




Complete Genome Sequence of a New Zealand Isolate of the Bovine Pathogen *Streptococcus uberis*

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ABSTRACT *Streptococcus uberis* forms part of the native microbiota of cattle and is able to opportunistically infect the mammary gland; as such, it is a leading cause of bovine mastitis globally. Here, we report the complete genome sequence of *S. uberis* NZ01, isolated in New Zealand from a cow with a clinical case of bovine mastitis.

Streptococcus uberis is a Gram-positive bacterium with a global distribution, being commonly found as part of the native microflora in cattle (1, 2). Opportunistic infection of the bovine mammary gland by *S. uberis* can lead to the bacterium acting as a major pathogen, causing the inflammatory disease mastitis (3). Economic losses associated with bovine mastitis have been estimated at \$35 billion per year globally, with *S. uberis* being the leading cause of bovine mastitis in New Zealand (4) and the United Kingdom (5) and a major cause in the United States (6), Canada (7), and Chile (8), among other countries.

As of this writing, there has been one complete genome of *S. uberis* assembled, which originated from the United Kingdom (2). Here, we report a second complete genome, that of New Zealand strain NZ01, which was isolated from a cow with a clinical case of bovine mastitis in Palmerston North, New Zealand. This complete genome will support efforts to manage bovine mastitis and further our understanding of the evolutionary responses of *S. uberis* to antimicrobial use.

DNA extraction and next-generation sequencing were performed at the Microbiological Diagnostic Unit Public Health Laboratory of the University of Melbourne. Genomic DNA was prepared from a culture grown from a single colony using a JANUS Chemagic workstation and Chemagic DNA/RNA kit (PerkinElmer, USA). DNA libraries were created using the Nextera XT DNA preparation kit (Illumina, USA). Next-generation sequencing was performed using the Illumina NextSeq platform.

The assembly involved a preliminary assembly in Geneious version 10.1.3 (9), followed by repeat spanning and gap closure with Sanger sequencing of PCR products. The complete genome was compared to that of *S. uberis* 0104J (GenBank accession number AM946015) by progressiveMauve alignment (10). Genomic features and coding DNA sequences (CDSs) were predicted with the NCBI Prokaryote Genome Annotation Pipeline (PGAP) (11).

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The complete NZ01 genome comprises a single chromosome of 1,863,842 bp, with 1,808 CDSs and 1,886 predicted genes. Approximately 146 CDSs found in the NZ01 genome are novel, compared to those of strain 1040J from the United Kingdom. Conversely, approximately 163 CDSs found in the UK strain do not appear in NZ01, further illustrating the genomic flexibility of this species (12). Estimates of the *S. uberis* pangenome have been made on a geographically limited set of strains (13), with many of the above-described novel genes identified in NZ01 being found in this pangenome.

An identified prophage in NZ01 (1,520,084 to 1,560,140 bp) has been shown as active, with a subset of next-generation sequencing reads highlighting the presence of a circular phage particle. This could be of interest for the control of bovine mastitis, as the phage encodes multiple holin and lysin genes and may be able to actively lyse *S. uberis* (14).

As further efforts to control *S. uberis* are made, it will be increasingly useful to track the emergence of resistance to these measures, with complete genomes such as that presented here providing a resource for such investigations. A detailed phylogenetic study of this and other New Zealand *S. uberis* isolates will follow, with analysis of both horizontally acquired elements and antimicrobial resistance determinants.

Accession number(s). This complete genome sequence has been deposited at GenBank under the accession number [CP022435](https://doi.org/10.3389/fvets.2017.00063).

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