E. coli O157 super-shedding in cattle and mitigation of human risk

Area of research interest: Foodborne pathogens
Study duration: 2014-09-01
Conducted by: Food Standards Agency and Food Standards Scotland

Background

This research was funded to investigate Escherichia coli O157 high level excretion (super-shedding) from cattle and the threat this poses to human health.

Cattle are a reservoir of a specific type of E. coli bacteria known as E. coli O157 and it is shed in the faeces of ruminant animals.

These bacteria can produce toxins (Shiga toxins) that can cause life-threatening human infections. It has been implicated in outbreaks of human disease via the cross-contamination of foods and direct contact with the faeces of affected animals.

Research Approach

Previous work has shown that there are different subtypes of E. coli O157 and that the particular subtypes excreted from the cattle in the highest amounts are those which are directly associated with the most severe human infections.

A significant part of the programme was based on surveys of the prevalence of E. coli O157 in faecal pats across 110 farms in Scotland and 160 in England & Wales which were completed between September 2014 and November 2015.

The work in this programme had four main objectives, which were to:

- examine how common E. coli O157 is across cattle farms in both Scotland and England & Wales.
- then compare (by genome sequencing) the E. coli O157 subtypes isolated from cattle with those isolated from human infections to understand if specific subtypes in animals pose more of a threat to human health.
- test if high level excretion (known as ‘super-shedding’) is associated with the bacteria being able to produce a specific type of Shiga toxin
- test a vaccine developed to limit E. coli O157 excretion from cattle and determine if its use can be a way to prevent transmission of the bacteria between cattle and humans.

Results

Our research has established that levels of E. coli O157 in cattle have remained relatively constant in Scotland over the last decade and are equivalent to those in England & Wales. Approximately 20% of farms and 10% of animals were positive for E. coli O157 based on faecal pat sampling.

The diversity of E. coli subtypes in cattle was, however, much greater in England & Wales compared to Scotland which had a high level of a certain subtype associated with super-shedding and severe human infection. Local exposure to this subtype may explain the higher human incidence in Scotland compared to England & Wales.

The accuracy of whole genome sequencing helps define which specific subtypes are associated with an outbreak; it can help trace the origin of an outbreak and can be used to make predictions about the threat to human health posed by specific isolates.

The research established that Shiga toxin subtype 2a is important for transmission of E. coli O157 between cattle as it enabled bystander animals in a group to become colonised following introduction of an animal excreting E. coli O157. The trialled vaccine limited both excretion from cattle as well as transmission to cattle and our modelling indicates that such a vaccine should be of significant benefit in terms of reducing human exposure and infection from E. coli O157.

Research Report

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