



2022年第37期总360期

动物营养专题

本期导读

► 学术文献

1. 猪DNA甲基转移酶基因家族进化分析
2. 槲皮素对PEDV感染幼龄仔猪的生长性能、血液生化指标和肠道吸收与屏障功能的影响
3. 富含游离氨基酸的日粮中含有快速但不缓慢消化的碳水化合物，促进了氨基酸从肠道的吸收和通过猪骨骼肌的净流量
4. 猪群体一步法基因组选择应用效果评估
5. 肠道微生物群和宿主遗传有助于常规和高纤维饲料喂养的生长猪消化和饲料效率性状的表型变异

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
2022年9月12日

更多资讯 尽在农业专业知识服务系统：<http://agri.ckcest.cn/>

学术文献

1. 猪DNA甲基转移酶基因家族进化分析

简介: 【目的】探究猪DNA甲基转移酶 (DNMT) 基因家族的基因特性及表达模式。【方法】利用生物信息学方法鉴定猪全基因组范围的DNMT基因家族, 并对其染色体定位、理化性质、蛋白质结构、亚细胞定位、基因结构、保守基序、系统进化关系、共线性关系和基因表达模式进行分析。【结果】共鉴定得到5个猪DNMT基因家族成员: PigDNMT1、PigDNMT2、PigDNMT3、PigDNMT4和PigDNMT5, 分别位于2、3、13、14、17号染色体上。猪DNMT基因家族进化树分析发现, PigDNMT1和PigDNMT4、PigDNMT2和PigDNMT5的亲缘关系较近。PigDNMT2和PigDNMT5具有相同数量和排列顺序的保守基序, 但在基因结构上差异较大。系统进化树结果揭示, 猪、人、小鼠和牛的DNMT基因家族分为4个亚族, 其中猪与牛的DNMT基因家族亲缘关系更近。基因共线性分析显示, 猪与人、小鼠、牛之间都具有4对直系同源DNMT基因, 表明4个物种的DNMT基因间存在较强的共线性关系。猪DNMT家族蛋白长度在228~1 706个氨基酸之间, 分子质量在26 133.32~192 267.80 u之间, 等电点在6.00~9.06之间。二级结构预测分析结果显示, 猪DNMT蛋白主要由无规则卷曲组成。亚细胞定位分析发现, 5个猪DNMT蛋白定位于细胞核。母猪性腺轴的转录组数据分析发现, PigDNMT1在下丘脑、垂体和卵巢组织中随着初情启动过程而展现出不同的表达模式。【结论】本研究在猪基因组上共鉴定出5个DNMT基因, 并发现性腺轴组织中的PigDNMT1在初情启动过程中呈现出不同的表达模式, 为解析猪DNMT基因家族功能提供一些参考。

来源: 中国知网

发布日期: 2022-08-25

全文链接:

http://agri.ckcest.cn/file1/M00/03/3D/Csgk0Ydr_yAXuF5AA1802B4cnw234.pdf

2. 槲皮素对PEDV感染幼龄仔猪的生长性能、血液生化指标和肠道吸收与屏障功能的影响

简介: 【目的】试验旨在探讨槲皮素在防治仔猪感染猪流行性腹泻病毒 (PEDV) 中的作用。【方法】选取18头体重相近、健康的7日龄仔猪 (杜×长×大), 随机分为3组 (对照组、PEDV组和PEDV+槲皮素组), 每组6个重复, 每个重复1头猪, 试验期共11 d。经过3 d适应期后, 于试验第4~10天给PEDV+槲皮素组仔猪口腔灌服10 mg/kg BW的槲皮素, 其他组仔猪口腔灌服等体积的人工乳, 于试验第8天给PEDV组与PEDV+槲皮素组仔猪口腔灌服 $1 \times 10^{4.5}$ TCID₅₀的PEDV, 对照组灌服等体积的PBS溶液。试验第11天早上空腹称重, 全部仔猪灌服D-木糖 (0.1 g/kg BW), 1 h后经前腔静脉采血, 检测血液生化指标、血浆二胺氧化酶 (DAO) 活性和D-木糖含量; 将所有仔猪屠宰取空肠黏膜, 检测肠道屏障相关基因, 包括肠绒毛蛋白 (villin), 紧密连接蛋白-1 (claudin-1), 闭合蛋白 (occludin) 和肠型脂肪酸结合蛋白 (iFABP) 的相对表达量。【结果】与对照组相比, PEDV组仔猪平均日增重显著下降 ($P < 0.05$), 粪便评分显著升高 ($P < 0.05$); 血液中高密度脂蛋白含量显著降低 ($P < 0.05$), 肌酐和尿素氮的含量显著提高 ($P < 0.05$); 血浆中D-木糖含量显著降低 ($P < 0.05$); 空肠claudin-1、iFABP基因的相对表达量显著下调 ($P < 0.05$)。与PEDV组相比, PEDV+槲皮素组仔猪平均日增重和血浆D-木糖含量显著升高 ($P < 0.05$); 血液中肌酐和尿素氮的含量显著降低 ($P < 0.05$); 空肠claudin-1、villin和iFABP基因

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

的相对表达量显著上调 ($P < 0.05$)。【结论】10 mg/kg BW 槲皮素可在一定程度上缓解 PEDV 感染导致的仔猪生长抑制和肾功能损伤，增强肠道吸收与屏障功能。

来源：中国知网

发布日期:2022-08-25

全文链接:

<http://agri.ckcest.cn/file1/M00/10/0F/Csgk0GMVUnKAIi13AAWd0zGIzAk949.pdf>

3 . Free Amino Acid-enriched Diets Containing Rapidly but Not Slowly Digested Carbohydrate Promote Amino Acid Absorption from Intestine and Net Fluxes across Skeletal Muscle of Pigs (富含游离氨基酸的日粮中含有快速但不缓慢消化的碳水化合物，促进了氨基酸从肠道的吸收和通过猪骨骼肌的净流量)

简介: BACKGROUND: The approach to matching appropriate carbohydrates alongside free amino acids to achieve optimal muscle growth remains unclear. OBJECTIVES: We investigated whether the consumption of a diet containing rapidly digested carbohydrate and free amino acids can enhance intestinal absorption and muscular uptake of amino acids in pigs. METHOD: Twelve barrows (28 kg; 11 wk old) with catheters installed in the portal vein, mesenteric vein, femoral artery, and femoral vein were randomly assigned to consume one of two free amino acid-enriched diets (3.34%) containing rapidly [waxy corn starch (WCS)] or slowly [pea starch (PS)] digested carbohydrate for 27 d. Blood was collected to determine the fluxes of plasma glucose and amino acids across the portal vein and the hindlimb muscle. Dietary in vitro carbohydrate digestive rates were also determined. Data were analyzed using repeated measures (Time \times Group) ANOVA. RESULTS: Carbohydrate in vitro cumulative digestibility at 30 and 240 min was 69.00% and 95.25% for WCS and 23.25% and 81.15% for PS, respectively. The animal experiment presented WCS increased individual amino acids (Lys, 0.67 vs. 0.53 mmol/min; Thr, 0.40 vs. 0.29 mmol/min; Ile, 0.33 vs. 0.22 mmol/min; Glu, 0.51 vs. 0.35 mmol/min and Pro, 0.51 vs. 0.27 mmol/min), essential amino acid (EAA; 3.26 vs. 2.65 mmol/min), and branched-chain amino acid (BCAA; 0.86 vs. 0.65 mmol/min) fluxes across the portal vein during 8 h postprandial, as well as individual amino acids (Ile, 0.08 vs. 0.02 mmol/min; Leu, 0.06 vs. 0.02 mmol/min and Gln, 0.44 vs. 0.25 mmol/min), EAA (0.50 vs. 0.21 mmol/min), and BCAA (0.17 vs. 0.06 mmol/min) net fluxes across the hindlimb muscle during 8 h postprandial compared with PS ($P < 0.05$). CONCLUSIONS: A diet containing rapidly digested carbohydrate and free amino acids can promote intestinal absorption and net fluxes across hindlimb muscle of amino acids in pigs.

来源：中国知网

发布日期:2022-08-02

全文链接:

http://agri.ckcest.cn/file1/M00/03/3D/Csgk0YdsBFGAR5_UACpa0nQTtZY747.pdf

4. 猪群体一步法基因组选择应用效果评估

简介: 【背景】在提高畜牧生产效率中，遗传育种的贡献率占比最高。通过育种可使畜牧企业提高生产效率，获得最大的经济效益。目前，基因组选择已经成为动植物育种中

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

广泛应用的技术手段。基因组选择能够利用覆盖全基因组的高密度标记对育种值进行估计，与系谱信息相比，利用这些标记得到的个体间平均亲缘关系更加准确，从而能更准确地估计育种值 (Estimate breeding values, EBV)，对个体进行选育。在实际育种中，对所有个体进行基因分型是不现实的，尤其是猪这种个体经济价值较小的物种，这限制了基因组选择在猪育种中的应用。一步法 (single-step genomic best linear unbiased prediction, ssGBLUP) 能够同时利用系谱和基因型信息，允许只测定部分个体的基因型，在保持较高预测准确性的同时，大大降低基因分型成本。目前，已经有很多研究表明，在猪育种中使用基因组选择方法能够提高预测准确性，但在实际育种中，育种成本也是畜牧企业考虑的一个重要问题。因此，如何经济有效地实施育种方案，具有重大的研究价值。【目的】通过对一步法基因组选择在杜洛克猪群体评估效果的研究，为基因组选择育种方案提供依据。【方法】以福建某猪场2009—2018年出生的杜洛克猪群体的3个重要经济性状为研究对象，比较了BLUP、GBLUP和一步法等方法在杜洛克猪生长性状上的基因组预测准确性与估计育种值预测可靠性，探究了当参考群中具有不同比例的基因型个体时，一步法预测准确性的变化规律。【结果】(1) 达100 kg日龄、背膘厚和眼肌面积的遗传力分别为 0.257 ± 0.038 、 0.250 ± 0.039 和 0.399 ± 0.040 ；(2) ssGBLUP相比于BLUP准确性提升14.7%—51.1%；相比于GBLUP准确性提升13.4%—45.7%；(3) 10%—30%的个体有基因型时，ssGBLUP预测的准确性超过BLUP；在40%—60%的个体有基因型时，准确性提升速度降低，趋于平缓。【结论】(1) 与BLUP相比，一步法能提高各性状估计育种值的准确性和可靠性；与GBLUP方法相比，只有无基因型个体的系谱信息时一步法略低于GBLUP，但在加入无基因型个体的表型信息后，一步法表现优于GBLUP。(2) 随着参考群中测定基因型个体的比例逐渐提高，不管使用哪种筛选测定基因型个体的方式 (随机选取和筛选关键个体)，一步法预测效果都逐渐提高。表明，在企业育种预算有限时，即使只测定部分个体基因型，一步法可提高基因组选择的预测效果。

来源：中国知网

发布日期:2022-08-01

全文链接:

http://agri.ckcest.cn/file1/M00/10/0F/Csgk0GMVUBGAQ1qoABFa_dM-bHU987.pdf

5 . Gut microbiota and host genetics contribute to the phenotypic variation of digestive and feed efficiency traits in growing pigs fed a conventional and a high fiber diet (肠道微生物群和宿主遗传有助于常规和高纤维饲料喂养的生长猪消化和饲料效率性状的表型变异)

简介: Background: Breeding pigs that can efficiently digest alternative diets with increased fiber content is a viable strategy to mitigate the feed cost in pig production. This study aimed at determining the contribution of the gut microbiota and host genetics to the phenotypic variability of digestive efficiency (DE) traits, such as digestibility coefficients of energy, organic matter and nitrogen, feed efficiency (FE) traits (feed conversion ratio and residual feed intake) and growth traits (average daily gain and daily feed intake). Data were available for 791 pigs fed a conventional diet and 735 of their full-sibs fed a high-fiber diet. Fecal samples were collected at 16 weeks of age to sequence the V3–V4 regions of the 16S ribosomal RNA gene and predict DE with near-infrared spectrometry. The proportions of phenotypic variance

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

explained by the microbiota (microbiability) were estimated under three OTU filtering scenarios. Then, microbiability and heritability were estimated independently (models Micro and Gen) and jointly (model Micro+Gen) using a Bayesian approach for all traits. Breeding values were estimated in models Gen and Micro+Gen. Results: Differences in microbiability estimates were significant between the two extreme filtering scenarios (14,366 and 803 OTU) within diets, but only for all DE. With the intermediate filtering scenario (2399 OTU) and for DE, microbiability was higher (> 0.44) than heritability (< 0.32) under both diets. For two of the DE traits, microbiability was significantly higher under the high-fiber diet (0.67 ± 0.06 and 0.68 ± 0.06) than under the conventional diet (0.44 ± 0.06). For growth and FE, heritability was higher (from 0.26 ± 0.06 to 0.44 ± 0.07) than microbiability (from 0.17 ± 0.05 to 0.35 ± 0.06). Microbiability and heritability estimates obtained with the Micro+Gen model did not significantly differ from those with the Micro and Gen models for all traits. Finally, based on their estimated breeding values, pigs ranked differently between the Gen and Micro+Gen models, only for the DE traits under both diets. Conclusions: The microbiota explained a significant proportion of the phenotypic variance of the DE traits, which was even larger than that explained by the host genetics. Thus, the use of microbiota information could improve the selection of DE traits, and to a lesser extent, of growth and FE traits. In addition, our results show that, at least for DE traits, filtering OTU is an important step and influences the microbiability.

来源: 中国知网

发布日期:2022-07-27

全文链接:

http://agri.ckcest.cn/file1/M00/10/0F/Csgk0GMVW_OAN21KAA9Wb6Tdpf0101.pdf