

Associations between antimicrobial use and antimicrobial resistance in *E. coli* isolates of Canadian turkey flocks



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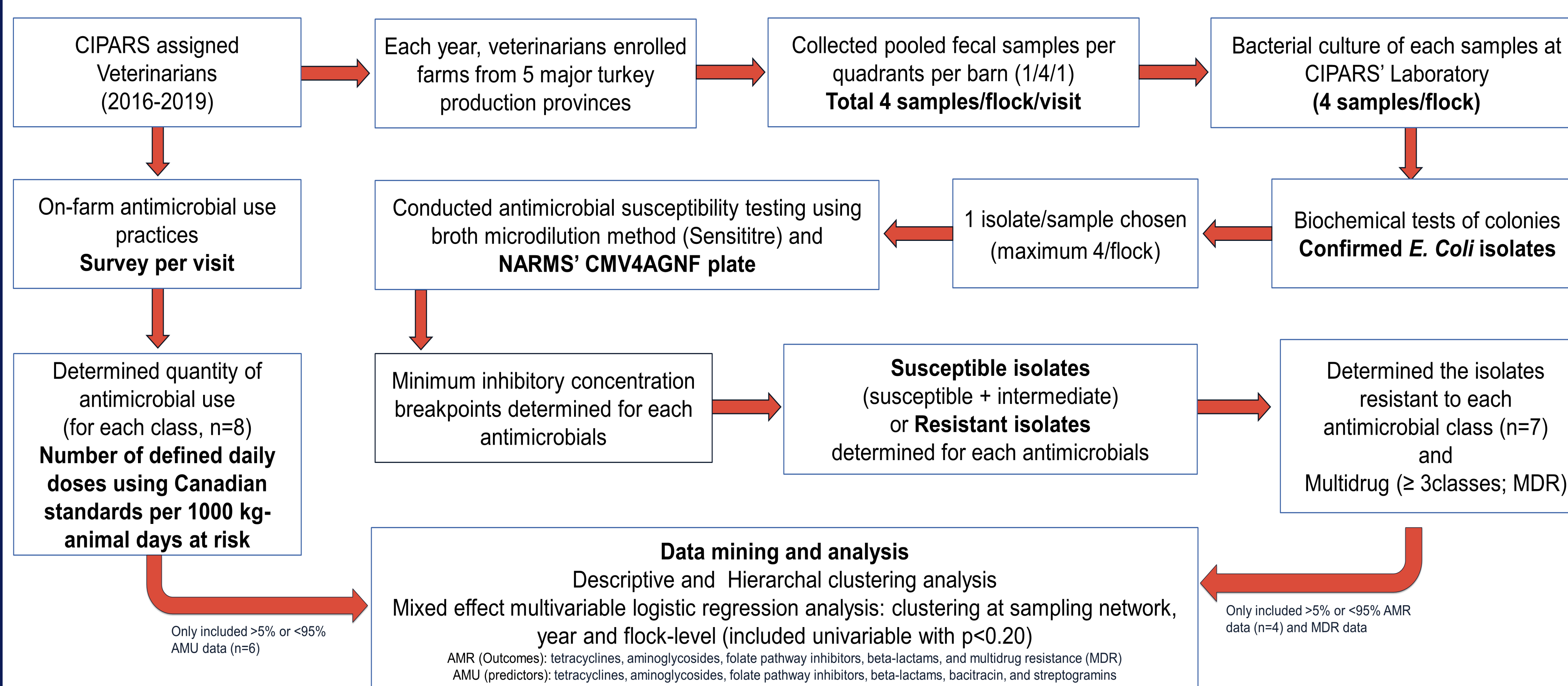
INTRODUCTION

- Antimicrobial resistance (AMR) in enteric bacteria is a global health threat that requires urgent attention.
- Antimicrobials have been used effectively to treat or prevent diseases in turkey flocks; however, antimicrobial use (AMU) is the main driver for the emergence of antimicrobial resistance (AMR) in commensal and pathogenic enteric bacteria (1-3).
- Commensal *Escherichia coli* (*E. coli*) is frequently used in surveillance systems to monitor the emergence and spread of AMR at the animal-human-environment interface (4-5).

OBJECTIVES

- To estimate the prevalence and determine the associations between the resistance to individual antimicrobial classes in *E. coli* isolated from turkey flocks and the flock-level antimicrobial use.

METHODS



CONCLUSIONS

- Flock-level use of antimicrobials impacted the emergence of phenotypic AMR to the same or unrelated antimicrobial classes.
- The resistance to unrelated AMU could be due to co-selection for AMR or the presence of resistance genes in the environment.
- Flock-level interventions and stewardships should be implemented to prevent and control infections in the turkey flocks.
- Continuous on-farm AMU and AMR surveillance with molecular epidemiological studies (e.g., metagenomics) are needed to provide insights on how the AMR occurs in the turkey flocks.

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RESULTS

- 1317 *E. coli* isolates were detected from 334 turkey flocks collected by 16 veterinarians
- Common antimicrobials used on turkey flocks were tetracyclines, aminoglycosides, folate pathway inhibitors, beta-lactams, bacitracins, and streptogramins.
- E. coli* isolates were mainly resistant to four antimicrobial classes: tetracyclines (62%), aminoglycosides (45%), folate pathway inhibitors (30%) and beta-lactams (31%), and 31% isolates had multidrug resistance.
- Multidrug resistance of *E. coli* isolates of turkey flocks (27%) was influenced by the use of folate antagonists (OR=1.01, 95% CI:1.006-1.016)
- The highest variances were observed at the flock-level and low to moderate level variances found at the sampling year level.
- Correlations and interactions terms were not significant.

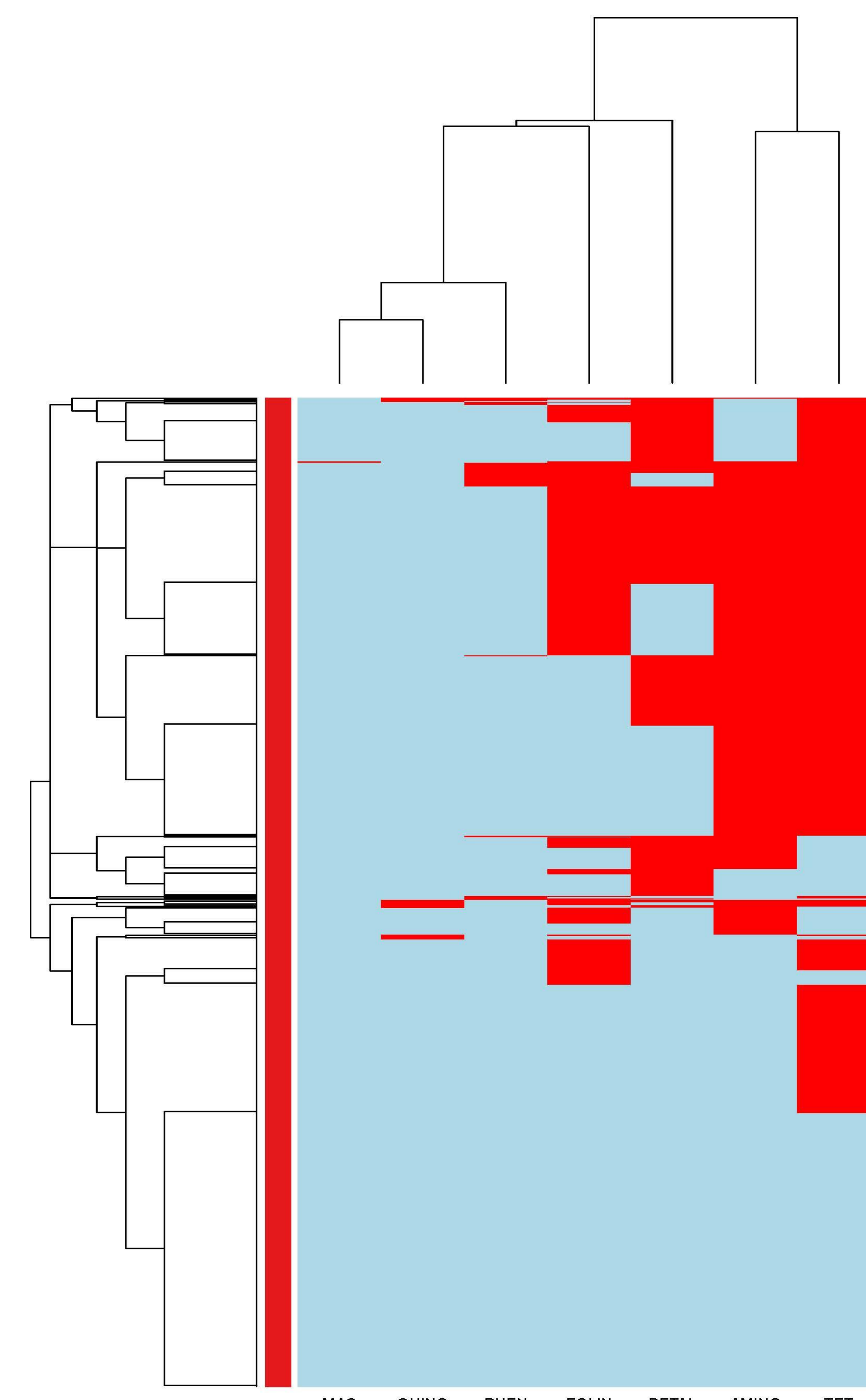


Figure 1: Resistance patterns of *Escherichia coli* isolates to seven antimicrobial classes (2016-2019)
 X-axes of heatmaps represent the antimicrobial classes: macrolides (MAC), fluoroquinolones (QUINO), phenicols (PHEN), folate pathway inhibitors (FOLIN), beta-lactams (BETAL), aminoglycosides (AMINO), tetracyclines (TET), ketolides (KETOL), lincosamides (LINCO). Y-axes of heatmaps represent the isolates of this study.

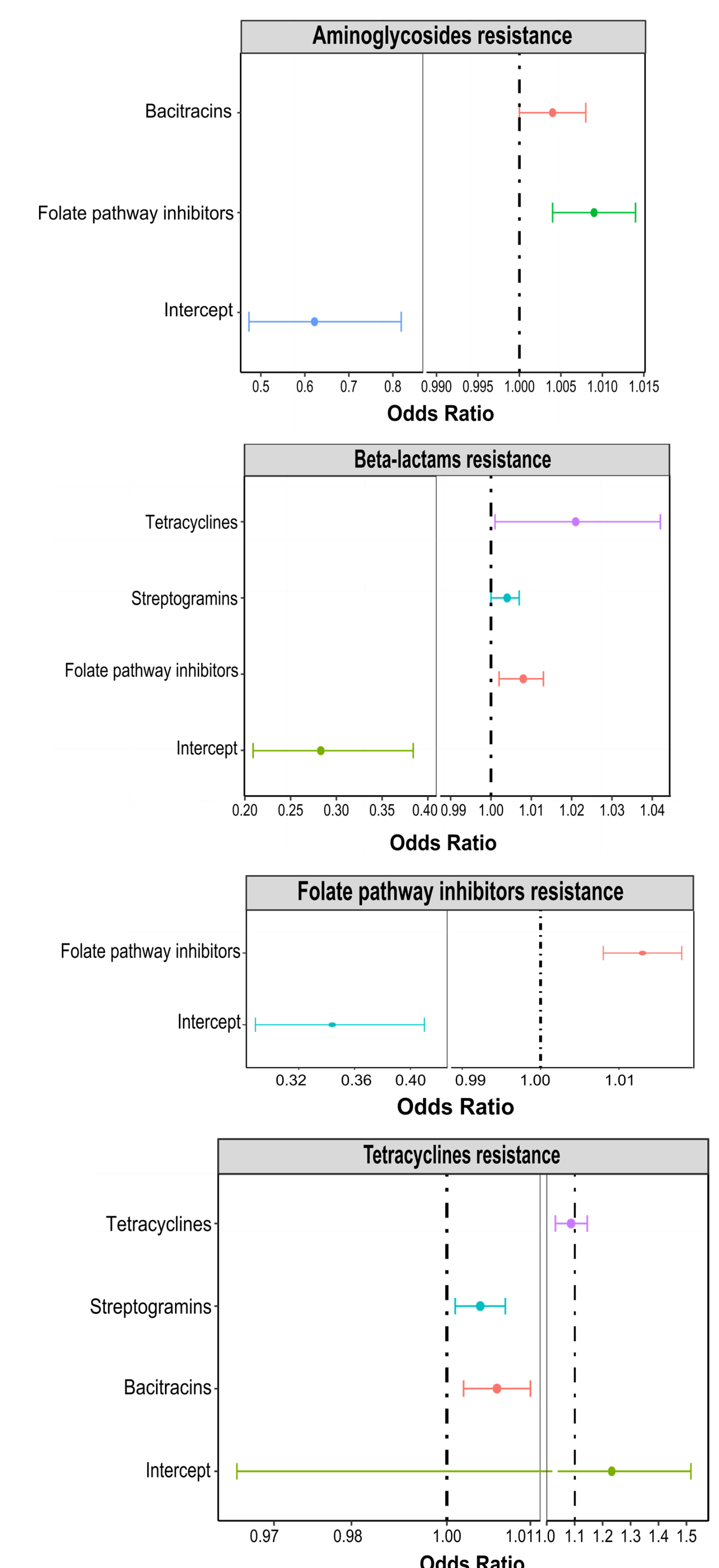


Figure 2: AMU associations with AMR in *E. coli* isolates of turkey flocks (n=1317)

ACKNOWLEDGEMENTS

Turkey farmers
 Veterinarians



Public Health
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CIPARS



Government
 of Canada

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College of
 Veterinary Medicine
 UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN

Associations among antimicrobial use and phenotypic antimicrobial class resistance in *E. coli* isolates of turkey flocks

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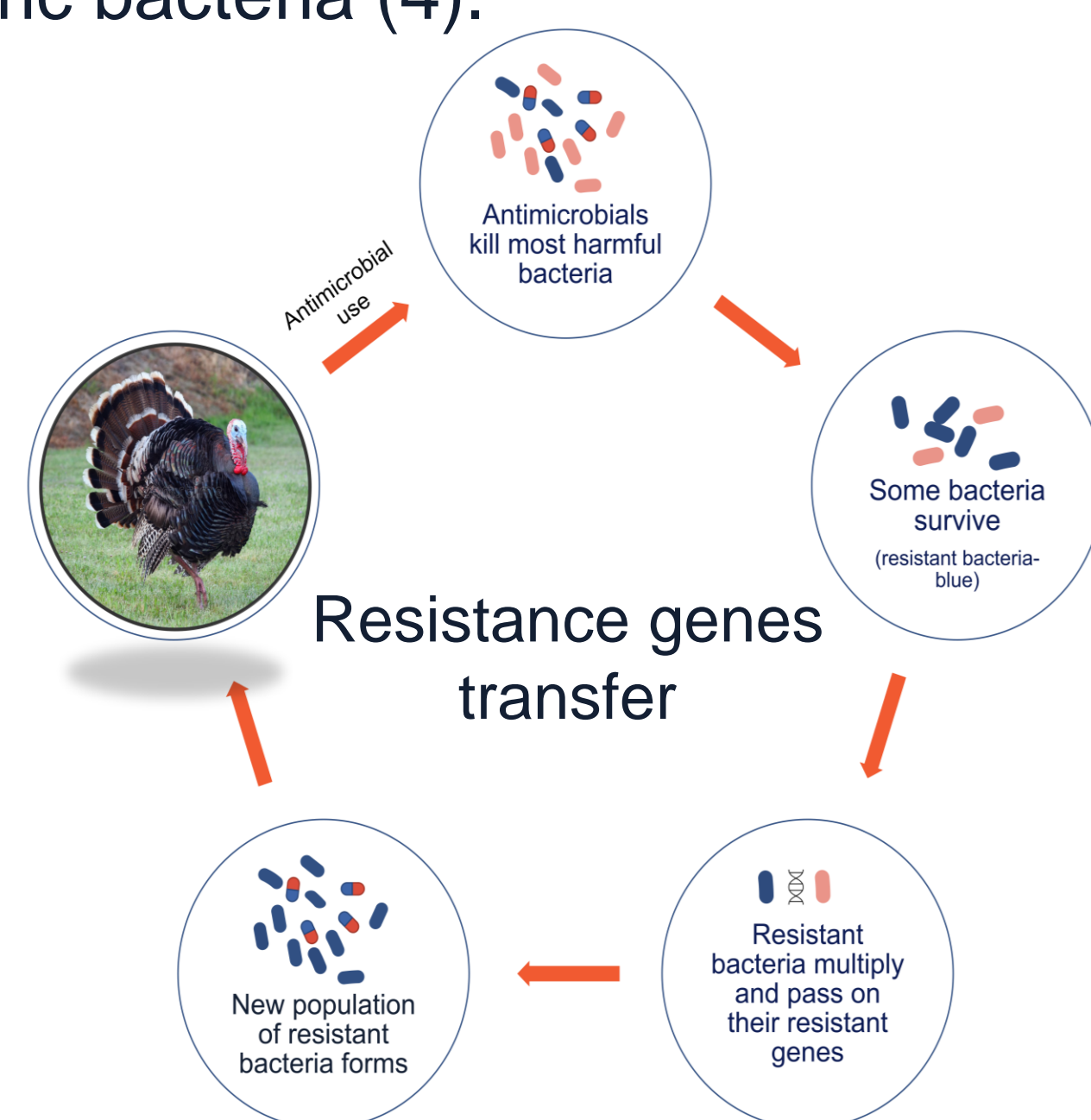
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INTRODUCTION

- Antimicrobial resistance (AMR) in enteric bacteria is a human and animal health threats world-wide.
- Antimicrobials are essential for disease prevention, treatment in turkey flocks (1).
- Since antimicrobial use (AMU) drives the emergence of AMR, turkey flocks could be a potential source of mobile genetic elements containing antimicrobial resistant genes (ARGs) that could pose a food safety risk (2, 3).
- The presence and spread of ARGs in mobile genetic elements could impact the development of resistance to other antimicrobials that are not used (2, 3).
- E. coli* is an organism that can transmit ARGs to other pathogenic and commensal enteric bacteria (4).



OBJECTIVES

- To determine the associations between the resistance to individual antimicrobial classes in *E. coli* isolated from turkey flocks and the flock-level antimicrobial use.

METHOD

- Veterinarians involved with the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) conducted the sentinel turkey farm surveillance.

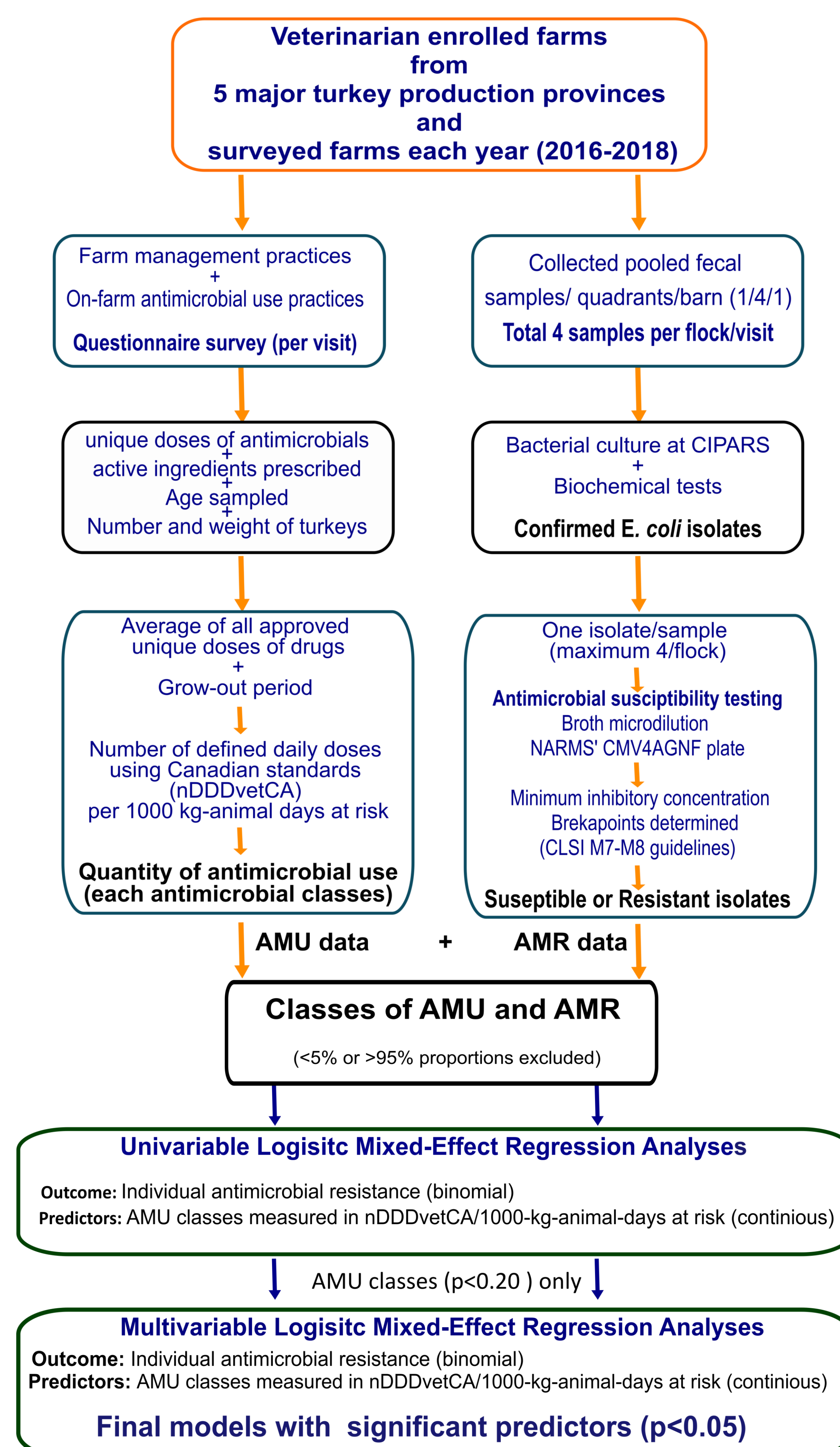


Figure 1: Schematic diagram showing sample collection, laboratory analyses, data management and statistical analysis

- All statistical analysis was conducted in R software and R studio platform.

RESULTS

- 1317 *E. coli* isolates from 334 turkey flocks were collected by 16 veterinarians and were tested for antimicrobial susceptibility.
- Common antimicrobials used on turkey flocks were tetracyclines, aminoglycosides, folate pathway inhibitors, beta-lactams, bacitracins, and streptogramins.
- E. coli* isolates were mainly resistant to four antimicrobial classes: tetracyclines, aminoglycosides, folate pathway inhibitors, and beta-lactams.

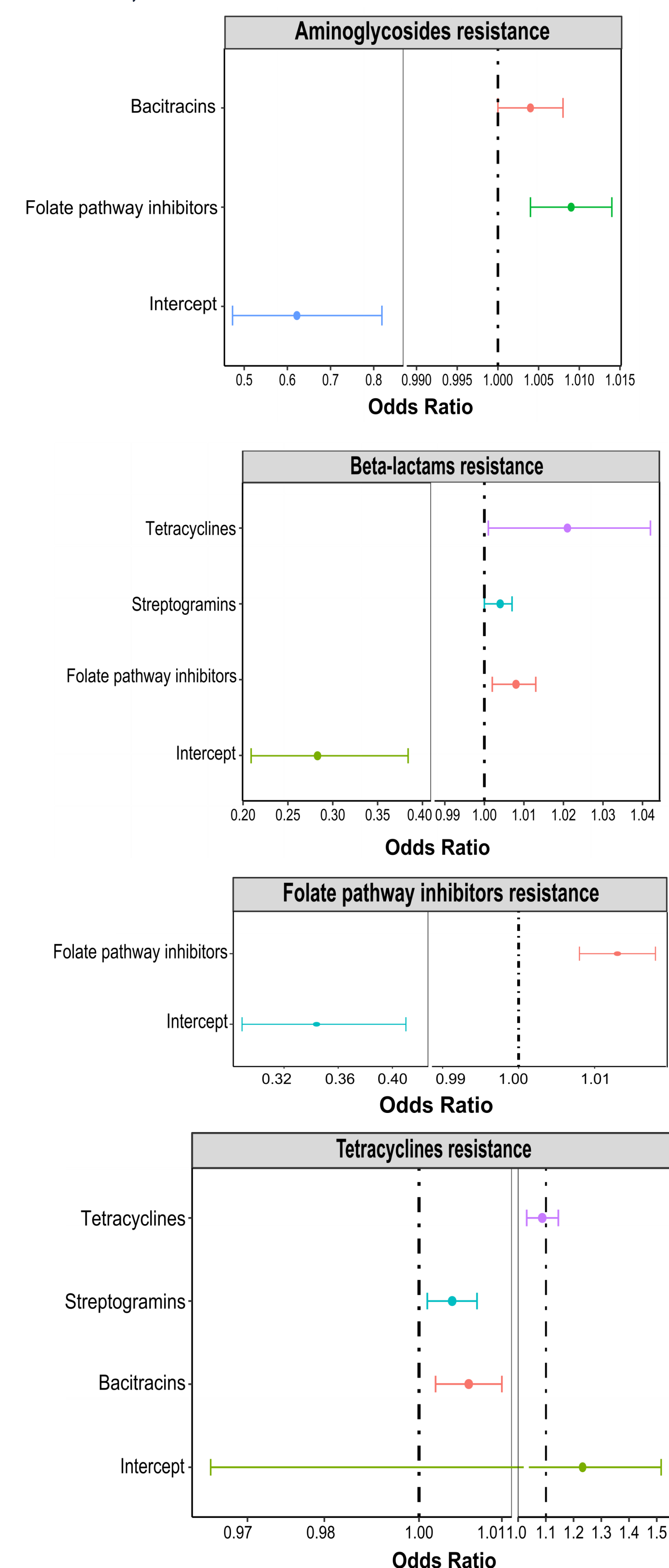


Figure 2: AMU associations with AMR in *E. coli* of turkey

CONCLUSIONS

- Flock-level use of antimicrobials impacted the emergence of phenotypic AMR to the same or unrelated antimicrobial classes.
- The resistance to unrelated AMU could be due to co-selection for AMR or the presence of resistance genes in the environment.
- Continuous on-farm AMU and AMR surveillance is needed to better understand the relationships between AMU and AMR.
- Future molecular epidemiological surveillance studies are needed to provide insights on how the AMR occurring in the turkey flocks.

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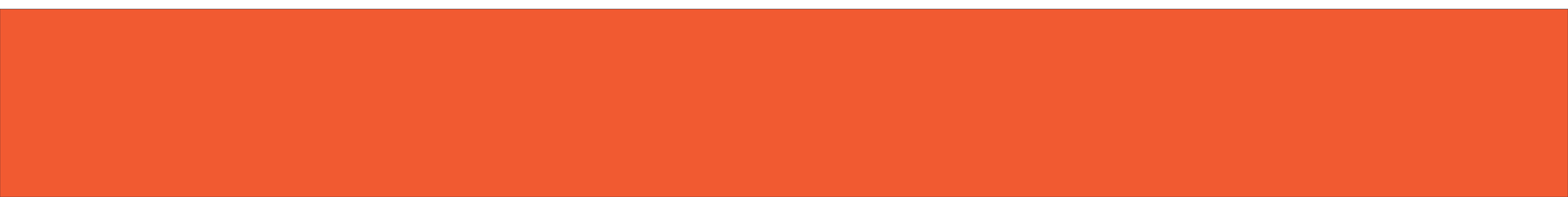
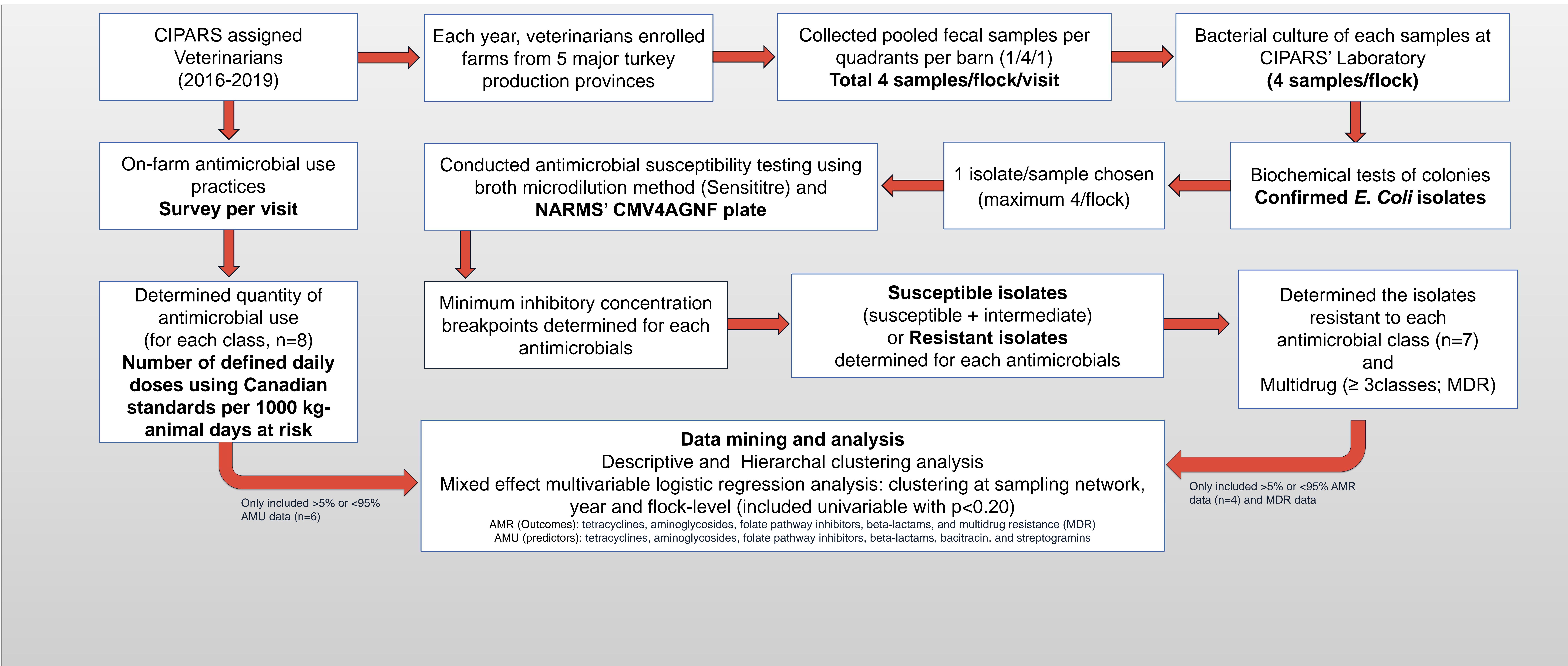
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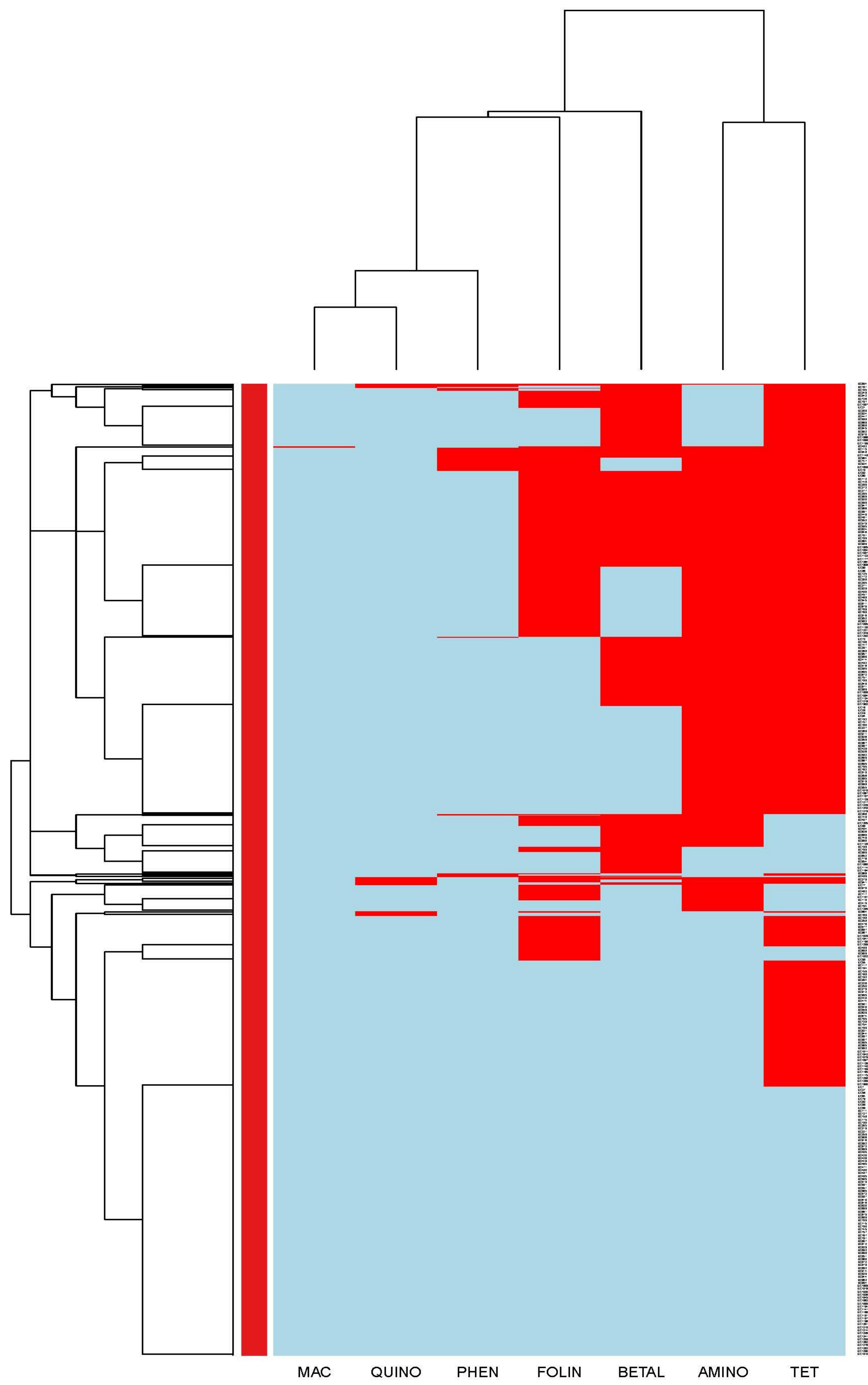


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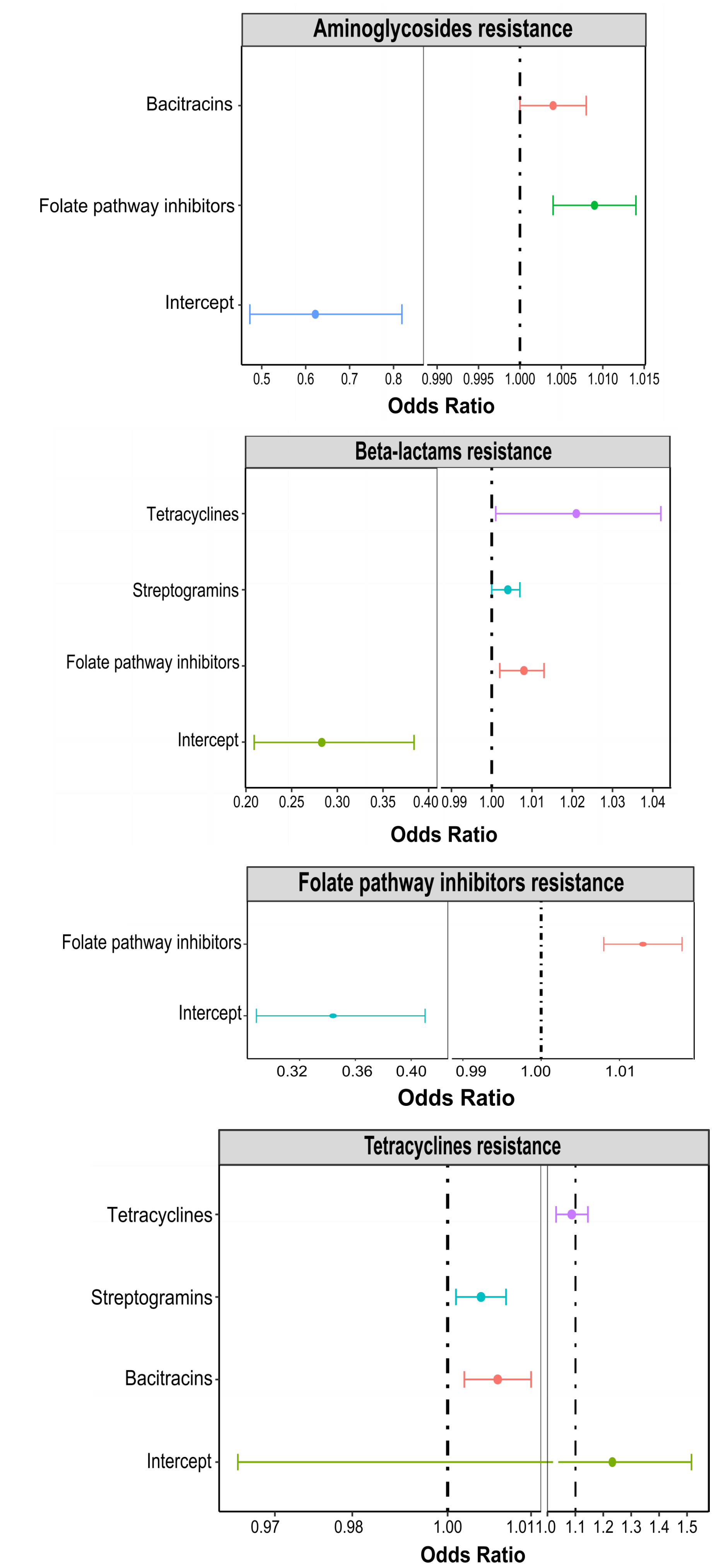


Figure 2: AMU associations with AMR in *E. coli* isolates of turkey flocks (n=1317)