Draft Genome Sequences of Four Commensal Strains of *Staphylococcus* and *Pseudomonas* Isolated from Healthy Human Skin

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ABSTRACT  *Staphylococcus* spp. and *Pseudomonas* spp. are widely distributed bacteria in the environment and are found in association with animals and humans. Here, we present the draft genome sequence data of the healthy human skin commensal strains *Staphylococcus aureus* MFP03, *Staphylococcus epidermidis* MFP04, *Staphylococcus capitis* MFP08, and *Pseudomonas fluorescens* MFP05.

*Staphylococcus* and *Pseudomonas* are among the most abundant genera of *Firmicutes* and *Proteobacteria*, respectively, which are major phyla of the skin microbiota (1–3). Although *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Staphylococcus capitis* are species that reside abundantly on the skin (4), they are described mainly as pathogens. Therefore, it seems relevant to sequence skin commensal strains of these species. Moreover, no sequences of *Pseudomonas fluorescens* cutaneous commensal isolates had been reported yet.

In healthy individuals, skin microbiota bacteria are harmless to the host and play a central role in skin homeostasis (5); therefore, they should possess few virulence factors. Nevertheless, exoenzymes, often considered virulence factors in pathogens (6), are also secreted by commensals contributing to host innate defense mechanisms (7). Here, we report the draft genome sequences of four skin commensal bacterial strains previously isolated from healthy volunteers (8), i.e., *Staphylococcus aureus* MFP03, *Staphylococcus epidermidis* MFP04, *Staphylococcus capitis* MFP08, and *Pseudomonas fluorescens* MFP05. A particular focus was given to virulence and exoenzyme genes.

Cryo-frozen isolates were grown 24 h in LB medium at 180 rpm and 37°C for *Staphylococcus* strains or at 28°C for the *Pseudomonas fluorescens* MFP05 strain. Genomic DNA was extracted using the GeneJET genomic DNA purification kit (Thermo Fisher Scientific, USA), following the manufacturer’s instructions, directly on the *Pseudomonas fluorescens* pellet or after a 60-min treatment of *Staphylococcus* strain pellets with lysis solution (400 μg/ml lysostaphin, 20 mg/ml lysozyme, 20 mM Tris-HCl [pH 8.0], 2 mM EDTA, and 1.2% Triton X-100). The quality and concentration of DNA were determined on a Nanodrop spectrophotometer and a Qubit 4.0 fluorometer (Thermo Fisher Scientific). Libraries were prepared using the Illumina Nextera XT or the Nextera Flex DNA library prep kits (Table 1) and sequenced on the MiSeq platform (Illumina) according to the manufacturer’s protocol, with the MiSeq reagent cartridge V3 (600 cycles, 250-bp or 300-bp dual-index paired-end reads).

Default parameters were applied for all software unless otherwise specified. FastQC v.0.11.9 (9) was utilized to check read quality, and Trimmomatic v.0.39 (10) was used to quality trim the generated reads. Genome assembly was achieved de novo with Unicycler v.0.4.8 (11), and CheckM v.1.1.3 (12) was used to assess contamination. QUAST v.5.0.2 (13) was used to check the consistency of the obtained assemblies (i.e.,...
### TABLE 1 Sequencing metrics and genomic data

| Parameter | Data for: |
|-----------|-----------|
|           | *S. aureus* MFP03 | *S. epidermidis* MFP04 | *S. capitis* MFP08 | *P. fluorescens* MFP05 |
| **Site of isolation** | Human, cheekbone | Human, cheekbone | Human, scapula | Human, scapula |
| **DNA library prep kit (bp)** | Nextera XT (2 × 250) | Nextera Flex (2 × 300) | Nextera XT (2 × 250) | Nextera XT (2 × 250) |
| **Sequencing metrics** | | | | |
| No. of reads | 899,406 | 854,508 | 874,656 | 1,812,096 |
| Mean coverage (×) | 79.37 | 95.08 | 86.39 | 59.6 |
| **Accession no.** | GenBank SRR12339019 | GenBank SRR1239018 | GenBank SRR12339016 | GenBank SRR1239017 |
| **Genomic data** | | | | |
| Genome size (bp) | 2,694,498 | 2,477,229 | 2,471,586 | 6,610,034 |
| G+C content (%) | 32.77 | 31.94 | 32.71 | 59.83 |
| No. of contigs | 25 | 48 | 50 | 100 |
| N50 value (bp) | 607,734 | 256,159 | 249,048 | 250,027 |
| No. of CDS | 2,484 | 2,309 | 2,340 | 6,072 |
| No. of rRNAs | 59 | 49 | 59 | 56 |
| No. of tRNAs | 4 | 4 | 5 | 2 |
| **CheckM** | | | | |
| Completeness (%) | 98.82 | 99.61 | 99.81 | 99.53 |
| Contamination (%) | 0.48 | 0.10 | 0.00 | 1.46 |
| Strain heterogeneity (%) | 0.00 | 0.00 | 0.00 | 6.25 |
| Virulence factors(s) | adxA, aur, cap8A to cap8P, chp, clfAB, ebp, T7SS, fnbAB, hly/hla, hlb, hld, hlgABC, icaA to icaD, sspA, sspBC, isd, hysA, sbi, geh, coa, spa, map, scn, sak, vWbp | None | None | None |
| Antibiotic resistance(s) | blaZ, ImRS, mepA, mepR, tet(38), norA, dha1, aph | blaZ, dfrC, fosB, norA | norA | mexF |
| MLST profile | 45 | 65 | NA | 111 |
| **Exoenzymatic activities** | | | | |
| Lipase/esterase | + | + | + | + |
| Urease | -- | -- | -- | + |
| Sialidase | -- | -- | -- | -- |
| Hyaluronidase | -- | -- | -- | -- |
| Sphingomyelinase | -- | -- | -- | -- |
| Ceramidase | -- | -- | -- | -- |
| Protease | + | + | -- | -- |

### Notes

- **CheckM:** coding DNA sequences.
- **CDS:** coding genes involved in the corresponding enzymatic activity.
- **Genome size, number of contigs, N50 value, and G+C content.** Annotation was carried out using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (14). Sequence type (ST) identification was performed using the program MLST v.2.19.0 (15). The contig-based search method abricate v.0.8.13 was used to identify virulence factors and antibiotic resistance genes (16). Custom abricate databases were created for the following enzymes,
based on downloaded NCBI reference sequences from *Pseudomonas* and *Staphylococcus*
keywords: lipase, esterase, urease, sialidase, hyaluronidase, sphingomyelinase, ceramidase,
and protease. The obtained metrics and results are presented in Table 1.

These draft annotated genome sequences of human skin isolates will improve the
understanding of genetic diversity and enzymatic activities as well as the mechanisms
involved in microbiota-human skin interactions.

**Data availability.** MiSeq sequencing reads and draft genome assemblies and anno-
tations have been deposited in the Sequence Read Archive (SRA) and GenBank, respec-
tively, under the accession numbers listed in Table 1. The abricate custom databases
used in this study are available from the corresponding authors upon request.

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