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GENOME ANNOUNCEMENT

Complete Genome Sequences of Three *Propionibacterium acnes* Isolates from the Type IA_2 Cluster

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***Propionibacterium acnes* is an anaerobic Gram-positive bacterium that has been linked to a wide range of opportunistic human infections and conditions, most notably acne vulgaris (I. Kurokawa et al., Exp. Dermatol. 18:821–832, 2009). We now present the whole-genome sequences of three *P. acnes* strains from the type IA_2 cluster which were recovered from ophthalmic infections (A. McDowell et al., Microbiology 157:1990–2003, 2011).**

Propionibacterium acnes is a member of the resident microbiota on the human skin and has been linked to various infections and conditions, most notably acne vulgaris. To date, complete and draft genome sequences available for *P. acnes* (1, 2, 5, 6) have identified numerous virulence factors, thus highlighting the pathogenic potential of the organism. This is further supported by *in vitro* studies demonstrating that distinct *P. acnes* strains trigger the secretion of various effector molecules from numerous cell types (4, 7, 8, 13, 14).

Recently, multilocus sequence typing (MLST) identified a distinct cluster of sequence types (STs) (ST9, ST22, and ST27) within the type I clade that were provisionally classified as type IB_2 pending further analysis (10). Placement in the type IB division was based on a number of observations, including the consistent presence of key core housekeeping and virulence gene sequences previously used to define type IB strains (11, 12), clustering with known type IB strains upon eBURST analysis (ST9; ST22), and infection profile, in particular an apparent lack of association with acne (10). These STs did, however, express dermatan-sulfate adhesins, a common feature of type IA strains but not of type IB, II, or III strains (10). On this basis, whole-genome sequencing was performed to ascertain the exact nature of this group and its relationship to other *P. acnes* organisms.

Genome sequencing of strains P.acn33 (ST9), P.acn17 (ST22), and P.acn31 (ST27) (10) was performed by SOLiD (Life Technologies) sequencing technology. We generated 43,880,983, 33,313,255, and 47,628,010 reads, respectively, which yielded >400-fold coverage. Assembly was performed using Genomics Workbench 4.8 and the Omixon Gapped SOLiD Alignment 1.3.2 plugin (3) provided by CLC Bio and Omixon, respectively. Gap closing was accomplished using PCR followed by Sanger sequencing on a 3500 genetic analyzer instrument (Life Technologies). Automatic annotation was performed by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), which utilizes GeneMark, Glimmer, and tRNAscan-SE searches.

The lengths of the single circular chromosomes of the three strains are as follows: 2,489,626 bp containing 2,236 putative coding sequences (CDSs) for P.acn33; 2,522,885 bp containing 2,266 putative CDSs for P.acn17, and 2,498,766 bp containing 2,247 putative CDSs for P.acn31. Each strain has 45 tRNAs and 6 rRNA loci with a GC content of 60%.

Based on whole-genome comparisons, isolates P.acn33, P.acn17, and P.acn31 belong to the type IA division. However, due to consistent phylogenetic and genomic differences in comparisons with other type IA strains, we propose this significantly distinct cluster as type IA_2, with all other type IA strains as IA_1. Currently, the type IA_2 grouping comprises six STs (ST2, ST22, ST23, ST24, ST36, and ST57) based on an expanded eight-locus MLST scheme. While not normally isolated from acne patients, type IA_2 strains appear to be associated with ophthalmic infections, along with type IA_1 and some type IB strains (10).

Nucleotide sequence accession numbers. The complete nucleotide sequences of strains P.acn33, P.acn17, and P.acn31 have been deposited in DDBJ/EMBL/GenBank under accession numbers CP003195, CP003196, and CP003197, respectively.

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