

Genomic Analysis of a Novel Antarctic Bacterium, *Cryobacterium* sp. SO2 Provides Insights into its Genomic Potential for Production of Antimicrobial Compounds

ABSTRACT

A novel strain of *Cryobacterium* designated as SO2, was isolated from the Antarctic. Hence, this study was undertaken to gain further insight into the antimicrobial compounds and secondary metabolites produced by *Cryobacterium* sp. SO2. It was found that strain SO2 is a Gram-positive that exhibits an irregular rod shape, which formed yellow to orange pigmented colonies on semi-solid media. Strain SO2 grows at temperatures ranging from 4 to 25 °C. It has a complete genomic size of 4.097 Mb. SO2 has a DNA G+C content of 68.43%, and genomic annotation showed that the genome contained 3,862 CDS, 10 rRNA, 55 tRNA and 1 tm-RNA. Phylogenetic and OrthoANI analysis suggested *Cryobacterium* sp. strains SO1, N22, TMB1-8, LW097, TMN39-1, *C. zongtaii* TMN-42, *C. arcticum* PAMC27867 and *C. soli* GCJ02 as its closest phylogenetic neighbour. Genome annotation shows that strain SO2 confers β -lactamase class A, cephalosporin-C deacetylases, and 27 drug-resistance or efflux coding genes, and allows resistance to ceftazidime. Functional annotation identifies 28.74% of predicted genes are of unknown functions. Genome mining indicates that there are six putative secondary metabolite gene clusters in strain SO2. They are made up of RRE-containing, terpene, beta-lactone, T3PKS, NAPAA, and 2dos. This finding shows strain SO2 harbours genes that may be involved in the production of compounds with antibacterial and antioxidant activities.