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Gastrointestinal microbiome–nutrition interactions in livestock: Linking feed chemistry, microbial metabolism, host physiology and productivity with an Indian perspective

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ABSTRACT

The gastrointestinal microbiome has emerged as a major biological determinant of nutrient utilization, animal health, feed efficiency and productive performance. Livestock do not digest feeds through host enzymes alone; microorganisms transform dietary substrates into volatile fatty acids, short-chain fatty acids, microbial protein, bile-acid derivatives, indole compounds and other metabolites that can influence epithelial integrity, immunity and systemic metabolism. The nutritional contribution of this ecosystem differs between ruminants and monogastrics. In ruminants, the rumen microbiome is central to the conversion of plant cell-wall carbohydrates and nitrogen into fermentation products and microbial biomass. In pigs and poultry, intestinal microbiota contribute mainly through hindgut fermentation, nutrient salvage, epithelial nutrition, immune regulation and pathogen ecology. Modern sequencing and metabolomics technologies have shifted the field from descriptive lists of taxa toward functional interpretation of microbial pathways and metabolites. Increasing evidence suggests that feed efficiency is an emergent property of diet–microbiome–host interactions rather than a simple feed-intake-to-output ratio. Nutritional strategies including fibre management, probiotics, prebiotics, synbiotics, postbiotics, phytochemicals, enzymes, fermented feeds and selected methane-mitigating additives can modulate microbial functions, although effects depend strongly on species, diet, dose, age, genotype and production environment. This is particularly relevant to India, where livestock feeding frequently depends on crop residues, cereal straws, green forages and agro-industrial by-products of variable quality. Indian metagenomic studies in cattle and buffaloes have demonstrated that diet can reshape rumen microbial composition and carbohydrate-active enzyme potential. Future research should integrate feed chemistry, microbial genes and transcripts, metabolite profiles, host phenotype and environmental measurements through longitudinal field studies. Microbiome-informed precision nutrition may therefore provide a route to more efficient, resilient and sustainable livestock production.

Keywords: Gastrointestinal microbiome, Rumen microbiome, Animal nutrition, Feed efficiency, Microbial metabolites, Probiotics, Prebiotics, Postbiotics, Methane, Precision nutrition, Indian livestock

1. Introduction

Animal nutrition has traditionally focused on feed composition, nutrient requirements, digestibility and the quantity of nutrients ultimately available to the animal. These variables remain fundamental, but they do not fully explain the biological conversion of feed into milk, meat, eggs, growth or reproductive output. The gastrointestinal tract contains a densely populated and metabolically active ecosystem in which bacteria, archaea, fungi, protozoa and viruses interact with dietary substrates and the host. Collectively, these microorganisms provide enzymatic activities that complement host digestion and generate metabolites capable of altering energy supply, nutrient absorption, intestinal barrier function, immune activity and systemic metabolism (Tardiolo *et al.*, 2025; Weimer, 2022; Palmonari *et al.*, 2024; Qi *et al.*, 2024) [1, 2, 3, 4].

The distinction between microbiota and microbiome is useful in this context. *Microbiota* refers primarily to the microorganisms inhabiting a defined ecological niche, while *microbiome* is generally used to encompass the microorganisms together with their collective genetic and functional potential (Tardiolo *et al.*, 2025) [1]. This functional perspective is particularly important in livestock because microbial communities can differ substantially among animals receiving similar diets, whereas some metabolic functions remain conserved because multiple taxa can perform overlapping biochemical roles.

The ruminant digestive system illustrates the nutritional significance of these interactions most clearly. The rumen provides an anaerobic fermentation chamber in which microbial consortia degrade structural carbohydrates, ferment starch and soluble carbohydrates, transform nitrogen and carry out hydrogen transfer. The products include acetate, propionate, butyrate, microbial protein and gases. In monogastric species such as pigs and poultry, host enzymatic digestion accounts for a larger proportion of nutrient absorption, yet microbial fermentation in the distal gut contributes to fibre utilization, SCFA generation, barrier maintenance, immune regulation and metabolic signalling (Tardiolo *et al.*, 2025; Jha *et al.*, 2019) [1, 5]. An important shift in recent literature is the movement from asking which microbial taxa are present toward asking which microbial functions are active and which metabolites mediate host phenotypes. A 2026 perspective in *Frontiers in Physiology* argues that feed efficiency should be viewed as an emergent property of diet–microbiome–host interactions, highlighting microbial mediation of nutrient transformation, methane loss, epithelial stability and inflammation (Ogwu *et al.*, 2026) [6]. This framework is highly relevant to practical nutrition because microbial functions are potentially modifiable through feed ingredients and management even when host genetics are fixed.

Abbreviation	Meaning
CAZymes	Carbohydrate-active enzymes
FCR	Feed conversion ratio
GIT	Gastrointestinal tract
H ₂	Hydrogen
N ₂ O	Nitrous oxide
NSP	Non-starch polysaccharides
RFI	Residual feed intake
SCFA	Short-chain fatty acid
SARA	Subacute ruminal acidosis
VFA	Volatile fatty acid

The Indian livestock context provides an especially valuable setting for this research. Feeding systems vary widely in forage availability, crop residues, agro-industrial by-products, concentrate use, season, climate and management intensity. Indian metagenomic studies in Mehsani and Jaffrabadi buffaloes and in crossbred cattle have already shown that diet can alter microbial composition and the repertoire of carbohydrate-active enzymes (Parmar *et al.*, 2014; Singh *et al.*, 2014; Jose *et al.*, 2017; Kala *et al.*, 2017) [7, 8, 9, 10]. These findings create an opportunity to connect conventional feed evaluation with microbial functional assessment.

The integrated feed–microbiome–host framework is summarized in Figure 1.

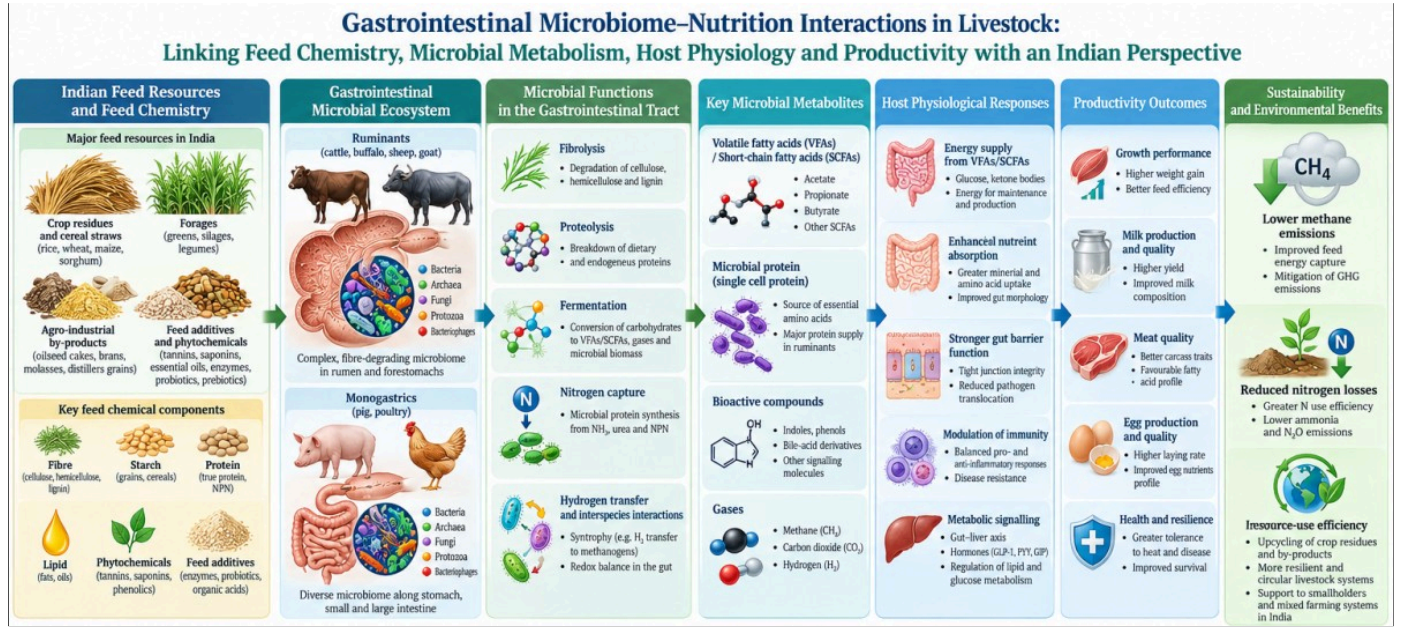


Figure 1. Integrated feed–microbiome–host framework linking feed chemistry, microbial metabolism, host physiology, livestock productivity and environmental outcomes.

Source: Conceptual schematic prepared for this review based on the cited literature.

2. Literature search and scope

This manuscript was developed as a structured narrative review with emphasis on peer-reviewed literature indexed in PubMed and major scientific publisher databases. Recent literature published during 2024–2026 was preferentially considered for emerging concepts, while earlier landmark studies were retained when they established foundational evidence. Search concepts included combinations of livestock gut microbiome, rumen microbiome, animal nutrition, feed efficiency, microbial metabolism, diet–microbiome interactions, SCFA, microbial protein, methane mitigation, probiotics, prebiotics,

postbiotics, metagenomics, metabolomics, precision nutrition, Indian cattle, Indian buffalo and crop residues.

The purpose was not to perform a quantitative *meta*-analysis, but to synthesize mechanistic relationships and identify translational gaps. Particular emphasis was placed on studies that connected microbial profiles to measurable animal outcomes rather than on studies reporting microbiome composition alone.

3. The gastrointestinal microbiome as a nutritional organ

The gastrointestinal microbiome can be considered a functional nutritional organ because microorganisms contribute enzymes, metabolic pathways and signalling molecules unavailable to the host alone. This concept is particularly strong in ruminants, where the rumen micro

biome determines how much of the plant cell-wall carbohydrate pool becomes metabolically useful to the animal. In monogastrics, the microbiome occupies a more distal role but remains important in nutrient salvage and gut homeostasis (Tardiolo *et al.*, 2025; Jha *et al.*, 2019) [1, 5].

Bacteria constitute the best-characterized component of livestock microbiomes, but archaea, anaerobic fungi, protozoa and bacteriophages are biologically relevant. In the rumen, fibrolytic bacteria such as *Ruminococcus* and *Fibrobacter* participate in plant fibre degradation; anaerobic fungi help disrupt recalcitrant plant tissues; protozoa contribute to carbohydrate metabolism and microbial predation; and

methanogenic archaea consume hydrogen during methanogenesis (Weimer, 2022; Qi *et al.*, 2024; Pitta *et al.*, 2022) [2, 4, 11].

The microbial ecosystem is spatially organized. Rumen liquid, fibre-adherent communities and epithelial-associated microbes are not identical, and whole-gut studies in cattle show clear regional differences along the gastrointestinal tract. Consequently, faecal samples may be useful for some questions but should not automatically be interpreted as a complete representation of the upstream rumen or small-intestinal microbiome (Akanmu, 2026) [12].

The principal microbial groups and their nutritional functions are summarized in Table 1.

Table 1. Major microbial groups in the livestock gastrointestinal tract and their nutritional functions

Microbial group	Representative examples	Principal nutritional functions	Main relevance
Bacteria	<i>Ruminococcus</i> ; <i>Fibrobacter</i> ; <i>Prevotella</i> ; <i>Bacteroides</i> ; <i>Lactobacillus</i>	Fibre and starch degradation; fermentation; SCFA/VFA production; vitamin metabolism; microbial protein	Abundant in both ruminants and monogastrics
Archaea	<i>Methanobrevibacter</i> ; <i>Methanosphaera</i>	Hydrogen utilization and methanogenesis	Major in rumen; smaller role in hindgut
Anaerobic fungi	<i>Neocallimastix</i> ; <i>Piromyces</i>	Disruption and degradation of recalcitrant plant cell walls; synergy with bacteria	Important in ruminants consuming fibrous diets
Protozoa	<i>Entodinium</i> ; <i>Isotricha</i> ; <i>Diplodinium</i>	Fermentation; starch utilization; predation on bacteria; hydrogen production	Common in rumen; limited importance in monogastrics
Bacteriophages	Diverse viral communities	Regulation of bacterial populations; horizontal gene transfer	Present throughout GIT; functional importance increasingly recognized

4. Nutritional roles in ruminants and monogastrics

4.1 Ruminants: foregut fermentation

Ruminants depend heavily on microbial fermentation before host enzymatic digestion. Microbial glycoside hydrolases, carbohydrate esterases and other CAZymes hydrolyse cellulose, hemicellulose and other plant polysaccharides. The resulting soluble carbohydrates enter microbial fermentation pathways and generate VFAs, microbial biomass and gases (Weimer, 2022; Qi *et al.*, 2024) [2, 4].

The nutritional implications are profound. Acetate contributes to energy metabolism and lipogenesis; propionate is a major gluconeogenic precursor; butyrate supports epithelial metabolism; and microbial biomass provides a substantial source of absorbable amino acids after passage to the small intestine. At the same time, methanogenesis represents a loss of feed-derived energy and redirects hydrogen away from alternative sinks (Pitta *et al.*, 2022; Kú-Vera *et al.*, 2020) [11, 13].

4.2 Monogastrics: hindgut fermentation and signalling

Pigs and poultry absorb much of their starch, fat and protein before the large intestine. Nevertheless, resistant starch, non-starch polysaccharides and other fermentable substrates can reach distal regions where microbiota produce SCFAs and other compounds. Butyrate is particularly relevant to epithelial energetics and barrier regulation, whereas microbial transformation of amino acids, bile acids and other molecules creates signalling pathways linking the gut to systemic physiology (Jha *et al.*, 2019; Lai *et al.*, 2026; Xiong, 2025) [5, 14, 15].

This distinction means that the same dietary intervention should not be expected to act through identical microbial mechanisms in all livestock. In ruminants, the primary endpoint may be fermentation efficiency and microbial protein supply; in monogastrics, outcomes may be driven more strongly by intestinal barrier integrity, pathogen ecology, immune regulation and metabolite signalling.

The contrasting nutritional pathways in ruminants and monogastrics are illustrated in Figure 2.

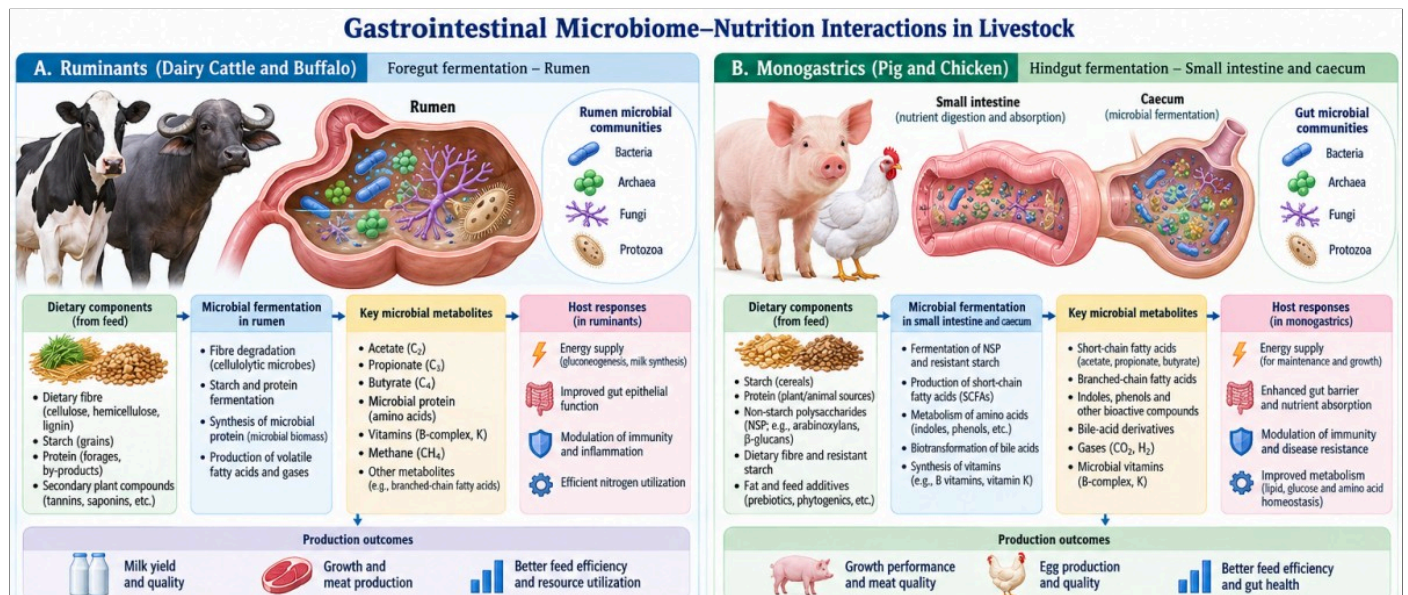


Figure 2. Comparative microbiome-mediated nutritional pathways in ruminant and monogastric livestock, highlighting fermentation sites, microbial functions, metabolites and host responses.

Source: Conceptual schematic prepared for this review based on the cited literature.

5. Feed as a major determinant of microbial community structure

Diet is among the strongest controllable determinants of gastrointestinal microbial ecology. By changing substrate availability, pH, osmotic conditions, retention time, redox status and host secretions, the diet selects microorganisms and metabolic pathways that can exploit the prevailing environment (Palmonari *et al.*, 2024; Henderson *et al.*, 2015) [3, 16].

5.1 Fibre and carbohydrates

Fibre quality matters as much as fibre quantity. Cellulose, hemicellulose, pectin, resistant starch and soluble fermentable fibre support different microbial guilds and generate different metabolite profiles. In ruminants, increasing forage availability generally favours fibre-associated microbial functions, whereas rapidly fermentable starch can shift fermentation toward acid-producing pathways. When dietary fermentability exceeds the capacity of rumen buffering and epithelial adaptation, microbial shifts contribute to SARA (Zhang *et al.*, 2026) [17].

In non-ruminants, fibre should not be evaluated only through apparent digestibility. Poorly digested fibre can be biologically valuable if selectively fermented to SCFAs in the hindgut. A 2026 review emphasizes the interaction among dietary fibre, intestinal microbiota and bile-acid metabolism, extending the nutritional interpretation of fibre beyond simple fermentation (Lai *et al.*, 2026) [14].

5.2 Protein and nitrogen

In ruminants, microbial degradation of dietary protein releases nitrogenous substrates that can be incorporated into microbial protein when sufficient fermentable energy is available. Synchronizing nitrogen supply with carbohydrate fermentation can therefore improve microbial protein synthesis and reduce ammonia losses. In pigs and poultry, excess protein reaching the distal intestine can undergo microbial putrefaction and generate ammonia, amines, phenolics and other metabolites, supporting the rationale for precision protein and amino-acid nutrition.

5.3 Lipids and bioactive compounds

Dietary lipids can alter microbial membranes and fermentation pathways, while phytochemicals such as tannins, saponins, essential oils and polyphenols may selectively inhibit or stimulate microbial

groups. Their practical use requires careful dose-response assessment because strong antimicrobial activity can suppress beneficial functions along with undesirable organisms (Ntsongota *et al.*, 2025) [18].

6. Microbial metabolism: The central link between feed and performance

Microbial taxa are only an indirect indicator of biological activity. Metabolites often provide a closer mechanistic link to nutrition and host phenotype.

6.1 Volatile fatty acids and short-chain fatty acids

Acetate, propionate and butyrate are central ruminal products and important signalling molecules in the intestine. Their relative proportions depend on carbohydrate source, rate of fermentation, forage-to-concentrate ratio and other dietary factors. The goal of nutritional manipulation should therefore be productive fermentation rather than indiscriminate maximization of total fermentation (Weimer, 2022; Ogwu *et al.*, 2026) [2, 6].

6.2 Microbial protein

Microbial protein is a central bridge between rumen nitrogen and host amino-acid supply. The efficiency of microbial protein synthesis depends on fermentable energy, nitrogen availability, ruminal pH, passage rate and microbial growth efficiency. Omics-based approaches are being explored because conventional estimates of microbial protein flow contain important uncertainty (Lima *et al.*, 2023) [19].

6.3 Bile acids and lipid signalling

Intestinal microbes deconjugate and otherwise transform bile acids. These modified bile acids can influence receptors involved in glucose metabolism, lipid metabolism and immune signalling. This helps explain why dietary fibre and microbial metabolism can affect physiological processes beyond the gut lumen (Lai *et al.*, 2026; Xiong, 2025) [14, 15].

6.4 Tryptophan and indole metabolites

Gut microorganisms convert tryptophan into indole and related compounds that can interact with host receptors such as the aryl hydrocarbon receptor. These pathways have potential effects on epithelial integrity and immune homeostasis. Recent reviews in swine nutrition identify microbial tryptophan metabolism as an emerging nutritional target, while emphasizing the need for better causal evidence (Wen, 2026) [20].

6.5 Methane and hydrogen transfer

In ruminants, methanogenic archaea act as hydrogen sinks. This interaction stabilizes fermentation but produces methane, representing an energetic and environmental loss. Redirecting hydrogen through alter-

native pathways is therefore a major objective of nutritional methane mitigation (Pitta *et al.*, 2022; Kú-Vera *et al.*, 2020) [11, 13].

The major microbial metabolites and their host-level implications are summarized in Table 2.

Table 2. Key microbial metabolites, nutritional pathways and their implications for livestock productivity

Metabolite/process	Major microbial source	Host-level effect	Production or sustainability relevance
Acetate (C ₂)	Fibre-fermenting bacterial pathways, including many Ruminococcus-associated pathways	Energy supply; substrate for lipid synthesis	Ruminant milk-fat synthesis and overall energy capture
Propionate (C ₃)	Starch- and fibre-fermenting bacterial pathways, including Prevotella-associated pathways	Major gluconeogenic precursor; influences energy metabolism	Growth, lactation and feed efficiency in ruminants
Butyrate (C ₄)	Fibre and resistant-starch fermentation; several Firmicutes-associated pathways	Colonocyte/epithelial energy; barrier support; signalling	Gut health, resilience and nutrient utilization
Microbial protein	Bacterial, protozoal and fungal biomass in the rumen	Major source of absorbable microbial amino acids after small-intestinal digestion	Growth, milk and meat protein production; nitrogen-use efficiency
Indoles and related aromatic metabolites	Microbial tryptophan metabolism	Immune and epithelial signalling through host receptors	Gut resilience and metabolic regulation; emerging target
Bile-acid derivatives	Microbial deconjugation and transformation of primary bile acids	Modulation of lipid, glucose and immune signalling	Nutrient metabolism and intestinal homeostasis
Methane (CH ₄)	<i>Methanogenic archaea</i> using H ₂ and CO ₂	Represents energetic loss from ruminant fermentation	Environmental greenhouse-gas emission; target for mitigation
Ammonia (NH ₃)	Protein deamination and urea-related microbial processes	Required substrate at controlled levels for microbial protein synthesis; excess is lost	Nitrogen-use efficiency and environmental nitrogen losses

7. Gut microbiome and feed efficiency

Feed efficiency is a critical economic and environmental trait. FCR and RFI are useful but largely describe outcomes rather than underlying mechanisms. They do not directly account for microbial enzyme production, fermentation stoichiometry, maintenance costs associated with intestinal inflammation, or energy lost through methane and nitrogen excretion (Ogwu *et al.*, 2026; Cantalapiedra-Hijar *et al.*, 2018) [6, 21].

Studies in cattle have identified differences in rumen microbiota between animals with divergent feed efficiency. Importantly, microbial associations with efficiency are often population- and diet-dependent. The same genus may correlate with efficiency in one system and not in another because the actual causal variable may be a pathway or metabolite rather than the taxon itself (Myer *et al.*, 2015; Li *et al.*, 2019) [22, 23].

Host genetics also contributes. Large cattle cohorts have demonstrated heritable microbial features and associations between microbial traits and feed efficiency, supporting the idea that host genetics can shape microbial ecology (Li *et al.*, 2019) [23]. A later direction of research is therefore co-selection of host and microbial traits rather than independent treatment of nutrition and breeding.

Poultry studies provide a parallel example. In laying hens with divergent residual feed intake, caecal microbial differences were observed, but microbial–efficiency relationships changed with diet. This finding cautions against searching for a universal microbial signature of feed efficiency (Bernard *et al.*, 2024) [24].

8. Microbiome, gut barrier, immunity and animal health

Productive efficiency cannot be separated from gut health. A damaged intestinal barrier increases microbial translocation and inflammatory stimulation, potentially redirecting nutrients toward immune maintenance

instead of growth, lactation or reproduction. Microbial metabolites including butyrate can support epithelial cells and influence inflammatory signalling (Mann *et al.*, 2024) [25].

In poultry, probiotics have been associated with changes in microbial ecology, intestinal morphology, barrier-related gene expression and immune responses, although effects are strain-, dose- and environment-dependent (Naeem *et al.*, 2025) [26]. In pigs, the weaning transition is a particularly sensitive period because dietary and environmental changes occur simultaneously and can destabilize the intestinal ecosystem (Wang *et al.*, 2025) [27].

9. Nutritional strategies for microbiome modulation

9.1 Probiotics

Probiotics are live microorganisms administered to confer a health benefit. Lactobacilli, Bacillus species and *Saccharomyces products* have been widely studied. Potential mechanisms include competitive exclusion, antimicrobial metabolite production, immune modulation, barrier support and changes in fermentation. Consistency across trials remains a limitation because strain, viability, dose and diet matter (Naeem *et al.*, 2025) [26].

9.2 Prebiotics

Prebiotics are selectively utilized substrates that benefit the host. Fructo-oligosaccharides, inulin, mannan-oligosaccharides and related oligosaccharides can alter microbial fermentation, although the response depends on the pre-existing community and chemical structure of the substrate.

9.3 Synbiotics

Synbiotics combine a live microbial component and a substrate intended to support beneficial microbial activity. The combined response should be tested against each component individually before concluding that a true synergistic effect exists.

9.4 Postbiotics

Postbiotics have gained attention because they deliver inanimate microorganisms or microbial constituents rather than requiring the survival of a live microorganism. A 2026 systematic review in sows and piglets found promising effects on gut health and performance while emphasizing heterogeneity among preparations and the still limited evidence base (Polimeni *et al.*, 2026) [28].

9.5 Phytogetic feed additives

Tannins, saponins, essential oils and polyphenols may selectively alter microbial metabolism, oxidative status and immune activity. Their effects are dose-sensitive and should be evaluated jointly for perfor-

mance, digestibility and microbiome outcomes rather than solely for antimicrobial activity (Ntsongota *et al.*, 2025) [18].

9.6 Enzymes, organic acids and fermented feeds

Exogenous enzymes modify substrate flow into microbial ecosystems; organic acids can alter intestinal conditions and pathogen ecology; fermented feeds may pre-process nutrients and alter the microbial inoculum entering the gut. These technologies can produce useful responses but require control of feed matrix, fermentation quality and inclusion rate.

The principal microbiome-modulating approaches and their research considerations are summarized in Table 3.

Table 3. Practical microbiome-modulating approaches and research considerations

Strategy	Primary purpose	Potential benefit	Key limitation or research question
Probiotics	Introduce functional live microorganisms	Gut barrier support; pathogen exclusion; fermentation modulation	Strain-, dose- and diet-specific responses
Prebiotics	Provide selective microbial substrates	SCFA production and beneficial microbial selection	Depends on baseline microbiome and substrate chemistry
Synbiotics	Combine microbes and supportive substrates	Potential complementary or synergistic effects	True synergy must be experimentally demonstrated
Postbiotics	Deliver inanimate microbes or microbial constituents	Stability; immune and epithelial modulation	Heterogeneous preparations; standardization needed
Phytogenics	Selectively modulate microbial metabolism	Potential antimicrobial, antioxidant and immunomodulatory actions	Dose-response and consistency remain major issues
Enzymes	Change digestible substrate flow	Improved nutrient release and altered microbial substrate supply	Depends strongly on feed matrix and enzyme specificity
Methane inhibitors	Reduce methanogenic energy loss	Lower methane intensity and potentially improved energy retention	Must maintain fermentation and animal performance
Microbiome-informed precision feeding	Match intervention to microbial function	Potential individualized feed efficiency and resilience	Requires affordable biomarkers and external validation

10. Early-life microbiome programming

The microbiome of newborn and young animals is dynamic. Microbial colonization, dietary transition and immune maturation occur simultaneously, creating a developmental window in which nutrition may influence the trajectory of the microbial ecosystem (Song *et al.*, 2026; Animal Microbiome, 2026) [29, 30].

In calves, lambs and kids, colostrum, maternal contact, environmental exposure and the introduction of starter feeds shape microbial succession and rumen development. A 2026 review concluded that early interventions may be more effective than interventions in the relatively stable adult microbiome, but also noted that long-term mechanisms remain incompletely understood (Song *et al.*, 2026) [29].

Early-life programming should therefore be approached as a resilience strategy rather than a guarantee of permanent microbial remodeling. Longitudinal research should ask whether early interventions generate durable improvements in feed efficiency, disease resistance, methane intensity and productivity across later life stages.

11. Host genetics and microbiome interactions

Host genotype influences the gastrointestinal environment through feed intake, rumen and intestinal physiology, epithelial responses, immune phenotype and metabolism. The microbiome in turn produces metabolites that can modify host physiology. This bidirectional interaction provides a biological basis for host-microbiome co-optimization (Li *et al.*, 2019; Marie-Etancelin *et al.*, 2026) [23, 31].

The discovery of heritable microbial features in cattle is particularly important because it suggests that some microbial traits may be incorporated into breeding objectives. However, microbial phenotypes are highly context-dependent and may change with diet and management. Routine selection should therefore await stronger cross-population validation and standardized phenotyping.

12. Microbiome, methane and sustainability

Methanogenic archaea use hydrogen and carbon dioxide to generate methane. The pathway is an integral component of anaerobic rumen fermentation but also represents loss of feed-derived energy. Nutritional methane mitigation aims to reduce methanogenesis or redirect hydrogen to alternative sinks without compromising animal productivity (Pitta *et al.*, 2022; Kú-Vera *et al.*, 2020) [11, 13].

Strategies include dietary lipids, plant secondary metabolites, nitrate, selected hydrogen sinks and methane-inhibiting compounds such as 3-nitrooxypropanol. Meta-analytic evidence indicates that several diet-based strategies can reduce methane, but the size of the response varies with animal, diet and experimental system (PubMed Central, 2024) [32].

Indian buffalo research is especially relevant. A recent study of a composite feed additive reported reductions in enteric methane together with changes in archaeal, bacterial and fungal profiles and improvements in nutrient utilization, illustrating the potential of combined microbial and nutritional approaches under buffalo production conditions (Paul *et al.*, 2026) [33].

13. Indian livestock perspective

Indian livestock systems present a distinct combination of nutritional variability, climatic stress and heterogeneous resource availability. Crop residues and cereal straws may form a major component of cattle and buffalo diets, especially where high-quality forage is seasonally limited. From a microbiome perspective, these feeds represent complex polysaccharide substrates whose effective utilization depends strongly on microbial fibrolytic capacity.

Indian crossbred cattle fed finger millet straw have been used to characterize rumen microbial fibrolytic enzyme repertoires, demonstrating that metagenomic approaches can reveal enzymatic potential that conventional proximate analysis cannot (Jose *et al.*, 2017) [9].

Mehsani buffalo studies have similarly shown strong effects of diet on rumen microbial community structure and functional classification, while work in Jaffrabadi buffaloes has demonstrated diet-related changes in microbial and CAZyme profiles (Parmar *et al.*, 2014; Singh *et al.*, 2014; Kala *et al.*, 2017) [7, 8, 10]. These studies provide an important country-specific foundation for microbiome-informed feed evaluation.

For Indian animal nutrition, an especially attractive framework is to characterize feed resources through four linked layers: chemical composition, *anti*-nutritional factors, fermentability and microbial response. Such a system could help identify which crop residues, agro-industrial by-products and local forages are likely to generate productive microbial fermentation rather than merely classify them according to crude nutrient content.

Indigenous cattle and buffaloes also deserve more attention. Their adaptation to local climates, feed resources and management conditions may be partly related to stable host–microbe interactions.

14. Omics technologies for microbiome-based nutrition

16S rRNA sequencing is useful for describing bacterial community structure but does not directly measure metabolic activity. Shotgun metagenomics provides broader functional information by characterizing microbial genes, while metatranscriptomics measures expressed RNA and metaproteomics identifies microbial proteins. Metabolomics measures the chemical outputs that arise from host and microbial metabolism (Qi *et al.*, 2024; Lima *et al.*, 2023) [4, 19].

The greatest interpretive value may come from integrating these layers. Metagenomics identifies pathway capacity; metatranscriptomics indicates which pathways are active; metaproteomics identifies enzymes; metabolomics shows the resulting chemical products; and host phenotype determines whether the response is biologically meaningful.

Recent methodological reviews caution that microbiome analysis faces important issues involving sampling site, compositionality, contamination, batch effects and the distinction between relative and absolute abundance (Akanmu, 2026) [12]. These issues are especially important when comparing field animals across breeds and seasons.

15. Microbiome-informed precision animal nutrition

Precision nutrition traditionally matches nutrient supply to the requirements of the individual animal or production group. A next-generation approach could add microbial function as another layer of personalization. An animal could be characterized by host genotype, feed intake, production stage, microbial profile, metabolite pattern, health status and environmental exposure before selecting a diet or feed additive.

For example, two cows consuming the same ration may differ in fibrolytic activity, microbial protein synthesis or methane formation. A microbial intervention that works in one animal may have little effect in another because the ecological starting point is different. Thus, the future target should be a functional state—such as efficient fibre degradation, productive SCFA formation, improved nitrogen capture or reduced methanogenesis—rather than a universal bacterial genus (Ogwu *et al.*, 2026) [6].

Machine learning offers a potential route for integrating multi-omics with feed composition, animal phenotype and farm-level data. However, external validation across breeds, diets, seasons and commercial farms is essential before predictive models can be translated into routine feeding decisions.

16. Research gaps and challenges

Causality. Many microbiome studies remain observational. Demonstrating that a microorganism or pathway causes a production phenotype requires intervention experiments, targeted manipulation or mechanistic validation.

Sampling and spatial heterogeneity. Microbial profiles differ markedly along the gastrointestinal tract. Rumen fluid, fibre-associated microbes, epithelial communities and faeces answer different biological questions (Akanmu, 2026) [12].

Compositionality. Relative-abundance sequencing data can produce misleading conclusions when one organism changes and others consequently appear to change. Absolute quantification is increasingly important.

Context dependence. Diet, breed, age, health status, management and climate can modify microbial responses. A universally applicable microbial biomarker remains unlikely without strong cross-environment validation.

Product standardization. Probiotic and postbiotic products can differ in strain identity, viability, composition and manufacturing, limiting cross-study comparison (Polimeni *et al.*, 2026) [28].

Indian evidence gap. Although Indian buffalo and cattle studies are increasingly informative, large longitudinal datasets across species, regions, production systems and seasons are still needed.

Field translation. Multi-omics methods remain expensive and technically demanding. Low-cost biomarkers that can be deployed under field conditions will be necessary for practical microbiome-informed feeding.

17. Future research priorities

Future work should prioritize longitudinal, mechanistic studies that simultaneously measure feed chemistry, microbial function, metabolite production, animal performance and environmental outcomes. The research question should move from “Which taxa differ?” to “Which microbial function changes, what metabolite does it produce, and does that change improve an actionable animal trait?”

Promising areas include early-life programming, host–microbiome genetics, microbiome-guided methane mitigation, microbial protein optimization, Indian crop-residue utilization, agro-industrial by-product valorization and low-cost precision nutrition tools.

For India, multi-institutional datasets covering cattle, buffalo, sheep, goats and poultry under tropical and subtropical production conditions would be particularly valuable. Such datasets could help separate universal microbial principles from context-specific responses and support the development of regionally adapted feeding recommendations.

18. Integrative framework for livestock nutrition

The overall evidence can be represented as a systems pathway: feed chemistry determines the substrates available; microbial communities select for appropriate enzymatic and fermentation pathways; microbial metabolism generates VFAs, SCFAs, microbial protein, indoles, bile-acid derivatives and gases; these molecules alter host energy metabolism, epithelial integrity, immunity and signalling; and the combined response emerges as productivity, health, feed efficiency and environmental performance.

This framework is more informative than a taxonomy-only approach because it preserves the causal sequence and highlights where nutritional intervention can occur. It also makes it possible to integrate conventional ration formulation with modern omics without abandoning practical measures such as digestibility and animal performance.

19. Conclusion

The gastrointestinal microbiome is a functional component of the livestock nutritional system. In ruminants, it is central to fibre digestion, VFA formation, microbial protein synthesis and hydrogen transfer. In monogastrics, it contributes to hindgut fermentation, SCFA formation, epithelial maintenance, immune regulation and metabolic signalling. Across species, these activities can influence feed efficiency, growth, milk and meat production, health and environmental sustainability.

The field is moving from descriptive microbiome catalogues toward functional, metabolite-centered and multi-omics approaches. The

most useful nutritional targets will therefore be reproducible microbial functions that can be manipulated through diet and verified using animal-level outcomes. Probiotics, prebiotics, postbiotics, phytochemicals, enzymes, fermented feeds and methane-mitigating strategies each provide potential tools, but responses remain context-dependent.

Indian livestock production offers a particularly relevant setting for microbiome-informed nutrition because of diverse feed resources, widespread use of crop residues, agro-industrial by-products, buffalo production and strong environmental variation. A research program that connects feed chemistry, microbial metabolism, host physiology and field-level productivity could support more efficient use of local resources and more resilient production.

Ultimately, the value of a feed should be understood not only by what it contains, but also by how the gastrointestinal microbiome transforms it and how those microbial products are used by the animal. This perspective provides a foundation for future precision nutrition in which feed, microbes and the host are treated as parts of one biological system.

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