UNIVERSITY of GUELPH

ONTARIO AGRICULTURAL COLLEGE

DEPARTMENT OF ANIMAL BIOSCIENCES

PhD Defence

Therapeutic Antimicrobials in Modulation of Gut Health, Growth Performances, Crude Protein and Amino Acid Utilization and Gut Microbiome in Weanling Pigs

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Date: May 29th 2023 at 10:00am

The PhD Defence for Wenyi Fan has been scheduled for May 29th, 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_ZDczZjM3NDktZWI1My00MzFhLTllNzEtYzEyMWQ4ZjMyMmQ0%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. David Huyben

Advisor: Dr. Ming Fan

Advisory Committee Member: Dr. Lee-Anne Huber

Additional Committee Member: Dr. Elijah Kiarie

External Examiner: Dr. Sung Woo Kim

Abstract:

Antibiotics are among the best medicine discoveries. Antimicrobials have been used for enhancing pig gut health and growth performances for the past seven to eight decades but have also contributed to the development of antimicrobial resistance (AMR). The major mode of antimicrobial actions for growth promotion is often linked to improved efficiency of utilization of dietary crude protein (CP) and amino acids (AA) but with less convincing data and unraveled biological mechanisms. Three studies were conducted to investigate the impacts of therapeutic antimicrobials on modulation of gut health, growth performances, CP and AA utilization and gut microbiome via the high-resolution and high accuracy Loop-Seq™ synthetic full-length 16S-rRNA gene sequencing platform in weanling pigs. Study-1 results showed that therapeutic chlortetracycline dramatically altered (P<0.05) the distal ileal relative abundances of the two most populous bacterial species, i.e., *Lactobacillus* sp. and *Streptococcus* sp., respectively. Chlortetracycline was also shown to substantially reduce (P<0.05) the distal ileal relative abundances of the zoonotic *Campylobacter lanienae* and the pancreatic and colonic carcinogenic *Fusobacterium* spp. Chlortetracycline improved the weanling pig gut health endpoint by enhancing the distal ileal colonization of the chlortetracycline-producing *Streptomyces aureofaciens*, providing a new understanding of the antimicrobial resistance associated with this antibiotic. Chlortetracycline could improve (P<0.05) the apparent ileal Lys digestibility via modulating relative abundances of several specific ileal bacterial species; however, it had limited effects (P>0.05) on the efficiency of digestive and post-digestive utilization of dietary CP in the weanling pigs. Thus, high-resolution sequencing the 16S-rRNA gene unravels species-level of the gut microbiome changes in the weanling pigs administered with the therapeutic chlortetracycline in providing important One Health implications to humans. The Study-2 results showed that therapeutic antimicrobials could selectively regulate (P<0.05) host gut gene expression and mediate gut digestibility and AA utilization in the small and the large intestines via modulating relative abundances of some specific bacterial species in the weanling pigs. In Study-3, we discovered that even when the last-resort human therapeutic macrolide-lincosamide-streptogramin (MLS) antibiotics were never used in the study pigs and their prior source swine herds, the fecal tetracycline resistome core AMR genes and the fecal last-resort human therapeutic MLS antibiotic AMR genes were equally enriched in their relative abundances. And these examined AMR gene abundances were not further enhanced (P>0.05) by the therapeutic tetracycline administration in the weanling pigs. We also found that *Syntrophococcus* sp. and *Enterobacter hormaechei* were responsible for explaining the relative abundances of *tet*M and *mcr*-1, respectively. Our results support the notion that the elevated AMR gene prevalence and abundances in the porcine commensal and pathogenic bacteria have been reaching plateau levels because of the globe-wide antimicrobial use over the past seven to eight decades. Realistic resistome mitigation strategies should be emphasized on developing disruptive means to remodel and optimize the porcine gut microbiome and to evolve and enrich specific taxa that are affiliated with reduced AMR impacts.