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动物营养专题

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学术文献

1. CRISPR/Cas9技术在畜禽育种中的研究进展

简介: 利用传统方法在畜禽特定基因座上进行基因组修饰时, 只能通过在体细胞中进行同源重组再经细胞核移植实现。传统同源重组方法的困难性和低效性阻碍了基因修饰在畜禽遗传育种中的广泛应用。近年来, 位点特异性核酸内切酶的发现为靶向基因修饰提供了一条更直接的途径, 主要由于这些酶能直接在DNA序列上进行一步式的基因编辑。成簇规律间隔短回文重复序列/Cas关联蛋白9 (clustered regularly interspaced short palindromic repeat/CRISPR associated protein 9, CRISPR/Cas9) 是一种RNA导向的DNA内切酶, 精准定位于特定的靶位点, 高效完成RNA导向的DNA识别及编辑。CRISPR/Cas9技术作为精准而强大的第3代基因组编辑工具, 已经成功应用于猪、牛、山羊、绵羊和鸡上, 这些CRISPR/Cas9基因编辑畜禽可作为研究人或畜禽生理和病理的生物模型、生产功能性蛋白质的生物反应器或器官移植的供体。特别是在畜禽生产方面, CRISPR/Cas9基因编辑可用于改善生产遗传特性及畜产品质量, 提高畜禽对疾病的抵抗力。作者对当前畜禽中特定位点基因组修饰的CRISPR/Cas9技术的原理及基因组编辑在畜禽育种中应用的最新进展进行了综述, 以为推进CRISPR/Cas9技术在畜禽育种中的研究提供参考。

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<http://agri.ckcest.cn/file1/M00/0F/FD/Csgk0GJNQwKAOPiqAATi7EGolfs248.pdf>

2 . Effect of different dosage of sodium butyrate and niacin on growth, fecal microbiota and vitamin B metabolism in weaned piglets (不同剂量丁酸钠和烟酸对断奶仔猪生长、粪便微生物及维生素B代谢的影响)

简介: AIMS: Our study aimed to evaluate the effects of different dosages of sodium butyrate and niacin on the growth performance, fecal vitamin B and microbiota in weaned piglets. METHODS AND RESULTS: Seventy-two weaned piglets (Duroc×Landrace×Yorkshire, age of 21d) were randomly assigned to 1 of 6 treatments (12 pigs / treatment): the control (CT) group was administered a basal diet. The groups which concentration ratio of sodium butyrate to niacin were 100: 1, 100: 2, 100: 4, 100: 8 and 100: 16 (BN1, BN2, BN4, BN8, BN16) were administered a basal diet supplemented with 2000 mg·kg⁻¹ sodium butyrate and 20 mg·kg⁻¹, 40 mg·kg⁻¹, 80 mg·kg⁻¹, 160 mg·kg⁻¹ or 320 mg·kg⁻¹ niacin. After 14-d treatment, the samples were collected. The results showed that feed conversion rate (FCR) was reduced and average daily gain (ADG) was increased in BN2 (P < 0.05). The diarrhea index of pigs decreased with the low supplement. Additionally, compared with CT group, other groups significantly increased (P < 0.05) the abundance of Firmicutes (BN4, phylum), Lactobacillaceae (BN8, family), Megasphaera (BN8, genus), and Lactobacillus (BN8, genus). Furthermore, the sodium butyrate and niacin supplementation influence vitamin B1, vitamin B2, pyridoxine, niacin, nicotinamide, and vitamin B12 (P < 0.05). Correlation analysis of the association of

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microorganisms with vitamin B indicated that changes of vitamin B metabolism have potential correlation with alterations of fecal microbiota in weaned piglets. CONCLUSIONS: The results indicated that adding of sodium butyrate and niacin in the diet could promote the performance and improve the fecal microbiota and vitamin B metabolism in weaned piglets. SIGNIFICANCE AND IMPACT OF THE STUDY: Our study might provide clues to the research of correlations between fecal bacteria and fecal vitamin B, and these findings will contribute to the direction of future research in weaned piglets.

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<http://agri.ckcest.cn/file1/M00/0F/FD/Csgk0GJNSVGAd8EbABV9eRS-fik453.pdf>

3 . Orally active bivalent VHH construct prevents proliferation of F4+ enterotoxigenic Escherichia coli in weaned piglets (口服活性二价VHH构建阻止断奶仔猪F4肠毒素大肠杆菌的增殖)

简介: A major challenge in industrial pig production is the prevalence of post-weaning diarrhea (PWD) in piglets, often caused by enterotoxigenic Escherichia coli (ETEC). The increased use of antibiotics and zinc oxide to treat PWD has raised global concerns regarding antimicrobial resistance development and environmental pollution. Still, alternative treatments targeting ETEC and counteracting PWD are largely lacking. Here, we report the design of a pH, temperature, and protease-stable bivalent VHH-based protein BL1.2 that cross-links a F4+ ETEC model strain by selectively binding to its fimbriae. This protein inhibits F4+ ETEC adhesion to porcine epithelial cells ex vivo and decreases F4+ ETEC proliferation when administrated as a feed additive to weaned F4+ ETEC challenged piglets. These findings highlight the potential of a highly specific bivalent VHH-based feed additive in effectively delimiting pathogenic F4+ ETEC bacteria proliferation in piglets and may represent a sustainable solution for managing PWD while circumventing antimicrobial resistance development.

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4. 基于SNP芯片的海南猪全基因组选择信号分析

简介: 旨在通过检测海南猪全基因组上的选择信号,以挖掘与海南猪重要经济性状相关的候选基因,并解析讨论海南猪在进化驯化历史中的受选择情况。本研究利用68头海南猪的GeneSeek Genomic Profiler Procine SNP 80K芯片数据,使用整合单倍型分数(integrated haplotype score, iHS)的方法进行全基因组选择信号检测,并进行了全基因组长片段纯合(runs of homozygosity, ROH)检测分析;以“标准化iHS分数>1.96 (P<0.05)”为阈值筛选候选位点,并向上、下游各延伸200 kb作为iHS方法检测到的候选区域,定义其中与ROH检测得到的片段发生“完全重叠”的区段为潜在受选择区域。为进一步探索海南猪选择信号的生物学功能,本研究进行了包含基因注释、QTL

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(quantitative trait locus) 探索和富集分析在内的生物信息学分析。该研究对经过质量控制后剩余的44 578个SNPs, 使用iHS方法共检测到395个潜在受选择位点, 检测得到172个ROH片段, 获得136个潜在受选择区域, 注释到469个候选基因。对潜在受选择区域进行QTLs探索分析, 结果揭示了海南猪的选择信号多与其肉质性状、生长性状、抗病性状相关; 此外, 与海南猪的初情期启动日龄相关的QTL主要被报道与SSC12(Sus Scrofa chromosome 12)上的潜在受选择区域重叠。此外, 通过候选基因的GO(gene ontology)和KEGG(kyoto encyclopedia of genes and genomes)通路富集分析发现, 有91个候选基因在21项功能条目(P<0.05)上显著富集, 主要集中在生长代谢、免疫应答和雌激素信号通路相关的条目上。本研究揭示了海南猪群体在其驯化历史上可能受到的选择情况。研究表明, 在海南猪全基因组范围内进行选择信号检测, 有助于进一步了解海南猪的进化历史及其重要经济性状的遗传机制, 在一定程度上为华南型地方猪种种质资源的保存利用和相关研究提供参考。

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5. 菌糠饲料资源开发研究进展

简介: 中国食用菌产业迅速发展, 随之产生了大量的食用菌副产物——菌糠。菌糠含有丰富的营养成分, 是一类优质的非常规饲料原料。该文就菌糠的营养价值、加工调制方法、菌糠饲料化开发利用情况以及在动物生产中的应用进展进行综述, 旨在为高效开发利用菌糠资源提供参考依据。

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