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Which one accounts for more human exposure to Extended-spectrum cephalosporin-resistant *Escherichia coli*, *Salmonella* & Fluoroquinolone -resistant *Campylobacter* in Canada?

The Chicken? *The Cow?* *The Pig?*

CP Murphy[1], J Marleau[2], C Carson[1], B Smith[3], B Chapman[3], R Reid-Smith[1], A Deckert[1], and EJ Parmley[1]

Canadian Integrated Program for Antimicrobial Resistance Surveillance, Public Health Agency of Canada[1]; Department of Biology, McGill University[2], National Microbiology Laboratory, Public Health Agency of Canada[3]

Background

- Agricultural antimicrobial use (AMU) may be linked with antimicrobial-resistant infections in people.
- Integrated assessment models (IAM) have the capacity to synthesize data from complex systems to support decision making or policy development.
- IAMs are able to integrate data reported on different scales, using different methods of measurement and sources of uncertainty, including surveillance derived data.
- These results are a component of a larger project to build a framework to assess human exposure to resistant bacteria from food animals using an IAM

Methods

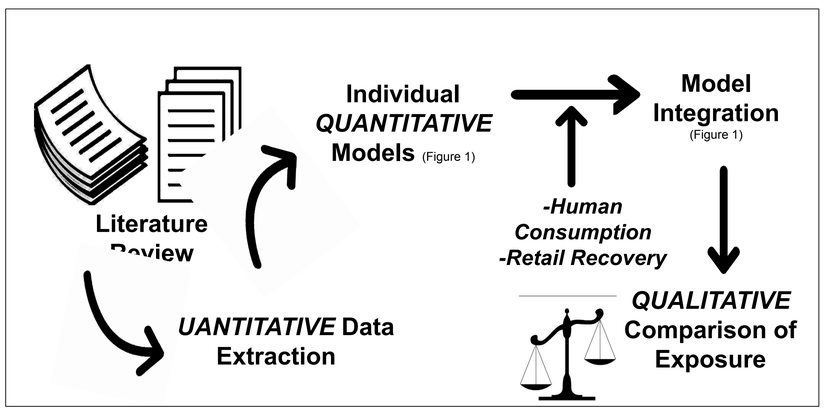
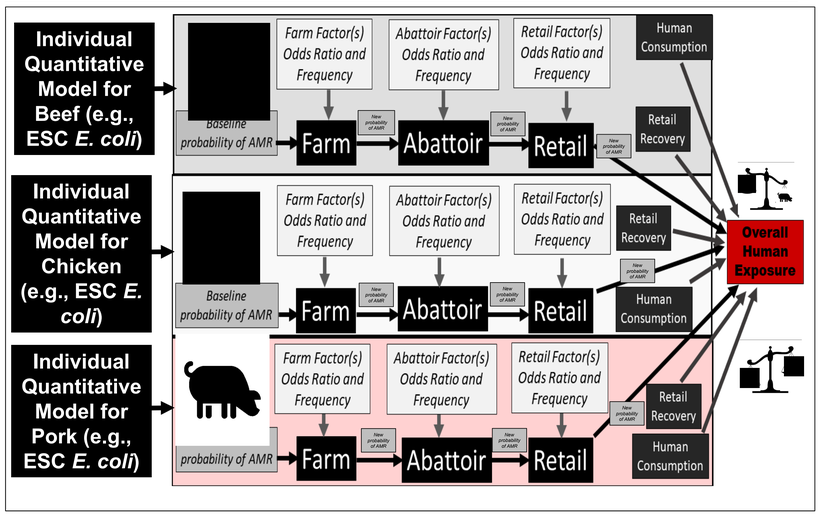


Figure 1 : Individual quantitative models and integration at consumption.

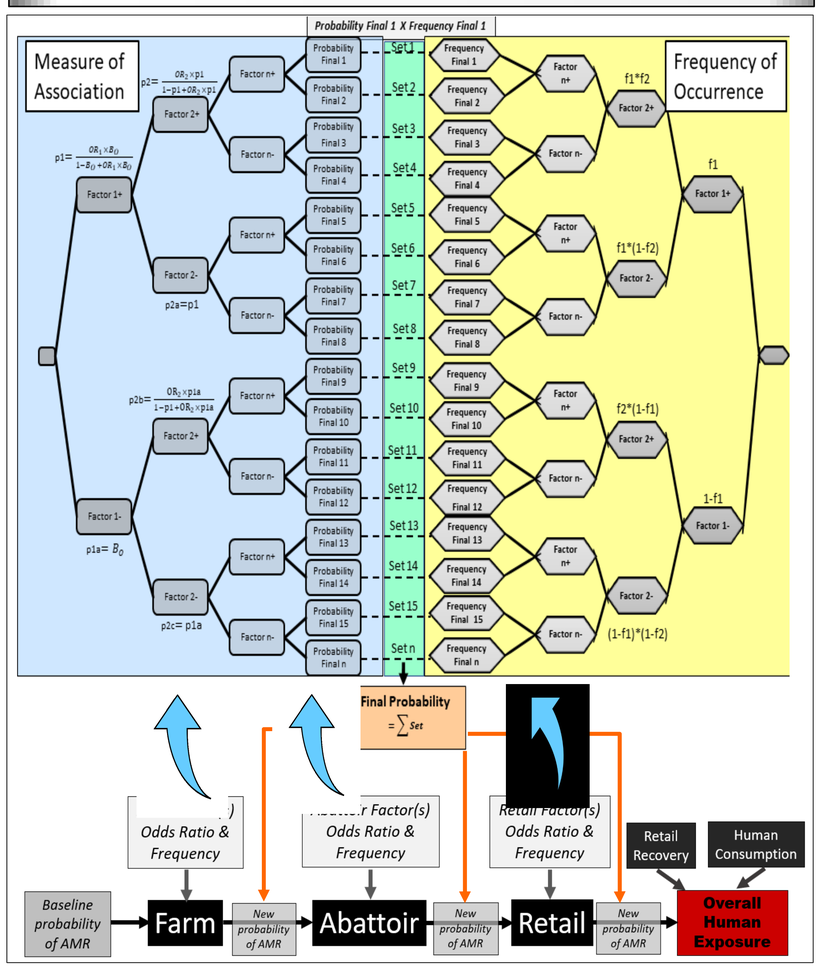


- Odds ratios between factors and AMR were calculated from data extracted from the literature.
- The Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) provided the baseline probabilities of AMR (phenotypic: susceptible, resistant) and bacterial retail recovery rates
- Human consumption data on beef, chicken, and pork were obtained from the Foodbook Report.
- Individual models were integrated at consumption.

Methods (continued)

- Probability of AMR was adjusted by the odds ratio between factors and AMR and the frequency of occurrence of factors and was propagated using a branching tree approach at each site (farm, abattoir and retail) (Figure 2).

Figure 2 : Propagation of probability of AMR adjusted by the odds ratio between factors and AMR, and frequency of occurrence of factors.



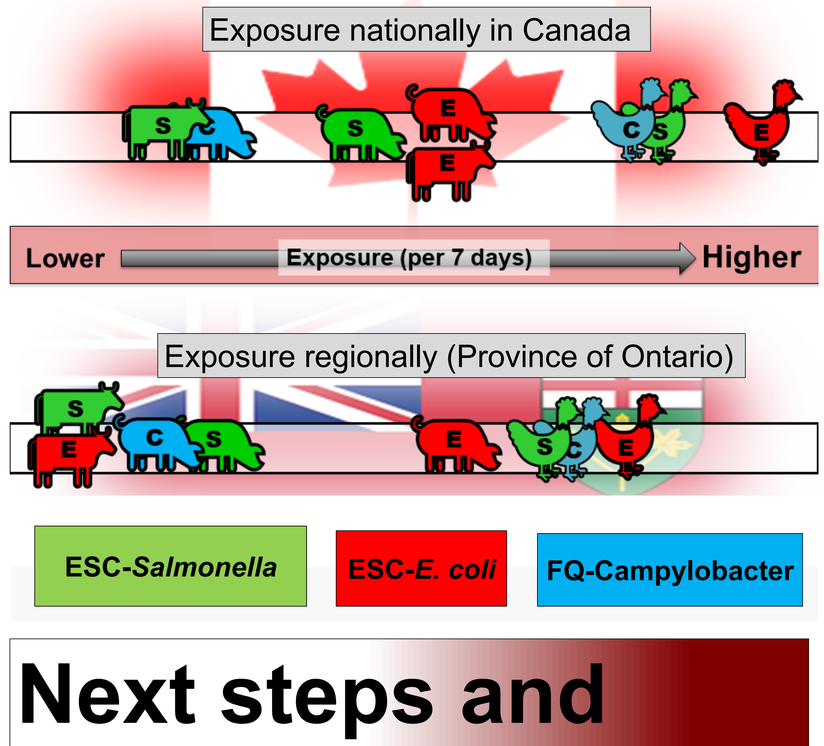
Results

- Potential human exposure to ESC-*E. coli*, ESC-*Salmonella* and FQ-*Campylobacter* was comparatively higher through chicken (Figure 3).
- The relative potential human exposure through pork varied by AMR-bacteria and region (Figure 3).

Additional information:

- The number of references identified through the literature search, contributing data to the models ranged from 2-7.
- A beef FQ-*Campylobacter* model could not be constructed as no factors relevant to Canadian beef production were identified.
- Most studies were performed in populations outside of Canada.
- With the exception of the model for chicken, factors were only identified at the farm level.
- Most of the factors in the model were exposure to or use of antimicrobials followed by management system (conventional, antibiotic free).

Figure 3 : Qualitative comparison of potential human exposure to ESC-*E. coli*, ESC-*Salmonella* and FQ-*Campylobacter* through chicken, beef and pork



Next steps and research gaps

Future refinements and Additions:

- Incorporate whole genome sequence data.
- Post-processing factors (e.g., cooking, cross-contamination)
- Commodity-specific production stage factors (e.g., parent flocks and hatcheries, feedlots, nursery pigs)
- Quantifiable AMU metrics
- Human and environmental factors
- Additional data from future research, stakeholders or other sources (e.g., grey literature).

Research gaps and needs:

- Specific AMU metrics
- Data from Canadian populations including interventions such as vaccination, animal/farm density, intensity of management.
- Additional interventions along the agri-food chain including farm, abattoir and retail
- Relationships between factors associated with animal illness (e.g., vaccination) and AMU and AMR
- Better understanding of the relationships between measurements along the agri-food chain (e.g., measurement of AMR on farm and its relationship to AMR in retail meats).
- Pathogen reduction interventions on reducing AMR bacteria through the agri-food chain.

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