

# Complete Genome Sequence of *Kosakonia* sp. Strain CCTCC M2018092, a Fucose-Rich Exopolysaccharide Producer

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**ABSTRACT** *Kosakonia* sp. strain CCTCC M2018092 is a fucose-rich exopolysaccharide producer that was isolated from spring water in Chongqing, Southwest China. In this study, the whole-genome sequence and genetic characteristics of this strain were elucidated. This genome contained 4,789,478 bp, with a G+C content of 56.08% (excluding the plasmid). The genome information in this study will facilitate understanding of the mechanism of high yield of fucose-rich exopolysaccharide produced by *Kosakonia* sp. CCTCC M2018092.

*Kosakonia* sp. strain CCTCC M2018092 was determined to be a Gram-negative, facultatively anaerobic bacterium with a rod cell shape. Most *Kosakonia* species are isolated from soil or trees, and several of them can promote plant growth. However, some other *Kosakonia* species, such as *Kosakonia cowanii*, are associated with human beings (1, 2). To date, several genera of bacteria have been reported to produce fucose-containing exopolysaccharides, while no literature has reported the production of fucose-containing polysaccharides by *Kosakonia* strains. Fucose-containing oligosaccharides and polysaccharides currently show enormous potential in foods, cosmetics, and pharmaceuticals because of the notable properties of L-fucose, a rare and functional sugar. It has been reported that approximately 50% of human milk oligosaccharides are fucosylated (3) and exhibit efficient prebiotic (4), bacteriostatic (5), and antifungal (6) properties.

*Kosakonia* sp. strain CCTCC M2018092 was cultured aerobically on Sabouraud medium at 30°C. Genomic DNA was extracted using a TIANamp bacterial DNA kit (Tiangen Biotech., Beijing, China). Whole-genome sequencing of strain CCTCC M2018092 was carried out on PacBio RS and Illumina sequencing platforms (Biozeron Biotechnology Co., Ltd., Shanghai, China). A TruSeq DNA sample prep kit and a TruSeq sequencing by synthesis (SBS) kit v3-HS (200 cycles) were used for library construction and DNA sequencing (Illumina HiSeq platform), respectively. The genomic DNA was disrupted into 8- to 10-kbp fragments by the g-TUBE method, followed by PacBio RS platform sequencing on two single-molecule real-time (SMRT) cells. After adapter trimming, 40,025 total reads from PacBio data and 18,637,752 total reads from Illumina data, with 548-fold average coverage, were obtained. The FastQC tool was used to assess the read quality (7). Illumina data were used to evaluate the complexity of the genome and correct the PacBio long reads. ABySS (<http://www.bcgsc.ca/platform/bioinfo/software/abyss>) was used to perform genome assembly with multiple kmer parameters in order to obtain optimal assembly results (8). Then, Canu (<https://github.com/marbl/canu>) was used to assemble the corrected PacBio long reads. The GapCloser software (<https://sourceforge.net/projects/soapdenovo2/files/GapCloser/>) was subsequently applied to fill the remaining local inner gaps and correct the single-base polymorphisms for the final assembly results (9). The whole genome of strain CCTCC

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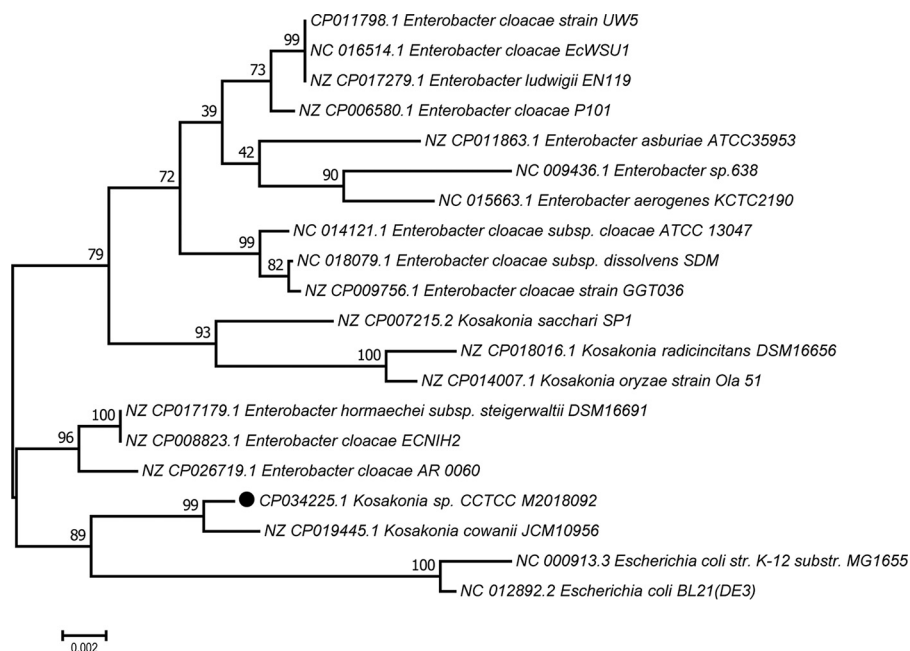
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**FIG 1** Phylogenetic relationships of the strain CCTCC M2018092. The scale bar represents the distance corresponding to 0.002 changes per nucleotide position. str., strain; substr., substrain.

M2018092 was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (10). Protein-coding sequences were annotated with a BLASTp search against the NCBI database (<https://www.ncbi.nlm.nih.gov/>), Kyoto Encyclopedia of Genes and Genomes (KEGG) database (<http://www.genome.jp/kegg/>), and Clusters of Orthologous Groups (COG) of proteins database (<https://www.ncbi.nlm.nih.gov/COG/>). All software programs were used with default parameters, unless otherwise stated.

The 16S rRNA genes were used to construct a phylogenetic tree with the MEGA 7.0 software (11). The neighbor-joining method and 1,000 bootstrap replicates were performed to assess the evolutionary relationships between different strains (Fig. 1). The result showed that *Kosakonia* sp. CCTCC M2018092 is closest to *Kosakonia cowanii* JCM10956 (GenBank accession number CP019445), and the two of them are classified in the same branch. Furthermore, the two strains are far from the other strains of the genus *Kosakonia* in classification, which indicates that they may not belong to the genus *Kosakonia*.

**Data availability.** The whole-genome sequence has been deposited in the NCBI GenBank database under accession number CP034225. The raw data were submitted to the SRA under accession number PRJNA506809.

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We declare no conflicts of interest.

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