R. Bras. Zootec., 49:e20190096, 2020
https://doi.org/10.37496/rbz4920190096

Non-ruminants
Full-length research article

Revista Brasileira de Zootecnia

Brazilian Journal of Animal Science
e-ISSN 1806-9290
www.rbz.org.br

Effect of fermented soybean meal supplementation on some growth performance, blood chemical parameters, and fecal microflora of finishing pigs

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ABSTRACT - This study evaluated the effect of fermented soybean meal (FSBM) supplementation on growth performance, meat quality, blood biochemical parameters, and fecal microflora of finishing pigs. Thirty-two crossbred pigs (Duroc × Landrance × Yorkshire) (66-day-old, 67.95±0.25 kg) were randomly allocated to two treatments and fed diets containing soybean meal and FSBM. The average daily gain (ADG), average daily feed intake (ADFI), feed conversion ratio (FCR), blood biochemical parameters, and meat quality index were measured. At the end of experiment, the fecal microflora of finishing pigs was analyzed with 16S rDNA techniques. Results revealed that pigs fed FSBM had a greater ADG and lower cooking loss relative to control group (basal diets). Compared with the control group, the triglyceride content in the serum of the group fed FSBM increased significantly, and the creatinine content in the serum decreased notably. Fermented soybean meal enhanced the abundance of *Bacteroidetes*, *Prevotellaceae*, *Bcteroidales*, *Bacteroidia*, but inhibited the growth of *Firmicutes*, *Clostridia*, *Clostridiales*, and *Ruminococcaceae* in the intestine of pigs. Therefore, we can speculate that FSBM may play an important role in animal production. Dietary FSBM supplementation may be beneficial to some aspects of growth performance and the diversity of fecal microflora in finishing pigs.

Keywords: 16S rDNA, fermentation, meat quality, pig, production performance, soybean meal

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Received: July 3, 2019
Accepted: November 11, 2019

How to cite: Feng, H.; Qu, H.; Liu, Y.; Shi, Y.; Wu, S. and Bao, W. 2020. Effect of fermented soybean meal supplementation on some growth performance, blood chemical parameters, and fecal microflora of finishing pigs. Revista Brasileira de Zootecnia 49:e20190096. https://doi.org/10.37496/rbz4920190096

Introduction

Soybean meal (SBM) is widely used as a protein source in poultry and swine industries because of its high nutritional value, good palatability, and ease of digestion and absorption. Relatively balanced amino acids in SBM can sustain the nutrition of pigs and poultry (Kishida et al., 2000). However, untreated soybean meal contains numerous anti-nutritional factors that adversely affect the intestinal health and digestion, absorption, and utilization efficiency of nutrients (Dunsford et al., 1989; Liu et al., 2014). Thus, alternative ingredients for reducing the content of anti-nutritional factors are needed.

Anti-nutritional factors in SBM can be eliminated by microbial fermentation, thus increasing nutrient absorption and utilization (Li, 2009). Protease generated during fermentation can decompose soybean proteins into small peptides and free amino acids, thereby improving the SBM utilization and lymphocyte activity (Fernandez-Orozco et al., 2007). Various beneficial bacteria such as yeasts, lactic acid bacteria, and *Bacillus* dominate the flora of fermented SBM (FSBM), thus improving intestinal microecological balance and immune function (Yamauchi and Suetsuna, 1993). Hirabayashi et al.

(1998) also reported that FSBM led to the complete degradation of phytate phosphorous of chicks, thus decreasing phosphorous excretion.

Current studies have mainly concentrated on the effects of FSBM supplementation on the production performance of weaning pigs. Adding FSBM to feed can increase the digestive enzyme activity in the intestine, improving the feed conversion ratio (FCR) and growth performance of weaned piglets (Feng et al., 2007). Upadhaya and Kim (2015) also found that dietary supplementation of SBM fermented with *Bacillus* significantly increased the digestibility of amino acid in weaned piglets. Kim et al. (2010a) showed that mortality from diarrhea decreased significantly in weaned piglets fed FSBM and that immune effects increased significantly.

Overall, fermentation can significantly enhance the nutritional values of SBM in animal diets, thereby improving the production performance and immunity of piglets. However, reports on using FSBM in the diet of finishing pigs are scarce. Therefore, we aimed with present study to assess the nutritive values of FSBM as a partial replacement for SBM by evaluating the growth performance, meat quality, and blood biochemical parameters. Illumina MiSeq sequencing platform and 16S rDNA were used to investigate the effect of FSBM on fecal microbial flora in finishing pigs. It may provide theoretical evidence for using FSBM in the diet of finishing pigs.

Material and Methods

The animal study proposal was approved by the Institutional Animal Care and Use Committee (IACUC) (SYXK (Su) IACUC 2012-0029). The animal experiment was conducted in Suzhou (31°18'20.88" N and 120°35'43.3" E), located in Jiangsu Province, China.

The SBM obtained from Jiangyin, located in Jiangsu province, China, was fermented with *Aspergillus oryzae* strain GB-107 (kept in the laboratory) in a packed bed solid-state fermentor for 48 h. The SBM was mixed with water at a ratio of 3:1, autoclaved at 120 °C for 20 min, and cooled at room temperature as describe by Feng et al. (2007).

Thirty-two crossbred (Duroc × Landrace × Yorkshire) pigs (16 males and 16 females), with an average weight of 67.95±0.25 kg, were randomly allotted to two treatments: control group (basal diet) and FSBM group (replacing 8% SBM with FSBM). Each treatment consisted of four replicates with four pigs per replicate. Diets were formulated according to NRC (2012) (Table 1).

The feeding trial, carried out in a fattening house (20 °C and 60-80% relative humidity), lasted for 66 d. Pigs were fed their respective diets twice daily (7.00-8.00 and 16.30-17.30 h) and allowed free access to feed and water. At the end of experiment, pigs were fasted for 12 h, then weighed in the morning. The fresh fecal samples were collected directly by rectal massage into plastic sample bags from all experimental pigs. The pigs were then killed humanly at a local commercial slaughterhouse. Blood samples (approximately 5 mL) were taken from anterior *venae cava*, and serum was separated by centrifugation at 3000 × *g* for 10 min, then stored at −20 °C until use. The *longissimus dorsi* muscle at the 6th-7th rib of the right carcass was collected to assess meat quality.

The following growth performance parameters were evaluated: initial and final weights of the individual pigs (kg), average daily feed intake (ADFI; kg day^{-1}), and FCR (ADFI:ADG).

Routine blood examinations were performed. Relative indexes containing the red blood cell counts (RBC), white blood cell counts (WBC), hemoglobin (Hb), platelet count (PLT), hematocrit (HCT), lymphocyte percentage (LYM %), and total number of lymphocytes were measured. The following serum biochemical indices were measured using CX9ALX automatic biochemical analyzer (Beckman Coulter, Brea, CA, USA): the alanine aminotransferase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP or AKP), serum albumin (ALB), total protein (TP), globulin (GLB), urea nitrogen (BUN), insulin, blood glucose (GLU), triglyceride, low-density lipoprotein (LDH), high-density lipoprotein (HDH), and total cholesterol (CHO).

Table 1 - Composition and nutrient levels of diets

Item	Group	
	Control	FSBM
Ingredient (g kg^{-1})		
Corn (g kg^{-1})	441.18	441.18
Soybean meal (g kg^{-1})	164.62	111.94
Wheat bran (g kg^{-1})	26.33	26.33
Fermented soybean meal (g kg^{-1})	0	52.68
$CaHPO_4$ (g kg^{-1})	7.97	7.97
L-threonine (g kg^{-1})	0.07	0.07
L-tryptophan (g kg^{-1})	0.07	0.07
Phytase (g kg^{-1})	0.07	0.07
Vitamin premix[1] (g kg^{-1})	1.32	1.32
Mineral premix[2] (g kg^{-1})	1.98	1.98
DL-methionine (g kg^{-1})	0.07	0.07
Salt (g kg^{-1})	2.30	2.30
Limestone (g kg^{-1})	9.68	9.68
Zeolite (g kg^{-1})	2.83	2.83
Nutrition levels[3]		
Metabolizable energy (kcal kg^{-1})	3410	3410
Crude protein (%)	16.55	16.55
Calcium (%)	0.59	0.59
Total phosphorous (%)	0.55	0.55
Available phosphorous (%)	0.33	0.33
Digestible lysine (%)	0.85	0.85
Digestible Met+Cys (%)	0.60	0.60
Digestible methionine (%)	0.27	0.27
Digestible threonine (%)	0.61	0.61
Digestible tryptophan (%)	0.16	0.16

Control group: basal diet; FSBM: basal diet, replacing partial SBM with fermented soybean meal.
[1] The vitamin premix provided the following, as mg/kg diet: vitamin A, 4480 IU; vitamin D_3, 500 IU; vitamin E, 20 IU; vitamin K_3, 2.20 mg; vitamin B_1, 1.80 mg; vitamin B_2, 2.20 mg; vitamin B_6, 1.50 mg; vitamin B_{12}, 12 µg; folic acid, 0.30 mg; biotin, 0.05 mg; calcium pantothenate, 8 mg; nicotinic acid, 10 mg.
[2] The mineral premix provided the following, as mg/kg diet: Fe (as ferrous sulfate), 80 mg; Cu (as copper sulfate), 15 mg; Zn (as zinc sulfate), 80 mg; Mn (as manganese sulfate), 5 mg; Se (as sodium selenite), 0.10 mg; I (as potassium iodide), 0.10 mg.
[3] Nutrient levels were calculated values.

The following meat quality parameters were evaluated: pH value, meat color values (CIE L*, a*, b*), water holding capacity (WHC), shear force, drip loss, and cooking loss. Muscle pH was measured as described by Schilling et al. (2008) at 45 min and 24 h (pH 45 min and pH 24 h) using a pH meter (HI9023, Hanna Instruments, Padova, Italy) equipped with an insertion glass electrode (FC 230B, Hanna Instruments). Meat color was measured in duplicate at 24 h referred to Cao et al. (2012); drip loss, as described by Young et al. (2004); and shear force and cooking loss, as described by Vasanthi et al. (2007).

The total bacteria DNA was extracted from fecal samples using a microbial DNA extraction kit (Qiagen Company, Germany) according to manufacturer's instructions. The Thermo Nano-Drop 2000 UV microspectrophotometer (Thermo Scientific Inc., Wilmington, USA) and 1% agarose gel electrophoresis were used for total DNA quality testing. The 16S rDNA V3 – V4 region was amplified by PCR using bacterial universal primers 338F 5 ' -ACTCCTACGGGAGGCAGCA-3 '; 806R 5 ' - GGACTACHVGGGTWTCTAAT- 3 '. The PCR amplification was carried out under these conditions: 95 °C for 2 min, 25 cycles of 95 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s, with a last step of 72 °C for 5 min. The PCR products were purified

with the QIA quick Gel Extraction Kit (QIAGEN, Dusseldorf, Germany), then the library was subjected to quality inspection. On-board sequencing was performed using the Illumina MiSeq platform according to standard protocols. Downstream data were filtered to remove low-quality reads, leaving high-quality clean data for further analysis.

The USEARCH software (v7.0.1090, http://drive5.com/uparse/) (Edgar, 2013) was used to cluster clean data at 97% similarity with a 0.8 threshold to obtain representative sequences of OTU (Operational Taxonomic Units). The OTU sequences were then aligned to the database for species annotation using the Mothur method and the SSUrRNA database of SILVA (http://www.arb-silva.de/) (Wang et al., 2007; Quast et al., 2013). The phylogenetic relationships of all the sequences of OTU were obtained according to the Muscle (v3.8.31, http://www.drive5.com/muscle/) software. Alpha diversity values were calculated using Mothur (v1.31.2) software. Beta diversity analysis was performed by QIIME (v1.80) software according to iterative algorithm. Based on the weighted and unweighted species taxonomic abundance information, 75% of the reads in each sample was randomly sampled for dissimilarity calculation, separately. The PCoA (Principal Coordinates Analysis) plot and statistical analysis results were obtained after integrated statistics up to 100 iterations.

Analysis of significant differences between groups was performed using Metastats (http://metastats.cbcb.umd.edu/) software. This corrected P-value using the "BH" (Benjamini-Hochberg) procedure (White et al., 2009) by the *p.adjust* command in the R (v3.1.1) package for significant differences between taxonomic ranks of groups at phylum, class, order, family, genus, and species level. The cluster tree plot was then plotted using online LEfSE (LDA Effect Size) package (https://huttenhower.sph.harvard.edu/galaxy/). Microbial function was predicted by using PICRUSt (Langille et al., 2013). The predicted genes and their respective functions were aligned with the Kyoto Encyclopedia of Genes and Genomes (KEGG) database, and differences between treatment groups were examined in STAMP software (http://kiwi.cs.dal.ca/Software/STAMP) (Parks and Beiko, 2010).

All experimental data were statistically analyzed using independent-samples t test model, using with or without fermentation as fixed factors, then growth performance and blood chemical parameters as the dependent variables, respectively. The SPSS 18.0 (SPSS Inc., Chicago, IL, USA) software was used to analyze the differences between groups regarding growth performance and blood chemical indices of the finishing pigs fed untreated or fermented soybean meal. Significance was set at $P<0.05$, with highly significant differences set at $P<0.01$. All data were expressed as mean ± standard deviation.

Results

Dietary supplementation of FSBM notably increased the ADG of finishing pigs compared with the control group ($P<0.05$). The FCR of pigs fed FSBM decreased by 0.16, which helped to increase economic efficiency (Table 2). Analysis of effect on meat quality between two treatments showed that the L* and b* values of the pork in FSBM decreased by 1.49 and 0.08, respectively, whereas the a* value increased by 0.75. Moreover, the meat of pigs of the FSBM group exhibited lower WHC and shear force values not significantly different from those of the control group. The pork cooking loss of the pigs fed FSBM was significantly lower than pork from control pigs ($P<0.05$) (Table 3).

Table 2 - Effect of fermented soybean meal on growth performance in finishing pigs

Item	Control	FSBM
Initial weight (kg)	67.94±0.26	67.96±0.12
Final weight (kg)	114.29±0.93	117.75±0.75
Average daily gain (ADG) (g day^{-1})	826.38±11.92*	900.67±13.92
Average daily feed intake (ADFI) (kg day^{-1})	2.95±0.07	3.07±0.04
F:G	3.57±0.13	3.41±0.02

Control group: basal diet; FSBM: basal diet, replacing partial SBM with fermented soybean meal.
* in a row indicate significant difference ($P<0.05$).
All data were expressed as mean ± standard deviation.

Analysis of the blood biochemical parameters showed that FSBM significantly increased the concentration of triglyceride and decreased creatinine concentration of pigs compared with the control group (P<0.05) (Table 4).

Analysis of alpha diversity (Figure 1) indices containing ACE, Chao, Observed Species, Shannon, and Simpson indicated the differences of microbiota richness, diversity, number of species, and genetic diversity between the two treatments. The result showed that the ACE index of pigs fed FSBM was significantly higher than that of control group (P<0.05).

Table 3 - Effect of fermented soybean meal on meat quality of finishing pigs

Item	Control	FSBM
Lightness (L*)	37.30±1.72	35.81±0.67
Redness (a*)	3.91±0.38	4.66±0.45
Yellowness (b*)	3.00±0.47	2.92±0.14
pH24	5.68±0.02	5.67±0.01
Muscle water loss (%)	43.99±1.14	42.27±0.94
Shear force (kgf)	2.82±0.07	2.64±0.07
Drip loss 24 h	3.02±0.14	3.01±0.18
Drip loss 48 h	5.95±0.17	5.96±0.19
Cooking loss (%)	43.62±0.72*	41.22±0.71

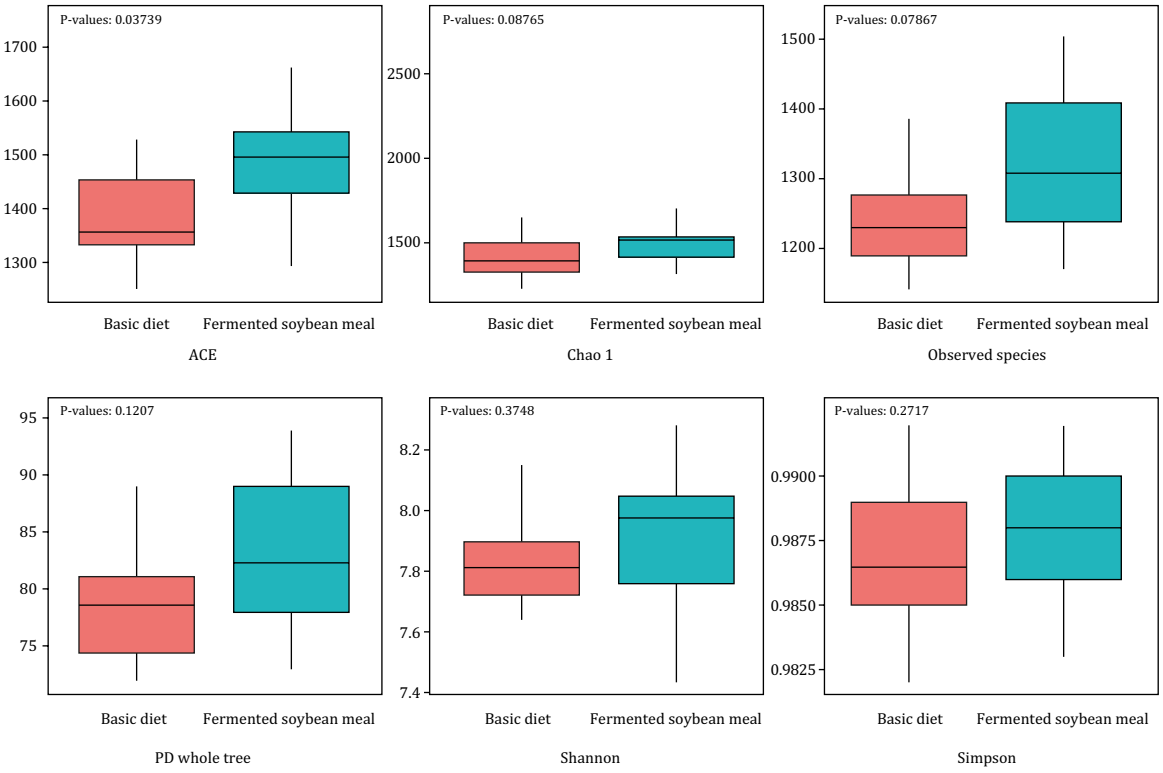
Control group: basal diet; FSBM: basal diet, replacing partial SBM with fermented soybean meal.
* in a row indicate significant difference (P<0.05).
All data were expressed as mean ± standard deviation.

Table 4 - Effect of fermented soybean meal on blood index of finishing pigs

Item	Control	FSBM
Glutamic-pyruvictransaminase (ALT)	50.50±3.87	56.83±5.56
Aspartate transaminase (AST)	49.00±4.67	43.07±5.26
AST:ALT	0.91±0.07	0.78±0.09
Total protein	68.32±1.63	70.57±1.89
Albumin (ALB)	35.52±0.52	36.37±0.95
Globulin (GLB)	31.80±1.62	34.20±1.96
ALB:GLB	1.17±0.06	1.08±0.07
Alkaline phosphatase	122.67±8.23	124.50±14.13
Gamma-glutamyl transpeptidase	33.00±2.80	34.67±2.60
Lactic dehydrogenase	446.80±20.15	438.67±22.35
Cholinesterase	573.33±51.07	662.83±24.48
Creatinine	158.67±1.91*	138.83±7.08
Urea nitrogen	7.32±0.61	8.17±0.66
Glucose	5.15±0.47	8.17±0.49
Total cholesterol	2.14±0.05	2.15±0.09
Triglyceride	0.38±0.02*	0.68±0.12
High-density lipoprotein	0.85±0.04	0.84±0.05
Low-density lipoprotein	1.07±0.05	1.04±0.04
Creatine phosphate kinase	3764.50±124.90	3529.00±17.44

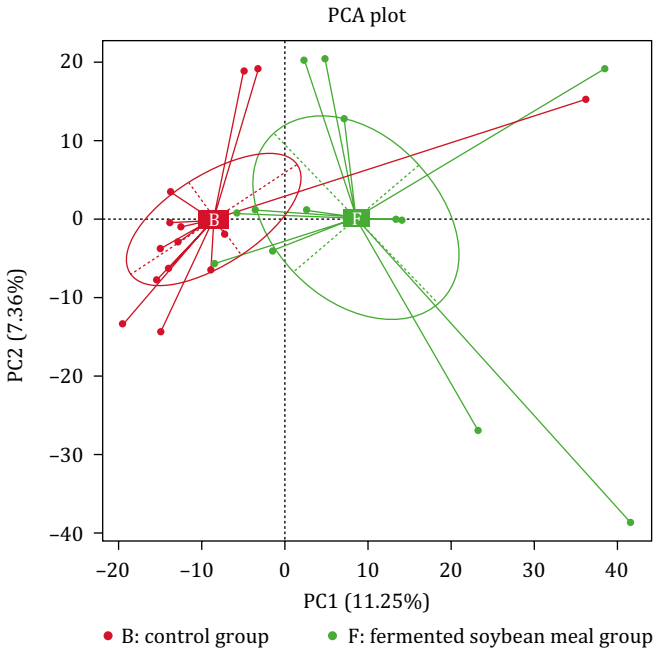
Control group: basal diet; FSBM: basal diet, replacing partial SBM with fermented soybean meal.
* in a row indicate significant difference (P<0.05).
All data were expressed as mean ± standard deviation.

The PCA analysis (Figure 2) showed that two treatments could be clearly distinguished: the microbial structure and abundance of the FSBM-fed group were significantly different from those of the control. A species profiling histogram of samples at the phylum level (Figure 3) evidenced that the dominant



Five statistics are displayed in the box diagram (minimum value, the first quartile, median, the third median, and maximum value; they are five lines from bottom to top).

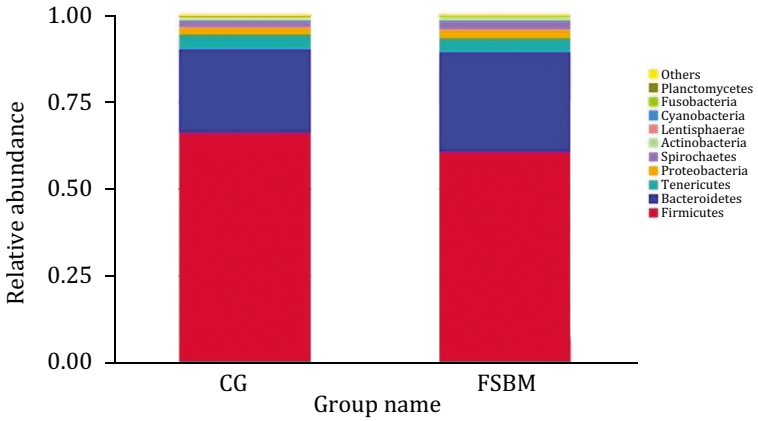
Figure 1 - Alpha diversity box shape among groups.



Each point represents each sample, and different colors represent different groups.

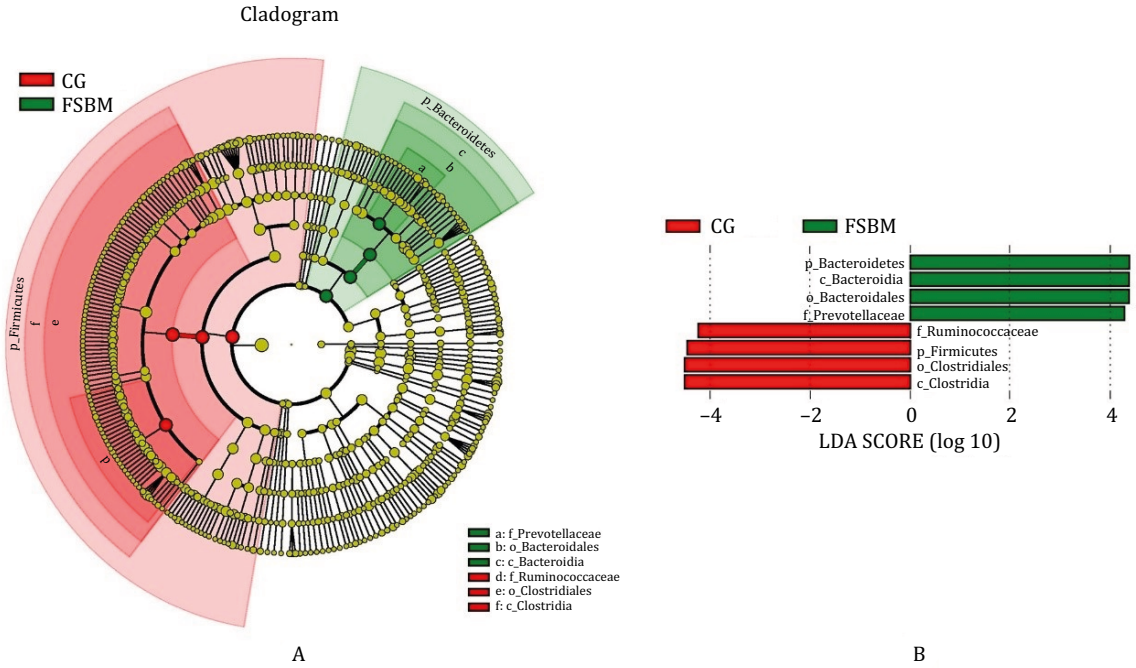
Figure 2 - Principal component analysis.

species in the feces of both groups were *Firmicutes*, *Bacteroidetes*, *Tenericutes*, *Proteobacteria*, *Spirochaetes*, and *Actinobacteria*. The LEfSE (LDA Effect Size) analysis (Figure 4) revealed that the biomarker with a statistically significant difference in FSBM group was *Bacteroidetes* at the phylum level, *Prevotellaceae* at the family level, *Bacteroidales* at the order level, and *Bacteroidia* at the class level. However, the dominant bacteria with the highest abundance in the control group were *Firmicutes* at the phylum level, *Ruminococcaceae* at the family level, *Clostridiales* (*Clostridium*) at the order level, and *Clostridia* at the class level.



CG - control group; FSBM - fermented soybean meal group.
The abscissa is the sample name; the ordinate represents the relative abundance; and others represents the sum of the relative abundances of all other phyla except these 10 phyla in the figure.

Figure 3 - Species profiling histogram of samples in phylum level (top 10).



CG - control group; FSBM - fermented soybean meal group.
The figure on the left is LEfSe cluster tree; circles radiating from inside to outside represent taxonomic levels from phylum to genus (or species). Each small circle at a different taxonomic level represents a taxon at that level, and the small-diameter-size circle is proportional to the relative abundance size. Coloring principle: species with no significant difference are uniformly colored in yellow, differential species biomarker follows the group for coloring, red nodes indicate microbial groups that play an important role in the red group, and green nodes indicate microbial groups that play an important role in the green group. The figure on the right indicates species with significant difference in two treatments ($P<0.05$).

Figure 4 - LEFSE analysis chart.

Discussion

Soybean meal has been widely used as the main source of plant protein in animal production. Nevertheless, some anti-nutritional factors, such as antigen protein, can reduce its nutritional value and production performance. The microbial fermentation of SBM can help reduce the content of these anti-nutritional factors. Therefore, using FSBM as a potential alternative to expensive protein sources has become a topic of great interest in meat production.

Several studies have reported that fermentation can degrade anti-nutritional factors contained in SBM into small peptides and free amino acids, which will facilitate gastrointestinal digestion and absorption in animals. Hong et al. (2004) showed that dietary FSBM supplementation increased the utilization ratio of crude protein in the fodder and significantly reduced the molecular size of the peptides (less than 10 kDa). The peptides in SBM are generally in the range from 20 to 250 kDa. A reduction in the molecular size of peptides may contribute to decreasing the gastric acid secretion for protein digestion (Cranwell, 1985) and increasing the absorption of composing glycinin and β-conglycinin (Kim et al., 2010b). The research by Jeong et al. (2016) also demonstrated this and further confirmed that FSBM contributed to improving the nutrient digestibility and growth performance of pigs. In the present study, pigs fed FSBM had greater ADG than the control group ($P<0.05$). The result indicated that addition of FSBM to the feed of finishing pigs accelerated their growth to some extent. The FCR also decreased by 0.16 in finishing pigs fed FSBM, which would help to reduce animal production costs and improve the economic efficiency.

Consumers and producers consider that quality is one of the most important indicators when selecting meat, its main factors for assessment being tenderness, meat color, and WHC. Bright red pork is considered an important factor in the evaluation of pork quality (Troy and Kerry, 2010). In this study, the pork from the group fed FSBM exhibited lower L* and b* values and higher a* value than that from the control group, which indicated that adding FSBM may increase the redness of the pork. The texture of the meat is usually measured by the tenderness value, as evaluated by its negative correlation with shear force. Tenderness (shear force) is probably the most important dietary quality parameter determining consumer acceptance (Miller et al., 2001). In the present study, the shear force of pork from the pigs fed FSBM tended to be lower than that from the control animals. This indicated that feed supplemented with FSBM improved the tenderness of pork from finishing pigs.

The WHC of meat is directly related to its intramuscular lipid and moisture content. Lower WHC indicates a loss of nutritional value through exudates leading to drier and harder meat (Dabes, 2001). The muscle water loss, cooking loss, and drip loss are usually used for a comprehensive assessment of WHC. Muscle water loss is linearly negatively correlated with WHC: the lower the drip loss and cooking loss, the higher the WHC. The present study showed that the cooking loss of meat from pigs fed FSBM was significantly lower than that from the control animals ($P<0.05$). The water loss from this group also tended to be less than that of the control. These results revealed that adding FSBM increased the WHC of pork, which affected its juiciness, tenderness, and color. Therefore, we speculated that dietary FSBM supplementation may improve the meat tenderness of finishing pigs.

Fermented soybean meal increased the concentration of triglyceride and decreased creatinine concentration. Triglyceride combined with proteins may generate HDL and LDL. Research has shown that HDL is able to impede the oxidation of LDL and can also transfer cholesterol from the macrophage back to the plasma in a process known as reverse cholesterol transport (Kwiterovich, 2000). Creatinine is a marker of the renal detoxification function, can be resolved by creatine, and is closely related to a variety of diseases (Wyss and Kaddurah-Daouk, 2000). Therefore, we speculated that the addition of FSBM may affect the lipoprotein metabolism and accelerate kidney detoxification of finishing pigs.

A previous study has shown that FSBM helped to increase the number of beneficial microbes and inhibit the proliferation of pathogenic microbial (Yin et al., 2012). Feng et al. (2007) found that FSBM could improve the intestinal morphology and enhance the intestinal digestive enzyme activity of crossbred pigs (Duroc × Landrace × Yorkshire). Dietary FSBM supplementation can also play an important role in

relieving diarrhea and producing immune-related effector cells such as IgA and haptoglobin (Kim et al., 2010b). The reason that FSBM can decrease the rate of diarrhea and change the intestinal morphology and intestinal digestive enzyme activity may be the fermentation of SBM that regulates the composition of the intestinal flora.

In the experiment, FSBM significantly increased the abundance of *Bacteroidetes*, *Prevotellaceae*, *Bcteroidales*, and *Bacteroidia* of pigs compared with the control diet. Generally, *Bacteriodes*, important components of the gut flora, are involved in regulating nutrition and maintaining physiological function. Seksik et al. (2003) found that many plant polysaccharides in the diet could not be degraded but could be absorbed and degraded by *Bacteroides*. Matsuda et al. (2000) also reported that *Bacteroides* can hydrolyze and ferment various exogenous fibrils, endogenous mucins, and also metabolize bile acids and steroids. *Bacteroides* compounds have also been shown to play important roles in modulating bacterial toxin production (Zoetendal et al., 2002) and enhancing the ability of host-specific immune responses (Macfarlane et al., 2004). We speculated that the increased abundance of *Bacteroidetes* at the phylum, class, and order levels may improve the decomposition ability of finishing pigs for various indigestible and absorbable substances.

The present study also indicated that *Prevotellaceae* was the dominant species in FSBM. *Prevotella* has been reported to be closely related to the immune system and can significantly reduce the content of mucopolysaccharides and glycoproteins in the intestinal mucosal glands (Arumugam et al., 2011; Wu et al., 2011; Kang et al., 2013; Scher et al., 2013). A recent study suggested that *Prevotella*, one of the human intestinal type classifications, may facilitate the synthesis of various vitamins such as riboflavin, pantothenate, ascorbate, and thiamine (B1) (Arumugam et al., 2011). Forsyth et al. (2011) and Brown et al. (2011) also reported that the lower abundance of *Prevotella*, the lower the mucin composite content, which would increase intestinal permeability and the susceptibility of the regional intestine to systemic exposure to bacterial toxins. Zhu et al. (2014) also found that lower abundance of *Prevotellaceae* may cause constipation. Therefore, the increased abundance of *Prevotellaceae* (*Prevalence*) in FSBM may be conducive to improving the immune capacity of finishing pigs, but the specific mechanism needs to be further detected.

Furthermore, FSBM significantly reduced the abundance of *Firmicutes*, *Clostridia*, *Clostridiales*, and *Ruminococcaceae* of pigs compared with the control treatment. Setlow et al. (2017) confirmed that *Clostridiales* may accelerate the spoilage of food and trigger disease. *Clostridium difficile* infection has been recognized as a major public health problem, producing toxins A and B that can damage the intestinal mucosa (Shrestha et al., 2018). Therefore, we can speculate that FSBM may increase the abundance of beneficial microbes and decrease the intestinal pathogens abundance of pigs, which would help to reduce the incidence of intestinal diseases in the livestock.

Conclusions

Our study revealed the effects of fermented soybean meal supplementation on the production performance of finishing pigs. It can potentially not only improve the growth performance and meat quality of the finishing pigs, but also modulate the composition diversity of intestinal microbial population. Specifically, dietary fermented soybean meal supplementation contributed to increasing the abundance of *Bacteroidetes*, *Prevotellaceae*, *Bcteroidales*, and *Bacteroidia* in finishing pigs.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: H. Feng and W. Bao. Data curation: H. Qu. Investigation: Y. Liu and Y. Shi. Methodology: S. Wu. Resources: H. Feng. Software: H. Qu. Supervision: W. Bao. Validation: Y. Liu, Y. Shi and S. Wu. Writing-original draft: H. Feng. Writing-review & editing: H. Feng.

Acknowledgments

This work was supported by Yangzhou University International Academic Exchange Fund, an independent innovation fund project of agricultural science and technology in Jiangsu [grant number CX (16)1003]; Qing Lan Project of Yangzhou University, Natural Science Foundation of Jiangsu province, China (Grant number BK20180899); and the Natural Science Foundation of Yangzhou City, China (Grant number YZ2018102).

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