Draft Genome Sequence of *Saccharomonospora piscinae* KCTC 19743<sup>T</sup>, an Actinobacterium Containing Secondary Metabolite Biosynthetic Gene Clusters

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**ABSTRACT** The draft genome sequence of *Saccharomonospora piscinae* KCTC 19743<sup>T</sup>, with a size of 4,897,614 bp, was assembled into 11 scaffolds containing 4,561 open reading frames and a G+C content of 71.0 mol%. Polyketide synthase and nonribosomal peptide synthetase gene clusters, which are responsible for the biosynthesis of several biomolecules, were identified and located in different regions in the genome.

The actinobacterial group has been recognized for its extensive secondary metabolism, and members produce approximately two-thirds of all antibiotics used in clinical, industrial, and biotechnological processes (1). There are two classes of bacterial bioactive secondary metabolites, namely, the polyketides and the nonribosomal peptides, which are biosynthesized by multifunctional enzymes, i.e., polyketide syntheses (PKSs) and nonribosomal peptide synthetases (NRPSs), respectively (2).

*Saccharomonospora piscinae* KCTC 19743<sup>T</sup> is the type strain of the most recently described species of the genus *Saccharomonospora*. It was isolated from the sediment of a fishpond in southern Taiwan, and it is characterized by its ability to grow at 0 to 8% (wt/vol) NaCl and between 20°C and 40°C (3). The aims of this work were to obtain the genome sequence of *Saccharomonospora piscinae* KCTC 19743<sup>T</sup> and to determine the presence of secondary metabolite biosynthetic gene clusters.

The type strain of *Saccharomonospora piscinae* was obtained from the Korean Collection for Type Cultures (KCTC) and grown for 7 days at 37°C on HM medium (4) with 10% salts, under aerobic conditions. Genomic DNA was isolated as described elsewhere (5). In brief, cells were lysed with a mixture of lysozyme and sodium lauryl sulfate, and nucleic acids were extracted with chloroform-isoamyl alcohol (24:1 [vol/vol]), followed by DNA precipitation with ethyl alcohol. Subsequently, DNA was purified using the MEGAquick-spin Plus kit (iNtRON Biotechnology) and quantified by spectrophotometry (DeNovix DS-11 FX spectrophotometer) and fluorometry (Qubit 3.0 fluorometer). Library construction was performed using the KAPA HyperPrep kit (Roche), according to the manufacturer’s instructions. The draft genome sequence of *Saccharomonospora piscinae* KCTC 19743<sup>T</sup> was obtained by following a complete-genome shotgun strategy (6) on an Illumina NovaSeq 6000 platform (2 × 150-bp paired-end reads) (Stab Vida, Portugal), with an output of 23,534,814 reads and a sequencing depth of 733×. Downstream analyses were carried out using default parameters for all software unless otherwise specified. BBduk from the BBTools v.38.44 package (7) was employed for read quality trimming (qtrim = rl, trimq = 18) and adapter trimming (k = 21, tbo ordered cardinality). Genome assembly was performed using SPAdes v.3.13.0 (8) (option–careful). The
NCBI Prokaryotic Genome Annotation Pipeline (9) was used to provide functional annotation. To determine the presence of secondary metabolite biosynthetic gene clusters, the assembled genome was analyzed using antiSMASH server v.5.0 (10).

The draft genome sequence of *Saccharomonospora piscinae* KCTC 19743T contained 4,897,614 bp, with a G+C content of 71.0 mol%. The reported coding density was 91.82%, with 0.93 genes per kbp. The assembly resulted in 11 scaffolds (>940 bp), with an N50 value of 1,086,926 bp and L50 value of 3. A total of 4,561 putative open reading frames (ORFs) were predicted, with an average size of 986 bp, including 4,508 coding sequences, a complete rRNA operon, 47 tRNA genes, and 3 noncoding RNA genes. The presence of the secondary metabolite biosynthetic gene clusters PKS-T1, PKS-T2, PKS-T3, and NRPS, as well as hybrid clusters, was localized in nine genomic regions within the genome sequence (Table 1). Our results suggest a high potential for *Saccharomonospora piscinae* to produce a variety of secondary metabolites related to the PKS and NRPS systems.

**Data availability.** This whole-genome shotgun project has been deposited in GenBank under accession number VCEK00000000. The version described in this paper is the first version, VCEK00000000.1. The raw Illumina data from BioProject PRJNA544002 were submitted to the NCBI Sequence Read Archive (SRA) under accession number SRX7473633.

**ACKNOWLEDGMENTS**

This study was supported by the National Council of Science and Technology with a scholarship granted to N. Ramírez-Durán (application 2018-000007-01EXTV-00289) for a sabbatical stay at the University of Sevilla, the Spanish Ministry of Science, Innovation, and Universities (project CGL2017-83385-P), and Junta de Andalucía (grants BIO-213 and US-1263771), Spain, which included FEDER funds.

| Contig | Genomic region (nucleotide position, start to stop) | Biosynthetic gene cluster(s) | Most similar known cluster | Similarity (%) | MIBiGa accession no. |
|--------|--------------------------------------------------|-----------------------------|----------------------------|----------------|----------------------|
| 1      | 132953 to 205507                                 | T2-PKS                      | Curamycin                  | 71             | BGC0000215           |
|        | 314548 to 421784                                 | NRPS, T1-PKS                | Collisymycin A             | 7              | BGC0000973           |
|        | 519335 to 560387                                 | T3-PKS                      | Alkyl-O-dihydrogeranyl-methoxyhydroquinones | 57 | BGC0001077 |
|        | 705947 to 724544                                 | Terpene                     | Isorenieratene             | 36             | BGC0001227           |
|        | 873907 to 899995                                 | Terpene                     | Hopene                     | 46             | BGC0000663           |
| 2      | 226982 to 268169                                 | Arylpolyene                 | A201A                      | 8              | BGC0001138           |
|        | 286693 to 307703                                 | Indole                      | Fortimicin                 | 9              | NDb                  |
|        | 820634 to 841380                                 | Homoserine lactone          | Albachelin                 | 40             | BGC0001211           |
| 3      | 1 to 9615                                        | Ectoine                     | Ectoine                    | 100            | BGC0000853           |
|        | 60896 to 82094                                   | Linaridin                   | Lomaivitcin                | 6              | BGC0000241           |
|        | 207856 to 250926                                 | NRPS                        | Sporolide                  | 36             | BGC0000150           |
|        | 251706 to 297528                                 | T1-PKS                      | Amycolamycin A/amycolamycin B | 10 | BGC0001503 |
|        | 990976 to 1014377                                | Linaridin                   | ND                         | ND             | ND                   |
| 4      | 559645 to 802161                                 | T1-PKS, T3-PKS              | Concanamycin A             | 42             | BGC0000040           |
| 5      | 47510 to 115116                                  | β-Lactone, NRPS             | Herboxidiene               | 8              | BGC0001065           |
| 6      | 25520 to 47697                                   | Terpene                     | Geosmin                    | 100            | BGC0000661           |
|        | 168655 to 218283                                 | Siderophore, T1-PKS         | Ficellomycin               | 14             | BGC0001593           |
| 9      | 1 to 13562                                       | T1-PKS                      | Mediomyacin A              | 28             | BGC0001662           |

*a* MIBiG, Minimum Information about a Biosynthetic Gene cluster.

*b* ND, not determined.
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