

NON RUMINANT NUTRITION

Potential use of ground brown rice for weanling pigs

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Abstract

The purpose of the current study was to assess the effects of substituting corn with ground brown rice on growth performance, immune status, and gut microbiota in weanling pigs. Seventy-two weanling pigs (28 d old with 6.78 ± 0.94 kg body weight [BW]) were randomly allotted to two dietary treatments with six pens and six pigs (three barrows and gilts) per pen within a randomized complete block design. The control pigs were fed a typical diet for weanling pigs based on corn and soybean meal diet (control diet: CON), and the other pigs were fed a formulated diet with 100% replacement of corn with ground brown rice for 35d (treatment diet: GBR). Growth performance, immune status, and gut microbiota of weanling pigs were measured. The substitution of corn with GBR did not affect growth performance or diarrhea frequency. Additionally, there were no differences in white blood cell number, hematocrit, cortisol, C-reactive protein, and serum tumor necrosis factor- α levels between pigs fed CON or GBR for the first 2 wk after weaning. However, weanling pigs fed GBR had lower ($P < 0.05$) serum transforming growth factor- β 1 level than those fed CON. Furthermore, weanling pigs fed GBR had increased ($P < 0.05$) relative abundance of phylum Firmicutes and genus *Lactobacillus* and *Streptococcus* and decreased ($P < 0.05$) relative abundance of phylum Bacteroidetes and genus *Clostridium* and *Prevotella* in the gut microbiota compared with those fed CON. In conclusion, there was no significant difference in growth performance when corn was replaced with ground brown rice in diets for weanling pigs. Furthermore, the substitution of corn with ground brown rice in weaning diet modulated immune status and gut microbiota of pigs by increasing beneficial microbial communities and reducing harmful microbial communities. Overall, ground brown rice-based diet is a potential alternative to corn-based diet without negative effects on growth performance, immune status, and gut microbiota changes of weanling pigs.

Key words: ground brown rice, growth performance, gut microbiota, immune status, weanling pigs

Abbreviations

ADFI	average daily feed intake
ADG	average daily gain
BW	body weight
G:F	gain to feed ratio
OTUs	operational taxonomic units
PCoA	principal coordinates analysis
SCFAs	short-chain fatty acids
TGF- β 1	transforming growth factor-beta 1
TNF- α	tumor necrosis factor-alpha

Introduction

Rice is grown in many Asian countries and is consumed as a staple grain in human diets. Many studies have examined the starch properties of rice that are related to the variety or processing method (Arns et al., 2015; Chelliah et al., 2019; Kim et al., 2021a); polished white rice contains more than 75% starch and has low fiber content (Li et al., 2004). Paddy rice is processed in several steps to produce polished final products such as brown and white rice for human consumption (Kaur et al., 2016). However, rice byproducts generated during processing and stale rice that cannot be used for human consumption may be used in the feeding of animals (Farrell and Hutton, 2017). Replacing corn with rice in diets for weanling (Devi et al., 2015; Casas and Stein, 2016; Yagami and Takada, 2017) or growing pigs (Casas et al., 2018; Fan et al., 2020; Kim et al., 2021b) improved growth performance and nutrient digestibility without negative effects. It has also been reported that rice feeding prevents diarrhea in weanling pigs (Pluske et al., 2003). In particular, brown rice is more nutritious than corn, containing 3,801 kcal/kg of gross energy and 8.0% crude protein (Piao et al., 2002), with higher starch content and more essential amino acids, minerals, and fatty acids than corn (Li et al., 2006). In addition, brown rice is cheaper to process than white rice (Saleh et al., 2019), and brown rice byproducts are also relatively cheaper in price than corn (Piao et al., 2002). The bioactive compounds such as phenolic acids, flavonoids, aminobutyric acid, γ -oryzanol, α -tocopherol, and γ -tocotrienol in brown rice have beneficial effects on immune functions and gut health (Pluske et al., 2003; Wu et al., 2013a; Saleh et al., 2019; Liang et al., 2020). Due to these properties, brown rice can potentially replace corn in swine diets without negatively affecting growth performance, nutrient digestibility, and gut health.

The nutritional quality and functionality of brown rice have beneficial effects on human health in food nutrition (Wu et al., 2013b; Lin et al., 2019; Saleh et al., 2019). Most studies examining the replacement of corn with brown rice in pig diets have focused on nutrient utilization and growth performance. However, information about corn replacement with brown rice on growth performance, immune status, and gut microbiota of weanling pigs is limited. Thus, it was hypothesized that when ground brown rice completely replace corn in diets for weanling pigs, there would be alters in the gut microbiota without negative effects on growth performance and immune responses. Therefore, the purpose of this study was to investigate the effects of substituting corn with ground brown rice in weaning diets on growth performance, immune status, and gut microbiota of weanling pigs.

Materials and Methods

All animal protocols of this experiment were reviewed and approved by the Institutional Animal Care and Use Committee of the Chungnam National University, Daejeon, Korea (approval no. CNU-00780). The animal study was conducted based on the guidelines of the Declaration of Helsinki.

Experimental animals and design

Pigs (Duroc \times Landrace \times Yorkshire) were weaned at 28 d old with an initial average body weight (BW) of 6.78 ± 0.94 kg. Seventy-two weanling pigs were randomly allotted to two dietary treatments of CON- and GBR-based diets with six pens and six pigs (three barrows and gilts) per pen in a randomized complete block design with BW as blocking criteria.

Diets

Pigs in the control group were fed a typical diet for weanling pigs based on corn–soybean meal (CON), and pigs in the treatment group were fed a formulated diet with 100% replacement of corn with ground brown rice for 35d (GBR). Experimental diets were made from the same base mix and formulated to meet nutrient requirements for weanling pigs (NRC, 2012) with both diets having comparable concentrations of crude protein, calcium, and phosphorus contents (Table 1). All diets were provided in mash form and did not contain animal plasma, antibiotics, or zinc oxide to prevent the antibacterial and the physiological effects. Experimental diets were fed to weanling pigs for 5 wk. All pigs were housed in an environmentally controlled room and had free access to diets and water during the entire period.

Experimental process and sample collection

Pigs and feeder were weighted at days 1, 14 and 35, in order to obtain the average daily gain (ADG), average daily feed intake (ADFI), and gain to feed ratio (G:F). Because postweaning diarrhea affects weanling pigs during the first 2 wk after weaning, each pig was monitored daily for 20 d after weaning, and its feces visually assessed and assigned a diarrhea score ranging from 1 to 5 by two independent evaluators (1 = well-formed feces, 2 = damp feces, 3 = shapeless feces, 4 = runny feces, and 5 = watery severe diarrhea). Diarrhea frequency was calculated by counting pig days with a pen average diarrhea score of 3 or higher (Lee et al., 2020a). Blood samples were collected at days 1, 3, 7, and 14 after weaning through the jugular vein of one selected pig (average BW of 7.8 ± 0.59 kg; a barrow) in each pen within a treatment via vacuum tubes (BD, Franklin Lakes, NJ, USA) with or without an anticoagulant (ethylenediaminetetraacetic acid). The serum samples were obtained after centrifuging the coagulated blood for 15 min at $3,000 \times g$ at room temperature and then stored at -80 °C. Feces samples for verifying microbiota changes were obtained from randomly selected three pigs per dietary treatment on the last day (day 35 after weaning) and then stored at -80 °C. Evaluation of gut microbiota was conducted using the metagenome analysis (Guevarra et al., 2018) and designed according to previous studies (Lin and Yu, 2020; Park et al., 2020; Xu et al., 2020; Kim et al., 2021b).

Sample analysis

White blood cells and hematocrit counts were measured using a hematology analyzer (scil Vet abc hematology analyzer, scil animal care company, F-67120 Altorf, France) calibrated with porcine blood (Lee et al., 2020b). The enzyme-linked immunosorbent assay (ELISA) kits were used to determine concentrations of serum cortisol (Cusabio, Wuhan, China), C-reactive protein (Abnova Corp., Taipei City, Taiwan),

Table 1. Composition of experimental diet of weaning pigs

Items	Diets ¹	
	CON	GBR ⁴
Ingredient, %		
Corn	49.86	—
Ground brown rice	—	49.86
Whey powder	12.50	12.50
Soybean meal (44%)	25.00	25.00
Soy protein concentrate	6.25	6.25
Soybean oil	3.00	3.00
Limestone	1.14	1.14
Monocalcium phosphate	1.05	1.05
Vitamin premix ²	0.20	0.20
Mineral premix ³	0.20	0.20
L-lysine-HCl (78.8%)	0.45	0.45
D,L-methionine	0.16	0.16
L-threonine	0.13	0.13
L-valine	0.06	0.06
Total	100.00	100.00
Analyzed value		
Dry matter, %	95.93	95.42
Crude protein, %	22.04	22.53
Gross energy, kcal/kg	3,988	4,112
Calculated energy and nutrients		
Metabolizable energy, kcal/kg	3,465	3,574
Crude protein, %	21.26	21.52
Calcium, %	0.81	0.81
Phosphorus, %	0.65	0.67
Lysine, %	1.53	1.57
Methionine, %	0.47	0.48
Total sulfur amino acid, %	0.83	0.82
Threonine, %	0.95	0.97
Tryptophan, %	0.25	0.31

¹CON, weaning diet based on corn and soybean meal; GBR, diet with 100% replacement of corn with ground brown rice.

²Vitamin premix provided the following quantities of vitamin per kilogram of complete diet: vitamin A, 12,000 IU; vitamin D₃, 2,500 IU; vitamin E, 30 IU; vitamin K₃, 3 mg; D-pantothenic acid, 15 mg; nicotinic acid, 40 mg; choline, 400 mg; and vitamin B₁₂, 12 µg.

³Mineral premix provided the following quantities of mineral per kilogram of complete diet: Fe, 90 mg from iron sulfate; Cu, 8.8 mg from copper sulfate; Zn, 100 mg from zinc oxide; Mn, 54 mg from manganese oxide; I, 0.35 mg from potassium iodide; and Se, 0.30 mg from sodium selenite.

⁴Analyzed value of ground brown rice: dry matter, 85.5%; crude protein, 9.13%; crude fat, 2.71%; ash, 1.38%; crude fiber, 6.68%; and calcium, 0.03%.

transforming growth factor-β1 (TGF-β1; R&D Systems, Inc., Minneapolis, MN, USA), and tumor necrosis factor-α (TNF-α; R&D Systems, Inc., Minneapolis, MN, USA) following the manufacturer's protocol.

16S rRNA sequencing for gut microbiota

Genomic DNA was extracted from fecal samples by QIAamp DNA Stool Mini Kit (Qiagen, Hilden, Germany) according to their protocol. The concentration and quality of genomic DNA were evaluated using NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, DE, USA). Genomic DNA was stored for analysis at -20 °C. The V4 region of the 16S rRNA gene was amplified by the polymerase chain reaction (PCR) step using featured primers as listed previously (Kozich et al., 2013). The amplicons were sequenced by the Illumina MiSeq platform based on the directions of the manufacturer. All sequencing

was conducted at MacroGen Inc. (Seoul, Korea). Raw sequence data were processed by the Mothur software and low-quality sequences were eliminated (Schloss et al., 2009). Sequencing errors and chimeras were eliminated using the UCHIME during Mothur processing (Kozich et al., 2013). The remaining high-quality sequences were categorized into operational taxonomic units (OTUs) clustering according to an identity cutoff of 97% (Caporaso et al., 2010). The sequence number was normalized by random subsampling for downstream analyses of microbial alpha diversity such as phylogenetic information; observed OTUs; Chao1, Shannon, and Simpson indices; and beta diversity (principal coordinates analysis [PCoA]).

Statistical analysis

Analyses of data were performed using the MIXED procedure of SAS statistical software (Version 9.4, 2013, SAS Inc., Cary, NC, USA; Gonçalves et al., 2016). The statistical model for growth performance, white blood cell and hematocrit counts, C-reactive protein, serum cytokines (TNF-α and TGF-β1), and cortisol included effects of dietary treatments as a fixed effect, initial BW as a random effect, and pen as the experimental unit. The χ^2 test was used to analyze data for diarrhea frequency. Alpha and beta diversities of taxonomic classification and microbial populations were analyzed using the STAMP and Prism software (Prism 5.00, GraphPad Software, La Jolla, CA, USA) as well as MicrobiomeAnalyst (<https://www.microbiomeanalyst.ca/>). Alpha diversity data were presented as mean ± SE. Significant differences and tendency were considered based on $P < 0.05$ and $0.05 \leq P < 0.10$, respectively.

Results

Growth performance

No differences in growth performance and final BW of pigs were observed between dietary treatments throughout the experiment (Table 2). During the first 20 d after weaning, no treatment effects were observed in the diarrhea frequency between CON and GBR groups (Table 2).

Blood profiles, cortisol, C-reactive protein, and serum cytokines

No differences were observed between dietary treatments in the number of white blood cells, hematocrit, C-reactive protein, and serum TNF-α of weaning pigs in the first 2 wk after weaning (Table 3). However, 3 d after weaning, the concentration of serum TGF-β1 decreased ($P < 0.05$) in the weaning pigs fed GBR diet compared with those fed CON diet.

Diversity of gut microbiota

The fecal microbiota community diversity results are presented in Table 4. The mean total sequence numbers were $238,515 \pm 62,593$ reads in the CON group and $225,497 \pm 117,166$ reads in the GBR group. In addition, the mean of observed OTUs was 257.33 ± 27.21 in the CON group and 239.33 ± 24.70 in the GBR group. No differences in Chao, Shannon, and Simpson diversity indices were observed between the GBR and CON groups.

The PCoA plot illustrates the composition of microbial communities between the CON and GBR groups (Figure 1). During the weaning period, the distinct separation of microbial communities was not visually found between CON and GBR groups.

A comparison of the relative abundance of taxonomic groups at the phylum and genus levels between CON and GBR

Table 2. Growth performance of weanling pigs fed corn- or ground brown rice-based diets¹

Items	Diets ²		SEM	P-value
	CON	GBR		
Initial BW ³ , kg	6.77	6.78	0.40	0.980
Final BW, kg	22.45	23.56	0.72	0.267
Day 1 to 14				
ADG ³ , g/d	175.00	228.00	26.16	0.182
ADFI ³ , g/d	315.00	335.00	25.37	0.587
G:F ³ , g/g	0.54	0.68	0.06	0.108
Day 15 to 35				
ADG, g/d	630.00	647.00	17.63	0.527
ADFI, g/d	925.00	950.00	29.76	0.566
G:F, g/g	0.68	0.68	0.01	0.932
Day 1 to 35				
ADG, g/d	448.00	479.00	15.40	0.183
ADFI, g/d	681.00	704.00	21.08	0.457
G:F, g/g	0.66	0.68	0.01	0.277
Diarrhea frequency ⁴ ,%	3.84	3.87	0.43	0.674

¹Data are least squares means of six replicates (six pigs per pen).

²CON, weanling diet based on corn and soybean meal; GBR, diet with 100% replacement of corn with ground brown rice.

³ADFI, average daily feed intake; ADG, average daily gain; BW, body weight; G:F, gain to feed ratio.

⁴Diarrhea frequency during the 20 d after weaning = (diarrhea number/days) × 100. The χ^2 test was used to analyze data for diarrhea frequency.

is shown in [Figure 2](#). The relative abundance of Firmicutes increased ($P < 0.05$) at the phylum level in GBR pigs compared with CON pigs ([Figure 2A](#)). However, weanling pigs fed GBR diet had a lower ($P < 0.05$) relative abundance of Bacteroidetes at the phylum level than those fed CON diet ([Figure 2A](#)). At the genus level, the GBR group had an increased ($P < 0.05$) relative abundance of *Lactobacillus* and *Streptococcus* compared with the CON group ([Figure 2B](#)). However, weanling pigs fed GBR diet had a lower ($P < 0.05$) relative abundance of *Clostridium* and *Prevotella* at the genus level than those fed CON diet ([Figure 2B](#)).

Discussion

During the paddy rice milling process, brown rice is obtained when only the husk layer is removed and the outer bran layers, which contain a large amount of nutrients, remain on the grain ([Kaur et al., 2016](#)). Brown rice contains more protein, lipids, minerals, and vitamins than white rice and is not significantly different from corn nutritionally ([Li et al., 2006](#); [Amagliani et al., 2017](#); [Saleh et al., 2019](#)). In addition, brown rice has higher starch content and well-balanced amino acid composition compared with corn ([Li et al., 2004](#)). The starch in brown rice is stored within the inner endosperm of rice kernel, existing as glucose polymers composed of amylose and amylopectin ([Takeda et al., 1993](#)). After starch, protein is the main component of brown rice, found in albumin, globulin, and glutelin in the outer bran layers ([Amagliani et al., 2017](#)). These nutritional properties of brown rice provide a good substitute to completely replace corn in the swine diets.

The present study showed the effects of completely replacing corn with ground brown rice in weaner diets. The BW, ADG, ADFI, and G:F ratio of weanling pigs were not different between dietary treatments during the experimental period. These observations are consistent with previously published results

Table 3. Immune status of weanling pigs fed corn- or ground brown rice-based diets¹

Items	Diets ²		SEM	P-value
	CON	GBR		
White blood cells, × 10 ³ /μL				
Day 1	14.07	13.07	1.46	0.232
Day 3	12.27	11.63	1.12	0.836
Day 7	15.97	15.77	1.27	0.229
Day 14	23.50	19.53	1.88	0.486
Hematocrit, %				
Day 1	33.07	32.93	1.87	0.965
Day 3	32.30	35.07	2.03	0.721
Day 7	34.92	37.02	1.34	0.615
Day 14	33.25	33.65	0.77	0.624
Cortisol, ng/mL				
Day 1	25.72	10.23	5.42	0.071
Day 3	36.35	11.81	16.71	0.324
Day 7	61.43	13.00	26.30	0.222
Day 14	10.18	10.88	4.20	0.908
C-reactive protein, ng/mL				
Day 1	70.13	85.58	19.76	0.593
Day 3	92.29	97.96	19.98	0.845
Day 7	123.22	98.70	26.45	0.527
Day 14	102.64	51.53	29.78	0.253
Serum TGF-β1 ³ , pg/mL				
Day 1	1,473	1,470	5.36	0.732
Day 3	1,458	881	182.00	0.049
Day 7	654	267	257.00	0.305
Day 14	992	450	350.00	0.583
Serum TNF-α ³ , pg/mL				
Day 1	113	115	7.74	0.870
Day 3	134	132	8.44	0.825
Day 7	121	118	10.16	0.872
Day 14	102	106	7.60	0.710

¹Data are least squares means of six replicates (one pig per pen).

²CON, weanling diet based on corn and soybean meal; GBR, diet with 100% replacement of corn with ground brown rice.

³TGF-β1, transforming growth factor-beta 1; TNF-α, tumor necrosis factor-alpha.

([Mateos et al., 2006](#); [Li et al., 2019](#)), showing that the replacement of corn with GBR in the weaning diets does not disrupt pig performance. Additionally, some studies have reported that pigs fed rice-based diets had better or no difference in growth performance than those fed the corn-based diets due to the type, the dietary composition, and the processing method of rice and rice byproducts ([Vicente et al., 2008](#); [Gekara et al., 2014](#)). Generally, the fiber content of brown rice is less than that of corn (1.87% vs. 2.86%); fiber inhibits starch hydrolysis by forming a physical barrier that limits amylase access to starch granules ([Li et al., 2004](#)). High-fiber diets reportedly had negative effects on growth performance and nutrient digestibility of weanling pigs ([Berrococo et al., 2015](#)). Moreover, starch is a major component of brown rice and corn, and the differences in starch content, composition, and structure are related to growth performance and nutrient digestibility. The digestibility of starch is inversely proportional to the amylose content and granule size, which are associated with digestive enzymes activity on the surface area ([Li et al., 2019](#)). Brown rice has less amylose content (15% to 19% vs. 25% to 35%) and smaller granule size (2 to 8 μm vs. 5 to 20 μm) than corn ([Riaz, 2006](#)). Despite these nutritional advantages of brown rice, the reason that there was no difference in growth performance in the current study might be due to the relatively

Table 4. Alpha diversity analysis for gut microbiota of weanling pigs by 16S rRNA sequencing¹

Diversity index	Diets ²		P-value
	CON	GBR	
Total number of sequence reads	238,515 ± 62,593	225,497 ± 117,166	
Observed OTUs ³	257.33 ± 27.21	239.33 ± 24.70	0.444
Chao1	281.83 ± 18.83	251.03 ± 20.98	0.132
Shannon	4.93 ± 0.53	4.50 ± 0.42	0.335
Simpson	0.905 ± 0.05	0.868 ± 0.06	0.447

¹Data are least squares means of three replicates (one pig per pen) and presented as mean ± standard deviation.

²CON, weanling diet based on corn and soybean meal; GBR, diet with 100% replacement of corn with ground brown rice.

³OTUs, operational taxonomic units.

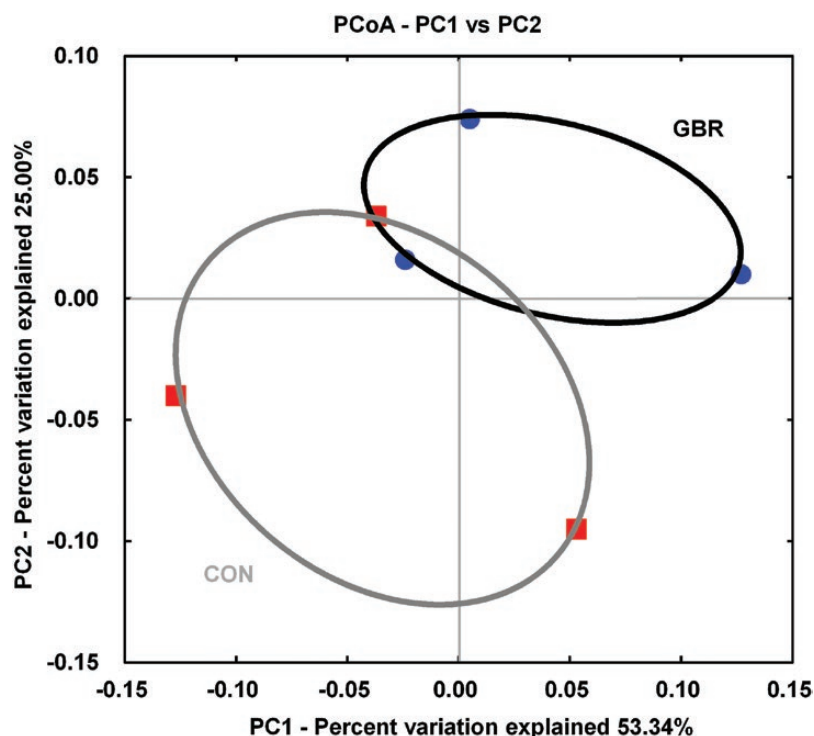


Figure 1. Biplot of principal coordinates analysis (PCoA) weighted UniFrac distances in gut microbiota communities from piglets' feces. Weanling pigs were regarded as the experimental units, $n = 3$ for each treatment group. CON, weanling diet based on corn and soybean meal (red square); GBR, diet with 100% replacement of corn with ground brown rice (blue circle).

poorer palatability of brown rice compared with corn during weaning period, which was mentioned in previous study (Li et al., 2002). Based on previous and present studies, it is possible to use brown rice without negative effects as a complete substitute for corn in weaner diets.

During the weaning period, piglets often suffer the stress during diet changes due to immature intestinal function. Changes in the immune status resulting from intestinal inflammation have been reported in pigs after weaning (Rhouma et al., 2017; Lee et al., 2020b). Therefore, we tested the blood profiles, cortisol, and serum cytokines of weanling pigs in two dietary treatments. Postweaning diarrhea can be considered the early symptom by the pathogenic *Escherichia coli* infection, which can stimulate the immune system, and we observed no difference in the diarrhea frequency between dietary treatments; however, the cortisol level in the CON group tended to be higher at the beginning of the study, which might be related to the weaning event. The functional ingredients such as phenolic acids, flavonoids, aminobutyric acid, γ -oryzanol,

α -tocopherol, and γ -tocotrienol in brown rice ameliorated the inflammatory response (Saleh et al., 2019). Inflammatory cytokines provide indicators for immune and inflammatory status and are closely associated with intestinal disease caused by weaning stress. In particular, TGF- β 1 has both pro- and anti-inflammatory properties and thus can enhance and repress immunities (Kany et al., 2019; Lee et al., 2019). Regulation of pro-inflammatory cytokines in the intestinal mucosa may alleviate gut dysfunction due to weaning stress (Liu et al., 2008). The outer bran layers in brown rice contain bioactive compounds, including phenolic compounds such as isoferulic, *p*-coumaric, vanillic, and ferulic acid (Pang et al., 2018), which enhance antioxidant activity and immune status (Wu et al., 2013a; Liang et al., 2020). In another study, a brown rice and rice bran-supplemented diet reduced liver inflammation and fibrosis in rats (Wunjuntuk et al., 2016). As an antioxidant plant extract, brown rice-derived extracts also have anti-inflammatory effects. A previous study reported that brown rice extract contains a natural anti-inflammatory agent,

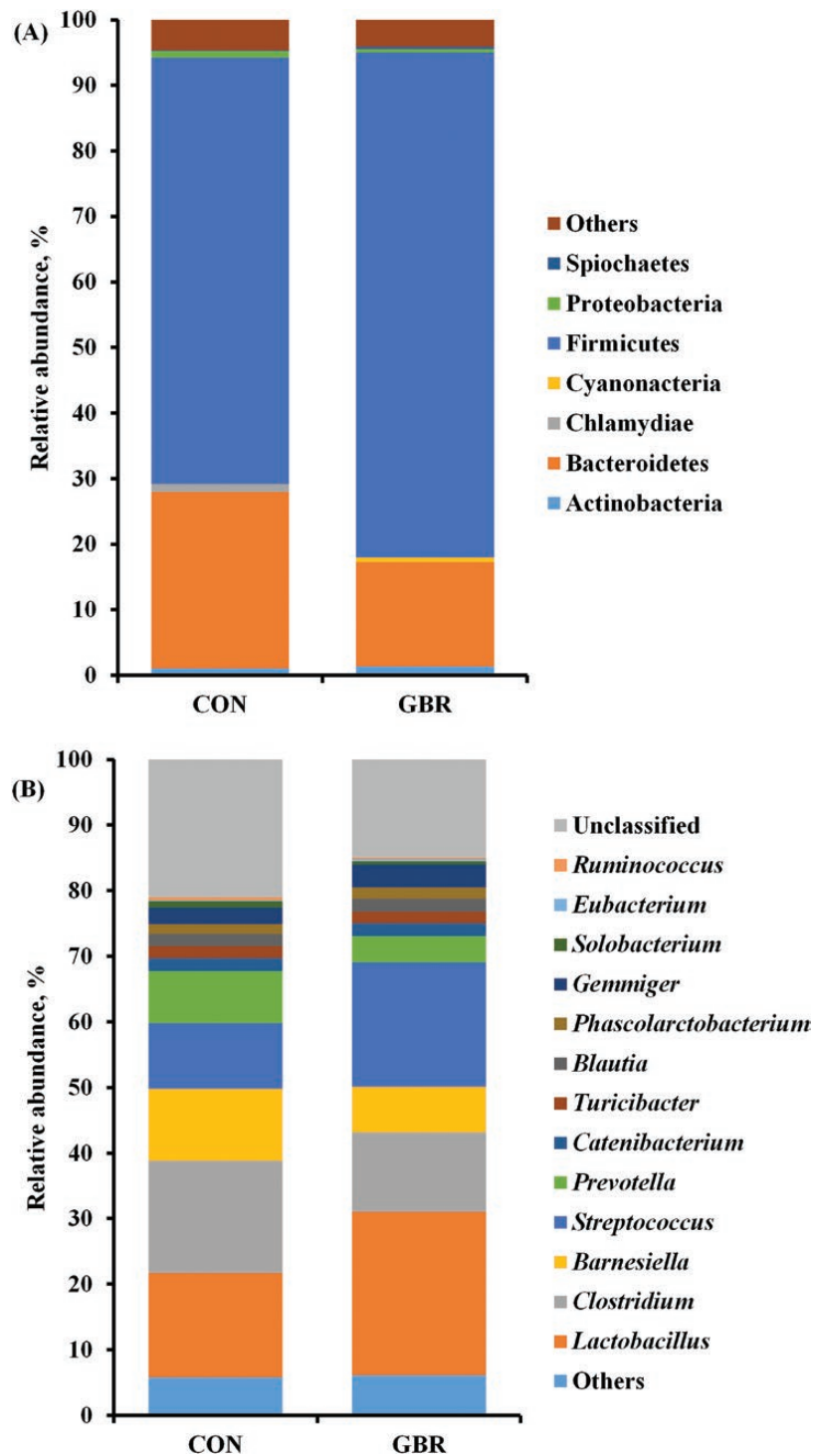


Figure 2. Taxonomic composition shows the relative abundance of fecal microbiota in each treatment group at the phylum level (A) and genus level (B). Weanling pigs were regarded as the experimental units, $n = 3$ for each treatment group. CON, weanling diet based on corn and soybean meal; GBR, diet with 100% replacement of corn with ground brown rice.

which inhibits gene expression and interleukin production of colon cancer cells (QuagliarIELlo et al., 2016). The results of a recent study have shown that the combinations of brown rice and probiotics such as *Lactobacilli* strains in a rat model inhibited colorectal carcinogenesis by regulating antioxidant activity (Lin et al., 2019). This symbiotic produces exopolysaccharides, which

have antioxidative properties via upregulating the expression of antiangiogenic genes and inactivating the inflammatory pathway (Deepak et al., 2016). Therefore, the reduced serum TGF- β 1 resulting from the complete replacement of corn with ground brown rice in the weanling diets suggests effects on autoimmunity and inflammation responses.

Brown rice supplementation can modulate intestinal microbiota and enhance innate immunity, which in turn improves gut health in nursery piglets (Yang et al., 2015). We used Illumina sequencing to perform 16S rRNA gene analysis on the fecal microbiota of piglets. Intestinal microbiota is directly or indirectly involved in the gut disease by affecting digestion and absorption of nutrients as well as resistance to infection and supporting animal health. It has been reported that fermentable carbohydrates such as dietary fiber, resistant starch, and oligosaccharide within whole grain rice may improve gut health by regulating the microbial fermentation pathway in the intestine (Han et al., 2018). Dietary rice bran increased beneficial microbial communities such as *Lactobacillus* and *Bifidobacterium* in the gut microbiota of pigs (Yang et al., 2015). Fermentation of indigestible carbohydrates in brown rice by native intestinal probiotics such as *Lactobacillus* and *Bifidobacterium* generates short-chain fatty acids (SCFAs), including acetic acids, propionic acids, and butyric acids (Lin et al., 2019). SCFAs reduce intestinal pH, thereby inhibiting the growth of pathogens to maintaining intestinal health and play an important role in the prevention of intestinal inflammation and diseases and served as a primary energy source for the colonic mucosa (Han et al., 2018). It is possible that ground brown rice supplementation attributes fermentation and SCFAs production in the colon, and thus improves the formation of mucins and gut health. Ground brown rice supplementation decreased the relative abundance of genera *Clostridium* and *Prevotella* caused by increased genera *Lactobacillus* in the current study, which is in agreement with results of previous data (So et al., 2016; Han et al., 2018), suggesting that brown rice supplementation suppresses pathogenic bacteria that cause intestinal diseases and promotes beneficial probiotic bacteria (So et al., 2016). Therefore, ground brown rice supplementation may improve immune status and gut health of weanling pigs by increasing the relative abundance of *Lactobacillus*.

Conclusions

There was no significant difference in growth performance when corn was replaced with ground brown rice in diets for weanling pigs. Furthermore, the substitution of corn with ground brown rice in weaning diet modulated immune status and gut microbiota of pigs by increasing beneficial microbial communities and reducing harmful microbial communities. Overall, ground brown rice is a potential alternative to traditional feed ingredients such as corn without negative effects on pigs, as demonstrated by the growth performance, immune status, and gut microbiota changes of weanling pigs on a ground brown rice-based diet. To our knowledge, the present study is the first to demonstrate that a complete replacement of corn with ground brown rice in nursery diets correlates with growth performance, immune status, and gut microbiota of weanling pigs during the weaning period. However, more research is needed to understand the benefits and biological effects of ground brown rice as an alternative feed ingredient.

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Conflict of interest statement

The authors declare that there are no competing interests.

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