

# Genome Sequences of *Amycolatopsis orientalis* subsp. *orientalis* Strains DSM 43388 and DSM 46075

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**Strains of *Amycolatopsis orientalis* produce vancomycin or other related glycopeptide antibiotic compounds. Here we report the draft genome sequences of glycopeptide nonproducers *Amycolatopsis orientalis* subsp. *orientalis* DSM 43388 and DSM 46075. Their genome information will provide insights into the acquisition and regulation of glycopeptide antibiotic resistance genes.**

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*Amycolatopsis orientalis* is known to produce glycopeptide antibiotics, including vancomycin (1) and other related antibiotic compounds such as orienticins (2), eremomycin (3), and chloroeremomycin (also known as A82846B and LY264826) (4). We previously reported the genome sequence of vancomycin-producing *Amycolatopsis orientalis* strain KCTC 9412<sup>T</sup> (5). In this study, the strains DSM 43388 and DSM 46075 (ATCC 35164), which do not produce vancomycin and were obtained from the public culture collection, were chosen for sequencing with a view to understanding the diversification of glycopeptide antibiotic biosynthesis and resistance genes.

Cells were grown in tryptic soy broth containing wheat starch at 30°C. Cells were harvested and resuspended with 50 mM EDTA (pH 8.0) and were subsequently treated with achromopeptidase (5 mg/ml) and lysozyme (10 mg/ml) for cell disruption (6). Genomic DNA (gDNA) was purified by use of a gDNA isolation kit (Promega). Illumina library construction and genome sequencing were performed by the Human Derived Material Center in KRIBB, Daejeon, Republic of Korea, using an Illumina HiSeq 2000 system. A total of 2 × 10<sup>1</sup>-nucleotide (nt) paired reads (47,213,684 and 49,370,206 bp) were produced for a total of 4.77 and 4.99 gb for DSM 43388 and DSM 46075, respectively.

Quality trimming of reads and *de novo* assembly were done using the CLC Genomics Workbench ver. 6.0.1 (CLC Bio). For DSM 43388, 197 contigs with a G+C content of 70.0% were obtained (total contig length, 8,920,384 bp; *N*<sub>50</sub>, 114,355 bp). The DSM 46075 assembly resulted in 182 contigs with a G+C content of 69.4% (total contig length, 9,445,329 bp; *N*<sub>50</sub>, 123,184 bp). The assembled sequences were automatically annotated using the RAST server (7). The numbers of protein-coding genes were 8,636 and 9,082.

Unexpectedly, the average nucleotide identities (ANI) of these two strains with the type strain KCTC 9412<sup>T</sup>, calculated by using the JSpecies program (8), were too low (76.6% and 76.5% for DSM 43388 and DSM 46075, respectively), suggesting these two

strains should be reclassified to other species. The two strains are rather close to each other, with a high ANI value (>91%). Vancomycin biosynthetic gene clusters were not identified in the assemblies of DSM 43388 and DSM 46075. Vancomycin resistance genes *vanH*, *vanA*, and *vanX* (9) were located in the front of the vancomycin synthetic modules in the genome of KCTC9412<sup>T</sup> (5). However, the *vanHAX* genes in DSM 46075 were located next to genes encoding a VanS/VanR two-component system, which might regulate the expression of glycopeptide antibiotic resistance genes.

**Nucleotide sequence accession numbers.** These whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers [ASXG000000000](https://www.ncbi.nlm.nih.gov/nuccore/ASXG000000000) and [ASXH000000000](https://www.ncbi.nlm.nih.gov/nuccore/ASXH000000000) for DSM 43388 and DSM 46075, respectively. The versions described in this paper are [ASXG010000000](https://www.ncbi.nlm.nih.gov/nuccore/ASXG010000000) and [ASXH010000000](https://www.ncbi.nlm.nih.gov/nuccore/ASXH010000000).

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