

Draft Genome Sequence of *Micrococcus* sp. Strain MS-AsIII-49, an Arsenate-Reducing Isolate from Tropical Metal-Rich Sediment

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***Micrococcus* sp. strain MS-AsIII-49, which was isolated from a tropical metal-polluted stream sediment in Brazil, has the ability to reduce AsV to AsIII. Analysis of its draft genome revealed 186 contigs with a total size of 2,440,924 bp encoding several metal resistance genes.**

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Members of the *Micrococcus* genus are found in the environment as saprophyte or commensal in a wide variety of ecosystems, such as human skin, water, dust, and soil, among others (1–8). This genus consists of nine recognized species. So far, only the *M. luteus* species has been sequenced, and its whole genome revealed a small size (2,501,097 bp) with only a few adaptation genes, leading to a very strict ecological niche (9). In this context, the *Micrococcus* sp. strain MS-AsIII-49, described in the present study, was isolated from a tropical metal-rich stream sediment, affected by human settlement, especially arsenic, NO₃⁻ and NH₄⁺ (10). This strain was phenotypically characterized as AsV-reducing bacteria. In addition, the genome sequencing of *Micrococcus* sp. strain MS-AsIII-49 provided insight into the genomic diversity and evolution of the *Micrococcus* genus.

For the genome sequencing of *Micrococcus* sp. strain MS-AsIII-49, a mate pair library was constructed and sequenced on an Illumina HiSeq 2000 platform at the Beijing Genomics Institute. The reads were subjected to preprocessing consisting of screens for errors and quality-based trimming using the *prinseq-lite* algorithm (11). The reads obtained were assembled using *de novo* assembly tool in the MIRA 4 software. After the assembly, the contigs were automatically annotated using the Rapid Annotations using Subsystems Technology (RAST) server (12).

The size of the *Micrococcus* sp. MS-AsIII-49 draft genome is 2,440,924 bp, comprising 186 contigs with a G+C content of 73.08%. The *N*₅₀ contig length was 27,810 bp, the largest contig length was 82,396 bp, and the smallest was 198 bp. In total, the numbers of putative coding sequences (CDS) was 2,189 in *Micrococcus* sp. MS-AsIII-49. Only one copy of the 5S rRNA, 16S rRNA, and 23S rRNA genes were found. Additionally, 43 tRNA sequences were found in *Micrococcus* sp. MS-AsIII-49. The subsystem analysis revealed predominance of subsystems related to cell maintenance, such as amino acids and derivatives, carbohydrates, and protein metabolism, among others. A comparison between the genome sequence of *Micrococcus* sp. MS-AsIII-49 and *M. luteus*, using the SEED comparative tool, revealed 165 genes found

only in *Micrococcus* sp. MS-AsIII-49, and 55.15% (91/165) of these genes were annotated as hypothetical proteins. The identified genes were related to mobile elements as integrase and normal cell function as glycosyltransferase, acetyltransferase, and DNA-methyltransferase, among others. The presence of several genes in the virulence, disease, and defense and stress response subsystems in the *Micrococcus* sp. MS-AsIII-49 genome suggests that this strain harbors a genomic repertory able to deal with metals and other environmental toxicants, which would provide an advantage in sediment impacted by human settlement. The analysis of the virulence, disease, and defense subsystem provided insight into *Micrococcus* sp. MS-AsIII-49 metal resistance identifying specific proteins related to arsenic resistance as ArsR, ArsC, and ACR3; mercury resistance as MerR and MerA; copper resistance as CopZ, CopC, CopB, multicopper oxidase, and CtpA; and cobalt-zinc-cadmium resistance as CzcD protein.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JXSP000000000](https://www.ncbi.nlm.nih.gov/nuccore/JXSP000000000). The version described in this paper is version JXSP01000000.

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REFERENCES

- Kloos WE, Tornabene TG, Schleifer KH. 1974. Isolation and characterization of micrococci from human skin, including two new species: *Micrococcus lylae* and *Micrococcus kristinae*. *Int J Syst Bacteriol* 24:79–101. [http://dx.doi.org/10.1099/00207713-24-1-79](https://doi.org/10.1099/00207713-24-1-79).
- Liu H, Xu Y, Ma Y, Zhou P. 2000. Characterization of *Micrococcus antarcticus* sp. nov., a psychrophilic bacterium from Antarctica. *Int J Syst Evol Microbiol* 50:715–719. [http://dx.doi.org/10.1099/00207713-50-2-715](https://doi.org/10.1099/00207713-50-2-715).
- Liu XY, Wang BJ, Jiang CY, Liu SJ. 2007. *Micrococcus flavus* sp. nov., isolated from activated sludge in a bioreactor. *Int J Syst Evol Microbiol* 57:66–69. [http://dx.doi.org/10.1099/ijs.0.64489-0](https://doi.org/10.1099/ijs.0.64489-0).

4. Chen HH, Zhao GZ, Park DJ, Zhang YQ, Xu LH, Lee JC, Kim CJ, Li WJ. 2009. *Micrococcus endophyticus* sp. nov., isolated from surface-sterilized *Aquilaria sinensis* roots. *Int J Syst Evol Microbiol* 59:1070–1075. <http://dx.doi.org/10.1099/ijs.0.006296-0>.
5. Zhao GZ, Li J, Qin S, Zhang YQ, Zhu WY, Jiang CL, Xu LH, Li WJ. 2009. *Micrococcus yunnanensis* sp. nov., a novel actinobacterium isolated from surface-sterilized *Polyspora axillaris* roots. *Int J Syst Evol Microbiol* 59:2383–2387. <http://dx.doi.org/10.1099/ijs.0.010256-0>.
6. Zhang JY, Liu XY, Liu SJ. 2010. *Agrococcus terreus* sp. nov. and *Micrococcus terreus* sp. nov., isolated from forest soil. *Int J Syst Evol Microbiol* 60:1897–1903. <http://dx.doi.org/10.1099/ijs.0.013235-0>.
7. Chittipurna K, Singh PK, Verma D, Pinnaka AK, Mayilraj S, Korpole S. 2011. *Micrococcus lactis* sp. nov., isolated from dairy industry waste. *Int J Syst Evol Microbiol* 61:2832–2836. <http://dx.doi.org/10.1099/ijs.0.028043-0>.
8. Rieser G, Scherer S, Wenning M. 2013. *Micrococcus cohnii* sp. nov., isolated from the air in a medical practice. *Int J Syst Evol Microbiol* 63: 80–85. <http://dx.doi.org/10.1099/ijs.0.036434-0>.
9. Young M, Artsatbanov V, Beller HR, Chandra G, Chater KF, Dover LG, Goh EB, Kahan T, Kaprelyants AS, Kyrpidis N, Lapidus A, Lowry SR, Lykidis A, Mahillon J, Markowitz V, Mavromatis K, Mukamolova GV, Oren A, Rokem JS, Smith MC, Young DI, Greenblatt CL. 2010. Genome sequence of the Fleming strain of *Micrococcus luteus*, a simple free-living actinobacterium. *J Bacteriol* 192:841–860. <http://dx.doi.org/10.1128/JB.01254-09>.
10. Costa PS, Scholte LL, Reis MP, Chaves AV, Oliveira PL, Itabayana LB, Suhadolnik ML, Barbosa FA, Chartone-Souza E, Nascimento AM. 2014. Bacteria and genes involved in arsenic speciation in sediment impacted by long-term gold mining. *PLoS One* 9:e95655. <http://dx.doi.org/10.1371/journal.pone.0095655>.
11. Schmieder R, Edwards R. 2011. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* 27:863–864. <http://dx.doi.org/10.1093/bioinformatics/btr026>.
12. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42: D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.