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THE MICROBIAL ECOLOGY OF  
*CAMPYLOBACTER JEJUNI* IN  
NEW ZEALAND WITHIN A  
SPATIAL-TEMPORAL FRAMEWORK

A thesis presented in partial fulfilment of the  
requirements for the degree of  
Doctor of Philosophy  
in  
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New Zealand

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The journey is the reward.

---

Chinese proverb

Look deep into nature, and then you will understand everything better.

---

Albert Einstein

## Abstract

*Campylobacter jejuni* (*C. jejuni*) is an important cause of gastroenteritis internationally; it is a complex bacterium carried by multiple hosts, showing phenotypic and genotypic variation. This thesis systematically examines the molecular ecology and evolution of *C. jejuni* in New Zealand from the levels of population movement, phenotype, genome and metabolism.

First, the demographic history of cattle, sheep and poultry importations into New Zealand (1860-1979) was quantified. Australia was the most common reported source of cattle sheep and poultry, with large numbers of cattle and sheep being imported in the 1860s, and large numbers of poultry imported from the 1960s onwards. This suggests the population structure of cattle and sheep and the microbial organisms they carried may exhibit a founder effect.

The second level investigated the phenotypes of related sequence types (ST) with generalist and specialist lifestyles and compared them at 42°C and 22°C on the basis of carbon source utilisation in Biolog phenotypic microarrays. The isolates utilised a total of 29 carbon sources in a pattern that clustered them together on the basis of ST at 42°C more than lifestyle and host. At 22°C they utilised a limited palette of carbon sources (9) related to the tricarboxylic acid cycle (TCA).

The third level, used genomic comparisons to identify a putative new species *C. sp. nov.* 4 spp. in the Australian purple swamphen (*Porphyrio porphyrio melanotus*). Overall, the pattern of relationship between isolates associated with the pukeko (*Porphyrio porphyrio melanotus*), takahe (*Porphyrio hochstetteri*) and the Australian swamphen isolates suggested a recent common ancestor and then divergence after separation. Despite high levels of recombination in *C. jejuni*, the genomes grouped by clonal complex and ST, this suggests there are factors restricting regular recombination between more distant *C. jejuni* STs. The draft genomes for the wild-bird and agricultural-related isolates clustered by lineages in a host(s).

The fourth level involved the comparison of *C. jejuni* metabolic pathways (subsystems) to identify host association. Type VI secretion system, Coenzyme A biosynthesis and *Campylobacter* spp. iron metabolism were identified as important pathways in distinguishing between wild-bird and livestock associated isolates.

We stand on the shoulders of giants.

---

used by Sir Isaac Newton

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## Abbreviations

AFLP: Amplified fragment length polymorphism  
AMOVA: Analysis of molecular variance  
AU: Australia  
blood agar: Columbia horse blood agar  
bp: base pair  
BIGSdb: Bacterial Isolate Genome Sequence Database.  
BRENDA: Bacterial restriction endonuclease DNA analysis  
contigs: contiguous reads of DNA sequence  
CPS: capsular polysaccharides  
CDC: Centers for Disease Control, USA  
cfu: colony forming unit  
CC: Clonal complex  
CRISPR: Clustered regularly interspaced short palindromic repeats  
DNA: Deoxyribonucleic acid  
D.O.C: New Zealand Department of Conservation  
ELISA: Enzyme-linked immunosorbent assay  
ESCMID: European Society of Clinical Microbiology and Infectious Diseases  
ESGEM: Study Group on Epidemiological Markers  
ERIC: Enterobacterial repetitive intergenic consensus  
ESR: Environmental Science and Research Ltd.  
EU: European Union  
FAME: Fatty acid methyl ester analysis  
FAFLP: fluorescent AFLP  
G+C%: guanine–cytosine content as a percent of nitrogenous bases in a DNA molecule  
gDNA: genomic Deoxyribonucleic acid.  
HGT: Horizontal gene transfer  
HL: Heat labile antigens  
hr: hour  
HS: Heat stable antigens  
IF0a: Omnilog inoculating fluid IF-0a GN/GP  
kbp: Kilobase pairs (of DNA)  
LOS: lipooligosaccharide mCCDA: Modified Cefoperazone Charcoal Desoxycholate agar  
MLEE: Multilocus enzyme electrophoresis  
MLST: Multilocus sequence typing  
mrp: Macrorestriction profiling  
MYA: million years ago

NCTC: National Collection of Type Cultures (UK)  
nt: Nucleotides  
NGS: Next generation sequencing  
NZFSA: New Zealand Food Safety Authority  
OIE: World Organisation for Animal Health  
Omnilog bags: Biolog Gas Bag (P/N 3032)  
PBS: Phosphate Buffer solution  
PCR: Polymerase Chain Reaction  
peg: protein encoding gene, plural pegs  
PFGE: Pulsed Field Gel Electrophoresis  
PM plates: Biolog Phenotypic Microarray plates.  
PM1: Biolog Phenotypic Microarray plate 1.  
PM2A: Biolog Phenotypic Microarray plates 2A.  
16S rRNA: 16S ribosomal  
RAPD: Randomly amplified polymorphic DNA  
RAPD-PCR: Random amplified polymorphic DNA Polymerase Chain Reaction  
rDNA: Ribosomal DNA  
RE: Restriction enzyme  
REA: Restriction endonuclease analysis  
RFLP: Restriction fragment length polymorphism  
rMLST: ribosomal Multilocus Sequence Typing  
RNA: Ribonucleic acid  
RNAT: RNA thermometers  
rps: ribosomal protein subunit  
SD: Standard deviation  
SNP: single nucleotide polymorphism  
ST: Sequence type, plural STs  
sp: Species (single)  
spp.: Species (multiple)  
subsp.: subspecies  
SVR: short variable repeats  
VBNC: Viable but Nonculturable State  
wgMLST: whole genome MLST  
WGS: Whole genome sequencing  
WHO: World Health Organisation  
WTO: World Trade Organisation



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