0.2% BP at the expense of the BP carriers in the control diet. The energy and nutrient concentrations in all diets met or exceeded the requirement estimates suggested by the NRC [16]. All experimental diets contained chromic oxide at 0.5% as an indigestible index. The BP product was obtained from CTCBIO Inc. (Seoul, Republic of Korea). The product contained a mixture of BP consisted of *Clostridium perfringens* types A and C, *Escherichia coli* (f41, k88, and k99), *Salmonella* spp. (*Salmonella choleraesuis*, *Salmonella derby*, *Salmonella enteritidis*, and *Salmonella typhimurium*), and *Staphylococcus aureus*. The BP product contained 10^9 plaque-forming units per gram.

Feeding and sample collection

The animals were fed the experimental diets at 3 times the daily maintenance requirement for energy (i.e., 197 kcal metabolizable energy/kg $BW^{0.60}$; [16]). The amount of feed allowance per pig was divided into 2 equal meals and provided to pigs at 0800 and 1700 h. Water was freely available. An experimental period was consisted of 4 days of adaptation to the experimental diet, 1 day of fecal collection, and 2 days of ileal digesta collection. Fecal samples were collected from 0900 to 1800 on day 5 by grab sampling, and rectal massage was carried out to acquire fresh fecal samples for microbial community analysis. Ileal digesta samples were collected from 0900 to 1630 on days 6 and 7 using a wired plastic bag fixed to a T-cannula. The plastic bags were replaced whenever filled with ileal digesta, or at least every 30 min. Collected feces and ileal digesta were immediately stored at −20℃ for further analyses. After the termination of the first period, 4 days of buffering period was used to prevent potential carryover effects.

Microbial community and chemical analyses

Bacterial genomic DNA were extracted from fresh ileal and fecal samples and the V4 region of the 16S rRNA gene was amplified. Amplicons were sequenced on an Illumina MiSeq, and microbial communities and alpha diversity were analyzed using Quantitative Insights into Microbial Ecology as described by Han et al. [17].

Fecal samples were dried in a forced-air drying oven and ileal digesta samples were lyophilized in a freeze dryer and finely ground (< 1 mm) before chemical analysis. Diet, feces, and ileal digesta samples were analyzed for dry matter (AOAC [18]; method 930.15), crude protein (AOAC [18]; method 990.03), and chromium (AOAC [18]; method 990.08) contents. The fibers were analyzed (D200; Ankom Technology, Macedon, NY, USA) for neutral detergent fiber (Ankom Technology, 1998a; method 13) and acid detergent fiber (Ankom Technology, 1998b; method 12) contents. All samples and diets were analyzed for gross energy using bomb calorimetry (Model C2000, IKA® , Germany).

Calculations and statistical analyses

The apparent ileal digestibility (AID) and ATTD of energy and nutrients were calculated using the index method [19]. Experimental data were analyzed using the MIXED procedure of SAS 9.4 (SAS

Institute. Inc., Cary, NC, USA). The statistical model included dietary treatment as the fixed variable and replication, period within replication, and animal within replication as random variables. The proportion of microbial communities in each treatment was expressed as a percentage of the total 16S rRNA gene sequences. Least squares means for the response variables were calculated for each treatment. Orthogonal contrasts were used to compare the control versus the AB and BP groups and the AB group versus the BP group. An individual pig was the experimental unit. Statistical significance and trend were determined at $p \leq 0.05$ and $0.05 < p \leq 0.10$, respectively.

Results

One pig that was provided with the control diet declined to consume the diet during the collection period and was subsequently excluded from the data for statistical analysis.

Microbial communities at different gut locations

A total of 528,719 (mean = 11,494 ± 575) 16S rRNA reads were generated, with an average of 12,361 (±1,465) and 9,970 (±1,627) reads in ileal digesta and feces from the pigs fed the control diet, 12,787 (±699) and 10,633 (±1,627) reads in ileal digesta and feces from the pigs fed the AB diet and 12,932 (±1,761) and 10,198 (±1,059) reads in ileal digesta and feces from the pigs fed the BP diet, respectively.

The alpha diversity of the microbial communities in the ileum and feces was not affected by AB or BP supplementation (Fig. 1 and 2). At the phylum level, *Firmicutes* accounted for the largest proportion of the microbiota in the ileal and fecal samples of all groups, followed by *Bacteroidetes* (Table 2). The proportion of *Bacteroidetes* in the ileal digesta tended to be less ($p = 0.099$) in the pigs fed the AB- or BP-supplemented diets compared with the control group, but there was no difference between AB and BP groups. The proportion of *Firmicutes* in the ileal digesta tended to be greater ($p = 0.059$) in the pigs fed the AB or BP diets than in the control group but there was no difference between the AB and BP groups. In the feces, there were no differences in the relative proportions of *Bacteroidetes* and *Firmicutes* among all treatments.

At the genus level, the proportion of *Lactobacillus* in the ileal digesta was the most dominant and tended to be greater ($p = 0.062$) in the pigs fed the AB- or BP-supplemented diets than in the control group, with no difference between the AB and BP groups (Table 3). The proportions of *Bacteroides* ($p = 0.074$) and *Streptococcus* ($p = 0.088$) in the ileal digesta tended to be less in the AB and BP groups compared to the control group with no difference between the AB and BP groups. In the fecal samples, the relative proportion of *Lactobacillus* was the most dominant. The relative proportion of *Bifidobacterium* tended to be less ($p = 0.029$) in the AB and BP groups compared with the control group with no difference between the AB and BP groups. In contrast, the relative proportions of *Parabacteroides* and *Succinivibrio* were less ($p<0.05$) in the AB group compared with the BP group.

Energy and nutrient digestibility at different gut locations

The AID and ATTD of energy and nutrients were not affected by the supplemental AB or BP (Table 4).

Discussion

The BP bind to specific receptors on the surface of bacteria prior to introducing their genetic materials [20, 21]. The relationship between BP and bacteria is either lytic or lysogenic. During lytic infection, the phages adhere to the surface of bacteria and they inject their chromosomes into the bacterial cells. After that, the phages reproduce and release virulent phages. In the lysogenic cycle, the genetic materials of phages incorporate into bacterial chromosomes. This incorporation permits bacteria to reproduce generally along with phage genetic material known as prophages. Consequently, temperate phages are released, and these have the potential to convert into virulent phages at any time [22]. Thus, the antimicrobial potential of virulent phages is greater than that of temperate phages. Each type of BP can efficiently infect specific bacteria more efficiently than others [23]. As the BP product used in this study contained a cocktail of BP for *Clostridium perfringens* types A and C, *Escherichia coli* *Salmonella* spp., and *Staphylococcus aureus*, the phage product may be specifically effective against these bacteria. Kim et al. [24] reported that supplemental BP at 0.1% or 0.15% decreased ileal *Escherichia coli* and *Clostridium* proportion in pigs. Furthermore, a previous study found that supplemental BP against *Salmonella typhimurium* increased the body weight gain and feed efficiency in *Salmonella*-challenged growing pigs [25].

Avilamix containing 20 g/kg avilamycin was used in the present study. Avilamycin is an antibiotic that inhibits protein synthesis by selectively targeting bacterial ribosomes. This action disrupts protein production, effectively suppressing bacterial growth and demonstrating antibacterial activity [26]. A previous study observed a significant reduction in *Salmonella* count in chicks treated with 100 ppm avilamycin compared to the control group [27].

The overall microbial diversity comprised prevalent intestinal microbial groups, with *Firmicutes* (35%), *Bacteroidetes* (21%), *Proteobacteria* (3%), and *Spirochaetes* (2%) dominating the total 16S rRNA gene sequences, as previously observed in pigs [28, 29]. However, according to a meta-analysis to define the core microbiota in the gastrointestinal tract of pigs, the ileal digesta primarily consisted of *Firmicutes* and *Proteobacteria*, whereas the phylum composition in the cecum and colon exhibited a high level of consistency [30]. In the ileal digesta in the present study, *Bacteroidetes* were 10 percentage unit greater than that reported in the literature. This inconsistency might be explained by different ileal digesta sampling methods. Most studies in the meta-analysis obtained ileal samples by necropsy at the end of the experiment [31-33]. In contrast, the collection of ileal digesta in this study used a T-cannula inserted into the terminal ileum, approximately 15 cm from the ileocecal valve [14].

Because the flow of ileal digesta in the small intestine is not consistent in one direction, the ileal digesta collected using a T-cannula may contain some cecal digesta. The analytical procedure, such as the targeted region of the 16S rRNA gene and DNA purification methods, also affects the composition of the microbial community [34].

Intestinal microbiota plays a critical role in maintaining immune function, nutritional status, and physiology in pigs. [35, 36]. Accordingly, major or frequent changes in intestinal microbiota are often associated with ill health [37-39]. *Firmicutes* and *Bacteroidetes* are the 2 dominant phyla in the intestine of pigs [40]. The proportions of *Firmicutes* and *Bacteroidetes* in the intestine are associated with the maintenance of homeostasis and changes in their proportions can lead to various pathologies. It has been reported that a decrease in the proportion of *Bacteroidetes* together with an increase in the proportion of *Firmicutes* can create an intestinal environment conducive to energy production and absorption in the intestine [41, 42]. To our knowledge, we first report the effects of BP on microbiota at the phylum level in the ileal digesta of pigs. The effects of BP on the alteration of microbiota at the phylum level in the ileal digesta were similar to those of AB. However, the effects of AB or BP on fecal microbiota at the phylum level have shown inconsistent results compared to the ileal digesta, which may be explained by the experimental period. Fecal samples were collected after 4 days of the adaptation period, which could be insufficient to detect noticeable changes. However, ileal digesta samples were collected after 5 days of adaptation and the fecal collection period, which might be sufficient to detect the effects of supplemental AB or BP.

Bifidobacterium and *Lactobacillus* exert beneficial effects on the intestinal environment of animals [43-45]. The growth of these beneficial bacteria was enhanced by the addition of AB. Because the antimicrobial action of AB reduces the colonization of harmful bacteria, it is likely to result in an increase in probiotics in a less competitive intestinal environment [46]. The avilamycin used in this study is recognized for its primary targeting of *Staphylococcus aureus*, *Streptococcus pneumoniae*, and *Streptococcus pyogenes* [26]. However, our study did not detect these specific harmful bacteria and previous research indicated no significant impact on the normal gut flora [47]. This aligns with our findings, suggesting that microbial diversity remains unaffected by avilamycin administration. In this study, we hypothesized that microbes affected by avilamycin could be found among the low-abundance microbes.

The increased proportion of *Lactobacillus* in the ileum with supplemental AB or BP was likely due to the inhibitory action of AP or BP on pathogenic bacteria. To our knowledge, only one study determined the effect of BP on the microbiota of this genus in the ileal digesta of pigs. Kim et al. [24] reported that supplemental BP at 0.10% or 0.15% increased the ileal *Lactobacillus* proportion but had no effect on the fecal *Lactobacillus* proportion in pigs, which agrees with the present results. However, previous studies have reported that supplemental BP increased the fecal *Lactobacillus* proportion in pigs [8, 12, 13]. The reason for the inconsistency between the present and previous studies is unclear.

The less proportion of *Bifidobacterium* in the feces observed in the AB or BP group compared with the control group was inconsistent with previous studies [8, 12, 24], the reason for which remains unclear. However, another study reported that a supplemental AB mixture consisting of ampicillin, gentamycin, and metronidazole resulted in decreased *Bifidobacterium* abundance in the feces of pigs [48], which agrees with the present study. They observed that the fecal *Bifidobacterium* proportion was positively correlated with branched-chain fatty acid concentration in the feces of pigs fed AB. Branched-chain fatty acids are formed from branched-chain amino acids that originate exclusively from the breakdown of proteins and thus serve as indicators of microbial branched-chain amino acid deamination. Thus, they suggested that the reduction in branched-chain fatty acids due to the effect of AB on microbial nitrogen results in a decreased *Bifidobacterium* proportion in the feces [48].

At the genus level in the gut, the target bacteria of BP containing *Clostridium perfringens*, *Escherichia coli*, *Salmonella* spp., and *Staphylococcus aureus* were not detected in this study. However, the proportion of *Streptococcus* in the ileal digesta decreased with the addition of AB or BP. *Streptococcus* is a genus of bacteria and certain species within this genus are known to cause various diseases. However, the results of this observation are unclear because of the known host specificity of BP.

The ATTD of energy and nutrients in the control diet was within the range of previous data [49, 50]. The index method used to calculate digestibility in this study relies greatly on the accurate chemical analysis of index compounds in the feed and digesta, which requires sufficient adaptation to achieve a constant fecal index concentration. Choi and Kim. [51] suggested that a minimum adaptation time of 3.5 days is needed to achieve a constant fecal index concentration if a high-fiber diet containing 30% neutral detergent fiber is fed, whereas 5.5 days are needed for a low-fiber diet containing 5% neutral detergent fiber. Because the neutral detergent fiber concentration of the experimental diets in this study was greater than 5%, an adaptation period of 4 days was sufficient.

The intestinal microbiota helps the host utilize nutrients and defend against pathogens [52]. However, in the present study, BP supplementation did not affect nutrient digestibility despite having positive effects on the intestinal microbial community. There are two potential reasons for these results. First, the species of microbes are critical for significant changes in nutrient digestibility. Niu et al. [53] suggested that only specific microbial species improve nutrient digestibility. In their study, the proportions of 3 phyla of *Proteobacteria*, *Tenericutes*, and *TM7*, and 11 genera including *Anaeroplasma*, *Campylobacter*, and *Clostridium* were positively correlated with apparent crude fiber digestibility. However, in the present study, there were no differences in the abundance of these phyla or genera among the treatments. Second, the experimental conditions, such as the use of a variety of AB, experimental diet composition, and experimental period, differed among the studies. There are discrepancies among studies on the relationships between microbial communities and nutrient digestibility in pigs. A strong relationship between the intestinal microbiota and nutrient digestibility in pigs has been reported in multiple studies [12, 13, 48] whereas no relationship was observed in other

studies [54, 55]. These discrepancies were attributed to the fact that the magnitude of microbial changes was not large and perhaps would not improve nutrient digestibility because of the short experimental period compared to previous studies. Previous studies fed diets containing 0.05% [13] or 0.1% [12] BP for more than 30 days, whereas this experiment was conducted for only 7 days. In addition, Kim et al. [24] reported that supplementation with BP at 0.15% resulted in increased apparent total tract dry matter digestibility for 35 days, but had no effect when fed for 7 days.

In conclusion, although BP supplementation had no effect on energy and nutrient digestibility and seemed to require a relatively long adaptation time to improve digestibility, the alteration of the intestinal microbiota in the ileal digesta and feces in the BP group was similar to that in the AB group. This might be the basis for supplemental BP to show a function similar to that of antibiotics. However, the effects of supplemental BP on the intestinal microbiota were inconsistent with those reported in previous studies. In addition, studies on the effect of BP on ileal microbiota at the phylum level and ileal digestibility in pigs are scarce. Therefore, further studies to determine the effects of BP on the ileal microbiota should be conducted to bridge this gap.

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Tables and figures

Table 1. Ingredient and analyzed nutrient composition of experimental diets (as-fed basis, %)

Item	Treatment		
	Control	Antibiotic (AB)[1)]	Bacteriophage (BP)[2)]
Ingredient composition			
Corn, yellow dent	64.35	64.35	64.35
Soybean meal, 48% crude protein	30.00	30.00	30.00
Soybean oil	2.00	2.00	2.00
AB	-	0.10	-
BP	-	-	0.20
BP carrier[3)]	0.20	0.10	-
L-Lys·HCl, 78.8 %	0.10	0.10	0.10
Dicalcium phosphate	1.10	1.10	1.10
Limestone	0.85	0.85	0.85
Vitamin-mineral premix[4)]	0.50	0.50	0.50
Salt	0.40	0.40	0.40
Chromic oxide	0.50	0.50	0.50
Analyzed nutrient composition			
Dry matter	92.2	92. 6	92.6
Organic matter	86.5	87.0	87.1
Crude protein	20.2	20.2	20.2
Neutral detergent fiber	11.9	11.8	11.8
Acid detergent fiber	3.6	3.7	3.6
Gross energy, kcal/kg	4,175	4,198	4,198

[1)] Avilamix (CTCBIO Inc., Seoul, Republic of Korea) contained 20 g of avilamycin/kg.
[2)] BacterPhage (CTCBIO, Inc., Seoul, Republic of Korea) contained contained a mixture of BP consisted of *Clostridium perfringens* types A and C, *Escherichia coli* (f41, k88, and k99), *Salmonella* spp. (*Salmonella choleraesuis*, *Salmonella derby*, *Salmonella enteritidis*, and *Salmonella typhimurium*), and *Staphylococcus aureus*. The BP product contained 10^9 plaque-forming units per gram.
[3)] Consisted of ground corn cob and wheat shorts.
[4)] Provided the following quantities per kg of complete diet: vitamin A, 25,000 IU; vitamin D_3, 4,000 IU; vitamin E, 50 IU; vitamin K, 5.0 mg; thiamin, 4.9 mg; riboflavin, 10.0 mg; pyridoxine, 4.9 mg; vitamin B_{12}, 0.06 mg; pantothenic acid, 37.5 mg; folic acid, 1.10 mg; niacin, 62 mg; biotin, 0.06 mg; Cu, 25 mg as copper sulfate; Fe, 268 mg as iron sulfate; I, 5.0 mg as potassium iodate; Mn, 125 mg as manganese sulfate; Se, 0.38 mg as sodium selenite; Zn, 313 mg as zinc oxide; butylatedhydroxytoluene, 50 mg.

Table 2. Effects of supplemental antibiotic (AB) and bacteriophage (BP) on relative proportion of phylum and *Firmicutes*-to-*Bacteroidetes* ratio (F:B) in the ileal and fecal microbiota of growing pigs[1)]

Item[2)]	Treatment			SEM[5)]	*p*-values	
	Control	AB[3)]	BP[4)]		Control vs. AB and BP	AB vs. BP
Ileum, %						
Actinobacteria	4.5	4.9	10.3	3.1	0.395	0.179
Bacteroidetes	18.4	14.2	11.9	3.0	0.099	0.492
Firmicutes	60.5	68.7	68.8	3.6	0.059	0.987
Proteobacteria	5.9	6.6	3.8	1.8	0.686	0.172
Others[6)]	10.5	6.1	5.1	2.4	0.102	0.741
Feces, %						
Actinobacteria	5.2	2.3	2.6	1.3	0.056	0.867
Bacteroidetes	27.2	26.9	26.1	4.1	0.892	0.895
Firmicutes	56.9	60.0	59.4	3.5	0.525	0.900
Proteobacteria	2.5	2.9	4.2	0.9	0.275	0.226
Others[6)]	7.6	8.4	7.5	0.9	0.796	0.530

[1)] Each least squares mean represents 8 observations except the control diet (n = 7).
[2)] The taxa at the phylum level with more than 3% average proportion in all samples were selected.
[3)] Avilamix (avilamycin 20 g/kg, CTCBIO Inc., Seoul, Republic of Korea) was supplemented at 0.1%.
[4)] BacterPhage (CTCBIO Inc., Seoul, Republic of Korea) was supplemented at 0.2%. The product contained a mixture of BP consisted of *Clostridium perfringens* types A and C, *Escherichia coli* (f41, k88, and k99), *Salmonella* spp. (*Salmonella choleraesuis*, *Salmonella derby*, *Salmonella enteritidis*, and *Salmonella typhimurium*), and *Staphylococcus aureus*. The BP product contained 10^9 plaque-forming units per gram.
[5)] SEM, standard error of the means.
[6)] Phylum less than 0.1% of the average in all groups.

Table 3. Effects of supplemental antibiotic (AB) and bacteriophage (BP) on relative proportion of genus in the ileal and fecal microbiota of growing pigs[1)]

Item[2)]	Treatment			SEM[5)]	*p*-values	
	Control	AB[3)]	BP[4)]		Control vs. AB and BP	AB vs. BP
Ileum, %						
Clostridium	1.7	1.9	1.5	0.5	0.915	0.496
Lactobacillus	28.0	36.6	38.4	4.1	0.062	0.729
Bacillus	2.7	1.2	1.5	0.6	0.105	0.702
Bacteroides	4.6	3.0	2.4	0.8	0.074	0.560
Bifidobacterium	4.0	4.5	9.7	2.9	0.345	0.142
Megasphaera	2.8	4.1	3.7	0.8	0.295	0.751
Mitsuokella	1.9	1.4	1.7	0.6	0.697	0.762
Prevotella	7.0	6.0	4.9	1.3	0.246	0.407
Streptococcus	2.2	1.4	1.6	0.3	0.088	0.702
Veillonella	0.4	1.2	1.5	0.7	0.277	0.782
Others[6)]	44.4	38.7	33.1	4.0	0.110	0.320
Feces, %						
Clostridium	0.6	0.6	0.6	0.1	0.954	0.734
Lactobacillus	20.2	20.5	20.6	3.7	0.933	0.988
Bacteroides	3.9	4.9	4.0	1.1	0.688	0.484
Bifidobacterium	3.5	1.6	2.0	0.8	0.029	0.589
Faecalibacterium	1.5	1.3	1.2	0.2	0.262	0.737
Megasphaera	3.3	3.4	7.6	2.2	0.386	0.142
Oscillospira	1.4	1.5	1.2	0.2	0.723	0.107
Parabacteroides	1.0	1.4	5.5	1.6	0.245	0.080
Prevotella	7.0	6.5	6.5	1.4	0.801	0.997
Streptococcus	3.4	0.7	0.6	1.4	0.152	0.985
Ruminococcus	1.4	2.4	1.6	0.5	0.344	0.293
Succinivibrio	0.8	0.7	2.3	0.8	0.417	0.090
Treponema	1.4	0.8	1.6	0.5	0.830	0.215
Others[6)]	50.1	54.0	44.4	3.1	0.784	0.032

[1)] Each least squares mean represents 8 observations except the control diet (n = 7).
[2)] The taxa at the genus level with more than 1% average proportion in all samples were selected.
[3)] Avilamix (avilamycin 20 g/kg, CTCBIO Inc., Seoul, Republic of Korea) was supplemented at 0.1%.
[4)] BacterPhage (CTCBIO Inc., Seoul, Republic of Korea) was supplemented at 0.2%. The product contained a mixture of BP consisted of *Clostridium perfringens* types A and C, *Escherichia coli* (f41, k88, and k99), *Salmonella* spp. (*Salmonella choleraesuis*, *Salmonella derby*, *Salmonella enteritidis*, and *Salmonella typhimurium*), and *Staphylococcus aureus*. The BP product contained 10^9 plaque-forming units per gram.
[5)] SEM, standard error of the means.
[6)] Genus less than 0.1% of the average in all groups and the unclassified genera.

Table 4. Effects of supplemental antibiotic (AB) and bacteriophage (BP) on apparent ileal and total tract digestibility of energy and nutrients in growing pigs[1)]

Item	Diet			SEM[4)]	*p*-values	
	Control	AB[2)]	BP[3)]		Control vs. AB and BP	AB vs. BP
Ileal digestbility, %						
Energy	80.7	79.1	79.5	1.4	0.347	0.818
Dry matter	79.6	78.2	78.5	1.5	0.413	0.845
Organic matter	81.5	79.9	80.3	1.6	0.426	0.809
Crude protein	83.8	82.4	81.0	1.4	0.109	0.276
Neutral detergent fiber	45.8	42.1	41.7	3.7	0.411	0.929
Acid detergent fiber	26.9	28.4	30.2	3.9	0.570	0.708
Total tract digestibility, %						
Energy	81.4	82.5	82.4	0.9	0.206	0.917
Dry matter	82.0	82.9	83.0	0.7	0.199	0.966
Organic matter	84.1	84.7	85.0	0.7	0.376	0.752
Crude protein	80.7	82.5	81.9	1.2	0.242	0.626
Neutral detergent fiber	49.8	49.6	52.8	2.5	0.403	0.100
Acid detergent fiber	39.1	37.7	39.9	3.9	0.886	0.380

[1)] Each least squares mean represents 8 observations except the control diet (n = 7).
[2)] Avilamix (avilamycin 20 g/kg, CTCBIO Inc., Seoul, Republic of Korea) was supplemented at 0.1%.
[3)] BacterPhage (CTCBIO Inc., Seoul, Republic of Korea) was supplemented at 0.2%. The product contained a mixture of BP consisted of *Clostridium perfringens* types A and C, *Escherichia coli* (f41, k88, and k99), *Salmonella* spp. (*Salmonella choleraesuis, Salmonella derby, Salmonella enteritidis*, and *Salmonella typhimurium*), and *Staphylococcus aureus*. The BP product contained 10^9 plaque-forming units per gram.
[4)] SEM, standard error of the means.

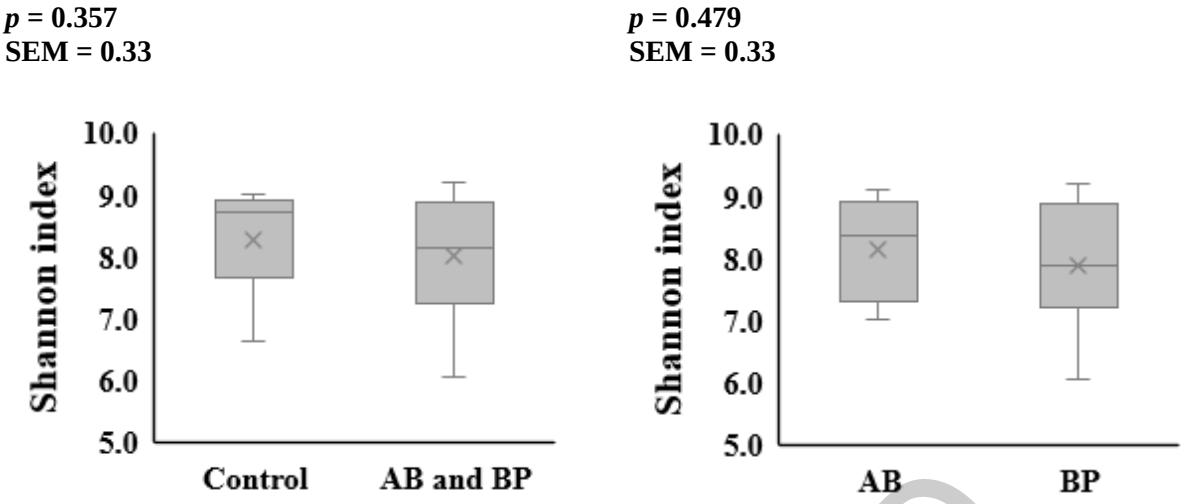

Fig. 1. The alpha diversity of Shannon index for ileum microbial community in pigs fed control, antibiotic (AB), or bacteriophage (BP) diet. SEM, standard error of the means. The X symbols represent the mean values.

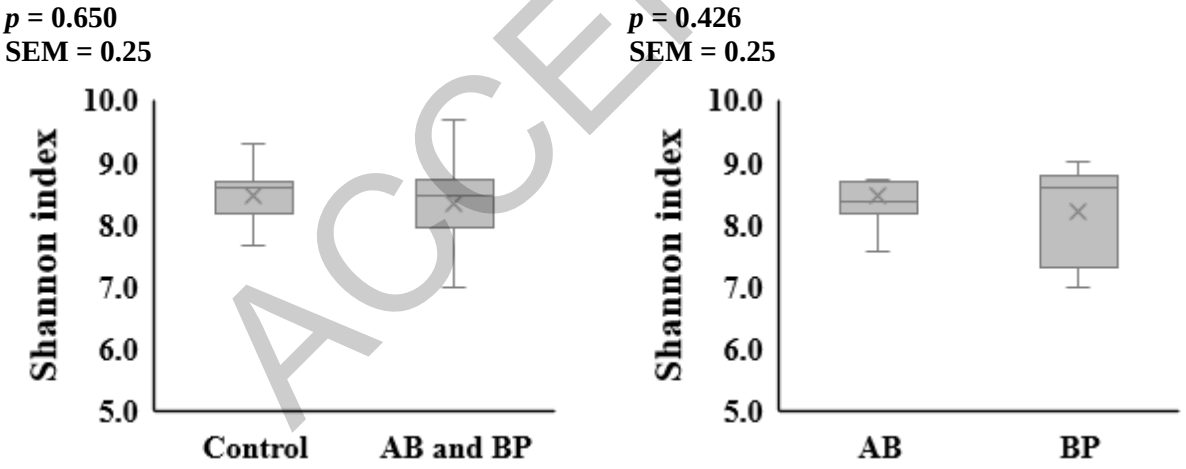

Fig. 2. The alpha diversity of Shannon index for fecal microbial community in pigs fed control, antibiotic (AB), or bacteriophage (BP) diet. SEM, standard error of the means. The X symbols represent the mean values.