



# Draft Genome Sequence of *Propionibacterium acnes* subsp. *elongatum* Strain Asn12

Andrew McDowell,<sup>a,b</sup> Judit Hunyadkürti,<sup>c</sup> Márta Magyari,<sup>c</sup> Andrea Vörös,<sup>d,e</sup> Balázs Horváth,<sup>e</sup> Sheila Patrick,<sup>b</sup> István Nagy<sup>c,d</sup>

<sup>a</sup>Northern Ireland Centre for Stratified Medicine, School of Biomedical Sciences, Ulster University, Londonderry, United Kingdom

<sup>b</sup>Centre for Experimental Medicine, School of Medicine, Dentistry & Biomedical Sciences, Queen's University, Belfast, United Kingdom

<sup>c</sup>Institute of Biochemistry, Biological Research Centre of the Hungarian Academy of Sciences, Szeged, Hungary

<sup>d</sup>SeqOmics Biotechnology Ltd., Mórahalom, Hungary

<sup>e</sup>ATGandCo Biotechnology Ltd., Mórahalom, Hungary

**ABSTRACT** *Propionibacterium acnes*, a non-spore-forming anaerobic Gram-positive bacterium, has been linked to a wide range of opportunistic human infections and conditions, most notably acne vulgaris. Here, we present the draft genome sequence of *P. acnes* subsp. *elongatum* strain Asn12, isolated from spinal disc tissue (in the United Kingdom).

The Gram-positive anaerobic bacterium *Propionibacterium acnes* forms part of the normal microbiota on human skin and mucosal surfaces. While normally associated with skin health, *P. acnes* is also an opportunistic pathogen linked with a range of human infections and clinical conditions, such as acne vulgaris (1), prosthetic joint infection (2), prostate cancer (3), sarcoidosis (4), progressive macular hypomelanosis (PMH) (5), and degenerative disc disease (6). Ever since we showed that distinct strains of *P. acnes* induce different gene expression patterns in human keratinocytes (7) and sebocytes (8), further advances in our understanding of the intraspecies phylogeny of *P. acnes* have occurred. Distinct phylogroups have been discovered and specific strains or sequence types (STs) associated with human health or disease revealed (9). In-depth studies of the phylogenetic and taxonomic heterogeneity of *P. acnes* have ultimately led to the recent proposal of the type I, II, and III phylogroups as distinct subspecies known as *P. acnes* subsp. *acnes*, *P. acnes* subsp. *defendens*, and *P. acnes* subsp. *elongatum*, respectively.

Here, we present the draft genome sequence of *P. acnes* subsp. *elongatum* strain Asn12 (10) that was isolated from spinal disc tissue (in the United Kingdom). The culture conditions and genomic DNA isolation methods were as published previously (11, 12). Sequencing libraries with ~500-bp inserts were prepared from 500 ng of input DNA using the NEBNext DNA library prep master mix for Illumina. Genome sequencing was performed on an Illumina MiSeq instrument, which generated 1,380,920 2 × 250-bp reads and yielded ~95-fold coverage. Assembly was performed using the Genomics Workbench 11.0 (Qiagen). Gap closing was accomplished using PCR (primers are available on request), followed by Sanger sequencing, as described previously (13). Automatic annotation of the genome was performed using the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) version 4.5 (<https://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). We have assembled the genome of *P. acnes* subsp. *elongatum* strain Asn12 into 2 contigs, with 2,484,878 bp, 2,422 putative coding sequences, 45 tRNAs, and 9 rRNAs.

To date, the majority of the *P. acnes* genomes sequenced belong to *P. acnes* subsp. *acnes*, with only four genomes of *P. acnes* subsp. *elongatum* strains (HL201PA1,

Received 14 June 2018 Accepted 19 June 2018 Published 19 July 2018

**Citation** McDowell A, Hunyadkürti J, Magyari M, Vörös A, Horváth B, Patrick S, Nagy I. 2018. Draft genome sequence of *Propionibacterium acnes* subsp. *elongatum* strain Asn12. *Microbiol Resour Announc* 7:e00801-18. <https://doi.org/10.1128/MRA.00801-18>.

**Editor** J. Cameron Thrash, Louisiana State University

**Copyright** © 2018 McDowell et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to István Nagy, [nagy@baygen.hu](mailto:nagy@baygen.hu).

JCM18909, PMH5, and PMH7) available (14, 15). This is not surprising since this subspecies has rarely been cultured from healthy facial skin, which is a primary skin sampling site, or from opportunistic infections or acne patients; strains from this subspecies, however, have been recently linked with the skin condition PMH (5, 16). Furthermore, type III strains are more frequently found on the back and abdomen than on other body sites, suggesting that this may be their preferred niche (16). *P. acnes* subsp. *elongatum* strain Asn12 belongs to ribotype 9 and, on the basis of our eight-gene multilocus sequence typing (MLST<sub>8</sub>) scheme (17), belongs to the ST33 lineage and clonal complex 77. As isolates PMH5 and PMH7 also belong to ST33, it will be of particular importance to sequence *P. acnes* subsp. *elongatum* isolates from other STs.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [QKRC00000000](https://doi.org/10.1093/j.1600-0625.2009.00890.x). The version described in this paper is version QKRC01000000.

## ACKNOWLEDGMENTS

This work was supported, in part, by a grant from the National Research, Development and Innovation Office (grant number GINOP-2.3.2-15-2016-00039). I.N. was supported by the János Bolyai Research Scholarship of the Hungarian Academy of Sciences. A.M. is funded under the European Union Regional Development Fund (ERDF) EU Sustainable Competitiveness Program for Northern Ireland & the Northern Ireland Public Health Agency (HSC R&D).

## REFERENCES

- Kurokawa I, Danby FW, Ju Q, Wang X, Xiang LF, Xia L, Chen W, Nagy I, Picardo M, Suh DH, Ganceviciene R, Schagen S, Tsatsou F, Zouboulis CC. 2009. New developments in our understanding of acne pathogenesis and treatment. *Exp Dermatol* 18:821–832. <https://doi.org/10.1111/j.1600-0625.2009.00890.x>.
- Tunney MM, Patrick S, Curran MD, Ramage G, Hanna D, Nixon JR, Gorman SP, Davis RI, Anderson N. 1999. Detection of prosthetic hip infection at revision arthroplasty by immunofluorescence microscopy and PCR amplification of the bacterial 16S rRNA gene. *J Clin Microbiol* 37:3281–3290.
- Cohen RJ, Shannon BA, McNeal JE, Shannon T, Garrett KL. 2005. *Propionibacterium acnes* associated with inflammation in radical prostatectomy specimens: a possible link to cancer evolution? *J Urol* 173: 1969–1974. <https://doi.org/10.1097/01.ju.0000158161.15277.78>.
- Negi M, Takemura T, Guzman J, Uchida K, Furukawa A, Suzuki Y, Iida T, Ishige I, Minami J, Yamada T, Kawachi H, Costabel U, Eishi Y. 2012. Localization of *Propionibacterium acnes* in granulomas supports a possible etiologic link between sarcoidosis and the bacterium. *Mod Pathol* 25:1284–1297. <https://doi.org/10.1038/modpathol.2012.80>.
- Barnard E, Liu J, Yankova E, Cavalcanti SM, Magalhães M, Li H, Patrick S, McDowell A. 2016. Strains of the *Propionibacterium acnes* type III lineage are associated with the skin condition progressive macular hypomelanosis. *Sci Rep* 6:31968. <https://doi.org/10.1038/srep31968>.
- Stirling A, Worthington T, Rafiq M, Lambert PA, Elliott TSJ. 2001. Association between sciatica and *Propionibacterium acnes*. *Lancet* 357: 2024–2025. [https://doi.org/10.1016/S0140-6736\(00\)05109-6](https://doi.org/10.1016/S0140-6736(00)05109-6).
- Nagy I, Pivarcsi A, Koreck A, Széll M, Urbán E, Kemény L. 2005. Distinct strains of *Propionibacterium acnes* induce selective human  $\beta$ -defensin-2 and interleukin-8 expression in human keratinocytes through toll-like receptors. *J Invest Dermatol* 124:931–938. <https://doi.org/10.1111/j.0022-022X.2005.23705.x>.
- Nagy I, Pivarcsi A, Kis K, Koreck A, Bodai L, McDowell A, Seltsmann H, Patrick S, Zouboulis CC, Kemény L. 2006. *Propionibacterium acnes* and lipopolysaccharide induce the expression of antimicrobial peptides and proinflammatory cytokines/chemokines in human sebocytes. *Microbes Infect* 8:2195–2205. <https://doi.org/10.1016/j.micinf.2006.04.001>.
- McDowell A. 2017. Over a decade of *recA* and *tly* gene sequence typing of the skin bacterium *Propionibacterium acnes*: what have we learnt? *Microorganisms* 6:1. <https://doi.org/10.3390/microorganisms6010001>.
- McDowell A, Perry AL, Lambert PA, Patrick S. 2008. A new phylogenetic group of *Propionibacterium acnes*. *J Med Microbiol* 57:218–224. <https://doi.org/10.1099/jmm.0.47489-0>.
- Nagy E, Urbán E, Becker S, Kostrzewa M, Vörös A, Hunyadkúrti J, Nagy I. 2013. MALDI-TOF MS fingerprinting facilitates rapid discrimination of phylotypes I, II and III of *Propionibacterium acnes*. *Anaerobe* 20:20–26. <https://doi.org/10.1016/j.anaerobe.2013.01.007>.
- Barnard E, Nagy I, Hunyadkúrti J, Patrick S, McDowell A. 2015. Multiplex touchdown PCR for rapid typing of the opportunistic pathogen *Propionibacterium acnes*. *J Clin Microbiol* 53:1149–1155. <https://doi.org/10.1128/JCM.02460-14>.
- McDowell A, Gao A, Barnard E, Fink C, Murray PI, Dowson CG, Nagy I, Lambert PA, Patrick S. 2011. A novel multilocus sequence typing scheme for the opportunistic pathogen *Propionibacterium acnes* and characterization of type I cell-surface associated antigens. *Microbiology* 157: 1990–2003. <https://doi.org/10.1099/mic.0.049676-0>.
- Tomida S, Nguyen L, Chiu B-H, Liu J, Sodergren E, Weinstock GM, Li H. 2013. Pan-genome and comparative genome analyses of *Propionibacterium acnes* reveal its genomic diversity in the healthy and diseased human skin microbiome. *mBio* 4:e00003-13. <https://doi.org/10.1128/mBio.00003-13>.
- Petersen R, Lomholt HB, Scholz CFP, Brüggemann H. 2015. Draft genome sequences of two *Propionibacterium acnes* strains isolated from progressive macular hypomelanosis lesions of human skin. *Genome Announc* 3:e01250-15. <https://doi.org/10.1128/genomeA.01250-15>.
- Petersen RLW, Scholz CFP, Jensen A, Brüggemann H, Lomholt HB. 2017. *Propionibacterium acnes* phylogenetic type III is associated with progressive macular hypomelanosis. *Eur J Microbiol Immunol* 7:37–45. <https://doi.org/10.1556/1886.2016.00040>.
- McDowell A, Barnard E, Nagy I, Gao A, Tomida S, Li H, Eady A, Cove J, Nord CE, Patrick S. 2012. An expanded multilocus sequence typing scheme for *Propionibacterium acnes*: investigation of “pathogenic”, “commensal” and antibiotic resistant strains. *PLoS One* 7:e41480. <https://doi.org/10.1371/journal.pone.0041480>.