The evolution of *Campylobacter*

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mEpiLab, Infectious Disease Research Centre
Institute of Veterinary, Animal and Biomedical
Sciences
at Massey University,
New Zealand.

Shoukai Yu

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Abstract of : The evolution of *Campylobacter*

Author : Shoukai Yu

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The genus *Campylobacter* is a major cause of human gastroenteritis worldwide, so understanding the evolution of *Campylobacter* has important implications. This multidisciplinary project unifies developments from statistics, genetics, bioinformatics and computer science and creates a good opportunity to investigate the evolution of *Campylobacter* by focusing on the factors which affect genetic exchange.

In order to understand how *Campylobacter* evolves, a mathematical method is put forward to estimate the relative rates of recombination and mutation in generating new alleles that lead to single locus variants (SLVs), and examine the effect of selection, recombination and mutation. This analysis shows the importance of recombination in the evolution of *Campylobacter* and larger contribution made by recombination, compared to mutation, in the evolution of *Campylobacter jejuni*, and *Campylobacter coli*. In addition, this research demonstrates that purifying selection plays an important role in the evolution of *Campylobacter*. For comparison, this analysis also examined the role played by recombination in the evolution of other bacteria. This application highlighted the importance of recombination for creating diversity in closely related isolates.

A range of phylogenetic and population genetic tools were applied to investigate the effect of geographical isolation on the evolution of *Campylobacter* by comparing datasets from two geographically separated countries, New Zealand and the United Kingdom, this is the first time this has been attempted. Analysing sequence data at different levels of resolution provided evidence that geographical isolation affects the evolution of *Campylobacter* genotypes over short time-scales, but that this effect diminishes over longer time-scales. Furthermore, this analysis estimates the time for divergence of NZ specific lineages of *Campylobacter* strains.

In New Zealand, *Campylobacter jejuni* strain type 474 (ST-474) is responsible for more than a quarter of human campylobacteriosis notifications, but has been rarely found outside NZ. Knowing the clonal relationships of ST-474 strains is helpful for inferring the origin and the evolutionary mechanism of *Campylobacter*. This research accessed 59 isolates of *Campylobacter*. It applied a range of phylogenetic tools to targeted gene reference set to compare estimations of the clonal genealogy inferred for *Campylobacter* datasets.

These findings have implications for identifying the origin of *Campylobacter*, developing disease intervention strategies, predicting the emergence of pathogens, and reducing the occurrence of campylobacteriosis in the food supply chain.

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