



# Draft Genome Sequences of Three Novel *Staphylococcus arlettae* Strains Isolated from a Disused Biological Safety Cabinet

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**ABSTRACT** The genome sequences of three new strains of *Staphylococcus arlettae* named Bari1, Bari2, and Bari3 are presented. The strains exhibited tolerance to hexavalent chromium ions. An *sprC* gene encoding a putative chromium transporter was present in each of the three draft genome sequences.

*Staphylococcus arlettae*, a coagulase-negative, Gram-positive bacterium, has been isolated from different samples, including those from human blood (1), horse and cow skin (2, 3), contaminated soil (4), and seawater (5). Here, we report the draft genome sequences of three novel *Staphylococcus arlettae* strains isolated from a disused biological safety cabinet.

A Nunc bioassay plate containing LB agar supplemented with 0.2 mM potassium chromate and chloramphenicol was deposited on the worktop of a disused but functional class II biological safety cabinet. After the airflow was switched on for 1 h, the plate was incubated for 16 h at 37°C. About 60 colonies were grown.

Colonies were replicated on LB agar containing 150 mM Cr<sup>+6</sup>. Only five colonies survived, three of which, recognized as distinct by 16S rRNA sequencing and designated Bari1, Bari2, and Bari3, were submitted for whole-genome sequencing.

Genomic DNA was extracted with the DNeasy blood and tissue kit (Qiagen). Libraries were prepared using the Nextera XT library prep workflow (Illumina), and 2 × 250-nucleotide (nt) paired-end reads were generated on an Illumina MiSeq instrument. A total of 1.9 million, 1.6 million, and 0.84 million reads were obtained for Bari1, Bari2, and Bari3, respectively. The preprocessing and assembly of reads and the functional annotation of contigs were performed using a modified version of the “Fosmid1” pipeline in the A-GAME (6) Galaxy (7) framework (the assignment of assembled contigs to presumed fosmids was deactivated).

Quality trimming was executed using the sliding-window operation in Trimmomatic (8) with default parameters. Overlapping reads were merged using PEAR (9) with standard parameters. The final assembly was performed using the SPAdes (10) assembler (version 3.50) using kmers of 33, 55, 77, 99, and 121 nt. Annotation was performed with PROKKA (11) using default parameters. Final assemblies consisted of 72 contigs for Bari1, 82 for Bari2, and 102 for Bari3, with  $N_{50}$  values of 109,514 bp, 83,737 bp, and 50,607, respectively, and theoretical coverage values of 364×, 313×, and 170×, respectively.

The draft genomes of Bari1, Bari2, and Bari3 were 2,612,388 bp (G+C content of 33.32%), 2,498,899 bp (G+C content of 33.56%), and 2,490,148 bp (G+C content of

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33.23%) long, respectively. A total of 2,601 (10 rRNAs, 62 tRNAs, and 2,529 coding sequences [CDS]), 2,464 (10 rRNAs, 62 tRNAs, and 2,392 CDS), and 2,447 (9 rRNAs, 62 tRNAs, and 2,376 CDS) genes were annotated for Bari1, Bari2, and Bari3, respectively. Following 16S rRNA analysis, the *dnaJ* gene sequences were compared with those of the NCBI nucleotide database (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) (12). Bari1, Bari2, and Bari3 all showed ~99% similarity with *Staphylococcus arlettae* GTC383 (GenBank accession number [AB234056](https://doi.org/10.1128/JB.01732-12)).

For each draft genome, functional annotation revealed an *srpC* homologue encoding a putative chromate transporter of the chromate ion transporter (CHR) superfamily (13). The *emrA* and *emrB* genes, implicated in chromate and ampicillin coresistance in *Staphylococcus aureus* LZ 01 (14), as well as loci specifying chloramphenicol resistance, were also identified in each isolate.

**Data availability.** The draft genome sequences were deposited in GenBank under the accession numbers [QLIZ00000000](https://doi.org/10.1128/JB.01732-12), [QLJA00000000](https://doi.org/10.1128/JB.01732-12), and [QLJB00000000](https://doi.org/10.1128/JB.01732-12). The versions described in this paper are the first versions, QLIZ01000000, QLJA01000000, and QLJB01000000. Raw sequences are available under the SRA study accession number [SRP158573](https://doi.org/10.1128/JB.01732-12).

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## REFERENCES

- Dinakaran V, Shankar M, Jayashree S, Rathinavel A, Gunasekaran P, Rajendhran J. 2012. Genome sequence of *Staphylococcus arlettae* strain CVD059, isolated from the blood of a cardiovascular disease patient. *J Bacteriol* 194:6615–6616. <https://doi.org/10.1128/JB.01732-12>.
- Schnellmann C, Gerber V, Rossano A, Jaquier V, Panchaud Y, Doherr MG, Thomann A, Straub R, Perreten V. 2006. Presence of new *mecA* and *mph(C)* variants conferring antibiotic resistance in *Staphylococcus* spp. isolated from the skin of horses before and after clinic admission. *J Clin Microbiol* 44:4444–4454. <https://doi.org/10.1128/JCM.00868-06>.
- Verdier-Metz I, Gagne G, Bornes S, Monsallier F, Veisseire P, Delbès-Paus C, Montel MC. 2012. Cow teat skin, a potential source of diverse microbial populations for cheese production. *Appl Environ Microbiol* 78:326–333. <https://doi.org/10.1128/AEM.06229-11>.
- Srivastava S, Verma PC, Chaudhry V, Singh N, Abhilash PC, Kumar KV, Sharma N, Singh N. 2013. Influence of inoculation of arsenic-resistant *Staphylococcus arlettae* on growth and arsenic uptake in *Brassica juncea* (L.) Czern. Var. R-46. *J Hazard Mater* 262:1039–1047. <https://doi.org/10.1016/j.jhazmat.2012.08.019>.
- Krishnaveni M, Jayachandran S. 2009. Inhibition of MAP kinases and down regulation of TNF-alpha, IL-beta and COX-2 genes by the crude extracts from marine bacteria. *Biomed Pharmacother* 63:469–476. <https://doi.org/10.1016/j.biopha.2008.09.005>.
- Chiara M, Placido A, Picardi E, Ceci LR, Horner DS, Pesole G. 2018. A-GAME: improving the assembly of pooled functional metagenomics sequence data. *BMC Genomics* 19:44. <https://doi.org/10.1186/s12864-017-4369-z>.
- Goecks J, Nekrutenko A, Taylor J, Galaxy Team T. 2010. Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biol* 11:R86. <https://doi.org/10.1186/gb-2010-11-8-r86>.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btt593>.
- Zhang J, Kobert K, Flouri T, Stamatakis A. 2014. PEAR: a fast and accurate Illumina paired-end reAd merger. *Bioinformatics* 30:614–620. <https://doi.org/10.1093/bioinformatics/btt593>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
- Shah MM, Iihara H, Noda M, Song SX, Nhung PH, Ohkusu K, Kawamura Y, Ezaki T. 2007. *dnaJ* gene sequence-based assay for species identification and phylogenetic grouping in the genus *Staphylococcus*. *Int J Syst Evol Microbiol* 57:25–30. <https://doi.org/10.1099/ijs.0.64205-0>.
- Aguilar-Barajas E, Jerónimo-Rodríguez P, Ramírez-Díaz MI, Rensing C, Cervantes C. 2012. The ChrA homologue from a sulfur-regulated gene cluster in cyanobacterial plasmid pANL confers chromate resistance. *World J Microbiol Biotechnol* 28:865–869. <https://doi.org/10.1007/s11274-011-0883-3>.
- Zhang H, Ma Y, Liu P, Li X. 2016. Multidrug resistance operon *emrAB* contributes for chromate and ampicillin co-resistance in a *Staphylococcus* strain isolated from refinery polluted river bank. *SpringerPlus* 5:1648. <https://doi.org/10.1186/s40064-016-3253-7>.