantly affect rumen microbiota structure and function; some cellulolytic bacteria decrease, and some starch-utilizing bacteria increase. Some metabolic diseases, such as ketosis, also affect the internal rumen environment and microecology of dairy cows, resulting in significant changes in the abundance of some rumen microbes; for instance, Christensenellaceae_R-7 increases, and *Prevotella* species decrease. Such changes induce a decrease in glucose and glycogenic substances and an increase in BHBA and other ketogenic substances in the rumen. In addition to host genetic factors, some dietary nutrition programs can modulate the rumen microbiota and function. Nevertheless, our existing knowledge mainly stems from isolatable and culturable microbes, and little is known about changes in rumen protozoa, fungi, and other uncultured microbes during the perinatal period. Several gaps exist in understanding the changes in rumen microbial function in perinatal dairy cows, as well as the relationship between rumen microbiota and production phenotype traits and the underlying interaction mechanisms, especially in perinatal dairy cows under different physiological conditions. Further research should focus on addressing these gaps and on minimizing the influence of other factors. Understanding the changes in the rumen microbial community throughout the perinatal period has practical implications for improving feeding and management and optimizing the postpartum lactation performance of dairy cows.

Author contributions

Xiaowei Zhao: Writing-Original Draft. **Yangdong Zhang, Ashikur Rahman, Meiqing Chen, Ning Li, Tao Wu, Yunxia Qi, Nan Zheng, and Shengguo Zhao:** Writing-Review and Editing. **Jiaqi Wang:** Proofreading and Supervision.

Declaration of competing interest

We declare that we have no financial and personal relationships with other people or organizations that can inappropriately influence our work, and there is no professional or other personal interest of any nature or kind in any product, service and/or company that could be construed as influencing the content of this paper.

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References

Abbas W, Howard JT, Paz HA, Hales KE, Wells JE, Kuehn LA, Erickson GE, Spangler ML, Fernando SC. Influence of host genetics in shaping the rumen bacterial community in beef cattle. *Sci Rep* 2020;10:15101.

Abdelmegeid MK, Elolimy AA, Zhou Z, Lopreiato V, Mccann JC, Loor JJ. Rumen-protected methionine during the periparturient period in dairy cows and its effects on abundance of major species of ruminal bacteria. *J Anim Sci Biotechnol* 2018;9:17.

Abuelo A, Hernandez J, Benedito JL, Castillo C. Redox biology in transition periods of dairy cattle: role in the health of periparturient and neonatal animals. *Antioxidants* 2019;8:20.

Aguerre MJ, Wattiaux MA, Powell JM, Broderick GA, Arndt C. Effect of forage-to-concentrate ratio in dairy cow diets on emission of methane, carbon dioxide, and ammonia, lactation performance, and manure excretion. *J Dairy Sci* 2011;94:3081–93.

Bach A, Lopez-Garcia A, Gonzalez-Recio O, Elcoso G, Fabregas F, Chaucheyras-Durand F, Castex M. Changes in the rumen and colon microbiota and effects of live yeast dietary supplementation during the transition from the dry period to lactation of dairy cows. *J Dairy Sci* 2019;102:6180–98.

Bekele AZ, Koike S, Kobayashi Y. Genetic diversity and diet specificity of ruminal *Prevotella* revealed by 16s rRNA gene-based analysis. *FEMS Microbiol Lett* 2010;305:49–57.

Benchaar C, Petit HV, Berthiaume R, Ouellet DR, Chiquette J, Chouinard PY. Effects of essential oils on digestion, ruminal fermentation, rumen microbial populations, milk production, and milk composition in dairy cows fed alfalfa silage or corn silage. *J Dairy Sci* 2007;90:886–97.

Busquet M, Calsamiglia S, Ferret A, Kamel C. Screening for effects of plant extracts and active compounds of plants on dairy cattle rumen microbial fermentation in a continuous culture system. *Anim Feed Sci Technol* 2005;123:597–613.

Busquet M, Calsamiglia S, Ferret A, Kamel C. Plant extracts affect in vitro rumen microbial fermentation. *J Dairy Sci* 2006;89:761–71.

Cainzos JM, Andreu-Vazquez C, Guadagnini M, Rijpert-Duvivier A, Duffield T. A systematic review of the cost of ketosis in dairy cattle. *J Dairy Sci* 2022;105: 6175–95.

Calsamiglia S, Busquet M, Cardozo PW, Castillejos L, Ferret A. Invited review: essential oils as modifiers of rumen microbial fermentation. *J Dairy Sci* 2007;90: 2580–95.

Carpinelli NA, Halfen J, Trevisi E, Chapman JD, Sharman ED, Anderson JL, Osorio JS. Effects of periparturient yeast culture supplementation on lactation performance, blood biomarkers, rumen fermentation, and rumen bacteria species in dairy cows. *J Dairy Sci* 2021;104:10727–43.

Cersosimo LM, Bainbridge ML, Kraft J, Wright AD. Influence of periparturient and postpartum diets on rumen methanogen communities in three breeds of primiparous dairy cows. *BMC Microbiol* 2016;16:78.

Chaucheyras-Durand F, Walker ND, Bach A. Effects of active dry yeasts on the rumen microbial ecosystem: past, present and future. *Anim Feed Sci Technol* 2008;145:5–26.

Chiquette J, Allison MJ, Rasmussen MA. *Prevotella bryantii* 25a used as a probiotic in early-lactation dairy cows: effect on ruminal fermentation characteristics, milk production, and milk composition. *J Dairy Sci* 2008;91:3536–43.

Chuang ST, Ho ST, Tu PW, Li KY, Kuo YL, Shiu JS, Wang SY, Chen MJ. The rumen specific bacteriome in dry dairy cows and its possible relationship with phenotypes. *Animals* 2020;10:1791.

Cobellis G, Trabalza-Marinucci M, Marcotullio MC, Yu ZT. Evaluation of different essential oils in modulating methane and ammonia production, rumen fermentation, and rumen bacteria in vitro. *Anim Feed Sci Technol* 2016;215: 25–36.

Contreras GA, Strieder-Barboza C, De Koster J. Symposium review: modulating adipose tissue lipolysis and remodeling to improve immune function during the transition period and early lactation of dairy cows. *J Dairy Sci* 2018;101: 2737–52.

Contreras GA, Strieder-Barboza C, De Souza J, Gandy J, Mavangira V, Lock AL, Sordillo LM. Periparturient lipolysis and oxylipid biosynthesis in bovine adipose tissues. *PLoS One* 2017;12:e0188621.

Creevey CJ, Kelly WJ, Henderson G, Leahy SC. Determining the culturability of the rumen bacterial microbiome. *Microb Biotechnol* 2014;7:467–79.

Dalbly FR, Svane S, Sigurdarson JJ, Sorensen MK, Hansen MJ, Karring H, Feilberg A. Synergistic tannic acid-fluoride inhibition of ammonia emissions and simultaneous reduction of methane and odor emissions from livestock waste. *Environ Sci Technol* 2020;54:7639–50.

Davidson S, Hopkins BA, Odle J, Brownie C, Fellner V, Whitlow LW. Supplementing limited methionine diets with rumen-protected methionine, betaine, and choline in early lactation Holstein cows. *J Dairy Sci* 2008;91:1552–9.

Deniz A, Aksoy K, Metin M. Transition period and subclinical ketosis in dairy cattle: association with milk production, metabolic and reproductive disorders and economic aspects. *Medycyna Weterynaryjna-Veterinary Medicine-Science and Practice* 2020;76:495–502.

Derakhshani H, Tun HM, Cardoso FC, Plaizier JC, Khafipour E, Loor JJ. Linking periparturient dynamics of ruminal microbiota to dietary changes and production parameters. *Front Microbiol* 2016;7:2143.

Deusch S, Camarinha-Silva A, Conrad J, Beifuss U, Rodehutsord M, Seifert J. A structural and functional elucidation of the rumen microbiome influenced by various diets and microenvironments. *Front Microbiol* 2017;8:1605.

Difford GF, Plichta DR, Lovendahl P, Lassen J, Noel SJ, Hojberg O, Wright ADG, Zhu ZG, Kristensen L, Nielsen HB, Guldbrandtsen B, Sahana G. Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows. *PLoS Genet* 2018;14:e1007580.

Doreau M, Ollier A, Michalet Doreau B. An atypical case of ruminal fermentations leading to ketosis in early lactating cows [rumen pH, ruminal volatile fatty acids]. *Revue de Medecine Veterinaire (France)* 2001;152:301–6.

Drackley JK. Adsa foundation scholar award. Biology of dairy cows during the transition period: the final frontier? *J Dairy Sci* 1999;82:2259–73.

Drackley JK. Advances in transition cow biology: new frontiers in production diseases. Production disease in farms animals. Wageningen, The Netherlands: Wageningen Academic Publishers; 2006. p. 24–34.

- Durmick Z, Blache D. Bioactive plants and plant products: effects on animal function, health and welfare. *Anim Feed Sci Technol* 2012;176:150–62.
- Eom JS, Kim HS, Lee SJ, Choi YY, Jo SU, Kim J, Lee SS, Kim ET, Lee SS. Metabolic profiling of rumen fluid and milk in lactating dairy cattle influenced by sub-clinical ketosis using proton nuclear magnetic resonance spectroscopy. *Animals* 2021;11:2526.
- Gebreyesus G, Difford GF, Buitenhuis B, Lassen J, Noel SJ, Hojberg O, Plichta DR, Zhu Z, Poulsen NA, Sundekilde UK, Lovendahl P, Sahana G. Predictive ability of host genetics and rumen microbiome for subclinical ketosis. *J Dairy Sci* 2020;103:4557–69.
- Giannenas I, Skoufos J, Giannakopoulos C, Wiemann M, Gortzi O, Lalas S, Kyriazakis I. Effects of essential oils on milk production, milk composition, and rumen microbiota in chios dairy ewes. *J Dairy Sci* 2011;94:5569–77.
- Gleason CB, White RR. Variation in animal performance explained by the rumen microbiome or by diet composition. *J Anim Sci* 2018;96:4658–73.
- Golder HM, Thomson J, Rehberger J, Smith AH, Block E, Lean IJ. Associations among the genome, rumen metabolome, ruminal bacteria, and milk production in early-lactation holsteins. *J Dairy Sci* 2023;106:3176–91.
- Gu F, Liang S, Zhu S, Liu J, Sun HZ. Multi-omics revealed the effects of rumen-protected methionine on the nutrient profile of milk in dairy cows. *Food Res Int* 2021;149:110682.
- Gu FF, Zhu SL, Tang YF, Liu XH, Jia MH, Malmuthuge N, Valencak TG, Mcfadden JW, Liu JX, Sun HZ. Gut microbiome is linked to functions of peripherical immune cells in transition cows during excessive lipolysis. *Microbiome* 2023;11:40.
- Guo C, Xue Y, Yin Y, Sun D, Xuan H, Liu J, Mao S. The effect of glycerol or rumen-protected choline chloride on rumen fermentation and blood metabolome in pregnant ewes suffering from negative energy balance. *Anim Feed Sci Technol* 2020;268:114594.
- Hansen HH, El-Bordeny NE, Ebeid HM. Response of primiparous and multiparous buffaloes to yeast culture supplementation during early and mid-lactation. *Anim Nutr* 2017;3:411–8.
- Hausler S, Sadri H, Ghaffari MH, Sauerwein H. Symposium review: adipose tissue endocrinology in the periparturient period of dairy cows. *J Dairy Sci* 2022;105:3648–69.
- Henderson G, Cox F, Ganesh S, Jonker A, Young W, Janssen PH. Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. *Sci Rep* 2015;5:14567.
- Henning PH, Horn CH, Leeuw KJ, Meissner HH, Hagg FM. Effect of ruminal administration of the lactate-utilizing strain *Megasphaera elsdenii* (me) ncimb 41125 on abrupt or gradual transition from forage to concentrate diets. *Anim Feed Sci Technol* 2010;157:20–9.
- Huang S, Ji S, Suen G, Wang F, Li S. The rumen bacterial community in dairy cows is correlated to production traits during freshening period. *Front Microbiol* 2021;12:630605.
- Indugu N, Vecchiarelli B, Baker LD, Ferguson JD, Vanamala JKP, Pitta DW. Comparison of rumen bacterial communities in dairy herds of different production. *BMC Microbiol* 2017;17:190.
- Jami E, Mizrahi I. Similarity of the ruminal bacteria across individual lactating cows. *Anaerobe* 2012;18:338–43.
- Jami E, White BA, Mizrahi I. Potential role of the bovine rumen microbiome in modulating milk composition and feed efficiency. *PLoS One* 2014;9:e85423.
- Kang SH, Evans P, Morrison M, Mcsweeney C. Identification of metabolically active proteobacterial and archaeal communities in the rumen by DNA- and rna-derived 16s rRNA gene. *J Appl Microbiol* 2013;115:644–53.
- Khafipour E, Li S, Tun HM, Derakhshani H, Moossavi S, Plaizier JC. Effects of grain feeding on microbiota in the digestive tract of cattle. *Animal Frontiers* 2016;6:13–9.
- Kim H, Jung E, Lee HG, Kim B, Cho S, Lee S, Kwon I, Seo J. Essential oil mixture on rumen fermentation and microbial community - an in vitro study. *Asian-Australas J Anim Sci* 2019;32:808–14.
- Krause DO, Denman SE, Mackie RI, Morrison M, Rae AL, Attwood GT, Mcsweeney CS. Opportunities to improve fiber degradation in the rumen: microbiology, ecology, and genomics. *FEMS Microbiol Rev* 2003;27:663–93.
- Kumar S, Indugu N, Vecchiarelli B, Pitta DW. Associative patterns among anaerobic fungi, methanogenic archaea, and bacterial communities in response to changes in diet and age in the rumen of dairy cows. *Front Microbiol* 2015;6:781.
- Leblanc SJ, Lissimore KD, Kelton DF, Duffield TF, Leslie KE. Major advances in disease prevention in dairy cattle. *J Dairy Sci* 2006;89:1267–79.
- Li S, Zeng H, Wang C, Han Z. Effect of methionine hydroxy analog on hu sheep digestibility, rumen fermentation, and rumen microbial community in vitro. *Metabolites* 2023;13:169.
- Lima FS, Oikonomou G, Lima SF, Bicalho ML, Ganda EK, Filho JC, Lorenzo G, Trojancanec P, Bicalhoa RC. Prepartum and postpartum rumen fluid microbiomes: characterization and correlation with production traits in dairy cows. *Appl Environ Microbiol* 2015;81:1327–37.
- Liu H, Zhao K, Liu J. Effects of glucose availability on expression of the key genes involved in synthesis of milk fat, lactose and glucose metabolism in bovine mammary epithelial cells. *PLoS One* 2013;8:e66092.
- Liu JH, Zhang ML, Xue CX, Zhu WY, Mao SY. Characterization and comparison of the temporal dynamics of ruminal microbiota colonizing rice straw and alfalfa hay within ruminants. *J Dairy Sci* 2016;99:9668–81.
- Lovendahl P, Difford GF, Li B, Chagunda MGG, Huhtanen P, Lidauer MH, Lassen J, Lund P. Selection for improved feed efficiency and reduced methane emissions in dairy cattle. *Animal* 2018;12:3336–49.
- Macrae AI, Burrough E, Forrest J, Corbishley A, Russell G, Shaw DJ. Prevalence of excessive negative energy balance in commercial United Kingdom dairy herds. *Vet J* 2019;248:51–7.
- Mann S. Symposium review: the role of adipose tissue in transition dairy cows: current knowledge and future opportunities. *J Dairy Sci* 2022;105:3687–701.
- Mann S, Yepes FA, Overton TR, Wakshlag JJ, Lock AL, Ryan CM, Nydam DV. Dry period plane of energy: effects on feed intake, energy balance, milk production, and composition in transition dairy cows. *J Dairy Sci* 2015;98:3366–82.
- Mccartney CA, Bull ID, Dewhurst RJ. Chemical markers for rumen methanogens and methanogenesis. *Animal* 2013;7:409–17.
- Mcfadden JW. Review: lipid biology in the periparturient dairy cow: contemporary perspectives. *Animal* 2020;14:s165–75.
- Minuti A, Palladino A, Khan MJ, Alqarni S, Agrawal A, Piccioli-Capelli F, Hidalgo F, Cardoso FC, Trevisi E, Looor JJ. Abundance of ruminal bacteria, epithelial gene expression, and systemic biomarkers of metabolism and inflammation are altered during the periparturient period in dairy cows. *J Dairy Sci* 2015;98:8940–51.
- Moraís S, Mizrahi I. Islands in the stream: from individual to communal fiber degradation in the rumen ecosystem. *FEMS Microbiol Rev* 2019;43:362–79.
- Morotomi M, Nagai F, Watanabe Y. Description of *Christensenella minuta* gen. Nov., sp. Nov., isolated from human faeces, which forms a distinct branch in the order Clostridiales, and proposal of *Christensenellaceae* fam. Nov. *Int J Syst Evol Microbiol* 2012;62:144–9.
- Mulligan FJ, Doherty ML. Production diseases of the transition cow. *Vet J* 2008;176:3–9.
- Neave HW, Lomb J, Von Keyserlingk MaG, Behnam-Shabahang A, Weary DM. Parity differences in the behavior of transition dairy cows. *J Dairy Sci* 2017;100:548–61.
- Nehme R, Andres S, Pereira RB, Ben Jemaa M, Bouhallab S, Ceciliani F, Lopez S, Rahali FZ, Ksouri R, Pereira DM, Abdennebi-Najar L. Essential oils in livestock: from health to food quality. *Antioxidants* 2021;10:330.
- Nishimura S, Manabe I, Nagasaki M, Eto K, Yamashita H, Ohsugi M, Otsu M, Hara K, Ueki K, Sugiura S, Yoshimura K, Kadowaki T, Nagai R. Cd8+ effector t cells contribute to macrophage recruitment and adipose tissue inflammation in obesity. *Nat Med* 2009;15:914–20.
- Pang K, Chai S, Yang Y, Wang X, Liu S, Wang S. Dietary forage to concentrate ratios impact on yak ruminal microbiota and metabolites. *Front Microbiol* 2022;13:964564.
- Patra AK, Yu Z. Effects of essential oils on methane production and fermentation by, and abundance and diversity of, rumen microbial populations. *Appl Environ Microbiol* 2012;78:4271–80.
- Pinloche E, Mcweeney N, Marden JP, Bayourthe C, Auclair E, Newbold CJ. The effects of a probiotic yeast on the bacterial diversity and population structure in the rumen of cattle. *PLoS One* 2013;8:e67824.
- Pinnell LJ, Reyes AA, Wolfe CA, Weinroth MD, Metcalf JL, Delmore RJ, Belk KE, Morley PS, Engle TE. Bacteroidetes and Firmicutes drive differing microbial diversity and community composition among micro-environments in the bovine rumen. *Front Vet Sci* 2022;9:897996.
- Pitta DW, Kumar S, Vecchiarelli B, Shirley DJ, Bittinger K, Baker LD, Ferguson JD, Thomsen N. Temporal dynamics in the ruminal microbiome of dairy cows during the transition period. *J Anim Sci* 2014;92:4014–22.
- Pitta DW, Pinchak WE, Indugu N, Vecchiarelli B, Sinha R, Fulford JD. Metagenomic analysis of the rumen microbiome of steers with wheat-induced frothy bloat. *Front Microbiol* 2016;7:689.
- Puniya AK, Singh R, Kamra DN. Rumen microbiology: from evolution to revolution. Springer; 2015.
- Rainard P. Mammary microbiota of dairy ruminants: fact or fiction? *Vet Res* 2017;48:25.
- Redfern EA, Sinclair LA, Robinson PA. Dairy cow health and management in the transition period: the need to understand the human dimension. *Res Vet Sci* 2021;137:94–101.
- Reynolds CK, Huntington GB, Tyrrell HF, Reynolds PJ. Net metabolism of volatile fatty acids, d- β -hydroxybutyrate, nonesterified fatty acids, and blood gases by portal-drained viscera and liver of lactating holstein cows. *J Dairy Sci* 1988;71:2395–405.
- Russell JB. Rumen microbiology and its role in ruminant nutrition. Department of Microbiology. Cornell University; 2002.
- Russell JB, Hino T. Regulation of lactate production in *Streptococcus bovis*: a spiraling effect that contributes to rumen acidosis. *J Dairy Sci* 1985;68:1712–21.
- Saint-Georges-Chaumet Y, Edeas M. Microbiota-mitochondria inter-talk: consequence for microbiota-host interaction. *Pathog Dis* 2016;74:ftv096.
- Sasson G, Ben-Shabat SK, Seroussi E, Doron-Faigenboim A, Shterzer N, Yaacoby S, Margret EBM, Bryan AW, Eran HC, Mizrahi I. Heritable bovine rumen bacteria are phylogenetically related and correlated with the cow's capacity to harvest energy from its feed. *mBio* 2017;8:e00703–17.
- Scharen M, Drong C, Kiri K, Riede S, Gardener M, Meyer U, Hummel J, Ulrich T, Breves G, Danicke S. Differential effects of monensin and a blend of essential oils on rumen microbiota composition of transition dairy cows. *J Dairy Sci* 2017;100:2765–83.
- Scharen M, Frahm J, Kersten S, Meyer U, Hummel J, Breves G, Danicke S. Interrelations between the rumen microbiota and production, behavioral, rumen fermentation, metabolic, and immunological attributes of dairy cows. *J Dairy Sci* 2018;101:4615–37.
- Shabat SKB, Sasson G, Doron-Faigenboim A, Durman T, Yaacoby S, Berg Miller ME, White BA, Shterzer N, Mizrahi I. Specific microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. *ISME J* 2016;10:2958–72.

- Shen JS, Liu Z, Yu ZT, Zhu WY. Monensin and nisin affect rumen fermentation and microbiota differently in vitro. *Front Microbiol* 2017;8:1111.
- Snelling TJ, Wallace RJ. The rumen microbial metaproteome as revealed by sds-page. *BMC Microbiol* 2017;17:9.
- Sofyan A, Uyeno Y, Shinkai T, Hirako M, Kushibiki S, Kanamori H, Mori S, Katayose Y, Mitsumori M. Metagenomic profiles of the rumen microbiota during the transition period in low-yield and high-yield dairy cows. *Anim Sci J* 2019;90:1362–76.
- Sordillo LM, Raphael W. Significance of metabolic stress, lipid mobilization, and inflammation on transition cow disorders. *Veterinary Clinics: Food Animal Practice* 2013;29:267–78.
- Stevenson DM, Weimer PJ. Dominance of *Prevotella* and low abundance of classical ruminal bacterial species in the bovine rumen revealed by relative quantification real-time PCR. *Appl Microbiol Biotechnol* 2007;75:165–74.
- Stokes MR, Bull LS, Halteman WA. Rumen liquid dilution rate in dairy cows fed once daily: effects of diet and sodium bicarbonate supplementation. *J Dairy Sci* 1985;68:1171–80.
- Tong J, Zhang H, Yang D, Zhang Y, Xiong B, Jiang L. Illumina sequencing analysis of the ruminal microbiota in high-yield and low-yield lactating dairy cows. *PLoS One* 2018;13:e0198225.
- Trevisi E, Minuti A. Assessment of the innate immune response in the periparturient cow. *Res Vet Sci* 2018;116:47–54.
- Uyeno Y, Akiyama K, Hasunuma T, Yamamoto H, Yokokawa H, Yamaguchi T, Kawashima K, Itoh M, Kushibiki S, Hirako M. Effects of supplementing an active dry yeast product on rumen microbial community composition and on subsequent rumen fermentation of lactating cows in the mid-to-late lactation period. *Anim Sci J* 2017;88:119–24.
- Wallace RJ, Sasson G, Garnsworthy PC, Tapio I, Gregson E, Bani P, Huhtanen P, Bayat AR, Strozzi F, Section FB, Snelling TJ, Saunders N, Potterton SL, Craigon J, Minuti A, Trevisi E, Callegari ML, Cappelli FP, Cabezas-Garcia EH, Vilkki J, Pinares-Patino C, Fliegerová KO, Mrázek J, Sechovcová H, Kopecny J, Bonin A, Boyer F, Taberlet P, Kokou F, Halperin E, Williams JL, Shingfield KJ, Mizrahi I. A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. *Sci Adv* 2019;5:eaav8391.
- Wang L, Li Y, Zhang Y, Wang L. The effects of different concentrate-to-forage ratio diets on rumen bacterial microbiota and the structures of holstein cows during the feeding cycle. *Animals* 2020;10:957.
- Wang MM, Li Y, Yang ZL, Shen YZ, Cao YF, Li QF, Gao YX, Li JG. Effects of rumen-protected lysine and methionine supplementation in low-crude protein diets on lactation performance, nitrogen metabolism, rumen fermentation, and blood metabolites in holstein cows. *Anim Feed Sci Technol* 2022;292:115427.
- Wang X, Li X, Zhao C, Hu P, Chen H, Liu Z, Liu G, Wang Z. Correlation between composition of the bacterial community and concentration of volatile fatty acids in the rumen during the transition period and ketosis in dairy cows. *Appl Environ Microbiol* 2012;78:2386–92.
- Xiang K, Shen P, Mu R, Li S, Wang Y, Zhao C, Zhang N, Hu X, Fu Y. Rumen microbiota alterations during subclinical ketosis is associated with the development of subclinical mastitis in dairy cows. 2022.
- Xue MY, Sun HZ, Wu XH, Liu JX, Guan LL. Multi-omics reveals that the rumen microbiome and its metabolome together with the host metabolome contribute to individualized dairy cow performance. *Microbiome* 2020;8:64.
- Xue MY, Xie YY, Zhong Y, Ma XJ, Sun HZ, Liu JX. Integrated meta-omics reveals new ruminal microbial features associated with feed efficiency in dairy cattle. *Microbiome* 2022;10:32.
- Yang CJ, Rooke JA, Cabeza I, Wallace RJ. Nitrate and inhibition of ruminal methanogenesis: microbial ecology, obstacles, and opportunities for lowering methane emissions from ruminant livestock. *Front Microbiol* 2016;7:132.
- Zang XW, Sun HZ, Xue MY, Zhang Z, Plastow G, Yang TF, Guan LL, Liu JX. Heritable and nonheritable rumen bacteria are associated with different characters of lactation performance of dairy cows. *mSystems* 2022;7:113248.
- Zhang J, Jin W, Jiang Y, Xie F, Mao S. Response of milk performance, rumen and hindgut microbiome to dietary supplementation with *Aspergillus oryzae* fermentation extracts in dairy cows. *Curr Microbiol* 2022;79:113.
- Zhao ZW, Ma ZY, Wang HC, Zhang CF. Effects of rumen-protected methionine and lysine supplementation on milk yields and components, rumen fermentation, and the rumen microbiome in lactating yaks (*Bos grunniens*). *Anim Feed Sci Technol* 2021;277:114972.
- Zhou M, Hernandez-Sanabria E, Guan LL. Assessment of the microbial ecology of ruminal methanogens in cattle with different feed efficiencies. *Appl Environ Microbiol* 2009;75:6524–33.
- Zhou R, Wu J, Zhang L, Liu L, Casper DP, Jiao T, Liu T, Wang J, Lang X, Song S, Gong X. Effects of oregano essential oil on the ruminal pH and microbial population of sheep. *PLoS One* 2019;14:e0217054.
- Zhou Z, Bulgari O, Vailati-Riboni M, Trevisi E, Ballou MA, Cardoso FC, Luchini DN, Looor JJ. Rumen-protected methionine compared with rumen-protected choline improves immunometabolic status in dairy cows during the periparturient period. *J Dairy Sci* 2016;99:8956–69.
- Zhu Z, Difford GF, Noel SJ, Lassen J, Løvendahl P, Højberg O. Stability assessment of the rumen bacterial and archaeal communities in dairy cows within a single lactation and its association with host phenotype. *Front Microbiol* 2021;12:636223.
- Zhu Z, Kristensen L, Difford GF, Poulsen M, Noel SJ, Abu Al-Soud W, Sorensen SJ, Lassen J, Lovendahl P, Højberg O. Changes in rumen bacterial and archaeal communities over the transition period in primiparous holstein dairy cows. *J Dairy Sci* 2018;101:9847–62.
- Zhu Z, Noel SJ, Difford GF, Al-Soud WA, Brejnrod A, Sorensen SJ, Lassen J, Lovendahl P, Højberg O. Community structure of the metabolically active rumen bacterial and archaeal communities of dairy cows over the transition period. *PLoS One* 2017;12:e0187858.