Complete Genome of *Pseudomonas mendocina* NK-01, Which Synthesizes Medium-Chain-Length Polyhydroxyalkanoates and Alginate Oligosaccharides[▽]

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***Pseudomonas mendocina* NK-01 can synthesize medium-chain-length polyhydroxyalkanoate (PHA_{MCL}) and alginate oligosaccharides (AO) simultaneously from glucose under conditions of limited nitrogen. Here, we report the complete sequence of the 5.4-Mbp genome of *Pseudomonas mendocina* NK-01, which was isolated from farmland soil in Tianjin, China.**

Polyhydroxyalkanoates (PHAs) are a family of biopolyesters produced by numerous bacteria as intracellular carbon and energy polymers under unfavorable growth conditions, such as limited nitrogen, phosphorus, oxygen, or magnesium, in the presence of excess carbon (1). Due to their biodegradability, biocompatibility, and thermoprocessibility, PHAs have been used in environmentally friendly bioplastics and biomedical materials (4, 14). Alginate oligosaccharides (AO) can be obtained from the degradation of alginate by alginate lyase (from *Vibrio* sp. 510) as described by Zhang et al. (15) or from mollusks in the natural world (3). In detailed studies, it was found that AO has many biological activities, such as antioxidation (13), anticoagulation (8), and immune regulation (10), and could be developed as a drug for enhancing human immunity. *Pseudomonas mendocina* NK-01 can synthesize medium-chain-length polyhydroxyalkanoate (PHA_{MCL}) and AO simultaneously from glucose under conditions of limited nitrogen (6).

The strain was grown in Luria-Bertani (LB) medium, and the genomic DNA was extracted from the cultured bacteria. We then sequenced the genome of *Pseudomonas mendocina* NK-01. The complete genome sequence of the strain was obtained using 454 pyrosequencing technology. The annotation was done by merging the results obtained from the RAST (Rapid Annotation using Subsystem Technology) server (2), the Glimmer 3.02 modeling software package (5), tRNAscan-SE 1.21 (9), and RNAmmer 1.2 (7).

The complete genome of *P. mendocina* NK-01 is made up of a circular chromosome of 5,434,353 bp with 62.51% G+C content and no plasmid. The genome size is bigger than that

of *P. mendocina* ymp (5,072,807 bp; GenBank accession number NC_009439), and the genome's G+C content of *P. mendocina* NK-01 is lower than that of *P. mendocina* ymp (64%). The genome of *P. mendocina* NK-01 encodes 4,958 proteins, 65 tRNAs, and 12 rRNA operons which account for 89.04% of the genome. Among the 4,958 open reading frames (ORFs), 3,732 (75.27%) have a clear function, 1,077 (21.72%) have high similarity with putative proteins, and the remaining 149 (3.01%) have no match with the protein database of the National Center for Biotechnology Information (NCBI).

The genome of *P. mendocina* NK-01 encodes PHA_{MCL} and AO synthesis-related genes. Two putative PHA_{MCL}- and AO-biosynthetic pathways have been identified in this strain. The PHA_{MCL} production pathway has been very clearly described in *Pseudomonas* species (11). The genes encoding PHA_{MCL} synthases (PhaC1 and PhaC2) of *P. mendocina* NK-01, which are located at locus MDS_0568 and locus MDS_0566 of the genome, respectively, and flank the PhaZ gene (PHA_{MCL} depolymerase, locus MDS_0567), have been identified. The alginate production pathway in *Pseudomonas* species has also been clearly demonstrated (12). For *P. mendocina* NK-01, the key enzymes mannuronan acid polymerase (MP, encoded by *alg8* at locus MDS_1081), mannuronan C-5 epimerase (AlgG, encoded by *algG* at locus MDS_1077), and alginate lyase (AlgL, encoded by *algL* at locus MDS_1075) have also been clearly confirmed.

Nucleotide sequence accession number. The complete genome sequence of *P. mendocina* NK-01 is available in GenBank under accession number CP002620.

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