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## 动物营养专题

### 本期导读

#### ► 学术文献

1. 北京市种猪基因组选择育种平台的构建与应用
2. 益生元和 $\beta$ -葡聚糖作为肠道改良剂饲料添加剂对断奶仔猪生长性能、蛋白质利用状态及干物质和乳糖消化率的调节作用
3. 肠道菌群及其代谢产物调节动物线粒体功能的研究进展
4. 国内种养复合循环农业模式应用现状
5. 以枯草芽孢杆菌为基础的多菌株直接饲喂微生物对断奶仔猪免疫指标和肠道形态的影响

中国农业科学院农业信息研究所  
联系人：熊本海；郑姗姗；顾亮亮  
联系电话：010-62816017  
邮箱：[agri@ckcest.cn](mailto:agri@ckcest.cn)  
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## 学术文献

### 1. 北京市种猪基因组选择育种平台的构建与应用

**简介:** 2006年,北京市建立了种猪遗传评估数据平台。截止到2021年底,平台共收录371.46万头种猪系谱信息,51.23万条达100 kg体重日龄记录,50.90万条达100 kg活体背膘厚记录和45.15万条窝产仔记录。2015年,北京市将常规育种与基因组育种相结合,启动了种猪基因组选择育种平台构建工作,北京市种猪遗传评估进入基因组选择时代。截止到2021年底,平台建立了大白猪基因组选择参考群体,规模达到5 335头;开发基因组遗传评估系统,实现了将复杂的基因组选择计算过程转化为“一键式”操作;利用一步法(ssGBLUP)对9个种猪场的4 631头大白猪进行基因组遗传评估。基因组选择实施后,选择准确性大幅提高。早期选择时,达100 kg体重日龄的育种值准确性由0.56提高至0.66,达100 kg活体背膘厚的基因组育种值准确性由0.56提高至0.70,总产仔数育种值准确性由0.41提高至0.60。终选时,达100 kg体重日龄的育种值准确性由0.69提高至0.79,达100 kg活体背膘厚的基因组育种值准确性由0.72提高至0.80,总产仔数性状育种值准确性由0.41提高至0.61。基因组选择技术的应用实现了种猪早期选择,减少了饲养成本和常规测定成本,提高了选育效率,增强了企业的市场竞争力。

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### 2 Prebiotics and $\beta$ -Glucan as gut modifier feed additives in modulation of growth performance, protein utilization status and dry matter and lactose digestibility in weanling pigs (益生元和 $\beta$ -葡聚糖作为肠道改良剂饲料添加剂对断奶仔猪生长性能、蛋白质利用状态及干物质和乳糖消化率的调节作用)

**简介:** There are growing interests in developing novel gut modifier feed additives and alternative therapeutics to replace antimicrobials to enhance efficiency of nutrient utilization and to address the antimicrobial resistance threat to public health facing the global pork production. Biological mechanisms of supplementing lactose for enhancing weanling pig growth and nitrogen utilization are unclear. Thus, this study was prompted to determine effects of dietary supplementation of 3 prebiotics and oat  $\beta$ -glucan vs. a sub-therapeutic antibiotic on growth performance, whole-body protein utilization status, the apparent total tract dry matter (DM) and lactose digestibility in weanling pigs fed corn and soybean meal (SBM)-based diets. Six experimental diets were formulated with corn (40%), SBM (28%) and supplemented with dried whey powder (20%) and fish meal (9%) with titanium oxide (0.30%) as the digestibility marker. Diet 1 (NC, negative control), as the basal diet, contained no antibiotics and no supplemental prebiotics or  $\beta$ -glucan. Diet 2 (PC, positive control), contained an antibiotic premix (Lincomix-44 at 0.10%) in the basal diet at the expense of cornstarch. Diets 3, 5 and 6 contained 0.75% of the three test prebiotics of retrograded cornstarch (Diet 3), Fibersol-2 (Diet 5, a modified digestion-resistant maltodextrin) and inulin (Diet 6), and the viscous soluble fiber oat  $\beta$ -glucan (Diet 4),

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respectively, at the expense of cornstarch. A total of 144 Yorkshire pigs, at the age of 21 days (d) and an average body weight (BW) of 5.5 kg, were allocated to 12 floor pens with 3 barrows and 3 gilts per pen, and fed one of the 6 diets for 21 d in 2 study blocks according to a completely randomized block design. Initial and final pig BW, average daily gain (ADG), average daily feed intake (ADFI), representative pig plasma urea concentration as well as the apparent total tract DM and lactose digestibility during d 8-15 were measured. Analyses of variances, Dunnett's and Tukey's tests were conducted on the endpoints by using the SAS mixed model. There were no differences ( $P > 0.05$ ) in ADG, ADFI, feed to gain ratio, plasma urea concentration, the apparent total tract apparent DM and lactose digestibility and the predicted whole-gut lactase digestive capacity among the diets, as examined by the Tukey's test. There were no differences ( $P > 0.05$ ) in these endpoints between each of the four treatment diets and the NC or the PC diet as examined by the Dunnett's test. The total tract lactose digestibility was determined to be at 100%. The predicted whole-gut lactase digestive capacity was about eight times of the daily lactose intake when dietary lactose contents were supplemented at 10 - 12% (as-fed basis). In conclusion, dietary supplementation (at 0.75%) of the prebiotics and the oat  $\beta$ -glucan did not significantly affect the major growth performance endpoints, whole-body protein utilization status as well as the apparent total tract DM and lactose digestibility in the weanling pigs fed the corn and SBM-based diets. The promoting effect for growth and nitrogen utilization associated with dietary supplementation of lactose is due to the fact that lactose is a completely and rapidly digestible sugar rather than acting as an effective prebiotic in weanling pig nutrition.

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### 3. 肠道菌群及其代谢产物调节动物线粒体功能的研究进展

**简介:** 线粒体是动物细胞生产能量的主要场所,可参与三磷酸腺苷的产生、细胞线粒体Ca<sup>2+</sup>稳态的维持,在调节动物机体能量代谢方面发挥重要的作用。目前,研究发现肠道微生物及其代谢产物可影响细胞线粒体代谢水平和功能,参与调节机体营养物质代谢周转速度,最终影响畜禽生长发育及饲料转化效率等。本文在总结线粒体生物学功能的基础上,重点阐述了肠道微生物及其代谢产物对线粒体功能的调节作用及影响因素,旨在为饲料营养手段介导肠道微生物-宿主线粒体途径调节动物生长发育和肠道健康提供理论参考。

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### 4. 国内种养复合循环农业模式应用现状

**简介:** 基于农业生态系统与种养生产体系特征,综述了种植业与生猪养殖业、草食动物养殖业相结合的种养结合循环农业模式及稻田种养循环模式,系统阐述了“猪-沼/肥-

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农田种植系统”、“猪-沼/肥-园种植系统”、“猪-沼/肥-草”、“猪-沼/肥-藻”与“牧草（秸秆）-草食动物养殖（牛、羊）-沼/肥-种植系统”循环模式及“稻-鱼”种养、稻鸭共生、稻虾共作等循环模式应用现状。指出了饲料转化及养殖废弃物还田利用是调控种养复合循环模式养分流动的关键环节,参考种植系统作物种类与养分需求、养殖系统对饲料质量需求特点及种植系统对养殖废弃物养分的消纳能力等,合理配置种养复合系统生物结构及时空结构,提高种养复合系统养分循环利用效率是实现种养平衡的关键。提出了在传统循环农业模式的基础上,创新发展环境保育型种养复合循环农业模式,并构建种养复合循环系统养分资源综合管理体系是实现国内种植业、畜禽养殖业绿色生产与可持续发展的重要途径。

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## **5 . Effects of a multi-strain Bacillus subtilis-based direct-fed microbial on immunity markers and intestinal morphology in diets fed to weanling pigs. (以枯草芽孢杆菌为基础的多菌株直接饲喂微生物对断奶仔猪免疫指标和肠道形态的影响)**

简介: The objective of this experiment was to evaluate the effects of a multi-strain Bacillus subtilis-based direct-fed microbial (DFM) on nursery pig health as indicated by intestinal mucosal and blood plasma immunological markers and intestinal morphology. Eighty pigs, of equal number of barrows and gilts (initial BW: 7.0  $\pm$  0.60 kg), weaned at 21  $\pm$  1 d of age were randomly allotted to sixteen pens, with five pigs per pen. Two dietary treatments were implemented, a basal control (CON) and a basal control plus DFM (CDFM). Both diets were corn, soybean meal, and distillers dried grains based and were formulated to meet or exceed all nutritional requirements (NRC, 2012) and manufactured on site. Diets were fed for 42 d. On d 21 and 42 of the experiment, one pig per pen was randomly selected and euthanized, with equal number of males and females represented. Blood samples were collected prior to euthanasia for assessment of plasma concentrations of immunoglobulin A (IgA) and intestinal fatty acid binding protein. Segments of the gastrointestinal tract including duodenum, jejunum, ileum, ascending and distal colon were removed for analysis of intestinal morphology, and levels of interleukin 6, interleukin 10 (IL-10), and tumor necrosis factor alpha. Jejunal villus height was greater in the CDFM pigs as compared with CON pigs ( $P = 0.02$ ) and ascending colon crypt depth tended to be greater on d 21 ( $P = 0.10$ ). Compared to CON, CDFM significantly increased overall plasma IgA ( $P = 0.03$ ) (0.58 vs. 0.73  $\pm$  0.05 mg/mL, respectively), while it tended to increase plasma IgA ( $P = 0.06$ ) on d 21 (0.34 vs. 0.54  $\pm$  0.07 mg/mL, respectively) and tended to increase overall IL-10 ( $P = 0.10$ ) in the jejunum (113 vs. 195  $\pm$  35 pg/mL, respectively). Addition of a multi-strain Bacillus subtilis-based DFM may have an early benefit to nursery pig health status, observed through specific changes in morphology and both systemic and localized immunological markers.

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