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**Complete Genome Sequence of *Staphylococcus aureus* 6850, a Highly Cytotoxic and Clinically Virulent Methicillin-Sensitive Strain with Distant Relatedness to Prototype Strains**

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*Staphylococcus aureus* is a frequent human commensal bacterium and pathogen. Here we report the complete genome sequence of strain 6850 (*spa* type t185; sequence type 50 [ST50]), a highly cytotoxic and clinically virulent methicillin-sensitive strain from a patient with complicated *S. aureus* bacteremia associated with osteomyelitis and septic arthritis.

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**Staphylococcus aureus** is a Gram-positive human commensal bacterium persistently colonizing the anterior nares of about 30% of the human population. Diverse virulence factors render the bacterium a versatile pathogen that causes a variety of diseases ranging from soft tissue infections to severe conditions (e.g., endocarditis, osteomyelitis, bacteraemia, and sepsis). *S. aureus* strain 6850 is a well-characterized prototype strain isolated from a patient with a skin abscess which had progressed to *S. aureus* bacteraemia, osteomyelitis, septic arthritis, and multiple systemic abscesses (1). This bacterium is strongly hemolytic on rabbit (2) and sheep blood agar, has a high propensity for cellular invasiveness (3–5), and displays phagosomal escape (5,6) as well as prominent cytotoxicity (1, 3–5, 7, 8). The strain has been used in a number of studies. Anaerobically grown *S. aureus* 6850 formed minute non-pigmented colonies with reduced hemolytic activity (2). A menadione auxotroph variant, JB1, was generated by a single *in vitro* passage of *S. aureus* 6850 in tryptic soy broth containing gentamicin (2, 9) and has been used to investigate so-called small-colony variants (SCV), noncytotoxic, auxotrophic persister cells (10, 11). A *hemB* mutant of 6850, Ib1 (12), behaving like a stable SCV, has been shown to persist intracellularly and causes less cytotoxicity, resembling the JB1 SCV phenotype (13). Phenotype switching (13), as well as intracellular gene expression in lung epithelial cells (14), has been investigated. *S. aureus* 6850 has also been observed to efficiently escape from endosomes/phagosomes of mammalian cells upon internalization (5). Intravenous infection with strain 6850 resulted in osteomyelitis in a mouse model (15).

Here we report the complete genome sequence of *Staphylococcus aureus* strain 6850. Whole-genome sequencing of the strain 6850 (*spa* type t185; sequence type 50 [ST50]), a highly cytotoxic and clinically virulent methicillin-sensitive strain from a patient with complicated *S. aureus* bacteremia associated with osteomyelitis and septic arthritis.

The draft genome *Staphylococcus aureus* strain 6850 was available in GenBank under the accession number CP006706.

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