ECM 2025 Conference
The 3rd International Electronic Conference on Microbiology
01–03 April 2025 | Online
MDPI

Evaluation of impacts from exposure to antimicrobial residues in the environment on the gut microbiome and resistome using a mouse mode

Amer Abdelgany[1,3], Tamara Morrill[3], Alex Wong[1], Catherine Carrillo[2],and Jiewen Guan[3]

Biology Department, Carleton University; [2] Ottawa Laboratory (Carling) - Research and Development, CFIA; [3] Ottawa Laboratory (Fallowfield) - Animal Health Research and Development, CFIA

INTRODUCTION

Antimicrobial resistance poses a serious public health threat, with antimicrobial resistant bacteria (ARB) and their genes (ARGs) distributed in diverse environments such as farms and water systems. These bacteria can reach humans through contaminated food, water, or direct contact, colonizing our gut upon ingestion. We hypothesize that exposure to clinical antimicrobials and environmental residues of antimicrobials, such as ampicillin and tetracycline, exacerbates ARB colonization, leading to microbial dysbiosis and enhanced ARG spread. Ampicillin is clinically relevant, while tetracycline is widely used in agriculture and animal husbandry and is extensively distributed in the environment.

AIM

The aim of this study is to investigate the persistence of *Salmonella Heidelberg* carrying ARGs on an IncA/C plasmid within the gut microbiota, and to examine the horizontal transfer of these ARGs among Enterobacteriaceae under varying levels of antimicrobial exposure, including sub-inhibitory and clinically relevant concentrations using a mouse model

METHOD

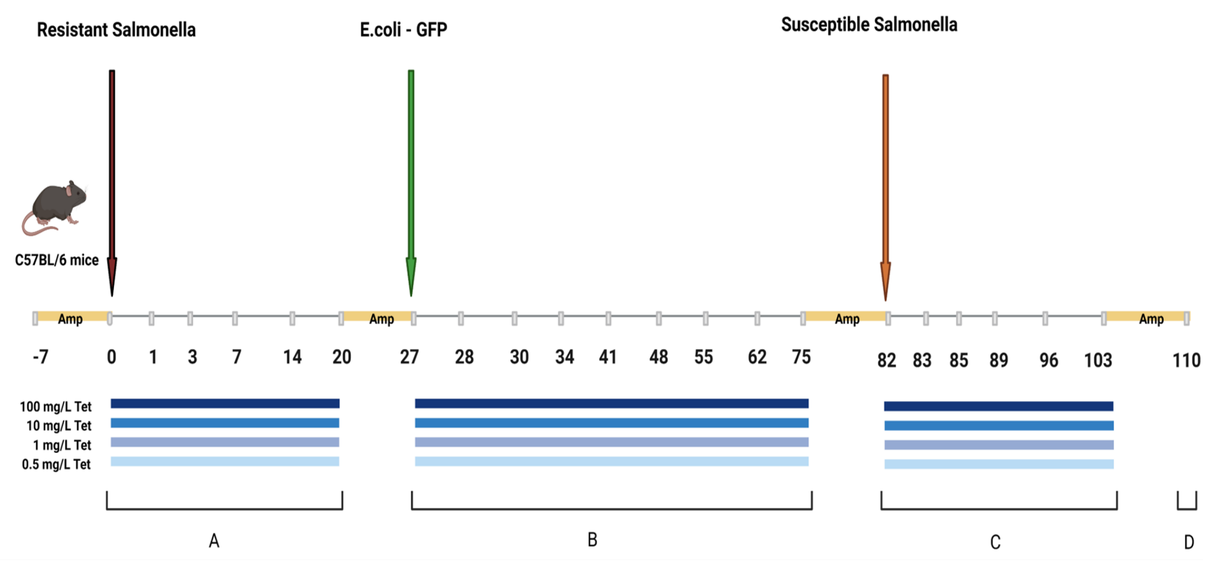

Fig.1 Shows the experiment design of the mouse experiment, including antimicrobial exposure and inoculations at different time points

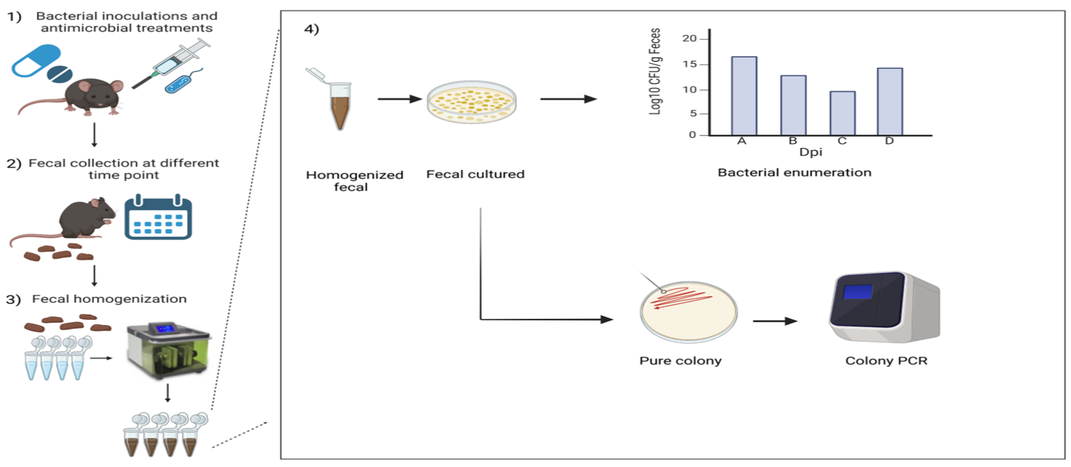

Fig.2 The schematic summaries all experiments in the mouse model study

RESULTS

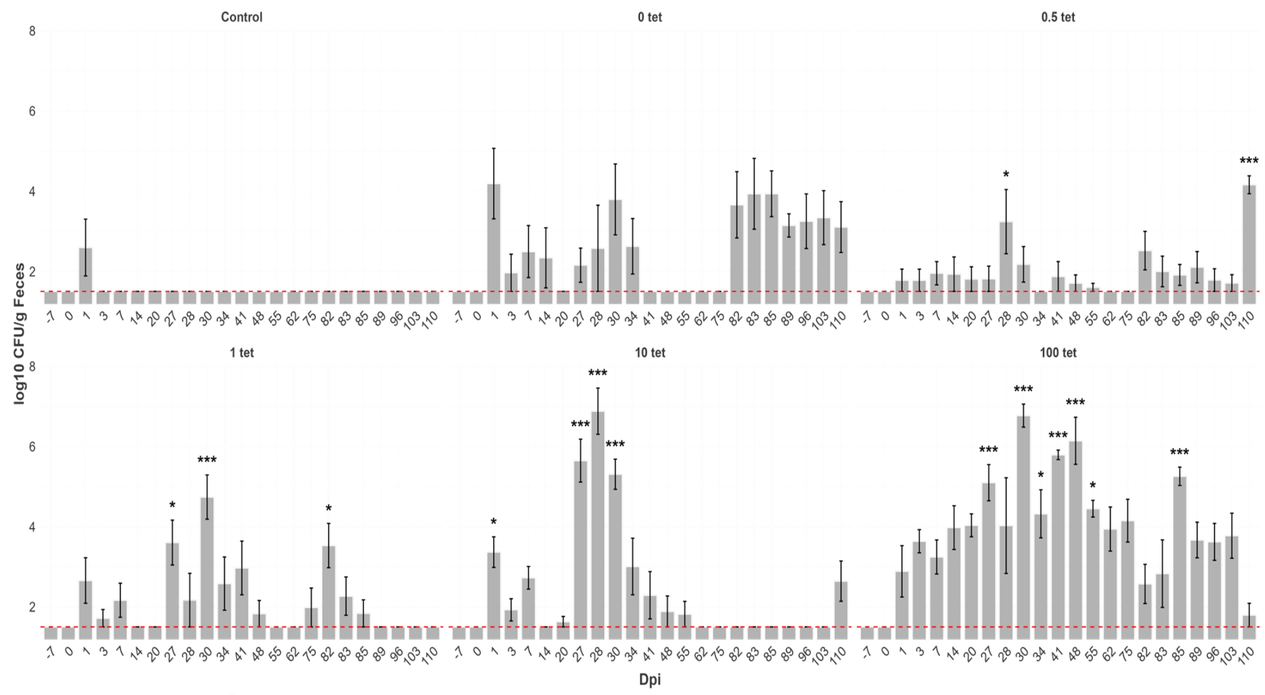

Fig.3 Persistence of donor Salmonella Heidelberg in all treatment groups over time in the mouse experiment. The Bar group represents the mean of log10 CFU/g feces. The dashed line is the detection limit. DPI: days post-inoculation.

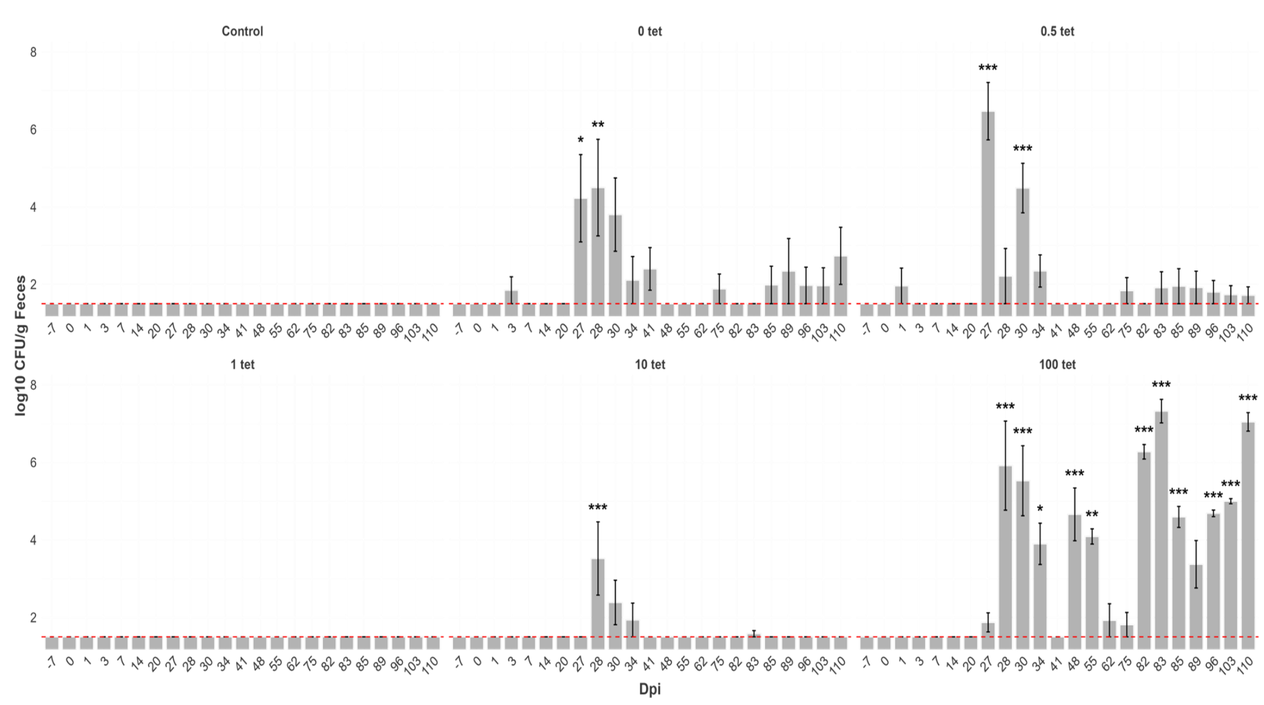

Fig.4 Transconjugant commensal E. coli in all groups in the mouse experiment. The Bar group represents the mean of log10 CFU/g feces. The dashed line is the detection limit.

DISCUSSION

- The donor *Salmonella Heidelberg* persisted in the gut microbiome and thrived in a cyclic pattern following each clinical dosage of ampicillin treatment. The tetracycline significantly increased the persistence in concentration depended pattern.
- Commensal *E.coli* received the AMR plasmid from SH and persisted in the gut microbiome after intermittent clinical dosage of ampicillin treatment. The tetracycline increased the persistence at higher subclinical doses.

CONCLUSION

Our This study demonstrated that *Salmonella Heidelberg* harboring ARGs on an IncA/C plasmid can persist in the gut microbiota and transfer resistance genes to other Enterobacteriaceae under various tetracycline exposure levels, with no transfer observed at the MIC. These findings underscore the influence of antimicrobial concentration on horizontal gene transfer dynamics.