



Genomics/technical resources

## Complete genome sequence of *Serinicoccus* sp. JLT9, an actinomycete isolated from the shallow-sea hydrothermal system



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### ABSTRACT

*Serinicoccus* sp. JLT9 was a novel rare actinomycete, isolated from the shallow-sea hydrothermal system. Here, we present the complete genome sequence of *Serinicoccus* sp. JLT9, which consists of 3,610,932 bp with a GC content of 72.43%. The genome data provides insight into microbial adaptation to the shallow-sea hydrothermal system and facilitates the discovery of natural compounds in the future.

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## 1. Introduction

Hydrothermal vents represent a unique habitat in the marine ecosystem and occur over a wide depth range, from the intertidal to the abyssal (Tarasov et al., 2005). Deep-sea hydrothermal systems are known to harbor numerous metabolically diverse microorganisms with potential biotechnological and environmental implications thus have received a great deal of attention (He and Zhang, 2016). However, comparatively few investigations on microbial community have been conducted in the shallow-sea hydrothermal systems (Tang et al., 2013). Shallow-sea hydrothermal systems (at the depth < 200 m) provide more instant access to investigate microbial genetic resource, which usually occur near active coastal or submarine volcanoes (Tang et al., 2013). The hydrothermal fluids vary greatly in their temperature, pH, and chemical composition due to seafloor physical and chemical processes such as fluid–rock interactions, and the mixture of fluids and seawaters (Tarasov et al., 2005).

The genus *Serinicoccus* was a rare actinomycete taxon and the majority of isolates were collected at surface seawater and marine sediment (Traiwan et al., 2011; Xiao et al., 2011a; Yi et al., 2004). Marine actinomycete is underexploited source for the discovery of natural compounds (Bull et al., 2005). A potentially useful antitumor agent (seriniquinone) (Trzoss et al., 2014) and six bioactive compounds

(Yang et al., 2013) were isolated from the representatives of the genus *Serinicoccus*. Here we present the complete genome sequence of *Serinicoccus* sp. JLT9. *Serinicoccus* sp. JLT9 was an aerobic, non-motile, non-sporulating, coccoid-shaped and yellow-colored, Gram-positive bacterium, which was obtained from the shallow-sea hydrothermal system, Kueishan Islet, offshore northeast of Taiwan. 16S rRNA gene in *Serinicoccus* sp. JLT9 showed 98% sequence similarity with that in *Serinicoccus marinus* DSM15273 (Yi et al., 2004) within the phylum *Actinobacteria*. To our knowledge, this study represents the first genome information of a cultivated actinomycete isolated from the shallow-sea hydrothermal system.

## 2. Data description

General features of *Serinicoccus* sp. JLT9 and the MixS mandatory information were show in Table 1. Whole genome sequencing of *Serinicoccus* sp. JLT9 was accomplished using a hybrid approach (Koren et al., 2012), combining Illumina short read data (Illumina, USA) with PacBio long read data (Pacific Biosciences, USA). The genome sequences were de novo assembled by the HGAP2 program in the SMRT analysis server (v2.3). Illumina pair end reads were mapped to the assembled contigs to improve the accuracy of genome sequences. The final assembled genomes were automatically annotated and analyzed through the Joint Genome Institute Integrated Microbial Genomics (IMG) site (<http://img.jgi.doe.gov>) (Table 2). The genomes was comprised of a single 3,610,932 bp long circular chromosome, harboring a total of 3386 predicted protein-coding

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**Table 1**  
General features of *Serinicoccus* sp. JLT9 and MlxS mandatory information (Field et al., 2008).

Items	Description
General features	
Classification	Domain <i>Bacteria</i> Order <i>Micrococcales</i> Family <i>Intrasporangiaceae</i>
Particle shape	Cocci
Gram stain	Positive
Pigmentation	Yellowish-pigmented
Temperature	4–40 °C
Salinity	0–15‰
pH range	4–12
Motility	Non-motile
MlxS data	
Submitted_to_insd	CP014989 (GenBank)
Investigation_type	Bacteria
Project_name	<i>Serinicoccus</i> sp. JLT9 genome sequencing and assembly
Geo_loc_name	Kueishantao Islet, Taiwan, China
Lat_lon	24°50' N, 121°57' E
Depth	25 m
Collection_date	2014–4
Env_biome	Marine hydrothermal vent (ENVO:01000122)
Env_feature	Coastal water body (ENVO: 02000049)
Env_material	Sea water (ENVO: 00002149)
Env_package	Missing
Ref_biomaterial	PMID: 20118285
Source:mat_id	JCM 31502; CGMCC 1.15779
Biotic_relationship	Free living
Trophic_level	Chemoorganotroph
Rel_to_oxygen	Aerobic
Isol_growth_condt	PMID: 20118285
Number of contigs	1
Seq_meth	Pacific Biosciences RS II; Illumina HiSeq 2000
Assembly method	RS HGAP v2
Finishing_strategy	125×, complete
Annot_source	IMG ER

sequences with a GC content of 72.43%. There were 45 tRNA genes and 6 rRNA genes predicted in the genome. The average nucleotide similarity between *Serinicoccus* sp. JLT9 and *S. marinus* DSM 15273 (AY382898), *S. chungangensis* CAU 9536 (HM068886; Chander et al., 2016) and *S. profundus* MCCC 1A05965 (EU603762; Xiao et al., 2011b) was 88.9%, 84.6% and 83.4% respectively, indicating a genomic divergence at the species level. Furthermore, the BLAST analysis showed that there were 2949 genes, 2882 genes and 2839 genes exhibited sequence homologous relationships between them,

respectively. *Serinicoccus* sp. JLT9 genomes contained 258 non-homologous genes to those other *Serinicoccus* genomes (>30% amino acid identity).

Reduced sulfur compounds, especially for hydrogen sulfide (H<sub>2</sub>S) and elemental sulfur (S<sup>0</sup>), are naturally enriched in the shallow-sea hydrothermal fluids (Tang et al., 2013). Sulfur-oxidizer bacteria were dominant in the shallow-sea hydrothermal systems (Tang et al., 2013). *Serinicoccus* sp. JLT9 possessed the complete repertoire of genes the oxidation of reduced sulfur compounds, which increased niches-specialization competitiveness in the shallow-sea environments. These genes encoded enzymes for the oxidation of reduced sulfur compounds including sulfide quinone oxidoreductase, mediating the oxidation of sulfide to elemental sulfur, rhodanese sulfurtransferase for oxidation of thiosulfate (S<sub>2</sub>O<sub>3</sub><sup>2-</sup>) to sulfite (SO<sub>3</sub><sup>2-</sup>), and reverse dissimilatory sulfite reductase for oxidation of elemental sulfur to sulfite, adenosine 5-phosphosulfate reductase and sulfate adenylyltransferase for oxidation of sulfite to sulfate (SO<sub>4</sub><sup>2-</sup>). Some common or different genetic features within *Serinicoccus* genus were shown in Fig. 1. For example, genes associated with sulfur oxidation functions were found in other *Serinicoccus* genomes. In contrast, genes encoding arsenical, copper and cadmium resistance proteins in *Serinicoccus* sp. JLT9 were more abundant than others (Fig. 1), which were beneficial for microbial survival in the heavy metal enriched shallow-sea hydrothermal system (Tang et al., 2013). A total of 57 genes encoding proteins were assigned to secondary metabolites biosynthesis, transport and catabolism COG (clusters of orthologous groups of proteins) category. The genome contained a gene cluster for the biosynthesis of aromatic carotenoid (isorenieratene) including genes encoding enzymes phytoene synthase, phytonene desaturase dehydrogenase, methyltransferase, lycopene cyclase, β-Carotene dehydrogenase, isopentenyl diphosphate isomerases, geranylgeranyl diphosphate synthase. Bacterial carotenoid genetic resources have been applied in biotechnological production of different carotenoids that are colored terpenoids with antioxidative properties (Venil et al., 2014). The genome data reveals functional adaptation in *Serinicoccus* sp. JLT9 to the shallow-sea environment and hints the potential application of this strain in the exploiting natural compounds.

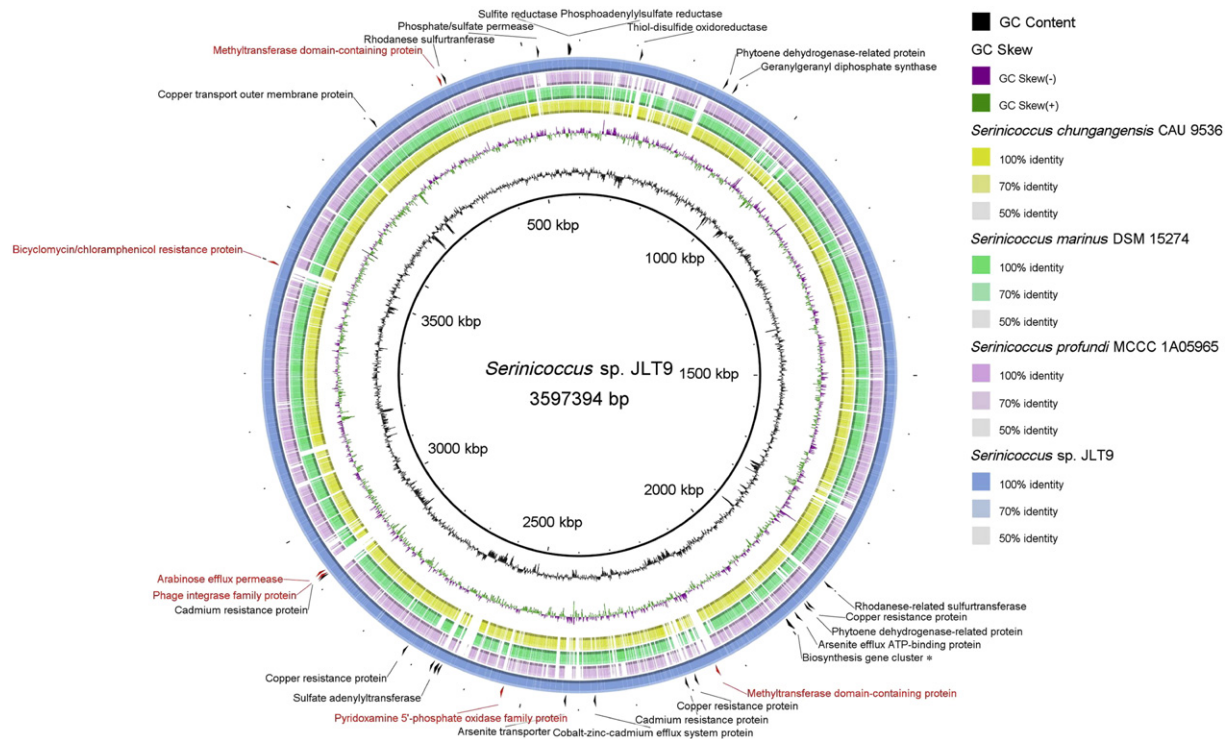
#### Nucleotide sequence accession numbers

The complete genome sequence of *Serinicoccus* sp. JLT9 (=JCM 31502<sup>T</sup>, =CGMCC 1.15779<sup>T</sup>) has been deposited at DDBJ/EMBL/GenBank under the accession number of CP014989.

**Table 2**  
General genomic features of *Serinicoccus* sp. JLT9.

Attributes	Values	% of total <sup>a</sup>
Genome size (bp)	3,610,932	100
DNA coding region (bp)	3,341,892	92.55
DNA G + C content (bp)	2,615,472	72.43
Total genes	3444	100
Protein-coding genes	3386	98.32
RNA count	58	1.68
rRNA count	6	0.17
tRNA count	45	1.31
Pseudo genes count	0	0
Genes in internal clusters	337	9.79
Genes with function prediction	2639	76.63
Genes assigned to COGs	2259	65.59
Genes with Pfam domains	2774	80.55
Genes with peptide signals	129	3.75
Genes with transmembrane helices	841	24.42

<sup>a</sup> The total is based on either the size of genome in base pairs or the total number of protein coding genes in the annotated genome.



**Fig. 1.** Circular plot of the genome comparison between *Sericinococcus* sp. JLT9 with *S. marinus* DSM 15273 (AY382898), *S. chungangensis* CAU 9536 (HM068886), and *S. profundus* MCCC 1A05965 (EU603762) strains using BRIG Version 0.95 (BLAST options > 0.00001, Alikhan et al., 2011) From the innermost to the outermost: GC content, GC skew, *S. chungangensis* CAU 9536, *S. marinus* DSM 15273, *S. profundus* MCCC 1A05965, *Sericinococcus* sp. JLT9. The main common genetic information within *Sericinococcus* genomes were highlighted with black color, whereas the unique genes in *Sericinococcus* sp. JLT9 were highlighted with red color.

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