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Review Article

Bacteriophages in the Rumen Ecosystem: Diversity, Ecological Functions, and Implications for Ruminant Health and Production

Javier Piloni-Martini[1], Aurora Quintero-Lira[1]*, María-Guadalupe Torres-Cardona[1], J Jesús-Germán Peralta-Ortiz[1], Mario-Antonio Cobos-Peralta[2] and Verónica-Azucéna Ibarra-Medina[1]

[1]Universidad Autónoma del Estado de Hidalgo, Instituto de Ciencias Agropecuarias, Avenida Universidad #133, Col. San Miguel Huatengo, C.P. 43775, Santiago Tulantepec de Lugo Guerrero, Hidalgo, México

2Colegio de Posgraduados Montecillo Campus, México-Texcoco Highway Km. 36.5, Montecillo, Texcoco, México

***Corresponding Author:** Aurora Quintero Lira, Universidad Autónoma del Estado de Hidalgo, Instituto de Ciencias Agropecuarias, Avenida Universidad #133, Col. San Miguel Huatengo, C.P. 43775, Santiago Tulantepec de Lugo Guerrero, Hidalgo, México.

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Abstract

Background: Viruses are abundant components of the rumen microbiome, but their diversity and ecological roles remain incompletely characterized.

Objective: This narrative review synthesizes current evidence on the diversity, ecology, virus-host interactions, and potential functional roles of rumen bacteriophages, while distinguishing them from viruses that infect archaea.

Methodology: We searched PubMed/MEDLINE, Web of Science, Scopus, Google Scholar, and bioRxiv for records published from 2001 through December 2025, using combinations of terms related to the rumen, bacteriophages, viromes, metagenomics, ecology, fermentation, methane, and production. We synthesized evidence qualitatively and classified findings as experimentally demonstrated, computationally predicted, or statistically associated.

Development: The Rumen Virome Database contains 397,180 species-level viral operational taxonomic units, most of which lack close homologs in existing databases. Recent studies also report large catalogs of rumen phage genomes and computationally inferred virus-host interactions. Bacteriophages may contribute to bacterial population regulation, microbial diversification, horizontal gene transfer, and metabolic processes, while auxiliary metabolic genes have been identified mainly through genomic annotation and computational analyses. Researchers have also reported associations between virome composition and feed efficiency, milk production, and methane emissions, but causality remains unresolved.

Conclusion: The rumen virome represents a substantial and diverse component of the rumen ecosystem. Current evidence is strongest for viral diversity and statistical or computational associations, whereas direct experimental evidence for specific ecological functions and effects on animal performance remains limited. Future work should prioritize controlled infection studies, functional validation of viral genes, and longitudinal experiments linking virome dynamics with rumen physiology and animal phenotypes.

Keywords: Bacteriophages; Rumen Virome; Metagenomics; Ruminal Fermentation; Auxiliary Metabolic Genes

Abbreviations

VFAs: Volatile Fatty Acids; AMGs: Auxiliary Metabolic Genes; HGT: Horizontal Gene Transfer; RVD: Rumen Virome Database; URPC: Unified Rumen Phage Catalog; SBSEC: *Streptococcus bovis/ Streptococcus equinus* Complex

Introduction

The rumen constitutes one of the most complex anaerobic microbial ecosystems. Its microbial community comprises bacteria, archaea, anaerobic fungi, ciliated protozoa, and viruses, including bacteriophages that infect bacteria. These communities act synergistically to degrade plant structural polysaccharides such as cellulose, hemicellulose, pectins, and lignin, converting them into metabolites usable by the host, principally volatile fatty acids (VFAs), microbial protein, and B vitamins [1-4]. This symbiotic system is fundamental to ruminant productive efficiency and the sustainability of livestock systems. Bacteriophages are abundant biological entities that can regulate microbial populations through cell lysis, influence nutrient recycling, and contribute to horizontal gene transfer (HGT) through mechanisms such as transduction [5-7]. In the rumen, viral particles are abundant and are increasingly recognized as components of the microbial ecosystem; however, the extent and direction of their effects on bacterial communities involved in fiber fermentation, methanogenesis, and nitrogen flux remain under active investigation [8,9]. Advances in high-throughput sequencing and culture-independent metagenomic approaches have expanded characterization of the rumen virome, revealing substantial sequence diversity and many viral genomes without close homologs in existing databases [10,14].

Literature Review Methodology

This manuscript is a narrative review of the scientific literature on rumen viruses, with primary emphasis on bacteriophages. We conducted the literature search in PubMed/MEDLINE, Web of Science, Scopus, Google Scholar, and bioRxiv. The search strategy combined ("rumen" OR "ruminal") AND ("bacteriophage*" OR "phage*" OR "virome" OR "viral" OR "virus") AND ("metagenom*" OR "metavirom*" OR "diversity" OR "ecology" OR "fermentation" OR "methane" OR "production"). Searches covered publications from 2001 through December 2025, with greater emphasis on peer-reviewed literature published from 2017 onward. Eligible records addressed viral diversity, ecology, virus-host interactions, functional roles, or potential applications in domestic ruminants and were published in English or Spanish. We included review articles for contextual synthesis. No formal meta-analysis or quantitative effect-size synthesis was performed; evidence was synthesized qualitatively and classified, where possible, as experimental, computationally predicted, or statistically associated. This literature-review methodology is distinct from the experimental methods used in the primary studies included in the review. We considered preprints identified during the search for contextual assessment but restricted the final reference list to published journal articles in accordance with the target journal's author guidelines.

The rumen and its microbiome

The rumen is the first and largest compartment of the ruminant digestive system and functions as a highly efficient anaerobic fermentation chamber. Its multi-kingdom microbial ecosystem comprises bacteria, methanogenic archaea, ciliated protozoa, anaerobic fungi, and viruses, including bacteriophages that infect bacteria. The synergy among these microorganisms allows ruminants to ferment structural polysaccharides and produce VFAs, microbial protein, and B vitamins [1,2,4]. Methanogenic archaea are also central to enteric methane production because they consume hydrogen generated during fermentation [11,12].

Bacteriophage diversity in the rumen

Abundance and richness of the rumen virome

Within the rumen virome, bacteriophages represent an important and frequently detected component, but the virome also contains viruses associated with other microbial hosts. Yan., *et al*. [14] developed the Rumen Virome Database (RVD) by analyzing 975 rumen metagenomes and identified 397,180 species-level viral operational taxonomic units (vOTUs). Most classified vOTUs lacked close homologs in existing viral databases, highlighting the extent of the rumen viral 'dark matter'. Wu., *et al*. [15] subsequently compiled 64,922 non-redundant phage genomes from 2,333 samples spanning eight ruminant species and multiple gastrointestinal regions, providing evidence of substantial cross-host viral diversity.

Taxonomic composition and heterogeneity

Among classified rumen viral sequences, many belong to tailed bacteriophages. Older literature commonly used the order *Caudovirales* and the families *Siphoviridae*, *Myoviridae*,

and *Podoviridae*; these names should not be used as current formal ICTV ranks unless the historical context is specified. The manuscript therefore uses current ICTV terminology when discussing formal classification and retains older names only as historical or morphological descriptors. *Fischettivirus* phages infecting members of the *Streptococcus bovis/Streptococcus equinus* complex (SBSEC) have been experimentally demonstrated [23]. Sato., *et al*. [16] identified 7,175 unique viral sequences in Japanese Black cattle, including 1,019 complete genomes, and reported differences among breeds and individuals; these observations support geographic and host-associated heterogeneity but do not by themselves demonstrate coevolution.

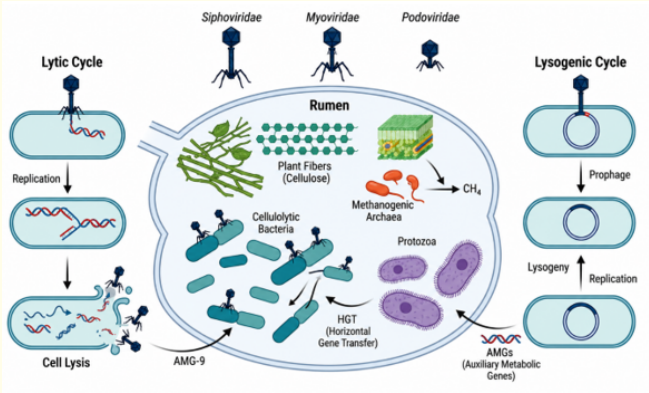

Figure 1: Schematic representation of interactions between bacteriophages and the rumen ecosystem via lytic and lysogenic cycles, which favor horizontal gene transfer (HGT) and the transport of auxiliary metabolic genes (AMGs). Figure generated using artificial intelligence and edited for scientific purposes based on specialized literature.

Proportion of lytic phages vs. temperate phages

In the ruminant gastrointestinal dataset analyzed by Wu., *et al*. [15], approximately 60% of phage genomes were classified as lytic (Figure 1). This finding indicates a substantial representation of lytic lifestyles in that dataset, but it should not be generalized to all rumen phages or to the highest proportion across all ecosystems. Differences in sampling, host age, sequencing strategy, and prediction criteria may also influence estimates of lytic versus temperate lifestyles (Table 1).

Reference/ Year	Animal Species	Sample Type	Sample Size	Sequencing Approach	vOTUs / Genomes Identified	Main Findings	Main Limitations
Berg Miller., *et al*. 2012 [5]	Bovine	Rumen contents	Not reported	Shotgun metagenomics (CRISPR spacer survey)	N/A (CRISPR-based)	First large-scale phage-host linkage study via CRISPR spacers in the bovine rumen microbiome	Small sample size; limited viral sequence annotation
Anderson., *et al*. 2017 [8]	Bovine (dairy)	Rumen contents	Not reported	Shotgun metagenomics	Not reported	Viral communities respond dynamically to changes in dietary energy concentration.	Limited diversity metrics; observational design
Gilbert., *et al*. 2020 [9]	Multiple ruminants	Narrative review	N/A	Literature synthesis	N/A	Comprehensive synthesis of rumen virome diversity and ecological roles	Review, not primary data; no novel sequencing
Stewart., *et al*. 2019 [10]	Bovine	Rumen contents	Not reported	Hi-C proximity metagenomics	4,941 MAGs (bacterial + archaeal)	High-resolution phage-host linkage map; viral integration patterns	Hi-C proximity ligation introduces chimeric assembly bias

Yan., *et al*. 2023 [14]	Multiple domestic ruminants	Rumen metagenomes	975 metagenomes	Shotgun metagenomics (Illumina)	397,180 vOTUs (species level)	Largest rumen virome database (RVD); >90% vOTUs lack known homologs (viral dark matter)	Most vOTUs uncharacterized; predominantly Illumina short-reads
Wu., *et al*. 2024 [15]	8 species (bovine, ovine, caprine, camel, deer, yak, buffalo, reindeer)	Rumen samples	2,333 samples	Shotgun metagenomics	64,922 phage genomes	Cross-species phage diversity; phages with potential lytic effects on methanogens identified	Predominantly computational predictions; limited direct experimental validation
Sato., *et al*. 2024 [16]	Japanese Black cattle	Rumen contents	Not reported	Hybrid sequencing (long-read + short-read)	7,175 viral sequences; 1,019 complete genomes	High-quality complete genomes; characterization of Japanese cattle-specific rumen virome	Single geographic region; breed-specific results may not generalize
Cook., *et al*. 2025	Dairy cattle	Rumen samples	Not reported	Hybrid sequencing (PacBio HiFi + Illumina)	30,321 vOTUs; 1,338 complete genomes (URPC)	Unified Rumen Phage Catalog (URPC); highest genome completeness to date	Limited temporal/longitudinal follow-up data
Yan and Yu 2024 [19]	Dairy cattle	Rumen virome	Not reported	Shotgun metagenomics	Not reported	Significant correlations between virome composition and milk yield, feed conversion ratio	Correlation only; no causal mechanism demonstrated
Liu., *et al*. 2025 [22]	Dairy cows	Rumen contents	Not reported	Shotgun metagenomics	Not reported	Rumen DNA virome composition associated with feed efficiency traits	Preliminary association data; mechanistic pathways unclear

Table 1: Major studies on the rumen virome and metavirome: study design, sequencing approach, findings, and limitations.

Discussion: Ecological roles and functions of rumen viruses

Regulation of bacterial populations

A plausible ecological role of bacteriophages is top-down regulation of bacterial populations through selective lysis. The 'kill-the-winner' model provides a useful ecological framework, but direct experimental evidence demonstrating this mechanism in the rumen remains limited [18,19]. Park., *et al*. [23] isolated and characterized two lytic phages infecting SBSEC and demonstrated inhibition of planktonic growth and biofilm formation *in vitro*, supporting their potential as experimental biocontrol candidates rather than establishing an *in vivo* rumen intervention.

Microbial diversification and lysogenic conversion

Rumen viruses may contribute to microbial diversification through antagonistic interactions, prophage integration, and other virus-host processes [19]. Yan and Yu [19] used metagenomic evidence, CRISPR-Cas spacer matching, and co-occurrence analyses

to infer virus-microbe relationships and prophage-associated diversification. These observations support a potential role in bacterial genetic diversification, but experimental validation is needed to determine the causal contribution of individual phages.

Horizontal gene transfer and auxiliary metabolic genes

Bacteriophages can mediate horizontal gene transfer, including transduction between bacterial hosts [5-7]. In the rumen, however, researchers have inferred the extent of phage-mediated HGT largely from genomic and metagenomic evidence, and direct demonstrations of transfer under ruminal conditions remain limited [13,19]. Auxiliary metabolic genes (AMGs) detected in rumen viral genomes provide evidence that some viruses carry genes capable of modifying host metabolism [14,22]. Such assignments should be described as computationally inferred unless the encoded function and its transfer or expression have been experimentally demonstrated (Figure 2).

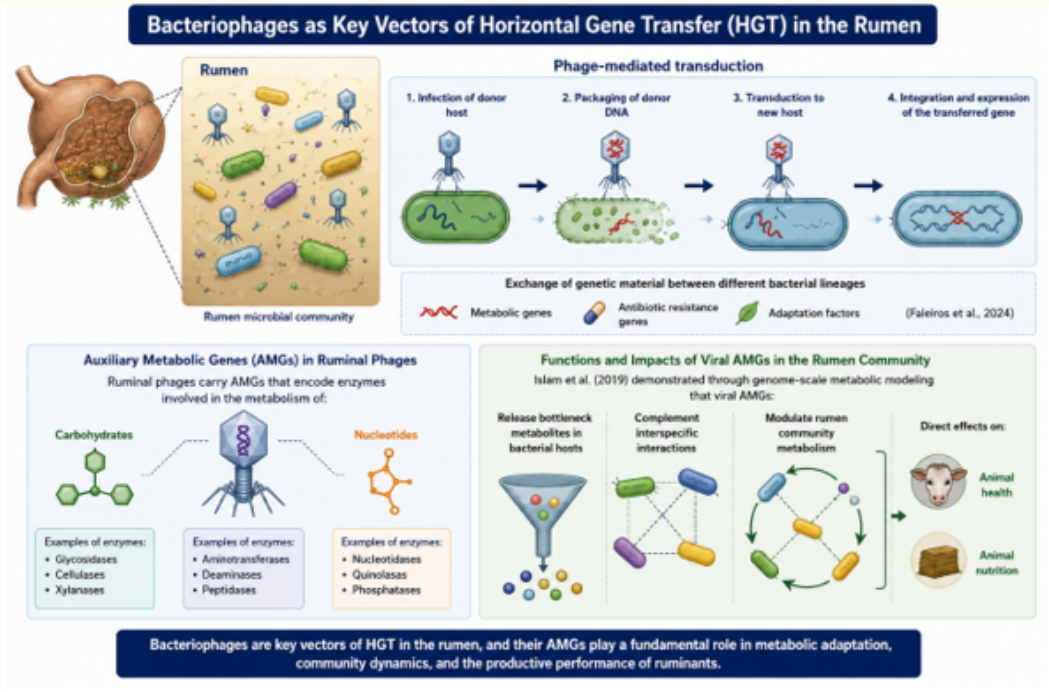

Figure 2: Schematic representation of bacteriophage-mediated transduction and the role of auxiliary metabolic genes (AMGs) in the rumen ecosystem. Phages facilitate genetic exchange between bacteria and contribute to the microbial community's metabolic and functional adaptation. Figure generated using artificial intelligence and edited for scientific purposes based on specialized literature.

Modulation of methane production

Viruses that infect methanogenic archaea should be described as archaeal viruses, not bacteriophages, because bacteriophages infect bacterial hosts. Wu., *et al*. [15] reported viral sequences with predicted associations with methanogenic archaea, including *Methanobrevibacter*, but these host assignments were computational. Such predictions may support hypotheses about methane production, but they do not demonstrate infection, lysis, or methane reduction *in vivo*. Consequently, archaeal viruses should be considered a research opportunity rather than an established methane-mitigation tool.

Phage-bacteria interactions in the rumen

Virus-host interaction networks

Characterizing specific virus-host interactions are fundamental to understanding rumen viral ecology. Current studies have used

CRISPR-Cas spacer matching, co-occurrence analysis, sequence homology, and prophage detection to infer host associations [14,19]. Most inferred interactions remain computationally predicted rather than experimentally confirmed by direct infection assays. Accordingly, table 2 separates experimentally demonstrated interactions from computationally inferred associations and distinguishes bacteriophages from archaeal viruses (Table 2).

Phage / Virus Type	Proposed Host	Interaction Basis	Method Used	Reference	Confirmation Status
Butyrivibrio phages (Siphoviridae-like)	*Butyrivibrio* spp.	Experimental	Phage isolation, electron microscopy, host-range assay	[20]	Experimentally confirmed
SBSEC-infecting phages	*Streptococcus bovis*/ *Streptococcus equinus* complex (SBSEC)	Experimental	Phage isolation, genome sequencing, infection assay	[21]	Experimentally confirmed
Fibrobacter/ *Ruminococcus* phages	*Fibrobacter succinogenes*; *Ruminococcus flavefaciens*	Computational	CRISPR spacer matching; co-occurrence network analysis	[16,22]	Computationally predicted (not experimentally verified)
Archaeal viruses (*methanophages*)	*Methanobrevibacter ruminantium*	Computational	Metagenomic co-occurrence; sequence homology to archaeal virus markers	[17,19]	Computationally predicted (not experimentally verified)
Prevotella-associated phages	*Prevotella* spp.	Computational	CRISPR spacer analysis; metagenomic co-abundance	[16]	Computationally predicted (not experimentally verified)

Table 2: Virus-host interactions in the rumen: experimental and computational confirmation status.

Antiviral defense systems in the rumen microbiome

The relentless evolutionary arms race between phages and their hosts has driven the emergence of a remarkable breadth of antiviral defense strategies in rumen bacteria. Sáenz., *et al*. [21] identified 14,241 defense systems and 31,948 genes related to antiviral defense in 89% of 3,038 high-quality bacterial and archaeal genomes from the rumen, grouped into 114 types belonging to 49 families. The modification-restriction systems, Abi and Cas, were the most prevalent. CRISPR-Cas systems, which provide adaptive immunity by storing memories of previous infections, were found in 21.9% of the genomes, with subtype I-C being the most common. Although most defense systems are rarely present, the rumen's collective set may represent a reservoir of shareable mechanisms, consistent with the "pan-immune system" model described in other environments [21].

Life cycle: Lysis vs lysogeny

Whether a phage enters a lytic or lysogenic pathway depends on viral, host, and environmental factors. The high proportion of lytic phages reported in the ruminant gastrointestinal dataset [15] suggests that lytic lifestyles are common there. In contrast, Yan and Yu [19] reported differences in viral life strategies across host developmental stages. These observations are consistent with dynamic phage-host interactions, but they do not establish that rumen maturation directly causes shifts in viral lifestyle.

Impact on rumen fermentation

Associations with animal production traits

Recent studies have reported associations between rumen virome composition and animal production traits. Yan and Yu [19]

identified statistical associations with feed efficiency, lactation performance, weight gain, and methane emissions. At the same time, Liu., *et al*. [22] reported differences in the rumen DNA virome between dairy cows with different feed-efficiency phenotypes. These findings are hypothesis-generating: they do not establish that viruses cause differences in production traits, and potential confounding by diet, host genetics, physiology, and management must be considered.

Influence on fermentation processes and dietary response

Bacterial lysis by bacteriophages can release intracellular compounds that become available to other members of a microbial community, providing a conceptual basis for a viral-shunt effect. However, direct evidence that phage-mediated lysis quantitatively changes VFA production in the rumen remains limited. Anderson., *et al*. [8] demonstrated that dietary energy changes bovine rumen viral communities, showing that the virome responds to dietary conditions. Still, this association should not be interpreted as proof that viruses actively drive fermentation efficiency (Figure 3).

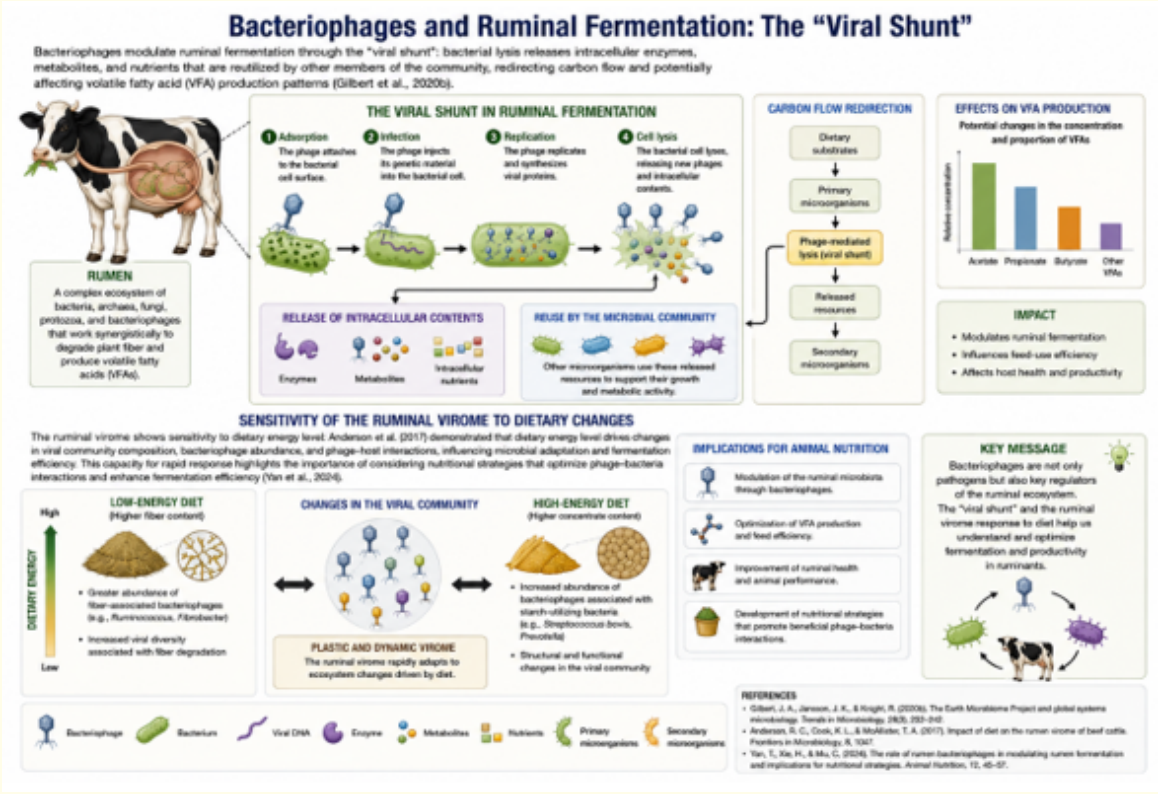

Figure 3: The image shows how bacteriophages modulate ruminal fermentation through viral shunting, promoting nutrient release and reuse after bacterial lysis. It also illustrates how diet influences ruminal virome composition and its effects on carbon flux, volatile fatty acid (VFA) production, fermentative efficiency, and ruminant productivity.

Methods used in primary studies: Metagenomics and metaviromics

Metagenomics and high-throughput sequencing

Shotgun metagenomics has revolutionized rumen virome research by enabling characterization of viral communities without culturing. Typical workflows include: DNA extraction from rumen samples, high-throughput sequencing, contig assembly, identification of viral sequences with specialized tools (VirSorer, VirFinder, VIBRANT), clustering into vOTUs, functional annotation, and diversity analysis [14,15]. To enrich the viral signal and reduce

bacterial contamination, researchers use filtration protocols (0.22 - 0.45 µm), DNase treatment, and viral particle concentration by ultracentrifugation or polyethylene glycol precipitation [16].

Hybrid sequencing, databases, and linkage inferences

Hybrid sequencing has improved the recovery of complete viral genomes in rumen studies. The RVD [14] and the ruminant phage genome catalog reported by Wu., *et al*. [15] provide important reference resources for comparative analyses. Virus-host linkage inference commonly relies on CRISPR-Cas spacer matching, integrated prophages, co-occurrence patterns, and sequence homology [14,19]. Genome-scale metabolic modeling can also generate hypotheses about potential virus-host metabolic interactions [20], but these are predictions rather than experimental demonstrations.

Implications and potential applications

Biocontrol and phage therapy

Targeted phage interventions have been proposed as a possible alternative to broad-spectrum antimicrobial approaches in the rumen. Park., *et al*. [23] demonstrated *in vitro* that lytic SBSEC phages can inhibit bacterial growth and biofilm formation, supporting further investigation of their biocontrol potential. Translation to animal use requires evidence of efficacy under ruminal conditions, host specificity, stability, resistance development, effects on non-target microbiota, and safety.

Methane mitigation and improved production efficiency

Identifying viral sequences computationally associated with methanogenic archaea supports a hypothesis for future methane-mitigation research [15]. However, because these are archaeal viruses rather than bacteriophages and because infection and methane reduction have not been demonstrated *in vivo*, no practical methane-mitigation recommendation can yet be made. Likewise, associations between the virome and feed efficiency [19,22] should not be interpreted as evidence that manipulating the virome will improve animal performance.

Challenges for practical implementation

Translating phage-based strategies into field practice remains challenging. The ecological complexity of the rumen means that targeted interventions may produce indirect effects that are difficult to predict; phage host specificity may require cocktails; bacterial resistance may arise through receptor changes or CRISPR-Cas defenses [21]; phages must remain stable under ruminal conditions; and any intervention requires appropriate regulatory and safety evaluation, including assessment of non-target effects and potential gene transfer (Table 3).

Functional Role	Mechanism	Evidence Type	Key References	Level of Support
Regulation of bacterial populations	Top-down lysis; 'kill-the-winner' dynamics; selective predation	Experimental + computational	[5,8,17]	Moderate - experimental evidence in analogous ecosystems (marine, gut); rumen evidence primarily metagenomic
Horizontal gene transfer (HGT)	Generalized and specialized transduction; prophage integration and excision	Computational + experimental	[6,7]	Moderate - mechanistically demonstrated; rumen-specific *in vivo* evidence mainly computational
Metabolic modulation via AMGs	Phage-encoded carbohydrate-active enzymes and metabolic genes complement host metabolism.	Computational modeling (metagenomics)	[11,12,16]	Low-to-moderate - inferred from metagenomic annotation; limited direct functional validation
Methane modulation	Lysis of methanogenic archaea or H2-producing bacteria; disruption of methanogenesis pathway	Computational prediction	[17,19]	Low - correlational and in silico; no direct experimental *in vivo* evidence available

Viral shunt (fermentation carbon cycling)	Bacterial lysis releases dissolved organic carbon and nutrients back into fermentation pool	Experimental (established in marine systems; emerging in rumen)	[20]	Moderate - well-established in marine virology; direct rumen evidence emerging but limited
Association with production traits	Virome composition correlates with milk yield, feed conversion ratio, and methane emissions.	Statistical correlation (metagenomic epidemiology)	[22]	Low - association without demonstrated causation; confounders not fully controlled

Table 3: Proposed functional roles of rumen viruses: mechanisms, evidence type, and level of support.

Conclusion

Current evidence, derived predominantly from metagenomic and metaviromic studies, indicates that the rumen contains a highly diverse viral community, including bacteriophages and viruses associated with other microbial hosts. More than 397,000 species-level vOTUs have been reported in the RVD [14], but most remain poorly characterized. The available literature therefore best describes viral diversity and associations and is substantially weaker for demonstrating specific mechanisms or causal effects *in vivo*.

Available evidence supports several plausible roles for rumen bacteriophages, including bacterial lysis, potential contributions to microbial diversification and HGT, and carriage of AMGs. However, the strength of evidence differs markedly among these functions. Interpret associations between virome composition and feed efficiency, milk production, or methane emissions as statistical associations, not evidence that phages directly determine host performance.

Phage-bacteria interactions are complex and involve antiviral defense systems, including CRISPR-Cas and restriction-modification systems [21]. These observations are consistent with ongoing virus-host evolutionary interactions, but the ecological consequences of individual defense systems *in vivo* remain incompletely resolved.

The growing body of metagenomic and computational evidence is valuable for generating hypotheses about rumen viral ecology. Before applications can be considered reliable, however, experimental studies are needed to validate host range, infection, lysis, gene expression, effects on fermentation, methane production, and animal performance under controlled and realistic ruminal conditions.

Strengths of the Study

Methodological advances in metagenomics

High-throughput sequencing and metagenomic workflows have substantially expanded rumen virome characterization, allowing viral sequences to be recovered without culturing. Rumen-specific viral databases and bioinformatic pipelines have increased the number of viral genomes that can be detected and compared [10,14,15].

Extraordinary diversity of the rumen virome

Recent studies have documented extensive viral diversity in the rumen, including many sequences that do not closely match previously characterized viruses [14,15]. This represents an important strength of the current literature, although the absence of database homologs also limits functional and taxonomic interpretation.

Understanding phage-bacteria interactions

Phage-host interaction analyses have enabled increasingly detailed hypotheses about virus-microbe relationships. CRISPR-Cas matching, prophage detection, and network analyses provide useful evidence, but predicted host links should be distinguished from experimentally demonstrated infection. AMG annotations likewise provide hypotheses about metabolic functions rather than direct evidence of activity.

Associations with productive traits

Associations have been reported between virome composition and traits such as feed efficiency, milk production, and methane emissions [19,22]. These findings can inform hypothesis generation, but they do not establish the virome as a causal zootechnical factor or biomarker without independent validation and control of confounding variables.

Weaknesses of the Study

Uncharacterized "viral dark matter"

A large proportion of viral sequences identified in the rumen have no close homology to known viruses, limiting inference about ecological and metabolic functions. Fragmented assemblies can further hinder reconstruction of complete pathways and accurate taxonomic classification.

Predominance of descriptive studies

Functional and experimental research demonstrating causality remains limited. Reported correlations between virome composition and production traits cannot, by themselves, establish molecular mechanisms or causal relationships. Likewise, researchers often infer many virus-host interactions from CRISPR-spacer matching, sequence homology, co-occurrence, or prophage detection rather than direct infection assays. AMG-related functional inferences generally depend on sequence annotation or metabolic modeling rather than biochemical or physiological validation. This distinction between computational prediction and experimental demonstration is central to interpreting the current literature.

Technical difficulty in isolation and culture

Experimental work with rumen phages is technically demanding because the rumen is strictly anaerobic and many potential bacterial hosts remain difficult to culture. These constraints limit isolation, controlled infection experiments, and direct testing of predicted virus-host interactions.

Geographic and species bias

The literature is heavily skewed toward cattle, while sheep, goats, buffalo, camels, and animals managed in extensive or pastoral systems remain less represented. Geographic and management differences may therefore limit the generalizability of current findings.

Research Priorities

Phage therapy for methane mitigation

Viruses that infect methanogenic archaea represent a potential research direction for methane mitigation, but they are archaeal viruses rather than bacteriophages. Experimental confirmation of host range, infection, lysis, and effects on methane production is required before their use as mitigation agents can be considered.

Targeted manipulation of the ruminal microbiome

Bacteriophages may eventually provide targeted modulation of selected bacterial populations. Still, their specificity, resistance development, host-range limitations, and possible non-target effects must be resolved experimentally before they can be considered more precise or safer than conventional interventions.

Integration of multi-omics approaches

Integrating metagenomics with metatranscriptomics, metaproteomics, and metabolomics could help move the field from descriptive virome inventories toward mechanistic understanding of virus-host interactions and their relationship with rumen metabolism and animal phenotypes.

Viral database development and standardization

Viral databases need to be continuously updated with sequences from underrepresented regions and species, incorporate standardized methods, and harmonize bioinformatics protocols to facilitate comparative meta-analyses between studies.

Longitudinal and heritability studies

Longitudinal studies could clarify virome stability and plasticity in response to dietary, physiological, and environmental changes. Studies of host-virome heritability may also help determine whether viral community features are reproducibly associated with host genetics and production phenotypes.

Conflicts of Interest

The authors declare they have no conflicts of interest regarding the work presented in this review article.

Use of Artificial Intelligence (AI)

The figures presented in this manuscript were generated with the assistance of ChatGPT (OpenAI) and subsequently reviewed and edited by the authors to ensure their scientific accuracy and consistency with the relevant literature. The AI-generated figures are intended solely for illustrative purposes and should not be interpreted as experimental data.

In addition, ChatGPT (OpenAI) was used as a support tool for organizing and formatting the references. Grammarly was used for English-language proofreading, including grammar, syntax, spelling, punctuation, and stylistic adjustments, with the aim of

improving the clarity of the manuscript and ensuring consistency with the journal's formatting requirements. The authors retain full responsibility for the accuracy, integrity, and scientific content of the manuscript.

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