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Background

The emergence of antimicrobial resistance (AMR) in *Salmonella* from turkeys has raised a food safety concern in Canada as certain serovars have been implicated in human salmonellosis outbreaks in recent years. While several studies evaluated AMR in broiler chickens in Canada, there are limited studies that assess AMR in turkey flocks. Therefore, this study includes a comprehensive data set collected from multiple turkey-producing provinces, and surveillance years (2013-2021).

Objectives

This study aimed: a) To determine the prevalence of AMR and multidrug resistance (MDR) among *Salmonella* serovars recovered from turkey flocks; b) To compare the individual AMR status of *Salmonella* serovars using hierarchical clustering dendrograms; and c) To evaluate differences in the probability of resistance between *Salmonella* serovars using generalized estimating equation logistic regression.

Methodology

1. Study design and data source

- Data were obtained between 2013 and 2021 through a prospective on-farm surveillance study of turkey flocks conducted by CIPARS across four regions of Canada (British Columbia, Ontario, Québec, and a region including the provinces of Alberta and Saskatchewan).
- One flock from each farm (n=421) was randomly selected from each producer per year.
- From each of the four quadrants of the selected flock's barn, one pooled fecal sample (10 fecal droppings per pool) were collected.

2. Laboratory methods

- Isolation of *Salmonella* was performed at the National Microbiology Laboratory (NML) at Saint-Hyacinthe, Québec. A modified MFLP-75 method was applied to isolate viable and motile *Salmonella* from fecal samples.
- Salmonella* isolates were tested for susceptibility to 14 antimicrobials using a microbroth dilution method with the Sensititre Antimicrobial Susceptibility Testing System.

3. Statistical analysis

- Statistical analyses were performed using STATA Intercooled software (Version 17, Stata Corporation, College Station, TX) and R software (R Core Team, 2020) in the RStudio platform (Version 1.4.1106 © 2009–2021 RStudio, PBC).
- To determine differences in the probability of resistance between *Salmonella* serovars generalized estimating equation logistic regression models were used to account for farm-level clustering.
- To compare each antimicrobial for their similarity in the resistance status of major *Salmonella* serovars, hierarchical single-linkage clustering dendrograms (heatmaps) were constructed.

Results

- 1,367 *Salmonella* isolates were recovered from collected samples.
- 55.3% of the isolates were resistant to at least one antimicrobial and 25.3% were MDR (resistant to ≥ 3 antimicrobial classes).
- The three most frequently occurring serovars were *S. Uganda* (22.9%), *S. Hadar* (13.5%), and *S. Reading* (12.0%).
- The three most frequently MDR serovars were *S. Uganda* (43.1%), *S. Hadar* (11.3%), and *S. Agona* (10.1%).
- Streptomycin-sulfisoxazole-tetracycline (n=204) was the most frequent MDR pattern identified.

Heatmaps showed co-resistance to:

- Quinolone class antimicrobials (ciprofloxacin and nalidixic acid) among *S. Reading* isolates.
- Gentamicin and sulfisoxazole in the *S. Heidelberg* isolates.
- Ampicillin and ceftriaxone among *S. Agona* isolates.
- Gentamicin and ampicillin in the *S. Senftenberg* isolates.

Our regression model revealed:

- Salmonella* Hadar isolates had higher odds of resistance to tetracycline (OR:152.1, 95% CI:70.6-327.4) compared to the other serovars.
- Salmonella* Senftenberg showed a higher probability of being resistant to gentamicin (OR = 5.80, 95% CI = 3.11-10.78) and ampicillin (OR = 2.14, 95% CI = 1.13-4.06).
- Salmonella* Uganda had the highest odds of being MDR (OR: 4.7, 95% CI: 3.7-6.1).

Resistance of *Salmonella* isolates to 14 antimicrobial agents

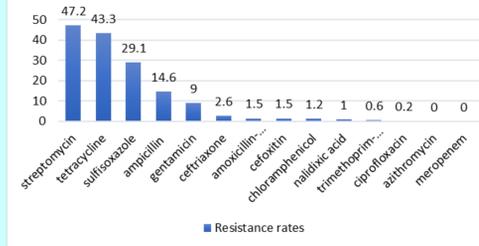


Figure 1. Resistance (%) of *Salmonella* isolates (n= 1367) to 14 antimicrobial agents.

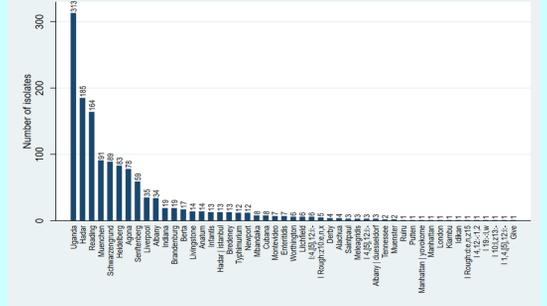


Figure 2. The frequency of *Salmonella enterica* serovar isolates (n=1367) of Canadian turkey flocks, 2013– 2021.

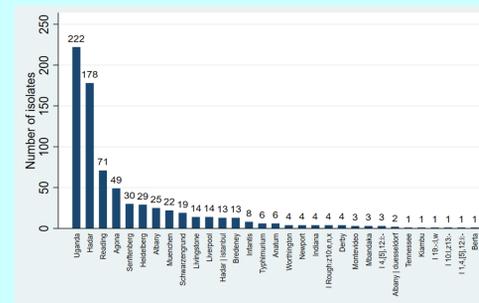


Figure 3. Number of isolates resistant to at least one antimicrobial agent (n=756) in *Salmonella* serovars recovered from Canadian turkey flocks (2013-2021).

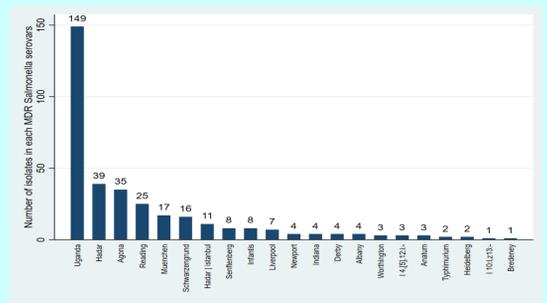


Figure 4. The number of MDR *Salmonella* serovars (n=346) isolated from turkey pooled fecal samples in Canada from 2013 to 2021.

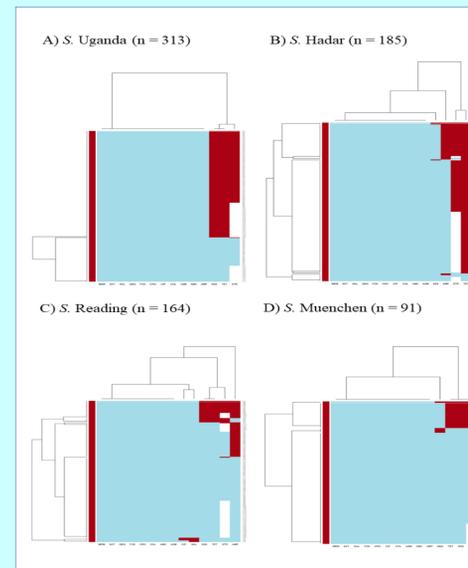


Figure 5. Antimicrobial resistance clustering dendrogram of *Salmonella* serovars isolated from turkey pooled fecal samples (2013-2021). Red color = resistant; blue color = susceptible.

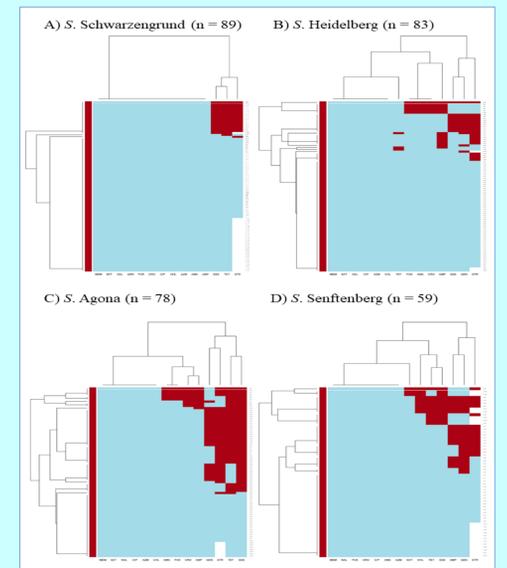


Figure 6. Antimicrobial resistance clustering dendrogram of *Salmonella* serovars isolated from turkey pooled fecal samples (2013-2021). Red color = resistant; blue color = susceptible.

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Conclusion

- Our results showed moderate to high levels of resistance to antimicrobials of lower importance used in human medicine in the major detected *Salmonella* serovars.
- A low level of resistance to critically important antimicrobials, notably Category I and Category II antimicrobials in Canadian human medicine was also observed in some of the *Salmonella* serovars in this study.
- The high resistance to antimicrobials commonly used to treat poultry bacterial infections as well as the presence of resistance in critical antimicrobials highlights the necessity of judicious antimicrobial use to limit the emergence of MDR *Salmonella* in the Canadian turkey industry.
- Differences in AMR patterns among the most frequently recovered *Salmonella* serovars highlight the need to implement serovar-specific mitigation strategies.
- Our results provide useful data that will benefit our understanding of AMR among different *Salmonella* serovars of turkey farms. These findings may also aid in the development of effective national antimicrobial stewardship programs to monitor AMR in *Salmonella* serovars and to reduce the presence of multidrug-resistant *Salmonella* serovars in the turkey industry in Canada.

Acknowledgments

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