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动物营养专题

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前沿资讯

1．法国报刊高度评价越南成功研制非洲猪瘟疫苗

简介：在越南宣布成为世界上第一个成功研发、商业生产和签发非洲猪瘟疫苗上市许可的国家后，法国《费加罗报》认为，越南的这一成就有助于击退非洲猪瘟疫情。该报称，越南首次宣布与美国研究人员合作开发猪用疫苗来抗击非洲猪瘟疫情，其给越南乃至世界的畜牧业带来希望。此前，6月3日，越南农业与农村发展部在河内举行仪式，对外公布非洲猪瘟疫苗研究生产成果，同时颁发疫苗上市许可。越南中央动物药业股份公司（Navetco）研发和生产的非洲猪瘟疫苗的商品名为NAVET-ASFVAC。越南农业与农村发展部副部长冯德进表示，非洲猪瘟疫苗可有效预防疾病6个月。该疫苗的安全性和有效性也得到了美国农业部农业研究局的证实。非洲猪瘟是一种对人类无害，但对牲畜具有破坏性影响，致死率几乎为100%的病毒感染性疾病。2019年2月，非洲猪瘟病毒在越南发现，致使越南要摧毁数百万头病猪。 越南成功研制非洲猪瘟疫苗给越南和其他国家带来有效控制非洲猪瘟疫情的希望。

来源：食品伙伴网

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http://agri.ckcest.cn/file1/M00/03/34/CsgkOYb9O3iAUUTOAApGrchzSPY192.pdf

2．家畜营养与调控团队揭示早期营养干预提高仔猪生长性能和肠道健康的机制

简介：近日，中国农业科学院北京畜牧兽医研究所家畜营养与调控科技创新团队揭示了早期营养干预通过调节肠道微生物组成提高仔猪生长性能和肠道健康的机制。相关研究成果发表在知名期刊《营养前沿（ Frontiers in Nutrition ）》（IF=6.576）上。断奶仔猪腹泻是引起仔猪死亡的重要原因之一，每年有高达20-30%的仔猪腹泻，直接经济损失达2400亿元，严重制约我国养猪业的发展。本研究通过早期营养干预调节仔猪肠道菌群组成，改善仔猪生长性能和肠道健康，为解决出生仔猪腹泻以及营养不足导致的生长缓慢提供了新思路。研究发现，通过对初生仔猪补饲合成奶进行早期营养干预，显著提高了断奶仔猪生长性能、肝重、脾重，降低了仔猪断奶前后腹泻率；显著上调了仔猪结肠黏膜 ZO-1 、 Occludin 、 Claudin4 、 GALNT1 、 B3GNT6 和 MUC2 mRNA 表达水平，并降低了血清AKP活性和血浆LPS含量。早期营养干预后仔猪杯状细胞数量和结肠隐窝深度显著提高，并且炎性因子表达水平显著降低。另一方面，早期营养干预也显著提高了仔猪结肠食糜和黏膜中乳酸杆菌的相对丰度。 Lactobacillus 的丰度与 ZO-1 、 Claudin4 和 GALNT1 mRNA相对表达量呈正相关，与结肠食糜和黏膜中 MCP-1 水平呈负相关。综上所述，早期营养干预可通过调节仔猪肠道菌群组成改善仔猪生长性能、结肠屏障和结肠炎症。

来源：中国农业科学院北京畜牧兽医研究所官网

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http://agri.ckcest.cn/file1/M00/03/34/CsgkOYb9VOeAYpjLAAk2X4pwQfU852.pdf

学术文献

1．鉴别非洲猪瘟野毒株与基因缺失疫苗株的三重TaqMan探针荧光定量PCR检测方法的建立

简介：为建立一种鉴别非洲猪瘟野毒株与基因缺失疫苗株的TaqMan探针荧光定量PCR检测方法，根据非洲猪瘟病毒（ASFV）的B646L、EP402R、MGF360-13L基因序列，分别设计PCR引物和TaqMan探针，绘制标准曲线，并进行重复性试验、特异性试验、敏感性试验与临床样品检测，建立三重TaqMan探针荧光定量PCR检测方法。结果显示，以B646L、EP402R和MGF360-13L重组质粒为标准品绘制的标准曲线具有良好的线性关系，线性相关系数(R2)分别为0.995、0.997和0.997；建立的方法与多种猪常见病原不存在交叉反应，特异性良好；对B646L、MGF360-13L与EP402R基因的检测下限均为10 copies/μL，变异系数均＜2%，该方法灵敏度高；当临床样品稀释至10-5时，即滴度为102.5 TCID50/mL时仍能检测到病毒粒子，具有较高的临床使用价值。本研究建立了一种高效、灵敏、特异的ASFV分子检测方法，对ASF风险预警具有重要意义。

来源：中国知网

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http://agri.ckcest.cn/file1/M00/10/06/CsgkOGKmn5mAIpnMAAkfTp5NizQ850.pdf

2．Effect of supplemental myo-inositol on growth performance and apparent total tract digestibility of weanling piglets fed reduced protein high phytate diets and intestinal epithelial cell proliferation and function(补充肌醇对饲喂低蛋白高植酸日粮的断奶仔猪生长性能和表观全肠道消化率的影响及肠上皮细胞增殖和功能的影响)

简介：Myo-inositol is a breakdown product of phytate produced in the gut through the action of phytase. Although the effect of phytase-released phosphorus (P) on growth performance of animals has been well characterized, there is still little understanding of effect of myo-inositol. The first objective of this study was to determine the effects of added myo-inositol to a phytate rich low protein diet on growth performance and apparent total tract digestibility (ATTD) in growing piglets. The second objective was to determine whether myo-inositol could directly affect intestinal epithelial cell proliferation and function for which we used intestinal porcine epithelial cells (IPEC-J2). A total of 128 weanling piglets were allotted to four dietary treatments consisting of eight replicates per treatment and four piglets per replicate in a randomized complete block design for four weeks. The four experimental diets comprised the positive control (PC; 20% crude protein (CP), negative control (NC; 17% CP), negative control plus 2.0g/kg myo-inositol (NC+INO; 17% CP) and negative control plus 3000FTU/kg phytase (NC+PHY; 17% CP). Average daily feed intake (ADFI), average daily gain (ADG), gain-feed ratio (G: F) were recorded. Phytase supplementation in the protein-deficient NC diet increased the G:F ratio ($P < 0.05$) without myo-inositol effect on growth performance. Phosphorus digestibility in the phytase supplemented group increased compared to the PC, NC, and NC+INO groups whereas plasma myo-inositol concentration was significantly higher ($P < 0.05$)

in the NC+INO group. Due to lack of myo-inositol effect on growth performance, an additional in vitro study was conducted to determine direct effect of myo-inositol on the intestinal epithelium that might not be reflected in growth performance. Myo-inositol increased the mRNA abundance of selected nutrient transporters in a concentration-dependent manner ($P < 0.05$). Myo-inositol also enhanced barrier integrity in the IPEC-J2 monolayer by increasing the transepithelial electrical resistance (TEER) with reduced paracellular permeability of FITC-dextran ($P < 0.05$). In conclusion, despite the lack of myo-inositol effect on animal performance, the in vitro data indicates that myo-inositol may directly regulate gut barrier integrity. Addition of myo-inositol to pig diets at levels that enhance intestinal epithelial cell function may result in effects on growth performance and gut health of pigs.

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http://agri.ckcest.cn/file1/M00/03/34/CsgkOYb9WRyAZ81ZABIR6y7KOwU612.pdf

3．Genetic relationships between efficiency traits and gut microbiota traits in growing pigs fed a conventional or a high fiber diet(饲喂常规或高纤维日粮的生长猪的效率性状与肠道菌群性状之间的遗传关系)

简介：In pigs, the gut microbiota composition plays a major role in the process of digestion, but is influenced by many external factors, especially diet. To be used in breeding applications, genotype by diet interactions on microbiota composition have to be quantified, as well as their impact on genetic covariances with feed efficiency (FE) and digestive efficiency (DE) traits. This study aimed at determining the impact of an alternative diet on variance components of microbiota traits (genera and alpha diversity indices) and estimating genetic correlations between microbiota and efficiency traits for pigs fed a conventional (CO) or a high fiber (HF) diet. Fecal microbes of 812 full-siblings fed a CO diet and 752 pigs fed the HF diet were characterized at 16 weeks of age by sequencing the V3-V4 region of the 16S rRNA gene. A total of 231 genera were identified. Digestibility coefficients of nitrogen, organic matter and energy were predicted analyzing the same fecal samples with near infrared spectrometry. Daily feed intake, feed conversion ratio, residual feed intake and average daily gain (ADG) were also recorded. The 71 genera present in more than 20% of individuals were retained for genetic analyses. Heritability (h²) of microbiota traits were similar between diets (from null to 0.38 ± 0.12 in the CO diet and to 0.39 ± 0.12 in the HF diet). Only three out of the 24 genera and two alpha diversity indices with significant h² in both diets had genetic correlations across diets significantly different from 0.99 ($P < 0.05$), indicating limited genetic by diet interactions for these traits. When both diets were analyzed jointly, 59 genera had h² significantly different from zero. Based on the genetic correlations between these genera and ADG, FE and DE traits, three groups of genera could be identified. A group of 29 genera had abundances favorably correlated with DE and FE traits, 14 genera were unfavorably correlated with DE traits, and the last group of 16 genera had abundances with correlations close to zero with production traits. However, genera

abundances favorably correlated with DE and FE traits were unfavorably correlated with ADG, and vice versa. Alpha diversity indices had correlation patterns similar to the first group. In the end, genetic by diet interactions on gut microbiota composition of growing pigs were limited in this study. Based on this study, microbiota-based traits could be used as proxies to improve FE and DE in growing pigs.

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