Penka M Petrova et al., J Biotechnol Biomater 2018, Volume 8
DOI: 10.4172/2155-952X-C5-101

De novo whole genome sequencing of 2,3-butanediol producing *Bacillus* sp. strain 5RB

Penka M Petrova[1], **Petya V Velikova**[1], **Flora V Tsvetanova**[2] and **Kaloyan K Petrov**[2]
[1]Institute of Microbiology - BAS, Bulgaria
[2]Institute of Chemical Engineering - BAS, Bulgaria

Compared to the chemical synthesis, the biotechnological route for 2,3-BD production has numerous economical and ecological advantages. Microbial synthesis by non-pathogenic strains allows the use of renewable raw materials during cheaper and less complex industrial fermentation process. In the present work, the whole genome sequence (WGS) of a novel isolate *Bacillus* sp. strain 5RB, capable to produce 2,3-BD was completed. WGS was based on TruSeq DNA PCR-library, Illumina SBS technology and Prokka pipeline identifying the locations of protein-coding sequences, tRNA, and rRNA genes (Macrogen Inc.). The genome of *Bacillus* sp. strain 5RB is 3.91 Mbp in size, without plasmids, and contains 3839 genes. The largest part of the genome is connected with amino acid transport and metabolism (289 genes), carbohydrate transport and metabolism (225), inorganic ion transport (176), and energy production and conversion (170 genes). Cell wall, the membrane, and envelope were encoded by 176 genes; translation, ribosomal structure and biogenesis - by 161; post translational modifications and chaperones - by 96 genes. Interestingly, 871 genes are with unknown functions (23% of the genome). Considering the species affiliation of the novel strain, the sequences of 5S, 16S and 23S rRNAs showed that *Bacillus* sp. 5RB is a member of *B. amyloliquefaciens* group, closely related to *B. velezensis*, *B. siamensis* and *B. tequilensis*. Its carbohydrates utilization profile, however, is substantially different from these of the mentioned species, giving convincing evidence that the new isolate represents a new species, promising producer of 2,3-BD. The genes, involved in 2,3-BD synthesis by Bacullus sp. 5RB were identified in the chromosome. For the first step, the decarboxylation of pyruvate to α-acetolactate, is responsible α-acetolactate synthase (EC 2.2.1.6), encoded by alsS gene, and putatively - by ilvB, and ilvH genes. Acetolactate conversion to acetoin is performed by α-acetolactate decarboxylase (EC 4.1.1.5), encoded by alsD, adjacent to alsS. The last step, the reversible reduction of acetoin to 2,3-BD is putatively catalyzed by the enzyme 3-hydroxybutyrate dehydrogenase (EC 1.1.1.30), acting as acetoin reductase, and encoded by two remote genes - *bdhA*1 and *bdhA*2. Large spectrum of genes, encoding glycoside-hydrolases was presented: *amyE* and *malL* (amylases), *xynA* (xylanase), *xynB* (xylosidase), *xynD* (arabinoxylan arabinofuranohydrolase), *xynC* (glucuronoxylanase), *eglS* encoding endoglucanase (cellulase), *etc*.

Biography

Penka M Petrova is Head of Gene Expression Laboratory at the Institute of Microbiology, Bulgarian Academy of Sciences. Her main interests are in the area of microbiology and molecular biology of Gram-positive bacteria, including isolation and genetic characterization of LAB, searching for new enzymatic activities, prebiotics utilization and synthesis, genes cloning and expression. She is author of more than 60 scientific publications and book chapters, cited more than 530 times. She is a leader of a number of research projects, funded by the National Scientific Fund, Republic of Bulgaria, Chr. Hansen A/S, and State Key Laboratory of Dairy Biotechnology of Bright Dairy & Foods Co. Ltd.

petq_v_@abv.bg

Notes: