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Rumen microbial establishment and adaptation to various anti-nutritional factors (ANFs): An overview

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Abstract

The rumen is the foremost and largest of the four chambers within the ruminant foregut. Its microbial ecosystem involves intricate interactions among anaerobic inhabitants, including bacteria, protozoa, fungi, archaea, and bacteriophage. Within the rumen, these microorganisms thrive in an environment conducive to producing the enzymes required for nutrient digestion. Key factors such as temperature, pH, buffering capacity, osmotic pressure, and redox potential significantly influence the growth and function of these microbes. Ruminant diets are predominantly plant-based, containing various toxic compounds that can adversely affect their health. Rumen microbes are crucial for digesting these diets, but how they establish themselves after birth and adapt to anti-nutritional factors (ANFs) such as tannins, cyanogens, saponins, etc. in their diet, remains poorly understood. This review provides an overview of rumen microbial establishment, the impact of ANFs on rumen microbes, and the strategies employed by these microbes to counteract ANFs. The resilience of the rumen microbiota to ANFs is highlighted, focusing on adaptation mechanisms such as microbial tolerance, enzymatic detoxification by specific bacteria, and shifts in microbial community composition. Understanding these interactions could improve feed efficiency, lessen environmental impact, and enhance animal health outcomes.

Keywords: Rumen microbes, anti-nutritional factors, tannins, saponin, gossypol, cyanogens

Introduction

The ruminant livestock includes cattle, buffalo, sheep and goats. Ruminants are hoofed mammals with a unique digestive system that allows them to better use nutrients from plant sources than other herbivores. The rumen, a specialized compartment in the stomach of ruminant animals hosts a diverse microbial community. The establishment of microbes in rumen is a fascinating process that begins at birth and continues throughout the animal's life. The rumen has billions of microbes, encompassing bacteria, protozoa, fungi, and archaea. Bacteria are pre-dominant (up to 10^{11} viable cells per gram comprising up to 1000 phylotypes) but a variety of ciliate protozoa occur widely (10^4 – 10^6 g⁻¹ distributed over 25 genera). The anaerobic fungi are also widely distributed (zoospore population densities of 10^3 – 10^5 g⁻¹ distributed over six genera). The occurrence of bacteriophage is well documented (10^7 – 10^9 particles per gram). These rumen microbes play a crucial role in animal nutrition, and their adaptation to anti-nutritional factors (ANFs) is essential for maintaining efficient feed utilization and animal health. ANFs can negatively impact nutrient availability, digestibility, and utilisation. Understanding rumen microbial adaptation to ANFs is crucial for developing strategies to improve feed efficiency, reduce environmental impact, and enhance animal health. Research in this area can lead to the development of novel feed additives, probiotics, or other nutritional interventions that promote rumen microbial resilience and functionality.

1. Rumen Microorganisms

The rumen is a complex ecosystem where nutrients consumed by microorganisms such as bacteria, protozoa, and fungi are digested anaerobically. The main end products of

fermentation are VFAs and microbial biomass, which are used by the host ruminant. The interaction between microorganisms and the host animal results in a symbiotic relationship that allows ruminants to digest diets rich in fibre and low in protein (Reddy, 2016) [29]. The rumen supports microorganisms that generate the enzymes required for nutrient digestion. Ruminants can convert low-quality fibrous materials into products such as meat, milk, and fibres, which are useful to humans. The ability of ruminal microorganisms to produce the enzymes necessary for fermentation processes allows ruminants to efficiently obtain the energy contained in forages (Burns, 2008) [5]. However, the ruminal fermentation process is not completely efficient because it produces some final products such as methane gas (Kingston-Smith *et al.*, 2012) [16] and excess ammonia (Russell *et al.*, 2001) [31]. Ruminants such as cattle, sheep, and goats have evolved to use fibrous food efficiently (Oltjen *et al.*, 1996) [24]. The anatomical adaptation of their digestive system allows them to use cellulose as an energy source without requiring external sources of the vitamin B complex (Russell *et al.*, 2001) [31] or essential amino acids because ruminal microorganisms can produce such products (Cole *et al.*, 1982) [7]. Thus, a symbiotic relationship exists within the rumen providing the necessary environment for the establishment of

microorganisms and substrates required for their maintenance. In turn, the microorganisms provide nutrients to the host ruminant to generate energy (Russell *et al.*, 2001) [31].

1.1 Establishment of Microbes in Rumen

When a young ruminant is born, its rumen is considered a sterile environment that contains no bacteria or other microbial life. The young ruminant is naturally exposed to different microbes through the dam’s birth canal and vagina, saliva, skin, and faeces. The first bacteria that developed most abundantly in the rumen were *Escherichia coli* and *Streptococci sp.* (Minato *et al.*, 1992) [2].

- Anaerobic bacteria appear a few hours after birth.
- Cellulolytic bacteria and methanogenic archaea appear at 2 - 4 days of age.
- Anaerobic fungi colonise the rumen during the second week.
- Ciliate protozoa begin to be established only after the third week.

The diversity of microbial communities in the rumen depends largely on diet composition (Fonty *et al.*, 1983) [9].

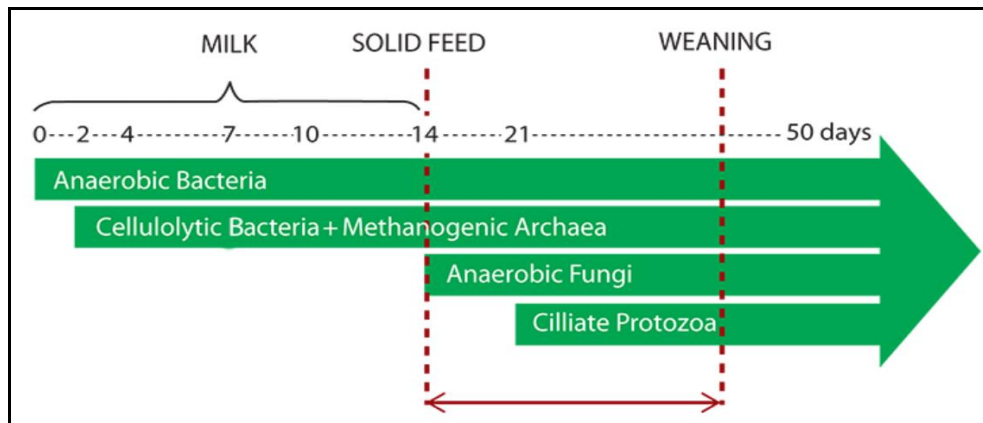


Fig 1: Progressive establishment of rumen microbes with increasing age of young ruminant

Table 1: Establishment of Rumen Microbes at Different Age Intervals in Young Ruminants

Age (weeks)	Group	Species
1 week	Anaerobic bacteria	<i>Escherichia coli</i>
		<i>Propionibacterium acnes</i>
		<i>Clostridium chauvoei</i>
		<i>Clostridium ramosum</i>
		<i>Bacteroides sp.</i>
		<i>Clostridium clostridioforme</i>
		<i>Eubacterium sp.</i>
		<i>Peptostreptococcus products</i>
		<i>Lachnospira multiparus</i>
		<i>Streptococcus bovis</i>
<i>Lactobacillus sp.</i>		
2 weeks	Anaerobic fungi	<i>Neocallimastix frontalis.</i>
		<i>Sphaeromonas communis</i>
3 weeks	Anaerobic bacteria	<i>Megasphaera elsdenii</i>
4 weeks		<i>Bifidobacterium sp.</i>
		<i>Selenomonas sp.</i>
		<i>Veillonella sp.</i>
8 weeks	Ciliate protozoa	<i>Entodinium sp.</i>
10 weeks		<i>Diplodinium sp.</i>

(Minato *et al.*, 1992) [2], (Fonty *et al.*, 1983) [9]

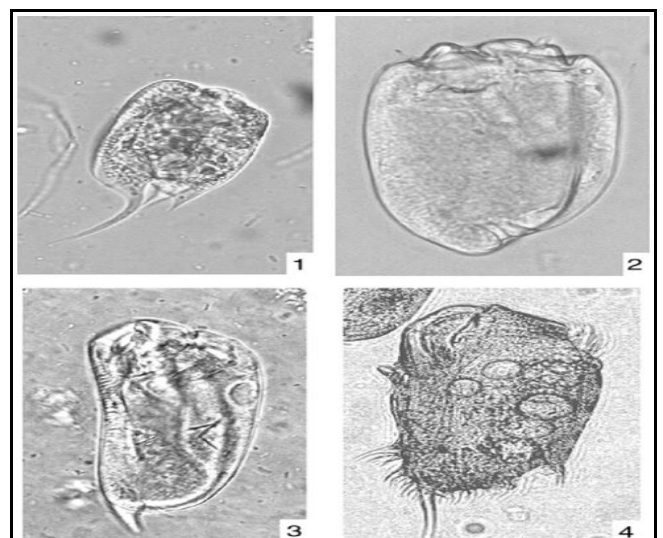


Fig 2: Microphotographs of some common Entodiniomorphid ciliates
 1. *Entodinium caudatum*; 2. *Eudiplodinium maggii*;
 3. *Epidinium ecaudatum* f. *caudatum*; 4. *Ophryoscolex caudatus*
 (Adapted from Michaiowski, 2005) [21]

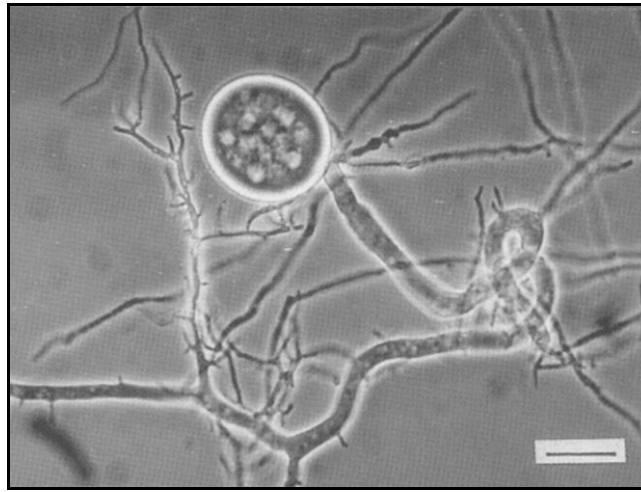


Fig 3: An anaerobic rumen fungus *N. frontalis* with filamentous myceloid rhizoids (Adapted from Ho *et al.*, 2000) ^[13]

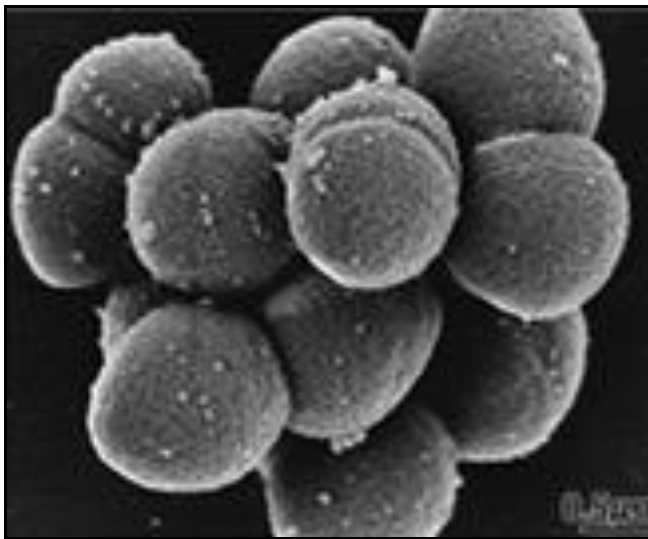


Fig 4: An anaerobic rumen bacteria *Megasphaera elsdenii* (Adapted from Kobayashi, 2019) ^[17]

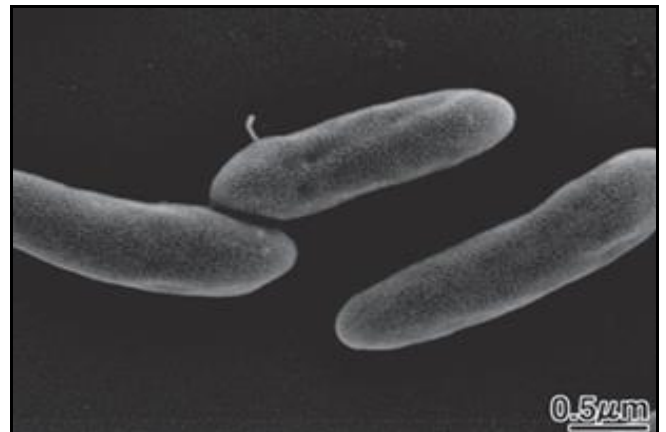


Fig 6: A rumen bacteria *Selenomonas ruminantium* (Adapted from Kobayashi, 2019) ^[17]

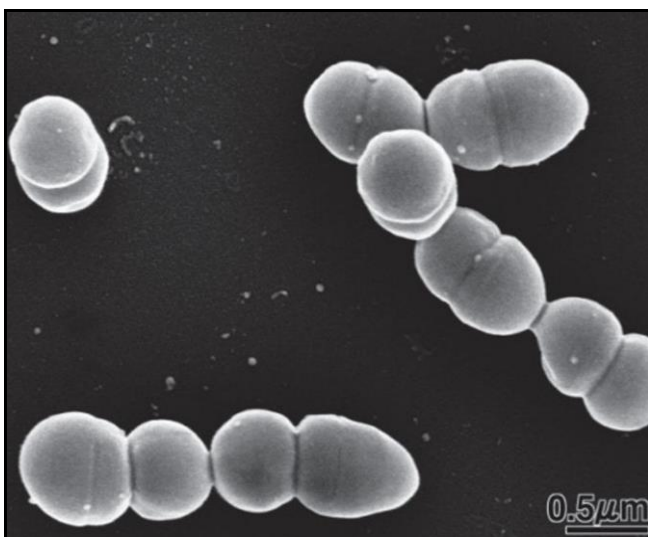


Fig 5: A rumen bacteria *Streptococcus bovis* (Adapted from Kobayashi, 2019) ^[17]

2. Anti-Nutritional Factors

Anti-nutritional factors are defined as those substances present in the diet which by themselves or their metabolic products arising in the system interfere with the feed utilization, reduce production, or affect the health of the animal. These antinutritive substances are often referred to as ‘toxic factors’ because of the deleterious effects they produce when eaten by animals (Reddy, 2016) ^[29]. The antinutritional factors may be regarded as a class of compounds, that are generally not lethal but reduce animal productivity and may cause toxicity during periods of scarcity or confinement when the feed rich in these substances, is consumed by animals in large quantities.

Many anti-nutrients (oxalate, phytate, etc.) and toxic substances (cyanide, nitrate, phenols, etc.) are present in many plants and vegetables. Anti-nutrients in foods are responsible for deleterious effects related to the absorption of nutrients and micronutrients. Phytic acid, lectins, tannins, saponins, amylase inhibitors and protease inhibitors have been shown to reduce the availability of nutrients and cause growth inhibition. Being an ANF is not an intrinsic characteristic of a compound but depends upon the digestive process of the ingesting animal (Cheeke *et al.*, 1985) ^[6].

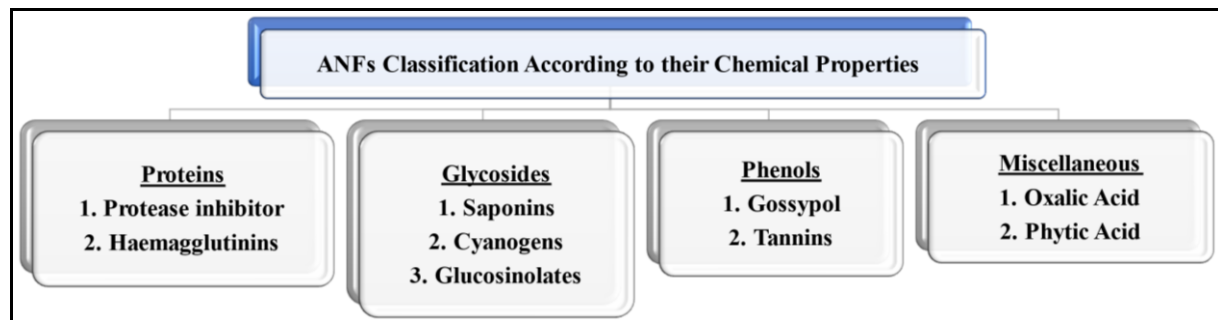


Fig 7: Classification of important anti-nutritional factors in plant-derived nutrient source

2.1 Rumen Microbial Adaptation to Various Anti-Nutritional Factors (ANFs)

The adaptation of rumen microbes to diverse anti-nutritional factors (ANFs) plays a pivotal role in facilitating ruminant animals' efficient digestion and utilization of plant-based feeds. ANFs, inherent in plant materials, exert effects that diminish nutrient availability to the animal, thereby influencing its performance and health outcomes significantly.

Rumen microbe's adaptation to Protease inhibitor

Rumen microbes can adapt to protease inhibitors over time, but the effects vary depending on the type and dose of inhibitors, animal species, diet composition, and microbial community structure. Based on the research it was found that rumen microbes can adapt to protease inhibitors over time. The rumen microbes, including certain bacteria like *Prevotella bryantii*, can alter their cell wall structure in response to protease inhibitors, showcasing an adaptation mechanism. Rumen protozoa are generally more susceptible to these inhibitors than bacteria. Targeted inhibition of protozoal lysozyme and peptidases can decrease protozoal populations and change fermentation profiles. Nevertheless, rumen protozoa can also adapt over time, limiting long-term effects (Belanche *et al.*, 2021) [2]. Adaptation mechanisms enable rumen microbes to tolerate and metabolize protease inhibitors over time. Initially, protease inhibitors can significantly affect rumen microbes, especially protozoa, within the microbial community. However, over time, adaptation mechanisms such as inhibitor degradation and structural modifications allow the rumen microbiome to lessen these impacts. The specific responses are influenced by the characteristics of the inhibitors and the composition of the rumen microbiota.

Rumen microbe's adaptation to Tannins

Rumen microbes can adapt to tannins in the diet, though the extent of adaptation varies by ruminant species and tannin type. Studies have shown that ruminants like goats and sheep, which naturally consume tannin-rich plants, have developed physiological adaptations, such as producing salivary enzymes that bind to tannins, enhancing their ability to tolerate and utilize them (Bueno *et al.*, 2020) [4]. Found that after 75 days of feeding lambs diets containing 4% hydrolyzable or condensed tannins, the rumen microbiome adapted, showing increases in tannin-tolerant bacteria. Conversely, rumen microbes from species not adapted to tannins, like dairy cattle, may initially be more vulnerable to tannin's antimicrobial effects. However, these microbes can gradually adapt over time through changes in microbial community composition and metabolic pathways. One adaptive mechanism that allows rumen microbes to tolerate

high tannin levels is the protection of key membrane proteins by strategically deploying lipids (Pell *et al.*, 2000) [27]. The degree of adaptation also depends on the tannin type. While rumen microbes can degrade hydrolyzable tannins, they cannot hydrolyze condensed tannins (Makkar, 2003) [19]. Although microorganisms resistant to high levels of condensed tannins are present in ruminants consuming high-tannin feeds, there is no evidence of rumen microorganisms capable of degrading condensed tannins (Nelson *et al.*, 1995) [23].

Rumen microbe's adaptation to Saponin

Saponins, which are plant-derived bioactive compounds, have been shown to affect the rumen microbiome and fermentation in ruminant animals. Saponins can modify the rumen microbial population and activity, often by suppressing rumen protozoa numbers (Kholif, 2023) [14]. However, this antiprotozoal effect is typically transient, as the ruminal bacteria can degrade and metabolize the saponins over time. The rumen microbes, including bacteria, fungi, and archaea, can adapt to the presence of saponins through various mechanisms. Some bacteria, such as *Fibrobacter succinogenes*, can effectively deglycosylate saponins and are more resistant to saponins than other cellulolytic bacterial species. This resistance is attributed to the presence of 2-aminomethyl phosphonic acid in their cell walls, which likely enhances membrane stability and promotes the longevity of these organisms. The covalent linkage of 2-aminoethyl phosphonic acid to membrane polymers contributes to this resistance and longevity by protecting the membrane from enzymatic degradation suggested that *F. succinogenes* deglycosylated the saponins from *Y. schidigera*. Further, an increase in the thickness of the cell wall of *Prevotella bryantii* was noted when these bacteria were grown in the presence of *Yucca* saponins, indicating an adaptation to saponins. The rumen microbiome demonstrates the ability to adapt to the presence of saponins over time, with the microbial community composition and metabolic activities shifting in response to saponin exposure. This adaptation allows the rumen to maintain its normal function despite the introduction of saponins in the diet. The mechanisms and effects of saponins on the rumen microbial community and fermentation are interdependent depending upon the types and levels of saponins, the composition of diets, the microbial populations affected and the adaptation of microbiota to saponins (Patra *et al.*, 2009) [26].

Rumen microbe's adaptation to Cyanogens

Rumen microbes play a crucial role in digesting plant materials in herbivorous animals and have evolved various adaptations to handle cyanogenic compounds found in certain plants. When these cyanogenic compounds break down, they

release cyanide, which are toxic. Rumen microbes have developed enzymatic mechanisms for cyanide detoxification, including cyanide hydratase and rhodanese enzymes. Cyanide hydratase converts cyanide into less toxic compounds like formamide, while rhodanese facilitates the conversion of cyanide into thiocyanate, a harmless compound that can be excreted safely. These adaptations underscore the microbial community's ability to mitigate the risks associated with cyanogenic plant consumption by herbivores (McSweeney *et al.*, 2002) [20]. Majak and Cheng (1984) [18] demonstrated that rumen microbes primarily transform cyanide-rich substrates, such as cyanogenic glycosides and chemical cyanides, to produce thiocyanate. Certain strains of enterococci bacteria found in the rumen of ruminant animals play a key role in the detoxification of cyanogenic compounds. The recent study conducted by Khota *et al.*, (2023) [15], identified 6 strains of *Enterococcus faecium* and *E. gallinarum* isolated from the rumens of domestic buffalo, dairy cattle, and beef cattle that exhibited high rhodanese enzyme that is responsible for transforming cyanide into the less toxic compound thiocyanate. These indicate that certain strains of rumen enterococci are particularly well-adapted to detoxifying cyanogenic compounds in ruminants.

Rumen microbe's adaptation to Glucosinolates

Rumen microbes can adapt to glucosinolates, which are antinutritional compounds found in the Crucifera family and Genus *Brassica*. These substances are present in cabbage, turnips, rapeseed, and mustard. Rumen microbes can detoxify a wide variety of plant toxins, including glucosinolates, by utilizing them as an energy source. The ability of the rumen microbiome to adapt and increase its capacity to detoxify a plant toxin is a key factor determining the pathogenesis of plant toxicity. The glucosinolates occur in the root, stem, leaf and seed and are always accompanied by the enzyme myrosinase, which is capable of hydrolysing them to thiocyanates, glucose and isothiocyanates or nitriles depending on the pH of the rumen (Reddy, 2016) [29]. *Bacteroides thetaiotaomicron*, *Peptostreptococcus* spp. and *Bifidobacterium* spp. reportedly produce enzymes with myrosinase-like activities, which hydrolyses glucosinolates. *Peptostreptococcus* and *Bifidobacterium* spp. are two prevalent rumen bacteria (Oshio *et al.*, 1987) [25]. Increasing the proportion of rapeseed cake, which is rich in glucosinolates, in rations of ruminants tended to decrease the relative abundances of *Ruminobacter amylophilus* and *Ruminococcus albus* but did not affect the relative abundances of methanogens, protozoa, anaerobic, fungi, *Ruminococcus flavefaciens*, *Butyrivibrio fibrisolvens* or *Fibrobacter succinogenes* (Gao *et al.*, 2021) [11]. This suggests most of the rumen bacteria can adapt to the presence of glucosinolates. Further research is needed to fully understand the mechanisms and microbial species involved in glucosinolate detoxification in the rumen.

Rumen microbe's adaptation to Gossypol

Rumen microbes, particularly those found in the digestive system of ruminant animals have remarkable adaptations to compounds like gossypol. Gossypol is a polyphenolic compound naturally present in cottonseed and cottonseed products, which can be toxic to non-ruminant animals and humans in high concentrations. The rumen microbial community contains some gossypol-degrading bacteria that can convert free gossypol into protein-gossypol complexes that are not absorbed in the digestive tract (Zhou *et al.*, 2021)

[11]. This protects ruminants from gossypol toxicity compared to monogastric animals (Wang *et al.*, 2022) [43]. The rumen hosts specific gossypol-degrading bacteria, such as *Bacillus subtilis* strain RBS, which can utilise gossypol as a carbon source. These bacteria, isolated from cow rumen, have been optimized to degrade gossypol in cottonseed meal. When these bacteria are present, free gossypol and total gossypol levels in cottonseed meal decrease by 78.86% and 49%, respectively, after 72 hours of fermentation at 39°C, pH 6.5, and 50% moisture, this indicates the efficiency of rumen microbes in degrading gossypol (Zhang *et al.*, 2023) [39]. Presented a study that highlights the potential of *Lactobacillus mucosae* LLK-XR1, isolated from sheep rumen liquid, as a promising candidate for the bio-degradation of free gossypol and as a probiotic. This suggests multiple species of rumen bacteria have adapted to gossypol. Ruminants-fed diets containing cottonseed meal show an increase in the prevalence of gossypol-degrading bacteria. This adaptation enables ruminants to better tolerate gossypol as compared to monogastric animals.

Rumen microbe's adaptation to Phytic acid

Rumen microbes can adapt to diets containing phytic acid, an anti-nutritional compound found in plant-based feeds. Phytic acid is the major storage form of phosphorous in cereals, legumes, oil seeds and nuts. Phytic acid is known as a food inhibitor that chelates micronutrients and prevents them from being bioavailable for monogastric animals, including humans because they lack enzyme phytase in their digestive tract (Gupta *et al.*, 2015) [12] but ruminants can effectively hydrolyze the phytate present in high grain diets through microbial phytases living in their rumen, rendering phosphorous supplementation unnecessary conducted a qualitative screening of 101 pure rumen bacterial cultures for phytase activity, identified by clearing zones on phytate-containing plates. They found phytase activity in strains of *Prevotella ruminicola*, *Ruminobacter amylophilus*, *Selenomonas ruminantium*, and *Streptococcus bovis*, with nearly all *Selenomonas ruminantium* strains showing activity. Additionally, *Megasphaera elsdenii*, another anaerobic rumen bacterium, also produces phytase (Rizwanuddin *et al.*, 2023) [30]. This demonstrates that rumen microbes exhibit a high degree of adaptability in metabolizing anti-nutritional compounds like phytic acid through enzyme production. This adaptability can be harnessed to enhance nutrient utilization and reduce environmental impacts in ruminant production systems.

Rumen microbe's adaptation to Oxalic acid

Rumen microbes exhibit an adaptive response to oxalic acid, an organic compound prevalent in certain plants and potentially toxic to ruminants. This compound is commonly found in leafy greens, vegetables, fruits, cocoa, nuts, and seeds, where it is often bound to minerals forming oxalates such as potassium, sodium, calcium, and magnesium oxalate (Reddy, 2016) [29]. The bacterium *Oxalobacter formigenes* is capable of degrading oxalate (Duncan *et al.*, 2000) [8] and plays a pivotal role in the rumen's microbial adaptation to oxalic acid. Belenguer *et al.* (2013) [3] demonstrated that rumen microbial exposure to oxalic acid through diets leads to a rapid increase in the abundance of *O. formigenes* within the rumen bacterial community, significantly rising from approximately 0.002% to much higher levels. This increase facilitates the degradation of oxalate, aiding in the detoxification of oxalic acid present in the diet of ruminants.

The enhanced presence of this oxalate-degrading bacterium allows ruminants to better tolerate and metabolize oxalic acid-containing forage, highlighting a crucial adaptive mechanism of the rumen microbiome (Duncan *et al.*, 2000)^[8].

Rumen microbe's adaptation to Mimosine

Rumen microbes can adapt to degrade mimosine, a toxic amino acid found in *Leucaena leucocephala* leaves, through gradual exposure and changes in the microbial community. Subabul green forage contains mimosine at concentrations of 2-5% in the leaves on a dry matter basis (DMB). When fresh leaves are chewed and acted upon by rumen microbes, mimosine is converted into a goitrogenic compound, 3,4-dihydropyridone (3,4-DHP) (Reddy, 2016)^[29]. Specific rumen bacteria, such as *Synergistes jonesii* from the phylum Synergistetes, have been identified for their ability to degrade mimosine and 3,4-dihydropyridone (3,4-DHP) to less toxic substances which are then excreted in the urine. This degradation process helps detoxify mimosine within the rumen, making it safer for ruminant animals to consume mimosine-containing plants as part of their diet (Ramli *et al.*, 2017)^[28]. Artiles-Ortega *et al.* (2021)^[1] have identified additional bacteria capable of breaking down mimosine, including *Streptococcus lutetiensis*, *Clostridium butyricum*, and *Lactobacillus vitulinus*. Gradually introducing *Leucaena* to animals results in a shift in the rumen microbiome, promoting the growth of mimosine-degrading bacteria over time. Probiotics, such as yeast supplements, can further enhance the colonization of these bacteria, especially in young ruminants. Regular consumption of mimosine-rich forage allows rumen microbes to adapt effectively to mimosine.

Conclusions and Future Perspectives

The adaptation of rumen microbial communities to anti-nutritional factors (ANFs) is a fascinating field with significant implications for animal nutrition and health. Over time, these microorganisms have evolved complex mechanisms to metabolize and neutralize the harmful effects of ANFs present in feed. This adaptation not only enhances feed utilization efficiency but also improves the overall health and productivity of ruminant animals. Future research should focus on exploring the diversity and resilience of rumen microbial populations in response to different types and concentrations of ANFs. Moreover, studying the practical applications of these microbial adaptations could lead to the development of more efficient and environmentally sustainable livestock diets. By deepening our understanding of these adaptive processes, we can refine nutritional strategies and promote sustainable agricultural practices, ultimately benefiting animal welfare, productivity, and environmental sustainability in livestock farming.

Conflict of Interest

Not available

Financial Support

Not available

References

1. Artiles-Ortega E, Portal O, Jeyanathan J, Reguera-Barreto B, de la Fé-Rodríguez PY, Lima-Orozco R, Fievez V. Performance, rumen microbial community and immune status of goat kids fed *Leucaena leucocephala* post-weaning as affected by prenatal and early life

- nutritional interventions. *Frontiers in Microbiology*. 2022;12:769438. doi: 10.3389/fmicb.2021.769438.
2. Belanche A, Patra AK, Morgavi DP, Suen G, Newbold CJ, Yáñez-Ruiz DR. Editorial: Gut microbiome modulation in ruminants: Enhancing advantages and minimizing drawbacks. *Frontiers in Microbiology*. 2021;11:622002. doi: 10.3389/fmicb.2020.622002. PMID: 33505388; PMCID: PMC7829182.
3. Belenguer A, Ben Bati M, Hervás G, Toral PG, Yáñez-Ruiz DR, Frutos P. Impact of oxalic acid on rumen function and bacterial community in sheep. *Animal*. 2013 Jun;7(6):940-7. doi: 10.1017/S1751731112002455. PMID: 23298534.
4. Bueno ICS, Brandi RA, Fagundes GM, Benetel G, Muir J. The role of condensed tannins in the *in vitro* rumen fermentation kinetics in ruminant species: Feeding type involved? *Animals (Basel)*. 2020 Apr;10(4):635. doi: 10.3390/ani10040635. PMID: 32272600; PMCID: PMC7222832.
5. Burns JC. ASAS Centennial Paper: Utilization of pasture and forages by ruminants: A historical perspective. *Journal of Animal Science*. 2008;86(12):3647-3663. doi: 10.2527/jas.2008-1104.
6. Cheeke PR, Shull LR. Natural toxicants in feeds and livestock. Westport: AVI Publishing Inc; c1985. p. 1-2.
7. Cole NA, McLaren JB, Hutcheson DP. Influence of preweaning and B-vitamin supplementation of the feedlot receiving diet on calves subjected to marketing and transit stress. *Journal of Animal Science*. 1982;54(5):911-917. doi: 10.2527/jas1982.545911x.
8. Duncan AJ, Young SA. The effect of rumen adaptation to oxalic acid on a selection of oxalic-acid-rich plants by goats. *British Journal of Nutrition*. 2000 Jan;83(1):59-65. doi: 10.1017/S000711450000009X.
9. Fonty G, Gouet P, Jouany JP, Senaud J. Ecological factors determining establishment of cellulolytic bacteria and protozoa in the rumens of meroxenic lambs. *Journal of General Microbiology*. 1983 Jan;129(1):213-223. doi: 10.1099/00221287-129-1-213. PMID: 6403660.
10. Fonty G, Gouet P, Jouany JP, Senaud J. Establishment of the microflora and anaerobic fungi in the rumen of lambs. *Journal of General Microbiology*. 1987 Jul;133(7):1835-1843. doi: 10.1099/00221287-133-7-1835.
11. Gao J, Sun Y, Bao Y, Zhou K, Kong D, Zhao G. Effects of different levels of rapeseed cake containing high glucosinolates in steer ration on rumen fermentation, nutrient digestibility, and the rumen microbial community. *British Journal of Nutrition*. 2021 Feb;125(3):266-274. doi: 10.1017/S0007114520002767.
12. Gupta RK, Gangoliya SS, Singh NK. Reduction of phytic acid and enhancement of bioavailable micronutrients in food grains. *Journal of Food Science and Technology*. 2015 Feb;52(2):676-684. doi: 10.1007/s13197-013-0978-y.
13. Ho YW, Abdullah N, Jalaludin S. The diversity and taxonomy of anaerobic gut fungi. *Fungal Diversity*. 2000;4(3):65-87.
14. Kholif AE. A review of the effect of saponins on ruminal fermentation, health and performance of ruminants. *Veterinary Sciences*. 2023 Jul;10(7):450. doi: 10.3390/vetsci10070450. PMID: 37505855; PMCID: PMC10385484.
15. Khota W, Kaewpila C, Kimprasit T. The isolation of rumen enterococci strains along with high potential

- utilizing cyanide. *Scientific Reports*. 2023 Aug;13:13176. doi: 10.1038/s41598-023-40488-9.
16. Kingston-Smith AH, Marshall A, Moorby JM. Breeding for genetic improvement of forage plants in relation to increasing animal production with reduced environmental footprint. *Animal*. 2012;1:1-10.
 17. Kobayashi Y. Improvement of livestock productivity and prevention of metabolic disorders through the control of gastrointestinal environments. *Journal of Livestock Infectious Diseases*. 2019;8(1):43-50.
 18. Majak W, Cheng KJ. Cyanogenesis in bovine rumen fluid and pure cultures of rumen bacteria. *Journal of Animal Science*. 1984 Sep;59(3):784-790. doi: 10.2527/jas1984.593784x.
 19. Makkar HP. Effects and fate of tannins in ruminant animals, adaptation to tannins, and strategies to overcome detrimental effects of feeding tannin-rich feeds. *Small Ruminant Research*. 2003;49(3):241-256. doi: 10.1016/S0921-4488(03)00142-1.
 20. McSweeney CS, Odenyo A, Krause DO. Rumen microbial responses to antinutritive factors in fodder trees and shrub legumes. *Journal of Applied Animal Research*. 2002;21(1):181-205. doi: 10.1080/09712119.2002.9706369.
 21. Michaiowski T. Rumen protozoa in the growing domestic ruminant. In: *Biology of Growing Animals*. Biology of Growing Animals. 2005;2:54-74.
 22. Minato H, Otsuka M, Shirasaka S, Itabashi H, Mitsumori M. Colonization of microorganisms in the rumen of young calves. *Journal of General and Applied Microbiology*. 1992;38(5):447-456. doi: 10.2323/jgam.38.447.
 23. Nelson KE, Pell AN, Schofield P, Zinder S. Isolation and characterization of an anaerobic ruminal bacterium capable of degrading hydrolysable tannins. *Applied and Environmental Microbiology*. 1995;61(9):3293-3298.
 24. Oltjen JW, Beckett JL. Role of ruminant livestock in sustainable agricultural systems. *Journal of Animal Science*. 1996;74(6):1406-1409. doi: 10.2527/1996.7461406x.
 25. Oshio S, Tahata I, Minato H. Effect of diets differing in rations of roughage to concentrate on microflora in the rumen of heifers. *Journal of General and Applied Microbiology*. 1987;33(2):99-111. doi: 10.2323/jgam.33.99.
 26. Patra AK, Saxena J. The effect and mode of action of saponins on the microbial populations and fermentation in the rumen and ruminant production. *Nutrition Research Reviews*. 2009 Dec;22(2):204-219. doi: 10.1017/S0954422409990163.
 27. Pell AN, Woolston TK, Nelson KE, Schofield P. Tannins: biological activity and bacterial tolerance. In: Brooker JD, editor. *Tannins in Livestock and Human Nutrition*. ACIAR Proceedings. 2000;92:111-116.
 28. Ramli N, Jamaludin AA, Ilham Z. Mimosine toxicity in *Leucaena* biomass: A hurdle impeding maximum use for bioproducts and bioenergy. *International Journal of Environmental Sciences & Natural Resources*. 2017;6(2):555700. doi: 10.19080/IJESNR.2017.06.555700.
 29. Reddy DV. *Applied Nutrition* (3rd ed.). New Delhi: CBS Publishers & Distributors Pvt Ltd; c2016. p. 543-57.
 30. Rizwanuddin S, Kumar V, Singh P, Naik B, Mishra S, Chauhan M, *et al.* Insight into phytase-producing microorganisms for phytate solubilization and soil sustainability. *Frontiers in Microbiology*. 2023 Aug;14:1103920. doi: 10.3389/fmicb.2023.1103920.
 31. Russell JB, Rychlik JL. Factors that alter rumen microbial ecology. *Science*. 2001 Jun;292(5519):1119-1122. doi: 10.1126/science.1058830.
 32. Saratsis A, Henriksson A, Mueller-Harvey I. Condensed tannins, prion disease and human health. *Journal of the Science of Food and Agriculture*. 2002;82(9):1074-1079. doi: 10.1002/jsfa.1169.
 33. Shu Z, Ma J, Huang H, Zeng Y. Effects of different levels of inclusion of *Sophora alopecuroides* in the ration on nutrient digestibility, rumen fermentation, and intestinal bacterial communities in sheep. *Frontiers in Veterinary Science*. 2022;9:873177. doi: 10.3389/fvets.2022.873177. PMID: 36072073; PMCID: PMC9431852.
 34. Singh B, Lamba JS, Sharma V, Kaur S. Influence of certain toxicants on rumen microbial ecosystem and toxicological manifestations in ruminants: a review. *Environmental Science and Pollution Research*. 2016 Nov;23(22):21058-75. doi: 10.1007/s11356-016-7694-y. PMID: 27665107.
 35. Singh B, Sharma A, Gupta M, Gupta PK. Rumen metabolic adaptations and diverse microbiota are associated with long-term (25 years) continuous rearing of sheep on a highly tannin-rich diet of oak (*Quercus semicarpifolia*) leaves. *Scientific Reports*. 2023 Jul;13:10764. doi: 10.1038/s41598-023-37317-6. PMID: 37420711; PMCID: PMC10330594.
 36. Smith AH, Zoetendal EG, Mackie RI. Bacterial mechanisms to overcome inhibitory effects of dietary tannins. *Microbial Ecology*. 2005 Apr;50(2):197-205. doi: 10.1007/s00248-004-0180-x. PMID: 16052397.
 37. Van Soest PJ. *Nutritional ecology of the ruminant*. Cornell University Press; c1994. p. 476.
 38. Waghorn G, Ulyatt M, John A. Pasture intake and milk production by cows grazing white clover or perennial ryegrass pasture in late lactation. *New Zealand Journal of Agricultural Research*. 1990;33(4):479-490.
 39. Wei L, Lv C, Yao Z, Chen H, Wang F, Zhang L. The effects of replacing soybean meal with linseed meal in the ration on performance, ruminal fermentation, and rumen microbiota of weaned lambs. *Frontiers in Veterinary Science*. 2023 Mar;10:1096026. doi: 10.3389/fvets.2023.1096026.
 40. Williams AG, Withers SE, Joblin KN, Chen G. Effects of ciliate protozoa on the hydrogenation of unsaturated fatty acids in the rumen of steers fed red clover silage. *Journal of Applied Microbiology*. 2016 Feb;120(2):399-409. doi: 10.1111/jam.13006. PMID: 26792358.
 41. Wina E, Muetzel S, Becker K. The impact of saponins or saponin-containing plant materials on ruminant production: A review. *Journal of Agricultural and Food Chemistry*. 2005 Jul;53(21):8093-105. doi: 10.1021/jf048053d. PMID: 16190604.
 42. Wood TA, Wallace RJ, Rowe A, Price J, Yanez Ruiz DR, Murray P, Newbold CJ. Encapsulated fumaric acid as a feed ingredient to decrease methane emissions from ruminants. *Animal Feed Science and Technology*. 2009;152(1-2):62-71. doi: 10.1016/j.anifeedsci.2009.03.011.
 43. Xiao J, Liu X, Wei Y, Cui J, Wang Z, Liu Y, *et al.* Effects of hydrolyzable tannins on the rumen bacterial community and metabolome of dairy cows. *Frontiers in Microbiology*. 2022 Sep;13:964197.

doi: 10.3389/fmicb.2022.964197. PMID: 36161100; PMCID: PMC9496354.

44. Xu ZJ, Bai Y, Chen G, Fu ZH. Ecotoxicity of plant allelopathy on anaerobic fungi in rumen ecosystem. *Scientific Reports*. 2017 Sep;7:11469. doi: 10.1038/s41598-017-11437-8. PMID: 28916733; PMCID: PMC5599850.
45. Yáñez-Ruiz DR, Bannink A, Dijkstra J, Kebreab E, Morgavi DP, O’Kiely P, *et al.* Design, implementation and interpretation of *in vitro* batch culture experiments to assess enteric methane mitigation in ruminants—a review. *Animal Feed Science and Technology*. 2016;216:1-18. doi: 10.1016/j.anifeedsci.2016.03.016.

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