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GENOME ANNOUNCEMENT

Genome Sequence of *Propionibacterium acnes* Type II Strain ATCC 11828

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***Propionibacterium acnes* is an anaerobic Gram-positive bacterium that forms part of the normal human cutaneous microbiota and is occasionally associated with inflammatory diseases (I. Kurokawa et al., Exp. Dermatol. 18:821–832, 2009). Here we present the complete genome sequence for the commercially available *P. acnes* type II reference strain ATCC 11828 (I. Nagy et al., Microbes Infect. 8:2195–2205, 2006) recovered from a subcutaneous abscess.**

Propionibacterium acnes is considered a skin commensal which, under certain conditions, acts as an opportunistic pathogen and is thus associated with several diseases such as acne vulgaris (9). Even though the significance of the involvement of *P. acnes* in inflammatory diseases is still controversial, the first complete genome sequence of *P. acnes* uncovered the pathogenic potential of this bacterium (1). This is further supported by recent studies showing that distinct *P. acnes* strains trigger the secretion of antimicrobial peptides and proinflammatory mediators from various cell types *in vitro* (4, 7, 8, 13, 14). By comparison of *recA* and *tly* sequences, *P. acnes* isolates may be subdivided into phylotypes IA, IB, II, and III (12). Further subdivision came from the multilocus sequence typing (MLST) approach, resulting in the identification of 60 sequence types (STs) (11). Importantly, there is a clear association between some STs and certain diseases, such as the association of type IA clone ST6 with acne vulgaris; in contrast, other STs, such as ST10 isolates, seem to be nonpathogenic (10, 11). In order to identify factors responsible for the diversity, it is mandatory to compare genomes within and across phylogenetic clusters. Yet, only three complete *P. acnes* genomes are currently available: one type IA ST25 genome (2) and two type IB ST10 genomes (1, 6).

Genome sequencing of a type II strain, ATCC 11828, was performed by the SOLiD sequencing technology. We have generated 14,040,094 reads, which yielded >280-fold coverage. Assembly was performed using the Genomics Workbench 4.7 and the Omixon Gapped SOLiD Alignment 1.2 plug-in (3) provided by CLC Bio and Omixon, respectively. Gap closing was accomplished using PCR followed by Sanger sequencing. Automatic annotation of the genome 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. *P. acnes* strain ATCC 11828 has a single circular chromosome of 2,488,752 bp with a GC content of 60%. There are 2,260 putative coding sequences, 45 tRNAs, and 6 rRNA loci.

Previous phylogenetic analysis revealed that strain ATCC 11828 belongs to the *P. acnes* type II division (13). Based on the recently published MLST scheme for *P. acnes* (11), we have now determined that this strain belongs to the ST44 lineage. When cocultured with keratinocytes, *P. acnes* strain ATCC 11828 did not induce the expression of human β-defensin-2, nor did it have any effect on the viability of keratinocytes (14). Furthermore, type II strains do not produce immunoreactive proteins, such as dermatan-sulfate binding adhesions (5, 11), which may be important in the context of acne pathogenesis. These data suggest that type II isolates are part of the normal cutaneous flora.

Nucleotide sequence accession number. The complete nucleotide sequence of *P. acnes* strain ATCC 11828 has been deposited in GenBank under accession number CP003084.

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