

Whole genome sequence data of *Chromobacterium violaceum* WCH4, a human pathogenic strain from Sabah, Malaysia

ABSTRACT

Chromobacterium violaceum is a gram-negative, facultative anaerobic bacillus which is commonly found in soil. It can cause mild diarrhoea upon infection but can progress, although rarely, to fatal multi-organ failure and death. Here we report the whole genome sequence data of *Chromobacterium violaceum* WCH4 strain, a pathogenic strain that was obtained from a 78 year old male patient suffering from an eye infection. This is a rare case of human infection of the bacteria. Blood culture report as well as 16S rRNA confirmed the presence of *C. violaceum* WCH4. DNA sequencing using the Illumina HiSeq 4000 system revealed a genome size of 4,637,406 bp with a GC-content of 64.89%. We identified 4,572 protein coding sequences (CDS), 78 transfer RNA (tRNA) genes, and 3 ribosomal RNA (rRNA) genes. The CDS included 1,261 hypothetical proteins and 3,311 proteins with functional assignments. We also identified seven putative genes involved in efflux pump and conferring multidrug antibiotic resistance. The genome data has been deposited at NCBI under the accession number JAFBBB000000000 and consist of full annotated genome and raw sequence data. Our data resource will assist in further downstream analysis and understanding of the mechanism of rare human infection caused by *Chromobacterium violaceum* WCH4 strain.