# **Antimicrobial Resistance in Turkey Flocks**

## <u>Rima D. Shrestha<sup>1,</sup> Agnes Agunos<sup>2</sup>, Csaba Varga<sup>1,3</sup></u>

<sup>1</sup>Department of Pathobiology, College of Veterinary Medicine, University of Illinois Urbana-Champaign, Urbana, Illinois, 61802 <sup>2</sup>Center for Foodborne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada, Guelph, Ontario, ON N1H 7M7, Canada <sup>3</sup>Carl R. Woese Institute for Genomic Biology, University of Illinois Urbana-Champaign, Urbana, Illinois, 61801

# BACKGROUND

Antimicrobial resistance (AMR) is a global health threat worldwide that requires urgent attention. Previous studies have reported the presence of multidrug-resistant bacteria in samples obtained from turkey farms, slaughterhouses, and retail stores, indicating a public health risk. Surveillance systems include *E. coli* as an indicator bacteria for the selection pressure of antimicrobial use because they can acquire and transmit AMR genes to other enteric bacteria. Whereas, evaluating AMR in *Campylobacter* is important since *Campylobacter* is the most common human enteric pathogen. Therefore, the goal of this study is to estimate the prevalence and determine AMR patterns in *E.coli* and *Campylobacter* isolates of Canadian turkey flocks monitored by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) between 2013 and 2020.

# METHODS

CIPARS assigned

Each year, veterinarians enrolled farms from 5 major Collected pooled fecal samples per quadrants per barn (1/4/1)

Bacterial culture of each samples at CIPARS' Laboratory



turkey production provinces

## Total 4 samples/flock/visit

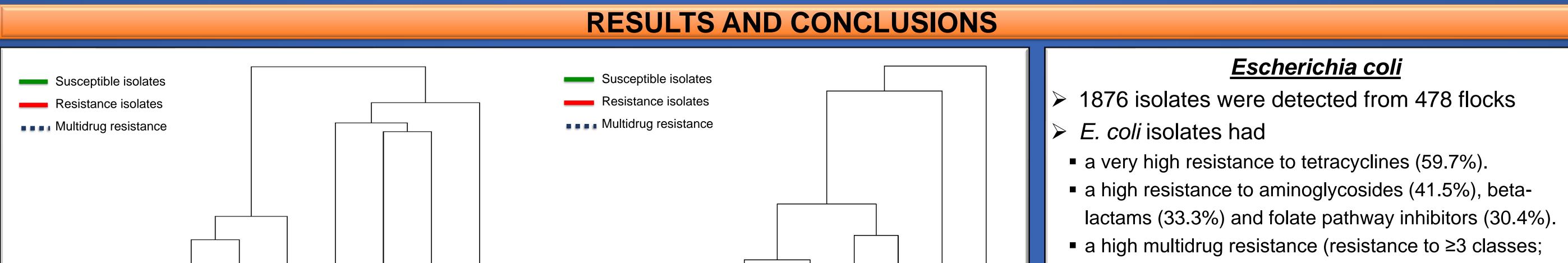
(4 samples/flock)

Conducted antimicrobial susceptibility testing using broth microdilution method (Sensititre) and NARMS' CMV4AGNF plate & NARMS' Campy plate

1 isolate/sample chosen (maximum 4/flock) Biochemical tests of colonies Confirmed E. Coli or Campylobacter isolates

Minimum inhibitory concentration breakpoints determined for each antimicrobials Susceptible isolates (susceptible + intermediate) or Resistant isolates determined Data mining and analysis Descriptive analysis and Hierarchal clustering analysis performed using R software in R-studio platform

Figure 1: Schematic flow diagram of sample collection, and laboratory and data analysis



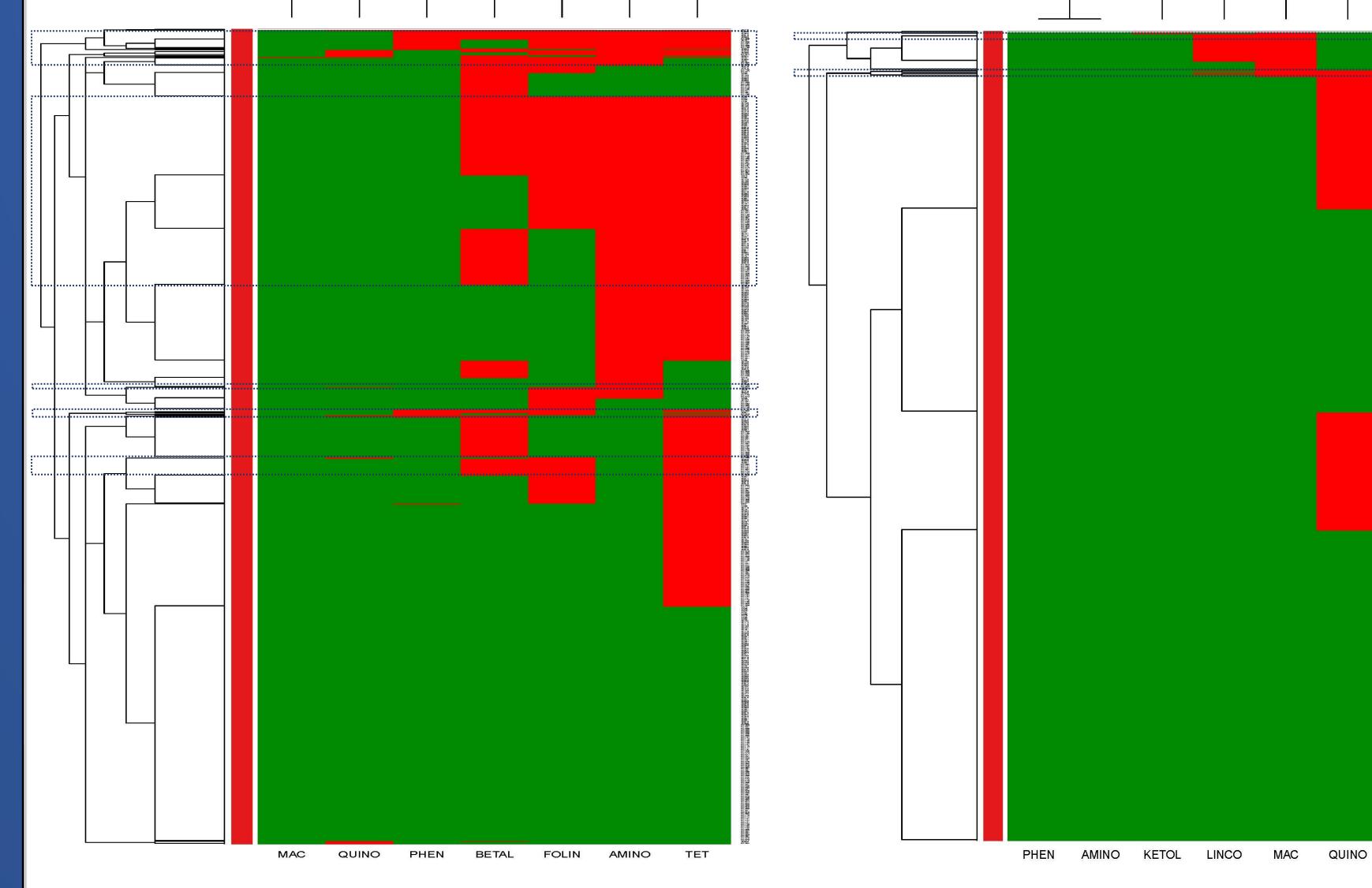


Figure 2: Resistance patterns of *Escherichia coli* isolates to seven antimicrobial classes

Figure 3: Resistance patterns of *Campylobacter* isolates to seven antimicrobial classes

30.9%).

 a very low resistance to phenicols (3.7%), quinolones (1.9%), and macrolides (0.16%).

#### **Campylobacter species**

- > 1094 isolates were detected from 298 flocks.
- 63.9% isolates were C. jejuni and 28.5% were C. coli.
- Campylobacter isolates had
  - a high resistance to tetracyclines (42.5%) and quinolones (31.5%).
  - a low resistance to macrolides (5.7%).
  - a very low resistance to lincosamides (3.7%) and ketolides (0.36%).
  - a low multidrug resistance (MDR; 17.8%).
  - MDR were lower in C. jejuni (17.1%) than C. coli (18.6%) isolates.

### E. Coli and Campylobacter species

- MDR in *E. Coli* and *Campylobacter* species significantly differed among years (p<0.001; p<0.001)</p>
- > MDR in the both bacteria were significantly higher

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.

Multidrug resistant isolates were those isolates resistant to  $\geq$ 3 classes. All the isolates of this study were collected between 2013 and 2020.

in turkey flocks from western than eastern

provinces (*E. Coli:* p=0.016 & *Campylobacter* species: p<0.001) of Canada.

