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Draft Genome Sequence of an Erythromycin-Resistant *Propionibacterium acnes* Isolate Recovered from Folliculitis of the Scalp

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ABSTRACT *Propionibacterium acnes* is now well-known and recognized for its implication in the pathogenesis of acne vulgaris. Here, we report the draft genome sequence of an erythromycin-resistant *P. acnes* strain isolated from a case of folliculitis of the scalp belonging to phylotype IA1 and sequence type 18 (ST18).

Propionibacterium acnes is an aerotolerant anaerobic Gram-positive bacterium constituting a significant part of the human skin microbiota (1). Although *P. acnes* is considered to be commensal and is likely to be found on all healthy adult skin (2), this bacterium is clearly well-known for its implication in the pathogenesis of acne or folliculitis (3–6). Moreover, *P. acnes* is clearly underestimated in medical device-related infections and sometimes considered a contaminant (7, 8). Using different molecular typing methods (multilocus sequence typing [MLST]/sequence-based strain typing [SLST]), *P. acnes* strains have been subdivided into six main phylogenetic types: IA1, IA2, IB, IC, II, and III (9, 10). In the acne field, phylotype/SLST type IA1/A1 is the most frequent lineage found (9, 11). In the context of this skin disorder, erythromycin, clindamycin, and tetracycline resistances have been extensively reported over the years (12, 13).

Here, we present the draft genome sequence of *Propionibacterium acnes* HB strain isolated from a patient suffering from folliculitis at Nantes University Hospital, France.

P. acnes HB was grown overnight at 37°C on a Schaedler agar plate (Oxoid, United Kingdom) under an anaerobic atmosphere. Genomic DNA was extracted using a DNeasy blood and tissue kit (Qiagen Gmbh, Germany), as described previously (14). A paired-end library was prepared with NEBNext Ultra DNA library prep kit for Illumina (NEB) and sequenced (2 × 150 bp) on a MiSeq sequencer (Illumina, USA). *De novo* assembly was performed with Velvet 1.2.10 and VelvetOptimiser 2.2.5 (optimal hash value = 127). A total of 4,394,492 reads were assembled into 21 contigs with an average coverage of 205×. Contig reordering and annotation were performed with Mauve 2.3.1 and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP), respectively (15, 16). Sequence alignment and comparison were performed with CLC Sequence Viewer 7.0 and BLAST. Average nucleotide identity (ANI) to the *P. acnes* reference strain KPA171202 was calculated using Oat 0.91 (17).

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The draft genome of strain HB (GenBank accession no. MDGS00000000) contains 2,328 genes, 2,275 coding sequences (CDSs), 45 tRNAs, four rRNAs, and four noncoding RNAs. The G+C content was 60.0%, and the ANI value was 99.1%.

Although *Propionibacterium* species on healthy human skin could be highly diverse (18, 19), an increased frequency of IA1/A1 phylotype/SLST has been observed, especially in case of severe acne (5). Despite a conserved core genome of 83% for *P. acnes* (20), with more than 100 genome sequences of *P. acnes* from different clonal complexes or sequence types at that time, genome analysis compared with clinical data can help to better understand how the inflammatory potential of *P. acnes* sequenced strains may influence the severity of skin lesions (4).

P. acnes HB belongs to ST18, phylotype IA1, and SLST A1. Sequence analysis revealed that the 23S rRNA gene is mutated at position 2059 (according to the *Escherichia coli* numbering), thus leading to a high-level resistance to erythromycin. This draft genome will be also used for studying the impact of different virulence factors, especially lipase or hyaluronate lyase on skin innate immunity (21).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number MDGS00000000.

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