

## Effect of Single Dose of Antimicrobial Administration at Birth on Fecal Microbiota Development and Prevalence of Antimicrobial Resistance Genes in Piglets

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### Keypoints:

- Early life antimicrobial prophylaxis had no effect on individual weight gain, or mortality but it was associated with minor shifts in the composition of fecal microbiota and noticeable changes in the abundance of selected Antimicrobial Resistant Genes
- The shifts in fecal microbiota structure caused by perinatal antimicrobial intervention are modest and limited to particular groups of microbial taxa
- Early life PPG and TUL intervention could promote the selection of Antimicrobial Resistant Genes in herds

Optimization of antimicrobial use in swine management systems requires full understanding of antimicrobial-induced changes on the developmental dynamics of gut microbiota and the prevalence of antimicrobial resistance genes (ARGs). The purpose of this study was to evaluate the impacts of early life antimicrobial intervention on fecal microbiota development, and prevalence of selected ARGs in neonatal piglets.

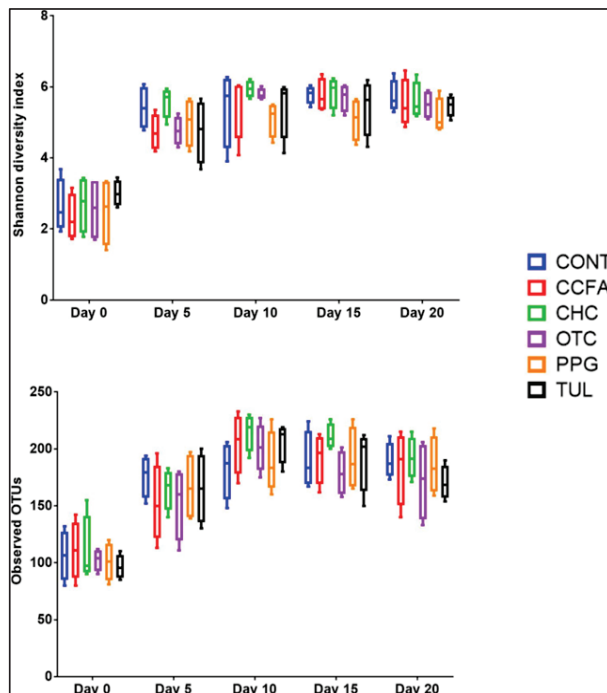
### Methods

A total of 48 litters were randomly allocated into one of six treatment groups soon after birth. Treatments were as follows: control (CONT), ceftiofur crystalline free acid (CCFA), ceftiofur hydrochloride (CHC), oxytetracycline (OTC), procaine penicillin G (PPG), and tulathromycin (TUL). Fecal swabs were collected from piglets at days 0 (prior to treatment), 5, 10, 15, and 20 post treatment. Sequencing analysis of the V3-V4 hypervariable region of the 16S rRNA gene and selected ARGs were performed using the Illumina Miseq platform.

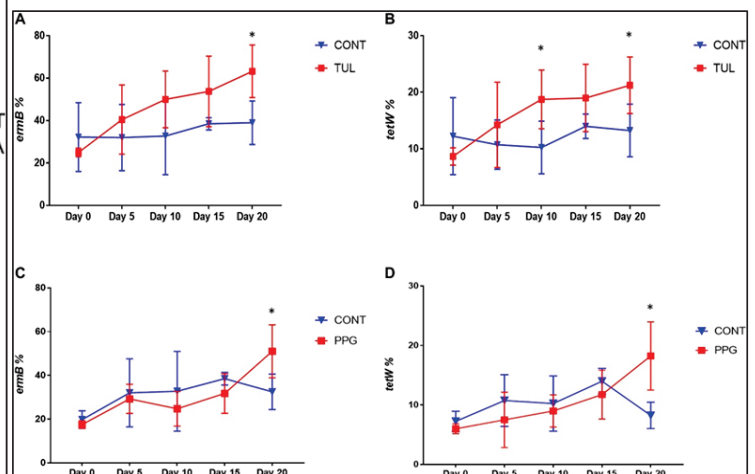
### Results

Our results showed that, while early life antimicrobial prophylaxis had no effect on individual weight gain, or mortality, it was associated with minor shifts in the composition of fecal microbiota and noticeable changes in the abundance of selected ARGs. Unifrac distance metrics revealed that the microbial communities of the piglets that received different treatments (CCFA, CHC, OTC, PPG, and TUL) did not cluster distinctly from CONT piglets. Compared to CONT group, PPG-treated piglets exhibited a significant increase in the relative abundance of the genes *ermB* and *tetW* at day 20 of life. Tulathromycin treatment also resulted in a significant increase in the abundance of *tetW* at days 10 and 20, and *ermB* at day 20.

Collectively, these results demonstrate that the shifts in fecal microbiota structure caused by perinatal antimicrobial intervention are modest and limited to particular groups of microbial taxa. However, early life PPG and TUL intervention could promote the selection of ARGs in herds. While additional investigations are required to explore the consistency of these findings across larger populations, these results could open the door to new perspectives on the utility of early life antimicrobial administration to healthy neonates in swine management systems.



**Figure 1:** Bacterial diversity indices by treatment groups demonstrated that there was an age but not a treatment effect on bacterial diversity (control (CONT, n = 4), ceftiofur crystalline free acid (CCFA, n = 4), ceftiofur hydrochloride (CHC, n = 4), oxytetracycline (OTC, n = 4), procaine penicillin G (PPG, n = 4), and tulathromycin (TUL, n = 4) at days 0, 5, 10, 15, and 20.



**Figure 2:** Line graphs illustrating the difference in relative abundance of two ARG (*ermB* and *tetW*) between the control (CONT, n = 4) and tulathromycin (TUL, n = 4) (A and B) control (CONT, n = 4) group and procaine penicillin G (PPG, n = 4) (C and D) treated piglets at each sampling day. \*P < 0.05.