Differential typing of Campylobacter

Campylobacter (C. jejuni/C. coli) is the major cause of human gastrointestinal illness in Australia, with rates of infection approximately double those for Salmonella each year. While poultry are a source of these infections, there is a considerable body of evidence which indicates that there are other origins.

A recent report, “Differential typing of Campylobacter”, has determined an effective typing scheme which will increase our capacity to identify specific sources of strains of Campylobacter, resulting in improved epidemiological investigations.

In this study, the genotyping results clearly show that there are sources other than poultry meat associated with human campylobacteriosis.

The issue

Campylobacter (C. jejuni/C. coli) is the major cause of human gastrointestinal illness in Australia, with rates of infection approximately double those for Salmonella each year. While poultry are a source of these infections, there is a considerable body of evidence which indicates that there are other sources, for example contaminated water, unpasteurised milk and pets.

The propagated view that raw or undercooked poultry products are the major source of human Campylobacter infections is based on research from the 1980s. However, it is now recognised worldwide that there are multiple non-poultry potential sources for transmission of Campylobacter into the human population.

The project

In order to determine the multiple sources for transmission of Campylobacter into the human population, this report examines methods for typing C. jejuni/C. coli. More specifically, this project applied a DNA-based typing scheme to over 500 Campylobacter isolates originating from six different host species: humans, chicken, dairy cattle, feedlot cattle, dogs and cats.

Multilocus Sequence Typing (MLST) has emerged as a key technique for discovering the source of Campylobacter infections as it is already in use in clinical typing applications in Australia. However, this method is expensive and requires DNA sequencing of at least seven different genes. There are now options for significant cost reduction through the use of a typing scheme combining MLST with single-nucleotide polymorphism (SNP) analysis which is user friendly, easily transportable between research groups and is relatively cheap.

An effective typing scheme, when supported by other information such as conventional epidemiological knowledge, will increase our capacity to identify specific sources of strains of Campylobacter, resulting in improved epidemiological investigations.
Results

This report concluded that the technique of using SNP typing is the preferred method for establishing the source of outbreaks of campylobacteriosis, and is a methodology that is relatively easy to implement and provides results which are comparable internationally. The specificity of this analysis will allow sources of outbreaks of campylobacteriosis in humans to be more correctly determined.

In this study, the genotyping results clearly show that there are sources other than poultry meat associated with human campylobacteriosis. While under-cooked poultry products continue to be accepted as a significant exposure method, there is now a better appreciation that other exposure methods exist and play a role in the overall picture of human campylobacteriosis.

Recommendations

A number of recommendations for food safety professionals, regulators and the industry research body have come from this study:

- SNP typing should be considered as a front line typing method when investigating outbreaks of campylobacteriosis or when looking for host associations with particular genotypes of Campylobacter
- Pets need to be considered as a source of C. jejuni for humans
- The preliminary evidence uncovered in this study of regional and company influences on Campylobacter genotypes in chickens requires further research.

For more information

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RIRDC publication no. 14/030 “Differential typing of Campylobacter” is available from the RIRDC website www.rirdc.gov.au or by phoning 1300 634 313