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Key Words: growing pig, immune system stimulation, plasma amino acid flux

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111 Effects of heat stress and zinc supplementation on the lipidome of growing pigs. L. Wang^{1,*}, P. E. Urriola², Z. Luo², Z. J. Rambo³, M. E. Wilson³, J. L. Torrison³, G. C. Shurson², C. Chen¹, ¹*Department of Food Science and Nutrition, University of Minnesota, St. Paul*, ²*Department of Animal Science, University of Minnesota, St. Paul*, ³*Zinpro Corporation, Eden Prairie, MN*.

Heat stress (HS) compromises growth performance and health status and is a major detrimental event in pig production. Zinc (Zn) has been explored as a supplement for protecting against the adverse effects of HS. In this study, metabolic effects of HS and Zn supplementation were evaluated by examining the lipidome of growing pigs fed with ZnNeg (no Zn supplementation), ZnIO (120 ppm ZnSO₄), or ZnAA (60 ppm ZnSO₄ + 60 ppm zinc amino acid complex) diets under diurnal HS (12 h at 37°C and 12 h at 25°C per day) or thermal-neutral (TN) condition (21°C). Diets were based on corn-soybean meal and formulated to meet NRC (2012) requirements. Following a 3 × 2 factorial design, crossbred gilts (71 ± 9 kg BW, n = 8/trt) were acclimated to experimental diets for 2 wk and then challenged with a diurnal HS treatment or maintained in a TN environment for 7 d. Liquid chromatography-mass spectrometry (LC-MS) based lipidomic analysis of serum, liver, cecal fluid, and fecal samples indicated that HS led to comprehensive changes in the lipidome while Zn supplementation selectively affected specific lipid species under HS. Compared to TN, HS decreased the levels of the phosphatidylcholines (PCs) containing odd chain fatty acids (pentadecanoic acid and heptadecanoic acid) (*P* < 0.05) while it increased PCs containing very long chain fatty acid (carbon number ≥ 22) or stearic acid in serum and the liver (*P* < 0.05). The HS group also had lower (*P* < 0.05) levels of oleic acid, linoleic acid, and their lysophosphatidylcholine and amide derivatives but higher (*P* < 0.05) levels of medium-chain dicarboxylic acids (suberic acid and sebacic acid) in cecal fluid and fecal samples than TN group. Moreover, under HS, ZnIO diet selectively increased acetic acid, propionic acid, and butyric acid in cecal fluid (*P* < 0.05). Considering microbial metabolism is responsible for generating many of these lipid markers, HS and Zn supplementation might affect the lipidome partly through changing the metabolic activities of gut microflora.

Key Words: heat stress, lipidomics, zinc supplementation

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112 Genetic parameters and genomic regions associated with piglet response to vaccination for porcine reproductive and respiratory syndrome (PRRS) virus and co-infection with PRRS virus and porcine circovirus type 2b (PCV2b). J. R. Dunkelberger^{1,*}, N. V. L. Serão^{1,2}, M. A. Kerrigan³, J. K. Lunney⁴, R. R. Rowland³, J. C. M. Dekkers¹, ¹*Iowa State University, Ames*, ²*North Carolina State University, Raleigh*, ³*Kansas State University, Manhattan*, ⁴*USDA, ARS, BARC, APDL, Beltsville, MD*.

Objectives of this research were to estimate genetic parameters and to identify genomic regions associated with PRRS viral load (VL), PCV2b VL, and average daily gain (ADG) in nursery pigs vaccinated or non-vaccinated for PRRS virus (PRRSV), followed by co-infection with PRRSV and PCV2b. Data used included 396 commercial crossbred pigs from two PRRS Host Genetics Consortium trials, all from the same genetic supplier. Pigs were sent to Kansas State University after weaning and randomly sorted into two rooms. All pigs in one room were vaccinated for PRRS, and 28 d later, pigs in both rooms were co-infected with PRRSV and PCV2b, followed for 42 d, and genotyped using the 80K BeadChip. PRRS VL after vaccination and post co-infection and PCV2b VL were calculated as area under the curve of serum viremia from –28 to 0, 0 to 21, and 0 to 42 d post co-infection, respectively. Genetic parameters were estimated by fitting multivariate animal models in ASReml4 with litter and pen (trial) as additional random effects. Trait-specific fixed effects of trial and weight and age at vaccination were also fitted. Genome-wide association (GWA) studies were performed by fitting SNPs as fixed effects one at a time in bivariate animal models for the non-vaccinated (Non-Vx) and vaccinated (Vx) groups for each trait. Heritability estimates following vaccination were 0.31, 0.07, and 0.10 for ADG Non-Vx, ADG Vx, and PRRS Vx, respectively. During the co-infection period, heritability estimates were slightly higher at 0.53, 0.57, 0.56, 0.20, 0.18, and 0.15 for ADG Non-Vx, ADG Vx, PRRS Non-Vx, PRRS Vx, PCV2b Non-Vx, and PCV2b Vx, respectively. Standard errors ranged from 0.14 to 0.22. A strong, positive genetic correlation (0.95 ± 1.01) was observed for PRRS VL post-vaccination with PRRS VL Non-Vx. Unique genomic regions were identified between Vx and Non-Vx pigs for each trait, the most significant of which was identified for PCV2b VL and located near the major histocompatibility complex, an important region for response to infection. The chromosome 4 region, which has been associated with VL following PRRS-V-only infection, was associated with PRRS VL Non-Vx but not PRRS Vx or PRRS VL post-vaccination. Together, these results suggest that selection for improved performance under co-infection of PRRS and PCV2b is possible. Additionally, identification of unique genomic regions between Vx and Non-Vx pigs may enable selection of pigs with better response to vaccination. This research was supported by USDA-NIFA

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Key Words: disease, GWAS, swine

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113 Optimizing cost and environmental impact of pig diets. J. Burek^{1*}, G. Thoma¹, C. V. Maxwell², J. Popp¹, R. Ulrich¹, ¹*University of Arkansas, Fayetteville*, ²*Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

Livestock production is one of the major causes of the world's environmental problems, such as climate change impact. Researchers are looking for sustainable pig diet formulations within the Climate Change Mitigation and Adaptation in Agriculture (CCMAA) program. The single-objective diets including least cost, least climate change impact, least water, and least land use were modeled using Windows-based User Friendly Feed Formulation (WUFFDA) linear models. Baseline U.S. pig diets for 1 nursery, 2 sow, and 5 grow phases formulated by the University of Arkansas' pig nutritionist included corn, soybean and fish meal, fat, lactose, dry whey, amino acids, minerals, vitamins, and additives. We added the U.S. pig industry top 80 most used feed ingredients to the WUFFDA models. Nutrient characteristics, inclusion limits, cradle-to-farm gate life-cycle assessment (LCA) environmental impacts, and cost data for feed ingredients were obtained from the U.S. Animal Feed Database available in the Pig Production Environmental Calculator (PPEC). Preliminary results show potential to lower cost and environmental footprint in pig producers' feeding systems (Table 113). The linear models input data are changeable including feed costs and availability, pig production practices, environmental footprints, and maximum inclusion rates. Thus, so far we can only conclude that the solution to increase sustainability of pig production for different criteria in the United States is to diversify feed ingredients, in particular for the least water and least land use diets. The formulated diets are currently being validated by swine nutritionists to check models and diets and propose recommendations to improve their economic and environmental feasibility. Nutritionists have an important role because they create connection between the scientific research, validation, and pig producers. Also, we will perform the multi-objective analysis and evaluate the potential to simultaneously reduce cost and environmental impacts. The proposed diets will be available in the PPEC for pig producers, which will allow pig producers to make informed decisions that can help reduce costs and environmental impacts throughout pig life-cycle.

Key Words: life cycle assessment, linear optimization, pig diets, pig production

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Table 113. Pig diet weight, cost, and environmental impact results for optimized diets per kg market pig, live weight

	Average U.S. pig diet	Least cost	Least climate change impact	Least water depletion	Least land use
Cradle-to-farm-gate LCA					
Diet weight (kg)	3.09	3.12	2.99	3.14	3.14
Total pig diet cost (\$)	0.91	0.87	1.13	2.04	1.46
Climate change impact (kg CO ₂ e)	3.08	2.80	1.99	3.14	2.60
Water depletion (m ³)	0.24	0.24	0.14	0.07	0.11
Land use (m ² a)	4.25	7.75	6.04	11.05	1.49

GRADUATE STUDENT COMPETITION: M.S. POSTER

114 Alterations of the rumen bacterial and archaeal communities in growing and finishing beef cattle and its effects on methane emissions.

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The rumen harbors a complex microbial community that is greatly influenced by diet composition. This microbial community is critical to the survival of the animal and provides up to 80% of the animals' energy needs. However, as a by-product, the rumen microbial community also produces methane. The sub-group of methane producing organisms in the rumen are called methanogens. The interactions between methanogens and the rumen microbial population is dictated by diet. As a result, the methane being released from cattle will be influenced by the diet being fed to the cattle. Therefore, evaluating the microbial community composition under different dietary conditions and relating these interactions to methane emissions is critical to methane mitigation. To evaluate the effects of diet on microbial community composition and methane emission, 120 animals were fed 10 different growing and 6 finishing diets. Growing diets included high and low quality forage, with and without monensin supplementation, and different inclusions of modified distillers grains plus solubles (MDGS), and finishing diets contained different fat sources (corn oil, tallow, and distillers) with and without monensin supplementation, and direct fed microbial (DFM). Microbial community composition and methane emission was monitored. Methane and CO₂ concentrations of respired air were taken during feeding in an individual feeding facility utilizing 120 individual bunks equipped with the Calan® gate system and an automated gas collection system. Rumen contents were collected via esophageal tubing for microbial community analysis. The V3 region of the 16S rRNA gene was sequenced using the Ion Torrent personal genome machine (PGM). When compared to the respective control diets, the microbial community composition differed in growing and