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巨菌草对育肥从江香猪生长性能及肠道健康的影响

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摘要:本试验旨在探究巨菌草替代不同水平基础饲料对育肥从江香猪生长性能及肠道健康的影响。选取6月龄体重相近的健康从江香猪30头,随机分为3组(每组5个重复,每个重复2头)。对照组饲喂100%基础饲料,试验I、II组分别用新鲜青绿巨菌草替代10%、20%基础饲料,试验期90 d。通过测定育肥从江香猪生长性能、肠道发育、肠道机械屏障和盲肠菌群结构,并进行经济效益分析,为巨菌草在猪的生产应用中提供理论依据。本试验主要结果如下:1)生长性能:与对照组相比,试验I、II组育肥从江香猪生长性能及胴体性状各指标无显著差异($P>0.05$)。巨菌草不计成本时,与对照组相比,试验I组的增重成本降低8.73%,试验II组降低11.59%;巨菌草按市场价格 $0.35\text{元}\cdot\text{kg}^{-1}$ 计算时,试验I组的增重成本降低2.78%,试验II组增加1.35%。2)肠道发育:与对照组相比,试验I、II组育肥从江香猪胃的相对重量显著提高($P<0.05$),小肠相对重量有升高的趋势($P=0.092$)。与对照组相比,试验I组育肥从江香猪回肠隐窝深度显著降低($P<0.05$),回肠绒毛高度/隐窝深度(V/C)、空肠GLP-2和回肠IGF-IR基因表达量显著提高($P<0.05$);试验II组育肥从江香猪回肠绒毛高度/V/C及空肠GLP-2基因表达量显著提高($P<0.05$)。3)肠道免疫及机械屏障:与对照组相比,试验I、II组育肥从江香猪回肠IFN- γ 含量显著降低,试验II组空肠TGF- β 含量显著提高($P<0.05$);试验I、II组回肠ZO-1基因表达量显著提高,试验II组空肠Occludin基因表达量显著提高($P<0.05$)。4)盲肠微生物区系:与对照组相比,试验I、II组育肥从江香猪Shannon指数显著提高,链球菌属相对丰度显著下降($P<0.05$)。试验I组和试验II组毛螺菌科未分类菌属有上升趋势($P=0.065$),螺旋体目($P=0.085$)、密螺旋体属($P=0.085$)有下降趋势。综上所述,巨菌草替代部分基础饲料对育肥从江香猪生长性能、胴体性状无显著影响,但可提高经济效益并促进胃肠道的发育,提升肠道屏障功能,有利于肠道健康。巨菌草不计成本时,替代20%基础饲料为宜,巨菌草按市场价格 $0.35\text{元}\cdot\text{kg}^{-1}$ 计算时,替代10%基础饲料为宜。

关键词:巨菌草;育肥从江香猪;生长性能;盲肠菌群;肠道健康

Effects of *Pennisetum giganteum* on the growth performance and intestinal health of finishing Congjiang Xiang pigs

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Abstract: The aim of this study was to determine the effects of dietary supplementation with *Pennisetum giganteum* on the growth performance and intestinal health of finishing Congjiang Xiang pigs. Thirty 6-month-old healthy Congjiang Xiang pigs of similar weight were selected and randomly divided into three groups (five replicates per group, two pigs per replicate). The control group was fed with a basal diet, and experimental groups I and II were fed with the basal diet with 10% and 20% (w/w) replaced with fresh *P. giganteum*. The experimental period was 90 days. The growth performance, intestinal development, and the structures of the intestinal mechanical barrier and cecal flora were analyzed, and the economic benefits were estimated. The main results were as follows: 1) Growth performance: Compared with the control group, groups I and II showed no significant differences in growth performance or carcass traits ($P > 0.05$). When the cost of *P. giganteum* was not considered, groups I and II had lower weight gain costs (reduced by 8.73% and 11.59%, respectively) than that of the control group. When the cost of *P. giganteum* was calculated according to the market price of 0.35 CNY·kg⁻¹, group I still had a lower weight gain cost (2.78% lower) than that of the control, but the weight gain cost of experiment group II was increased by 1.35%. 2) Intestinal development: Compared with the control group, groups I and II had significantly higher relative weight of the stomach ($P < 0.05$), and a trend of higher relative weight of the small intestine ($P = 0.092$). Compared with the control group, group I showed significantly decreased ileal crypt depth ($P < 0.05$), and significantly increased ileal height/crypt depth (V/C) and transcript levels of *GLP-2* in the jejunum and *IGF-1R* in the ileum ($P < 0.05$). Compared with the control group, group II showed significantly increased ileal villus height, V/C, and gene transcript level of jejunal *GLP-2* ($P < 0.05$). 3) Intestinal immunity and mechanical barriers: Compared with the control group, groups I and II showed significantly decreased ileal IFN- γ content, and group II showed significantly increased jejunal TGF- β content ($P < 0.05$). Comparing gene transcript levels with those in the control, groups I and II showed significantly increased transcript levels of *ZO-1* in the ileum ($P < 0.05$), and group II showed significantly increased transcript levels of *Occludin* in the jejunum ($P < 0.05$). 4) Cecal microbes: Shannon index was significantly higher in both experimental groups than in the control ($P < 0.05$). The relative abundance of *Streptococcus* was significantly lower in both experimental groups than in the control ($P < 0.05$). The experimental groups showed trends of increased abundance of *unclassified_f__Lachnospiraceae* ($P = 0.065$) and decreased abundance of Spirochaetota ($P = 0.085$) and *Treponema* ($P = 0.085$). In conclusion, replacing part of the basal diet with *P. giganteum* had no significant effect on the growth performance or carcass traits of finishing Congjiang Xiang pigs, but it improved the economic efficiency, promoted gastrointestinal tract development, and enhanced intestinal barrier function, which were conducive to intestinal health. These results show that 20% of the basal diet can be replaced with *P. giganteum* if its cost is not considered, and 10% of the basal diet can be replaced with *P. giganteum* if it is costed at the market price of 0.35 CNY·kg⁻¹. These findings provide scientific data for assessing the application of *P. giganteum* in pig production.

Key words: *Pennisetum giganteum*; finishing Congjiang Xiang pigs; growth performance; cecal microflora; intestinal health

饲料是畜牧业赖以发展的物质基础,饲料成本约占整个畜禽养殖成本的60%~70%^[1]。目前饲料以玉米(*Zea mays*)—豆粕型基础饲粮为主,但我国玉米、大豆(*Glycine max*)仍需进口,对外依存度较高,受国际影响较大。为保障饲料粮供需平衡、稳定粮食安全,2021年农业农村部畜牧兽医局发布了关于推进玉米豆粕减量替代

工作的通知,倡导充分挖掘利用现有饲料资源^[2],充分合理地开发利用饲草资源可以节约玉米、豆粕,降低饲养成本,提高经济效益。巨菌草(*Pennisetum giganteum*)作为饲草资源,优质、高产、抗逆性强、株高可达3~5 m,原产于非洲,由福建农林大学菌草研究所引进并选育,具有较大的发展潜力^[3]。黄晓飞等^[4]发现在奶牛日粮中添加22.3%的巨菌草青贮料可显著提升奶牛的产奶量,并提高经济效益。邓新为等^[5-6]的研究报道在七彩山鸡日粮中用巨菌草替代部分麸皮可提高七彩山鸡的生长性能、免疫器官指数及降低盲肠中沙门氏菌数量。裘博文等^[7]还表明在日粮中添加8%巨菌草可显著提升七彩山鸡肠道绒毛高度。巨菌草在反刍动物及家禽中已有较多研究,但在猪上的研究较少。从江香猪作为小型猪种,体型矮小、抗逆性强、耐粗饲,能较好地利用青绿饲料^[8-9]。因此,本试验通过探究巨菌草替代10%、20%基础饲粮对从江香猪的生长性能、肠道发育及肠道屏障功能的影响,并进行经济效益分析,以探究巨菌草替代部分基础饲粮的可行性,以期达到玉米豆粕减量替代效果,并为巨菌草养猪提供数据支撑。

1 材料与方法

1.1 试验设计

试验于2022年9至12月在南靖绿明生态农业有限公司进行。选取30头6月龄从江香猪,随机分为3组,每组5个重复,每个重复2头,公母各半,重复之间体重相近。巨菌草直接替代部分基础饲粮更符合农村养殖户应用青绿饲料饲喂猪的情况并便于养殖户现场应用,参照Raj等^[10]的试验设计,对照组饲喂基础饲粮,试验I组和试验II组用新鲜青绿巨菌草分别替代10%、20%的基础饲粮。巨菌草当天收割,用碎草机(45型,山东)切碎后与基础饲粮混合后进行饲喂,1.8~2.0 m新鲜青绿巨菌草干物质含量约为14.6%,饲料干物质含量约为88%,所以巨菌草按6:1的重量替代基础饲粮,即6 kg巨菌草替代1 kg基础饲粮。预饲期7 d,试验期90 d,由于猪胃容量有限,为使猪能够采食更多的巨菌草,参考王进波^[11]的试验设计对猪的基础饲粮进行限制饲喂,本试验对照组育肥从江香猪按体重的3.5%进行饲喂,试验组按比例进行替代饲喂,自由饮水,按正常免疫程序进行免疫接种。基础饲粮参照国家标准《猪营养需要量》(肉脂型,GB/T 39235-2020)^[12]营养需要配制粉状配合饲料,饲粮组成及营养水平见表1。

1.2 测定指标及方法

1.2.1 生长性能测定 记录试验猪每日喂料量和余料量,计算基础饲粮及巨菌草平均日采食量(average daily feed intake, ADFI)。试验期第1和91天8:00对猪空腹称重,在前一天20:00断料,记录试验初重、试验末重。

$$\text{平均日增重} = (\text{试验末重} - \text{试验初重}) / \text{试验天数}$$

1.2.2 经济效益分析 根据试验期基础饲粮及巨菌草的总采食量和价格、试验期增重,计算单位增重成本。

$$\text{单位增重成本}(\text{元} \cdot \text{kg}^{-1}) = \frac{\text{基础饲粮总采食量} \times \text{基础饲粮价格} + \text{巨菌草总采食量} \times \text{巨菌草价格}}{\text{试验末重} - \text{试验初重}}$$

$$\text{节约增重成本}(\%) = \frac{\text{各组别单位增重成本} - \text{对照组单位增重成本}}{\text{对照组单位增重成本}} \times 100$$

1.2.3 胴体性状测定 试验期结束后,每个重复选取一只接近每组平均体重的猪进行屠宰。猪放血屠宰后,参照《畜禽屠宰操作规程 生猪》(GB/T 17236-2019)^[13]去除头、蹄,开膛,剥离内脏,拆分胴体。参照《瘦肉型猪胴体性状测定技术规范》(NY/T 825-2004)^[14]测定屠宰率、板油率、背膘厚和眼肌面积。

1.2.4 胃肠道相对重量及长度 从江香猪屠宰分离胃和各肠段后,去除其中内容物,称量胃、小肠、大肠绝对重量,计算胃肠道相对重量。在自然伸展状态下,测量小肠、大肠绝对长度,计算各肠段相对长度。

$$\text{胃肠道相对重量}(\text{g} \cdot \text{kg}^{-1}) = \text{胃肠道绝对重量}(\text{g}) / \text{宰前活重}(\text{kg})$$

$$\text{肠道相对长度}(\text{cm} \cdot \text{kg}^{-1}) = \text{肠道绝对长度}(\text{cm}) / \text{宰前活重}(\text{kg})$$

1.2.5 肠道形态结构 空肠、回肠组织固定、脱水、包埋、切片、染色和封片等处理后,使用光学显微镜(Eclipse Ci-L, Nikon, 日本)测量其绒毛高度、隐窝深度,并计算绒毛高度/隐窝深度(villous height/crypt depth, V/C)值。

1.2.6 肠道发育相关基因表达 刮取空肠、回肠黏膜后按照 TRNzol Universal 总 RNA 提取试剂说明书提取黏膜的 RNA, 将提取的 RNA 按照 Evo M-MLV 反转录预混型试剂盒(长沙)说明书进行反转录制备 cDNA, 最后按照 Hieff UNICON® Universal Blue qPCR SYBR Green Master Mix 说明书进行荧光定量 PCR 检测胰岛素样生长因子-1(insulin-like growth factor 1, *IGF-1*)、胰岛素样生长因子-1受体(insulin-like growth factor 1 receptor, *IGF-1R*)、胰高血糖素样肽-2(glucagon-like peptide-2, *GLP-2*)基因表达水平, 肠道发育相关基因和内参基因的引物序列见表 2。采用 $2^{-\Delta\Delta Ct}$ 方法^[18] 计算基因的相对表达量。

1.2.7 肠道细胞因子含量测定 取 3 cm 空肠、回肠并用生理盐水将内容物冲洗干净, 灭菌剪刀剪开肠段, 用载玻片轻轻刮取黏膜。按照南京建成生物工程研究所酶联免疫(ELISA)试剂盒说明书测定空肠、回肠黏膜的白介素-1 β (interleukin-1 β , IL-1 β)、白介素-6(interleukin-6, IL-6)、白介素-10(interleukin-10, IL-10)、肿瘤坏死因子- α (tumor necrosis factor- α , TNF- α)、干扰素- γ (interferon- γ , IFN- γ)、转化生长因子- β (transforming growth factor- β , TGF- β)含量。

1.2.8 小肠黏膜紧密连接蛋白基因表达 刮取空肠、回肠黏膜后按照 TRNzol Universal 总 RNA 提取试剂说明书提取黏膜的 RNA, 将提取的 RNA 按照 Evo M-MLV 反转录预混型试剂盒说明书进行反转录制备 cDNA, 最后按照 Hieff UNICON® Universal Blue qPCR SYBR Green Master Mix 说明书进行荧光定量 PCR 检测闭合小环蛋白-1(Zonula occludens-1, *ZO-1*)、闭合蛋白-1(*Claudin-1*)、闭锁蛋白(*Occludin*)的基因表达水平, 采用 $2^{-\Delta\Delta Ct}$ 方法^[18] 计算基因的相对表达量。小肠紧密连接蛋白基因和内参基因的引物序列见表 3。

1.2.9 巨菌草对育肥从江香猪盲肠微生物的影响 从江香猪屠宰后, 取部分盲肠内容物于无菌冻存管中, 于 -80°C 冰箱保存待测, 通过 Illumina-MiSeq 高通量测序技术对育肥从江香猪的盲肠微生物菌群进行 Alpha 多样性分析、主坐标分析, 并测定门水平和属水平菌群相对丰度。

1.3 数据统计分析

采用 Excel 2019 整理试验数据, 用 SPSS 26.0 软件进行单因素方差分析(one-way ANOVA), 并采用 Duncan 氏法进行多重比较, 试验结果用平均值 \pm 标准误表示, $P < 0.05$ 为差异显著, $0.05 \leq P < 0.10$ 为有差异显著趋势。用 GraphPad Prism 9.4.1 软件对 qRT-PCR 数据分析结果作图。

表 1 饲料组成及营养水平(风干基础)

Table 1 Composition and nutrient levels of diets (air-dry basis)

项目 Items	含量 Content		
	对照组 Control group	试验 I 组 Experi- mental group I	试验 II 组 Experi- mental group II
原料 Ingredients			
玉米 Corn (%)	76.97	69.27	61.57
小麦麸 Wheat bran (%)	2.04	1.84	1.63
豆粕 Soybean meal (%)	18.02	16.22	14.42
巨菌草鲜草(干物质) Fresh <i>P. giganteum</i> (dry matter) (%)	0	10	20
食盐 NaCl (%)	0.30	0.27	0.24
石粉 Limestone (%)	0.86	0.77	0.69
磷酸氢钙 CaHPO ₄ (%)	0.70	0.63	0.56
L-赖氨酸盐酸盐 L-Lys·HCl (%)	0.11	0.10	0.09
预混料 Premix ¹⁾ (%)	1.00	0.90	0.80
合计 Total (%)	100.00	100.00	100.00
营养水平 Nutrient levels ²⁾			
消化能 Digestible energy (MJ·kg ⁻¹)	13.81	12.95	12.09
粗蛋白质 Crude protein (%)	14.50	13.88	13.25
中性洗涤纤维 Neutral detergent fiber (%)	10.91	15.04	19.18
酸性洗涤纤维 Acid detergent fiber (%)	4.36	7.47	10.58
钙 Calcium (%)	0.55	0.54	0.53
非植酸磷 Non-phytate phosphorus (%)	0.20	0.20	0.20
赖氨酸 Lysine (%)	0.74	0.71	0.67
蛋氨酸+胱氨酸 Methionine+cystine (%)	0.50	0.48	0.45

¹⁾ 预混料为每 kg 饲料提供 The premix provided the following per kg of diets: V_A 2250 IU, V_{D3} 270 IU, V_E 22.5 mg, V_{K3} 0.75 mg, V_{B1} 2.25 mg, V_{B2} 3.75 mg, V_{B5} 13.50 mg, V_{B6} 1.50 mg, V_{B12} 0.02 mg, 生物素 Biotin 0.12 mg, 叶酸 Folic acid 0.45 mg, 烟酸 Nicotinic acid 18 mg, 胆碱 Choline 680 mg, 铁 Fe 90 mg, 铜 Cu 6 mg, 锌 Zn 97.50 mg, 锰 Mn 4.50 mg, 碘 I 0.23 mg, 硒 Se 0.38 mg. ²⁾ 营养水平为计算值 Nutrient levels were calculated values.

表 2 肠道发育相关基因和内参基因的引物序列

Table 2 Primer sequences for genes related to intestinal development and reference gene

基因 Gene	引物序列 Primer sequence (5'–3')	参考文献 References
β -肌动蛋白 <i>β-actin</i>	F: CCAGCACGATGAAGATCAAGA R: AATGCAACTAACAGTCCGCCTA	[15]
胰岛素样生长因子-1 Insulin-like growth factor 1 (<i>IGF-1</i>)	F: CTGAGGAGGCTGGAGATGTACT R: CCTGAACTCCCTCTACTTGTGTTC	[16]
胰岛素样生长因子-1受体 Insulin-like growth factor 1 receptor (<i>IGF-1R</i>)	F: GGAGGAAGTGACAGGGACTAAAGG R: GGTGCCAGGTGATGATGATGC	[15]
胰高血糖素样肽-2 Glucagon-like peptide-2 (<i>GLP-2</i>)	F: ACTCACAGGGCAGTTCACCA R: AGGTCCCTCAGCATGTCTCT	[17]

表 3 小肠紧密连接蛋白基因和内参基因的引物序列

Table 3 Primer sequences for small intestinal tight junction protein genes and reference gene

基因 Gene	引物序列 Primer sequence (5'–3')	参考文献 References
β -肌动蛋白 <i>β-actin</i>	F: CCAGCACGATGAAGATCAAGA R: AATGCAACTAACAGTCCGCCTA	[15]
闭合蛋白-1 <i>Claudin-1</i>	F: TCTTAGTTGCCACAGCATGG R: CCAGTGAAGAGAGCCTGACC	[17]
闭锁蛋白 <i>Occludin</i>	F: ATGCTTTCTCAGCCAGCGTA R: AAGGTTCCATAGCCTCGGTC	[15]
闭合小环蛋白-1 Zonula occludens-1 (<i>ZO-1</i>)	F: GAGGATGGTCACACCGTGGT R: GGAGGATGCTGTTGTCTCGG	[16]

2 结果与分析

2.1 巨菌草对育肥从江香猪生长性能的影响

各组间育肥从江香猪生长性能指标差异不显著 ($P > 0.05$, 表 4)。

表 4 巨菌草对育肥从江香猪生长性能的影响

Table 4 Effects of *P. giganteum* on growth performance of finishing Congjiang Xiang pigs

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
初重 Initial weight (kg)	28.65 ± 0.34a	28.65 ± 0.23a	28.81 ± 0.16a	0.895
末重 Final weight (kg)	61.75 ± 1.20a	61.26 ± 1.48a	58.83 ± 0.57a	0.264
平均日增重 ADG (g)	367.78 ± 9.59a	362.33 ± 15.16a	333.61 ± 5.03a	0.140
基础饲粮平均日采食量 Basal diets ADFI ($\text{kg} \cdot \text{d}^{-1}$)	1.30	1.17	1.04	—
巨菌草平均日采食量 <i>P. giganteum</i> ADFI ($\text{kg} \cdot \text{d}^{-1}$)	0	0.78	1.55	—

同行不同小写字母表示差异显著 ($P < 0.05$); $0.05 \leq P < 0.10$ 表示有趋势。In the same row, the different lowercase letters mean significant difference ($P < 0.05$); $0.05 \leq P < 0.10$ indicates a trend. ADG: Average daily gain; ADFI: 平均日采食量 Average daily feed intake. 下同 The same below.

2.2 巨菌草对育肥从江香猪经济效益的影响

当巨菌草不计成本时(农民自己种植),与对照组相比,试验 I 组的增重成本降低 8.73%,试验 II 组的增重成本降低 11.59%。当巨菌草按市场价格 $0.35 \text{元} \cdot \text{kg}^{-1}$ 计算时,与对照组相比,试验 I 组的增重成本降低 2.78%,试验 II 组的增重成本增加 1.35%(表 5)。

表5 巨菌草对育肥从江香猪经济效益的影响

Table 5 Effects of *P. giganteum* on economic benefits of finishing Congjiang Xiang pigs

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II
巨菌草成本按 0 元·kg ⁻¹ 计算 <i>P. giganteum</i> are calculated at a cost of 0 CNY·kg ⁻¹			
单位增重成本 Unit weight gain cost (CNY·kg ⁻¹)	12.60	11.50	11.14
节约增重成本 Save weight gain costs (%)	0	8.73	11.59
巨菌草按市场价格 0.35 元·kg ⁻¹ 计算 <i>P. giganteum</i> are calculated at a cost of 0.35 CNY·kg ⁻¹			
单位增重成本 Unit weight gain cost (CNY·kg ⁻¹)	12.60	12.25	12.77
节约增重成本 Save weight gain costs (%)	0	2.78	-1.35

基础饲料价格为 3.56 元·kg⁻¹, 基础饲料按试验时的原料市场价计算得出。The price of the basal diet was 3.56 CNY·kg⁻¹. The basal diet was calculated based on the market price of raw materials at the time of the experiment.

2.3 巨菌草对育肥从江香猪胴体性状的影响

各组间育肥从江香猪胴体性状指标差异不显著 ($P > 0.05$, 表 6)。与试验 I 组相比, 试验 II 组育肥从江香猪屠宰率有下降趋势 ($P = 0.078$)。

2.4 巨菌草对育肥从江香猪胃肠道相对重量及长度的影响

与对照组相比, 试验 I 组和试验 II 组育肥从江香猪胃相对重量均显著提高 ($P < 0.05$, 表 7), 小肠相对重量有上升趋势 ($P = 0.092$)。各组间其他胃肠道相对重量及长度指标无显著差异 ($P > 0.05$)。

2.5 巨菌草对育肥从江香猪肠道形态结构的影响

与对照组相比, 试验 I 组育肥从江香猪回肠隐窝深度显著下降 ($P < 0.05$, 表 8), 回肠 V/C 显著上升 ($P < 0.05$)。试验 II 组回肠绒毛高度和 V/C 显著上升 ($P < 0.05$)。各组间育肥从江香猪空肠肠道形态结构各指标无显著差异 ($P > 0.05$)。

表6 巨菌草对育肥从江香猪胴体性状的影响

Table 6 Effects of *P. giganteum* on carcass traits of finishing Congjiang Xiang pigs

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
屠宰率 Dressing percentage (%)	67.44 ± 0.78a	68.14 ± 1.17a	64.93 ± 0.84a	0.078
板油率 Leaf lard percentage (%)	2.24 ± 0.50a	1.78 ± 0.29a	1.83 ± 0.34a	0.666
背膘厚 Backfat thickness (mm)	29.86 ± 0.98a	26.33 ± 2.49a	25.92 ± 3.33a	0.483
眼肌面积 Loin-eye area (cm ²)	31.10 ± 4.51a	30.35 ± 2.84a	27.56 ± 2.80a	0.754

表7 巨菌草对育肥从江香猪胃肠道相对重量及长度的影响

Table 7 Effects of *P. giganteum* on gastrointestinal tract (GIT) relative weight and relative length of finishing Congjiang Xiang pigs

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
胃肠道相对重量 Gastrointestinal tract relative weight (g·kg ⁻¹)				
胃相对重量 Stomach relative weight	8.88 ± 0.16b	11.38 ± 0.84a	11.21 ± 0.57a	0.008
小肠相对重量 Small intestine relative weight	17.36 ± 1.22a	18.77 ± 1.28a	22.42 ± 1.96a	0.092
大肠相对重量 Large intestine relative weight	15.50 ± 1.81a	16.40 ± 0.85a	17.90 ± 0.52a	0.384
胃肠道相对长度 Gastrointestinal tract relative length (cm·kg ⁻¹)				
小肠相对长度 Small intestine relative length	22.29 ± 1.10a	22.86 ± 0.94a	24.25 ± 0.69a	0.338
大肠相对长度 Large intestine relative length	6.24 ± 0.54a	6.32 ± 0.26a	7.00 ± 0.09a	0.275

表8 巨菌草对育肥从江香猪肠道形态结构的影响

Table 8 Effects of *P. giganteum* on intestinal morphology of finishing Congjiang Xiang pigs

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
空肠 Jejunum				
绒毛高度 Villous height (V, μm)	903.68 \pm 83.76a	859.67 \pm 51.07a	846.77 \pm 29.63a	0.780
隐窝深度 Crypt depth (C, μm)	539.08 \pm 19.42a	491.84 \pm 34.26a	489.05 \pm 37.78a	0.710
绒毛高度/隐窝深度 V/C	1.71 \pm 0.12a	1.82 \pm 0.11a	1.84 \pm 0.13a	0.473
回肠 Ileum				
绒毛高度 Villous height (V, μm)	806.74 \pm 28.02b	813.14 \pm 8.61b	910.38 \pm 29.87a	0.017
隐窝深度 Crypt depth (C, μm)	539.77 \pm 7.42a	447.13 \pm 27.26b	505.58 \pm 26.36ab	0.037
绒毛高度/隐窝深度 V/C	1.51 \pm 0.05b	1.90 \pm 0.10a	1.90 \pm 0.12a	0.017

2.6 巨菌草对育肥从江香猪肠道发育相关基因的影响

与对照组相比,试验 I 和试验 II 组空肠 *GLP-2* 基因表达量显著上升 ($P < 0.05$, 图 1), 各组间其他基因表达量无显著差异 ($P > 0.05$)。与对照组相比,试验 I 组回肠 *IGF-1R* 基因表达量显著上升 ($P < 0.05$, 图 2), 各组间其他基因表达量无显著差异 ($P > 0.05$)。

2.7 巨菌草对育肥从江香猪肠道细胞因子的影响

与对照组相比,试验 II 组育肥从江香猪空肠 TGF- β 含量显著上升 ($P < 0.05$, 表 9), 各组间空肠其他细胞因子含量无显著差异 ($P > 0.05$)。与对照组相比,试验 I 和 II 组育肥从江香猪回肠 IFN- γ 含量显著下降 ($P < 0.05$, 表 10), 回肠各组间其他细胞因子含量无显著差异 ($P > 0.05$)。

2.8 巨菌草对育肥从江香猪肠道紧密连接蛋白基因表达的影响

与对照组相比,试验 II 组育肥从江香猪空肠黏膜 *Occludin* 的基因表达量显著上升 ($P < 0.05$, 图 3), 各组间其他基因表达量无显著差异 ($P > 0.05$)。与对照组相比,试验 I 和 II 组育肥从江香猪回肠黏膜 *ZO-1* 的基因表达量均显著上升 ($P < 0.05$, 图 4), 各组间其他基因表达量差异不显著 ($P > 0.05$)。

2.9 巨菌草对从江香猪盲肠微生物的影响

2.9.1 测序数据及扩增子序列变异体 (amplicon sequence variant, ASV) 分析

对育肥从江香猪的 15 个盲肠食糜样本进行微生物测序, 经过降噪和优化处理, 获得 718739 个优化序列。运用 DADA 2 模型算法对这些序列进行进一步分析, 共得到

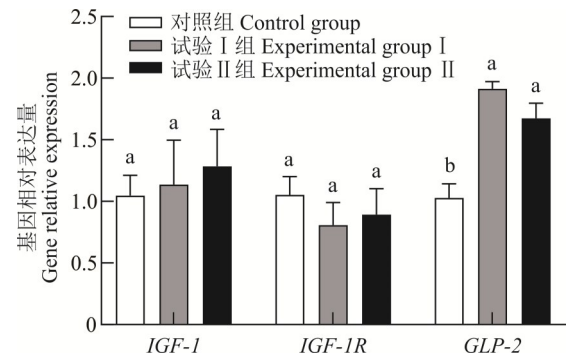


图1 巨菌草对育肥从江香猪空肠肠道发育相关基因表达的影响
Fig. 1 Effects of *P. giganteum* on gene expression level of intestinal development in jejunum of finishing Congjiang Xiang pigs

IGF-1: 胰岛素样生长因子-1 Insulin-like growth factor 1; *IGF-1R*: 胰岛素样生长因子-1受体 Insulin-like growth factor 1 receptor; *GLP-2*: 胰高血糖素样肽-2 Glucagon-like peptide-2. 不同小写字母表示不同处理间存在显著差异 ($P < 0.05$), $0.05 \leq P < 0.10$ 表示有趋势, 下同。Different lowercase letters mean significant differences among different treatments ($P < 0.05$); $0.05 \leq P < 0.10$ indicates a trend, the same below.

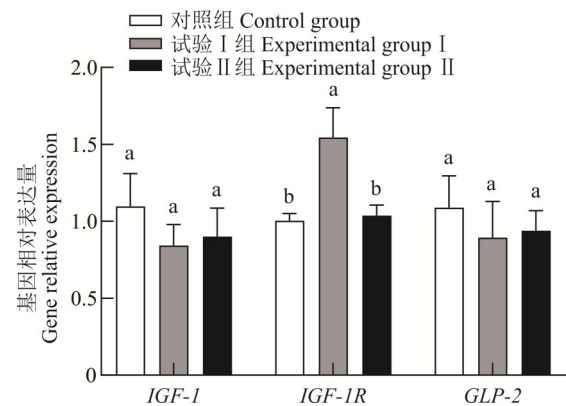


图2 巨菌草对育肥从江香猪回肠肠道发育相关基因表达的影响
Fig. 2 Effects of *P. giganteum* on gene expression level of intestinal development in ileum of finishing Congjiang Xiang pigs

表9 巨菌草对育肥从江香猪空肠细胞因子的影响

Table 9 Effects of *P. giganteum* on jejunum cytokines of finishing Congjiang Xiang pigs ($\text{pg} \cdot \text{mg}^{-1} \text{prot}$)

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
白介素-1 β Interleukin-1 β (IL-1 β)	338.19 \pm 26.39a	329.35 \pm 34.87a	375.16 \pm 54.05a	0.691
白介素-6 Interleukin-6 (IL-6)	482.70 \pm 27.33a	447.46 \pm 33.76a	468.63 \pm 36.22a	0.731
白介素-10 Interleukin-10 (IL-10)	136.96 \pm 6.48a	140.27 \pm 10.82a	147.66 \pm 17.72a	0.829
肿瘤坏死因子- α Tumor necrosis factor- α (TNF- α)	99.24 \pm 4.13a	97.67 \pm 4.60a	105.35 \pm 1.25a	0.323
干扰素- γ Interferon- γ (IFN- γ)	21.61 \pm 1.40a	22.91 \pm 1.92a	26.89 \pm 3.28a	0.289
转化生长因子- β Transforming growth factor- β (TGF- β)	4245 \pm 257b	5002 \pm 497ab	6427 \pm 602a	0.021

表10 巨菌草对育肥从江香猪回肠细胞因子的影响

Table 10 Effects of *P. giganteum* on ileum cytokines of finishing Congjiang Xiang pigs ($\text{pg} \cdot \text{mg}^{-1} \text{prot}$)

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
白介素-1 β Interleukin-1 β (IL-1 β)	728.76 \pm 85.09a	586.90 \pm 46.46a	723.17 \pm 58.09a	0.223
白介素-6 Interleukin-6 (IL-6)	1032.87 \pm 125.42a	834.07 \pm 41.41a	1043.27 \pm 81.61a	0.219
白介素-10 Interleukin-10 (IL-10)	313.59 \pm 33.99a	263.04 \pm 11.29a	332.65 \pm 22.38a	0.156
肿瘤坏死因子- α Tumor necrosis factor- α (TNF- α)	237.39 \pm 23.15a	196.57 \pm 4.92a	246.83 \pm 18.39a	0.134
干扰素- γ Interferon- γ (IFN- γ)	51.91 \pm 4.60a	37.17 \pm 1.88b	41.58 \pm 0.98b	0.011
转化生长因子- β Transforming growth factor- β (TGF- β)	1016.15 \pm 125.91a	954.25 \pm 79.64a	1095.24 \pm 100.36a	0.619

14773个不同的ASVs。随着不断增加抽取的样本数量,曲线呈逐渐平缓的趋势,这表明所测得的样本数据已足够丰富,能够充分反映样品中微生物的多样性(图5A)。此外,对照组、试验 I 组和试验 II 组各组间共有ASV数目为592个,各组特有ASV数目分别为:对照组4053个、试验 I 组4820个、试验 II 组4674个(图5B)。

2.9.2 Alpha多样性分析 与对照组相比,试验 I 组和试验 II 组育肥从江香猪盲肠微生物Alpha多样性中Shannon指数显著上升($P < 0.05$,表11)。Chao1指数和ACE指数各组间无显著差异($P > 0.05$)。

2.9.3 Beta多样性分析 基于Bray-Curtis距离的主坐标分析(principal co-ordinates analysis, PCoA)结果显示,对照组与试验 I、II组盲肠微生物组间距离较远,表明组间微生物群落结构具有差异性(图6)。

2.9.4 门和属水平相对丰度分析 在门水平上,育肥从江香猪盲肠微生物主要优势菌门为厚壁菌门、拟杆菌门和螺旋体门,其中与对照组相比,试验 I 组和试验 II 组螺旋体门相对丰度呈下降趋势($P = 0.085$,图7A和表12)。属水平菌群相对丰度排名前10的菌属为乳杆菌属、链球菌属、毛螺菌科未分类菌属、UCG-005、密螺旋体属、*norank_f__p-251-o5*、狭义梭菌属1、克里斯滕森菌科R-7群、普雷沃菌科_UCG-003菌属、土袍杆菌属(图7B和表12)。其中与对照组相比,试验 I 组和试验 II 组链球菌属相对丰度显著下降($P < 0.05$),试验 I 组和试验 II 组

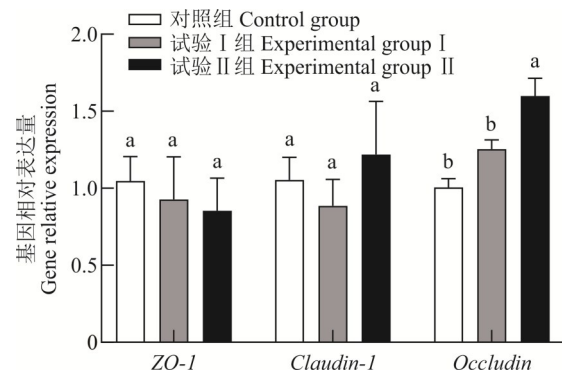


图3 巨菌草对育肥从江香猪空肠黏膜紧密连接蛋白基因表达的影响

Fig. 3 Effects of *P. giganteum* on gene expression level of tight junction proteins in jejunum mucosa of finishing Congjiang Xiang pigs

ZO-1: 闭合小环蛋白-1 Zonula occludens-1; Claudin-1: 闭合蛋白-1; Occludin: 闭锁蛋白. 下同 The same below.

毛螺菌科未分类菌属有上升趋势($P=0.065$),密螺旋体属有下降趋势($P=0.085$)。

3 讨论

3.1 巨菌草对育肥从江香猪生长性能的影响

生长性能是反映动物生长情况最直观的指标,受日粮组成、动物品种、畜禽生长环境等影响。本试验结果表明,巨菌草替代部分基础饲料对育肥从江香猪生长性能无显著影响。徐佳玉等^[19]研究表明在育肥黑猪饲料中添加 10% 巨菌草对黑猪平均日增重无显著影响。朱雷等^[20]研究发现黑麦草(*Lolium perenne*)替代 10%~20% 的基础饲料对生长育肥猪的生长性能无显著影响。项延润^[21]研究发现添饲 0.5 kg·d⁻¹皇

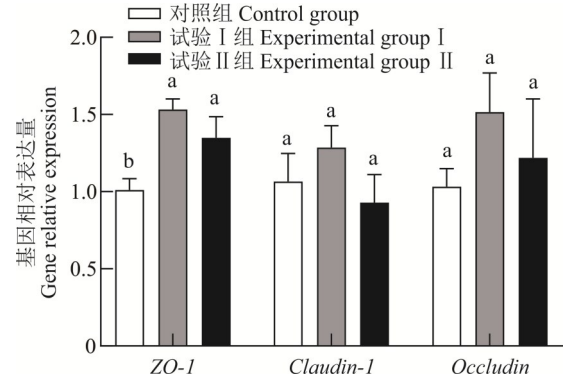


图 4 巨菌草对育肥从江香猪回肠黏膜紧密连接蛋白基因表达的影响

Fig. 4 Effects of *P. giganteum* on gene expression level of tight junction proteins in ileum mucosa of finishing Congjiang Xiang pigs

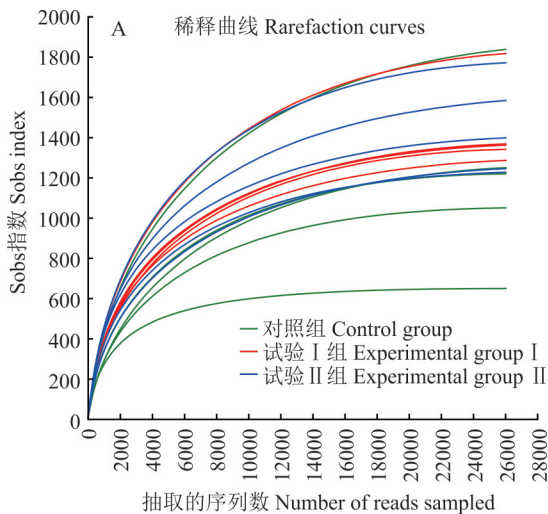


图 5 育肥从江香猪菌群稀释曲线和扩增子序列变异体韦恩图

Fig. 5 Rarefaction curves of observed species and Venn diagram of amplicon sequence variants (ASVs) in finishing Congjiang Xiang pigs

表 11 巨菌草对育肥从江香猪盲肠微生物 Alpha 多样性的影响

Table 11 Effects of *P. giganteum* on Alpha diversity of cecal microorganism of finishing Congjiang Xiang pigs

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
Chao1 指数 Chao1 index	1214±199.96a	1447±99.19a	1462±105.50a	0.275
ACE 指数 ACE index	1236±211.22a	1475±103.49a	1490±107.29a	0.275
Shannon 指数 Shannon index	5.14±0.19b	5.86±0.10a	5.86±0.21a	0.026

竹草(*Pennisetum sinense*)替代 3% 基础饲料,对育肥猪的日增重影响不显著。Wallenbecka 等^[22]研究表明在育肥猪饲料中以代谢能为基础用粉碎青贮料与基础饲料混合制粒替代 20% 基础饲料,对猪的平均日增重无显著影响。本研究结果与上述研究结果一致,可能因为育肥猪能够较好利用饲料中的纤维,饲料营养成分可满足猪的生长需要,使得替代部分基础饲料对猪的生长性能无显著影响^[23]。与上述研究结果不同的是,陈冬梅等^[24]研究发现在 20~50 日龄四川白鹅饲料中额外添加 10%、15% 的巨菌草粉可提高其生长性能。赵鹤青^[25]也研究表明在七彩山

鸡饲料中额外添加8%的巨菌草可提高其日增重。究其原因可能与巨菌草饲喂方式和饲喂量、饲养动物等不同有关。

3.2 巨菌草对育肥从江香猪经济效益的影响

饲料成本会影响经济效益,牧草与精料相比价格更低,为了提升经济效益,已有较多牧草在猪饲料中应用的研究。在一定条件下,在猪日粮中添加牧草可以提升经济效益,但牧草能够在多大程度上更加经济地为猪的生长发育提供营养,取决于猪对牧草的采食量、消化率以及与精料相比牧草的相对成本和可得性^[26]。赵静^[27]研究发现育肥猪饲料中添加10%和15%的苜蓿(*Medicago sativa*)草粉替代部分玉米和豆粕,分别可使单位增重成本下降0.74和0.46元·kg⁻¹,毛利润分别提高31.54和14.91元·头⁻¹。项延润^[21]研究表明在育肥猪饲料中用0.5 kg·d⁻¹皇竹草替代3%精饲料,每头平均可增加收益24.63元,但添饲

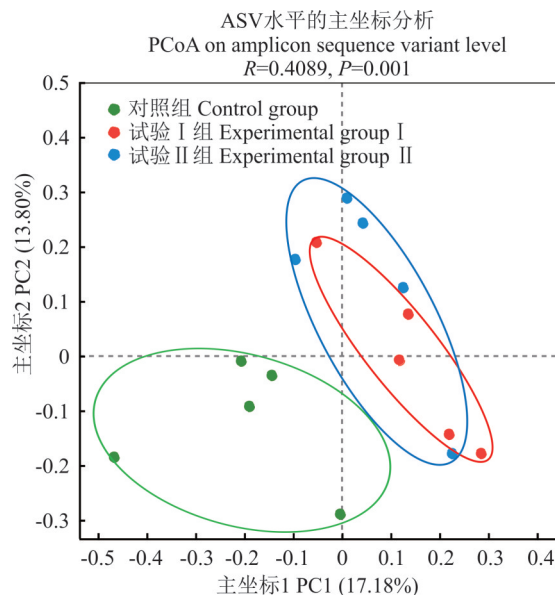


图6 基于 Bray-Curtis 距离的主坐标分析

Fig. 6 Principal co-ordinates analysis based on Bray-Curtis distance

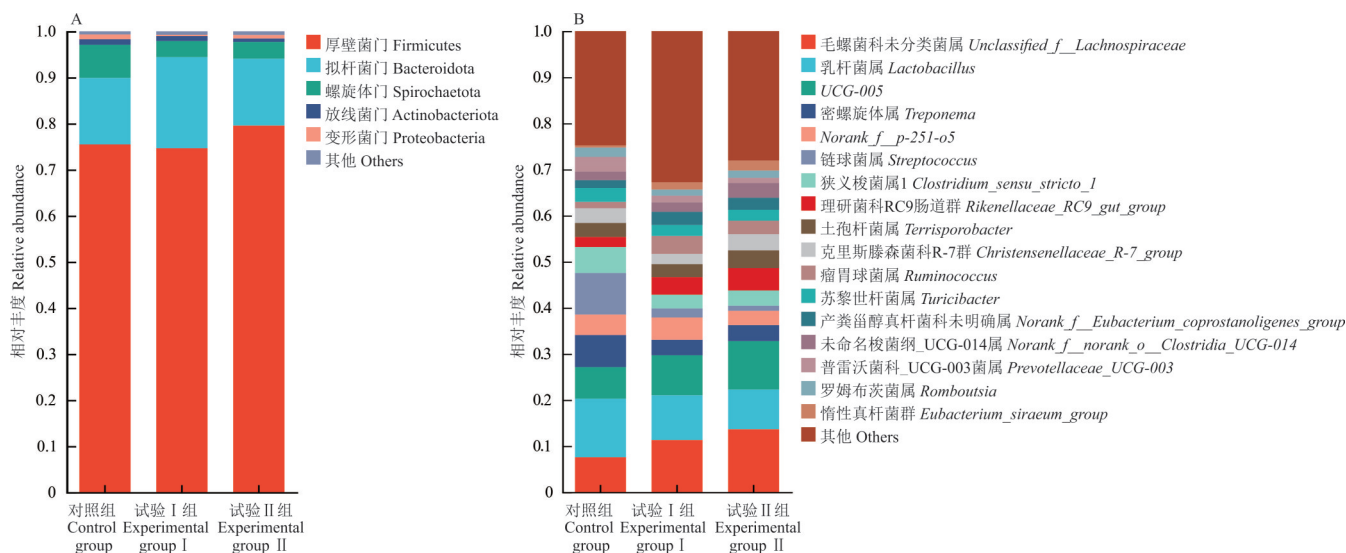


图7 盲肠微生物门水平(A)和属水平(B)上的物种相对丰度

Fig. 7 Relative abundance at phylum level (A) and genus level (B) in cecal microbiota

1.0 kg·d⁻¹皇竹草替代6%精料,头均减少收益31.87元。本试验结果表明,巨菌草不计入成本替代10%和20%基础饲料均能降低增重成本,巨菌草按市场价格0.35元·kg⁻¹计算时,替代10%基础饲料可降低增重成本,但替代20%基础饲料增重成本反而增加。经济效益受到基础饲料价格、牧草价格、猪的生长性能共同影响,适宜的替代量可以提高经济效益,替代量过大反而会使经济效益降低。

3.3 巨菌草对育肥从江香猪胴体性状的影响

胴体性状可反映肉用畜禽体组织营养物质沉积情况^[28]。胴体性状包括屠宰率、板油率、背膘厚、眼肌面积等指标。其中屠宰率可以反映猪的产肉性能进而影响经济效益,板油率、背膘厚和眼肌面积对评定胴体品质具有重要意义^[29]。本试验结果表明,巨菌草替代20%基础饲料与替代10%基础饲料相比,屠宰率有下降的趋势,其他指标无显著差异。Galassi等^[30]研究报道在育肥猪饲料中添加12%麦(*Triticum aestivum*)麸对屠宰率无显著影响,

表 12 育肥从江香猪盲肠内优势菌门和优势菌属的相对丰度

Table 12 Relative abundance of cecal dominant phyla and genera in finishing Congjiang Xiang pigs (%)

项目 Items	对照组 Control group	试验 I 组 Experimental group I	试验 II 组 Experimental group II	P 值 P-value
门水平 Phylum level				
厚壁菌门 Firmicutes	75.47±2.09a	74.64±2.02a	79.56±2.23a	0.275
拟杆菌门 Bacteroidota	14.43±2.06a	19.77±2.26a	14.52±0.90a	0.145
螺旋体门 Spirochaetota	7.18±0.92a	3.49±1.36a	3.63±1.40a	0.085
放线菌门 Actinobacteriota	1.21±0.57a	1.07±0.38a	0.74±0.15a	0.914
变形菌门 Proteobacteria	1.03±0.49a	0.28±0.12a	0.77±0.25a	0.281
属水平 Genus level				
乳杆菌属 <i>Lactobacillus</i>	12.72±4.50a	9.71±3.80a	8.62±6.11a	0.651
链球菌属 <i>Streptococcus</i>	9.01±3.70a	1.97±0.56b	1.10±0.23b	0.021
毛螺菌科未分类菌属 <i>Unclassified_f_Lachnospiraceae</i>	7.56±1.67a	11.30±1.30a	13.63±1.36a	0.065
<i>UCG-005</i>	6.84±1.82a	8.67±0.67a	10.50±1.17a	0.230
密螺旋体属 <i>Treponema</i>	6.96±0.93a	3.36±1.36a	3.47±1.36a	0.085
<i>Norank_f_p-251-o5</i>	4.44±1.73a	4.84±1.04a	3.10±0.47a	0.533
狭义梭菌属 1 <i>Clostridium_sensu_stricto_1</i>	5.63±1.09a	2.97±0.71a	3.30±1.32a	0.108
克里斯滕森菌科 R-7 群 <i>Christensenellaceae_R-7_group</i>	3.20±0.61a	2.21±0.22a	3.51±0.41a	0.164
普雷沃菌科 <i>UCG-003</i> 菌属 <i>Prevotellaceae_UCG-003</i>	3.19±2.37a	1.44±0.21a	1.12±0.26a	0.717
土孢杆菌属 <i>Terrisporobacter</i>	3.03±0.36a	2.83±0.33a	3.86±0.61a	0.497

但添加 24% 麦麸时屠宰率显著下降。徐佳玉等^[19]研究发现在育肥黑猪饲料中用粉碎巨菌草替代 10% 基础饲料可显著提高其屠宰率,显著降低其背膘厚,对眼肌面积无显著影响。王进波^[11]研究表明在生长育肥猪饲料中用黑麦草替代 10%、15%、20% 基础饲料其屠宰率均下降,眼肌面积无显著变化。赵静^[27]研究发现在育肥猪饲料中用苜蓿草粉替代 5%、10%、15%、20% 基础饲料可增加其眼肌面积,但对屠宰率、背膘厚均无显著影响。前人对于牧草替代部分饲料对猪胴体性状影响的结论不一致。造成这种差异的原因可能与牧草品种、牧草刈割长度、饲料营养水平、饲养品种等不同有关。

3.4 巨菌草对育肥从江香猪胃肠道相对重量及长度的影响

胃肠道在营养物质吸收和免疫应答中起重要作用,与机体健康密切相关^[31]。胃肠道相对重量及长度可以反映其发育情况。本试验结果表明,巨菌草替代部分基础饲料可显著提高育肥从江香猪胃的相对重量,小肠相对重量有上升趋势。李文新^[32]研究发现随着饲料粗纤维水平上升,生长猪胃和小肠的相对重量上升。Ngoc 等^[33]报道与低纤维饲料相比,高纤维饲料可显著提高猪胃的绝对重量。Raj 等^[34]研究表明在基础饲料中添加 20% 草粉,胃肠道绝对重量显著上升,小肠和大肠的绝对长度无显著差异。本试验结果与上述试验结果基本一致。表明高纤维饲料可以促进消化道膨大,其原因可能是:1)饲料纤维的含量增加使饲料体积增大;2)高纤维饲料的低能值效应,使动物的采食量代偿性增加,继而导致动物消化道体积的增加^[35-36]。

3.5 巨菌草对育肥从江香猪肠道形态结构的影响

小肠是营养物质吸收和代谢的主要器官。猪肠道上皮细胞包括吸收细胞、潘氏细胞、杯状细胞、内分泌细胞、微皱褶细胞,细胞间通过紧密连接、间隙连接、桥粒连接排列形成绒毛和隐窝^[37-38]。小肠中的绒毛呈现向肠腔内突出的手指状结构,扩大了小肠的表面积,有利于营养吸收和物质代谢^[39]。小肠隐窝是绒毛根部上皮陷入固有层形成的管状腺,位于隐窝中的肠道干细胞和祖细胞不断分裂和分化,以维持肠道稳态和组织完整性,隐窝深度可反映上皮细胞的生成率^[40-41]。V/C 增加可提升肠道对营养物质的消化吸收能力^[42]。赵鹤青^[25]研究发现在七彩

山鸡饲料中添加8%巨菌草,十二指肠、空肠、回肠绒毛高度均显著增加,添加12%巨菌草其十二指肠、空肠隐窝深度均显著下降。Adams等^[43]研究表明在断奶仔猪饲料中添加12%苜蓿可显著增加其空肠绒毛高度、V/C。Zhao等^[44]研究报道生长育肥猪饲料粗纤维水平为22.5%与粗纤维水平9%相比可显著提升十二指肠、空肠、回肠的绒毛高度和V/C。本试验结果显示,巨菌草替代部分基础饲料可显著提高回肠绒毛高度、V/C,降低隐窝深度。本试验结果与上述研究结果基本一致。其原因可能是巨菌草替代部分基础饲料使得在整体饲料中纤维含量上升,纤维经肠道内微生物发酵产生短链脂肪酸,为肠道细胞分化和增殖提供能量,进而促进绒毛和隐窝的增殖发育^[45-46]。

3.6 巨菌草对育肥从江香猪肠道发育相关基因的影响

肠道生长发育受其相关基因的调控。IGF-1的合成主要由垂体生长激素控制,IGF-1可促进有丝分裂和抑制细胞凋亡,IGF-1也可与胰岛素共同调节新陈代谢^[47]。在大多数促进有丝分裂和抗凋亡活动中,IGF-1由IGF-1R介导,IGF-1R也可影响细胞转化^[48]。GLP-2是一种肽类激素,可通过促进隐窝细胞增殖和抑制细胞凋亡促进肠道生长,也可在TGF- β 的介导下促进肠道伤口愈合,并通过增加肠系膜血流量,促进营养物质的消化吸收^[49-50]。本试验结果表明巨菌草替代10%基础饲料可提高育肥从江香猪空肠GLP-2、回肠IGF-1R基因表达量,替代20%基础饲料可提高空肠GLP-2的基因表达量。Diao等^[51]研究发现用甜菜(*Beta vulgaris*)浆作为纤维源[5.74%粗纤维(crude fiber, CF)]与基础日粮(1.5%CF)相比可显著增加生长猪空肠GLP-2和IGF-1的mRNA表达水平,但对回肠GLP-2、IGF1、IGF1R表达量无显著影响。Schedle等^[52]研究报道在断奶仔猪饲料中添加3%麦麸可提升空肠中IGF1的表达量。He等^[53]研究表明在生长猪日粮中额外添加0.5%的菊(*Chrysanthemum morifolium*)粉作为纤维源可显著提升猪回肠中GLP-2的基因表达量,但对IGF-1无显著影响。以上研究结果均表明日粮中纤维水平可提升部分肠道发育相关基因的表达量,本试验与其一致。其原因可能是饲料中纤维水平上升使得肠道内短链脂肪酸含量上升,促进肠内分泌L细胞产生GLP-2并诱导其他生长发育相关基因的表达^[54]。

3.7 巨菌草对育肥从江香猪肠道细胞因子的影响

肠道是重要的消化器官,也是最大的免疫器官^[55],许多细胞因子介导肠道炎症反应,IL-1 β 、TNF- α 、IL-6、IFN- γ 均属于促炎细胞因子^[56]。IL-1 β 可介导炎症并调节免疫反应、细胞增殖和分化^[57]。IL-6可参与调节造血、产生急性期反应以及诱导炎症和肿瘤的产生^[58]。TNF- α 主要由单核巨噬细胞产生,可通过诱导肠上皮紧密连接通透性增加,使肠道产生炎症^[59]。IFN- γ 主要由活化的T细胞和大颗粒淋巴细胞产生,可参与免疫反应,具有促凋亡和抗增殖功能^[60-61]。IL-10、TGF- β 属于抗炎细胞因子。IL-10可调节免疫反应,抑制促炎细胞因子的产生和功能的发挥^[62]。TGF- β 参与多种细胞过程,可参与免疫调节、维持细胞稳态、细胞凋亡和胚胎发育^[63]。Chen等^[64]研究发现在仔猪日粮中添加10%麦麸可降低肠道TNF- α 、IL-1 β 、IL-6基因表达量。Ding等^[65]在3个品种的生长猪中均分别设置低纤维日粮组和高纤维日粮组进行研究,与低纤维水平日粮相比,饲喂高纤维日粮杜洛克猪回肠IL-1 β 、IL-6、IL-10、IFN- γ 、TGF- β 和TNF- α 含量显著上升,但桃源黑猪和湘村黑猪饲喂不同纤维水平回肠细胞因子各指标均无显著差异。此外,Weber等^[66]发现在断奶仔猪日粮中添加7.5%大豆壳,对空肠、回肠中IL-6、IL-1 β 、TNF- α 的基因表达量无显著影响。本研究结果与前人^[64-66]探究日粮纤维水平对猪肠道细胞因子含量影响的结果不一致,可能与猪的品种和纤维组成有关。本试验结果表明巨菌草替代10%基础饲料可显著降低回肠IFN- γ 含量,替代20%基础饲料可显著提升空肠TGF- β 含量、显著降低回肠IFN- γ 含量。其原因可能是巨菌草替代部分基础饲料使得纤维含量上升,纤维发酵后挥发性脂肪酸含量上升,挥发性脂肪酸通过抑制组蛋白去乙酰化酶和激活G蛋白偶联受体来调节炎性细胞因子的产生,从而维持肠道稳态^[67]。

3.8 巨菌草对育肥从江香猪肠道紧密连接蛋白基因表达的影响

肠道机械屏障由肠道上皮细胞和细胞间的紧密连接构成^[68]。紧密连接是位于上皮细胞顶端的主要细胞间连接,以环状方式包裹细胞,将邻近的上皮细胞紧密连接,既是离子通道,也是抵御有害物质的屏障^[69-70]。ZO-1是紧密连接的重要组成部分,作为紧密连接的支架蛋白,具有多个专门用于与蛋白质相互作用的结构域,可与Claudins、Occludin等多种蛋白质结合^[71]。Claudin-1对紧密连接完整性具有重要作用,可调节离子和小分子在邻

近细胞中的细胞旁转运、细胞间通讯和上皮细胞稳态,并且 *Claudin-1* 表达的增加可促进细胞增殖^[72-73]。Occludin 是一种可调节内皮和上皮结构和功能的多功能紧密连接蛋白,可参与调节大分子的细胞旁转运,也可作为还原型烟酰胺腺嘌呤二核苷酸(nicotinamide adenine dinucleotide, NADH)氧化酶影响细胞代谢^[74-75]。饲料中纤维水平会影响猪肠道中紧密连接蛋白的表达。Liu 等^[76]研究表明在仔猪饲料中添加 4.3% 麦麸可增加空肠和回肠中 *ZO-1* 和 *Claudin-1* 基因表达。Chen 等^[77]研究报道用 10% 麦麸替代断奶仔猪饲料中 10% 膨化大豆可以显著提升仔猪回肠中 *ZO-1* 和 *Occludin* 的基因表达量。Liu 等^[78]分别用纤维含量为 3.14% 的基础饲料和 6.86% 的高纤维饲料饲喂桃园猪,研究发现饲喂高纤维饲料与基础饲料的猪相比只显著提升了空肠中 *Claudin-1* 和 *Occludin* 的表达量,并提高了回肠中 *ZO-1* 的表达量。本试验结果表明巨菌草替代 10% 基础饲料可显著提升育肥从江香猪回肠 *ZO-1* 的基因表达量,替代 20% 基础饲料可显著提升空肠 *Occludin* 和回肠 *ZO-1* 的基因表达量,与前人研究结果趋于一致。表明饲料中纤维水平上升,可以提高肠道紧密连接蛋白的表达,从而改善肠道屏障完整性。

3.9 巨菌草对育肥从江香猪盲肠微生物的影响

肠道菌群的生态系统是复杂且动态的,肠道菌群与宿主存在共生关系,在维持宿主肠道健康中起重要作用^[79]。饲料是影响猪肠道微生物群组成的重要因素^[80]。Alpha 多样性指标中 Chao1 指数和 ACE 指数可反映群落丰富度,Shannon 指数可反映群落多样性^[81]。本试验结果表明巨菌草替代部分基础饲料可显著提高育肥从江香猪盲肠微生物的 Shannon 指数且 PCoA 分析中的菌群位置距离较远,表明巨菌草替代部分基础饲料使菌群多样性提升,菌群结构发生改变。高崇敏等^[82]研究显示在育肥猪饲料中添加 10% 桂引象草(*Pennisetum purpureum* cv. *Guiminyin*)可显著提升 Chao1、ACE、Shannon 指数。Li 等^[83]研究也发现在生长猪饲料中添加 16% 麦麸可显著提升 Shannon 和 Chao1 指数。这些研究结果均表明饲料中纤维水平上升可使菌群多样性上升,本试验结果与其基本一致。

本试验 3 个组别优势菌门均为厚壁菌门、拟杆菌门和螺旋体门,与前人研究结果一致^[84-86]。厚壁菌门可以利用纤维产生短链脂肪酸,尤其是丁酸盐^[87]。拟杆菌门具有强降解蛋白质和碳水化合物的能力,并可分解日粮中多种难以消化的植物多糖,例如纤维素、果胶和木聚糖等^[88]。本试验还显示巨菌草替代部分基础饲料可使螺旋体门呈下降趋势。螺旋体门中含有多种常见于猪肠道的病原微生物,例如密螺旋体属^[89]。Yu 等^[81]研究报道妊娠母猪饲料中以甜菊(*Stevia rebaudiana*)渣为纤维源粗纤维含量 9.15% 和 10.68% 的组别与对照组相比可显著降低母猪粪便中 *Treponema_2* 的相对丰度。

本试验中排名前 10 的属为乳杆菌属、链球菌属、毛螺菌科未分类菌属、UCG-005、密螺旋体属、*norank_f__p-251-o5*、狭义梭菌属 1、克里斯滕森菌科 R-7 群、普雷沃菌科_UCG-003 菌属、土孢杆菌属。此外,与对照组相比,试验 I 组和试验 II 组在属水平上链球菌属相对丰度显著下降,密螺旋体属呈下降趋势,毛螺菌科未分类菌属呈上升趋势。链球菌属中部分菌群是致病菌,可能引起猪的多种疾病,如脑膜炎、败血症和关节炎^[42,90]。Gao 等^[91]研究表明在生长育肥藏猪饲料中添加 50% 苜蓿,结肠链球菌属丰度会显著下降。*Lachnospiraceae* 与纤维降解和短链脂肪酸的产生有关^[92]。Pu 等^[93]研究发现在育肥猪饲料中用脱脂米糠作为纤维源替代部分玉米可显著提升 *unclassified_f__Lachnospiraceae* 菌群相对丰度并显著降低链球菌属相对丰度。Petry 等^[94]研究发现在后备母猪中,与饲料中含有 7.5% 中性洗涤纤维的低纤维组相比,含有 21.9% 中性洗涤纤维的高纤维组 *unclassified_f__Lachnospiraceae* 中的部分菌群丰度上升,链球菌相对丰度下降。本试验中密螺旋体属、毛螺菌科未分类菌属变化与前人研究结果趋势一致。

本试验结果表明用巨菌草替代部分基础饲料可提升菌群多样性,降低链球菌属的丰度,有提高毛螺菌科未分类菌属丰度的趋势。其原因可能是巨菌草替代部分基础饲料使得饲料纤维水平上升,纤维在发酵过程中作为底物被微生物降解发酵成短链脂肪酸,并且形成酸性环境,有助于微生物群的选择性增殖,并且抑制致病菌的生长,提高有益菌的数量,使肠道微生物群组成改变^[46,79]。

4 结论

巨菌草替代部分基础饲料对育肥从江香猪生长性能及胴体性状无显著影响,可增加从江香猪胃的相对重量,增加绒毛高度、降低隐窝深度、提升绒毛比,并显著提高肠道 *GLP-2* 和 *IGF-1R* 基因表达量,有利于肠道发育。此外,可促进肠道 *Occludin* 和 *ZO-1* 基因表达,增强肠道机械屏障功能,降低链球菌属相对丰度并增加有益菌的丰度,有利于肠道健康。巨菌草不计成本时,替代 20% 基础饲料可获得最大经济效益,巨菌草按市场价格 0.35 元·kg⁻¹ 购买时,替代 10% 基础饲料为宜。

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