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GENOME SEQUENCES

Draft Genome Sequence of *Streptomyces* sp. Strain ventii, Isolated from a Microbial Mat near Hydrothermal Vents within the Axial Seamount in the Pacific Ocean, and Resequencing of the Type Strains *Streptomyces lonarensis* NCL 716 and *Streptomyces bohaiensis* 11A07

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ABSTRACT The draft genome of *Streptomyces* sp. strain ventii, an environmental isolate recovered from deep-sea hydrothermal vents in the Pacific Ocean, is presented along with the resequenced draft genomes of the type strains *Streptomyces bohaiensis* 11A07 and *Streptomyces lonarensis* NCL 716.

Members of the genus *Streptomyces* are Gram-positive, spore-forming, filamentous bacteria that often synthesize desirable antimicrobials, cytotoxins, and other lead compounds (1–4). The type strains *Streptomyces bohaiensis* 11A07 and *Streptomyces lonarensis* NCL 716 produce antimicrobials and an α-amylase, respectively (5–7). *Streptomyces* sp. strain ventii was isolated from the Juan de la Fuca Ridge in the Northeast Pacific Ocean. The draft genome of *Streptomyces* sp. ventii is presented, along with the resequenced draft genomes of *S. bohaiensis* 11A07 and *S. lonarensis* NCL 716.

Deep-sea samples were collected during the 2011 New Millennium Observatory expedition, run through the National Oceanic and Atmospheric Administration (NOAA) Vents Program at Oregon State University and the NOAA Pacific Marine Environmental Laboratory. A microbial mat near hydrothermal vents on the Axial Seamount (46.06°N, 130°W) at a depth of 2,190 m was collected with a custom syringe-based sampler on the remotely operated vehicle (ROV) Jason II (aboard the research vessel [R/V] *Thompson*). The sample was diluted 1:1,000 in sterile Instant Ocean, spread onto 1/10 Zobell marine agar 2216 with sterile swabs, and incubated at 28°C for 2 weeks. Strain maintenance was performed on International Streptomyces Project 2 (ISP2) medium supplemented with 0.1 M sodium phosphate buffer to a pH of 8.0 (buffered ISP2) at 28°C (8). Strains 11A07 (DSM 42125) and NCL 716 (DSM 42084) were obtained from the Leibniz Institute DSMZ and cultured on buffered ISP2 medium at 28°C. *Streptomyces* sp. ventii was confirmed as a member of the *Streptomyces* genus through 16S rRNA gene sequencing and BLAST analysis (9, 10). Following a 4-day incubation at 28°C in buffered ISP2 broth shaken at 120 rpm, DNA was isolated by phenol-chloroform extraction (11). The raw reads were obtained from the Microbial Genome Sequencing Center, LLC (Pittsburgh, PA), using 151-bp paired-end read libraries prepared with the Illumina Nextera kit (12). Libraries were run on the Illumina NextSeq 550 platform yielding 9,643,560, 12,101,213, and 14,343,200 pairs of raw reads for

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TABLE 1 Characteristics of the draft genome sequences from the *Streptomyces* strains described in this work and the previously published *Streptomyces bohaiensis* strain 11A07 and *Streptomyces lonarensis* strain NCL 716 genome sequences[a]

Relevant characteristic	Data for strain:						
	Streptomyces sp. ventii	*Streptomyces bohaiensis* 11A07	*Streptomyces lonarensis* NCL 716	*Streptomyces bohaiensis* 11A07[b]	*Streptomyces bohaiensis* 11A07 (>1,000 bp)[b,c]	*Streptomyces lonarensis* NCL 716[b]	*Streptomyces lonarensis* NCL 716 (>1,000 bp)[b,c]
Genome size (bp)	5,708,881	5,631,365	5,953,444	5,698,492	5,621,459	6,006,371	5,884,873
G+C content (%)	73.34	73.75	73.79	73.82	73.81	73.83	73.81
No. of scaffolds	474	547	482	883	649	1,154	745
No. of contigs	486	565	502	890	656	1,162	753
N_{50} (bp)	19,934	16,815	20,580	13,470	13,894	11,176	11,454
Mean coverage (fold)	67.9	72.6	86.7	13	13	14	14
No. of genes annotated with PGAP (15)	4,842	4,919	5,133	NA	NA	NA	NA
No. of RNAs from PGAP annotation	66	72	72	NA	NA	NA	NA
% of genome in scaffolds >50 kb	14.95	10.25	13.50	0.91	0.92	0.87	0.89
GenBank accession no. (version no.)	JAAVJB000000000 (JAAVJB010000000)	JAAVJC000000000 (JAAVJC010000000)	JAAVJD000000000 (JAAVJD010000000)	BHZH00000000 (BHZH00000000.1)	NA	BHZG00000000 (BHZG00000000.1)	NA
BioSample accession no.	SAMN14445373	SAMN14448217	SAMN14448297	SAMD00146571	NA	SAMD00146572	NA
SRA accession no.	SRS6438928	SRS6447757	SRS6447181	NA	NA	NA	NA

[a] The published assemblies were filtered with BBMap to remove scaffolds and contigs smaller than 1,000 bp, as was done for genome sequences presented in this work, and analyzed with the same software.
[b] Data taken from Terahara et al. (16).
[c] Data for the genome assemblies with all contigs/scaffolds <1,000 bp removed.

strains ventii, 11A07, and NCL 716, respectively. FastQC was used to assess the read quality (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/); adapter sequence removal, read quality trimming (removal and trimming parameters: ktrim = r, ordered, minlen = 50, mink = 11, tbo, rcomp = f, k = 21, ow = t, ftm = 5, zl = 4, qtrim = rl, trimq = 20), and analysis were performed using BBDuk in the BBMap package (http://sourceforge.net/projects/bbmap/), and genomes were assembled with SPAdes v. 3.14.0 using the "–careful" option and specifying kmers of 21, 33, 55, 77, 99, and 121 (13). Contigs and scaffolds greater than 1,000 bp were retained for analysis. Assemblies were analyzed with the Prokaryotic Genome Annotation Pipeline (PGAP), and DNA-DNA hybridization (DDH) was performed *in silico* using the DSMZ Genome-to-Genome Distance Calculator with default settings (14, 15).

The relevant genome characteristics are presented in Table 1. The resequenced *S. bohaiensis* and *S. lonarensis* genomes presented here are derived from the same strains (DDH = 99.50% and 99.40%, respectively, between the two versions of each genome) and display higher mean coverage in fewer contigs with more of the genomes in scaffolds greater than 50 kb (Table 1). Removal of contigs and scaffolds smaller than 1,000 bp from the published assemblies did not greatly alter their quality or statistics (16).

Data availability. The whole-genome shotgun projects, BioSample material, and raw reads have been deposited in DDBJ/ENA/GenBank under the accession numbers listed in Table 1.

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