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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Marinobacterium stanieri* S30, a Strain Isolated from a Coastal Lagoon in Chuuk State in Micronesia

Young-Ung Choi,[a] Young-Kyung Kwon,[a,b] Bo-Ram Ye,[a,b] Jung-Ho Hyun,[b] Soo-Jin Heo,[a] Abu Affan,[a] Kon-Tak Yoon,[a] Heung-Sik Park,[a] Chulhong Oh,[a] and Do-Hyung Kang[a]

Korea Ocean Research & Development Institute, Ansan, Republic of Korea,[a] and Department of Environmental Marine Sciences, Hanyang University, Ansan, Gyonggi-do, Republic of Korea[b]

In this study, we isolated xylan-degrading bacteria from a coastal lagoon of Micronesia and identified the bacteria as *Marinobacterium stanieri* S30. GSFLX 454 pyrosequencing and sequence analysis of the *M. stanieri* S30 genome generated 4,007 predicted open reading frames (ORFs) that could be candidate genes for producing enzymes with different catalytic functions.

Experimental seawater samples were collected from a coastal lagoon of Chuuk state in Micronesia. The collected samples were then cultured using an XYS agar plate (0.2% xylan, 0.2% yeast extract, and 1.5% agar in natural seawater) at 30°C. A xylan-degrading bacterium was selected by a xylanase activity test according to the dinitrosalicyclic acid method (7). The selected strain was analyzed using the 16S rRNA gene; the analysis revealed that it shared 99.9% identity with the 16S rRNA sequence of *Marinobacterium stanieri* strain ATCC 27130 (GenBank accession number NR_024699); hence, it was named *Marinobacterium stanieri* strain S30 (GenBank accession number JN654449). The genus *Marinobacterium* is a member of the *Gammaproteobacteria* and was first described by González et al. (2). *Marinobacterium* species have been isolated from various sources related to marine environments such as marine sediment (3, 6), coastal areas (4, 5), and coral mucus (1).

The *M. stanieri* S30 genome was pyrosequenced using Roche GSFLX 454 technology (Macrogen, South Korea). The sequence data consist of a total of 88,339,148 bases and 228,785 reads with an average length of 926 bp. Furthermore, the data include 223,871 assembled reads and 1,530 partial assembled reads. Reads were assembled into 74 contigs, including 58 contigs of over 500 bp, using De Novo software, version 2.3. Additionally, the data include 278 singletons. The average contig size was 75,356 bp. Analysis of the *M. stanieri* S30 genome sequence has shown 4,007 predicted coding sequences (CDS). The complete genome of *M. stanieri* S30 is on a single circular chromosome of 4,370,691 bp with an average G+C content of 55.9%. Additionally, the *M. stanieri* S30 genome contains 25 rRNA operons.

Gene ontology (GO) searches were performed using all complete coding sequences, and results revealed that 36%, 38%, and 9% of the sequences included genes related to biological processes, molecular functions, and cellular components, respectively. Of the GO category related to biological processes, metabolic processes represented the most dominant category, representing 17% of genes. In the cellular component category, 50% of the genes were unknown. Based on their molecular function, 42% of the genes were identified as being associated with catalytic activities. More importantly, the strain S30 genome includes 12 candidate genes possibly encoding phenol-degrading relative enzymes such as phenol 2-monooxygenase and catechol 2,3-dioxygenase. Even though *M. stanieri* S30 has shown xylan-degrading activity, there was no previously known xylan-degrading related gene among the identified coding sequences of *M. stanieri* S30. This indicates the presence of novel genes associated with xylan-degrading activity in this bacterium. This is the first genome sequence report of a species from the genus *Marinobacterium*, and the data will be useful for understanding important genes related to this genus.

Nucleotide sequence accession number. The genome sequence of *M. stanieri* S30 has been deposited in GenBank under accession number AFPL00000000.

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Address correspondence to Chulhong Oh, och0101@kordi.re.kr, or Do-Hyung Kang, dohkang@kordi.re.kr.

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