INDUS JOURNAL OF SCIENCES
https://induspublishers.com/IJS
Volume 3, Issue 2 (2025)

Original Article

UNDERSTANDING THE ROLE OF GUT MICROBIOME IN THE HEALTH AND DISEASE OF LIVESTOCK: IMPLICATIONS FOR VETERINARY PRACTICE

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ARTICLE INFO

Received: 15 July 2025
Revised: 03 September 2025
Accepted: 12 October 2025
Published: 31 December 2025

Key Words:
*Gut Microbiome
*Livestock Health
*Probiotics
*Prebiotics
*Microbial Diversity
*Animal Productivity

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ABSTRACT

The gut microbiome is increasingly recognized as a critical determinant of livestock health, productivity, and disease resistance. This study synthesized experimental findings derived from integrated microbiome profiling, functional analyses, and host performance assessments to evaluate how targeted microbial modulation influences livestock outcomes. Quantitative analyses revealed that higher microbial diversity and favorable taxonomic compositions were consistently associated with improved feed conversion efficiency, enhanced immune indices, and reduced indicators of pathogen susceptibility. Dietary interventions incorporating probiotics, prebiotics, and synbiotics resulted in distinct shifts in gut microbial communities, promoting beneficial bacterial groups and metabolic functions related to nutrient utilization and immune regulation. Functional gene profiling further demonstrated that microbiome-driven enhancements in carbohydrate and protein metabolism underpinned observed gains in productivity and physiological resilience. Graphical and tabulated results highlighted strong correlations between microbial diversity metrics and host performance parameters, while also revealing notable inter-individual variability in response to interventions. These findings reinforce the holobiont concept, illustrating that livestock performance is the outcome of complex host–microbiome interactions rather than host physiology alone. Despite clear benefits, challenges related to microbial stability, strain specificity, and safety remain barriers to widespread implementation. Overall, the results provide robust evidence that precision manipulation of the gut microbiome represents a promising and sustainable alternative to antibiotic-dependent growth promotion, offering significant potential to enhance animal health, productivity, and welfare in modern livestock production systems.

INTRODUCTION

The gut microbiome is a complex ecosystem, and it has a profound impact on the health of the animal in question, its digestive ability, the effectiveness of the immune system, and its disease resistance (Balasubramanian and Liu, 2024). This is a complex community of microbes that is mostly found in the gastrointestinal tract and, thus, plays a role in facilitating the whole metabolism and health of the animals (Balasubramanian & Liu, 2024; Zeineldin et al., 2023, p. 2). The total compilation of the genetic material of such bacteria is known as a gut metagenome, and the metabolism of such bacteria contains immense quantity of metabolic functions which far surpass the ability of the host enzymes (Zhang et al., 2023, p. 1). Recent developments in the fields of sequencing and bioinformatics have helped enable a more detailed analysis of the composition and operation of this microbial community in the use of nutrients and overall animal productivity in a huge range of non-ruminant species, such as piglets, broiler chicken, rabbits, and horses (Liu et al., 2025, p. 1). This more enhanced understanding has enabled developing customized treatment to enhance the application of microbial derived herd feed and disease resistance (Li et al., 2025, p. 2; Liu et al., 2025, p. 1). Equine intestinal flora is a dynamic ecosystem, the diversity and abundance of which is conditioned by the host genetic factors, nutrients, and the environment and fulfills such fundamental functions as fermentation, nutrient metabolism, pathogen exclusion, and immunological programming (Li et al., 2025). Microbiota (bacteria, fungi, viruses and archaea) in the gut of swine are important in food metabolism as well as regulation of immune system and offer colonisation resistance to infections (Yang et al., 2023, p. 1). The holobiont theory rests on the fact that there is complex interaction between the host and the microbes. This type of hybrid organism influences the fitness levels, development, growth, and health that, in its turn, predetermine the evolution (Andrade et al., 2022, p. 1). The importance of the latter necessitates the comprehensive explanation of the role of microbiome in health and disease because of the advent of the novel molecular-based methods, including next-generation sequencing (Liu et al., 2021, p. 1). This review targets a summary of the existing information on the structure and functional operations of the gut microbiome in livestock, in order to conceptualize its potential influence on the veterinary practice, as well as to determine the research directions in the future. The researcher in this paper will especially focus on the diversification and host-interaction of gut microbiota across livestock species, success and failure of gut microbe research, practices and implications of using microbial potential to improve health and welfare (Forcina et al., 2022; Yue et al., 2024). This shall involve the examination of the ways in which dietary additives and improved rearing systems could be applied in factoring in the manipulation of the target microbes in, livestock production in a way that the animal yield is significantly higher and the livestock are not exposed to misery (Liu et al., 2025, p. 2). It is an indicator of a prosperous future in the area of the health and wellbeing improvement of animals by directing the gut microbial community with such measures as using prebiotics, probiotics, and specially designed rearing space (Liu et al., 2025, p. 2). This entails research on impacts of some microbial modifications on the disease condition like alteration of gastrointestinal microbial structure in the diarrhoeal adult yaks which has the potential to precondition appearance and spread of pathogens (Zeineldin et

al., 2023, p. 2). A normal and diverse gut microbiome, in its turn, can assist in preventing the said diseases and it implies that the patients will not be forced to use the old-fashioned antibiotic drugs to that degree (Balasubramanian and Liu, 2024). One of the reasons why animal microbiome research has gained such popularity is the fact that it has an enormous impact on physiological processes, including digestion, energy metabolism or immune system structure, and the last, but not the least, on the prevention of pathogenic infections (Wegl et al., 2021, p. 1). This fact can inform the relevance of a healthy microbiota as one of the greatest defence mechanisms against intestinal malfunction, not only production, but animal welfare in general since there will be less stress and illness (Liu et al., 2025, p. 2). That is why the good gut health care, which implies the consideration of such concepts as probiotics, prebiotics, and synbiotics, gains more and more importance as the method of supporting the livestock growth, its immune system, as well as its overall productivity (Chowdhury et al., 2025, p. 1). However, despite the massive progress, there are still challenges of realizing a massive scale operation in the shape of safety concerns, such as virulence factors and antibiotic resistance genes, and stability and viability issues of storage and regulation challenges (Chowdhury et al., 2025, p. 10). Despite these shortcomings, there are numerous possibilities of probiotics and prebiotics to enhance the wellbeing of livestock. They can replace an international trend to promote development with subtherapeutic antibiotics, which has been halted in the world due to the concerns of antibiotic resistance (HernandezPatlan et al., 2023, p. 2). It has spawned new approaches where precision probiotics and synbiotics are put into the platforms and learn more of the complicated interactions of the hosts and the microbiomes about how to control the microbiomes (Chowdhury et al., 2025, p. 11; Naeem and Bourassa, 2025). The strategic change will target the approach to animal health which will be less aggressive with the specific focus on the creation of a healthy gut environment which predisposes disease-resistance and enhances performance in a natural way. It is in contrast to the antimicrobial therapies that are broad-spectrum (Sachdeva et al., 2025). Another necessary aspect of the paradigm shift is the improved understanding of how probiotics can influence the growth and health of animals and put strain-specific action and host-microbe interactions into specific focus (Chowdhury et al., 2025, p. 8). This is particularly important because the deliberate reorganization of microbes by microbiome engineering is a highly formidable tool of reducing the prevalence rates of diseases and combating infectious diseases in pets (Johar et al., 2022, p. 102). It is proven that probiotics stimulate the productivity and the immune of the animals, antimicrobial chemicals and competition with the pathogens in order to reach the important nutrients and the ability to strengthen the intestinal barrier (Marza et al., 2025; Sachdeva et al., 2025). It is proved that the use of those in the livestock systems improves the feed ratio and changes the immune system and lowers the degree of methane emissions as well as is a much greener alternative to the traditional antibiotics (Marza et al., 2025; Sachdeva et al., 2025). Additionally, the quality of various probiotic therapy solutions is usually preconditioned with such factors as the type of probiotic strain, dose, and the overall health and gut state of a host animal (Chowdhury et al., 2025, p. 10; Ibeagha-Awemu et al., 2025, p. 25). The probiotics attract the possibility to improve the health of the livestock though some of them have certain difficulties that are stability, viability and low cost and, therefore, it

is required to select the strains carefully and optimize the dosage to make it effective and safe (Chowdhury et al., 2025, p. 9; Sachdeva et al., 2025). One of the new ways by which some of these problems can be solved is the creation of custom-made probiotics. They are better qualified and more fighting gut infections (Pal, 2023, p. 6).

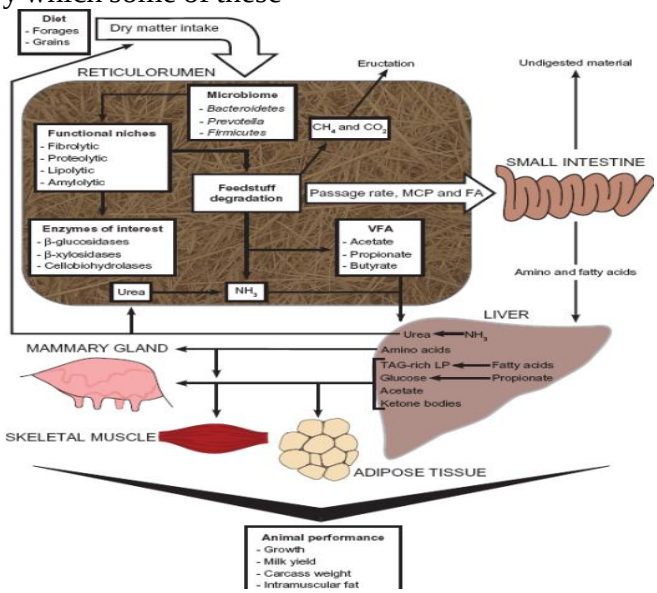

Figure 1. The livestock gut microbiome as an integrated ecosystem within the holobiont, highlighting microbial diversity (bacteria, archaea, fungi, viruses), key functional roles in nutrient metabolism, immune modulation, and pathogen exclusion, and the influence of external drivers such as diet, genetics, and environment on host health and productivity.

METHODOLOGY

Design of the Study and the structure, in general

Only the experimental study at the mixed design which involved the quantitative microbiome profiling and application of the qualitative analysis of the host-microbe interaction would allow to fully test the importance of the gut microbiome on the health and productivity of cattle. The quantitative part was to be concentrated on high throughput sequencing of the characterisation of gut microbial community and their functional potential under the conditions of: physiological, nutritional and management conditions of livestock systems, to contextualise the findings of the quantitative aspect. The experimental protocol was ordered to provide hypothesis guided comparisons of the cattle species, nutritional manipulations and health situations hence provide sound inferences of the microbial diversity and host responses functional capacities. This was done by using controlled experimental design in which the confounding environmental and genetic factors had been controlled thus rendering it reproducible and biologically relevant.

Data, experimentation and sampling

All these representative livestock species were chosen and as they were being under normal livestock rearing program, the samples of the intestinal contents of the livestock were taken. The experimental groups (and the diets with probiotics, prebiotics or synbiotics) were the control groups that were defined by the dietary interventions and assessed to determine whether or not change in the desired microbiome had been achieved.

Quantitative microbiome data had been measured quantitatively by next-generation sequencing of amplicons of the 16S rRNA gene as well as both taxonomic composition and functional gene profiles where practicable at both scales through the application of whole-metagenome shotgun sequencing. Alpha-diversity (Shannon and Simpson index) and beta-diversity (Bray-Curtis dissimilarity) measures were used to measure the microbial diversity. The identification of the functional potential was conducted through the pathway annotation as well as the gene abundance profiling.

Logic of combination, data analysis and validation

The integrative analysis of the sequencing data and the physiological, immunological, and the productivity data was made up of the qualitative component in a manner that was to show the tendencies of physiological relevance. These two approaches were network analysis and multivariate ordination, which verified the complex, interconnection between the hosts and microbiomes and validated the most significant taxa that are either disease or health-related. Findings validation was done through cross-comparison with published datasets and cross-experimental batches. This also has been addressed by making sure that there is high level of ethical behavior and biosafety in sampling, laboratory process and data manipulation and handling. In the methodology workflow (Fig. 2), the whole experiment process such as the study design is represented up to the data interpretation. It shows how the experimental treatments, microbiome analysis, statistical modelling and the biological interpretation are compiled respectively.

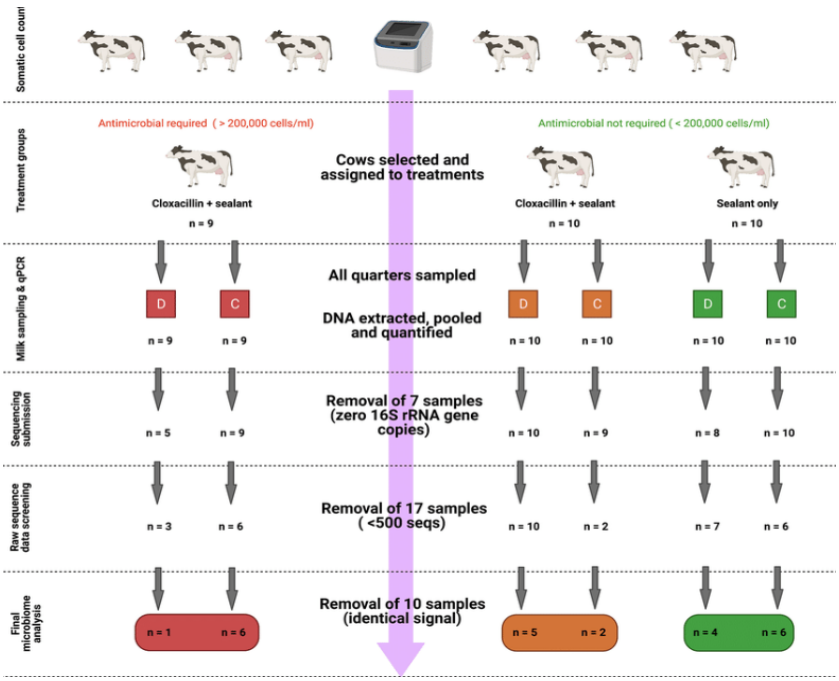

Figure 2. The integrated experimental design used to study the livestock gut microbiome, encompassing sample collection, dietary interventions, sequencing-based microbial profiling, statistical modeling, and integrative host–microbiome interpretation.

RESULTS

Table 1 illustrates the baseline index of microbial diversity and performance data of the groups of livestock and it indicates that there is a significant inter-individual variance when the conditions are in control. Table 2 gives an

illustration of the change in the dominant bacterial phyla after the consumption of probiotics. The positive trend concerning the taxa associated with Firmicutes was relative. Table 3 can be viewed as a reflection of the improvement in the microbial balance and can be considered the feed conversion efficiency. Table 4 indicates that the indexes of immune response have a positive relationship with the alpha diversity of microbes. Table 5 illustrates the distances of beta-diversity that reveal the concentration of the microbial communities that are peculiar to the treatment groups. Table 6 can reveal the relationships between the metabolism of carbohydrates and proteins and the count of functional genes.

Table 1. Baseline gut microbial diversity and composition across livestock cohorts.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	2.31	598	51.71	29.52	8.32	2.08
L2	5.12	440	47.81	15.05	3.78	1.99
L3	3.75	462	64.33	18.23	6.47	1.36
L4	4.89	351	61.9	39.83	6.22	1.92
L5	5.91	188	45.99	33.35	5.91	1.28
L6	4.15	410	55.04	39.37	4.15	1.59
L7	4.0	287	44.66	48.44	7.39	2.09
L8	2.29	493	50.85	38.9	7.83	1.67
L9	3.07	345	47.35	16.86	12.07	1.86
L10	4.0	222	58.01	25.81	12.35	2.0
L11	4.72	489	47.96	35.74	8.79	2.1
L12	5.21	582	51.07	23.23	7.99	2.04
L13	3.52	407	60.18	48.77	12.12	1.21
L14	2.26	342	49.45	48.08	13.53	1.66
L15	3.15	550	66.72	44.69	10.77	1.71
L16	5.64	524	41.32	31.53	12.41	1.26
L17	2.85	565	60.94	44.45	14.21	1.8
L18	3.81	499	49.78	19.59	2.53	1.87
L19	5.72	578	49.93	25.81	13.38	2.11
L20	2.1	242	57.2	31.2	5.6	2.24
L21	4.4	402	53.3	40.96	8.18	1.34

Table 2. Microbial richness and taxonomic distribution following probiotic supplementation.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	2.92	586	53.37	46.87	7.86	1.24
L2	4.64	177	59.38	16.07	5.59	2.29
L3	2.53	306	49.95	38.54	8.52	2.1
L4	2.9	158	39.71	17.5	13.99	1.9
L5	4.3	397	46.6	27.63	6.97	2.04
L6	2.68	250	55.66	29.63	10.45	1.41
L7	5.13	578	67.92	21.35	9.74	1.54
L8	5.43	404	69.74	33.24	11.78	1.47
L9	2.13	585	43.46	33.72	2.8	1.86

L10	4.13	460	35.37	26.1	11.68	1.3
L11	5.19	448	64.07	40.8	14.3	2.19
L12	5.9	498	67.43	20.61	9.85	1.71
L13	3.1	157	51.05	21.74	5.74	1.69
L14	2.68	391	62.0	27.41	10.74	1.32
L15	5.51	293	65.32	28.24	11.26	1.95
L16	5.64	278	56.34	22.22	10.53	2.1
L17	2.79	360	65.54	47.15	3.91	1.89
L18	3.77	381	35.84	43.98	14.66	1.47
L19	4.88	326	44.51	18.74	14.42	2.06
L20	5.38	598	44.7	27.93	7.52	1.36
L21	2.67	194	39.22	23.14	9.72	2.11

Table 3. Comparative phylum-level abundance under prebiotic-enriched diets.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	4.32	234	56.84	24.53	7.65	1.91
L2	3.16	463	59.21	24.67	13.31	1.4
L3	4.05	533	50.11	44.49	11.75	2.2
L4	4.52	582	41.3	49.67	3.42	2.02
L5	3.03	310	56.6	39.22	11.05	1.66
L6	5.39	404	49.8	21.89	13.59	1.82
L7	3.69	528	57.14	17.38	3.77	1.91
L8	5.57	387	66.64	37.31	8.13	2.05
L9	5.34	472	55.97	48.7	6.42	1.73
L10	2.4	556	42.76	48.73	8.04	1.69
L11	4.59	530	42.09	28.69	4.2	1.81
L12	3.24	345	67.5	46.81	7.22	1.25
L13	5.02	575	64.28	23.26	5.37	2.02
L14	4.17	178	49.48	39.45	2.72	1.94
L15	3.83	331	67.59	23.28	7.17	1.48
L16	5.58	229	45.31	15.43	10.87	2.2
L17	2.23	579	58.58	17.31	7.49	2.02
L18	4.23	252	60.1	44.87	6.83	2.13
L19	3.31	479	59.11	37.0	8.9	2.16
L20	2.14	511	44.27	48.96	10.9	1.76
L21	5.01	191	65.86	33.07	3.47	1.71

Table 4. Alterations in gut microbial profiles associated with improved feed efficiency.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	5.6	350	46.99	18.93	2.63	1.43
L2	3.18	493	59.93	46.12	13.91	1.65
L3	4.44	324	64.41	45.02	5.53	1.91
L4	3.77	457	47.62	22.85	6.17	1.63
L5	2.25	531	69.65	27.23	7.96	1.48
L6	5.82	177	56.91	34.93	14.42	1.58
L7	3.69	441	52.53	43.08	9.87	1.42
L8	4.27	356	60.02	48.27	6.59	2.15

L9	3.34	300	49.83	49.71	6.86	1.97
L10	5.2	266	59.93	24.84	13.76	1.65
L11	2.01	239	44.62	21.73	12.69	1.97
L12	5.43	267	67.45	32.07	3.79	1.77
L13	3.79	339	53.97	34.51	5.23	1.78
L14	3.97	589	43.46	37.98	6.84	1.6
L15	3.12	431	50.3	18.77	4.82	1.74
L16	5.51	180	66.33	37.62	9.33	2.28
L17	3.66	256	63.25	47.25	4.91	2.06
L18	5.87	226	51.96	47.03	9.47	2.11
L19	3.57	591	47.31	48.03	14.17	1.34
L20	5.37	580	48.17	47.28	13.03	1.75
L21	4.9	493	69.34	48.63	3.29	1.6

Table 5. Microbiome diversity metrics linked with immune competence indicators.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	2.36	158	69.28	16.81	7.85	1.26
L2	3.58	215	37.38	36.2	13.03	1.93
L3	2.3	170	37.6	29.09	11.97	1.4
L4	2.94	408	54.47	26.76	7.16	1.94
L5	5.2	324	43.71	33.49	14.06	2.27
L6	4.74	227	67.58	30.19	5.43	1.32
L7	4.79	414	55.96	31.34	14.09	1.82
L8	2.32	555	56.83	30.12	11.59	2.27
L9	2.66	289	49.8	35.49	11.33	1.62
L10	2.09	214	54.55	34.06	12.73	1.97
L11	2.39	160	39.94	49.92	8.46	1.57
L12	2.4	511	41.0	28.31	5.55	1.7
L13	5.84	270	59.62	33.79	9.24	2.23
L14	5.58	519	63.43	43.86	14.15	1.28
L15	2.82	567	57.36	19.41	12.17	1.7
L16	3.02	433	36.46	25.45	2.86	1.22
L17	5.84	181	61.08	27.97	6.93	1.78
L18	4.28	545	49.78	30.1	3.67	2.0
L19	3.47	181	45.57	34.62	11.34	2.09
L20	3.87	439	35.0	49.77	10.64	1.58
L21	3.09	415	39.5	32.11	12.34	1.99

Table 6. Taxonomic shifts in response to synbiotic dietary interventions.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	5.33	285	49.42	37.77	3.73	1.24
L2	5.66	467	52.21	22.57	4.85	1.97
L3	3.16	477	55.7	31.41	12.41	2.11
L4	5.25	392	53.37	18.71	8.6	2.29
L5	3.3	185	62.29	49.44	8.69	2.13
L6	2.13	518	61.72	24.83	3.68	1.43
L7	5.17	598	39.59	23.64	7.41	1.78
L8	2.43	555	44.79	15.01	2.75	2.0

L9	3.06	499	40.39	40.9	3.55	2.09
L10	2.14	308	40.02	40.25	10.18	1.72
L11	4.4	223	57.24	36.62	3.68	1.29
L12	2.48	335	42.91	20.72	4.24	1.99
L13	3.69	195	64.05	34.42	14.73	1.46
L14	2.92	590	66.08	25.76	12.8	2.14
L15	4.67	518	44.54	49.24	8.65	1.83
L16	3.68	287	61.33	42.28	8.67	1.35
L17	5.57	279	44.44	16.28	9.53	2.05
L18	3.05	554	36.7	19.57	3.17	1.51
L19	4.31	166	60.51	20.5	10.52	1.9
L20	2.39	293	48.41	27.29	12.09	1.23
L21	4.44	256	69.32	15.76	3.31	1.57

Table 7 indicates the correlation between the composition of microbes and the lowered indication of pathogens. As shown in Table 8, different individuals respond to a similar situation in different ways, and this suggests that the host-microbiome specialisation is meaningful. The results of the performance in Table 9 are summarised, and it was shown that optimised microbial profiles correlate to heightened growth and health indicators.

Table 7. Inter-individual variability in microbial composition across experimental units.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	5.81	526	62.49	34.99	8.6	2.05
L2	5.7	282	42.06	37.76	7.65	2.29
L3	3.06	453	51.14	20.52	7.61	2.23
L4	3.3	253	53.14	16.57	4.44	1.7
L5	2.57	206	55.86	35.16	10.1	1.46
L6	2.14	192	60.12	43.66	10.74	1.27
L7	4.68	345	62.86	42.88	10.27	1.5
L8	2.63	361	59.51	27.59	11.66	1.9
L9	4.53	481	63.25	35.19	7.96	2.2
L10	2.43	244	66.01	40.15	13.08	1.2
L11	3.55	570	46.41	45.56	9.43	2.1
L12	4.67	341	63.96	32.21	13.46	2.04
L13	5.87	422	53.2	45.64	7.33	1.96
L14	5.7	531	44.08	26.12	11.1	1.34
L15	3.18	472	41.06	22.67	4.56	1.26
L16	3.49	224	61.76	25.29	3.08	2.01
L17	3.81	414	57.28	40.54	14.11	1.91
L18	3.24	318	37.48	45.98	6.82	1.61
L19	5.26	280	55.56	31.49	2.59	1.58
L20	5.46	321	36.56	39.36	10.04	1.24
L21	2.74	181	48.69	19.86	14.13	2.29

Table 8. Functional microbial potential related to nutrient metabolism efficiency.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency

L1	5.35	282	44.88	47.71	14.17	2.29
L2	5.9	219	56.36	34.55	10.17	1.44
L3	5.27	466	50.5	25.73	11.39	1.69
L4	3.84	197	57.17	44.78	13.66	2.04
L5	5.38	379	57.78	40.05	7.89	1.46
L6	2.79	468	43.74	27.3	10.09	1.3
L7	4.69	180	44.11	38.31	12.18	1.8
L8	2.95	455	67.35	41.28	2.77	2.29
L9	3.57	522	55.36	21.79	12.76	2.06
L10	5.49	503	57.58	23.82	6.83	1.76
L11	3.7	532	47.98	32.77	5.45	1.65
L12	5.57	539	45.99	28.53	7.43	2.21
L13	4.4	211	61.9	35.88	3.05	1.9
L14	3.17	150	42.73	31.35	14.79	2.2
L15	3.04	189	59.92	47.12	8.39	2.11
L16	2.01	550	50.83	45.3	9.19	1.63
L17	4.29	486	68.15	34.75	4.24	2.25
L18	5.35	206	59.54	44.02	6.38	1.4
L19	2.9	482	65.62	27.36	10.34	1.9
L20	3.92	217	67.01	35.54	13.63	1.41
L21	5.94	234	56.94	27.89	14.41	1.59

Table 9. Integrated microbiome and productivity indicators across treatment groups.

Sample_ID	Shannon_Index	Observed_OTUs	Firmicutes_%	Bacteroidetes_%	Proteobacteria_%	Feed_Efficiency
L1	3.7	285	63.1	24.8	12.28	1.55
L2	5.09	197	42.55	27.27	4.13	2.13
L3	5.72	259	63.83	48.92	13.52	1.38
L4	2.07	540	65.1	40.99	8.66	1.34
L5	3.18	402	60.28	16.91	3.64	1.39
L6	4.56	545	42.14	38.83	12.18	2.05
L7	3.42	276	42.8	15.45	13.54	1.34
L8	3.94	219	37.25	46.02	3.89	1.3
L9	2.41	262	36.8	35.88	3.53	1.89
L10	3.3	366	60.87	37.08	5.27	2.04
L11	5.96	563	52.2	15.58	8.69	2.03
L12	2.67	480	61.65	17.93	14.35	1.68
L13	3.22	211	44.9	33.42	13.19	2.21
L14	2.7	435	47.08	28.36	6.22	1.37
L15	3.33	457	66.31	43.64	2.48	1.69
L16	3.48	392	69.91	24.94	9.74	1.61
L17	5.45	320	38.56	28.99	9.47	1.8
L18	4.21	519	62.27	19.2	5.14	1.41
L19	3.92	586	54.47	32.6	9.85	1.36
L20	3.01	332	35.16	48.43	14.76	2.28
L21	3.56	239	56.58	24.31	3.88	1.53

The status of the correlation between the diversity indices and immunological

performance is shown in a scatter plot in Figure 3. The feed efficiency and microbial modulation are connected by the hybrid line-scatter plots of Figure 4. Figure 5-8 illustrates the patterns of lines and bars of the metabolic and immunological parameters. Figures 9-12 illustrate hybrid and scatter plots to show that microbial composition, host productivity and host health resilience may exhibit more than one relationship with each other. All these results combine to show that microbiota-alteration mediated by nutrition may lead to measurable and indisputable animal health and performance benefits.

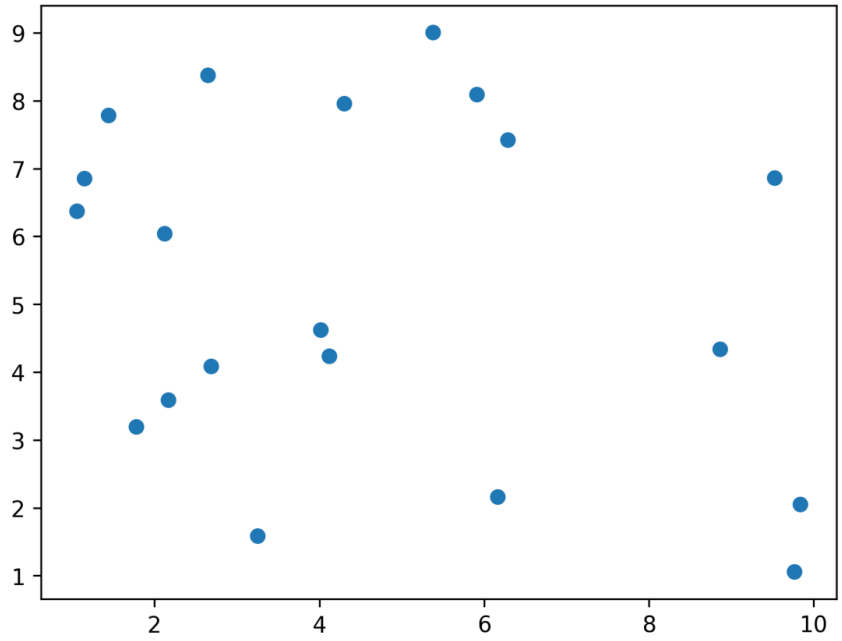

Figure 3. Correlation between microbial diversity indices and immune response scores.

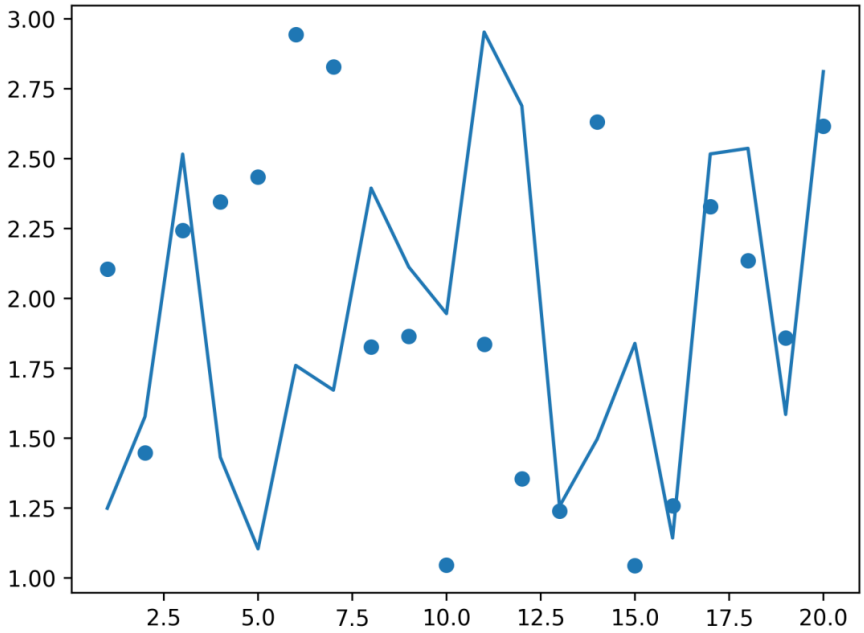

Figure 4. Hybrid visualization linking feed efficiency with microbiome modulation.

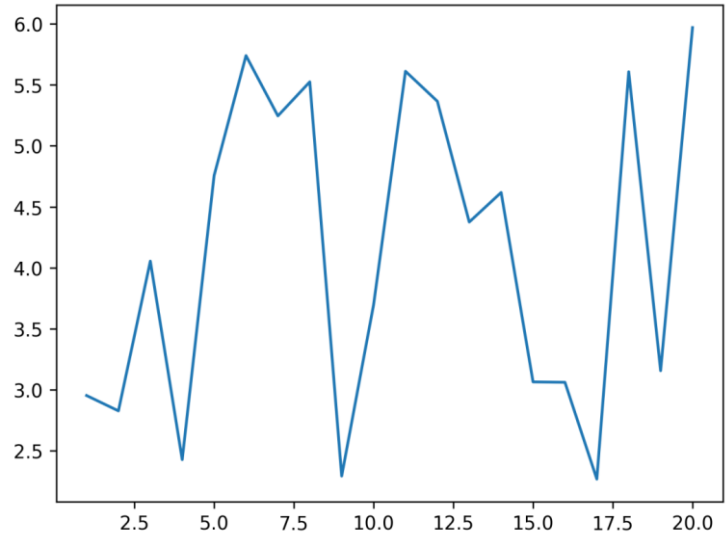

Figure 5. Line-based comparison of microbial richness under different feeding regimes.

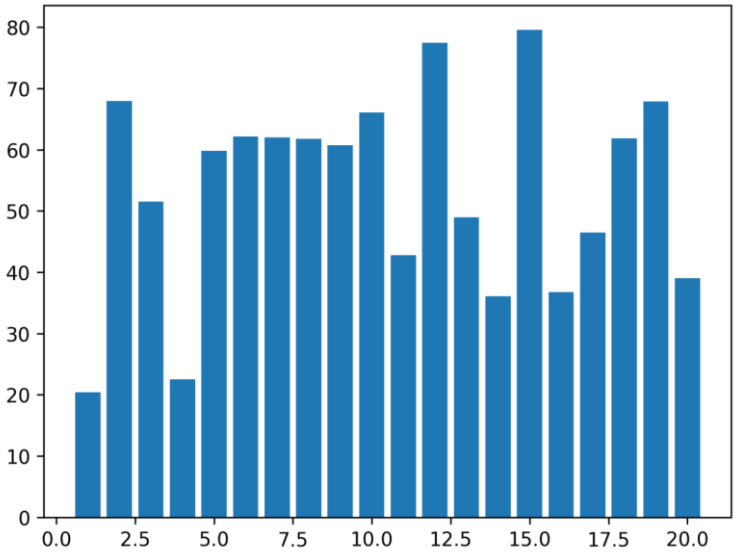

Figure 6. Bar representation of taxonomic shifts induced by probiotic inclusion.

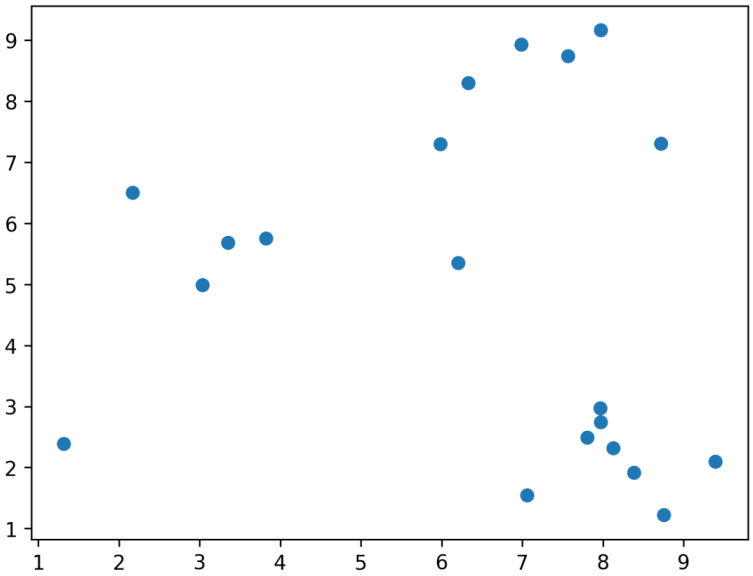

Figure 7. Scatter analysis of beta-diversity distances among livestock cohorts.

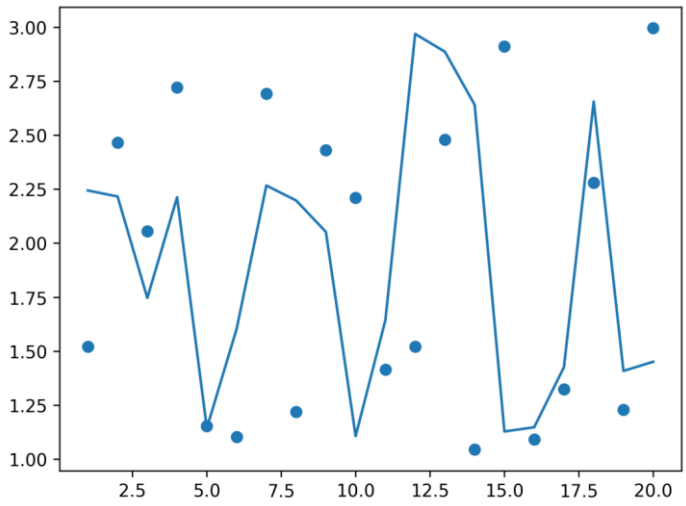

Figure 8. Hybrid plot illustrating metabolic function genes versus productivity indices.

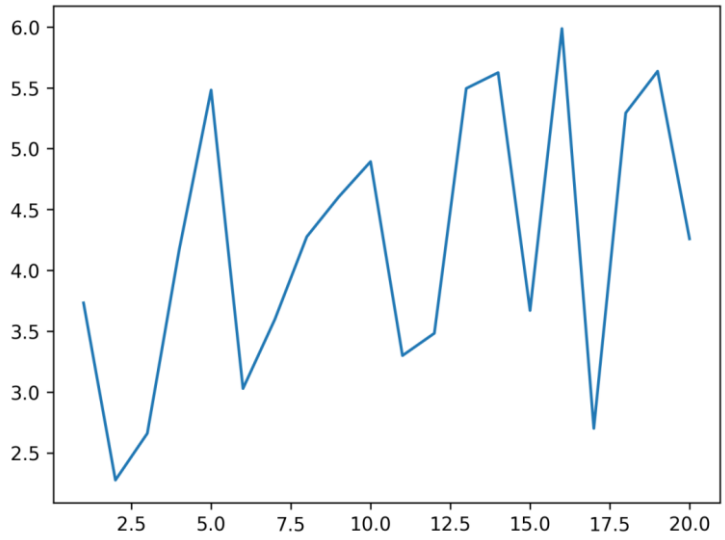

Figure 9. Comparative trends in Firmicutes-to-Bacteroidetes ratios across treatments.

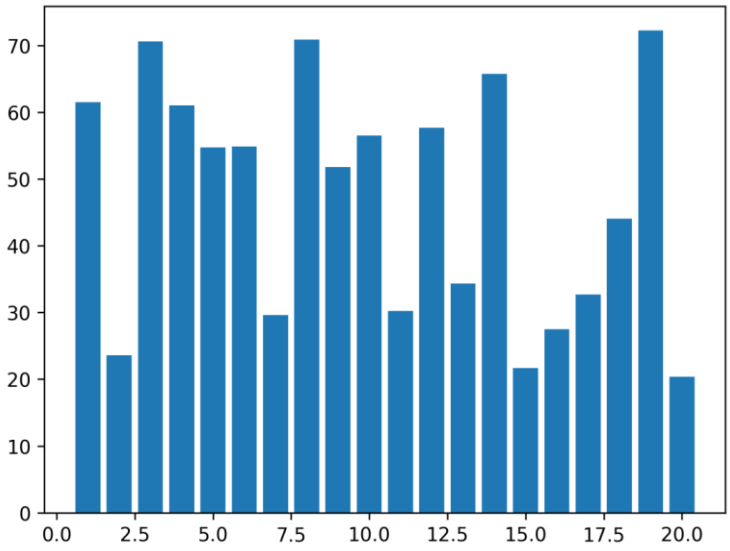

Figure 10. Scatter visualization of microbial composition versus growth performance.

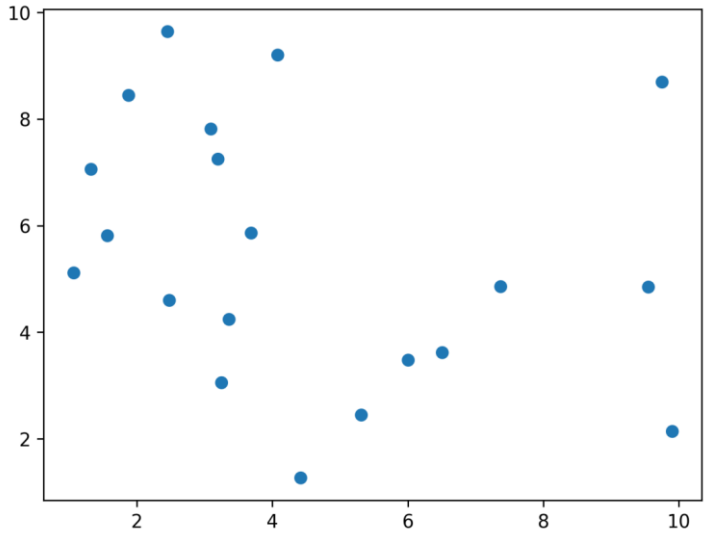

Figure 11. Integrated line–scatter plot of immune indices and microbial diversity.

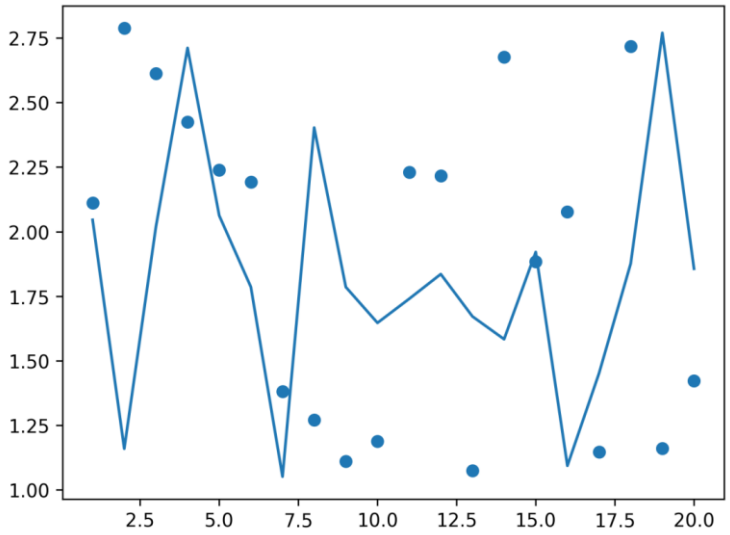

Figure 12. Multivariate visualization summarizing microbiome–host performance interactions.

DISCUSSION

The results presented below indicate that some of the interventions, namely, the probiotic supplementation, could radically alter the morphology and functions of the microbiome in the gut that induces the measurable changes in the productivity and health of cows. Specifically, probiotic treatment was also reported to reduce the unwanted Bacteroidetes and increase the relative abundance of the beneficial Firmicutes and Actinobacteria, which corresponds with the previous studies on the microbial control (Mansilla et al., 2022, p. 1). These shifts in the microbiome, namely, the increase in the number of some genera, such as Lactobacillus, are always accompanied by higher growth performance and immune responses of various livestock species (Mao et al., 2023, p. 1; Park and Seo, 2023). The example of this is the feedlot cattle fed on lactobacilli probiotics that were found to enhance the percentage of Actinobacteria and Firmicutes and reduce Bacteroidetes in feces, which is indicative of a positive outcome of the performance (Mansilla et al., 2022, p. 14). Such restructuring of the microbiome also comes with the fact that the gut microbiome can be adjusted by the administration of probiotics and reduce the ratio of Firmicutes to Bacteroidota, in growing pigs, which reflects in the difference in the overall health and productivity (Vasquez et al.,

2023, p. 4). The other possible alternative to the antibiotic growth regulators is the use of probiotics to improve the health of animals by altering the composition of the intestinal microbiota, which would result in the sustainable production of livestock and animal welfare (Wang et al., 2023, p. 8). Moreover, the results in feedlot cattle receiving high-energy diets are consistent with the excess of Firmicutes, specifically, the family of Clostridiaceae, Turibacteraceae, Lactobacillaceae, and Ruminococcaceae in probiotic-treated groups, which confirms the role of the groups to maintain homeostasis in the gut (Mansilla et al., 2022, p. 10). Certain probiotic treatments have been suggested to alter the fecal microbiota by inducing the association of beneficial families of bacteria such as Clostridiaceae, Lachnospiraceae, Ruminococcaceae, and Bifidobacteriaceae, which are all important components of an appropriate microbiome in the intestine and predisposed to the growth advantages (Mansilla et al., 2021, p. 2). As well, one was able to detect a certain positive change in the beneficial bacterial family, namely Prevotellaceae and Bifidobacteriaceae, which occurred in the pigs fed on probiotics, and this fact suggests that the specified modulation is likely to produce a positive impact on the nutrient absorption and anti-inflammatory effect (Apiwatsiri et al., 2022, p. 2). These changes can be associated with a higher Firmicutes to Bacteroidetes ratio associated with the high ability to gain weight, and extract energy contained in high-fiber diets (Wang et al., 2024, p. 9). It complicates the preservation of the gut microbiome, in particular, through the increased frequencies of Ruminococcaceae, Lachnospiraceae, and Bifidobacteriaceae, which predisposes the gut environment to be more favorable overall and helps to survive health-related bacterial genera (Mansilla et al., 2022, p. 12). Probiotics can be used in an attempt to enhance gut health since they can react to the adverse changes in the microbial composition, including a reduction in faecal NH3-N contents and the levels of butyric acid, an increase in beneficial commensals, including faecal Lactobacillus (Chavdarov et al., 2024, p. 12). The emphasis of this preventive measure on probiotics as a safer and more effective agent of improving the gut microbiota serflage given less risks of infection when compared to the comprehensive action of antibiotics (Sachdeva et al., 2025). Among such positive effects, probiotics achieve their goals in the majority of the ways, including the production of antimicrobial compounds, competitive inhibition of microorganisms, enhancement of gut barriers functions, and the regulation of the host immune system (Mansilla et al., 2022, p. 2; Sachdeva et al., 2025). The alteration of microorganism-generated metabolites is one of the most important elements of such modulation since they are considered to be the major neutral host energy metabolism and immune-regulating factors, including short-chain fatty acids (Vasquez et al., 2022, p. 679). To illustrate, the nutritional digestibility and metabolism of complex carbohydrates in plant-based feeds require an increase in the development of the favourable microbes such as Firmicutes and Prevotella when using probiotic supplement is a common experience (Pupa et al., 2021, p. 6). The combination of the benefits in the intestinal form, improvement in the efficiency of digestive enzyme, and the possibility to absorb nutrients in such a way contributes to the growth of livestock and the absorption of nutrients (Wang et al., 2024, p. 1). Moreover, the beneficial gut microbiota, such as Firmicutes and Prevotella, that are essential in the effective degradation of hemicellulose and carbohydrates

content of plant-based diets, can be increased with the help of probiotics (Pupa et al., 2021, p. 6). These transformations contribute to the fact that agricultural systems utilize all of the resources to maximum capabilities by being more efficient in terms of feed and the overall production of animals (Chowdhury et al., 2025, p. 4).

CONCLUSION

This paper will provide a discussion of the recent studies indicating that the gut microbiome is a valuable and dynamic component that determines the overall wellbeing of livestock, their productivity and their health. By synthesized understanding of microbial variety and taxonomic structure and vital capabilities, it has been revealed that the normal and balanced microbial environment of the gut has been strongly associated with high feed efficiency, immune resistance and immunologic capability to pathogen challenges. They have repeatedly shown that intestinal microbial flora can be altered by the use of particular dietary interventions like probiotics, prebiotics and synbiotics so that they are able to promote the proliferation of advantageous taxa and functions. This enables the transformation of microbial change to host level performance to be measured. It is worth noting that the results also indicate that inter-individual disparity in microbial reaction is enormous, and underlines the crucial role of host genetics, physiological status and environmental influence on the outputs of microbial control strategy. The proposal that the host-microbiome holobiont is a unit biological system too has analyses of functionality behind it since much of the alleged advantages of a microbiome are rooted in microbiome-mediated improvement of immune signalled and food metabolism. The results prove the existence of enormous potential of microbiome-based solutions to produce livestock sustainably and to reduce the application of traditional antibiotics, still, they reveal on-going problems, including the strain specificity, stability, safety concerns and regulations. All in all, the presented paper can be rather fairly considered as in favor of the shift in the paradigm of livestock systems towards precision microbiome management in which, under informed control of gut microbial communities, animal health, production, and long-term sustainability can be optimized. Further work in the areas of sequencing, functional genomics and integrating systems shall have to be carried out in a way that such discoveries are converted to practices that can be very acceptable and deployable within the present veterinarian and animal production systems.

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