



Review Article

Mechanism of action, benefits, and research gap in fermented soybean meal utilization as a high-quality protein source for livestock and poultry

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ABSTRACT

Animal nutritionists have incessantly worked towards providing livestock with high-quality plant protein feed resources. Soybean meal (SBM) has been an essential and predominantly adopted vegetable protein source in livestock feeding for a long time; however, several SBM antinutrients could potentially impair the animal's performance and growth, limiting its use. Several processing methods have been employed to remove SBM antinutrients, including fermentation with fungal or bacterial microorganisms. According to the literature, fermentation, a traditional food processing method, could improve SBM's nutritional and functional properties, making it more suitable and beneficial to livestock. The current interest in health-promoting functional feed, which can enhance the growth of animals, improve their immune system, and promote physiological benefits more than conventional feed, coupled with the ban on the use of antimicrobial growth promoters, has caused a renewed interest in the use of fermented SBM (FSBM) in livestock diets. This review details the mechanism of SBM fermentation and its impacts on animal health and discusses the recent trend in the application and emerging advantages to livestock while shedding light on the research gap that needs to be critically addressed in future studies. FSBM appears to be a multifunctional high-quality plant protein source for animals. Besides removing soybean antinutrients, beneficial bioactive peptides and digestive enzymes are produced during fermentation, providing probiotics, antioxidants, and immunomodulatory effects. Critical aspects regarding FSBM feeding to animals remain uncharted, such as the duration of fermentation, the influence of feeding on digestive tissue development, choice of microbial strain, and possible environmental impact.

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1. Introduction

Soybean (*Glycine max*), an annual crop belonging to the Leguminosae or Fabaceae family, is grown across a large geographic area

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worldwide and is economically the most important bean globally. It is used largely to produce oilseed meal or vegetable oil for livestock feeding, and its worldwide acceptance as a feedstuff results from its essential components, such as comparatively high digestible protein, dietary fiber, free sugar, minerals, and essential fatty acid composition (Esteves et al., 2010), and a high and well-proportioned amino acid (AA) profile, except for sulfur-containing amino acids (Czech et al., 2021). Soybean meal (SBM) is the material remaining after the mechanical and solvent extraction of oil from soybean, with about 46%–48% crude protein, 2.5%–3.5% lysine, 0.6%–0.7% tryptophan, 0.5%–0.7% methionine and 0.5%–0.8% cystine (Mukherjee et al., 2015a). It is available all year round, has a minimal change in nutrient composition, allows limited use of

animal protein like fish and blood meal, can be free from uncontrollable antinutrients if processed appropriately, and is often a preferred choice when formulating diets (Wilkinson and Young, 2020). As SBM becomes a more popular alternative high-quality plant protein source (HQPPS) in animal diets, the production and consumption of soybean protein products in food and feed are unquestionably rising (Dei, 2011); indisputably, it may become the primary sustainable protein source by 2050 (Zhu et al., 2022).

Even though SBM is frequently used because of its high nutritional profile, there are restrictions regarding its safe use in livestock diets. Early research shows that it is not recommended to feed unprocessed soybeans to monogastric animals and pre-ruminants under four months of age or weighing less than 136 kg (Lalman et al., 2017). Consuming raw soybeans reduced the feed intake and growth and increased pancreatic and duodenal size in chicks (Mogridge et al., 1996), reduced growth performance in pigs (Palacios et al., 2004), and diminished the growth performance and health of calves (Abdelgadir et al., 1984). These effects are mainly due to several soybean antinutrients coupled with the antigenic proteins interacting with the gastrointestinal tract, resulting in negative physiological responses of the digestive tract (Ansia and Drackley, 2020).

To combat these challenges and improve its overall quality, processing of soybeans, such as extrusion and expelling, flaking, cooking, roasting and jet-sploding, micronization, and enzyme treatment have been used to remove or reduce the antinutrients before inclusion in animal diets (Ansia and Drackley, 2020). Nevertheless, many of these techniques' high-temperature treatments often lead to protein denaturation, the formation of potentially harmful Maillard reaction products, and decreased nutrient digestibility (Hemetsberger et al., 2021). Recently, there has been much interest in adopting fermentation, which has a long history in human food, in processing livestock feed. Soybean fermentation involves applying microbial inoculants to break down the intrinsic antinutrients for better livestock production performance (Czech et al., 2021). Feeding fermented SBM (FSBM) improved nutrient digestibility and efficiency in pigs (Yuan et al., 2017), improved intestinal health in chicken (Jazi et al., 2019), and alleviated diarrhea incidence in calves (Feizi et al., 2020), amongst others. Therefore, this review extensively discusses the techniques involved in FSBM processing, the mechanism by which the

fermentation process impacts and improves the functional and nutritional quality of SBM, summarizes the research progress and findings on the application of FSBM in different livestock species, and highlights the research gaps and prospects of FSBM utilization in livestock feeding.

2. Limitations of the use of soybean meal in livestock nutrition

Despite the vast nutritional potential of SBM, the presence of antinutrients limits its utilization in livestock feeding (Fig. 1). These antinutrients inhibit the intake, digestibility, feed utilization, absorption, and metabolism of nutrients, the animal's physiological conditions, and growth performance, as well as the overall health status of the animal (Clarke and Wiseman, 2005).

2.1. Impact of trypsin inhibitors on livestock nutrition and health

One of the main limiting factors of SBM is the proteinaceous trypsin inhibitors (TIs), which cause the inactivity of trypsin and chymotrypsin and impair protein digestibility. Although most legumes have TIs, the amount could vary from plant to plant, with most leguminous plants containing less than 50% of those found in soybeans (Savage and Morrison, 2003). According to Chen et al. (2020), the level of trypsin inhibitors in SBM ranged from 2 to 6 mg/g. Inactivating soybean TIs can positively impact health by reducing pancreatic weight and enhancing enzymatic activity in the pancreas (García-Rebollar et al., 2016; Liu, 2019). Whereas the continuous daily intake of high TIs can ultimately reduce the digestibility of dietary protein (Rada et al., 2017). Heat treatment to reduce soybean TIs is limited because of the incidence of Maillard reactions, a form of non-enzymatic browning that occurs during excessive thermal processing involving the binding of amino groups to the carbonyl group of reducing sugars, thus reducing its nutritive value (González-Vega et al., 2011). A high amount of TIs in feed has been reported to cause pancreatic hypertrophy, resulting in growth deficiency and lower performance (Pacheco et al., 2014; Rackis et al., 1985). Pancreatic hypertrophy is the body's compensatory mechanism to counteract the effect of ingested TIs (Liener and Tomlinson, 1981). Also, TIs bind to trypsin and chymotrypsin, the key enzymes aiding dietary protein digestion in animals,

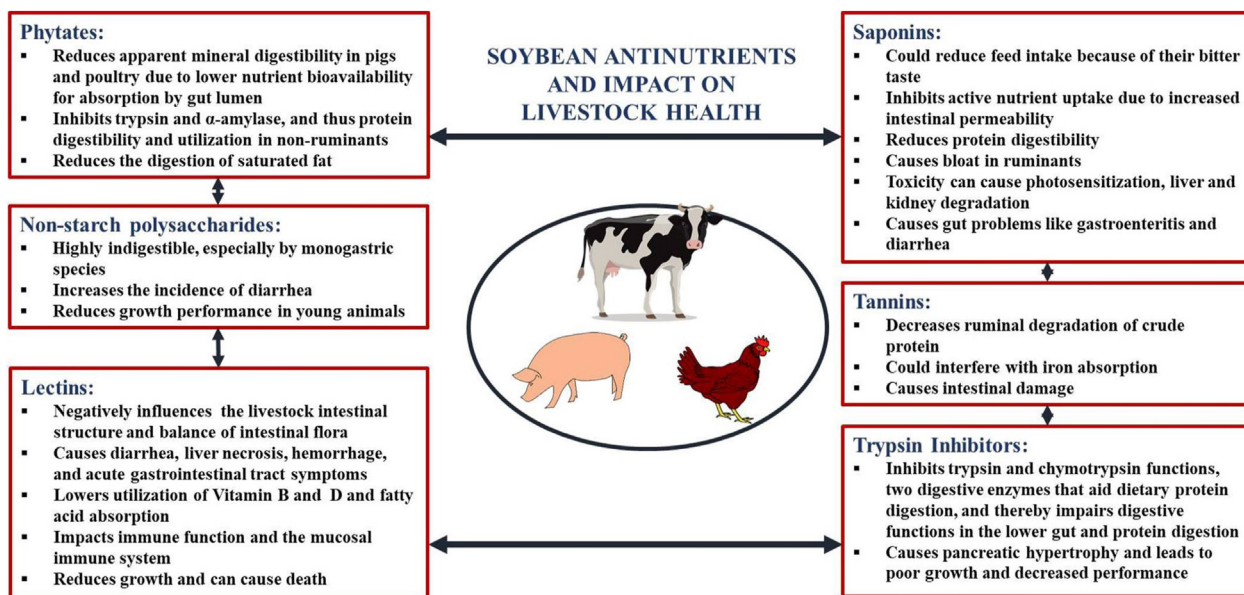


Fig. 1. Diagrammatic representation of some common soybean antinutritional factors and their impact on livestock health.

rendering them nonfunctional and impairing protein digestion (Mukherjee et al., 2015a). Their effect is more significant in non-ruminants such as poultry, swine, and immature ruminants (Adams, 1995; Mukherjee et al., 2015a).

2.2. Impact of saponins on livestock nutrition and health

Saponins naturally occur on surface-active glycosides in most plants (Shewangzaw and Aschalew, 2016), and their content ranges from 0.1% to 0.5% in SBM (Guang et al., 2014). They are a diverse chemical group in a grey area between antinutritional factors and beneficial plant constituents (Hill, 2003). They are heat-stable and alcohol-soluble. Saponin from some plants has been reported to benefit animals, such as anticoagulants, anti-inflammatory, immunomodulatory, hypocholesterolemic, anticarcinogenic, hepato-protective, and hypoglycemic. They can form complexes with cholesterol in the gastrointestinal tract (GIT), leading to increased excretion or elimination of cholesterol and thus reducing blood cholesterol levels. Cheeke (2009) noted that saponins lowered the ruminal protozoa population by complexing with cholesterol in the protozoa cell membrane. Nevertheless, they could affect livestock negatively by impacting rumen microorganisms, rumen fermentation, blood parameters, ruminant growth, and wool, egg, and milk production. Because of their bitter taste, one theory is that their effects are facilitated by feed intake being inhibited by bitter flavors (Shewangzaw and Aschalew, 2016), leading to low active uptake of nutrients such as vitamins and minerals in the intestine and reduced protein digestibility (Chen et al., 2011; Francis et al., 2002). They have also been associated with bloat in ruminants, photosensitization, and gut problems and are believed to cause cytoplasmic protein fractions, especially in animals grazing temperate legumes high in saponin (Hill, 2003).

2.3. Impact of lectins on livestock nutrition and health

Lectin (agglutinin) toxicity is typical of animals consuming soybeans. Lectins are multivalent glycoproteins representing 5%–7% of soybean antinutrients and can recognize and bind diverse carbohydrate structures like N-acetylgalactosamine or galactose (Pan et al., 2018) and could interfere with small intestinal nutrient absorption (Dias et al., 2015). While some are partially heat-stable and their biological activity can be lowered by thermal treatment, a significant amount is still present because most could pass through the GIT without changes to its functional and immunological state, where they interact with the surface epithelium and impair the gut dietary intake leading to digestive disorders (Pan et al., 2017). Also, they can impact the structure of the intestine (Fasina et al., 2004), barrier function (Pan et al., 2017), the mucosal immune system (Greer and Pusztai, 1985), and the balance of the intestinal microflora (Pan et al., 2018). It was reported that the effect of lectins on animals depends on the species, age, and lectin dosage. For instance, it was noted that their impact on monogastric animals is more pronounced than on ruminants. This could be because rumen fermentation reduces their activity (Pan et al., 2018). The impact of lectin toxicity in livestock includes reduced growth, diarrhea, interference with nutrient absorption, liver, local necrosis, fatty degeneration, local hemorrhage, depressed vitamin B and D utilization, reduced fatty acid absorption, acute gastrointestinal symptoms or even death.

2.4. Impact of some other important soybean meal antinutrients and their effect on livestock

Other limiting antinutrients in soybean which make it unfavorable for direct animal consumption include amylase inhibitors,

gossypols, tannin, antivitamins, phytate, non-starch polysaccharides, and so on. Non-starch polysaccharides such as verbascose, stachyose, and raffinose (Choct et al., 2010), for instance, are indigestible by monogastric animals' ileum because of certain enzyme's absence leading to a high incidence of diarrhea (Liyang et al., 2003) and hampering the growth of young animals (Hong et al., 2004). Their total concentration in SBM is about 15%–20% of the dry matter (Opazo et al., 2012). Soybean also contains about 0.7–5.2 mg/g of Isoflavones, which act as a phytoestrogen in animals and affect their reproductive health when consumed in high quantities (Azam et al., 2020; Grgic et al., 2021). Phytate is present in soybean at 1%–2% dry matter, making phosphorus and zinc less available to animals (Deak and Johnson, 2007; Mukherjee et al., 2015a), reducing protein bioavailability by attaching to peptides and AA and blocking proteolytic enzyme activities. Lipoygenases contribute up to 2% of soybean total protein content, and they catalyze lipid hydroperoxidation, causing the typical beany flavor and influencing SBM palatability and consumption (Hayward et al., 2017). Beta-conglycinin is a storage glycoprotein accounting for about 30% of total soybean protein (Hei et al., 2012) and induces intestinal damage by preventing enterocyte growth and inducing cytoskeleton breakdown, which leads to apoptosis (Escames et al., 2004) and damages the integrity of the intestinal epithelium, induces inflammation, and oxidation (Omosebi et al., 2018; Zhang et al., 2013). Many of these factors negatively impact directly or indirectly the health of animals. Therefore, soybeans require processing to remove intrinsic compounds negatively affecting the animal's digestive tract to ensure optimal feeding properties.

3. Fermented soybean meal: the multifunctional high-quality vegetable protein source for livestock

Various techniques have been researched for removing or reducing SBM antinutrients, including chemical, biotechnological, and physical methods (Kumar et al., 2012; Mukherjee et al., 2015b). A commonly adopted processing method is the thermal treatment, which could be roasting, toasting, or extrusion, enzymatic deactivation (Goebel and Stein, 2010), micronization (Berrocso et al., 2013), sieve separation, alcohol extraction (Lenehan et al., 2007), and both non-alcohol extraction and enzyme treatment (Oliveira and Stein, 2016) has also been used. However, conventional methods like heating do not easily deactivate some antinutrients (Miri et al., 2019) because some factors, such as saponins, non-starch polysaccharides, and some antigenic proteins, are heat-stable. Biotechnical strategies such as fermentation have, therefore, been one of the most widely accepted and successful approaches for inactivating or reducing such antinutrients, improving SBM nutritional quality (Bi et al., 2015; Chi and Cho, 2016), and effectively changing the physicochemical properties of feed (Mukherjee et al., 2015b).

3.1. Impact of fermentation on soybean meal processing

Fermentation is an old traditional food processing method to preserve or improve quality and has recently gained renewed attention in the livestock industry as a way of effective feed processing that can remove antinutrients and toxins, break down large substrate molecules by microorganisms, and produce bioactive compounds and metabolites. It is a metabolic process involving sugar oxidation into energy and enhances mineral uptake. Enzymes typically break down these complexes and require an optimum pH maintained by fermentation (Samtiya et al., 2020).

Interest in feeding fermented feedstuff to improve animal health skyrocketed following the European Union ban on the use of antibiotics as antimicrobial growth promoters for livestock

(Missotten et al., 2010; van Winsen et al., 2001). Fermented soybean meal processing involves incorporating fungi or bacteria inoculants, such as *Bifidobacterium bifidum*, *Bacillus subtilis*, *Lactobacillus plantarum*, *Lactobacillus brevis*, *Aspergillus oryzae*, *Rhizopus oligosporus*, *Neurospora crassa*, *Saccharomyces cerevisiae*, *Lactobacillus acidophilus*, *Enterococcus faecalis*, and *Bacillus licheniformis* (Li et al., 2019, 2020). An earlier investigation discovered that fermenting SBM with *L. plantarum* reduced SBMs' anti-nutrients, including protease inhibitors, phytate, and trypsin inhibitors (Adeyemo and Onilude, 2013). In a study on piglets, fermentation lowered SBM glycine and β -conglycinin content, two potentially allergic and antigenic compounds associated with crypt hyperplasia and villous atrophy in weaned piglet's ileum (Czech et al., 2021). Sanjukta and Rai (2016) reported that fermenting SBM with lactic acid bacteria (LAB) favored the production of antimicrobial peptides while facilitating lactic acid production, which enhanced feed acidity and improved palatability.

Therefore, the fermentation of soybeans serves two key purposes. One is the large-scale multiplication of probiotic bacteria during the fermentation process, which consumes and utilizes non-protein antinutritional factors such as phytic acid, oligosaccharide, thyroxin, etc., and produces metabolites with bioactive properties (de Oliveira et al., 2022) and at the same time, serves as a carrier of those microorganisms into the animal gut during feeding, where they alter the gastrointestinal microbial community to enhance digestibility (Cheng et al., 2019) subsequently. The other, more pronounced in most literature, is that microorganisms secrete some protease to degrade the antinutritional protein in SBM.

3.2. Techniques involved in fermented soybean meal processing

Numerous techniques are available for processing fermented feeds, such as ensiling, liquid fermentation, and solid-state fermentation, which have seen widespread application in recent decades (Dai et al., 2020). FSBM processing involves solid-state fermentation, a traditional method that uses several organisms and has a long history in food production. It is done under low-moisture conditions, which helps minimize the drying time for protein hydrolysates. According to published research, it produces metabolites like digestive enzymes, high-value-added bioproducts like bacterial antimicrobial peptides, and antibiotics than the submerged fermentation. The advantages of solid-state fermentation include a more extensive culture condition and relatively minimal

pre-treatment. Large-scale production is practicable because it is less capital-intensive and eco-friendly (Wang et al., 2021). Further, as documented by Dai et al. (2020), solid-state fermentation could be a one-step involving a single fermentation phase or a two-step process involving two stages of fermentation.

Although many studies adopted the one-step direct soybean fermentation by microbial additives (Seo and Cho, 2016; Zhang et al., 2018), recent studies have noted that fermentation involving two stages of solid-state fermentation is more effective. In two-step fermentation, the first stage is aerobic fermentation, and the second is anaerobic (Fig. 2). During the first stage of aerobic fermentation, aerobic microorganisms like *Bacillus* and fungi are promoted, producing many bioactive products such as vitamins and enzymes and as a result, fostering the proliferation of LAB. In practice, Shi et al. (2017) described that SBM is ground coarsely and sieved to pass through a 1-mm mesh, after which sterile water is added to a moisture content of about 40% and inoculated with aerobic microorganisms like *Bacillus* sp. The SBM is then fermented at 37 °C for 24 h. Followed by this is the second stage of fermentation involving anaerobic solid-state fermentation to facilitate the proliferation of LAB and generate large amounts of lactic acid. The microbes are forced to dissolve under the anaerobic conditions, and the intracellular enzymes and other bioactive components in the cells secrete. During this phase, SBM that has undergone aerobic fermentation is inoculated again with lactic acid metabolizing bacteria, sealed in plastic bags and fermented under an anaerobic condition at 37 °C for 48–96 h before drying or milling and storage. The effectiveness of solid-state fermentation in enhancing SBM nutritional quality and reducing its antinutrients was also ascertained by Amadou et al. (2010) and, more recently, Yang et al. (2021).

3.3. Mechanism of fermentation and its impact on SBM's physicochemical and functional properties and microbial ecology

A diagrammatic representation of the mechanism by which fermentation improves SBM is shown in Fig. 3. The nutritional value of SBM could be improved by fermentation via biodegradation, phytic acid, oligosaccharide reduction, and amino acid profile enrichment (de Oliveira et al., 2022; Rajabi et al., 2020). In recent years, research has been focusing on changes to the protein profile of the soybean as a result of fermentation (Zheng et al., 2017). The major biochemical changes that occur during fermentation depend

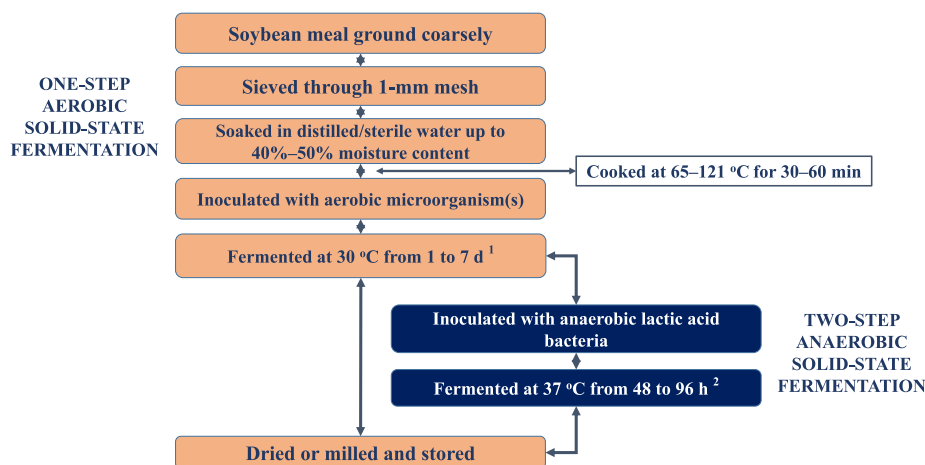


Fig. 2. Diagrammatic representation of the step-by-step solid-state fermentation of soybean meal indicating the one-step and two-step procedures. ¹The numerical range refers to fermentation time varying from 1 to 7 d as reported in different studies summarized in this paper. ²The numerical range refers to fermentation time varying from 48 to 96 h as reported in different studies summarized in this paper.

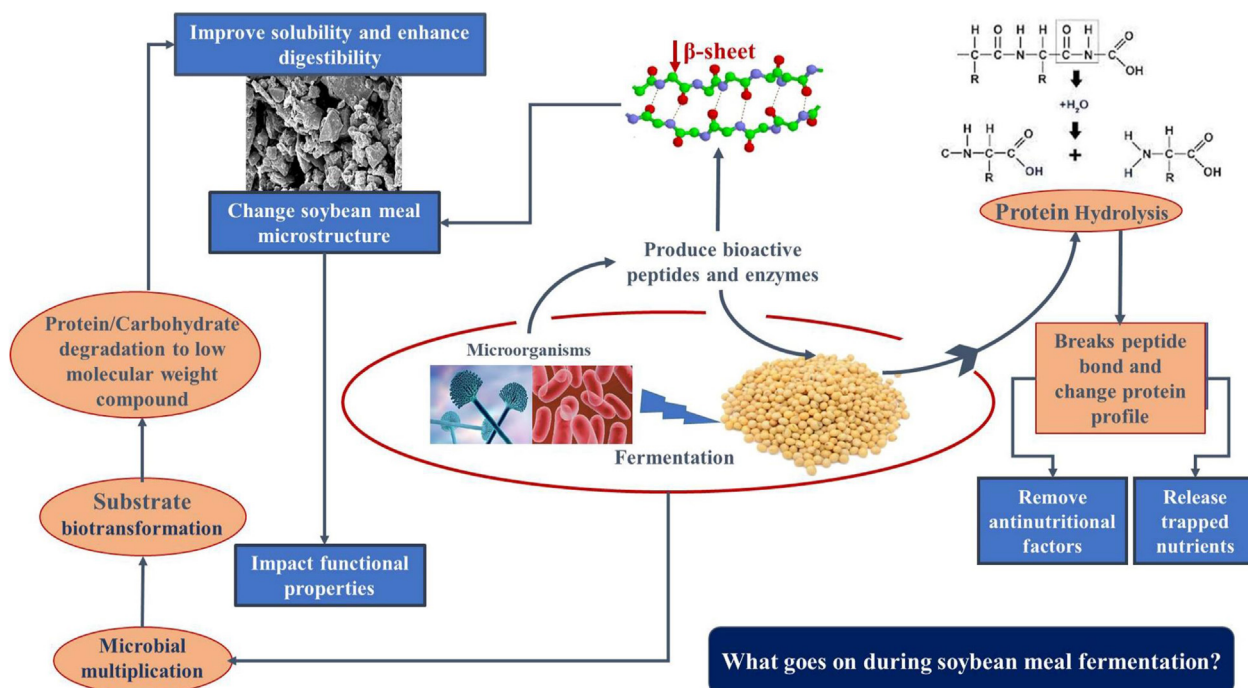


Fig. 3. Diagrammatic representation of the mechanism by which fermentation improves the value of soybean meal.

on the protein hydrolysis reaction of protease, which occurs due to different types of enzymes secreted from microorganisms (Rui et al., 2017). In the work of Seo and Cho (2016), proteomic tools were used to compare the protein profile of SBM before and after fermentation. The study adopted two-dimensional (2D) electrophoresis to investigate SBM's allergenic and antinutritional protein profiles during solid-state fermentation with *Bacillus*. According to the report, β -conglycinin, comprising of α -, α' -, and β -subunits, and interacting with trimeric glycoprotein, was found in the 2D gel of SBM, while it had been reduced by 59% in FSBM 12 h post-fermentation. Similarly, glycinin acid chains, which were about 22.2% in SBM 2D gels, were reduced by 54.6% 12 h post-fermentation.

Fermentation is also accompanied by microstructure destruction of SBM proteins, leading to changes in their functional or nutritional properties. Wang et al. (2011) found that the surface hydrophobicity of soybean protein isolate has a negative correlation with α -helix and a positive correlation with β -sheet and random coil. According to Peng et al. (2014), ruminant solubility and intestinal protein digestibility were associated with molecular structure characteristics. In Zheng et al. (2017), FSBM protein morphology and microstructure were evaluated by scanning electron microscope and Fourier-transform infrared spectroscopy, and it was revealed that fermentation might improve the nutritional value of FSBM by changing the structure of the β -sheet and obliterating the original SBM structure. In brief, FSBM peptides, particularly glycinin and β -conglycinin, either originate from protein hydrolysis or are released by the fermentation microbes as a result of microbial enzymatic activities and biochemical changes. Depending on the AA's arrangement and composition, these bioactive peptides have health benefits and can exhibit functional and metabolic properties such as antimicrobial, antioxidant, and immune modulation (de Oliveira et al., 2022; Sanjukta and Rai, 2016).

Substrate fermentation occurs at a certain temperature, moisture level, and redox, and these conditions foster microorganisms, leading to the biotransformation of different substrates at varying

rates. As explained by Wang et al. (2021), who used high-throughput sequencing to assess the microbial dynamics involved in SBM fermentation, FSBM quality has a close correlation with the bacteria community during solid-state fermentation. It was noted that *Pseudomonas*, the predominant bacteria pre-fermentation, was significantly and extensively replaced by the *Bacillus* 24 h post-fermentation, indicating that fermentation greatly impacted the bacterial community structure FSBM. More importantly, the author observed that bio-augmented inoculation elevated the water-soluble protein content of SBM by 110%, 47.2%, and 473.7% after 24, 72, and 96 h fermentation. The partial degradation of the soybean protein and carbohydrate by microbes to low-molecular-weight compounds makes them more soluble in water and enhances digestibility (Xu et al., 2012). Also, because acetic acid, lactic acid, ethanol, and formic acid constitute the majority of the low-molecular-weight fermentation products in FSBM, the microbes and their metabolic products influence the gut microbiome animal depending on the properties of the substrates, microbial strain, quantity of FSBM fed, and the fermentation processing technique (Mukherjee et al., 2015a; Yan et al., 2022). In addition, as nutrients decline and metabolites accumulate when the fermentation culture enters a stationary phase, and the generation of specific organic compounds is lowered, soluble protein and amino acids contents are elevated (de Oliveira et al., 2022).

Another mechanism by which fermentation improves the SBM quality is by impacting its functional properties. Functional properties, which are related to protein structure, hydration, rheological characteristics, and protein surface (Jideani, 2011), greatly impact the thermal stability, water-holding capacity, consistency, gel-forming ability, and emulsifying properties of SBM. At the same time, the complex SBM protein and peptides exhibit strong biological activities such as emulsification and emulsifying stability (Lu et al., 2022). Improving feed emulsion capacity is important to the feed industry because it improves feed stability and enhances the growth performance of livestock through an increment in FA digestibility (Saleh et al., 2020). Recently, Lu et al. (2022) observed that fermenting SBM naturally improved the emulsifying activity

Table 1
Benefits of feeding fermented soybean meal (FSBM) diet on swine health and productivity.

Fermentation microbe(s)	Inoculant dose	Duration of fermentation	Inclusion level, % (replacement of SBM with FSBM)	Animal physiological status	Benefits	Reference
<i>Bacillus subtilis</i> BS12	NS	24 h	10% replacement	Piglet	<ul style="list-style-type: none"> Lowered ileum macrophage infiltration Upregulated mucins and tight junction protein expression in the jejunum and ileum Lowered serum IL-6, IL-1β, and D-lactate FSBM-derived peptide improved the epithelial barrier function and suppressed inflammation. 	Zhang et al. (2020)
<i>B. subtilis</i> BS12	10 ⁷ to 10 ⁸ cfu/mL	24 h	10% replacement	Piglet	<ul style="list-style-type: none"> Improved ADG and FI Reduced jejunum and ileum mRNA expression of pro-inflammatory cytokines and reduced gut inflammation 	Zhang et al. (2018)
<i>Escherichia faecium</i> SLB120	1.0 \times 10 ⁸ cfu/g	NS	Total replacement (39% inclusion of FSBM on an as-fed basis)	Weaned piglet	<ul style="list-style-type: none"> Improved growth performance Improved apparent ileal digestibility of CP, DM, nitrogen, and ME 	Jeong et al. (2016)
<i>Lactobacillus plantarum</i> , <i>B. subtilis</i> , and <i>Saccharomyces cerevisiae</i>	10 ⁸ cfu/g	NS	10% replacement	Weaned pigs	<ul style="list-style-type: none"> Increased ADG with low feed consumption Elevated serum alkaline phosphatase and total serum protein levels and lowered serum urea nitrogen Increased serum IgG, IgM, and IgA concentrations Improved intestinal morphology of pigs via an enhanced villus height in the duodenum, jejunum, and ileum and lowered crypt depth. 	Zhu et al. (2017)
<i>Aspergillus oryzae</i> GB-107	NS	48 h	10%–15% replacement	Weaned pigs	<ul style="list-style-type: none"> No effect on the ADG and FI Elevated histidine, lysine, and methionine digestibility Enhanced feed efficiency and AA digestibility Elevated BUN and total protein concentrations 	Cho et al. (2007)
<i>A. oryzae</i> 3.042	10,000 cfu/g	48 h	Total replacement	Weaned piglets	<ul style="list-style-type: none"> Improved growth performance Decreased serum IgG Lowered whole blood and spleen lymphocyte proliferative response to concanavalin A and LPS 	Liu et al. (2007)
<i>A. oryzae</i> 3.042	10,000 cfu/g	48 h	Total replacement	Weaned piglets	<ul style="list-style-type: none"> Increased ADG and reduced F:G ratio Increased total protease and trypsin activities in the duodenum and jejunum Improved nutrient digestibility 	Feng et al. (2007a)

(continued on next page)

Table 1 (continued)

Fermentation microbe(s)	Inoculant dose	Duration of fermentation	Inclusion level, % (replacement of SBM with FSBM)	Animal physiological status	Benefits	Reference
<i>A. oryzae</i> and <i>B. subtilis</i>	NS	NS	Total replacement (28% inclusion of FSBM on an as-fed basis)	Weanling pigs	<ul style="list-style-type: none"> Increased feed DM, CP, NDF, and ADF Increased DE, ME, and NE Standardized ileal digestibility of all indispensable amino acids except lysine, threonine, and tryptophan 	Rojas and Stein (2013)
<i>B. subtilis</i> , <i>Hansenula anomala</i> , and <i>Lactobacillus casei</i>	1×10^6 cfu/g	48 h	3.75%–7.5% substitution for SBM and wheat bran	Piglets	<ul style="list-style-type: none"> No effect on suckling piglets' growth performance Increased ADG and FCR in weaned piglets Increased nutrient digestibility, fecal enzyme activity, and LAB counts and decreased fecal <i>Escherichia coli</i> counts 	Yuan et al. (2017)
<i>Streptococcus thermophilus</i> , <i>B. subtilis</i> MA139, and <i>S. cerevisiae</i>	NS	5 d	6% replacement	Weanling piglets	<ul style="list-style-type: none"> 6% FSBM increased growth performance Improved ADG and ADFI No effect on FCR, nutrient digestibility and plasma urea nitrogen concentration 	Wang et al. (2014a)
<i>B. subtilis</i> WB117	1×10^6 cfu/g	48 h	Total replacement (24.5% inclusion of FSBM on an as-fed basis)	Piglets	<ul style="list-style-type: none"> Increased duodenum and jejunum total protease and trypsin activities Decreased trypsin activity in the pancreas Improved intestinal morphology 	Feng et al. (2007b)
<i>A. oryzae</i> GB-107	10,000 cfu/g	48 h	6% inclusion	Nursery pigs	<ul style="list-style-type: none"> Improved nutrient utilization and efficiency for growth by newly weaned pigs No adverse effects on growth performance No adverse effect on the relative bioavailability of protein 	Kim et al. (2010b)
<i>B. subtilis</i> CP-9	NS	48 h	34% FSBM inclusion (as-fed basis) as only dietary protein source	Nursery pigs	<ul style="list-style-type: none"> Higher apparent ileal digestibility of DM, ash, CP, NDF, and ADF 	Akhtar et al. (2022)
<i>Streptococcus thermophilus</i> , <i>S. cerevisiae</i> , and <i>B. subtilis</i>	1×10^7 cfu/mL	5 d	3%–6% replacement (on an as-fed basis)	Weanling pigs	<ul style="list-style-type: none"> No effect on the energy value and standardized ileal digestibility of AA Improved performance after weaning Reduced immunological challenges 	Wang et al. (2014b)
<i>B. subtilis</i> , <i>Lactobacillus</i> , and yeast	NS	3 d	Total replacement (32% inclusion on an as-fed basis)	Weaned pigs	<ul style="list-style-type: none"> Improved nutrient digestibility of CP and AA Improved intestinal integrity, antioxidant capacity, and immune function 	Yan et al. (2022)
<i>B. subtilis</i> and <i>Lactobacillus fermentum</i>	NS	NS	2% FSBM + 6% fermented rapeseed replaced SBM	Weaned Piglets	<ul style="list-style-type: none"> Positively influenced the intestinal microbial composition and histology and resulted in improved nutrient digestibility coefficients (ATTD and AID) 	Czech et al. (2021)
<i>A. oryzae</i> GB-107	NS	48 h	8% replacement	Finishing pigs	<ul style="list-style-type: none"> Improved growth performance Improved meat quality Modulated intestinal microbial population diversity Increased <i>Bacteroidetes</i>, <i>Prevotellaceae</i>, <i>Bacteroidales</i>, and <i>Bacteroides</i> populations 	Feng et al. (2020)

<i>B. subtilis</i>	1×10^8 cfu/g	24 h	50% replacement	Finishing pigs	<ul style="list-style-type: none"> • Increased serum and muscle antioxidant capacity • Improved nutrient digestibility and growth performance • Improved carcass trait and meat quality via increased serum and muscle antioxidant capacity • Caused changes in metabolism-related gene expression in long-issimus thoracis 	Xie et al. (2022)
<i>B. subtilis</i> KC 101, <i>S. cerevisiae</i> JM 102, and <i>Bacillus lactis</i> RG 103	1.0×10^{10} , 1.0×10^9 , 2.5×10^9 cfu/g	4 d	7.33% wet FSBM and 5% dry FSBM inclusion	Piglets	<ul style="list-style-type: none"> • Improved growth performance, • Increased large intestine metabolites of carbohydrates and reduced metabolites of protein 	Zhang et al. (2018)
<i>S. thermophilus</i> , <i>S. cerevisiae</i> , and <i>B. subtilis</i>	1×10^7 cfu/mL	5 d	6% replacement	Enterotoxigenic <i>E. coli</i> -challenged piglets	<ul style="list-style-type: none"> • Altered large intestine microbiome • Improved growth performance • Alleviated diarrhea in <i>E. coli</i>-challenged piglets • Modulated the cecal microbial composition and down-regulated inflammatory cytokines production 	Wang et al. (2020)
<i>A. oryzae</i> GB-107	10,000 cfu/g	48 h	10% replacement	Lipopolysaccharide-challenged nursery piglets	<ul style="list-style-type: none"> • Increased expression of cytosolic glutathione peroxidase and glutathione S-transferase • Reduced expression of adiponectin, neonatal Fc receptor, and decreased tumor necrosis factor ligand • Modulated expression of gene related to inflammatory response and antioxidant activity 	Roh et al. (2015)
<i>L. plantarum</i> , <i>B. subtilis</i> , and <i>S. cerevisiae</i>	Mixed at ratio 1:2:2 and $> 10^8$ cfu/g	NS	15% FSBM inclusion replaced 57% SBM	Weaned piglets	<ul style="list-style-type: none"> • Reduced serum cortisol • Improved growth performance • Lowered diarrhea incidence • Improved intestinal morphology • Changed intestinal bacterial community structure • Increased butyrate-producing bacteria population in the cecum and colon 	Xie et al. (2017)
<i>S. thermophilus</i> , <i>S. cerevisiae</i> , and <i>B. subtilis</i>	Mixed at a ratio of 1:1:1	5 d	25% replacement	Enterotoxigenic <i>E. coli</i> -challenged piglets	<ul style="list-style-type: none"> • Enhanced growth performance • Reduced diarrhea incidence • Improved ileal barrier function • Reduced pro-inflammatory cytokine expression and ileal mucosal cell apoptosis 	Wang et al. (2020)
<i>Lactobacillus acidophilus</i> , <i>Lactobacillus delbrueckii</i> , <i>Lactobacillus salivarius</i> , and <i>Clostridium butyricum</i>	1×10^8 cfu/g	2 d	5% inclusion	Weaning piglets	<ul style="list-style-type: none"> • No effect on growth performance • Reduced diarrhea incidence • Increased fecal LAB population • Led to a high inhibitory effect on the fecal Enterobacteriaceae population • Elevated serum IgG and IgA 	Cheng et al. (2019)
<i>L. plantarum</i> , <i>B. subtilis</i> MA 139, and <i>S. cerevisiae</i>	Mixed at 1:2:2	72 h	10% inclusion replaced 38% SBM	Weaning piglets	<ul style="list-style-type: none"> • Increased ADG • No effect on the F:G ratio • Increased total protein • Lowered blood urea nitrogen • Reduced piggery NH_3 levels due to nitrogen conversion • Decreased piggery PM10 and PM2.5 levels 	Cheng et al. (2017)

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Table 1 (continued)

Fermentation microbe(s)	Inoculant dose	Duration of fermentation	Inclusion level, % (replacement of SBM with FSBM)	Animal physiological status	Benefits	Reference
<i>A. oryzae</i> and <i>Lactobacillus reuteri</i>	NS	48 h	2%–4% inclusion replaced up to 50% SBM	Sows and piglets	<ul style="list-style-type: none"> Attenuated gestation and lactation-associated oxidative stress by increasing serum superoxide dismutase activity and decreasing malondialdehyde, cortisol, and 8-isoprostaglandin F2α Enhanced the average weight Improved serum estrogen and growth factors Increased colostrum protein and IgG levels 	Luo et al. (2021)

SBM = soybean meal; FSBM = fermented soybean meal; ADG = average daily gain; FI = feed intake; ADFI = average daily feed intake; F:G = feed to gain ratio; CP = crude protein; DM = digestible energy; ME = metabolizable energy; NE = net energy; NS = not stated; IgG = immunoglobulin G; IgM = immunoglobulin M; IgA = immunoglobulin A; IL-6 = interleukin 6; IL-1 β = interleukin 1 β ; BUN = blood urea nitrogen; LPS = lipopolysaccharide; LAB = lactic acid bacteria; NDF = neutral detergent fiber; ADF = acid detergent fiber; FCR = feed conversion ratio; ATTD = apparent total tract digestibility; AID = apparent ileal digestibility; AA = amino acid.

index and emulsifying stability index, noting that the SBM protein structure loosened post-fermentation as a result of exposing the hydrophobic residues, which can bind with more hydrophobic molecules like oils. These properties can directly or indirectly affect animal health statuses after feeding on SBM, such as influence on bowel movement and health, fore- and hind-gut fermentation, and so on.

To sum up, SBM nutritional value after fermentation does not only improve by the removal of multiple antinutritional factors but by the decomposition of protein to produce multiple small peptides, serving as a carrier of multiple beneficial bacteria, antibiotics, and digestive enzymes, and by producing multiple bioactive factors and mycoprotein. Microorganisms break down complex large-molecule organic compounds in feed into small molecules that animals may easily utilize, while at the same time, several metabolic compounds and nourishing bacterial proteins are generated. The consumption of organic compounds by the microbes during feed fermentation also causes increased feed crude protein (CP), leads to the “concentration effect” of protein, and translates to a sour flavor that can stimulate an animal's appetite and increase feed intake. Fermentation-achieved protein solubility and increased emulsibility are essential for good functionality like emulsion stabilization (Zhu et al., 2022).

4. Application and emerging health benefits of fermented soybean meal utilization in livestock

4.1. Fermented soybean meal in swine nutrition

Research on applying FSBM in monogastric, especially pigs, has covered a good aspect. For instance, several authors have reported that partially or completely replacing SBM with FSBM in pigs' diets improved their production performance by enhancing nutrient CP, dry matter, ether extract digestibility, and feed efficiency at different growth stages and improved weight gain (Table 1) (Gebbru et al., 2010; Kim et al., 2010b; Shi et al., 2017; Yuan et al., 2017). Other studies also observed that feeding FSBM provided pigs with vitamins, probiotics, short-chain fatty acids, enzymes, and exoenzymes, improving digestion, absorption, and immune function (Palacios et al., 2004; Smiricky-Tjardes et al., 2003). FSBM fed to finishing pigs also elevated serum glucagon, an insulin counter-regulatory hormone critical in inducing glucose production and release from the liver (Wendt and Eliasson, 2020; Xie et al., 2022).

4.2. Fermented soybean meal in poultry nutrition

In chicken, it was also reported that FSBM improved weight gain and elevated the synthesis of high-density lipoprotein (HDL), which is responsible for cholesterol transport to the liver, where it is metabolized (Ooi and Liong, 2010; Xie et al., 2022), improved meat quality (Guo et al., 2020), improved growth performance, improved the morphology of intestines and immune function in *Salmonella typhimurium* challenged chicks and lowered *Salmonella* colonization (Jazi et al., 2019; Li et al., 2020; Soumei et al., 2019), and decreased jejunum's fungi and coliforms population (Chachaj et al., 2019). FSBM also improved the hepatic insulin-like growth factor-1 (IGF-1) expression (Soumei et al., 2019), improved serum immunity (Li et al., 2020), and increased blood total protein, high-density lipoprotein, aspartate aminotransferase activity, and protein and lipid metabolism (Sembratowicz et al., 2020) (Table 2).

4.3. Fermented soybean meal in ruminant nutrition

In ruminants, Kim et al. (2012) observed that FSBM could be used as a calf starter for improved health and growth in weaned

Table 2

Benefits of feeding fermented soybean meal (FSBM) diet on poultry health and productivity.

Fermentation microbe(s)	Inoculant dose	Duration of fermentation	Inclusion level, % replacement of SBM with FSBM	Animal physiological status	Benefits	Reference
<i>Lactobacillus acidophilus</i> and <i>Lactobacillus plantarum</i> <i>Bacillus subtilis</i> and <i>Aspergillus oryzae</i>	10 ⁸ cfu/mL 10 ⁶ spores/mL	7 d	Total replacement (35% inclusion in starter diet and 36% in grower diet)	Young broiler chickens	<ul style="list-style-type: none"> Lowered gut <i>Salmonella</i> colonization, and internal organ invasion Increased <i>Lactobacillus</i> counts and improved the morphology of intestinal mucosa Reduced the heterophil-to-lymphocyte ratio Improved growth performance Improved growth performance, dressing percentage 	Jazi et al. (2019)
<i>Lactobacillus</i>	Approximately 10 ⁶ cfu/g	NS	3%–6% FSBM inclusion replaced up to 17%–27% SBM	Chickens	<ul style="list-style-type: none"> Modulated the immune system Improved intestinal morphology Lowered jejunum fungi and coliforms population 	Chachaj et al. (2019)
<i>L. acidophilus</i> , <i>L. plantarum</i> , <i>B. subtilis</i> , and <i>A. oryzae</i>	10 ⁸ cfu/mL 10 ⁶ spores/mL	7 d	Total replacement (34%, 37%, and 32% inclusion of FSBM in starter, grower and finisher diet)	Broiler chickens	<ul style="list-style-type: none"> Enhanced BWG and feed efficiency throughout the grow-out period Increased duodenal and jejunum villus height and villus height to crypt depth Improved ileal CP and energy digestibilities, as well as the activities of the intestinal amylase and protease and pancreatic protease Reduced plasma 3-methylhistidine levels Upregulated hepatic <i>IGF-1</i> gene expression. 	Soumei et al. (2019)
<i>Bacillus amyloliquefaciens</i> , <i>L. acidophilus</i> and <i>S. cerevisiae</i>	NS	24 h	25% replacement of SBM	Broiler chickens	<ul style="list-style-type: none"> Influenced serum immunity by increasing serum IgA, IgG, and IgM Improved ADG and FCR Positively altered cecal microbial diversity and population 	Li et al. (2020)
<i>Bacillus stearothermophilus</i>	NS	48 h	Up to 39% and 42% replacement of SBM in starter and grower diet	Broiler chickens	<ul style="list-style-type: none"> Elevated feed organic acids & aroma Lowered residual solvents & off-flavor No effect on growth performance Improved thymus and bursa of fabricius weight Lowered serum level of glutamic-oxaloacetic transaminase Enhanced intestinal morphology and gut flora Suppressed duodenum and cecum digesta <i>Escherichia coli</i> population 	Wu et al. (2020)
<i>L. plantarum</i> and <i>B. subtilis</i> <i>A. oryzae</i>	10 ⁵ cfu/mL 10 ⁶ spores/mL	7 d	Total replacement (37% FSBM inclusion)	Japanese quail	<ul style="list-style-type: none"> Improve growth performance by lowering the FCR and improving weight gain Enhanced crop and ceca balance of desirable microbiota Improved small intestine morphology and serum lipid profile 	Jazi et al. (2018)
<i>Bacillus velezensis</i> and <i>Lactobacillus brevis</i>	NS	1st Stage: 60 h 2nd Stage: 24 h and 36 h	6% FSBM inclusion replaced 17% and 21% SBM in starter and finisher diets, respectively	Broiler chickens	<ul style="list-style-type: none"> Regulated immune expression Enhanced intestinal traits and repair during stress Maintained tight junction-related gene expression Induced Jejune inflammatory factor and MUC2 expression 	Tsai et al. (2021)

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Table 2 (continued)

Fermentation microbe(s)	Inoculant dose	Duration of fermentation	Inclusion level, % replacement of SBM with FSBM	Animal physiological status	Benefits	Reference
<i>A. oryzae</i>	10,000 cfu/g of SBM	48 h	Total replacement	Broiler chickens	<ul style="list-style-type: none"> Improved ADG, ADFI, and FCR in chicks during the growth phase. Improved serum phosphorus, IgA, and IgM Reduced serum urea nitrogen during the growing and finishing periods 	Feng et al. (2007)
<i>A. oryzae</i>	10,000 cfu/g of SBM	48 h	Total replacement (29.5% and 27% FSBM inclusion in starter and grower diets, respectively)	Broiler	<ul style="list-style-type: none"> Increased starter chicks' intestinal protease, trypsin, and lipase activities Improved growers' chicken protease activity No effect on amylase activity Lowered pancreatic trypsin activity Improved villus height and decreased jejunum mucosa crypt depth Increased starter chicks' duodenal villus height 	Feng et al. (2007)

SBM = soybean meal; FSBM = fermented soybean meal; ADG = average daily gain; ADFI = average daily feed intake; BWG = body weight gain; CP = crude protein; IgG = immunoglobulin G; IgM = immunoglobulin M; IgA = immunoglobulin A; FCR = feed conversion ratio; MUC2 = mucin2; IGF-1 = insulin-like growth factor-1; NS = not stated.

calves, as it could influence the weaning stress response through improved nutritional quality and because it contains various functional molecules (Table 3). In another study, Feizi et al. (2020) observed that up to 50% partial substitution of SBM with FSBM calves starter elevated ruminal ammonia-nitrogen content, improved starter intake and growth performance could enhance calf productivity by altering the fermentation products and rumen microbial community. Substituting FSBM for SBM in neonatal calves alleviated the incidence of diarrhea and improved immunocompetence by promoting immune-related serum protein production against microbial infection (Kim et al., 2010a). According to Kim et al. (2012), FSBM alleviated stress by reducing pro-inflammatory hormone cytokines and acute phase protein stimulation, besides improving health, growth, and feed consumption in pre-weaned calves. In lipopolysaccharide (LPS)-induced weaned calves, the FSBM starter diet lowered cortisol and improved LPS-specific haptoglobin, immunoglobulin G, and immunoglobulin A generation against LPS challenge (Kwon et al., 2011). Calves often risk diseases and impaired growth because of environmental stress, like abrupt weaning and extreme weather conditions. Rezazadeh et al. (2019) indicated that feeding abruptly-weaned calves FSBM starter diet during cold weather helped calves adapt to weaning stress, as they had a lower interleukin 1B and serum amyloid A associated with sudden weaning in cold weather.

Surprisingly, there is still little knowledge on applying FSBM in adult ruminant diets. Most research on the effects of FSBM application in cattle has focused on young calves' productivity and immunological response. As far as we are concerned, Wang et al. (2021), who looked into the effects of substituting FSBM for SBM in lactating cows' diets, was the only study on feeding FSBM to adult ruminants. It was found that switching from SBM to FSBM affected the rumen's bacterial flora and fermentation. To our knowledge, there are no studies on FSBM utilization in sheep and goats, and much is yet to be known regarding the response of adult ruminants to the inclusion of FSBM or the replacement of SBM with FSBM. It appears that there could be restraints in fermented feeds in adult ruminants, probably because of their complex digestive system and feed processing mechanisms, which are quite different from that of monogastric animals; moreover, young ruminants are still in their pre-ruminant stage with gastrointestinal tract similar to that of monogastric. Additionally, unlike pre-ruminants, the AA profile of vegetable protein is not so important to ruminants since their vast gut microflora can convert nitrogenous compounds and produce high-quality rumen microbial CP.

5. Highlighting the research gap and prospects of fermented soybean meal application in livestock

SBM as feed for livestock animals has been extensively studied for decades. However, recently, FSBM has been considered more and more as an alternative high-quality plant protein source in poultry, swine, and ruminant diets. Despite the obvious reported benefits FSBM provides when fed to livestock, the literature review highlights that several aspects need further investigation. Firstly, many studies investigating FSBM utilization in livestock adopted the inoculation of microorganisms belonging to the fungi kingdom, namely *Aspergillus* spp. and a few *Candida* spp., followed by gram-positive bacteria *Bacillus* spp. There appears to be a preference for these two microbial inoculants, while only a few studies have considered using *Lactobacillus* spp., which also has a high probiotic potential. In this regard and coupled with the current ban on using antimicrobial growth promoters in animal nutrition, it is essential to screen more microbial strains, either single or mixed, with the capacity to improve the value of SBM to have a high protein content, with strong antinutritional factor degradation potential

Table 3
Benefits of feeding fermented soybean meal (FSBM) diet on ruminant health and productivity.

Fermentation microbe(s)	Inoculant dose	Duration of fermentation	Inclusion level, % replacement of SBM with FSBM	Animal physiological status	Benefits	Reference
<i>Aspergillus oryzae</i> and <i>Bacillus subtilis</i>	NS	48 h	Total replacement (61.5% FSBM inclusion on an as-fed basis)	Calves	<ul style="list-style-type: none"> ■ No adverse effects on growth or digestive processes ■ No observable effect on feed digestibility and efficiency 	Wolfswinkel et al. (2009)
<i>Lactobacillus</i> spp., <i>B. subtilis</i> , and <i>Saccharomyces cerevisiae</i>	NS	NS	Total replacement (5.55% FSBM inclusion)	Lactating dairy cows	<ul style="list-style-type: none"> ■ Increased propionate and valerate levels ■ Increased ruminal total bacteria, <i>Fibrobacter succinogenes</i>, <i>Selenomonas ruminantium</i>, and <i>Prevotella</i> species ■ Enriched <i>Succiniclasticum ruminis</i> and <i>Saccharofermentans acetigenes</i> population 	Wang et al. (2021)
<i>A. oryzae</i>	NS	NS	Total replacement (13.36% FSBM inclusion)	<i>Salmonella typhimurium</i> LPS-induced neonatal calves	<ul style="list-style-type: none"> ■ No effect on growth performance and milk intake ■ Alleviated weaning stress and enhanced immune status by <ul style="list-style-type: none"> ● Increased LPS-specific blood IgG and IgA ● Increased serum haptoglobin level ● Lowered cortisol concentration 	Kwon et al. (2011)
NS	NS	NS	Total replacement	Cows	<ul style="list-style-type: none"> ■ Increased milk urea nitrogen, milk protein yield, fat-corrected milk, and milk fat yield ■ Decreased milk somatic cell count ■ Increased percentage of acetate and A:P ratio, elevated rumen pH ■ An increased population of phyla <i>Fibrobacterota</i> and <i>Spirochaetota</i> and lowered <i>Proteobacteria</i> ■ Upregulated AA biosynthesis functional genes 	Amin et al. (2022)
<i>A. oryzae</i>	NS	NS	5% FSBM inclusion replaced 5% SBM in the 15.43% SBM of calf starter diet	Neonatal calves	<ul style="list-style-type: none"> ■ No effect on calves' growth performance ■ Alleviated diarrhea incidence and severity ■ Promoted immune-related serum proteins, like antigen-specific IgA and haptoglobin, against microbial infection 	Kim et al. (2010)
<i>B. subtilis</i>	10,000 cfu/g of SBM	48 h	9%–13.5% FSBM inclusion replaced 33%–50% SBM	Calves	<ul style="list-style-type: none"> ■ Improved calf performance ■ Changed fermentation products ■ Modulated rumen bacterial community abundance ■ Increased starter intake 	Feizi et al. (2020)
<i>B. subtilis</i>	10,000cfu/g of SBM	48 h	9%–13.5% FSBM inclusion replaced 33%–50% SBM	Weaned calves	<ul style="list-style-type: none"> ■ Enhanced calf growth performance ■ Reduced weaning stress via pro-inflammatory mediator level reduction 	Rezazadeh et al. (2019)

SBM = soybean meal; FSBM = fermented soybean meal; IgG = immunoglobulin G; IgA = immunoglobulin A; LPS = lipopolysaccharide; A:P = acetate-to-propionate ratio; AA = amino acid; NS = not stated.

having the capacity to remove almost all SBM antinutrients, that can colonize the animal gastrointestinal tract and improve the gut microbial flora, that can improve digestion and absorption rate and can also produce rich metabolites.

Secondly, FSBM is known to be a lipid-rich feedstuff and a source of unsaturated lipids with the potential to influence the FA profile of animals (Mukherjee et al., 2015a), and data on its effect on the digestive function of the animal is limited. Therefore, more specific responses associated with lipid and protein metabolism need to be further investigated, especially the evaluating gene expression involved in their metabolism. Additionally, because fermentation decomposes large protein molecules into small peptides with nutritional properties that the animal can directly absorb, it has been observed that absorption of such active small peptides can facilitate the early maturation of the digestive system of young animals like chicks, piglets, and calves. Therefore, cytological and genetic studies on the development and absorption capacity of the intestinal epithelium of young animals fed FSBM are important to understand the physical changes to tissue growth that might occur during the feeding period. This knowledge will aid researchers in better understanding the sustainability and adaptability of feeding FSBM to young animals and probably adults.

Further, this review shows a wide inconsistency in the duration or length of time for fermenting SBM from study to study, ranging from 12 h to 7 d. Variations in fermentation time could influence the obtained FSBM. The total protein content is increased during fermentation due to microbial protein production and the modified protein fraction. Similarly, fraction A (non-protein nitrogen), which consists of free amino acids and small peptides, appears to increase with fermentation time. For instance, [Weng and Chen \(2011\)](#) found that the concentration of non-protein nitrogen in soybeans increased after 24 h of fermentation, while [Feizi et al. \(2020\)](#) observed an even greater percentage of fraction A after 48 h of fermentation of SBM. Therefore, more studies are required to explore microbial bacteria and fungal strains that can reduce fermentation time and increase production, which will reduce production costs.

Additionally, the competition for soybean use in human nutrition, livestock industries and biofuel has resulted in its high cost. According to [USDA \(2023\)](#), including SBM in feed continues to be hampered by its relatively high cost and limited returns in the swine and poultry industries. Replacing SBM with FSBM to a large extent in livestock diets could address this critical concern by improving feed efficiency. Yet, to our knowledge, no studies have evaluated the cost of producing and feeding FSBM against the potential benefit. Hence, future studies should consider feed cost analysis to understand the economic feasibility of partially or completely replacing SBM with FSBM in livestock diets, especially on a commercial and large-scale basis. Also, about 81% of the soybeans grown worldwide are genetically engineered varieties ([Van Eenennaam, 2013](#)) which has been a public concern. Even though much research has reported no or negligible adverse impact of feeding genetically modified feedstuff to livestock and their products ([Nicolia et al., 2014](#); [Van Eenennaam and Young, 2014](#); [Vicini, 2017](#)), some have reported some serious effects of genetically modified plants, especially on human health ([Shen et al., 2022](#)). Whether or not feed processing, such as fermentation, could address this issue requires in-depth study.

Finally, future studies need to consider the environmental impact of feeding livestock with FSBM on a short-term or long-term basis. In ruminants, altering enteric methane production by manipulating the population of rumen microbes has proven to be achieved by the dietary composition of the feed ([Beauchemin et al., 2020](#)). [Jazi et al. \(2018\)](#) highlighted that fermented feed like FSBM could elevate LAB populations throughout the gastrointestinal tract

by foregut acidification, thereby providing an environment that favors the establishment and proliferation of healthy bacteria like LAB, which in turn could lower enteric methane production. At the same time, microbes used in FSBM have been shown to produce proteases, peptidases, and enzymes that could enhance fiber digestibility and ultimately reduce ruminal acetate to propionate ratio and methane emission ([Eun and Beauchemin, 2007](#)). Interestingly, saponin and tannin at certain limits have methane mitigation potential, but the negative impact of higher concentrations poses a health risk, restricting their broad use in abating methane ([Haque, 2018](#)). FSBM could be a better alternative to making minimal antinutrients available for consumption without impacting the animal's health. Based on these factors, in-depth research to bridge the gap in knowledge regarding the use of FSBM in adult ruminants and its potential in modulating the rumen ecosystem and mitigating methane emissions is warranted.

6. Conclusions

A high-quality vegetable protein source that can make available high concentrations of essential AAs in the right proportion is essential as a substitute for animal protein sources in livestock and poultry feed formulation because they can be cheaper and safer. FSBM has proven to be an excellent protein source that can partially or completely replace SBM, which is limited by allergenic antinutrients such as trypsin inhibitors, saponin, and tannin, which pose a great health risk to animals. Fermenting SBM by beneficial bacteria with strong probiotic effects potentially increased its nutritional value. FSBM is superior to its unfermented counterpart by improving animal nutrient utilization, digestibility, and absorption, enhancing growth performance and animal productivity, elevating feed intake, improving gut morphology and balance of microflora, alleviating gut disorders, and improving livestock product quality. These benefits were elicited not only by antinutrient removal during fermentation but also because the microbes produce multiple bioactive compounds with antimicrobial, antioxidant, and immune-stimulatory effects. Also, the SBM microstructure is changed, leading to better solubility and digestibility and bettering its functional properties. Again, antinutrients are removed, and trapped nutrients are released via changes in protein profile during protein hydrolysis. Still, research needs to be extended into understanding their impact on young animal gut histomorphogenesis, screening microbial strains with stronger probiotic capacity and shorter fermentation time, and investigating possible environmental impacts.

Author contributions

Modinat T. Lambo: Writing – original draft preparation, Revision, Fund acquisition, and Investigation. **Haokai Ma, Haosheng Zhang, Peng Song, Hongxiang Mao:** Investigation and Revision. **Guowen Cui:** Validation and Revision. **Baisheng Dai:** Revision, Proofreading, and Fund acquisition. **Yang Li:** Proofreading, Fund acquisition and Oversight responsibility. **Yonggen Zhang:** Supervision – oversight and leadership responsibility, Fund acquisition.

Declaration of competing interest

We declare that we have no financial and personal relationships with other people or organizations that can inappropriately influence our work, and there is no professional or other personal interest of any nature or kind in any product, service and/or company that could be construed as influencing the content of this paper.

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