Data in Brief

High-quality draft genome sequence of *Kocuria marina* SO9-6, an actinobacterium isolated from a copper mine

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A B S T R A C T

An actinobacterial strain, designated SO9-6, was isolated from a copper iron sulfide mineral. The organism is Gram-positive, facultatively anaerobic, and coccoid. Chemotaxonomic and phylogenetic properties were consistent with its classification in the genus *Kocuria*. Here, we report the first draft genome sequence of *Kocuria marina* SO9-6 under accession JROM00000000 (http://www.ncbi.nlm.nih.gov/nuccore/725823918), which provides insights for heavy metal bioremediation and production of compounds of biotechnological interest.

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1. Direct link to deposited data

The draft genome sequence of *Kocuria marina* SO9-6 has been deposited at DDBJ/EMBL/GenBank under the accession JROM00000000 (http://www.ncbi.nlm.nih.gov/nuccore/725823918), and this paper describes its first version.

2. Experimental design, materials and methods

The genus *Kocuria*, which belongs to the Micrococcaceae family, was first proposed by Stackebrandt et al. [1]. These bacteria were formerly classified in the genus *Micrococcus*, but were subsequently separated from it based on phylogenetic and chemotaxonomic analyses. The members of this genus are coccoid, Gram-positive, non-encapsulated, and aerobic, but *Kocuria kristinae* and *Kocuria marina* are exceptions, since the first is facultatively anaerobic and the second can grow in 5% CO₂ [1,2]. Members of the *Kocuria* genus have been isolated from different environments including marine sediment [2], saline desert soil [3] and fermented food [4]. Our strain was isolated from a sulfite ore containing partially oxidized chalcopyrite, obtained from the Sossego mine (6°25’45"S, 50°3’58"W) in Canaã dos Carajás, Brazil. To date, there is only one complete published genome of *Kocuria rhizophila* DC2201 (GenBank/EMBL/DDBJ accession number AP009152) [5] and

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the possibility of genetic features that could be targeted in future bioremediation processes and especially copper), and siderophore biosynthesis (implying the capacity to acquire iron), which could explain the organism’s survival in extreme environments and raises the possibility of genetic features that could be targeted in future bioremediation studies.

According to RAST, K. rhizophila DC2201 is the closest neighbor of our strain, encoding a type III polyketide synthase (T3pks) and a nonribosomal peptide synthetase, and is probably capable of degrading the aromatic compounds phenylacetate, protocatechuate, and homoprotocatechuate [5]. The functional annotation of K. marina SO9-6 revealed genes related to the degradation of aromatic compounds including the industrial water contaminant phenylacetic acid [17], benzene (by means of hydroxylation), and phenylacetate. The antiSMASH v.2.0 [18] analysis revealed five known secondary metabolic clusters, one siderophore, two bacteriocins, one terpene, and one T3pks synthetis, in contigs KM0016, KM0022, KM0028, KM0045, and KM0055, respectively. A nearly complete route for butanol production from glycerol degradation was also identified, as well as genes involved in antibiotic resistance, tolerance to heavy metals (mercury, arsenic, zinc, and especially copper), and siderophore biosynthesis (implying the capacity to acquire iron), which could explain the organism’s survival in the high metal content environment. The genes for aromatic compound degradation and heavy metal tolerance suggest that K. marina SO9-6 could be used to improve bioremediation processes in contaminated areas.

Comparative genomics analyses of SO9-6 are in progress and will be published separately. This first genome of K. marina helps to provide insights into its survival in extreme environments and raises the possibility of genetic features that could be targeted in future bioremediation studies.

Table 1

| Attributes          | Value |
|---------------------|-------|
| Genome size (bp)    | 3,066,141 |
| Total contigs       | 62 |
| GC content (%)      | 68.82 |
| Protein-coding genes| 2818 |
| tRNA genes          | 48 |
| rRNA genes          | 9 |
| Genes assigned to subsystems | 1250 |

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D.B.A. Castro et al. / Genomics Data 5 (2015) 34–35