

DIVERSITY OF *SCHLEGELELLA THERMODEPOLYMERANS* REVEALED WITH NANOPORE SEQUENCING

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Schlegelella thermodepolymerans is a thermophilic bacterium known for more than two decades thanks to its ability to decompose polyhydroxyalkanoates (PHA), environment-friendly, biodegradable and renewable alternatives to petrochemical polymers. Recently, we proved that the type strain *S. thermodepolymerans* DSM 15344^T is also a potent PHA producer, which suggests its utilization for industrial production of bioplastics. Moreover, the strain prefers xylose over other sugars, including glucose. This is caused by unique *xyl* operon containing genes for xylose transport together with genes for its utilization as we found out from the complete genome assembly we had published previously. Here, we present genome comparisons of the type strain with additional strains *S. thermodepolymerans* DSM 15264, LMG 21645, and CCUG 50061 using nanopore sequencing. While genomes of all strains possessed gene machinery required for PHA metabolism, only strains DSM 15264 and LMG 21645 showed very high genome similarities, 98.6% and 96.1%, to the type strain, calculated as digital DNA-DNA hybridization (dDDH) values. On the contrary, the genome of the strain CCUG 50061 differed from the others not only in overall genome length but its dDDH value to the type strain was only 23.1%. Since the value is below the 70 % threshold for species delineation, the strain *S. thermodepolymerans* CCUG 50061 is probably misidentified. Nevertheless, resequencing with short reads is needed to polish inaccurate nanopore-based draft assemblies.

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