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# Complete genome sequence of a cellulose-producing bacteria *Komagataeibacter oboediens* BPZTR01

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*Komagataeibacter* is well-known genus consisting of impressive bacterial cellulose producers. In the present work, the complete genome sequence of *Komagataeibacter oboediens* BPZTR01 is presented to reveal the potential and the characteristics of this strain.

*Komagataeibacter*, formerly referred as *Gluconacetobacter*, is a Gram-negative and obligately aerobic bacteria (Yamada et al., 2012; Zhang et al., 2017).

This genus is classified in the acetic acid bacteria (AAB) family with fourteen species (Saichana et al., 2015; Ryngajłło et al., 2019). Many strains of the *Komagataeibacter* genus are efficient bacterial cellulose producers (Römling and Galperin, 2015; Pfeffer et al., 2017; Trache et al., 2017), excluding *Komagataeibacter medellinensis* NBRC3288 (Ogino et al., 2011).

Bacterial cellulose has a unique polymeric structure with its properties of high crystallinity, chemical modifiable capacity, biodegradability, biocompatibility, and high water retention capacity. Therefore, it is commonly used in many industrial fields including food and health (Esa et al., 2014; Chen et al., 2018; Portela et al., 2019).

*K. oboediens* BPZTR01, is a Gram-negative, cellulose-producing and rod-shaped cell which was isolated from a home-made vinegar. It was grown in HS medium (Hestrin and Schramm, 1954) at 28°C and 180 rpm for 24 hours. After the isolation of the corresponding DNA, it was sequenced via Illumina HiSeq 2500. Fastq file obtained as a result of sequencing is uploaded to Galaxy platform (https://usegalaxy.org/). A quality report of the sequence file (Blankenberg et al., 2010), base level sequence quality, distribution of quality values at the sequence level, GC content at the base and sequence level, unreadable sequence content, sequence length distribution, sequence repetition level and $K_{mer}$ content was generated using FastQC tool.

The format of the sequences suitable for filtering was performed on the Galaxy platform with the FastQ Groomer tool. After this process, the data was filtered with Filter Fastq tool and the filtered sequences were transferred to the Geneious Prime

2019.2.1 for mapping sequence ends, then mapping, combined with the Geneious de novo Assembler method, and a consensus sequence were finally obtained (Kearse et al., 2012). It was found that the genome exists 2.642,352 bp in size. The GC content of *K. oboediens* BPZTR01 as 62.90% is similar to *K. rhaeticus* AF1 (62.49%) (dos Santos et al., 2014), *K. xylinus* E25 (62.13%) (Kubiak et al., 2014) and *K. oboediens* 174Bp2 (61.26%) (Andrés-Barrao et al., 2011).

Gene, CDS, tRNA, rRNA and ncRNA annotations were performed with the Annotate from Database tool in the Geneious Prime 2019.2.1. Microbial Genomes BLAST (https://www.ncbi.nlm.nih.gov/) was used to compare *K. oboediens* strain BPZTR01 with related species in database. A total of 2,450 genes including 2,130 protein-encoding genes, 3 rRNA and 51 tRNA genes were described. In addition, 346 unidentified hypothetical protein coding sequences were also found.

*Acetobacter* cellulose synthesis operon (*acsABCD*) and BC synthesis operon (*bcsABCD*) are homologous operons to encode the required proteins for cellulose synthesis (Mehta et al., 2015).

A homology comparison to the *acsABCD* operon of *Komagataeibacter* strains in GenBank was additionally performed and resulted in a 100% identity to *acsD* (*Komagataeibacter* multispecies, WP_010513886.1), 100% identity to *acsC* (*K. intermedius* TF2, GAN87373.1), 100% identity to *bcsB* (*K. oboediens*, WP_010513889.1) and 100% identity to *bcsA* (*K. oboediens*, WP_010513890.1).

Additional investigations on the *Komagataeibacter oboediens* BPZTR01 genome may provide further information about the mechanisms for the requirement of cellulose biosynthesis. The whole genome sequencing project has been deposited at DDJB/EMBL/GenBank under the accession number CP043481.

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