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Draft genome sequence of *Kocuria* sp. SM24M-10 isolated from coral mucus

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ABSTRACT

Here, we describe the genomic features of the Actinobacteria *Kocuria* sp. SM24M-10 isolated from mucus of the Brazilian endemic coral *Mussismilia hispida*. The sequences are available under accession number LDNX01000000 (http://www.ncbi.nlm.nih.gov/nuccore/LDNX00000000). The genomic analysis revealed interesting information about the adaptation of bacteria to the marine environment (such as genes involved in osmotic and oxidative stress) and to the nutrient-rich environment provided by the coral mucus.

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Specifications	
Organism/cell line/tissue	*Kocuria* sp.
Strain	SM24M-10
Sequencer or array type	*Illumina HiSeq 2500*
Data format	Processed
Experimental factors	Laboratory cultivated strain
Experimental features	Draft genome sequence of *Kocuria* sp. SM24M-10
Consent	N/A
Sample source location	Brazilian Collection of Environmental and Industrial Microorganisms (CBMAI), accession number 1702

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/nuccore/LDNX00000000

2. Experimental design, materials and methods

The *Kocuria* genus was established in 1995 by a taxonomic dissection of the *Micrococcus* genus [1]. So far, it comprises the species *Kocuria rosea*, *Kocuria varians*, *Kocuria kristinae* [1], *Kocuria rhizophila*, *Kocuria palustris* [2], *Kocuria polaris* [3], *Kocuria marina* [4], *Kocuria atrinae* [5], *Kocuria koreensis* [6], *Kocuria gwangalliensis* [7], *Kocuria himachalensis* [8], *Kocuria aegyptia* [9], *Kocuria flava*, *Kocuria turfanensis* [10], *Kocuria salsicia* [11], *Kocuria halotolerans* [12], *Kocuria carniphila* [13], *Kocuria sediminis* [14], and *Kocuria assamensis* [15]. Members of the *Kocuria* genus can be found in soil, mammal skin, the rhizosphere, clinical samples, and several other ecological niches, such as the Antarctic cyanobacterial mat [3], marine sediment [4], fermented food [5,6], seawater [7], and sulfide ore [16]. Although isolated from various sources, the size of the *Kocuria* genus is relatively small among the *Actinomycetes*, which suggests that each species of *Kocuria* is highly adapted to its ecological niche [8,9]. Here, we report a draft genome of *Kocuria* sp. SM24M-10 isolated from coral mucus, adding new information about this genus and its adaptation to the marine environment.

Kocuria sp. SM24M-10 was grown overnight in 3 mL of liquid GASW (Glycerol Artificial Sea Water) medium [17] at 30 °C, followed by centrifugation. The supernatant was discarded and the cells were used for

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DNA extraction with the Wizard® Genomic DNA Purification Kit (Promega), according to the manufacturer's protocol. Sequencing of the genomic DNA was performed at the Life Sciences Core Facility (LaCTAD) at the State University of Campinas (UNICAMP), using a paired-end library of 400 bp in a HiSeq2500 Illumina sequencer, and yielded 65,536,228 paired-end reads of 100 bp. The estimated genome size was 4.56 Mbp, with coverage of 1437×, based on k-mer count [18,19]. All reads were preprocessed using NGS QC Toolkit v.2.2.3 [20], with quality and length cutoffs of 20 and 70 bp, respectively. The assembly was performed with Edena v.3 [21] (m = 41) and resulted in 177 contigs with a total length of 4,346,986 bp, N50 of 45,611 bp, and GC content of 72.35%. The identification of RNA genes, the open reading frames (ORFs), and the prediction of protein functions were performed using the Rapid Annotation Subsystem Technology (RAST) online server [22], with the gene caller GLIMMER 3.0 [23]. *Kocuria* sp. SM24M-10 presented 4013 coding sequences (CDSs), 49 tRNA genes, and 6 rRNA genes (two 5S RNA, two 16S, and two 23S). A total of 1650 (42%) protein-coding genes were classified in 404 subsystems, and a predicted function was assigned to 1574 of them (Table 1).

The genomic analysis of *Kocuria* sp. SM24M-10 revealed interesting information about its adaptation to the marine environment and to the nutrient-rich environment provided by the coral mucus. The genome presented 22 genes associated with osmotic stress, and 18 of these genes were classified as being involved in betaine uptake and biosynthesis. Betaine is an efficient osmolyte that is promptly accumulated in large amounts in response to osmotic stress [24,25]. Due to symbiosis with zooxanthellae algae [26], coral tissues may contain exceptionally high levels of oxygen, which can generate oxidative stress. For this reason, it is expected that bacteria associated with coral are able to produce enzymes to overcome the toxic effects of reactive oxygen species [26]. Several genes involved in the oxidative stress response were found in *Kocuria* sp. SM24M-10. Among these genes, 14 were related to the biosynthesis of glutathione and its analogs (e.g. mycothiol). Glutathione plays a role in preventing cellular damage caused by reactive oxygen species [27,28], while mycothiol provides protection against oxidative compounds as well as some classes of antibiotics [28]. Genes related to the catabolism of sugar alcohols, such as glycerol and inositol, were also observed in the bacteria genome. Both glycerol and inositol are important photosynthetic products that are released by symbiotic *Symbiodinium* algae and are used by corals [29]. The presence of genes related to the use of these compounds as energy sources demonstrates the adaptation of *Kocuria* sp. SM24M-10 to the microenvironment provided by the coral. The genome also presented genes related to mechanisms of resistance against antibiotics and toxic compounds. Considering the fact that *Kocuria* sp. SM24M-10 was isolated from a marine environment exposed to chemicals derived from high levels of cargo ship traffic, we suggest that some of the resistance genes found in the genome annotation might have contributed to the survival of the bacteria in the coral microenvironment. In addition, genes related to pathways of resistance to heavy metals (cobalt, copper, mercury, and arsenic) were found in the genome.

In conclusion, the first draft genome of *Kocuria* sp. SM24M-10 revealed a pool of functional categories related to central metabolism, together with characteristic properties associated with the response to osmotic and oxidative stress, carbohydrate metabolism, and resistance to antibiotics and toxic compounds. These data provide new insights into the adaptation and survival of microorganisms in marine environments, as well as the relationship between microorganisms and coral species.

Table 1
Features of the *Kocuria* sp. SM24M-10 draft genome.

Attributes	Values
Genome size (bp)	4,346,986
Total contigs	177
G + C content (%)	72.35
Protein-coding genes	4013
tRNA genes	49
rRNA genes	6
Genes assigned to subsystems	1650

3. Nucleotide sequence accession number

The draft genome sequence of *Kocuria* sp. SM24M-10 has been deposited at DDBJ/EMBL/GenBank under accession number LDNX01000000.

Conflicts of interest

The authors declare no conflicts of interest concerning the work published in this paper.

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