

Genome Sequence of the Abyssomicin- and Proximicin-Producing Marine Actinomycete *Verrucosipora maris* AB-18-032[∇]

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***Verrucosipora maris* AB-18-032 is a marine actinomycete that produces atrop-abyssomicin C and proximicin A, both of which have novel structures and modes of action. In order to understand the biosynthesis of these compounds, to identify further biosynthetic potential, and to facilitate rational improvement of secondary metabolite titers, we have sequenced the complete 6.7-Mb genome of *Verrucosipora maris* AB-18-032.**

Verrucosipora maris AB-18-032 was isolated from a deep marine sediment sample collected from the East Sea (Sea of Japan) (3, 9). It produces unique polycyclic type 1 polyketide antibiotics, namely, the abyssomicins, which are the first known natural-product inhibitors of the *para*-aminobenzoic acid biosynthetic pathway (6, 7). In particular, atrop-abyssomicin C is active against Gram-positive bacteria, including *Bacillus subtilis*, methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant *S. aureus* (6, 7, 9), and *Mycobacterium tuberculosis* (5). The strain also produces proximicin A, a furan analogue of netropsin with novel antitumor properties (4, 10). Here, we announce the genome sequence of *Verrucosipora maris* AB-18-032, the first member of this genus to be sequenced, which should provide fundamental understanding of the biosynthesis of these antibiotics and facilitate bioengineering and biodiversity efforts involving this strain.

The complete genome of *Verrucosipora maris* AB-18-032 was sequenced using Roche 454 genome sequencer (GS) FLX (9.4-, 9.9-, 6.7-, and 6.8-times coverage of single-end reads and 13.3-times coverage of paired-end reads having 3-kb inserts) and Solexa (Illumina genome analyzer [GA], 43-times coverage with ~350-bp inserts and paired-end reads) sequencing technology. To combine the GA library with 454 GS FLX libraries, reads were assembled into 1,730 contigs using the ABySS 1.20 assembler (11), and the contigs were shredded into 15,379 fake reads. The fake reads and 454 GS FLX reads were assembled into 5 scaffolds (116 contigs) by using a combination of Newbler gsAssembler 2.3 (454 Life Sciences, Branford, CT) and CABOG assembler (8). The actual order of the scaffolds was determined by a series of PCRs based on a permutation table, and gaps were filled by primer-walking PCR followed by sequencing using an ABI 3730

system (Applied Biosystems, CA). Finally, Polisher software (Alla Lapidus, unpublished data) was used with the Illumina data to correct for homopolymers in the 454 reads and increase consensus quality. Annotation was performed by the RAST server (2) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), and both annotations were scrutinized by manual inspection based on BLAST searches (1).

The genome of *Verrucosipora maris* AB-18-032 has a single circular chromosome of 6,673,976 bp with a GC content of 70.9%. A circular plasmid of 58,295 bp with a GC content of 70.3%, pVMKU, was also identified. The chromosome has 5,947 coding sequences (CDS), 51 tRNA genes, and 9 rRNA genes, and the plasmid has 55 CDS.

Nucleotide sequence accession numbers. The complete genome sequence of *Verrucosipora maris* AB-18-032 has been deposited in NCBI GenBank under accession numbers CP002638 and CP002639.

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