Campylobacter jejuni microevolution and phenotype:genotype relationships

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Anja Friedrich

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Massey University
mEpiLab | Infectious Disease Research Centre (IDReC)
Institute of Veterinary, Animal & Biomedical Science
Palmerston North, New Zealand

Abstract

Campylobacter spp. are a major cause of human gastroenteritis. Their wide host range, environmental distribution and high genetic diversity contribute to the complex molecular epidemiology of campylobacteriosis. The aim of this multidisciplinary thesis is to investigate the phenotype:genotype relationships of *C. jejuni* and how they influence the micro-evolution of these bacteria in New Zealand.

The first study used a time series of genotyped human campylobacteriosis cases from a region of New Zealand to investigate if the clonal complexes (CCs) identified in human cases showed a seasonal pattern. The analysis revealed a prevalent clonal complex (CC-45) which showed a consistent summer peak.

The second study applied phylogenetic and population genetic tools to describe the population structure and host associated genotypes within the *C. jejuni* population in wild and agricultural animals. The findings showed that the *C. jejuni* isolates from non-agricultural animals exhibit a higher number of mosaic alleles and fewer shared sequence types (STs) between the host groups, whereas the *C. jeuni* in agricultural animals show a higher number of shared STs and fewer occurrences of admixture.

The third study tested the ability of a variety of *C. jejuni* isolates to utilise 95 substrates as carbon sources and tested their tolerance to different osmotic conditions using phenotypic microarray (PM) technology. These phenotypic expressions were correlated with their genomes and a genome wide association study was used to identify genes associated with the observed phenotype.

The last study made use of data from a dual isolate chicken challenge. The study showed the out-competition of one challenge strain and genetic variations of 15 core single nucleotide polymorphisms (SNPs), 14 of which were non-synonymous point mutations. These SNPs were confined to nine genes all of which were associated with cell shape, chemotaxis or motility of the bacteria.

This thesis has furthered our understanding of the seasonality of human campylobacteriosis in New Zealand, the existing population structure of *C. jejuni*, its biochemical requirements and tolerance to osmolytes and novel insights into short-term evolutionary dynamics *in vivo*. Based on these findings and the recommendations for future directions, this could lead to a greater understanding of host-association and new intervention strategies.

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