

## Scientific Interpretive Summary: Dynamic modelling of *Campylobacter* sources in the Manawatu

Source attribution is the process of determining the proportions that the various pathways and sources contribute to the total disease incidence. This information is critical in creating targeted intervention strategies, and for assessing their effectiveness.

Traditional approaches to source attribution include quantitative risk assessments, analysis and extrapolation of surveillance or outbreak data, and analytical epidemiological studies. The molecular epidemiology of human campylobacteriosis was studied in the Manawatu (*Quantifying the proportion of human campylobacteriosis attributable to consumption of poultry meat in New Zealand: a Manawatu case study*). Using the advanced molecular genotyping technique of Multi-locus Sequence Typing (MLST), combined with novel statistical modelling tools, the relative contributions of different food and environmental sources to the incidence of human infection with *Campylobacter jejuni* was estimated.

There have been several models proposed for source attribution, each of which assesses the proportion of infections attributable to a particular source in various ways. These models, however, do not take into account temporal variation that may occur in the data, a factor of pivotal interest to a food regulator when control measures are being monitored. Of the existing models, the Modified Hald and Island models are most amenable to the incorporation of temporal variation. Each of these models attributes a human infection to a source with a certain probability, based on sequence type information, such as from MLST.

This project examines the suitability of various models to take account of temporal variation (dynamic) source attribution of human cases of potentially foodborne disease, using campylobacteriosis as the demonstration illness.

The modified Hald model was shown to be the most appropriate for dynamic source attribution of human cases to sources. This model allows factors associated with each source to change through time, such as adjusting for changes in food preparation practises or industry processing. The Island model should not be disregarded, however, being useful at assigning particular isolates to a source, allowing categorisation of human cases for further modelling purposes. These models may be applicable to other diseases as long as the distribution of source isolates is reasonably stable through time, and that a sufficient number of human isolates are available to balance the requirements of temporal resolution and model accuracy. A temporal resolution allowing an average of at least 20 isolates per time period would be an appropriate starting point.

This study was undertaken as part of the NZFSA foodborne illness surveillance strategy to further inform the aetiology of human campylobacteriosis, using novel approaches to food

source attribution in a particular geographical location. Linkage to human surveillance data was used to give new insight into the epidemiology of the disease in New Zealand.

The source attribution modelling identified poultry as the most important source of human infection. The estimated contribution of consumption of poultry using different attribution models was 52% (Dutch model), 67% (modified Hald model) and 75% (Island model). Ruminants contributed 17%, 23% and 17% of human cases respectively when these models were applied and smaller contributions came from wild birds and environmental sources. There was a small decline in the proportion of cases attributable to consumption of poultry meat in year three of the study than previously and an increase in the ruminant proportion.

A single MLST type, (ST-474) accounted for 28%, 34% and 27% of the human cases annually. To find such a dominant strain, and one that is relatively rare internationally, was surprising and unexpected. ST-474 was strongly associated with poultry and was particularly prevalent in the urban areas as were other poultry-associated strains. Other strains were associated with ruminant sources, and were prevalent in the rural areas. There were major age distribution and occupational differences; ruminant-associated cases being more common in young children and adults with occupations that would bring them into contact with ruminant faeces than were found in poultry-associated cases.

Using a sentinel surveillance site, this study has provided essential quantitative evidence on the importance of poultry as a source of human campylobacteriosis in New Zealand, especially in urban areas. It has underlined the importance of ruminants as a source of infection, especially in young children and rural dwellers. These data demonstrate that a hazard reduction programme aimed at significantly decreasing *C. jejuni* contamination of fresh poultry meat has the potential to at least halve the number of cases of human campylobacteriosis in Manawatu, and, given the demonstration of comparable findings in validation studies in Auckland and Christchurch, in New Zealand as a whole.

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