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*J. Bacteriol.* 2012, 194(5):1263. DOI: 10.1128/JB.06643-11.

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# Draft Genome Sequence of an Efficient Antibiotic-Producing Industrial Strain of *Saccharomonospora azurea*, SZMC 14600

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**Although certain rare actinomycetes have been recognized as prolific sources of bioactive natural products, their potential for producing biologically active metabolites still remains unexplored. With the aim of gaining global insights into the genetic background and the metabolic capability of *Saccharomonospora azurea* SZMC 14600, whole-genome sequencing was performed.**

*Saccharomonospora azurea* sp. nov. (synonym *Saccharomonospora caesia*) is a Gram-positive, soil-dwelling filamentous bacterium (4, 7) belonging to the family *Pseudonocardiaceae* proposed by Nonomura and Ohara (2) for monosporic actinomycetes. So far, only very limited knowledge exists or is publicly available concerning the relevance of *S. azurea* to produce biopharmaceutical compounds, e.g., antimicrobials and other active ingredients (3). *S. azurea* strain SZMC 14600 was selected for whole-genome sequencing based on its ability to (over)produce primycin in combination with a completely uncharacterized self-protective strategy(ies) (5; Á. Juhász, Á. Péntes, Z. Péteri, J. P. Pallos, D. Seffer, P. Feiszt, M. Pesti, C. Fekete, C. Vágvolgyi, Z. Gazdag, and G. Papp, 5 May 2011, WIPO patent application WO/2011/051741).

The genome sequencing of *Saccharomonospora azurea* strain SZMC 14600 was performed by combining cycled ligation sequencing on the SOLiD 3Plus system (Life Technologies) with 454 FLX pyrosequencing (Roche). We generated 17,192,716 mate-paired (2× 25-bp) and 8,254,794 fragment (50-bp) reads on SOLiD along with 187,566 ~400-bp reads on 454 FLX, which altogether yielded >270-fold coverage. The assembly was performed using the Genomics Workbench 4.8. *de novo* plug-in and the Omixon Gapped SOLiD Alignment 1.3.2 plug-in (1) provided by CLC Bio and Omixon, respectively, which generated 216 large (>200-bp) contigs. The automatic annotation of the genome was performed by using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which utilizes GeneMark, Glimmer, and tRNAscan-SE searches. The incomplete draft genome of *S. azurea* strain SZMC 14600 consists of 4,973,727 bp with a GC content of 70.3%. There are 4,555 putative coding sequences, 47 tRNAs, and 3 rRNA loci.

As the problem of antimicrobial resistance becomes more widespread, the need for new anti-infective agents is more urgent than ever. As a part of these efforts, massively parallel next-generation sequencing (NGS) technologies provide tremendous ability to typify microbes not only on the basis of readily observable characteristics but also upon their genetic (biosynthetic) potential (6). Due to its novel properties, *S. azurea* strain SZMC

14600 represents an excellent model to support further development of early-stage drug discovery and biopharmaceutical product improvement.

**Nucleotide sequence accession numbers.** The draft genome sequence of *S. azurea* strain SZMC 14600 (SZMC, Microbiological Collection of the University of Szeged) has been deposited at DDBJ/EMBL/GenBank under accession number [AHBX00000000](http://www.ncbi.nlm.nih.gov/nuccore/AHBX00000000). The version described in this paper is the first version, AHBX01000000.

## ACKNOWLEDGMENTS

This work was supported in part by grant TÁMOP-4.2.1.B-10/2/KONV-2010-0002, Baross grant DA07-DA TECH 07-2008-0045, and NKTH Teller program grant OMF0-00441/2007.

We thank Marianna Nagymihály and Judit Cseklye for their valuable work in sequencing.

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Received 9 December 2011 Accepted 19 December 2011

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doi:10.1128/JB.06643-11