



ACNE, ROSACEA, AND RELATED DISORDERS (INCLUDING HIDRADENITIS SUPPURATIVA)

COMPLETE DRAFT GENOME SEQUENCE OF CUTIBACTERIUM (PROPIONIBACTERIUM) ACNES TYPE STRAIN ATCC6919

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Background: The first draft genome sequence of ATCC 6919 was published in 2014 using whole-genome shotgun sequencing and Illumina Miseq. However, second generation sequencing technology revealed gap regions and errors. Here we resequenced ATCC 6919 genome by high-throughput deep sequencing methods and reannotated genome, providing high-quality, complete whole genome sequences in this study.

Objectives: Antibiotics widely used for acne is the main cause of drug-resistant Cutibacterium acnes (C. acnes), but we found that there is a lack of complete genetic sequence reference of the drug-resistant C. acnes. Here, we reported the complete genetic sequence of C. acnes type strain ATCC6919.

Methods: Whole-genome sequencing of C. acnes ATCC6919 was performed using both Illumina Hiseq4000 and PacBio RSII single-molecule real-time (SMRT) sequencing platforms. The generated sequence reads were de novo assembled using SMRT Analysis v.2.3.0 software. The draft genome was annotated and further analyzed by different bioinformatics tools.

Results: The total genome length of C. acnes ATCC6919 is 2495001bp (60.02% G+C content), with 2450 coding sequences including 2388 proteins, 45 tRNAs, 9 rRNAs, and 1 sRNA. The genome contains several resistance genes, such as thy associated with resistance to aminosalicylic. Antimicrobial susceptibility testing showed that except for metronidazole and trimethoprim/sulfamethoxazole, this isolate is sensitive to all the tested antimicrobials.

Conclusion: To our knowledge, this is the first report of complete genome sequence of C. acnes ATCC6919, which will be a valuable reference for comparative analysis with genomic characteristics and resistance gene diversity of C. acnes.

