



The Dietary Hemp–Gut Microbiome Interplay in Ruminants and Broilers: A Narrative Review in Livestock Nutrition

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Abstract | Although hemp-derived feed ingredients have recently been studied in relation to nutritional value, animal performance, product quality, safety, and regulatory constraints, their microbiota-specific effects in ruminants and poultry have not been reviewed as a distinct dietary hemp-gut microbiome axis. This review discusses current research on how dietary hemp compounds interact with the endocannabinoid system and gut microbiota in ruminants and poultry. Early evidence indicates that cannabinoids and hemp-based feeds might influence gut function, microbial communities, fermentation, and barrier health. However, responses may differ; for example, micronized hemp fiber supplementation increased total volatile fatty acid (VFA) in broiler cecal fermentation (from 29.2 to 37.5 mmol/mL), whereas industrial hemp extraction byproduct decreased ruminal total VFA in dairy cows (from 115.0 to 92.1 mmol/L). In ruminants, hemp supplements appear to have limited effects on overall ruminal diversity but may be associated with changes in microbial community structure, acetate:propionate balance, and methanogenic archaeal populations. Hemp seed products and micronized hemp fiber have been linked to modest microbiota changes in poultry, including an approximate 0.50 log₁₀ CFU increase in *Lactobacillus*/lactic acid bacteria and an approximate 0.80 log₁₀ CFU decrease in *E. coli*/coliform counts. Cannabidiol may also strengthen gut barrier function and immune response, especially during infections like *Clostridium perfringens*. Despite these promising signs, current research is limited by small sample sizes, short durations, inconsistent hemp product descriptions, and diverse microbiota assessment methods. Therefore, compounds derived from hemp are not presently recommended as routine feed additives targeting microbiota. The existing evidence should be regarded as hypothesis-generating rather than as a basis for altering current practices. Prioritizing standardized, comparative, and mechanistic studies is essential to better understand their potential in animal production.

Keywords | *Cannabis sativa*, Gut microbiota, Hemp-derived feed ingredients, Poultry, Ruminants, Cannabinoids

Received | April 20, 2026; **Accepted** | June 10, 2026; **Published** | July 28, 2026

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Citation | Sahin E, Bediz Sahin S (2026). The dietary hemp–gut microbiome interplay in ruminants and broilers: A narrative review in livestock nutrition. Adv. Anim. Vet. Sci., 14(8):1718-1730.

DOI | <https://dx.doi.org/10.17582/journal.aavs/2026/14.8.1718.1730>

ISSN (Online) | 2307-8316



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INTRODUCTION

Recent research has shed light on the pharmacological potential of hemp (*Cannabis sativa* L.), which is attributed to its diverse composition, including a variety

of phytocannabinoids, terpenes, phenolics, flavonoids, and alkaloids (Andre *et al.*, 2016; Radwan *et al.*, 2021). The non-psychoactive compound cannabidiol (CBD) and the psychoactive compound Δ^9 -tetrahydrocannabinol (THC) are currently the focus of significant research in

both human and veterinary medicine (Lima *et al.*, 2022), including growing interest in livestock species (Fallahi *et al.*, 2022; Irawan *et al.*, 2025).

The gut microbiota, whose composition and function are increasingly linked to cannabinoid signalling (Cani *et al.*, 2016; Silvestri and Di-Marzo, 2023), plays established roles in metabolic regulation, immune function, and intestinal barrier integrity (Khan *et al.*, 2025; Lynch and Pedersen, 2016). The endocannabinoid system (ECS), consisting of endogenous cannabinoids, their receptors (CB1R and CB2R), and metabolic enzymes, is particularly relevant to gastrointestinal physiology (Maccarrone *et al.*, 2023). CB1R in the enteric nervous system and intestinal epithelium is involved in motility and secretion (Izzo and Sharkey, 2010), while CB2R in gut-associated lymphoid tissue (GALT) modulates mucosal immune responses (Turcotte *et al.*, 2016). Both receptors have been characterized in the bovine gastrointestinal tract (Kent-Dennis and Klotz, 2024; Osiak-Wicha *et al.*, 2024; Zachut *et al.*, 2025) and chicken ileum (Ghazi Sahm *et al.*, 2026). The bidirectional interaction between the ECS and the gut microbiota, termed the endocannabinoidome–microbiome axis, may influence microbiota composition, intestinal barrier integrity, and microbial metabolite production (Cani *et al.*, 2016; Silvestri and Di-Marzo, 2023), though how dietary hemp compounds interact with this system in farm animals remains largely unexplored.

As the commercial use of hemp-derived supplements continues to increase in livestock (Fallahi *et al.*, 2022; Irawan *et al.*, 2025) animals, the mechanistic effects of cannabinoids on host physiology and gut microbiota remain incompletely understood. Existing studies suggest that cannabinoids may influence intestinal microbial composition, barrier integrity, and metabolic activity; however, current data are still somewhat limited and heterogeneous. This review aims to evaluate the existing literature on the effects of dietary hemp and hemp-derived products on the intestinal microbiota of ruminants and broilers, with emphasis on study designs, key findings, methodological limitations, and future research priorities.

LITERATURE SEARCH STRATEGY

A literature search was performed in Google Scholar, PubMed, Scopus, and Web of Science for records published from January 2008 to April 2026. The last search was performed on 15 April 2026. The search terms were adapted to the syntax of each database and combined into three groups of terms. The terms related to hemp and cannabinoids were *Cannabis sativa*, hemp, industrial hemp, hempseed, hemp seed cake, hemp seed meal, hemp oil, cannabinoids, CBD, and phytocannabinoids. The microbiota and fermentation-related terms included microbiota, microbiome, gut bacteria, rumen, cecum

(caecum), fermentation, short-chain fatty acids, SCFA, and methane. Species included poultry, broiler, chickens, ruminants, cattle, cows, goats, and sheep. Peer-reviewed conference proceedings and meeting abstracts, as grey literature, were also eligible and identified using Google Scholar and by hand-searching the reference lists of retrieved articles.

Records were eligible if they were original peer-reviewed studies reporting a direct gut microbiota or microbial outcome following dietary hemp-derived or cannabinoid exposure in ruminants or poultry. Studies in non-livestock species, those using non-dietary administration, and those reporting only performance, morphology, or immune endpoints without microbiota measurements were used only for supporting context. From the 412 records identified, 89 duplicates were removed and 323 were screened by title and abstract (287 excluded); of 36 full texts assessed, 20 were excluded at this stage (no direct microbiota or microbial outcome reported, reporting of performance, product quality, or agronomic endpoints only, or non-dietary administration), leaving 16 studies for the final narrative synthesis (9 ruminant or *in vitro* rumen and 7 poultry or *in vitro* gut studies).

CANNABINOIDS

Δ9-Tetrahydrocannabinol (THC) is acknowledged as the principal psychoactive compound found in *Cannabis sativa*. It plays a significant role in the regulation of gastrointestinal motility, secretion, and intestinal barrier function. This occurs through its interactions with both the central and enteric nervous systems, primarily via binding to CB1 receptors with a high affinity (Irawan *et al.*, 2025). Although THC activates CB1R in the central and enteric nervous systems at pharmacologically relevant concentrations, industrial hemp varieties contain THC below 0.3% by dry weight (Farinon *et al.*, 2020). Given this low concentration, the levels of THC that can be achieved in the gastrointestinal system from typical dietary intake in farm animals may fall short of the threshold necessary for significant activation of CB1 receptors. Cannabidiol (CBD) is a non-psychoactive phytocannabinoid that, despite exhibiting low affinity for CB1 and CB2 receptors (Table 1), exhibits a broad spectrum of biological effects through diverse molecular targets, including Transient Receptor Potential Vanilloid Type 1 (TRPV1), G Protein-Coupled Receptor 55 (GPR55), 5-Hydroxytryptamine (Serotonin) Receptor 1A (5-HT1A) receptors, and Peroxisome Proliferator-Activated Receptor Gamma (PPARγ) (Pertwee, 2008). Recent studies have shown that CBD influences intestinal PPARα expression, with PPAR-related responses correlating with tight-junction genes in broilers (Szkopek *et al.*, 2024). Furthermore, the bovine small intestine has been identified as containing CB1R, CB2R, and TRPV1, with notable increased

Table 1: Receptor targets and physiological effects of selected phytocannabinoids from *Cannabis sativa* L.

Compound	Receptor targets	Main biological effects	References
THC	CB1R (high affinity), CB2R (moderate)	Analgesia, appetite stimulation, antiemetic effects, regulation of gastrointestinal motility	Pertwee (2008)
CBD	GPR55, TRPV1, 5-HT1A, PPAR γ	Anti-inflammatory, antioxidant, anxiolytic, modulation of intestinal barrier function	Boehm <i>et al.</i> (2023); Brown <i>et al.</i> (2024); Ibeas <i>et al.</i> (2015)
CBG	CB1R/CB2R (weak), α 2-adrenergic receptors	Antimicrobial, neuroprotective, anti-inflammatory	Li <i>et al.</i> (2024)
CBC	TRP, PPAR γ	Anti-inflammatory, analgesic, antimicrobial	Sepulveda <i>et al.</i> (2024)
CBN	CB1R (weak), CB2R (moderate), TRP	Sedative effects, antibacterial activity	Farha <i>et al.</i> (2020); Morales <i>et al.</i> (2017)
THCV	CB1R antagonist/agonist (dose-dependent), CB2 partial agonist, TRP	Appetite suppression, potential anticonvulsant activity, anti-inflammatory	Walsh <i>et al.</i> (2021)
CBDA	COX-2 inhibition, PPAR γ , TRP, 5-HT1A	Anti-inflammatory, anti-emetic	Formato <i>et al.</i> (2020)
B-Caryophyllene	CB2 agonist (selective)	Anti-inflammatory, antimicrobial activity against rumen methanogens (<i>in vitro</i>)	Tabiś <i>et al.</i> (2024); Russo (2011)

Δ 9-tetrahydrocannabinol: THC, Cannabidiol: CBD, Cannabigerol: CBG, Cannabichromene: CBC, Cannabinol: CBN, Tetrahydrocannabivarin: THCV, Cannabidiolic acid: CBDA.

expression of TRPV1 in the jejunum (Osiak-Wicha *et al.*, 2024). However, the extent to which dietary hemp modulates microbiota through endocannabinoid system-related signaling in farm animals remains to be clarified. Additionally, minor phytocannabinoids such as cannabichromene (CBC), cannabigerol (CBG), and cannabinol (CBN) have been reported to exhibit anti-inflammatory properties and show protective effects in experimental models of intestinal inflammation (Borrelli *et al.*, 2013; Li *et al.*, 2024; Sepulveda *et al.*, 2024).

GUT MICROBIOTA AND GASTROINTESTINAL RELEVANCE IN RUMINANTS AND POULTRY

The gut microbiota, a complex ecosystem of host-associated microorganisms, plays established roles in metabolic regulation, immune function, and intestinal barrier integrity. Its composition varies substantially across animal species, and these differences carry direct functional implications for how diet-mediated effects may manifest in different production contexts.

In ruminants, the gastrointestinal microbial ecosystem is predominantly situated within the rumen, where cellulolytic microorganisms are predominant and aid in the breakdown of cellulose and other complex plant polysaccharides. The ruminal microbiota comprises eight bacterial phyla, which collectively account for approximately 99% of the sequences observed in 16S rRNA sequence analyses. Among these, Bacteroidota, particularly *Prevotella* spp., and Firmicutes, including *Butyrivibrio* and *Ruminococcus* spp., are recognized as dominant phyla (Henderson *et al.*, 2015; Mizrahi *et al.*, 2021). Key cellulolytic bacteria such as *Fibrobacter succinogenes* and *Ruminococcus flavefaciens*

play a crucial role in fiber digestion (Mizrahi *et al.*, 2021) while methanogenic archaea are responsible for methane synthesis (St-Pierre *et al.*, 2015). Rumen microorganisms also participate in broader physiological processes including nitrogen cycling and host energy utilisation, making the ruminal microbiota central to animal productivity (Liang *et al.*, 2024). In poultry, the gut microbiota contributes to digestive efficiency, immune function, and resistance to pathogen colonization (Choi *et al.*, 2014; Oakley *et al.*, 2014). The cecal microbiome is dominated by Firmicutes and Bacteroidetes, which together constitute 75–95% of classified sequences (Aruwa *et al.*, 2021; Kers *et al.*, 2018). Within Firmicutes, *Lactobacillaceae*, *Lachnospiraceae*, and *Ruminococcaceae* are the most prominent families (Aruwa *et al.*, 2021; Vacca *et al.*, 2020), while Proteobacteria, including potentially pathogenic genera such as *Escherichia*, *Campylobacter*, and *Salmonella*, remain below 10% in healthy birds but expand during dysbiosis (Yue *et al.*, 2024). These compositional characteristics are directly relevant to interpreting hemp supplementation effects, as the primary outcomes reported in poultry studies, increased *Lactobacillus* abundance, reduced *E. coli* counts, and altered short-chain fatty acids (SCFAs) profiles, reflect shifts within this established microbial framework.

Beyond structural composition, the gut microbiota in both species contributes to core physiological functions that are directly relevant to the outcomes observed in hemp supplementation studies. The gut microbiota contributes to a broad range of physiological processes, including the production of SCFAs via fermentation of complex carbohydrates (Flint *et al.*, 2012), preservation of epithelial barrier integrity through regulation of tight junction proteins

(Ulluwishewa *et al.*, 2011), and modulation of mucosal and systemic immune responses (Belkaid and Hand, 2014). In recent years, an increasing number of studies have explored the interactions between cannabinoids and microbiota (Varsha *et al.*, 2022). However, comparing findings across animals can present challenges due to significant variability in microbiota composition and the distinct metabolic and immune response capacities of each species (Tang *et al.*, 2026). Consequently, effects observed in one production system cannot be directly extrapolated to another, and species-specific interpretation remains essential when evaluating the gastrointestinal responses of ruminants and poultry to dietary hemp compounds.

HEMP-DERIVED FEED INGREDIENTS AND PRODUCTS FOR ANIMAL NUTRITION

Industrial hemp has gained increasing attention as a sustainable feed resource due to its high nutritional value and the availability of multiple co-products generated during seed oil processing and cannabinoid extraction. The most common hemp-derived feed ingredients include whole hemp seeds, hemp seed meal (also referred to as hemp seed cake), hemp seed oil, and spent hemp biomass from cannabinoid extraction, all of which have been investigated in different animal production systems (Irawan *et al.*, 2025). Hempseed and its derived fractions represent a nutritionally valuable and increasingly relevant option in animal feeding. Hemp seeds typically contain 20–25% highly digestible protein, characterized by albumin and a well-balanced profile of essential amino acids, including arginine, methionine, and cysteine (Fallahi *et al.*, 2022). They also provide 25–35% carbohydrates, significant levels of vitamins, particularly γ -tocopherol (~60.85 mg/100 g dry matter), and a range of essential minerals. Hempseed meal, in particular, contains elevated protein levels (typically 30–50%). The lipid composition is dominated by six major long-chain fatty acids: palmitic acid (6.73–7.75%), stearic acid (2.26–2.69%), oleic acid (12.77–13.98%), linoleic acid (53.82–56.55%), γ -linolenic acid (1.83–5.45%), and α -linolenic acid (14.60–16.84%). This profile results in an advantageous omega-6 to omega-3 ratio of approximately 3–3.5:1, making these products increasingly considered viable alternatives to conventional plant-based feed ingredients (Finet *et al.*, 2023; Irawan *et al.*, 2025).

In ruminant nutrition, hemp seed meal and cake have been extensively evaluated as alternative protein sources for cattle, sheep, and goats. Their excellent nutritional profile allows them to partially replace conventional sources like soybean meal, canola meal, dried distillers' grains, and alfalfa (Irawan *et al.*, 2025). Importantly, hemp-derived lipids may influence milk and meat fatty acid composition by increasing beneficial PUFAs, including omega-3 fatty acids. Nevertheless, the use of these by-

products in ruminant feed may remain limited by THC and CBD residues. No harmonised maximum residue limit for cannabinoids in ruminant meat or milk has been established across major jurisdictions; Switzerland has set a food product threshold of 10 ppm total THC, but no equivalent standard exist for ruminant products. Smith *et al.* (2023) detected no CBD or THC in muscle, liver, or kidney of heifers fed 20% hempseed cake for 111 days, with only trace levels in adipose tissue (6.3–10.1 ng/g) well below the EFSA acute reference dose (ARfD) of 0.001 mg THC/kg body weight, and Ran *et al.* (2024), similarly found no cannabinoid residues in meat of hemp-supplemented goats. Milk presents a greater concern: Wagner *et al.* (2022) detected up to 316 μ g Δ 9-THC/kg milk from dairy cows fed cannabinoid-rich hemp, with a feed-to-milk transfer rate of approximately 0.2%, concentrations that significantly exceeded the ARfD for several consumer groups, particularly children, making product-specific risk assessment essential when cannabinoid-rich hemp ingredients are used in lactating dairy cow diets.

In poultry production, hemp derivatives have been extensively investigated as sources of essential fatty acids and plant protein. The American Association of Feed Control Officials (AAFCO) has formally approved hemp seed meal for use in laying hen feeds (up to 20% inclusion) with strict limits of ≤ 2 ppm THC and ≤ 20 ppm CBD, marking the first federally approved hemp-based feed ingredient in the United States.

Research on laying hens and broiler chickens indicates that hemp derivatives can be safely utilized in poultry feed formulations. For laying hens, hemp seed inclusion at 20–25% does not impair health or productivity (Shariatmadari, 2023). Hemp seed cake or meal has also been evaluated at 15–20% inclusion levels, with no major adverse effects on laying rate or egg weight reported in several studies (Lanzoni *et al.*, 2024). Furthermore, hemp oil has been tested mainly at 4–12% inclusion levels, showing improved egg yolk fatty acid profiles without consistent negative effects on laying performance (Lanzoni *et al.*, 2024). For broilers, responses are product- and condition-dependent even within the same ingredient category: Eriksson and Wall (2012) reported no impairment of growth performance with hemp seed cake at tested inclusion levels (10–20%, organic production), whereas Darmawan and Ozturk (2025) found that 15% hemp seed cake was associated with reduced final body weight, poorer feed conversion, and decreased villus height and surface area, indicating that outcomes vary depending on experimental conditions.

Although direct evidence on hemp-specific applications in livestock remains limited, the combined nutritional profile and bioactive constituents of hemp, including dietary

fiber, polyunsaturated fatty acids, and phytocannabinoids, suggest a potential role in modulating gastrointestinal function. In particular, these components may interact with gut microbiota and intestinal physiology; however, current evidence is still fragmented and largely indirect. Therefore, a comprehensive evaluation of the effects of hemp-derived ingredients on gut microbiota is needed to better understand their functional implications in animal nutrition.

EFFECTS OF HEMP AND CANNABINOIDS ON GUT MICROBIOTA IN RUMINANTS

The genus *Methanobrevibacter* constitutes a significant proportion of the rumen archaeal community (60–70%) and is classified into two primary subclades: the ‘high-methane’ *smithii–gottschalkii–millerae–thauri* (SGMT) group and the ‘low-methane’ *ruminantium–olleyae* (RO) group. Research indicates that these clades are associated with distinct methane emission phenotypes (St-Pierre *et al.*, 2015). The interplay between protozoa and methanogenic archaea is particularly noteworthy; defaunation studies suggest that the removal of protozoa can lead to a reduction in methane emissions (Wallace *et al.*, 2015). Additionally, compounds such as rumen terpenes and polyphenols are recognized for their potential to suppress microbial populations (Ku-Vera *et al.*, 2020), forming a theoretical basis for the methane mitigation capabilities of plant-derived secondary metabolites.

In light of this, the impact of hemp and its by-products on rumen microbiota and fermentation processes has been the focus of investigation. In research utilizing whole hemp biomass, *Cannabis sativa* residue (CSR) powder, and hemp essential oils, a notable finding across both *in vivo* and *in vitro* models (Table 2) is the observed increase in ruminal propionate levels, accompanied by a reduction in the abundance of methanogenic archaea or methane production (Hnokaew *et al.*, 2025; Ran *et al.*, 2024; Silva *et al.*, 2023). *In vitro* studies indicate that hemp-derived essential oils and cannabinoids can influence the rumen bacterial community and may help reduce methane production (Silva *et al.*, 2023; Tabiś *et al.*, 2024). *In vivo* research has demonstrated that the incorporation of hemp seed cake or green hemp biomass can modify rumen fermentation parameters, microbial composition, and nutrient digestion in ruminants (Früge *et al.*, 2025; Ran *et al.*, 2024; Stevens *et al.*, 2022; Wang *et al.*, 2023; Winders *et al.*, 2023a, b). Across studies employing 16S rRNA amplicon sequencing, beta diversity shifts indicate that hemp supplementation reorganises community composition without reducing overall microbial richness, a pattern functionally distinct from a diversity-depleting intervention. Notably, alterations in populations of *Prevotella*, *Ruminococcus*, and methanogenic archaea suggest a possible association with reduced methane production under specific experimental

conditions within the rumen microbial ecosystem (Irawan *et al.*, 2025; Winders *et al.*, 2023a).

Observed modifications in microbial taxa such as *Succinivibrionaceae*, *Prevotella*, and *Lachnospiraceae*, alongside increased propionate and decreased methane production across independent studies using different hemp products (Hnokaew *et al.*, 2025; Ran *et al.*, 2024; Silva *et al.*, 2023; Tabiś *et al.*, 2024), are consistent with the well-established rumen fermentation principle that propionate synthesis and methanogenesis compete for available metabolic hydrogen (Hnokaew *et al.*, 2025; Ku-Vera *et al.*, 2020; Wallace *et al.*, 2015). The convergence of this pattern across methodologically distinct studies strengthens the mechanistic inference; however, as no study in the reviewed literature directly measured dissolved hydrogen partial pressure or quantified hydrogen flux through competing pathways in hemp-fed ruminants, a causal relationship cannot yet be confirmed. Hnokaew *et al.* (2025) reported a 34–38% reduction in *in vitro* methane production and a significant increase in the propionic acid molar proportion at 1–2% CSR inclusion, accompanied by decreased *Methanobacteriales* abundance; CBD and THC in CSR were further shown by molecular docking to bind the active site of methyl-coenzyme M reductase with binding energies of –8.8 and –5.5 kcal/mol, respectively.

Hemp-related secondary metabolites, particularly terpenes such as E-B-caryophyllene, α -pinene, and B-myrcene, have the capacity to directly inhibit specific rumen microorganisms, including those implicated in methanogenesis. This potential mechanism may elucidate why whole-plant extracts or fractions rich in essential oils frequently produce more consistent outcomes than isolated cannabidiol. Supporting this hypothesis, Tabiś *et al.* (2024) quantified terpene profiles by GC-MS and found E-B-caryophyllene to be the predominant compound in *Cannabis* essential oils (18.4% in *Cannabis sativa*, 24.1% in *Cannabis indica*), alongside α -pinene and B-myrcene, and demonstrated that these oils alter rumen microbial populations and reduce methane production *in vitro*. However, the remaining ruminant studies reviewed here characterized their hemp products for cannabinoid and nutritional content only, without reporting terpene profiles; the role of terpenes in the fermentation effects observed in those studies therefore remains speculative and warrants direct investigation through standardized phytochemical characterisation.

The currently available evidence indicates that hemp-based feeds and cannabinoid-containing products may influence selected fermentation outcomes through shifts in specific components of the ruminal microbial ecosystem (Ran *et al.*, 2024; Silva *et al.*, 2023; Wang *et al.*, 2023; Winders *et al.*, 2023b).

Table 2: Summary of the effects of cannabinoid and hemp applications in ruminant and poultry.

Animal species	Sample size/ duration	Product/ Cannabinoid	Method	Key microbiota findings	Other Key Results	Reference
Ruminants						
Beef cattle (Angus cross heifers)	n=16 111 days	Hempseed cake (20%)	16S rRNA amplicon sequencing, MCC; Tukey HSD and Benjamini-Hochberg	Rumen beta-diversity altered ($R^2=0.06-0.12$, $p<0.05$), Shannon diversity $\uparrow$ ($p<0.05$); dominant phyla Bacteroidota (62.2%), Firmicutes (16.9%), Proteobacteria (16.3%)	Nasopharyngeal microbiota, also significantly affected, suggesting gut-respiratory linkage	Winders, Holman, <i>et al.</i> (2023a)
Dairy cattle (Holstein)	n=9 21 days	Industrial hemp ethanol extraction byproduct (11%)	16S rRNA amplicon sequencing, CC; Duncan's multiple range tests	Alpha diversity: no change ($p>0.10$), Rumen: <i>Bacteroidota</i> , <i>Fibrobacterota</i> , <i>Prevotellaceae</i> $\uparrow$; <i>Firmicutes</i> $\downarrow$, Feces: <i>Firmicutes</i> , <i>Lachnospiraceae</i> , <i>Monoglobaceae</i> $\uparrow$	Butyrate (-19.3%) and total VFA (-19.9%) $\downarrow$; milk yield and digestibility unaffected; CBD/THC not detected in milk	Wang <i>et al.</i> (2023)
<i>In vitro</i> rumen model, (Brahman x Thai Indigenious)	<i>In vitro</i>	<i>Cannabis sativa</i> L. residue powder (2%)	qPCR MCC; Duncan's multiple range tests	<i>Ruminococcus flavefaciens</i> $\downarrow$, <i>Methanobacteriales</i> $\downarrow$, $p<0.05$, exact fold NR	Methane production (-35%) $\downarrow$, Acetate /Propionate $\downarrow$, Propionate $\uparrow$, $\text{NH}_3\text{-N}$ $\uparrow$, exact ratio NR	Hno-kaew <i>et al.</i> (2025)
<i>In vitro</i> rumen model (Angus x Holstein steers)	<i>In vitro</i>	CBD (different concentrations)	Culture MCC; Tukey HSD	The viable cell count of hyper-ammonia-producing bacteria and generalist amino acid-fermenting bacteria remained unchanged	Ammonia production: $\downarrow$ by ~10–15 mM at highest concentration (860 $\mu\text{g/mL}$) ($p < 0.05$)	Lakes <i>et al.</i> (2024)
<i>In vitro</i> rumen model	<i>In vitro</i>	CBD (different concentrations; hemp varieties) and alfalfa	16S rRNA amplicon sequencing, MCC; ANCOM testing	Alpha diversity: alfalfa highest; no difference between CBD levels Beta diversity: alfalfa clustered separately from all hemp groups. Dominant phyla: Firmicutes, Bacteroidetes, Proteobacteria, Fusobacteria Alfalfa > Hemp: <i>Aerococcaceae</i> and <i>Enterobacteriaceae</i> Alfalfa < Hemp: <i>Lactobacillales</i> , <i>Streptococcaceae</i> , <i>Succinivibrionaceae</i> , <i>Bacilli</i>	No diversity differences between CBD levels; substrate type (alfalfa vs hemp) more influential than CBD concentration on microbiome structure	Silva <i>et al.</i> (2023)*
<i>In vitro</i> rumen model	<i>In vitro</i>	Essential oils (EOs) from <i>Cannabis sativa</i> and <i>Cannabis indica</i> (50 μL or 100 μL)	qPCR MCC; Bonferroni	Modulation of rumen microbial populations; notable effects on <i>Lactobacillus</i> spp. ($p<0.01$) and <i>Butyrivibrio</i> spp. ($p<0.05$) $\downarrow$	Acetate ($\uparrow$, 6h, +15.4%, <i>C. Indica</i> 100 μL) and Propionate ($\uparrow$, 6h, +3%, <i>C. Indica</i> 100 μL) Acetate/propionate ratio $\downarrow$, 24h, <i>C. indica</i> 100, -20%, $p<0.05$). Methane production ($\downarrow$, 6h, -27.7%, <i>C. Indica</i> 100 μL)	Tabiś <i>et al.</i> (2024)
Goats (Xiangdong black goats)	n=10 60 days	Hemp forage (stems and leaves; 5%, 10%, or 20% in diet, substituting alfalfa hay)	16S rRNA amplicon sequencing, MCC; NR	Alpha diversity: No effect ($p>0.05$); <i>Prevotella_1</i> $\downarrow$ ($p=0.040$, exact ratio NR), <i>Rikenellaceae_RC9_gut_group</i> $\uparrow$ $p=0.017$, exact ratio NR), Tenericutes $\uparrow$	In 20% hemp forage group FCR $\downarrow$ (-18.4%), $\text{NH}_3\text{-N}$ $\uparrow$ (+25.1%) $\downarrow$, Propionate $\uparrow$ (+15.2%), VFAs $\uparrow$ (+34.4% in 10% hemp forage group), cannabinoids/metabolites detected in rumen fluid and plasma; none detected in meat.	Ran <i>et al.</i> (2024)

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Animal species	Sample size/ duration	Product/ Cannabinoid	Method	Key microbiota findings	Other Key Results	Reference
Goats (Alpine dairy goats)	n=6 140 days	Hemp seeds (9.3%)	16S rRNA amplicon sequencing MCC; NR	Hemp did not significantly alter major bacterial genera	ruminal linoleic acid ↑ (+63%), milk fat ↑ (from 3.39% to 3.69%)	Cremonesi <i>et al.</i> (2018)
Buffalo (dairy crossbred)	n=5 42 days	Hemp seed oil	16S rRNA amplicon sequencing MCC; NR	Alpha diversity: No effect <i>Engyodontium</i> ↑ (p=0.047) and <i>Sarocladium</i> ↑ (p=0.031)	Lactic acid ↑ (+80.5%), Acetate /Propionate ↓ (-21.4)	Zhou <i>et al.</i> (2022)
Poultry						
Ross 308 line male broilers (<i>C. perfringens</i> -challenged)	n=72 8 replicates 35 days	CBD (15 g/kg)	qPCR MCC; LSD	Abundance of Total bacteria, <i>C. perfringens</i> , <i>Lactobacillus</i> spp. <i>Bi-fidobacterium</i> spp. not changed in cecal digesta	ADG and final BW not changed	Kinsner <i>et al.</i> (2025)
Ross 308 line male broilers	n=25 42 days	10-30 g/kg Hemp leaves (242.5 µg/kg CBD)	Culture MCC; Bonferroni	Faecal <i>E. coli</i> ↓ (p<0.0001, from 5.53 to 3.13 log ₁₀ CFU)	CD4 ⁺ lymphocyte ↑ (p<0.0001, exact ratio NR), CD8 ⁺ lymphocyte ↑ (p<0.0001, exact ratio NR)	Baleno- vić <i>et al.</i> (2024)
Unsexed Ross 308 broilers	n=30 6 replicates 42 days	Hemp seed cake (15%), autoclaved (120°C)	Culture MCC; Duncan's multiple range tests	Caecal <i>E. coli</i> ↓ (p<0.01, from 4.00 to 3.47 log ₁₀ CFU), <i>Lactobacillus acidophilus</i> ↑ (p<0.01, from 3.62 to 4.32 log ₁₀ CFU)	Final BW ↓ (-22.1%, p<0.01), DFCR ↑ (+17.8%, p<0.01), villus height (-31.3%, p<0.01) and surface area ↓ (45.9%, p<0.01)	Dar- mawan and Ozturk (2025)
Cari- bro-Vishal broiler chicks	n=32 4 replicates 42 days	Hemp seed (0.2-0.3%)	Culture MCC; Tukey HSD	Jejunal total coliforms ↓ (p<0.01, from 7.32 to 6.35 log ₁₀ CFU) Caecal total <i>Lactobacillus</i> spp. ↑ (p<0.001, from 7.90 to 8.61 log ₁₀ CFU)	ADG, final BW and intestinal histomorphology not changed	Vispute <i>et al.</i> (2019)
<i>In vitro</i> cecal fermentation by broiler microbiota	<i>In vitro</i>	Micronized hemp fiber (0.75-1.5%)	Culture MCC; Duncan's multiple range tests	Total bacteria ↑ (p=0.005, from 9.10 to 9.30 log ₁₀ CFU), <i>Lactobacillus</i> spp. ↑ (p=0.001, from 8.10 to 8.60 log ₁₀ CFU), <i>Enterococcus</i> spp. ↑ (p=0.001, from 7.20 to 7.90 log ₁₀ CFU), <i>E. coli</i> ↓ (p=0.001, from 5.30 to 4.50 log ₁₀ CFU),	Lactic acid: ↑ (+19.6%, p=0.006); total VFA: ↑ (+28.4%, p=0.004); acetic acid: ↑ (+19.9%, p=0.002); propionic acid: ↑ (+22.9%, p=0.001); butyric acid: ↑ (+42.9%, p=0.001); final BW: ↑ (+13.7%, p<0.001); ADG: ↑ (+19.5%, p<0.001); FCR: ↓ (-14.3%, p<0.001)	Inchar- oen <i>et al.</i> (2025)
Ross 308 hybrid cockerels	n=50 37 days	2.5% Hemp seed expellers (0.03% CBD) or 1% hemp plant tops (0.015% CBD)	Culture MCC; Scheffé's test	Ileal <i>E. coli</i> , <i>Lactobacillus</i> spp. and <i>Enterococcus</i> spp not changed	FCR and final BW not changed	Štastník <i>et al.</i> (2016)*
Unsexed Ross 308 broilers, organic production	n=600 70 days	Hemp seed cake (10% for starter-20% for finisher)	Culture MCC: not required	Caecal content of <i>C. perfringens</i> not changed	FCR and final BW not changed	Eriksson and Wall (2012)

Average daily gain: ADG, Body weight: BW, Cannabidiol: CBD, cluster of differentiation: CD, Feed conversion ratio: FCR, Volatile fatty acids: VFA, Δ9-tetrahydrocannabinol: THC, not reported: NR, MCC: Multiple comparison correction, * Conference paper

and modulation of microbial metabolic activity (Hnokaew *et al.*, 2025), with the relative contribution of each pathway remaining unclear given the heterogeneity of available evidence. Interpretation remains difficult because product composition, dietary background, and analytical methodology vary substantially across studies, and no published study has directly measured ECS receptor activation as a mechanistic endpoint in the context of dietary hemp supplementation in ruminants. Accordingly, the present evidence base is insufficient to support the use of hemp-derived products as microbiota-targeted interventions in ruminant nutrition. Until controlled *in vivo* trials with standardised hemp preparations, quantified cannabinoid profiles, and direct microbiota endpoints, including, where feasible, receptor-level measurements, are conducted across multiple ruminant species, the fermentation and community composition changes reported to date should be interpreted as preliminary observations rather than actionable findings (Table 2).

EFFECTS OF HEMP AND CANNABINOIDS ON GUT MICROBIOTA IN POULTRY

Broiler production constitutes a significant sector for hemp-based feed supplementation, particularly in response to industry-wide pressures to diminish prophylactic antibiotic usage in accordance with global antimicrobial stewardship initiatives. Of the poultry studies reviewed, four reported reductions in *E. coli* or coliform counts and three reported increases in *Lactobacillus* populations (Balenović *et al.*, 2024; Darmawan and Ozturk, 2025; Incharoen *et al.*, 2025; Vispute *et al.*, 2019), while one reported no change in *Lactobacillus* or *C. perfringens* abundance under CBD supplementation (Kinsner *et al.*, 2025).

The effects of hemp derivatives on gastrointestinal health and the microbiota warrant further investigation. Some studies suggest that hemp products may not substantially affect the gut microbiota (beneficial or pathogenic) (Eriksson and Wall, 2012) whereas other findings indicate a potential role in promoting beneficial bacteria (Vispute *et al.*, 2019). These different results could be due to differences in how the products are made, how much is administered, the age of the animals being tested, and the experimental conditions. In broiler chickens, inclusion of hemp seed meal and micronized hemp fiber significantly increases *Lactobacillus* populations while reducing *Escherichia coli* counts in the cecum (Darmawan and Ozturk, 2025; Incharoen *et al.*, 2025). Hemp fiber may act via a possible prebiotic-like mechanism by supporting saccharolytic fermentation (Nissen *et al.*, 2023), thereby enhancing *Lactobacillus* spp. populations and increases the production of lactic acid and short-chain fatty acids. This process potentially lowers luminal pH and suppresses pathogen growth, as suggested by Incharoen *et al.* (2025). In

broiler chickens, micronized hemp fiber supplementation at 0.75–1.50% of diet significantly increased *in vitro* cecal SCFA concentrations ($p < 0.01$): total VFA increased from 29.2 to 37.5 mmol/mL (+28%), driven by +20% acetic acid, +23% propionic acid, and +43% butyric acid (Incharoen *et al.*, 2025).

CBD supplementation has been evaluated under *C. perfringens* challenge models designed to mimic necrotic enteritis. CBD exerted its effects mainly through modulation of intestinal barrier function, immune responses, and oxidative status (Bień *et al.*, 2024). CBD administration was linked to changes in tight-junction-related markers and expression and shifting bacterial enzyme activity toward increased energy uptake (Konieczka *et al.*, 2020). Hemp bioactives may indirectly support intestinal health by modulating immune functions in immune tissues rich in CB2R receptors, such as the gut-associated lymphoid tissue in chickens (Ghazi *et al.*, 2026). In this context, the immunomodulatory role of CB2R described by Turcotte *et al.* (2016), along with the increased CD4+ and CD8+ lymphocyte responses observed in broilers by Balenović *et al.* (2024), suggests that some microbiota-related benefits might arise not only from direct antimicrobial actions but also from improved mucosal immune surveillance. Sopian *et al.* (2024) reported that *Cannabis sativa* residue supplementation at 1% of diet significantly improved the villus height-to-crypt depth ratio in the ileum ($p = 0.011$) and reduced plasma malondialdehyde and total bilirubin concentrations, suggesting improved intestinal morphology and oxidative stability without adverse effects on growth performance or blood biochemistry at inclusion levels of 0.5–2%. Sana *et al.* (2024) reported that hemp seed inclusion at 15–20% significantly increased white blood cell counts ($p = 0.037$) and transiently elevated IgM and IgG production at 20% inclusion on day 28 ($p = 0.021$); however, these immune effects were not sustained to day 35, and jejunal histomorphology, including villus height, width, and crypt depth, was not significantly affected at any tested inclusion level ($p > 0.05$), with only a non-significant numerical trend toward increased villus height at higher inclusion levels.

The mechanism underlying CBD-mediated improvement of intestinal barrier function in poultry is not fully established. Szkopek *et al.* (2024) provided the most direct poultry-specific mechanistic evidence to date, demonstrating that CBD significantly modulates PPAR α expression in the broiler gut under both *C. perfringens* and LPS challenge conditions ($p = 0.001$), with PPAR activity positively correlated with tight junction gene expression. Cannabidiol-mediated improvement of intestinal barrier function may operate through targets such as TRPV1, GPR55, and inflammation-related signaling cascades (Brown *et al.*, 2024), thereby supporting tight junction

integrity and making epithelial colonization more difficult for opportunistic pathogens; this interpretation is consistent with the findings of Konieczka *et al.* (2022) in challenged chickens and with the barrier-protective effects of CBD on intestinal cells described by Boehm *et al.* (2023). However, TRPV1 and GPR55 have not been confirmed by receptor blockade studies in poultry and remain working hypotheses derived from mammalian pharmacology.

The poultry studies (Table 2) exhibit a more heterogeneous pattern than the ruminant data, reflecting greater diversity in hemp preparation type, inclusion level, and microbiota assessment methodology. Future studies should preferentially employ 16S rRNA amplicon sequencing (V3–V4 or V1–V3 regions) as a minimum standard for microbiota characterization to enable cross-study comparability and robust taxonomic resolution. The existing literature indicates that research on the effects of hemp-derived products on gastrointestinal microbiota and intestinal health in poultry has predominantly focused on broiler chickens, while data on laying hens remain limited (Table 2). Furthermore, microbiota-related evidence for other poultry species such as quail, turkey, goose, and duck is absent. In addition, current evidence is largely restricted to CBD and hemp seed by-products, and no published data exists on the effects of THC or minor cannabinoids on the poultry gut microbiota.

LIMITATIONS

Several methodological and empirical limitations impede our current understanding and render it challenging to draw definitive conclusions from existing research. Firstly, the available mechanistic evidence on cannabinoid–microbiota interactions in farm animals remains limited; this gap reflects the deliberate scope of the present review, which focuses on ruminants and poultry rather than extrapolating from preclinical mammalian models. Future studies should directly examine cannabinoid–microbiota mechanisms in the species relevant to livestock production. Secondly, most *in vivo* studies employed limited sample sizes and short durations. For cattle, the median sample size was 12.5 animals per group (range 9–16) and median duration was 66 days (21–111). For goats, median *n*=8 (6–10) and 100 days (60–140). For broilers, median *n*= 41 (25–600) and 42 days (35–70). These limited scales constrain insights into long-term microbiota adaptations and inter-individual variability (Table 2). Thirdly, a prevalent issue involves inconsistent standardization of preparations derived from hemp: discrepancies in botanical sources, extraction techniques, purity levels, and phytocannabinoid profiles across studies hinder direct comparisons. Seven studies reported only primary cannabinoid content (CBD and/or THC), and a single study (Tabis *et al.*, 2024) performed terpene profiling by GC-MS; the remaining studies

supplied no chemical characterization at all. Fourthly, the use of diverse microbiota assessment methods, including 16S rRNA sequencing, qPCR, and culture-based techniques, introduces substantial methodological heterogeneity and limits direct comparability across studies. We therefore did not exclude studies based on methodology alone, as the current literature remains too limited to permit such filtering without losing relevant evidence. While this inclusive approach is appropriate for a narrative review, it precludes meta-analysis and prevents any claim of quantitative synthesis. Finally, the available livestock studies do not provide sufficient paired data on gastrointestinal cannabinoid exposure and microbiota outcomes to assess concentration–response relationships. This absence of segment-specific exposure data limits mechanistic interpretation and should be addressed in future studies. Consequently, the mechanistic relationship between bioavailability and microbial response remains inadequately elucidated.

FUTURE DIRECTIONS

Despite increasing interest in the therapeutic and nutritional advantages of hemp-derived compounds, limited evidence remains regarding their impact on the gut microbiota of livestock animals. The effect of feeding hemp and its by-products on the animal microbiome is still insufficiently characterized, with extant research primarily concentrating on digestibility and growth performance rather than microbiome alterations. Furthermore, current available microbiome data are largely restricted to ruminants and poultry, thus leaving a substantial knowledge gap concerning monogastric animals such as pigs and horses. Future research should endeavor to execute controlled trials in pigs and horses employing techniques such as 16S rRNA sequencing and shotgun metagenomics. The hemp–microbiota interplay represents an emerging candidate mechanism, but current livestock evidence remains insufficient for routine application. Preliminary findings suggest *Lactobacillus* enrichment and *E. coli* suppression in poultry, together with SCFA and fermentation-related modulation in ruminants. However, practical antibiotic-sparing or sustainable production applications require confirmation through standardized, species-specific controlled trials.

CONCLUSION

The current evidence indicates that dietary hemp derivatives may affect certain microbiota-related outcomes in ruminants and broilers, but the effects are species-, product-, and context-dependent. In broilers, the most common findings are reductions in *E. coli* or coliform counts and increases in *Lactobacillus* abundance following supplementation with

hempseed products or hemp fiber. In ruminants, the most reported effects are changes in rumen fermentation, SCFA profiles, microbial groups involved in methanogenesis, and microbial community composition. Hempseed cake may be considered for use as a partial protein source for broilers only after product-specific formulation, regulatory compliance, and performance monitoring. For ruminants, no clear microbiota-based recommendation can be made at present because of heterogeneous fermentation responses and unresolved safety concerns regarding cannabinoid residues, particularly in milk. Future studies should address standardization of hemp product characterization, defined inclusion criteria, adequate sample size and experimental duration, comparable microbiota assessment methods, and concurrent phytochemical and performance analyses.

ACKNOWLEDGEMENT

The authors have no acknowledgements to declare.

NOVELTY STATEMENT

This review provides a focused synthesis of the dietary hemp–gut microbiome interplay in ruminants and broilers by integrating evidence on microbial composition, fermentation, intestinal barrier function, and endocannabinoid-related mechanisms.

AUTHOR'S CONTRIBUTION

ES wrote the original draft and reviewed the manuscript. SBS wrote parts of the original draft and reviewed the manuscript. All the authors read and approved the final manuscript.

DATA AVAILABILITY

Not applicable, as it is a review article and no datasets were generated.

GENERATIVE AI AND AI ASSISTED TECHNOLOGY STATEMENT

The authors utilized generative artificial intelligence (AI) exclusively for language editing and grammatical corrections.

CONFLICT OF INTEREST

The authors have declared no conflict of interest.

REFERENCES

- Andre CM, Hausman JF, Guerriero G (2016). *Cannabis sativa*: The plant of the thousand and one molecules. *Front. Plant Sci.*, 7: 19. <https://doi.org/10.3389/fpls.2016.00019>
- Aruwa CE, Pillay C, Nyaga MM, Sabiu S (2021). Poultry

- gut health-microbiome functions, environmental impacts, microbiome engineering and advancements in characterization technologies. *J. Anim. Sci. Biotechnol.*, 12(1): 119. <https://doi.org/10.1186/s40104-021-00640-9>
- Balenović M, Janječić Z, Savić V, Kasap A, Popović M, Šimpraga B, Sokolović M, Bedeković D, Kiš G, Zglavnik T, Špoljarić D, Krstulović F, Listić I, Zelenika TA (2024). Immunostimulatory and antibacterial effects of *Cannabis sativa* L. leaves on broilers. *Animals*, 14(8): 1159. <https://doi.org/10.3390/ani14081159>
- Belkaid Y, Hand TW (2014). Role of the microbiota in immunity and inflammation. *Cell*, 157(1): 121-141. <https://doi.org/10.1016/j.cell.2014.03.011>
- Bień D, Michalczyk M, Józwik A, Matuszewski A, Konieczka P (2024). Effects of *Cannabis sativa* extract on growth performance, meat physicochemical properties, and oxidative status in chickens challenged with *Clostridium perfringens* and lipopolysaccharide. *Anim. Sci. Pap. Rep.*, 42(1): 81-108. <https://doi.org/10.2478/aspr-2023-0024>
- Boehm E, Droessler L, Amasheh S (2023). Cannabidiol attenuates inflammatory impairment of intestinal cells expanding biomaterial-based therapeutic approaches. *Mater. Today Bio*, 23: 100808. <https://doi.org/10.1016/j.mtbio.2023.100808>
- Borrelli F, Fasolino I, Romano B, Capasso R, Maiello F, Coppola D, Orlando P, Battista G, Pagano E, Di Marzo V, Izzo AA (2013). Beneficial effect of the non-psychoactive plant cannabinoid cannabigerol on experimental inflammatory bowel disease. *Biochem. Pharmacol.*, 85(9): 1306-1316. <https://doi.org/10.1016/j.bcp.2013.01.017>
- Brown K, Funk K, Figueroa Barrientos A, Bailey A, Shrader S, Feng W, McClain CJ, Song Z-H (2024). The modulatory effects and therapeutic potential of cannabidiol in the gut. *Cells*, 13(19): 1618. <https://doi.org/10.3390/cells13191618>
- Cani PD, Plovier H, Van Hul M, Geurts L, Delzenne NM, Druart C, Everard A (2016). Endocannabinoids- at the crossroads between the gut microbiota and host metabolism. *Nat. Rev. Endocrinol.*, 12(3): 133-143. <https://doi.org/10.1038/nrendo.2015.211>
- Choi JH, Kim GB, Cha CJ (2014). Spatial heterogeneity and stability of bacterial community in the gastrointestinal tracts of broiler chickens. *Poult. Sci.*, 93(8): 1942-1950. <https://doi.org/10.3382/ps.2014-03974>
- Cremonesi P, Conte G, Severgnini M, Turri F, Monni A, Capra E, Rapetti L, Colombini S, Chessa S, Battelli G, Alves SP, Mele M, Castiglioni B (2018). Evaluation of the effects of different diets on microbiome diversity and fatty acid composition of rumen liquor in dairy goat. *Animal*, 12(9): 1856-1866. <https://doi.org/10.1017/S1751731117003433>
- Darmawan A, Ozturk E (2025). Effect of dietary heated hemp seed cake and phytase as soybean meal substitution on broiler chicken performance, carcass yield, visceral organ weight, intestinal health, and serum biochemical parameters. *Trop. Anim. Health Prod.*, 57(3): 162. <https://doi.org/10.1007/s11250-025-04416-5>
- Eriksson M, Wall H (2012). Hemp seed cake in organic broiler diets. *Anim. Feed Sci. Technol.*, 171(2): 205-213. <https://doi.org/10.1016/j.anifeedsci.2011.10.007>
- Fallahi S, Bobak Ł, Opaliński S (2022). Hemp in animal diets-cannabidiol. *Animals*, 12(19): 2541. <https://doi.org/10.3390/ani12192541>
- Farha MA, El-Halfawy OM, Gale RT, MacNair CR, Carfrae LA, Zhang X, Jentsch NG, Magolan J, Brown ED (2020).

- Uncovering the hidden antibiotic potential of cannabis. *ACS Infect. Dis.*, 6(3): 338-346. <https://doi.org/10.1021/acsinfectdis.9b00419>
- Farinon B, Molinari R, Costantini L, Merendino N (2020). The seed of industrial hemp (*Cannabis sativa* L.): Nutritional quality and potential functionality for human health and nutrition. *Nutrients*, 12(7): 1935.
- Finet S, He F, Utterback PL, Parsons CM, de Godoy MRC (2023). Nutrient profile, amino acid digestibility, true metabolizable energy, and indispensable amino acid scoring of whole hemp seeds for use in canine and feline diets. *J. Anim. Sci.*, 101: skad106. <https://doi.org/10.1093/jas/skad106>
- Flint HJ, Scott KP, Duncan SH, Louis P, Forano E (2012). Microbial degradation of complex carbohydrates in the gut. *Gut Microbes*, 3(4): 289-306. <https://doi.org/10.4161/gmic.19897>
- Formato M, Crescente G, Scognamiglio M, Fiorentino A, Pecoraro MT, Piccolella S, Catauro M, Pacifico S (2020). (–)-Cannabidiolic acid, a still overlooked bioactive compound: An introductory review and preliminary research. *Molecules*, 25(11): 2638. <https://doi.org/10.3390/molecules25112638>
- Früge G, Jessup R, Suter J, Fortunatti S, Drewery ML (2025). The effect of hemp leaves on intake, digestion, and rumen fermentation parameters in beef steers. *Livest. Sci.*, 300: 105782. <https://doi.org/10.1016/j.livsci.2025.105782>
- Ghazi Sahn S, Louei Monfared A, Sharoot H (2026). Immunofluorescence localization of cannabinoid receptor type 2 in the ileum of juvenile and adult chickens (*Gallus domesticus*) and its association with gga-miR-200a-3p and oxidative stress. *Iraqi J. Vet. Sci.*, 40(1): 131-139. <https://doi.org/10.33899/ijvs.2025.163438.4423>
- Henderson G, Cox F, Ganesh S, Jonker A, Young W, Global Rumen Census Collaborators, Janssen PH (2015). Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. *Sci. Rep.*, 5: 14567.
- Hnokaew P, Arjin C, Satsook A, Halder JN, Tateing S, Potapohn N, Sringarm K (2025). Harnessing bioactive compounds from *Cannabis sativa* residue to improve rumen fermentation and reduce methane production: *in silico*, *in vitro*, and *in situ* nylon bag studies. *BMC Vet. Res.*, 21(1): 611. <https://doi.org/10.1186/s12917-025-04985-5>
- Ibeas Bih C, Chen T, Nunn AV, Bazelot M, Dallas M, Whalley BJ (2015). Molecular targets of cannabidiol in neurological disorders. *Neurotherapeutics*, 12(4): 699-730. <https://doi.org/10.1007/s13311-015-0377-3>
- Incharoen T, Nopparatmaitree M, Kongkeaw A, Soisuwan K, Likittrakulwong W, Thongnum A, Norbu N, Tenzin J, Supatsaraphokin N, Loo JJ (2025). Dietary micronized hemp fiber enhances *in vitro* nutrient digestibility and cecal fermentation, antioxidant enzyme, lysosomal activity, and productivity in finisher broilers reared under thermal stress. *Front. Anim. Sci.*, 6: 1553829. <https://doi.org/10.3389/fanim.2025.1553829>
- Irawan A, Buffington H, Ates S, Bionaz M (2025). Use of industrial hemp byproducts in ruminants: A review of the nutritional profile, animal response, constraints, and global regulatory environment. *J. Cannabis Res.*, 7(1): 25. <https://doi.org/10.1186/s42238-025-00279-7>
- Izzo AA, Sharkey KA (2010). Cannabinoids and the gut: New developments and emerging concepts. *Pharmacol. Ther.*, 126(1): 21-38. <https://doi.org/10.1016/j.pharmthera.2009.12.005>
- Kent-Dennis C, Klotz JL (2024). The endocannabinoid system in bovine tissues: characterization of transcript abundance in the growing Holstein steer. *BMC Vet. Res.*, 20(1): 481. <https://doi.org/10.1186/s12917-024-04319-x>
- Kers JG, Velkers FC, Fischer EAJ, Hermes GDA, Stegeman JA, Smidt H (2018). Host and Environmental Factors Affecting the Intestinal Microbiota in Chickens. *Front. Microbiol.*, 9: 235. <https://doi.org/10.3389/fmicb.2018.00235>
- Khan MT, Zohair M, Khan A, Kashif A, Mumtaz S, Muskan F (2025). From Gut to Brain: The roles of intestinal microbiota, immune system, and hormones in intestinal physiology and gut-brain-axis. *Mol. Cell. Endocrinol.*, 607: 112599. <https://doi.org/10.1016/j.mce.2025.112599>
- Kinsner M, Szkopek D, Jaworska D, Kotlarska A, Przybylski W, Bień D, Michalczyk M, Cieślak A, Kozłowski K, Matusevičius P, Konieczka P (2025). Dietary cannabidiol and nanoselenium mediates post-infection changes in the profiles of fatty acids, sarcoplasmic proteins, and meat properties of *C. perfringens* challenged chickens. *Anim. Feed Sci. Technol.*, 329: 116487. <https://doi.org/10.1016/j.anifeedsci.2025.116487>
- Konieczka P, Szkopek D, Kinsner M, Fotschki B, Juśkiewicz J, Banach J (2020). Cannabis-derived cannabidiol and nanoselenium improve gut barrier function and affect bacterial enzyme activity in chickens subjected to *C. perfringens* challenge. *Vet. Res.*, 51(1): 141. <https://doi.org/10.1186/s13567-020-00863-0>
- Konieczka P, Wojtasik-Kalinowska I, Poltorak A, Kinsner M, Szkopek D, Fotschki B, Juśkiewicz J, Banach J, Michalczyk M (2022). Cannabidiol affects breast meat volatile compounds in chickens subjected to different infection models. *Sci. Rep.*, 12(1): 18940. <https://doi.org/10.1038/s41598-022-23591-1>
- Ku-Vera JC, Jiménez-Ocampo R, Valencia-Salazar SS, Montoya-Flores MD, Molina-Botero IC, Arango J, Gómez-Bravo CA, Aguilar-Pérez CF, Solorio-Sánchez FJ (2020). Role of secondary plant metabolites on enteric methane mitigation in ruminants. *Front. Vet. Sci.*, 7: 584. <https://doi.org/10.3389/fvets.2020.00584>
- Lakes JE, Davis BE, Flythe MD (2024). Activity of Cannabidiol on *ex vivo* amino acid fermentation by bovine rumen microbiota. *Fermentation*, 10(6): 267. <https://doi.org/10.3390/fermentation10060267>
- Lanzoni D, Skrivanova E, Pinotti L, Rebucci R, Baldi A, Giromini C (2024). Review: Nutritional aspects of hemp-based products and their effects on health and performance of monogastric animals. *Animal*, 18(2): 101058. <https://doi.org/10.1016/j.animal.2023.101058>
- Li S, Li W, Malhi NK, Huang J, Li Q, Zhou Z, Wang R, Peng J, Yin T, Wang H (2024). Cannabigerol (CBG): A comprehensive review of its molecular mechanisms and therapeutic potential. *Molecules*, 29(22): 5471. <https://doi.org/10.3390/molecules29225471>
- Liang J, Zhang R, Chang J, Chen L, Nabi M, Zhang H, Zhang G, Zhang P (2024). Rumen microbes, enzymes, metabolisms, and application in lignocellulosic waste conversion: A comprehensive review. *Biotechnol. Adv.*, 71: 108308. <https://doi.org/10.1016/j.biotechadv.2024.108308>
- Lima TM, Santiago NR, Alves ECR, Chaves DSA, Visacri MB (2022). Use of cannabis in the treatment of animals: a systematic review of randomized clinical trials. *Anim.*

- Health Res. Rev., 23(1): 25-38. <https://doi.org/10.1017/S1466252321000189>
- Lynch SV, Pedersen O (2016). The human intestinal microbiome in health and disease. N. Engl. J. Med., 375(24): 2369-2379. <https://doi.org/10.1056/NEJMra1600266>
- Maccarrone M, Di Marzo V, Gertsch J, Grether U, Howlett AC, Hua T, Makriyannis A, Piomelli D, Ueda N, van der Stelt M (2023). Goods and bads of the endocannabinoid system as a therapeutic target: Lessons learned after 30 years. Pharmacol. Rev., 75(5): 885-958. <https://doi.org/10.1124/pharmrev.122.000600>
- Mizrahi I, Wallace RJ, Morais S (2021). The rumen microbiome: Balancing food security and environmental impacts. Nat. Rev. Microbiol., 19(9): 553-566. <https://doi.org/10.1038/s41579-021-00543-6>
- Morales P, Hurst DP, Reggio PH (2017). Molecular targets of the phytocannabinoids: A complex picture. Prog. Chem. Org. Nat. Prod., 103: 103-131. https://doi.org/10.1007/978-3-319-45541-9_4
- Nissen L, Casciano F, Babini E, Gianotti A (2023). Beneficial metabolic transformations and prebiotic potential of hemp bran and its alcalase hydrolysate, after colonic fermentation in a gut model. Sci. Rep., 13(1): 1552. <https://doi.org/10.1038/s41598-023-27726-w>
- Oakley BB, Lillehoj HS, Kogut MH, Kim WK, Maurer JJ, Pedroso A, Lee MD, Collett SR, Johnson TJ, Cox NA (2014). The chicken gastrointestinal microbiome. FEMS Microbiol. Lett., 360(2): 100-112. <https://doi.org/10.1111/1574-6968.12608>
- Osiak-Wicha C, Muszyński S, Tomaszewska E, Kras K, Ropka-Molik K, Zhyla M, Arciszewski MB (2024). Gene expression level and immunohistochemical localization of cannabinoid and cannabinoid-related receptors in the small intestine of Holstein Bulls (*Bos Taurus Taurus*). Ann. Anim. Sci., 24(3): 779-789. <https://doi.org/10.2478/aoas-2024-0016>
- Pertwee RG (2008). The diverse CB1 and CB2 receptor pharmacology of three plant cannabinoids: delta9-tetrahydrocannabinol, cannabidiol and delta9-tetrahydrocannabivarin. Br. J. Pharmacol., 153(2): 199-215. <https://doi.org/10.1038/sj.bjp.0707442>
- Radwan MM, Chandra S, Gul S, ElSohly MA (2021). Cannabinoids, phenolics, terpenes and alkaloids of cannabis. Molecules, 26(9): 2774. <https://doi.org/10.3390/molecules26092774>
- Ran T, Xu Z, Yang W, Liu D, Wu D (2024). Partially substituting alfalfa hay with hemp forage in the diet of goats improved feed efficiency, ruminal fermentation pattern and microbial profiles. Anim. Nutr., 17: 49-60. <https://doi.org/10.1016/j.aninu.2024.01.003>
- Russo EB (2011). Taming THC: Potential cannabis synergy and phytocannabinoid-terpenoid entourage effects. Br. J. Pharmacol., 163(7): 1344-1364. <https://doi.org/10.1111/j.1476-5381.2011.01238.x>
- Sana B, Chand N, Naz S, Alhidary IA, Khan RU, Shamsi S, Losacco C, Tufarelli V (2024). Effects of hempseed (*Cannabis sativa* L.) in diet on growth, gut health, and immunity in broilers. Vet. Q., 44(1): 1-10. <https://doi.org/10.1080/01652176.2024.2367214>
- Sepulveda DE, Vrana KE, Kellogg JJ, Bisanz JE, Desai D, Graziane NM, Raup-Konsavage WM (2024). The potential of cannabichromene (CBC) as a therapeutic agent. J. Pharmacol. Exp. Ther., 391(2): 206-213. <https://doi.org/10.1124/jpet.124.002166>
- Shariatmadari F (2023). Emergence of hemp as feed for poultry. World's Poult. Sci. J., 79(4): 769-782. <https://doi.org/10.1080/00439339.2023.2234871>
- Silva A, Franco AM, Brody T, Frese S, Fonseca MA (2023). PSXIII-20 the effect of hemp varieties and cannabidiol concentrations on the *in vitro* ruminal microbiome. J. Anim. Sci., 101(Supplement_3): 647-648. <https://doi.org/10.1093/jas/skad281.753>
- Silvestri C, Di Marzo V (2023). The gut microbiome-endocannabinoidome axis: A new way of controlling metabolism, inflammation, and behavior. Function, 4(2): zqad003. <https://doi.org/10.1093/function/zqad003>
- Smith DJ, Serum EM, Winders TM, Neville B, Herges GR, Dahlen CR, Swanson KC (2023). Excretion and residue depletion of cannabinoids in beef cattle fed hempseed cake for 111 days. Food Addit. Contam. Part A, 40(4): 552-565. <https://doi.org/10.1080/19440049.2023.2187645>
- Sopian Y, Sartsook A, Arjin C, Lumsangkul C, Sringarm K, Sivapirunthep P, Chaosap C (2024). Dietary supplementation of *Cannabis sativa* residues in broiler chickens affects performance, carcass characteristics, intestinal morphology, blood biochemistry profile and oxidative stability. Poult. Sci., 103(10): 104117. <https://doi.org/10.1016/j.psj.2024.104117>
- Štastník O, Karásek F, Štenclová H, Burdová E, Kalhotka L, Trojan V, Vyhnánek T, Pavlata L, Mrkvicová E (2016). The effect of hemp by-products feeding on gut microbiota and growth of broiler chickens. Mendel. Net., 23: 289-293. <https://mendelnet.cz/pdfs/mnt/2016/01/52.pdf>
- Stevens SA, Krebs GL, Scrivener CJ, Noble GK, Blake BL, Dods KC, May CD, Tai ZX, Clayton EH, Lynch EE, Johnson KN (2022). Nutrient digestibility, rumen parameters, and (cannabinoid) residues in sheep fed a pelleted diet containing green hemp (*Cannabis sativa* L.) biomass. Transl. Anim. Sci., 6(4): txac141. <https://doi.org/10.1093/tas/txac141>
- St-Pierre B, Cersosimo LM, Ishaq SL, Wright A-DG (2015). Toward the identification of methanogenic archaeal groups as targets of methane mitigation in livestock animals. Front. Microbiol., 6: 776. <https://doi.org/10.3389/fmicb.2015.00776>
- Szkopek D, Mendel M, Kinsner M, Fotschki B, Juśkiewicz J, Kozłowski K, Matuszevičius P, Konieczka P (2024). Interaction between peroxisome proliferator-activated receptors and cannabidiol in the gut of chickens applied to different challenge conditions. Int. J. Mol. Sci., 25(21): 11398. <https://doi.org/10.3390/ijms252111398>
- Tabiś A, Szumny A, Bania J, Pacyga K, Lewandowska K, Kupczyński R (2024). Comparison of the effects of essential oils from *Cannabis sativa* and cannabis indica on selected bacteria, rumen fermentation, and methane production-*in vitro* study. Int. J. Mol. Sci., 25(11): 5861. <https://doi.org/10.3390/ijms25115861>
- Tang TWH, Ullah K, Lee J-J, Chen H-C, Hsieh PCH (2026). Comparative insights into the gut-heart axis: Cross-species and cross-population perspectives. Gut Microbes, 18(1): 2611617. <https://doi.org/10.1080/19490976.2025.2611617>
- Turcotte C, Blanchet M-R, Laviolette M, Flamand N (2016). The CB2 receptor and its role as a regulator of inflammation. Cell. Mol. Life Sci., 73(23): 4449-4470. <https://doi.org/10.1007/s00018-016-2300-4>
- Ulluwishewa D, Anderson RC, McNabb WC, Moughan PJ, Wells JM, Roy NC (2011). Regulation of tight junction permeability by intestinal bacteria and dietary components.

- J. Nutr., 141(5): 769-776. <https://doi.org/10.3945/jn.110.135657>
- Vacca M, Celano G, Calabrese FM, Portincasa P, Gobetti M, De Angelis M (2020). The controversial role of human gut lachnospiraceae. Microorganisms, 8(4): 573. <https://doi.org/10.3390/microorganisms8040573>
- Varsha KK, Nagarkatti M, Nagarkatti P (2022). Role of gut microbiota in cannabinoid-mediated suppression of inflammation. Adv. Drug Alcohol Res., 2: 10550. <https://doi.org/10.3389/adar.2022.10550>
- Vispute MM, Sharma D, Mandal AB, Rokade JJ, Tyagi PK, Yadav AS (2019). Effect of dietary supplementation of hemp (*Cannabis sativa*) and dill seed (*Anethum graveolens*) on performance, serum biochemicals and gut health of broiler chickens. J. Anim. Physiol. Anim. Nutr., 103(2): 525-533. <https://doi.org/10.1111/jpn.13052>
- Wagner B, Gerletti P, Fürst P, Keuth O, Bernsmann T, Martin A, Schäfer B, Numata J, Lorenzen MC, Pieper R (2022). Transfer of cannabinoids into the milk of dairy cows fed with industrial hemp could lead to Δ^9 -THC exposure that exceeds acute reference dose. Nat. Food, 3(11): 921-932. <https://doi.org/10.1038/s43016-022-00623-7>
- Wallace RJ, Rooke JA, McKain N, Duthie C-A, Hyslop JJ, Ross DW, Waterhouse A, Watson M, Roehe R (2015). The rumen microbial metagenome associated with high methane production in cattle. BMC Genom., 16(1): 839. <https://doi.org/10.1186/s12864-015-2032-0>
- Walsh KB, McKinney AE, Holmes AE (2021). Minor cannabinoids: Biosynthesis, molecular pharmacology and potential therapeutic uses. Front. Pharmacol., 12: 777804. <https://doi.org/10.3389/fphar.2021.777804>
- Wang Y, Yu Q, Wang X, Song J, Lambo MT, Huang J, He P, Li Y, Zhang Y (2023). Replacing alfalfa hay with industrial hemp ethanol extraction byproduct and Chinese wildrye hay: Effects on lactation performance, plasma metabolites, and bacterial communities in Holstein cows. Front. Vet. Sci., 10: 1061219. <https://doi.org/10.3389/fvets.2023.1061219>
- Winders TM, Holman DB, Schmidt KN, Luecke SM, Smith DJ, Neville BW, Dahlen CR, Swanson KC, Amat S (2023a). Feeding hempseed cake alters the bovine gut, respiratory and reproductive microbiota. Sci. Rep., 13(1): 8121. <https://doi.org/10.1038/s41598-023-35241-1>
- Winders TM, Neville BW, Swanson KC (2023b). Effects of hempseed cake on ruminal fermentation parameters, nutrient digestibility, nutrient flow, and nitrogen balance in finishing steers. J. Anim. Sci., 101: skac291. <https://doi.org/10.1093/jas/skac291>
- Yue Y, Luasiri P, Li J, Laosam P, Sangsawad P (2024). Research advancements on the diversity and host interaction of gut microbiota in chickens. Front. Vet. Sci., 11: 1492545. <https://doi.org/10.3389/fvets.2024.1492545>
- Zachut M, Butenko Y, dos Santos Silva P (2025). International symposium on ruminant physiology: The involvement of the endocannabinoid system in metabolic and inflammatory responses in dairy cows during negative energy balance. J. Dairy Sci., 108(7): 7643-7661. <https://doi.org/10.3168/jds.2024-25772>
- Zhou X, Zhang N, Zhang J, Gu Q, Dong C, Lin B, Zou C (2022). Microbiome and fermentation parameters in the rumen of dairy buffalo in response to ingestion associated with a diet supplemented with cysteamine and hemp seed oil. J. Anim. Physiol. Anim. Nutr., 106(3): 471-484. <https://doi.org/10.1111/jpn.13616>