



REVIEW

# Toward climate-smart livestock: The role of the microbiome in One Health approaches

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## Abstract

**Background:** Climate change poses critical challenges to global livestock systems, threatening productivity, food security, and environmental sustainability. The ruminant microbiome, particularly the rumen microbial community, plays a vital role in animal health, nutrition, and productivity, while also contributing to greenhouse gas emissions. Framing the microbiome within a One Health perspective highlights its importance for animal well-being, human nutrition, and environmental resilience. **Methods:** This review synthesizes evidence on the impacts of climate-related stressors, including heat, drought, and feed scarcity on the livestock microbiome. It examines interventions such as probiotics, prebiotics, fecal microbiota transplantation, dietary modifications, and synthetic biology approaches, alongside strategies to inhibit methanogenic archaea. Advances in microbiome analytics, including omics platforms, sensors, and machine learning, are discussed in relation to precision livestock farming and monitoring of animal health and emissions. **Results:** Findings indicate that microbiome shifts under climate stressors influence both livestock productivity and methane emissions. Meta-analyses and field trials demonstrate that feed and microbial additives and methanogenesis inhibitors can decrease enteric methane emissions by 20–80%, enhance feed conversion efficiency by 5–15%, and sustain milk production under heat stress conditions. While technological innovations enable more precise monitoring, significant gaps remain in understanding host–microbe–climate interactions, and barriers such as technical limitations, regulatory hurdles, and farmer adoption challenges persist. Integrated multi-omics methodologies now elucidate key genes and pathways that regulate fermentation resilience, facilitating precise microbiome engineering via probiotics, bacteriophages, and CRISPR-mediated modulation of methanogens. Beyond biological innovation, microbiome-focused approaches are consistent with international One Health frameworks (FAO–WHO–WOAH), facilitating the mitigation of antimicrobial resistance (AMR), reduction of zoonotic risks, and reporting of greenhouse gas emissions within climate-smart agricultural initiatives. Integrating microbiome metrics into national livestock, AMR, and climate policies can elevate them from experimental instruments to quantifiable sustainability strategies. **Conclusion:** Overall, this review demonstrates that harnessing the ruminant microbiome has the potential to reduce global agricultural methane emissions by up to 40%, while simultaneously enhancing animal resilience and productivity – positioning the microbiome as a critical biological and policy frontier for climate-smart, One Health-oriented livestock transformation. Microbiome-based strategies offer a promising pathway toward climate-smart livestock systems. Achieving this will require harmonized research methodologies, systems-based multi-omics approaches, cross-sectoral collaboration, and supportive policy frameworks. Integrating microbiome innovations into climate adaptation strategies can strengthen livestock productivity, improve food security, and support environmental resilience.

## One Health impact statement

This review underscores the centrality of the ruminant microbiome at the interface of animal, human, and environmental health. By shaping livestock productivity, methane emissions, and antimicrobial resistance dynamics, microbial communities act as critical levers for sustainable food systems. Integrating microbiome science into livestock management contributes to safer food, reduced zoonotic and AMR risks, and lower greenhouse gas outputs, thereby aligning with the global One Health agenda. Advancing microbiome-based interventions through selective breeding, dietary strategies, and precision livestock farming, offers practical opportunities to strengthen climate resilience, improve animal welfare, and safeguard public health.

**Keywords:** climate change, livestock microbiomes, emissions, One Health, methane mitigation

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## Introduction

Climate change is increasingly affecting livestock systems, exposing animals to more frequent heat waves, prolonged droughts, emerging diseases, and fluctuations in feed availability. These pressures already cause significant economic and productivity losses; for example, heat stress alone costs the US cattle industry billions each year, with an estimated US\$900 million loss in the dairy sector (Polsky and von Keyserlingk, 2017). Such figures underscore the limitations of conventional adaptation strategies. While approaches such as genetic selection for heat-tolerant breeds, improved housing, and optimized nutrition have provided some relief, they remain only partially effective in offsetting climate-induced stressors. Given these constraints, researchers are increasingly turning to the livestock microbiome as a promising frontier for resilience (Silpa *et al.*, 2025).

However, climatic pressures directly and indirectly disrupt these host–microbiome interactions. High ambient temperatures impair thermoregulation, reduce feed intake, and lower milk yield and growth rates. Heat stress also alters reproductive physiology by affecting estrus behavior and inducing hormonal imbalances (Degefu and Milkias, 2024). Moreover, it weakens immune function through glucocorticoid-mediated cytokine suppression, thereby heightening susceptibility to infectious diseases (Bagath *et al.*, 2019). In parallel, climatic variability degrades pasture quality and feed availability, intensifying nutritional stress and reducing livestock productivity (Agbeja *et al.*, 2021). Although conventional measures such as heat shelters, genetic selection, and adjusted feeding regimes are widely promoted, they carry inherent limitations and cannot fully address these complex challenges (Mondal, 2022).

The microbiome offers a novel opportunity to develop climate-smart livestock systems. Understanding how microbial communities respond to environmental stressors may not only improve resilience and productivity but also provide new avenues for mitigating climate-related disease risks and nutritional deficits.

Livestock systems are situated at the intersection of two converging pressures: they are becoming more vulnerable to the effects of climate change, and they are also making a substantial contribution to climate forcing. Productivity, welfare, and farm economics are already being challenged by heat stress, drought, altered pasture dynamics, and altering infectious disease patterns, particularly in areas where adaptive capacity is restricted (Króliczewska *et al.*, 2023). Global assessments suggest that livestock systems make a significant contribution to anthropogenic greenhouse gas emissions, with ruminant production accounting for the majority of this contribution as a result of enteric fermentation processes (Kelly and Kebreab, 2023).

Enteric fermentation is a primary contributor to methane emissions in agriculture and is on the rise, primarily as a result of the growing global demand for animal products (Sun *et al.*, 2023). Methane is a potent greenhouse gas with a higher warming potential than CO<sub>2</sub>. However, its relatively short atmospheric lifetime means that mitigation can yield rapid climate benefits (Khairunisa *et al.*, 2023). It is crucial to note that microbial processes associated with ruminant digestion are responsible for a significant portion of methane emissions from agriculture, which underscores the necessity of focusing on biological pathways for mitigation (Hosen *et al.*, 2025). Methane formation also represents a direct loss of feed energy from an animal–production perspective, which connects emission reduction strategies with potential improvements in production efficiency (Morgavi *et al.*, 2023).

It is crucial to note that the host does not solely determine these emission and efficiency outcomes; rather, they are the result of metabolic interactions between the host and microbes. The ruminant can be viewed as a holobiont, in which rumen microbial consortia regulate fermentation processes, hydrogen flux, and downstream methanogenesis (Gonzalez-Recio *et al.*, 2023). The activity of

methanogenic archaea, which utilize hydrogen and carbon dioxide produced during microbial fermentation, is reflected in methane production (Khairunisa *et al.*, 2023). This positions the microbiome as a concealed, mechanistic regulator of both productivity through nutrient harvesting and fermentation efficiency and emissions intensity through hydrogen routing pathways (López-García *et al.*, 2022). As a result, microbiome-targeted strategies, such as dietary additives, microbial modulation, and fermentation inhibitors, have risen as plausible methods for reducing methane emissions while maintaining productivity (Bature *et al.*, 2024).

A One Health framework is also inherently aligned with a microbiome-centered climate strategy for livestock. Interconnected pathways between environmental, animal, and human health are established by the circulation of microbial communities and antimicrobial resistance (AMR) genes through animals, manure, soil, water, and food systems (Ceh, 2021). By altering microbial ecology, climate-driven stressors have the potential to exacerbate these exchanges, thereby increasing the dissemination of resistance and the transmission of pathogens. This interconnectedness emphasizes the necessity of integrated strategies that simultaneously mitigate health risks, productivity, and emissions by means of microbiome-informed interventions (Lozano *et al.*, 2017).

This review synthesizes evidence on how climate-related stressors, such as heat stress, drought, and variability in feed resources, disrupt livestock-associated microbiomes, thereby affecting productivity, health, and methane emissions. It evaluates microbiome-targeted interventions dietary strategies, microbial and phyto-genic additives, and methane-inhibiting approaches for their potential to enhance resilience and reduce emissions intensity without compromising animal performance. It examines emerging technologies for microbiome monitoring and precision livestock farming, focusing on functional multi-omics, portable sequencing, and data-driven decision support. Finally, it analyzes how advancements in livestock microbiome science align with One Health priorities, including the mitigation of AMR, reduction of zoonotic risks, and the integration of livestock–environment surveillance and policy frameworks.

## Review methodology

To enhance transparency and reproducibility, we implemented a narrative, exhaustive literature review that was informed by PRISMA-style principles to synthesize the evidence on livestock microbiomes in the context of climate change and One Health. The evidence was synthesized narratively rather than through quantitative aggregation, as this article was not intended to be a comprehensive systematic review or meta-analysis.

The reference lists of relevant reviews, primary studies, and selected policy or technical documents were manually screened to identify additional eligible sources, in addition to the literature search conducted in Scopus, Web of Science, PubMed, and Google Scholar. The primary search concentrated on literature published between 2005 and 2025, with a small number of prior foundational studies retained as needed to provide historical or mechanistic context.

The search terms that were combined were those that were associated with the livestock microbiome, climate stressors, methane biology, microbiome-targeted interventions, omics technologies, precision livestock husbandry, and One Health. Representative Boolean search strings included the following: (“rumen microbiome” or “ruminant microbiome” or “livestock microbiota” or “rumen microbiota”) and (“climate change” or “heat stress” or drought or “feed scarcity” or “nutritional stress”) and (livestock or ruminant or cattle or dairy or sheep or goat or buffalo); (“enteric methane” or methanogenesis or “methane mitigation”) and (rumen or ruminant or livestock) and (probiotics or prebiotics or “fecal microbiota transplantation” or “feed additives” or “3-nitrooxypropanol” or “3-NOP” or Asparagopsis or

nitrate); (metagenomics or meta transcriptomics or “multi-omics” or metabolomics or sensors or “precision livestock farming” or “machine learning”) and (microbiome or microbiota) and (livestock or ruminant); and (“One Health” or “antimicrobial resistance” or AMR or “zoonotic risk”) and (microbiome or microbiota) and (livestock or ruminant). The same concept blocks were searched for on Google Scholar using simplified phrase combinations due to platform-specific search limitations.

Records were systematically evaluated through title and abstract examination, followed by a comprehensive assessment of full-text eligibility. Studies qualified if they: (i) concentrated on livestock or ruminant systems; (ii) investigated microbiome composition, function, or host–microbe interactions; (iii) presented outcomes pertaining to productivity, methane emissions, resilience, animal health, antimicrobial resistance, zoonotic risk, or policy significance; or (iv) assessed microbiome-targeted interventions or facilitating technologies. Records were excluded if they: (i) did not concentrate on livestock or ruminant systems; (ii) lacked significant relevance to microbiome composition or function; (iii) failed to address climate stress, methane, productivity, One Health, or policy aspects; (iv) were duplicate entries; (v) provided inadequate methodological detail; (vi) were non-English full texts that could not be evaluated; or (vii) consisted of opinion or commentary articles lacking direct scientific or policy significance.

## Climate change and its impact on livestock systems

Heat stress, when animals are exposed to temperatures beyond their thermoneutral zone, reduces fertility, milk yield, feed intake, and overall productivity. For example, dairy cows under heat stress may produce up to 38% less milk during mid-lactation, and even modest increases in temperature-humidity index (THI) above 72 can severely impair performance in high-yielding breeds (Poliquit, 2014).

The effects are particularly pronounced in tropical and subtropical regions. In Fiji, for instance, heat stress has emerged as a critical threat to both animal welfare and dairy productivity (Iqbal *et al.*, 2024). Water and forage scarcity represent another major, though sometimes overlooked, impact of climate change. Declining rainfall, coupled with higher evaporation rates, intensifies water shortages in semi-arid areas. In response, animals exhibit physiological adjustments such as reduced feed intake, altered excretion patterns, and even body weight loss to conserve water (Iqbal *et al.*, 2024). At the same time, declining fodder species diversity and forage quality reduce palatability and nutrient availability, thereby lowering growth and productivity. In countries like India, indiscriminate crossbreeding in drought-prone areas has further complicated resilience, as exotic breeds require higher levels of grain and water, resources that are becoming increasingly unreliable (Mahajan *et al.*, 2015).

Finally, while climate change adversely impacts livestock, the sector itself is also a major contributor to global warming. Animal agriculture accounts for 18% of global greenhouse gas emissions, primarily through enteric methane from ruminants and nitrous oxide from manure and feed production (Prasad *et al.*, 2015). However, estimates vary widely depending on system complexity, production intensity, and microbial fermentation processes in ruminants, which complicate conventional emission assessments (Röös and Nylander, 2013).

## Microbiome’s role in livestock health and productivity

Viewing livestock as holobionts integrated host-microbe systems redefines resilience from a static genetic characteristic to a dynamic process of microbial-host co-adaptation (Richardson, 2017). This perspective introduces microbial-engineering strategies that can simultaneously improve feed conversion efficiency, boost

immune responses, and reduce enteric methane emissions. Dietary and additive interventions targeting the rumen microbiome (e.g., phytogenic feed additives) have demonstrated significant reductions in methane emissions, thereby enhancing energetic efficiency and animal performance (Hassan *et al.*, 2020). Building upon these advancements, this review advocates a holobiont-based One Health framework for climate-smart livestock integrating microbial mechanisms, practical intervention strategies, and policy pathways to promote resilient, low-emission animal production amid environmental stress.

The host-associated microbiome, particularly gut and rumen communities, plays a decisive role in how livestock responds to environmental stressors. These microbial populations regulate digestion, energy metabolism, and immune defenses, making them central to animal health and productivity. Importantly, microbiota exhibits remarkable plasticity, adapting rapidly to fluctuating conditions, a trait that can be harnessed to strengthen climate resilience (Thriene and Michels, 2023). This has led to the growing view of livestock as “holobionts,” where resilience is shaped not only by host genetics but also by dynamic host–microbe interactions (Richardson, 2017).

Emerging interventions aim to deliberately shape microbial communities to improve resilience. Phytogenic additives, including essential oils, tannins, and probiotics, can modulate rumen fermentation, reduce methane emissions while improve feed efficiency (Hassan *et al.*, 2020). Selective breeding may even extend to microbiome-related traits, such as the presence of methanogen-inhibiting bacteria or fiber-degrading fungi associated with resilient breeds (Omondi *et al.*, 2024).

The ruminal microbiome underpins livestock nutrition by fermenting otherwise indigestible plant biomass into host-available nutrients. Dominated by *Firmicutes* and *Bacteroidetes*, these symbiotic bacteria hydrolyze cellulose and starch, producing volatile fatty acids (VFAs), i.e., acetate, propionate, and butyrate, as well as microbial protein (Silva *et al.*, 2024). Genera such as *Prevotella*, *Eubacterium*, and *Streptococcus bovis* specialize in fermenting non-fiber carbohydrates, while cellulolytic species including *Fibrobacter succinogenes* and *Ruminococcus flavefaciens* degrade plant fibers. Fermentation products from this system supply 70–80% of the ruminant’s energy and protein requirements, making the microbiome central to host productivity (Kibegwa *et al.*, 2023).

Methanogenic archaea also play a critical role in consuming hydrogen, a byproduct of fermentation, to produce methane. This process maintains anaerobic conditions necessary for digestion but simultaneously represents an energetic loss to the host. Overall, the tightly integrated rumen community enables efficient transformation of forage into usable energy; disturbances to this balance, such as abrupt dietary changes, can markedly alter fermentation efficiency (Morgavi *et al.*, 2006; Janssen and Kirs, 2008).

Microbiome composition is increasingly recognized as a determinant of feed efficiency. High-performing cattle and sheep often harbor higher abundances of *Prevotella* and *Fibrobacter*, taxa associated with fiber degradation and volatile fatty acids (VFA) production (Peraza *et al.*, 2024). Conversely, dysbiosis caused by sudden dietary shifts can impair digestion. For example, a rapid switch to grain-rich diets promotes lactic acid accumulation, collapse of Gram-negative populations, and endotoxin release, leading to acidosis and inflammation. Thus, the structure and stability of the rumen microbial population dictate how effectively ruminants convert feed into growth, milk, or meat (Du *et al.*, 2023).

Microbial ecology is the primary factor influencing feed efficiency in ruminant systems. Rumen communities regulate the rate and completeness of fibrolysis, the efficiency of fermentation end-product formation, and the stability of cross-feeding networks (e.g., lactate production and utilization) to prevent dysbiosis and

maintain ruminal pH and epithelial integrity (Ahmad *et al.*, 2025). In practical terms, a functionally diversified and stable rumen microbiome facilitates the consistent conversion of complex plant polysaccharides into host-usable energy, while simultaneously restricting the diversion of fermentation intermediates toward methane production (Indugu *et al.*, 2024).

Despite the fact that alpha diversity metrics do not consistently correlate with residual feed intake across studies, evidence suggests that (i) microbial community composition and metabolic function differ between efficient and inefficient animals, and (ii) ecological stability and functional redundancy are enhanced in response to dietary and environmental perturbations (Ceh, 2021). It is crucial to note that enhanced feed efficiency decreases the quantity of feed required per unit of animal product, thereby reducing the overall environmental footprint and emissions intensity of livestock systems. This reduction in upstream resource demand and associated emissions, including those from feed production and manure management, is a significant benefit (Palangi and Lackner, 2022).

Rumen microorganisms transform indigestible plant biomass into short-chain VFAs, which provide the predominant portion of the host's metabolizable energy. However, methanogenic archaea that utilize fermentation-derived hydrogen divert 2–12% of feed energy into methane, a direct emission of greenhouse gases and a metabolic loss (Samal and Kumar Dash, 2022). Climate-induced alterations in rumen conditions, including decreased pH and oxygen flux under heat stress, facilitate the proliferation of methanogens and diminish fibrolytic bacterial activity, thereby intensifying inefficiency and emissions (Pragna *et al.*, 2018).

### GUT MICROBIOME AND IMMUNE MODULATION

The gastrointestinal (particularly hindgut) microbiome plays a significant role in regulating gut barrier function and immune responses. A balanced microbial community (homeostasis) is essential for immune development, as the gut harbors a vast population of immune cells alongside diverse microorganisms (Du *et al.*, 2023). Fermentation of dietary fiber generates short-chain fatty acids (SCFAs), which exert significant host effects. For instance, acetate stimulates (Immunoglobulin A) IgA synthesis by gut B cells, while propionate contributes to gluconeogenesis (Baky *et al.*, 2024).

Fermentation-derived short-chain fatty acids like acetate, propionate, and butyrate modulate host metabolic processes and mucosal immune responses. Butyrate, the primary energy substrate for rumen epithelial cells, preserves the integrity of tight junctions and inhibits inflammatory signaling through (Nuclear Factor) NF- $\kappa$ B suppression (Luo *et al.*, 2019). Climate stress impacts feed intake and microbial composition, resulting in a reduction of butyrate-producing microbes and compromised gut barrier integrity, which subsequently facilitates endotoxin leakage and systemic inflammation. This dysbiosis-immunity feedback loop connects heat stress to diminished nutrient assimilation, immune dysregulation, and an increased risk of disease (He *et al.*, 2021).

### SKIN AND RESPIRATORY MICROBIOMES AND ENVIRONMENTAL RESILIENCE

The skin and respiratory tract microbiomes serve as the first line of defense against environmental infections in cattle. Commensal skin bacteria can outcompete or inhibit pathogens, particularly on the hooves and udders. For example, the composition of the bovine foot skin microbiome influences susceptibility to digital dermatitis: healthy animals display distinct microbial profiles, whereas early dysbiosis has been associated with the onset of bovine digital dermatitis lesions (Bay *et al.*, 2023).

The respiratory microbiome contributes to health in a comparable way. Studies on bovine respiratory disease (BRD) show that nasopharyngeal microbial populations shift during infection and

treatment. In calves treated for pneumonia, beneficial *Lactobacillus* increased in the upper airway following therapy, suggesting a role in recovery. By contrast, healthy cattle maintain stable nasal and lung microbial communities over time, which may help prevent colonization by BRD-associated pathogens (Centeno-Martinez *et al.*, 2023a, 2023b).

### MICROBIOME INFLUENCE ON REPRODUCTION AND GROWTH

The microbiome also plays a critical role in ruminant reproduction and development. Fertility has been strongly associated with the reproductive tract microbiota. Dysbiosis of uterine or vaginal bacterial communities is frequently linked to reduced conception rates and repeat-breeding syndrome in dairy cows (Gupta *et al.*, 2024). While the underlying mechanisms remain under investigation, a balanced vaginal microbiome is believed to support embryo implantation and reduce inflammation-related infertility (Patel *et al.*, 2022).

Beyond reproduction, the gut and rumen microbiota strongly influence growth trajectories. In calves, a stable intestinal microbiome supports immune system maturation, efficient nutrient absorption, and healthy weight gain. Conversely, disruptions caused by pathogen overgrowth or dietary imbalance often led to diarrhea, poor feed utilization, and stunted growth (Guo *et al.*, 2023). Interventions that focus on microbial ecology rather than host genetics alone provide scalable leverage points for climate-smart cattle growth, which can be explained by these perturbations at the microbiome level.

### Microbiome plasticity and adaptation to environmental stressors

Livestock microbiomes display remarkable plasticity, enabling them to adapt dynamically to environmental stressors. Among the most significant is heat stress, which disrupts rumen fermentation and microbial balance (Wang *et al.*, 2025). Nutritional stress, including undernutrition or poor-quality forage, likewise exerts strong selective pressure on gut flora. Feed quantity and quality remain among the most powerful determinants of rumen composition (Kibegwa *et al.*, 2023). Under nutrient scarcity, ruminants often increase the abundance of fiber-degrading taxa (Li *et al.*, 2024). Chronic heat stress also perturbs rumen chemistry, lowering pH, and acetate concentrations while elevating lactate levels in dairy cows (Kim *et al.*, 2022).

In addition to environmental factors, pathological conditions can induce dysbiosis. Rumen acidosis is a classic example, arising when high-concentrate diets overwhelm the rumen buffering system, causing fermentation imbalances and hindgut inflammation (Wu *et al.*, 2024a, 2024b). These microbial shifts occur in parallel with systemic metabolic disturbances, such as reduced serum niacin and amino acid levels reflecting broader host stress responses (Table 1) (Pedersen *et al.*, 2016).

### Leveraging microbiome interventions for climate resilience

Targeted microbiome interventions offer promising strategies to improve livestock resilience under climatic stressors such as heat waves, nutritional fluctuations, and oxidative challenges. Among these, probiotics, prebiotics, and microbial-based additives are gaining attention as tools to stabilize rumen fermentation, enhance host immunity, and mitigate metabolic stress (Kotsampasi *et al.*, 2024). In goats exposed to heat stress, yeast-based probiotics (*Saccharomyces cerevisiae* cultures) stabilized rumen function while enhancing milk fat and antioxidant content (Cai *et al.*, 2021).

Heat-tolerant lactic acid bacteria (LAB) represent another promising avenue. A strain of *Lactobacillus plantarum* (L19), isolated from cow milk, retained 16% viability at 65°C and exhibited strong

free-radical scavenging activity. Genomic analyses revealed multiple heat-shock and antioxidant-related genes, suggesting potential roles in protecting cattle against oxidative damage during thermal stress (Wang *et al.*, 2024a, 2024b).

Prebiotics, such as non-digestible fibers and oligosaccharides, further support resilience by selectively stimulating beneficial microbial growth. In transition cows, supplementation with  $\beta$ -glucan and fructo-oligosaccharides attenuated the rise in inflammatory cytokines and oxidative stress markers around calving (Jantzi, 2024).

Together, these interventions demonstrate that manipulating the microbiome through probiotics and prebiotics can enhance livestock adaptation to environmental stressors, improving both productivity and welfare (Table 2).

### Fecal microbiota transplantation (FMT)

A promising emerging strategy to improve resilience in young or weak animals is the transfer of microbiota from healthy donors. In neonatal dairy calves, early-life FMT has been shown to accelerate gut maturation and mitigate the adverse effects of weaning stress. Rosa *et al.* (2021) reported that administering 25 g of donor feces daily during the first 8–12 days of life enhanced microbial diversity in both rumen and feces, while also reducing acute-phase protein levels at weaning compared to controls. Specifically, FMT calves exhibited a smaller rise in haptoglobin and increased paraoxonase activity, indicating a more stable metabolic and immune response to dietary transitions. These findings suggest that early exposure to a diverse, adult-like microbiota strengthens gut health and immune function during critical developmental stages (Du *et al.*, 2023).

Together, these interventions highlight the potential of microbiome-based therapies to support growth, resilience, and productivity in ruminant livestock.

### Selective breeding for microbiome-associated traits

Host genetics exert a strong influence on the rumen microbiota, and emerging evidence suggests that these host–microbe interactions can be harnessed in breeding programs. Heritability studies indicate that a substantial proportion of rumen taxa and functions are genetically regulated.

Methane production, a key trait for climate resilience, illustrates this dual control. Difford *et al.* (2018) found that host genetics explained ~21% of the variation in methane emissions, while rumen microbiome composition accounted for ~13%, with independent effects. This implies that combining traditional selection for low-methane genotypes with microbiome-targeted interventions (e.g., diet optimization, microbial transplants) could maximize gains (Kamath *et al.*, 2023).

Further, Martínez-Álvaro *et al.* (2022) identified over 300 heritable microbial genes strongly linked to methanogenesis. Incorporating these microbial markers into breeding programs could reduce methane emissions by ~17% per generation, exceeding reductions achievable through selection on raw methane (CH<sub>4</sub>) output alone. An integrated host–microbiome breeding strategy could produce livestock that naturally ferments feed more efficiently and emits fewer greenhouse gases (Myer, 2019).

### Dietary interventions and microbiome engineering

Dietary strategies are among the most direct and effective tools for modulating the rumen ecosystem and reducing its climate footprint. For example, supplementing beef steers with a native

**Table 1.** Microbiome shifts under climate-related stressors in ruminants.

Stressor type	Observed microbial changes	Impact on host	Key studies
Heat stress	Decreased <i>Fibrobacter</i> , increased lactate-producers ( <i>Streptococcus</i> )	Reduced feed intake, altered rumen fermentation	Zhao <i>et al.</i> (2019); Kim <i>et al.</i> (2022)
Poor nutrition	Increase in fiber degraders ( <i>Prevotella</i> , fungi)	Enhanced fiber utilization under low nutrient availability	Wallace <i>et al.</i> (1997); Betancur-Murillo (2022)
Disease pressure	Increased opportunists ( <i>Proteobacteria</i> , <i>Enterobacteriaceae</i> )	Reduced barrier function, increased inflammation	Stevenson and Weimer (2009); Shinkai <i>et al.</i> (2024)
Drought conditions	Dominance of <i>Prevotella ruminicola</i> , elevated fungi	Increased fiber digestion, energy extraction	Lopes <i>et al.</i> (2015); Malik <i>et al.</i> (2020)

**Table 2.** Microbiome-based interventions for climate resilience in livestock.

Intervention type	Examples/agents used	Mechanism of action	Efficacy/effect	References
Probiotics	<i>Saccharomyces cerevisiae</i> , <i>Lactobacillus plantarum</i>	Rumen pH stabilization, enhanced immune function	Improved feed efficiency, reduced heat stress impacts	Abd El-Tawab <i>et al.</i> (2016); Wang <i>et al.</i> (2024a, 2024b)
Prebiotics	$\beta$ -glucans, fructooligosaccharides	Support beneficial microbiota	Improved gut barrier, reduced inflammation	Zapata <i>et al.</i> (2021)
Fecal microbiota transplantation	Adult rumen microbiota	Restoring microbial balance	Enhanced gut health, reduced disease incidence	Guo <i>et al.</i> (2024a, 2024b)
Feed additives	Seaweed ( <i>Asparagopsis</i> ), nitrate, 3-NOP	Methanogenesis inhibition	Reduced methane emissions, improved feed efficiency	Hendawy <i>et al.</i> (2021)
Synthetic biology	Engineered methanotroph consortia, phage therapy	Targeted microbial suppression/ modification	Potential high methane reductions, precision microbiome engineering	Krishnan <i>et al.</i> (2020)

methanotroph–methylotroph consortium (NC52PC) reduced enteric CH<sub>4</sub> emissions by ~12–14% compared to controls (Tseten *et al.*, 2025). Chemical feed additives have also shown promise: the methanogenesis inhibitor 3-nitrooxypropanol (3-NOP) consistently decreases CH<sub>4</sub> by 20–40%, while nitrate salts redirect hydrogen toward ammonia rather than methane (Lileikis *et al.*, 2023).

Beyond feed-based solutions, smart microbiome engineering is emerging as a frontier technology. Phage therapy, leveraging the host-specific nature of rumen phages, could selectively target methanogens or pathogens without disrupting beneficial microbes. A recent catalog of ~65,000 ruminant gut phage genomes revealed that ~60% are lytic, highlighting their therapeutic potential (Wu *et al.*, 2024a, 2024b). Microbiome engineering aims for precision rather than broad-spectrum shifts. Examples include CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)-guided phages that deactivate the methyl-coenzyme M reductase gene in archaea or engineered yeast that secrete enzymes to degrade heat-shock products in the rumen (Subedi *et al.*, 2022). Together, these approaches represent a new generation of interventions, moving beyond suppression of emissions toward reprogramming microbial functions for climate-smart livestock production.

## Integration of microbiome research with precision livestock farming

Precision livestock farming (PLF) uses continuous monitoring and data-driven decision making to optimize animal health, welfare, and productivity. Recent advances are extending PLF frameworks to incorporate microbiome data, recognizing the crucial roles of rumen and gut microbiota in digestion, feed conversion efficiency, and disease resilience (Zhou *et al.*, 2018). By integrating microbial profiles with sensor-based measurements, farmers can tailor nutrition and management strategies with unprecedented accuracy.

The field of livestock microbiome research is transitioning from descriptive profiling to real-time surveillance and actionable mechanism discovery because of the rapid emergence of “functional-first” technologies. Metagenomics facilitates the identification of functional pathways that are associated with fermentation efficiency, stress tolerance, pathogen carriage, and methanogenesis by enabling the exhaustive characterization of the collective gene content within rumen and gut microbial communities (Lawther *et al.*, 2025). In addition to this, metatranscriptomics offers a comprehensive understanding of the active expression of microbial genes in response to specific dietary conditions, environmental stressors, or mitigation interventions, thereby facilitating functional resolution that extends beyond taxonomic composition (Indugu *et al.*, 2024). In contexts relevant to methane, integrated metagenome–metatranscriptome analyses have shown that low- and high-methane phenotypes are differentiated not only by microbial composition but also by the differential abundance and expression of genes associated with hydrogenotrophic methanogenesis and competing hydrogen-utilizing pathways (Mrutu *et al.*, 2025).

Simultaneously, portable real-time sequencing technologies (e.g., nanopore-based platforms) are bringing genomic analysis closer to the point of need, allowing for near-real-time diagnostics and surveillance of environmental microbiomes, AMR genes, and livestock pathogens across soil and water systems (Ceh, 2021). These methods facilitate integrated One Health monitoring by identifying emergent risks in manure-impacted ecosystems and capturing microbial exchange across animal–environment interfaces (Hosen *et al.*, 2025). The operational value of these technologies is essential in their integration with farm-level decision systems.

Microbiome dynamics also provide early-warning biomarkers of disease or metabolic stress. For example, a longitudinal 16S rRNA study showed that fecal *Lactobacillus* and *Prevotella-9* abundances predicted clinical ketosis in dairy cows approximately 1 week before onset (Du *et al.*, 2024).

Such findings highlight the potential of routine or periodic microbiome surveillance via fecal, rumen, or nasal sampling as predictive health tools. Integrating microbial biomarkers into decision-support systems is still in its infancy, but promising evidence exists. For instance, longitudinal metagenomic and metabolomic surveillance in transition cows has already identified microbial signatures that forecast metabolic illness (Duarte *et al.*, 2025). In sum, linking microbiome data with PLF technologies opens the door to precision management strategies where microbial health is monitored alongside animal performance, creating a real-time, predictive model for resilient and sustainable livestock systems.

## One Health and policy dimensions

Microbiome science is increasingly being recognized as a pillar of the One Health framework, offering actionable insights for food safety, AMR, and zoonotic disease prevention.

### ONE HEALTH AND THE QUADRIPARTITE COMMITMENT

The OH Joint Plan of Action (2022–2026) established by FAO, WHO, WOA, and the United Nations Environment Programme (UNEP) serves as a framework for international collaboration at the human–animal–environment nexus to tackle zoonoses, AMR, food safety, ecosystem health, and the effects of climate change (*One Health Joint Plan of Action, 2022–2026*). The One Health paradigm explicitly acknowledges that the health of humans, animals, and ecosystems are intricately interconnected, necessitating coordinated multisectoral efforts across agriculture, public health, veterinary services, and environmental management (“One Health 2025”). By design, this framework facilitates the integration of innovations in livestock systems, including microbiome-based interventions into global health, environmental, and food-system policies, under a cohesive governance structure.

### CLIMATE ADAPTATION, EMISSIONS REDUCTION, AND SUSTAINABLE LIVESTOCK

The FAO’s One Health initiative encompasses the promotion of sustainable agrifood systems that harmonize animal productivity, environmental preservation, and ecosystem health. Microbiome interventions (e.g., feed additives, microbiome engineering, fermentation modulation) that decrease enteric methane emissions and enhance feed efficiency directly align with FAO’s objectives of reducing the environmental impact of livestock while sustaining productivity (“One Health”). Integrating these interventions within national or regional livestock–environment policies would support FAO’s mandate to incorporate climate-smart agricultural practices into sustainable development and food system transformation frameworks.

The way productivity interventions are conceptualized in livestock systems has been significantly altered by policy changes that are designed to mitigate AMR. The broader transition toward non-antibiotic strategies for sustaining livestock performance has been reinforced by evolving global guidance, such as the World Health Organization’s recommendations to restrict routine antibiotic use for growth promotion and disease prevention in healthy animals. The development and adoption of alternatives that modulate microbial ecology without relying on medically important antibiotics, such as probiotics, prebiotics, phytochemicals, organic acids, enzymes, vaccination, and enhanced management practices, have been accelerated by this regulatory momentum (Królczewska *et al.*, 2023).

It is crucial to note that a considerable number of these alternatives intersect mechanistically with rumen fermentation pathways, thereby establishing a convergence between climate mitigation objectives and AMR stewardship. In cases where hydrogen flux is diverted from methane production, strategies that modify microbial composition and metabolic function can simultaneously enhance feed utilization and decrease methanogenesis (Sun *et al.*, 2023).

Consequently, the advancement of targeted methanogenesis inhibitors and functional feed additives through regulatory approval pathways and safety evaluations has resulted in an increasing alignment between methane mitigation and feed-efficiency objectives and innovation in microbiome-directed feed additives and management, which was initially motivated by the necessity to reduce antibiotic reliance (Kelly and Kebreab, 2023).

### ANTIMICROBIAL RESISTANCE (AMR) MITIGATION

The fight against AMR is intricately linked to microbial ecology. Routine antibiotic use alters the gut and rumen resistome, favoring ARG (antimicrobial resistance gene) enrichment and horizontal transfer across commensals, pathogens, and environmental reservoirs. Metagenomic surveillance of livestock resistomes has revealed distinct ARG hotspots in farm effluents and manure-amended soils (Kraemer *et al.*, 2019). Policies that integrate microbiome endpoints into AMR monitoring, alongside stewardship measures and alternatives, such as probiotics or vaccines, may therefore reduce resistance pressure while safeguarding productivity (WHO, 2022).

The European Union's ban on antibiotics as growth-promoting feed additives, fully implemented on January 1, 2006, was a major policy action aimed at reducing the emergence of AMR linked to sub-therapeutic antibiotic use in livestock production. The ban eliminated the routine use of low-dose antibiotics to enhance growth and feed efficiency, due to concerns that such practices contribute to the development and spread of resistant bacteria in animals and humans (Pugh, 2002). This regulatory shift stimulated research into non-antibiotic alternatives that support animal health and productivity, including natural feed additives, probiotics, enzymes, and bioactive compounds that can modulate gut microbiota without promoting resistance (Millet and Maertens, 2011). Furthermore, the focus on reducing AMR coincided with growing research on enteric methane mitigation feed additives, which also target microbial pathways in the rumen to reduce methane emissions. The drive for sustainable and safe feed solutions has thus expanded the innovation landscape, encouraging the development and authorization of anti-methanogenic feed additives that are both environmentally beneficial and aligned with public health goals. The EU's precautionary stance has since been mirrored by other countries adopting similar restrictions on antibiotic growth promoters, reinforcing the global shift towards AMR-safe and climate-friendly feed additive technologies (Durmic *et al.*, 2025; Liu *et al.*, 2025).

### ANIMAL HEALTH, FOOD SAFETY AND ZONOSIS PREVENTION

Microbiome stewardship can help reduce zoonotic spillover risk. Destabilized gut or respiratory microbiota in livestock may increase pathogen shedding and transmission potential. For example, nasal microbiome profiling has shown predictive power for bovine respiratory disease cases, with higher prevalence of *Mannheimia* and *Mycoplasma* in affected cattle (Centeno-Martínez *et al.*, 2022). Stabilizing host microbiomes through nutrition, probiotics, or reduced antibiotic dependence could thus lower the probability of spillover at human–animal–environment interfaces. The OH JPA's mandates include strengthening capacity for zoonotic disease prevention and improving food-safety risk management across animal production and supply chains (“One Health Joint Plan of Action”).

### GOVERNANCE, SURVEILLANCE AND DATA SYSTEMS INTEGRATION

The OH JPA outlines six interconnected action paths, encompassing the enhancement of One Health capacities, integrated surveillance, and environmental health monitoring. Microbiome interventions can be integrated into these systems by offering novel metrics such as microbiome composition, fermentation efficiency, emission intensity, and health/resilience indicators for national and international monitoring frameworks. The implementation of microbiome-based practices can be facilitated through technical

support, capacity development, and policy guidance provided by FAO/WOAH/WHO, as outlined within the coordination and institutional development pathways of the OH JPA (“One Health Joint Plan of Action”).

Machine learning (ML) and predictive modeling offer practical frameworks for synthesizing microbiome, host, diet, and environmental variables into decision-relevant outputs. Regression and ensemble-based ML methods have been successfully implemented in the context of methane mitigation to forecast methane emissions from rumen microbiome profiles. Additionally, these methods have been employed to identify microbial taxa and functional signatures with biomarker capability (López-García *et al.*, 2022).

In a broader sense, predictive models facilitate a variety of high-value applications, such as: (i) predicting microbiome assembly trajectories in response to dietary transitions or climate stressors; (ii) identifying early-warning microbial signatures associated with metabolic disorders or dysbiosis; (iii) modeling the transmission dynamics of pathogens and AMR across animal–environment interfaces; and (iv) estimating emissions intensity under alternative feeding or management strategies (Królczewska *et al.*, 2023). Nevertheless, it is imperative to employ meticulous and rigorous framing. External validation of ML models is necessary to guarantee generalizability across a variety of herds, geographic regions, and production systems. These models should be interpreted as probabilistic decision-support instruments rather than deterministic outputs. This is of particular significance due to the fact that the relationships between microbiomes and phenotypes are extremely context-dependent and are significantly influenced by environmental conditions, host genetics, and diet (Morgavi *et al.*, 2023).

## Challenges and future directions

The ruminal microbiome is particularly important for making enteric methane; however, there are still numerous unclear connections between the host, bacteria, nutrition, and climate. Variation across microbiome studies makes it hard to put effective strategies into action (Frazier *et al.*, 2024a, 2024b). Long-term feedback is unclear. A recent review highlights the vital role of the ruminal microbiome; however, in extreme environments, the factors influencing its stability remain unclear (Guo *et al.*, 2024a, 2024b).

It is also not clear how interventions that lower methane levels affect the host–microbe ecology. This is because shifting methanogen populations could lead to novel digestive phenotypes (Saborio-Montero *et al.*, 2021). Experts also say integrating microbial processes in climate models is hard: “completely knowing how climate change and bacteria affect each other is a big problem” (“The Role of Microbes in Mediating Methane Emissions”).

The fact that there are no standard ways to sample the rumen and analyze microbiomes is a big technological problem. Different collecting methods (rumen cannula, stomach tube, or post-slaughter grab) and preservation methods can give different community profiles (Martinez-Fernandez *et al.*, 2019). But even when standard approaches are followed, datasets often do not have important metadata. According to Ortiz-Chura *et al.* (2024), who looked at 47,000 ruminant samples, over 40% were missing the essential metadata, such as age, breed, sex, etc., which limits its reusability. Table 3 outlines the major challenges in the microbiome-livestock-climate research along with possible solutions to address them.

The high financial and time demands of regulatory procedures often slow down the adoption of innovative farming practices (Subedi *et al.*, 2022). Gene editing of rumen archaea or cattle genomes, for instance, is promising but faces different standards around the world. Some nations do not apply GM rules to certain CRISPR modifications, while others like Europe do (Kupferschmidt, 2018).

In short, ethical acceptability, safety rules, economic incentives, and knowledge transfer all present problems. Rules need to be made more consistent and easier to understand, and on-farm trials and extension services should show real-world advantages (Middelveld and Macnaghten, 2021).

### Recommendations for future research

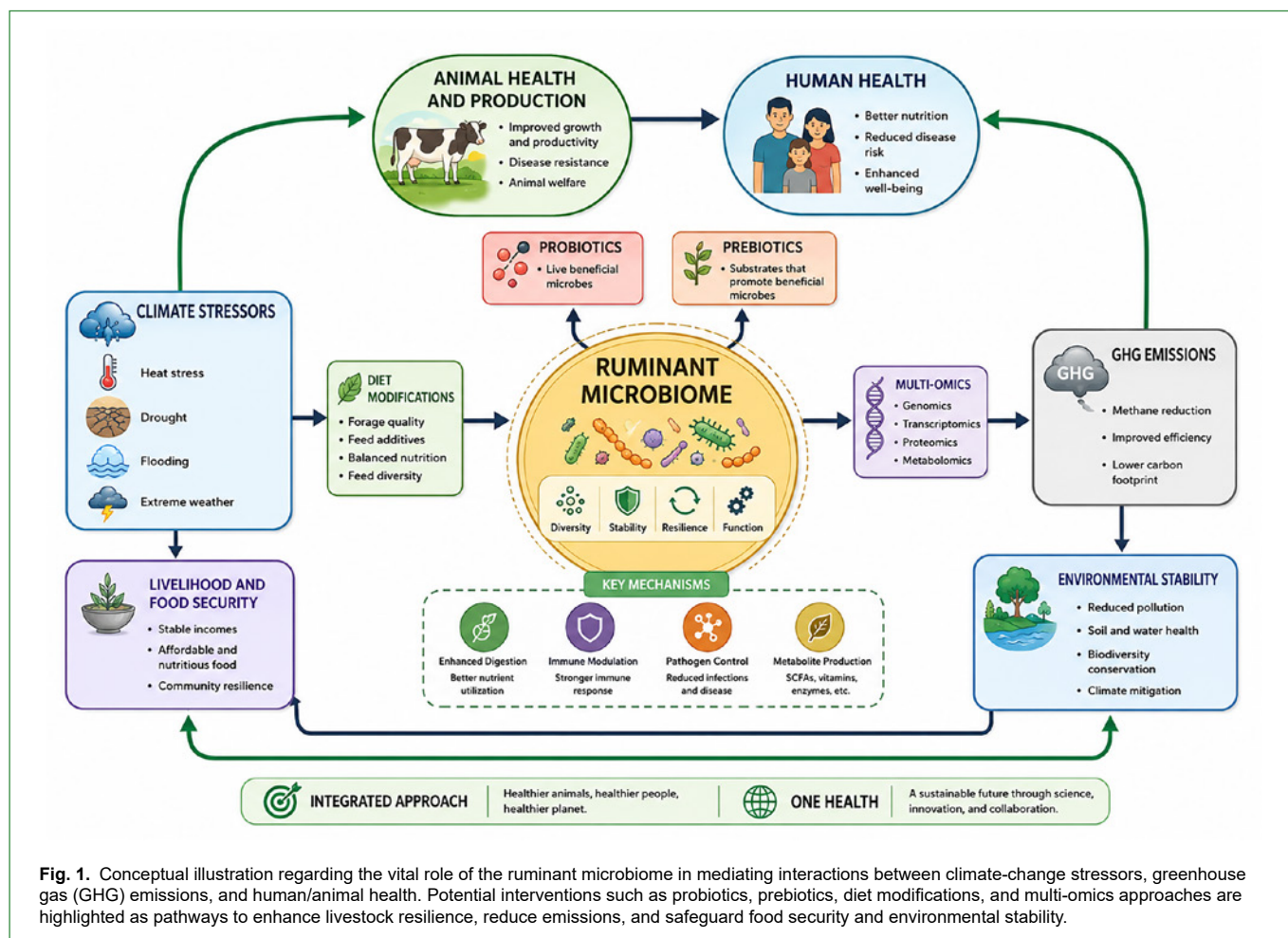
To bridge current knowledge and implementation gaps, coordinated, interdisciplinary research is essential to integrate microbial ecology with practical livestock management and policy development. Longitudinal, multi-generational studies are crucial for comprehending how diet, additives, and environmental factors impact microbiome inheritance and adaptation. Studying animals throughout various life phases and across multiple generations can elucidate the extent of microbiome trait heritability and the speed at

which these traits adapt to environmental or dietary modifications (Frazier *et al.*, 2024a, 2024b). These kinds of investigations could show features of the microbiome that can be passed down and how quickly they change. Combining ecological and evolutionary theories will make experimental design better. For instance, the “Red Queen” and “Eco-Evolutionary” frameworks imply that researchers should evaluate if switching between diverse ways of reducing the effects of microbes (such as changing diets or using intermittent inhibitors) causes them to adapt or stay stable (Bonachela *et al.*, 2017). This review presents a conceptual framework illustrating the role of the ruminant microbiome in mediating interactions between climate-change stressors, greenhouse gas (GHG) emissions, and human and animal health (Fig. 1).

In practical terms, this involves concurrently assessing methane yield, fiber digestibility, and feed efficiency to determine potential trade-

**Table 3.** Key Challenges and proposed solutions for microbiome-livestock-climate research.

Challenge area	Specific issues	Recommended solutions	References
Knowledge gaps	Unclear long-term host–microbiome–climate feedback	Multi-generation, longitudinal studies	Frazier <i>et al.</i> (2024a, 2024b); Wang <i>et al.</i> (2024a, 2024b)
Standardization	Variable sampling protocols, bioinformatic methods	Development of standardized protocols	Woodhams <i>et al.</i> (2020)
Regulatory and ethical	Genetically Modified Organisms (GMO) concerns, regulatory delays, public acceptance	Clear policy frameworks, transparent communication	Casadevall and Pirofski (2015); Joe (2022)
Practical adoption barriers	Economic viability, farmer acceptance, scalability	Economic modeling, stakeholder engagement	Liu <i>et al.</i> (2023); Omondi <i>et al.</i> (2024)



**Fig. 1.** Conceptual illustration regarding the vital role of the ruminant microbiome in mediating interactions between climate-change stressors, greenhouse gas (GHG) emissions, and human/animal health. Potential interventions such as probiotics, prebiotics, diet modifications, and multi-omics approaches are highlighted as pathways to enhance livestock resilience, reduce emissions, and safeguard food security and environmental stability.

offs between emission mitigation and productivity outcomes. Spatial ecology perspectives should likewise be embraced: Treating each animal as a dynamic ecological “patch” allows for the assessment of methanogen recolonization following suppression and the determination of whether hydrogenotrophic niches are occupied by alternative microbial populations (McGovern *et al.*, 2017). Advanced meta-omics and modeling are particularly important on the technical side. A new review says that combining metagenomics, metatranscriptomics, metaproteomics, and metabolomics can help find the microbial genes, pathways, proteins, and metabolites that are involved in producing methane (Zhao *et al.*, 2024).

Working with agricultural economics and policy academics can help make sure that modern technologies fit with what farmers need and what the climate needs. One new area of research is connecting rumen microbiome studies with global models of greenhouse gases, including Earth system models. The American Academy of Microbiology recently talked about how important this kind of work is: we can only completely understand how livestock and climate affect each other by “explicitly including microbial processes into Earth system models” (Tricarico *et al.*, 2022). By solving these problems, future research can use the ruminant microbiome in a way that is good for society and the environment without hurting the productivity of cattle.

## Conclusion

Microbiomes are increasingly recognized as pivotal allies in helping agricultural ecosystems adapt to the mounting pressures of climate change. In plants and soils, diverse microbial groups support hosts in coping with abiotic stresses, improving nutrient acquisition, and maintaining ecosystem stability under conditions of heat and drought (Addison *et al.*, 2024). Substantial evidence now shows that the organization and activities of microbial consortia are closely tied to both ecosystem resilience and host stress tolerance, highlighting microbiomes as essential components of climate-smart farming and livestock production.

In the livestock sector, however, challenges remain. Ruminants alone contribute nearly 80% of livestock-associated greenhouse gas emissions, primarily through methane release from cattle and sheep (Clemmons *et al.*, 2019). Addressing this burden requires moving beyond reductionist approaches. While studies of single microbial taxa or individual omics layers have been informative, they fall short of capturing the intricate web of host–microbe–environment interactions (Wadood *et al.*, 2025). Emerging integrative strategies that combine metagenomic, transcriptomic, metabolomic, and host genetic data are beginning to reveal how microbes influence critical processes such as feed digestion and immune function. Applying such systems biology frameworks holds promise for advancing selective breeding programs, improving animal health, and strengthening the resilience of livestock systems (Choudhary *et al.*, 2024).

The convergence of microbiome science and climate resilience research presents both an opportunity and a responsibility. Microbial communities offer innovative avenues to safeguard livestock and crops against climatic stressors, but their potential can only be realized through holistic, multi-omics-driven research, long-term field validation, and cross-disciplinary knowledge integration. Harnessing microbiomes at the system level may well determine the future sustainability, productivity, and climate resilience of global agriculture.

## CONSENT FOR PUBLICATION

This review article does not include any identifiable images or personal information of human participants. Therefore, consent for publication is not applicable.

## CONFLICT OF INTEREST

The authors declare that they have no competing interests or conflicts of interest relevant to this manuscript.

## ETHICS STATEMENT

Not applicable.

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## AUTHOR CONTRIBUTIONS

SMB was the major contributor to prepare the manuscript. AU provided her input in the manuscript by reviewing, adding data and corresponding for the publication. HSB proofread the whole manuscript and changed the manuscript formatting according to journal guidelines. All authors read and approved of the final manuscript.

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## DATA AVAILABILITY

This article does not contain data.

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