

GENOMIC AND FUNCTIONAL ANALYSIS OF POLYHYDROXYALKANOATES PRODUCER *RHODOSPIRILLUM RUBRUM* DSM 467

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Rhodospirillum rubrum is a bacterium capable of the production of polyhydroxyalkanoates (PHA). PHA are polyesters that bacteria primarily use as a storage of energy and carbon in a form of cytoplasmic granules. Nevertheless, PHA are also promising renewable and biodegradable alternatives to petrochemical polymers, which nowadays leads to extensive research of *R. rubrum*. In this study, we focused on the analysis of a genome sequence of *Rhodospirillum rubrum* DSM 467. We sequenced and assembled genome of *R. rubrum* DSM 467 by a hybrid approach using long (Oxford Nanopore) and short (Illumina) reads. Chromosome sequence is available under accession number CP077803.1 and plasmid sequence under CP077804.1 in the GenBank database. Chromosome sequence was 4,352,570 bp long, CG content was 65.4%, and 3919 open reading frames (ORF) belonged to protein-coding sequences. Plasmid sequence was 53,835 bp long, CG content was 59.8%, and a number of ORF was 49. Functional annotation revealed that protein-coding sequences can be assigned a clusters of orthologous genes group in 90% cases for chromosome sequence and 80% cases for plasmid sequence, respectively. From available genome sequences of *R. rubrum* species, we created its pangenome with 4,572 genes, where we identified the core genome with 1,765 genes, accessory genome with 2,808 genes and 890 genes were unique. Genome annotation was also used for the construction of the genome scale model of *R. rubrum* DSM 467 in Pathways tool. Our results will be used in further research of metabolic processes behind PHA biosynthesis in *Rhodospirillum rubrum* DSM 467.

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