Background:

Objective: *Salmonella* Enteritidis (SE) is a leading cause of foodborne illness in BC and Canada, and has known links to the agriculture/food industries (e.g. poultry, eggs)\(^1\). To better understand the degree of linkage, a genomic pilot study was launched using retrospective data from 2016, during a period where several known outbreaks occurred.

- Hypothesis: Performing surveillance of both human and animal/food/environmental SE, from the same time period, will help to quantify how much human SE illness is linked to the agriculture/food industries.
- This knowledge can assist with outbreak prevention and intervention strategies, inform policy development, and protect Canadian industries from financial loss (via inaccurate product recalls, etc).

Methods:

- Genome sequencing and wgMLST analysis was performed to identify the proportion of agricultural SE clustering with human SE (proportion of human illness potentially linked to the agri-food industry).
- The 2016 isolates were then compared to BC human isolates (2249 SE total) from other years (1998-2019) to assess how strains may persist and shift over time.
- Pure culture of 611 isolates of *Salmonella* enterica serovar Enteritidis were subjected to whole genome sequencing, from the study period:
  - March 1 – August 30, 2016 (Human isolates)
  - January 1 – August 30, 2016 (Animal/Environmental isolates, to account for any lag in product distribution for human consumption)
  - 445 human (405 passed WGS QC)
  - 160 agricultural/food/environment (93 Animal/Agricultural; 43 Food; 20 Environmental = 156 total, passed WGS QC)
  - 587 isolates, total, passed WGS QC
- Phylogenomic analysis: BioNumerics v7.6.2 wgMLST schema for *Salmonella*
  - Included isolates from 6 known BC outbreaks from the same time period as the study time frame (noted on clades at right).

Results:

For 2016 data:
- 28 clades (3+ isolates) were observed at <10 allele differences.
- Human SE were found in all clades, and 12 clades also contained agricultural SE (155/156 isolates).
- 61% of human SE were in clades containing agricultural SE.
  - The largest clade contained 31% of the total study isolates.
  - 39% of human SE were not associated with the 2016 agricultural isolates sampled.

When combined with SE from other years (2249 SE from 1998-2019):
- 57 clades (of 5+ isolates) were observed at <10 allele differences.
- Human SE (1326 isolates) were found in all clades, and 314 Agricultural SE were found in 10 clades.
- 49% of all human SE were contained in clades with agricultural isolates.
- Most clades (50/57) spanned multiple (2-9) years, the largest spanned 2009-2019.

Conclusions:

- Human SE was strongly linked to agriculture/food isolates via wgMLST analysis.
- Over 60% of human SE illness may be linked to the agri-food industry.
- Many strains also appeared to persist over several years.
- Some clusters appeared to have no links to agriculture, which may be indicative of other niches that contribute to human illness, and may be worth investigating further. Alternatively, this may also indicate a need to include other agricultural sectors not currently assessed.

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References: