Draft Genome Sequences of Four \textit{Propionibacterium acnes} Strains Isolated from Implant-Related Infections

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\textit{Propionibacterium acnes} was previously described as a potential implant-related pathogen. Here, we report the draft genome sequence of four \textit{P. acnes} strains, isolated from spine material, hip arthroplasty, and knee arthroplasty infections in France belonging to different sequence types (ST18, ST27, and ST36).

\textit{P. acnes} is a Gram-positive bacterium constituting a significant part of the human skin microbiota \cite{1}. It has been associated with skin diseases such as acne vulgaris or fulminans acne \cite{2}. The role of this microorganism in deep and medical device-related infections is underestimated \cite{3}. Besides shoulder prosthesis infections, spinal instrumentation infections have been reported \cite{4}. Using multiplex sequence typing (MLST) and single-locus sequence typing (SLST) schemes, the \textit{P. acnes} species has been subdivided into five main phylogenetic types: IA1, IA2, IB, IC, II, and III \cite{5,6}. In the context of device-related infections, \textit{P. acnes} antibiotic resistance may be a problem, especially when low- or high-level rifampin resistance is detected \cite{7,8}, as rifampin remains a key drug for eradicating \textit{P. acnes} biofilm infection \cite{9}.

Here, we present the draft genome sequences of four \textit{P. acnes} strains (2003-1719, NTS31306190, 2004-10708, and LRY\_BL) isolated from patients at Nantes University Hospital and La Roche/Yon Hospital, France, suffering from bone infection.

All \textit{P. acnes} strains were grown overnight at 37°C on 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 \cite{10}. A pair-end library was prepared with a 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 version 1/2/10 and VelvetOptimizer version 2.2.5 (optimal hash value = 127). Contig reordering and annotation were performed with Mauve version 2.3.1 and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP), respectively \cite{11,12}. Sequence alignment and comparison were performed with CLC Sequence Viewer version 7.0 and BLAST. Average nucleotide identity (ANI) with the \textit{P. acnes} reference strain KPA171202 was calculated using Oat version 0.91 \cite{13}.

The draft genome of strain NTS\textsubscript{2003}_1719 (GenBank accession no. MAUV00000000) contains 2,373 genes, 2,320 coding sequences (CDSs), 46 tRNAs, 3 rRNAs, and 4 noncoding RNAs, with an OrthoANI value of 99.1%; the draft genome of strain NTS\textsubscript{31306190} (accession no. MAUY00000000) contains 2,327 genes, 2,275 CDSs, 45 tRNAs, 3 rRNAs, and 4 noncoding RNAs, with an OrthoANI value of 99.1%; the draft genome of strain NTS\textsubscript{2004}_10708 (accession no. MAUW00000000) contains 2,322 genes, 2,270 CDSs, 45 tRNAs, 3 rRNAs, and 4 noncoding RNAs, with an OrthoANI value of 99.0%; and the draft genome of strain LRY\_BL (accession no. MAUX00000000) contains 2,376 genes, 2,327 CDSs, 45 tRNAs, 0 rRNAs, and 4 noncoding RNAs, with an OrthoANI value of 100.0% (Table 1).

According to the diversity of \textit{Propionibacterium} spp. on human skin \cite{14}, their potential involvement in prosthetic-related infections remains an open question for future research. The genome sequences of these four strains of \textit{P. acnes} will also provide a valuable resource for (comparative) bone cell–\textit{P. acnes} host relationship studies. Indeed, depending on their genetic background,

P. acnes cells seem to interact differently with the bone cell matrix (G. G. Aubin and S. Corvec, unpublished data). These draft genomes of P. acnes will also be used for studying virulence features associated with bone infection, especially hyaluronate lyase (15).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers listed in Table 1. The versions described in this paper are in the first versions, under the BioProject designations listed in Table 1.

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