UNIVERSITY of GUELPH
ONTARIO AGRICULTURAL COLLEGE
DEPARTMENT OF ANIMAL BIOSCIENCES

PhD Defence

Impacts of Antimicrobials on Host Responses and Gut Microbiome through Up-regulating the Gut Endogenous Alkaline Phosphatase Expression in Weanling Pigs

Jiali Chen

Date: September 6th 2023 at 10:00am

The PhD Defence for Jiali Chen has been scheduled for September 6th, 2023 at 10:00am. The defence will be held online via Teams and in room 141: https://teams.microsoft.com/l/meetup-join/19%3ameeting_MzE3MWMwZTYtMjU5OC00NDA0LWI0ZWMtMTVhNDRmNTM5Zjg0%40thread.v2/0?context=%7b%22Tid%22%3a%22be62a12b-2cad-49a1-a5fa-85f4f3156a7d%22%2c%22Oid%22%3a%22fbd28915-dda5-478f-8ecb-a3682dcf0c3a%22%7d

The exam committee will consist of:

Examining Chair: Dr. Elijah Kiarie

Advisor: Dr. Ming Fan

Advisory Committee Member: Dr. Yoshinori Mine

Additional Committee Member: Dr. Anna Kate Shoveller

External Examiner: Dr. Shengfa Liao

Abstract:

Administration of prescribed therapeutic antimicrobials for prophylactic purposes is still widely practiced in global swine production with the primary objectives of maintaining the gut health and growth of weanling pigs. Three studies were conducted to gain a comprehensive understanding the impacts of prescribed therapeutic antimicrobials on the digestive utilization of dietary starch, crude fat and dietary fiber, endogenous alkaline phosphatase (AP) activity and expression, bacterial species level of the gut microbiome changes and their interrelationships and contributions to the growth promotion and gut health in weanling pigs. In Study-1, therapeutic antimicrobials (ppm) of chlortetracycline (220), tiamulin (31.2) and ZnO (2358) improved ($P<0.05$) weanling pig growth performances. The growth-promoting effect of the antimicrobials were associated ($P<0.05$) with increased feed intake and reduced digestive utilization of dietary fiber rather than the unaffected ($P>0.05$) digestive utilization of dietary starch and crude fat. The high-resolution and high-accuracy full-length 16S rRNA gene sequencing data showed that the antimicrobials reduced or eliminated ($P<0.05$) the relative abundances of the bacterial pathogens such as *Streptococcus* spp. and the zoonotic *Campylobacter* spp. in the cecal digesta and feces. In addition, the antimicrobials were shown to decrease ($P<0.05$) the relative abundances of *Lactobacillus* spp. in the cecal digesta and feces. Specific bacterial species in the cecal digesta and feces were identified in association ($P<0.05$) with improved growth performances. Fecal relative abundance of *p-1088-a5* sp., *Parasutterella* sp., *Defluviitaleaceae* sp., *Parasutterella* sp.; *Selenomonas* sp., *Mitsuokella* sp., *Lachnoclostridium* sp. and *Streptococcus orisratti* displayed ($P<0.05$) the potential to serve as non-invasive biomarkers for the prediction of the growth performance endpoints. In Study-2, antimicrobials up-regulated ($P<0.05$) the AP maximal enzyme activity (i.e., V_{max}) along the small-large intestininal longitudinal axis and in the blood plasma. Increases in plasma AP V_{max} showed a positive and linear correlation ($P<0.05$) with both feed intake and growth rate, indicating the plasma AP V_{max} as a novel biomarker for predicting porcine growth performances. The antimicrobials were also shown to increase ($P<0.05$) the relative abundance of the bacterial endocellulase gene, GH5-p4818Cel5_2A, in the cecal digesta and feces and demonstrated a positive association with ($P<0.05$) the improved gut health.

Furthermore, specific bacterial species in the cecal digesta and feces were identified in association with the up-regulation of the endogenous AP activity and improved gut health. Specifically, the fecal relative abundance of the bacterial species of *Blautia obeum*, *Oribacterium* sp., *Lactobacillus salivarius*, *p-2534-18B5* sp., *dgA-11* sp., *Mucispirillum* sp. and *Streptococcus orisratti* exhibited a linear correlation ($P<0.05$) with gut health, suggesting their potential roles as biomarkers for predicting porcine gut health. In Study-3, antimicrobials down-regulated ($P<0.05$) the permeability and inflammation-related gene mRNA abundances in the hindgut which were also associated with ($P<0.05$) the growth performance and gut health endpoints as well as abundances of the identified specific bacterial species in the weanling pigs. Our findings provide insights into reducing the reliance on antimicrobials and in developing alternative strategies to antimicrobials in swine production.