ALBERTA **INNOVATES**

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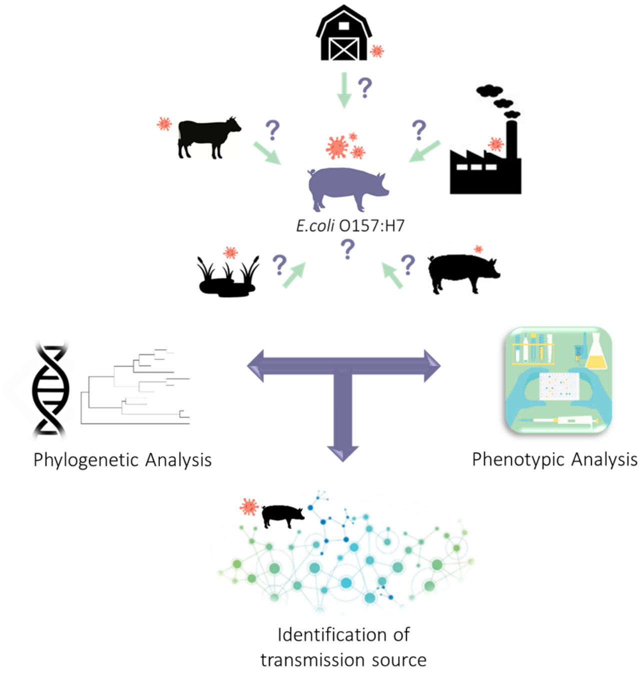
AGRICULTURE FUNDING CONSORTIUM

Comparative genetic characterization of *E. coli* O157:H7 from pigs and cattle, feces and carcasses

While Shiga toxin-producing *E. coli* (STEC) O157 prevalence is relatively low in pigs, nearly 25 per cent (three of 13) of all global outbreaks since 2014 occurred in Alberta licensed abattoirs, one of which was the second-largest outbreak in Canadian history. The underlying cause is not well understood and is of great concern to public health and the Alberta pork industry. Whole genome sequencing will be applied to determine similarities and differences in the genetic makeup of STEC O157 found in various sources (pigs, cattle, feces, and carcasses) to determine the root cause of STEC O157 outbreaks associated with pork in Alberta.



FUNDING DETAILS

RECIPIENT:

Agriculture and Agri-Food Canada
PI: Xianqin Yang

PARTNERS:

Alberta Agriculture and Forestry

TOTAL BUDGET:

$381,100

AI FUNDING:

$136,808

PROJECT DATES:

Mar 2019 - Sep 2023

PROJECT TRL:

Start: 3
End:5

APPLICATION

Understanding the route by which STEC O157 contaminates pork is of paramount importance in preventing future food contaminations. This work will fully characterize genomes and phenotypic properties associated with stress tolerance of STEC O157 from pigs, pork, cattle, and environmental sources to pinpoint the route of transmission of STEC O157 to pork. Information from this study will provide the industry and regulatory bodies science-based recommendations to mitigate risks associated with STEC O157 in pork.

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PROJECT GOALS

- Determine the genetic relatedness among STEC O157 isolates of various populations (swine, cattle, pork, environment, and outbreak isolates associated with pork) using core genome analysis to identify origins of foodborne contamination.
- Open ended pan-genome analysis to identify genomic content specific to each population of STEC O157.
- Profile mobile elements, antibiotic resistance genes, virulence genes, and stress tolerance related genes.
- Phenotypic characterization of STEC O157 from various populations in their response to desiccation, heat, biocides, and their biofilm-forming ability.
- Develop recommendations for STEC O157 control in pork based on the origin of the STEC O157 contaminating pork inferred from both phenotypic and WGS characterization of the populations.

BENEFITS TO ALBERTA

- Minimize outbreaks of STEC O157 associated with pork produced in Alberta, which in turn results in improved food safety in Alberta. This will be achieved through better understanding of the origin of STEC O157 on pork.
- This project will contribute to implementation of whole genome sequencing (WGS) for STEC outbreak investigations and Alberta-based researchers are currently developing capacities and becoming global experts in this area.

Up to 39 Industry Partnerships

3 Scientific Papers & 2 Presentations

6 Industry Communications

4 Highly Qualified Personnel

5 Public Health Partnerships

CURRENT STATUS

MAY 2021

Pig and pork production environmental STEC O157 isolates were classified into seven distinct yet related phylogenetic groups. The genomic characterization in the pig isolates may represent a branch of *E. coli* O157 originating from cattle but evolved to pig gut conditions, indicating that pigs can be a significant source of *E. coli* O157. Additionally, most of the isolates from pigs carry the more potent Shiga toxin subtype for human illness.