



Characterising the drinking water microbiome on campgrounds in New Zealand



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Summary

Whole-genome, 16S and 18S ribosomal RNA (rRNA) analyses combined with conventional isolation techniques are being applied to profile microbial community DNA associated with drinking water on campgrounds. The current study has a serial cross-sectional design and is being conducted on 15 campgrounds that are situated across New Zealand (Figure 1) and are managed by the Department of Conservation (DOC). Preliminary results generally show low *Escherichia coli* counts in water, suggesting minimal faecal contamination, and a low proportion of faecal samples were positive for *Campylobacter* and *Giardia*.

Introduction

Camping is a common activity in New Zealand and drinking water is freely available at most campgrounds. Water quality is therefore an important public health concern for campground management. *E. coli* can be used as an indicator of faecal contamination [1] while metagenomics can be used to not only investigate drinking water public health concerns [2] but also to perform microbial source tracking.

Study Objectives

- To investigate the composition of the aquatic microbial community genome associated with drinking water at DOC campgrounds
- To examine the influence of the activities within the water catchment area on the aquatic microbial community genomes composition
- To develop a protocol for assessing public health risks based on a metagenomics approach and new sequencing technology

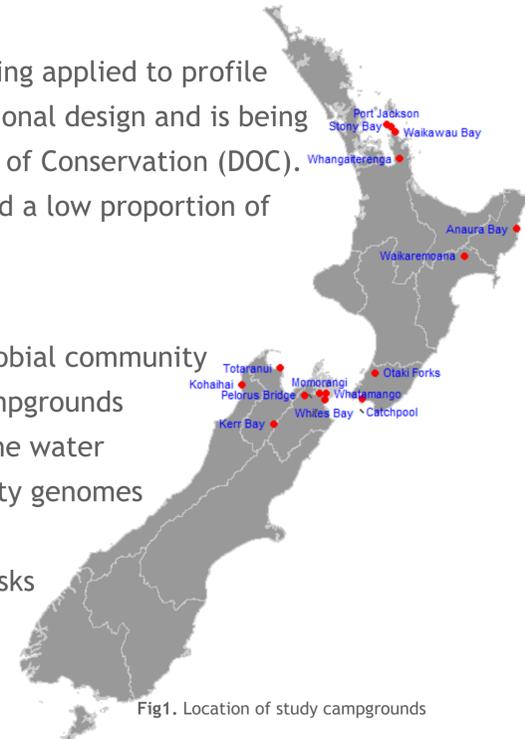


Fig1. Location of study campgrounds

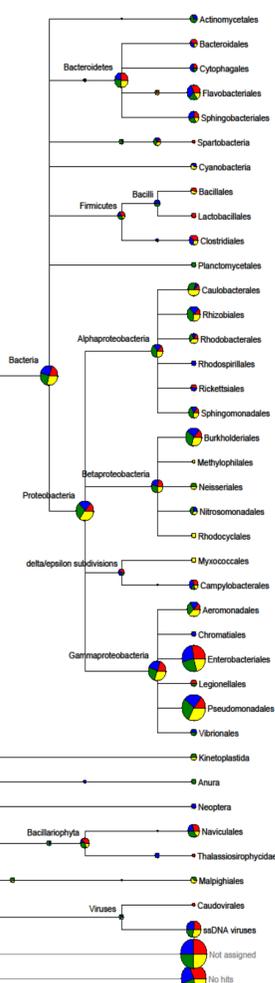


Fig2. MEGAN output showing four sequence quality thresholds having a similar effect on taxonomic classification at the level of order. The quality threshold sets the probability of finding an incorrect base pair in sequences, and the longest contiguous sequences were generated from the reads with probabilities at the threshold or lower. Ten thousand randomly selected sequences of length at least 75 bases were analysed for each threshold. The DNA was extracted from surface water sampled from a river in Manawatu.

Materials and Methods

- Risk based sampling is being conducted during peak camping season (November to March) for two consecutive years
- In the first year, both faecal and water samples were collected at each campground:
 - Faecal samples were screened for *Campylobacter*, *Cryptosporidium* and *Giardia*
 - Water samples were screened for *Campylobacter*, *Cryptosporidium* and *Giardia*
 - E. coli* was enumerated in water samples
 - DNA from water samples was processed using multiplexed 16S rRNA, 18S rRNA and shotgun whole genome sequencing
 - Sequence quality will be assessed using SolexaQA as shown in Figure 2 using data from a pilot study

Preliminary Results

- A total of 333 (284 faecal and 49 water) samples were collected during the first sampling season
- Twenty-five (8.8%) faecal samples were positive for *Campylobacter jejuni*
- Two campgrounds returned a positive *Campylobacter jejuni* test in water on a single occasion each
- A further two campgrounds returned a positive *Giardia* test in water on a single occasion each
- The median *E. coli* count in water was 33MPN/100mL (range: 0-2800)
- DNA extraction proved challenging because of low amounts of DNA in the water samples and difficulty in accessing some water sources to obtain larger volumes of the sample

Conclusion and Expectations

- The current study offers an opportunity to apply both culture-based laboratory methods and metagenomics to enhance the detection of water-borne pathogens in drinking water sources
- Generally, preliminary results indicate that drinking water sources for DOC campgrounds have minimal faecal contamination, but potential pathogens were isolated from four campgrounds
- Residual waterborne infection risk still exists despite evidence of minimal faecal contamination hence the need to strengthen contamination prevention and enhance water treatment
- Metagenomic data may reveal patterns across different water catchments to inform water contamination prevention programmes

Acknowledgements

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Presentation

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References

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