




Draft Genome Sequence of the Community-Associated *Staphylococcus aureus* Sequence Type 88 Strain LVP-7, Isolated from an Ocular Infection

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ABSTRACT We report a *de novo*-assembled draft genome sequence of the Indian *Staphylococcus aureus* sequence type 88 (ST88) strain LVP-7, isolated from an ocular infection. The genome harbors a Pantone-Valentine leukocidin phage, a type V staphylococcal cassette chromosome *mec* element, the delta-hemolysin-converting Newman phage Φ NM3, and the pathogenicity island SaPI3, encoding the superantigen enterotoxin B.

Staphylococcus aureus is among the most common pathogens causing ocular infection. Previous reports suggest that both hospital-associated (HA) and community-associated (CA) methicillin-resistant *Staphylococcus aureus* (MRSA) can cause eye infections (1–3). In India, CA MRSA and methicillin-sensitive *Staphylococcus aureus* (MSSA) strains belong to distinct clonal lineages carrying either type IV or V staphylococcal cassette chromosome *mec* (SCC*mec*) elements (4, 5). The sequence type 88 (ST88) lineage is more prevalent in India (4, 6), Africa (3, 7), and China (8), unlike other Indian CA-MRSAs such as ST772 that are globally disseminated (9–11).

Here, we report a draft genome sequence of an ST88 CA MRSA strain. Strain LVP-7 was isolated from an orbital abscess in a patient at LV Prasad Eye Institute, Bhubaneswar, India. This isolate is not part of a larger epidemiological study and is exempt from ethics committee approval. For genomic DNA (gDNA) extraction, LVP-7 glycerol stock stored at -80°C was streaked onto chromogenic agar medium (chromAgar, bioMérieux, Marcy-L'Etoile, France). A single colony was picked and grown overnight in brain heart infusion (BHI) broth under aerobic conditions. gDNA was prepared using the phenol-chloroform method (4). Sequencing libraries were prepared using the NEBNext DNA Ultra II library prep kit (New England Biolabs) and sequenced using v3 chemistry in an Illumina HiSeq 2500 instrument (2×100 -bp paired-end format). A total of 9,561,330 read pairs were demultiplexed to fastq format using bcl2fastq v2.20.0.422. The quality of the fastq files was ascertained using FastQC v0.11.7 (12). Adapter content and low-quality reads were removed using Trim Galore (13). *De novo* assembly was performed using SPAdes v3.14.1 (14) and assembly quality assessed using QUAST v4.5 (15). Gap filling, ordering of contigs, and optimal scaffolding were done using RagTag (16), with the *S. aureus* M013 genome as reference (17). The resulting assembly was annotated using PROKKA v1.14.6 (18), and downstream analyses were performed using SCC*mec*Finder, SPATyper v0.1.0, and TA finder (19–21). The NARA-curated enterotoxin database (22) was used to predict toxin gene clusters. ResFinder and PathogenFinder were used to identify the antibiotic resistance and virulence gene clusters, respectively (23, 24). Prophage Hunter and PhiSpy helped to identify prophage gene signatures (25, 26). Default parameters

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TABLE 1 Genome assembly statistics and annotation features of the *Staphylococcus aureus* ST88 strain LVP-7

Feature	Value
Draft <i>de novo</i> assembly statistics	
No. of contigs	69
No. of contigs >500 bp	16
Largest contig size (bp)	2,777,888
Genome size (bp)	2,858,759
G+C content (%)	32.73
N_{50} (bp)	2,777,888
No. of <i>N</i> s per 100 kbp	217.54
Genome annotation features	
No. of ORFs ^a	2,722
No. of mRNAs and rRNAs	2,668
No. of tRNAs	53
No. of tmRNAs ^b	1
Positive strand (bp)	1,323
Negative strand (bp)	1,399

^a ORFs, open reading frames.

^b tmRNAs, transfer-messenger RNAs.

were used for all software unless otherwise specified. Details of the assembled genome sequence and annotation are compiled in Table 1.

The draft genome sequence reveals that LVP-7 belongs to the *spa* (*Staphylococcus aureus* protein A) type t2526 and carries an SCCmec type V (5C2) cassette. This ST88

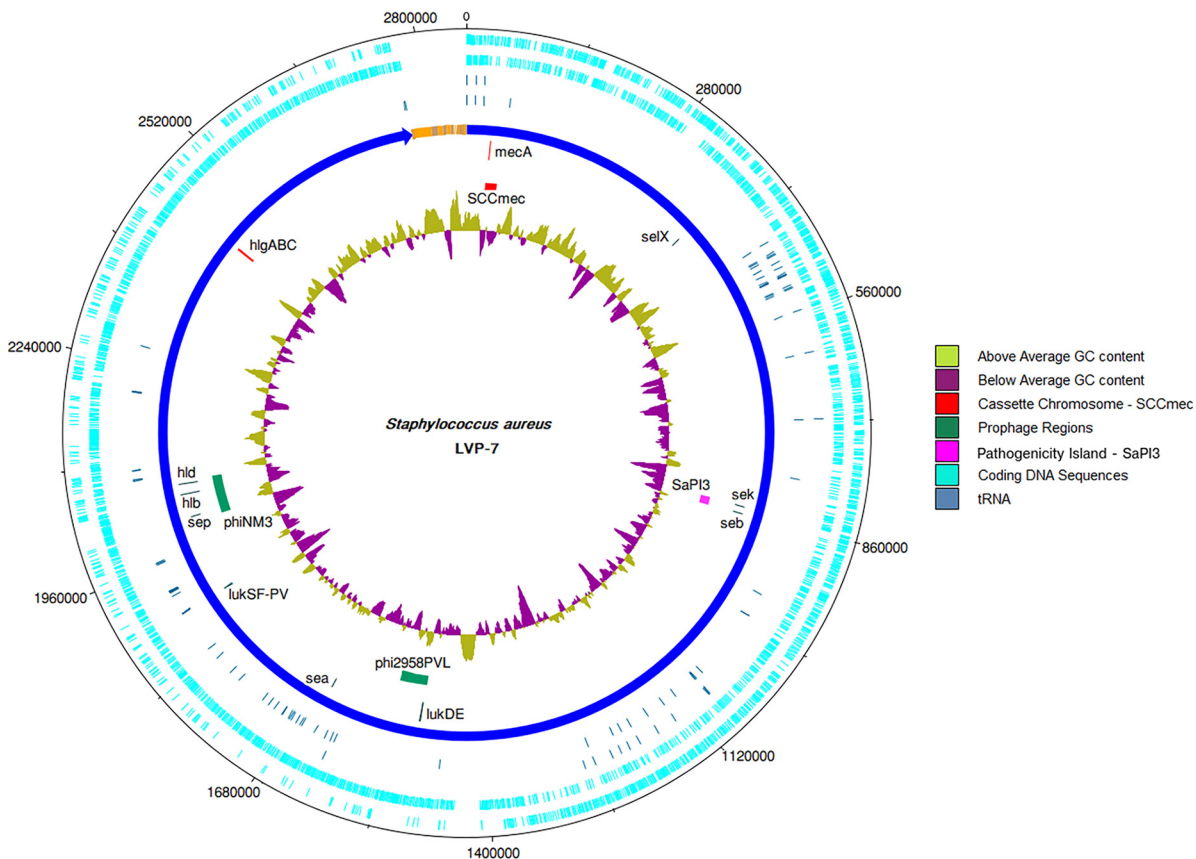


FIG 1 Major genetic elements in *Staphylococcus aureus* ST88 strain LVP-7. The innermost circular track (track 1) represents the G+C content. Track 2 displays select mobile genetic elements, including the staphylococcal cassette chromosome (SCCmec) element, the pathogenicity island SaPI3, and the Pantone-Valentine leukocidin (PVL) and phiNM3 prophages. Track 3 displays select virulence genes. While track 4 represents the major (blue) and minor (orange) contigs, tracks 5 and 6 show the location of the tRNAs. The outer tracks (7 and 8) represent coding sequences. This representation was made using DNAPlotter (29).

strain encodes Pantan-Valentine leukocidin (PVL) phage Φ 2958PVL, gamma-hemolysin components (hlgABC), and several super antigens such as *sea*, *sep*, *sek*, and *selX* (Fig. 1). A δ -hemolysin (*hIb*)-converting *S. aureus* Newman phage (Φ NM3) was also identified, as depicted in Fig. 1. The staphylococcal pathogenicity island (SaPI3; Fig. 1) in LVP-7 harbors the *seb* enterotoxin, which may contribute to systemic *S. aureus* infection (27). The accessory gene regulator (*agr*) quorum-sensing system in LVP-7 is part of *agr* allele group III and was confirmed using multiplex PCR (28). The role of these virulence genes in LVP-7 pathogenesis needs further assessment.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [JADRJK000000000](https://doi.org/10.1186/s12864-015-1599-9). The associated BioProject and BioSample accession numbers are [PRJNA679674](https://doi.org/10.1186/s12864-015-1599-9) and [SAMN16843707](https://doi.org/10.1186/s12864-015-1599-9), respectively. The raw reads from Illumina sequencing have been submitted to the Sequence Read Archive (SRA) and are available under the accession number [PRJNA679674](https://doi.org/10.1186/s12864-015-1599-9).

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