

Negligible Impact of Perinatal Tulathromycin Metaphylaxis on the Developmental Dynamics of Fecal Microbiota and Their Accompanying Antimicrobial Resistome in Piglets

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Keypoints:

- Fluctuations in antimicrobial resistance genes (ARGs) associated with the developing gastrointestinal microbiota have not been elucidated
- The swine fecal microbiota and their accompanying ARGs were diverse and established soon after birth
- Results indicate that the perinatal TUL metaphylaxis has no measurable beneficial or detriment impacts on fecal microbiota structure and abundance of ARGs in pre-weaned piglets

While the antimicrobial resistance profiles of cultured pathogens have been characterized in swine, the fluctuations in antimicrobial resistance genes (ARGs) associated with the developing gastrointestinal microbiota have not been elucidated. The objective of this study was to assess the impact of the perinatal antibiotic tulathromycin (TUL) metaphylaxis on the developmental dynamics of fecal microbiota and their accompanying antimicrobial resistome in pre-weaned piglets.

Sixteen litters were given one of two treatments [control group (CONT; saline 1cc IM) and TUL group (TUL; 2.5 mg/kg IM)] directly after birth. Deep fecal swabs were collected at day 0 (prior to treatment), and again at days 5 and 20 post treatment. Shotgun metagenomic sequencing was performed on the extracted DNA, and the fecal microbiota structure and abundance of ARGs were assessed.

Collectively, the swine fecal microbiota and their accompanying ARGs were diverse and established soon after birth. Across all samples, a total of 127 ARGs related to 19 different classes of antibiotics were identified. The majority of identified ARGs were observed in both experimental groups and at all-time points. The magnitude and extent of differences in microbial composition and abundance of ARGs between the TUL and CONT groups were not statistically significant. However, both fecal microbiota composition and ARGs abundance were changed significantly between different sampling days. In combination, these results indicate that the perinatal TUL metaphylaxis has no measurable beneficial or detrimental impacts on fecal microbiota structure and abundance of ARGs in pre-weaned piglets. Based on the results of this small study, it does not appear that TUL administration at birth has any implications on the amount of ARG present in the pigs or shed into the environment.

Figure 1: There were no differences in the structure of the bacterial communities between the treated and control groups as demonstrated by the taxonomic classification of shotgun metagenomic sequences at the phylum level for the control (CONT) and tulathromycin (TUL) treated piglets at each sampling time days (0, 5, and 20). Only those bacterial phyla that averaged more than 1% of the relative abundance across all samples are displayed.

