



Proposal of new combination, *Cutibacterium acnes* subsp. *elongatum* comb. nov., and emended descriptions of the genus *Cutibacterium*, *Cutibacterium acnes* subsp. *acnes* and *Cutibacterium acnes* subsp. *defendens*.

Dekio, I., Mc Dowell, A., Sakamoto, M., Tomida, S., & Ohkuma, M. (2019). Proposal of new combination, *Cutibacterium acnes* subsp. *elongatum* comb. nov., and emended descriptions of the genus *Cutibacterium*, *Cutibacterium acnes* subsp. *acnes* and *Cutibacterium acnes* subsp. *defendens*. *International Journal of Systematic and Evolutionary Microbiology*, 69(4), 1087-1092. Article 003274. Advance online publication. <https://doi.org/10.1099/ijsem.0.003274>

[Link to publication record in Ulster University Research Portal](#)

Published in:

International Journal of Systematic and Evolutionary Microbiology

Publication Status:

Published (in print/issue): 01/04/2019

DOI:

[10.1099/ijsem.0.003274](https://doi.org/10.1099/ijsem.0.003274)

Document Version

Publisher's PDF, also known as Version of record

General rights

Copyright for the publications made accessible via Ulster University's Research Portal is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy

The Research Portal is Ulster University's institutional repository that provides access to Ulster's research outputs. Every effort has been made to ensure that content in the Research Portal does not infringe any person's rights, or applicable UK laws. If you discover content in the Research Portal that you believe breaches copyright or violates any law, please contact pure-support@ulster.ac.uk.

Proposal of new combination, *Cutibacterium acnes* subsp. *elongatum* comb. nov., and emended descriptions of the genus *Cutibacterium*, *Cutibacterium acnes* subsp. *acnes* and *Cutibacterium acnes* subsp. *defendens*

Itaru Dekio,^{1,2,*} Andrew McDowell,³ Mitsuo Sakamoto,^{2,4} Shuta Tomida⁵ and Moriya Ohkuma²

Abstract

In 2016, division of the genus *Propionibacterium* into four distinct genera was proposed. As a consequence, the species *Propionibacterium acnes* was transferred to *Cutibacterium* gen. nov. as *Cutibacterium acnes* comb. nov. The three recently proposed subspecies of *P. acnes* were not, however, accommodated in this proposal. Following a very recent validation of a new combination for *C. acnes* subsp. *defendens* and an automatically created *C. acnes* subsp. *acnes*, we now propose the new combination, *C. acnes* subsp. *elongatum* comb. nov. The type strain of *Cutibacterium acnes* subsp. *elongatum* is JCM 18919^T (=NCTC 13655^T). On the basis of further genomic and phenotypic (haemolysis and MALDI-TOF mass spectrometry) analyses of these subspecies, we also provide emended descriptions of the genus *Cutibacterium* Scholz and Kilian 2016, *C. acnes* subsp. *acnes* (Gilchrist 1900) Nouioui et al. 2018, and *C. acnes* subsp. *defendens* (McDowell et al. 2016) Nouioui et al. 2018.

The bacterial species *Cutibacterium acnes* (basonym: *Propionibacterium acnes*) is one of the most abundant residents of the human skin microbiota. There has been a rich history of investigation into the medical relevance of this organism since its successful isolation from acne pus [1] and its proposal as a novel species in the late nineteenth century [2]. Three distinct groups of *C. acnes*, designated types I, II, and III, have been well described based on a combination of genetic, phenotypic, and morphological differences, as well as pathogenic profile [3–9] (Fig. 1). These differences have ultimately led to the proposal of *P. acnes* subsp. *acnes* for type I [10, 11], *P. acnes* subsp. *defendens* for type II [11], and *P. acnes* subsp. *elongatum* for type III [10].

In parallel to the proposal of these distinct phylogroups as subspecies, it has recently been proposed to divide the genus *Propionibacterium* into four genera based on whole genome sequence analysis and source of isolation [12]. As part of this proposal, *P. acnes* was placed within the new genus *Cutibacterium*, although this taxonomic re-appraisal has not met with universal acceptance [13]. Due to the simultaneous timelines of these independent proposals, the three

subspecies were not described under the proposal of *Cutibacterium acnes* comb. nov. However, very recently, *C. acnes* subsp. *defendens* was proposed [14] and validated with automatically created *C. acnes* subsp. *acnes* as part of the latest Validation List [15]. As a consequence, this leaves *P. acnes* subsp. *elongatum*, which we now propose as *C. acnes* subsp. *elongatum*.

The 16S rRNA gene dendrogram generated from the DDBJ/EMBL/GenBank database entries of type strains of all three *C. acnes* subspecies and all other *Cutibacterium* species and '*Propionibacterium humerusii*', which has not been validated yet, outlined the clade formation of the three *C. acnes* subspecies within genus *Cutibacterium* (Fig. 1). Upon phylogenetic analysis of concatenated protein-encoding gene sequences from all known *C. acnes* sequence types (STs) in the MLST₈ database (<http://pubmlst.org/pacnes/>), *C. acnes* subsp. *elongatum* clearly forms a highly distinct clade from *C. acnes* subsp. *acnes* and *C. acnes* subsp. *defendens* (Fig. 2), consistent with its proposal as a distinct subspecies [10].

Further analysis based on *in silico* DNA–DNA hybridization (using the Genome-to-Genome Distance Calculator 2.1) of

Author affiliations: ¹Skin Microbe Laboratory, Mildix Skin Clinic, Tokyo, Japan; ²Microbe Division/Japan Collection of Microorganisms, RIKEN BioResource Research Center, Tsukuba, Japan; ³Northern Ireland Centre for Stratified Medicine, Biomedical Sciences Research Institute, Altnagelvin Area Hospital, Ulster University, Londonderry, UK; ⁴PRIME, Japan Agency for Medical Research and Development (AMED), Tsukuba, Japan; ⁵Department of Biobank, Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama University, Okayama, Japan.

*Correspondence: Itaru Dekio, i@skinmicrobe.com

Keywords: *Cutibacterium*; *Cutibacterium acnes* subspecies *elongatum*; genome; haemolysis; subspecies; MALDI-TOF mass spectrometry.

Abbreviations: MALDI-TOF MS, matrix-assisted laser desorption and ionization time-of-flight mass spectrometry; MLST, multilocus sequence typing. The DDBJ/EMBL/GenBank accession numbers for the 16S rRNA gene and the draft genome sequence of the type strain of *C. acnes* subsp. *elongatum* comb. nov. (JCM 18919^T) are AB777861 and BFFM01000001–BFFM01000226, respectively. One supplementary figure is available with the online version of this article.

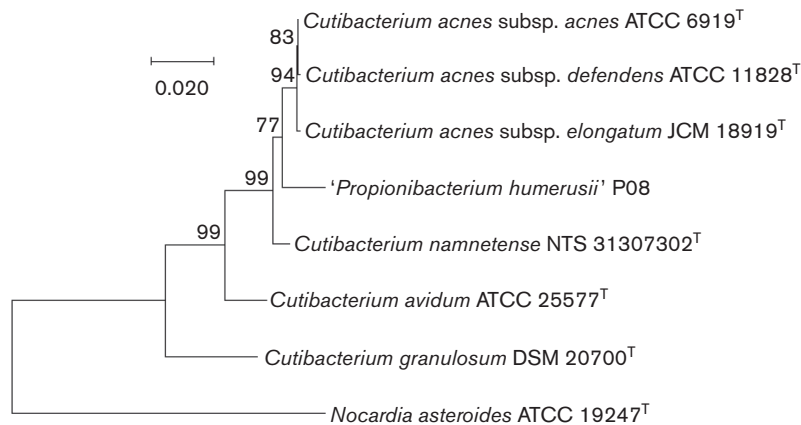


Fig. 1. Minimum evolution phylogenetic tree generated from 16S rRNA gene sequences of all three *Cutibacterium acnes* subspecies and all other *Cutibacterium* species.

the DDBJ/EMBL/GenBank database entries revealed that type strains representing *C. acnes* subsp. *elongatum* had DNA–DNA hybridization values that ranged from 72–74 % when analysed against type strains from types I and II, consistent with its proposal as a distinct subspecies based on a 79–80 % similarity boundary [16] (Table 1). Strains within each subspecies also shared high DNA–DNA hybridization scores (89–99 %) in keeping with their shared type or phylogroup status. While comparison of all 11 *C. acnes* genomes revealed DNA–DNA hybridization values above the 70 % cut-off value currently used for bacterial species demarcation, values of 36 % or lower were determined when compared to the type strains of bacterial species

Cutibacterium avidum, *Cutibacterium granulorum*, *Cutibacterium namnetense* and ‘*Propionibacterium humerusii*’. In line with their classification as *C. acnes*, all subspecies demonstrated high levels of synteny upon whole genome alignments, although some differences with respect to inversions and translocations were noted (Fig. S1, available in the online version of this article).

The genome analysis of the complete genome sequences of *C. acnes* subsp. *acnes* and *C. acnes* subsp. *defendens* and the draft whole genome of *C. acnes* subsp. *elongatum* revealed all three subspecies shared a similar G+C content of 60.0 mol%, but the genome length is slightly longer for

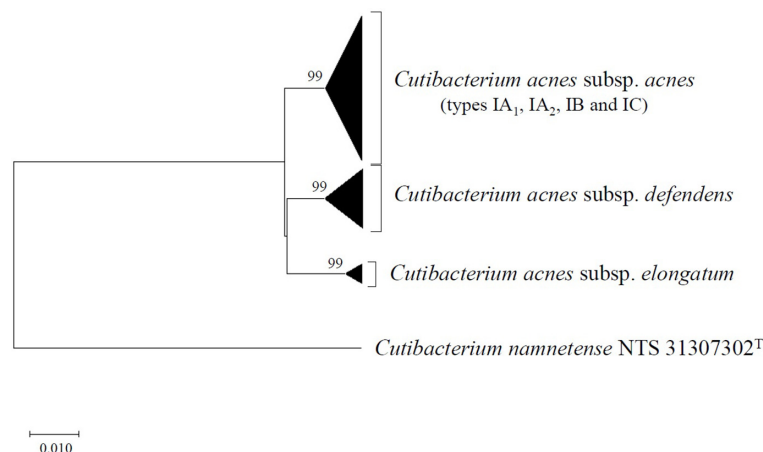


Fig. 2. Minimum-evolution phylogenetic tree of concatenated gene sequences (4253 bp) from all sequence types (STs) currently represented in the MLST₈ database (<http://pubmlst.org/pacnes/>). Genes analysed are *aroE*, *atpD*, *gmk*, *guaA*, *lepA*, *recA*, *sodA*, *tly* and *camp2*. The closely related sister taxon, *Cutibacterium namnetense* (NTS 31307302^T), was also analysed as an outgroup. Sequence input order was randomized, and bootstrapping resampling statistics were performed using 500 data sets. Bootstrap values (≥ 70 %) are shown on the arms of the tree. Horizontal bar represents genetic distance. The different subspecies of *Cutibacterium acnes* are indicated. All *C. acnes* strains analysed were as listed previously [6]. The MLST₈ scheme provides high resolution typing of *C. acnes* and strain clustering which is consistent with that obtained by whole genome analysis [6].

Table 1. *In silico* DNA–DNA hybridization values

Whole genome *in silico* DNA–DNA hybridization (using DSMZ site Genome-to-Genome Distance Calculator 2.1) was performed using genome data in DDBJ/EMBL/GenBank database. DNA–DNA hybridization value >70 % indicates same species, DDH value >79 % indicates same subspecies.

		<i>C. acnes</i> Type IA ₁ ATCC 6919 ^T	<i>C. acnes</i> Type II ATCC 11828 ^T	<i>C. acnes</i> Type III JCM 18919 ^T
<i>C. acnes</i>				
Type IA ₁	ATCC 6919 ^T	100	75.6	73.2
	JCM 18916	98.5	74.1	72.0
Type IA ₂	P.acn33	96.7	76.7	73.4
Type IB	KPA171202	93.1	78.4	73.8
	JCM 18918	91.2	76.8	72.4
Type IC	PRP-38	89.4	74.1	72.4
Type II	ATCC 11828 ^T	75.5	100	74.1
	JCM 18920	75.3	96.3	73.8
Type III	JCM 18919 ^T	73.1	74.1	100
	Asn12	73.1	74.0	98.7
	JCM 18909	72.0	72.9	97.6
<i>C. avidum</i>	ATCC 25577 ^T	19.6	23.5	23.3
<i>C. granulorum</i>	NCTC 11865 ^T	22.5	22.2	21.6
<i>C. namnetense</i>	NTS 31307302 ^T	36.0	35.3	35.1
' <i>P. humerusii</i> '	P08	31.6	32.3	31.4

C. acnes subsp. *elongatum* (Table 2). The results of *C. acnes* subsp. *acnes* and *C. acnes* subsp. *defendens* are consistent with the emended description of *C. acnes* by Nouioui et al. [14].

Previously, we described that some strains of *C. acnes* are haemolytic [10]. The description of the genus *Cutibacterium*, however, states that the species is non-haemolytic [12]. To clarify this, we examined the haemolytic features of 45 strains representing all three subspecies (Table 3). We observed that 23 out of 25 *C. acnes* subsp. *acnes* isolates were β-haemolytic under anaerobic conditions (92 %), while all 16 strains of *C. acnes* subsp. *defendens* and *C. acnes* subsp. *elongatum* were non-haemolytic. This finding is consistent with previous descriptions of *P. acnes* subspecies [10, 11], but not with the description of genus *Cutibacterium* [12].

We also examined differences between the proposed *C. acnes* subsp. *elongatum* and *C. acnes* subsp. *acnes* and *C. acnes* subsp. *defendens* based on MALDI-TOF mass spectrometry profiles previously reported [10, 17]. Analysis of three strains of type IA₁ within *C. acnes* subsp. *acnes* (strains K107=JCM 18916, M5, M18), using an MALDI Biotyper (Bruker), showed predominant peaks of 3450–3650 Da window at 3516 and 3589 Da, and those of 6950–7300 Da window at 7034 and 7180 Da (Table 4). The predominant peaks of three strains of types IA₂ and IB within *C. acnes* subsp. *acnes* (strains K115=JCM 18918, M1, W27) were also similar to type IA₁, but with differences, at 3503, 3516, and 3589 Da (3450–3650 Da window), and at 7005 and 7180 Da (6950–7300 Da window). This is also consistent with previous observations that type IA₂ and IB share other

characteristics including *recA* and *tly* alleles, which suggests conjugal transfer of large genomic regions [18].

The spectra of five strains of *C. acnes* subsp. *defendens* (strains K80=JCM 18911, K127=JCM 18920, M13, M17, M33) were largely different than *C. acnes* subsp. *acnes*, with predominant peaks at 3493 and 3632 Da (3450–3650 Da window), and 6985 and 7265 Da (6950–7300 Da window). This was also the case for five strains of *C. acnes* subsp. *elongatum* (strains K124=JCM 18919^T, K57=JCM 18909, K55), with predominant peaks at 3619 Da (3450–3650 Da window), and 7237 Da (6950–7300 Da window). The results added the description of the mass ion peaks of *C. acnes* subsp. *defendens* but not that of *C. acnes* subsp. *elongatum* (the two peaks are 2–3 Da different than previous description [10] but we concluded it is not worth amending this as the differences are relatively small.)

Table 2. Genome comparison of the type strains of three subspecies of *C. acnes*

Subspecies name	Strain	Size (Mb)	GC %	Gene number
<i>C. acnes</i> subsp. <i>acnes</i> (type I)	ATCC 6919 ^T	2.495	60.0	2509
<i>C. acnes</i> subsp. <i>defendens</i> (type II)	ATCC 11828 ^T	2.489	60.0	2477
<i>C. acnes</i> subsp. <i>elongatum</i> (type III)	JCM 18919 ^T	2.618*	60.0*	2660*

*Estimation based on the draft whole genome.

Table 3. β -Haemolysis features of *C. acnes* strains

UK, United Kingdom; JP, Japan; NG, no growth.

Isolate	Source	Type	β -Haemolysis	
			Anaerobic	Aerobic
<i>C. acnes</i> subsp. <i>acnes</i> (type I)				
NCTC 737 ^T	Facial acne, UK	IA ₁	+	–
JCM 6495	Unknown	IA ₁	+	–
K107=JCM 18916	Facial skin, JP	IA ₁	+	–
K161=JCM 18922	Facial skin, JP	IA ₁	+	–
K282=JCM 18924	Facial skin, JP	IA ₁	+	–
K51=JCM 18907	Facial skin, JP	IA ₂	+	–
K56=JCM 18908	Facial skin, JP	IA ₂	–	–
K72=JCM 18910	Facial skin, JP	IA ₂	+	–
K94=JCM 18912	Facial skin, JP	IA ₂	–	–
K12	Facial skin, JP	IB	+	–
K13	Facial skin, JP	IB	+	–
K24	Facial skin, JP	IB	+	–
K81	Facial skin, JP	IB	+	+
K86	Facial skin, JP	IB	+	+
K114=JCM 18917	Facial skin, JP	IB	+	–
K115=JCM 18918	Facial skin, JP	IB	+	–
K280=JCM 18923	Facial skin, JP	IB	+	–
S16=JCM 18927	Axilla skin, JP	IB	+	–
W27	Facial acne, JP	I	+	+
W31	Facial acne, JP	I	+	–
W32	Facial acne, JP	I	+	–
W33	Facial acne, JP	I	+	–
W34	Facial acne, JP	I	+	–
W35	Facial acne, JP	I	+	–
W36	Facial acne, JP	I	+	–
<i>C. acnes</i> subsp. <i>defendens</i> (type II)				
JCM 6473 ^T	Abscess	II	–	–
K80=JCM 18911	Facial skin, JP	II	–	–
K96=JCM 18913	Eczema skin, JP	II	–	–
K104=JCM 18914	Facial skin, JP	II	–	–
K106=JCM 18915	Facial skin, JP	II	–	–
K127=JCM 18920	Eczema skin, JP	II	–	–
K145=JCM 18921	Facial skin, JP	II	–	–
S13=JCM 18926	Axilla skin, JP	II	–	–
K15	Facial skin, JP	II	–	–
K79	Facial skin, JP	II	–	–
K128	Eczema skin, JP	II	–	–
S14	Axilla skin, JP	II	–	–
W37	Facial acne, JP	II	–	–
<i>C. acnes</i> subsp. <i>elongatum</i> (type III)				
K124 ^T = JCM 18919 ^T	Facial skin, JP	III	–	NG
K57=JCM 18909	Facial skin, JP	III	–	NG
K290=JCM 18925	Forearm skin, JP	III	–	NG

Table 4. Characteristic MALDI-TOF peaks of *C. acnes* subspecies

Subspecies	Prominent peaks (Da)	
	3450–3650 Da	6950–7300 Da
<i>C. acnes</i> subsp. <i>acnes</i> (type I)		
Type IA ₁	3516, 3589	7034, 7180
Types IA ₂ and IB	3503, 3516, 3589	7005, 7180
<i>C. acnes</i> subsp. <i>defendens</i> (type II)	3493, 3632	6985, 7265
<i>C. acnes</i> subsp. <i>elongatum</i> (type III)	3619	7237

DESCRIPTION OF *CUTIBACTERIUM ACNES* SUBSP. *ELONGATUM* COMB. NOV.

Cutibacterium acnes subsp. *elongatum* (e.lon.ga'tum. L. neut. part. adj. *elongatum* elongated, named after the characteristic cell shape).

Basonym: *Propionibacterium acnes* subsp. *elongatum* Dekio et al. 2015.

Description is as given for *Propionibacterium acnes* subsp. *elongatum* [10] with the following additions. Strains can be isolated from the human skin surface, but are infrequently recovered from the face and are more common on the back, especially the lower back, which appears the preferred habitat [19]. Strains are not associated with *acne vulgaris*, but have been shown to be associated with progressive macular hypomelanosis [19, 20]. The G+C content of the type-strain genome is approximately 60.0 mol% and its approximate size is 2.62 Mbp, based on the draft whole genome.

The type strain is K124^T (JCM 18919^T=NCTC 13655^T), isolated from normal-looking facial skin of an atopic dermatitis patient in Wako, Japan, 2003.

EMENDED DESCRIPTION OF *CUTIBACTERIUM SCHOLZ* AND KILIAN 2016

The description is as given before [12] with the following modification. Some strains of *C. acnes* are β -haemolytic under anaerobic condition, and in some cases, also under aerobic condition.

EMENDED DESCRIPTION OF *CUTIBACTERIUM ACNES* SUBSP. *ACNES* (GILCHRIST 1900) NOUIQUI ET AL. 2018

The description is as given for *Propionibacterium acnes* subsp. *acnes* [11] with the following modifications. The G+C content of the type-strain genome is 60.0 mol%, its approximate size 2.50 Mbp, Prominent mass ions obtained by MALDI-TOF MS at 3516, 3589, 7034, and 7179 Da are characteristic for type IA₁, and those at 3503, 3516, 3589, 7005, and 7179 Da are characteristic for type IA₂ and type IB.

EMENDED DESCRIPTION OF *CUTIBACTERIUM ACNES* SUBSP. *DEFENDENS* (MCDOWELL 2016) NOUIQUI ET AL. 2018

The description is as given before [14] with the following modifications. The G+C content of the type-strain genome is 60.0%, its approximate size 2.49 Mbp. Prominent mass ions obtained by MALDI-TOF MS at 3493, 3632, 6985 and 7265 Da are characteristic.

Funding information

I. D. is funded by a Researcher Invitation or Research Abroad Grant from Institution for Fermentation, Osaka (IFO), Japan and the British Council Japan Association Scholarship. A. M. is funded under the EU Regional Development Fund (ERDF) EU Sustainable Competitiveness Programme for N. Ireland and the N. Ireland Public Health Agency (HSC R&D).

Acknowledgement

We are grateful for Professor Aharon Oren at The Hebrew University of Jerusalem, Israel, for the helpful suggestions. We thank Dr. Vlad Serafim, Professor Haroun Shah and Professor Ajit Shah, at Middlesex University, London, UK, and Dr. Rikiya Endoh at RIKEN BioResource Reserch Centre, Tsukuba, Japan, for their kind help in obtaining MALDI-TOF mass spectrometry spectra. We also thank Professor Shinji Fukuda and Miss Mia Yoshikawa at Institute for Advanced Biosciences, Keio University, Tsuruoka, Japan, for their support in isolating bacterial materials, Dr. Tomohiro Watanabe at Medical Centre East, Tokyo Women's Medical University, Tokyo, Japan for his assistance in preserving and maintaining biological materials, and Dr. Yoshiyuki Murakami, Mildix Skin Clinic, Tokyo, for his overall support for this work.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

- Sabouraud R. La séborrhée grasse et la pelade. *Ann Inst Pasteur* 1897;11:134–159.
- Gilchrist TC. A bacteriological and microscopical study of over three hundred vesicular and pustular lesions of the skin, with a research upon the etiology of *acne vulgaris*. *Johns Hopkins Hosp Rep* 1900;9:409–430.
- McDowell A, Valanne S, Ramage G, Tunney MM, Glenn JV et al. *Propionibacterium acnes* types I and II represent phylogenetically distinct groups. *J Clin Microbiol* 2005;43:326–334.
- Valanne S, McDowell A, Ramage G, Tunney MM, Einarsson GG et al. CAMP factor homologues in *Propionibacterium acnes*: a new protein family differentially expressed by types I and II. *Microbiology* 2005;151:1369–1379.
- McDowell A, Perry AL, Lambert PA, Patrick S. A new phylogenetic group of *Propionibacterium acnes*. *J Med Microbiol* 2008;57:218–224.
- McDowell A, Nagy I, Magyari M, Barnard E, Patrick S. The opportunistic pathogen *Propionibacterium acnes*: insights into typing, human disease, clonal diversification and CAMP factor evolution. *PLoS One* 2013;8:e70897.
- Tomida S, Nguyen L, Chiu BH, Liu J, Sodergren E et al. Pan-genome and comparative genome analyses of *Propionibacterium acnes* reveal its genomic diversity in the healthy and diseased human skin microbiome. *mbio* 2013;4:e00003–00013.
- Johnson T, Kang D, Barnard E, Li H. Strain-level differences in porphyrin production and regulation in *Propionibacterium acnes* elucidate disease associations. *mSphere* 2016;1:e00023.
- Scholz CF, Brüggemann H, Lomholt HB, Tettelin H, Kilian M. Genome stability of *Propionibacterium acnes*: a comprehensive study of indels and homopolymeric tracts. *Sci Rep* 2016;6:20662.
- Dekio I, Culak R, Misra R, Gaulton T, Fang M et al. Dissecting the taxonomic heterogeneity within *Propionibacterium acnes*: proposal

- for *Propionibacterium acnes* subsp. *acnes* subsp. nov. and *Propionibacterium acnes* subsp. *elongatum* subsp. nov. *Int J Syst Evol Microbiol* 2015;65:4776–4787.
11. McDowell A, Barnard E, Liu J, Li H, Patrick S. Proposal to reclassify *Propionibacterium acnes* type I as *Propionibacterium acnes* subsp. *acnes* subsp. nov. and *Propionibacterium acnes* type II as *Propionibacterium acnes* subsp. *defendens* subsp. nov. (Emendation of *Propionibacterium acnes* subsp. *acnes* (Dekio, et al. 2015) and proposal of *Propionibacterium acnes* type II as *Propionibacterium acnes* subsp. *defendens* subsp. nov.) *Int J Syst Evol Microbiol* 2016; 66: 5358–5365. *Corrigendum Int J Syst Evol Microbiol* 2017;67:4880.
 12. Scholz CF, Kilian M. The natural history of cutaneous propionibacteria, and reclassification of selected species within the genus *Propionibacterium* to the proposed novel genera *Acidipropionibacterium* gen. nov., *Cutibacterium* gen. nov. and *Pseudopropionibacterium* gen. nov. *Int J Syst Evol Microbiol* 2016;66:4422–4432.
 13. Alexeyev OA, Dekio I, Layton AM, Li H, Hughes H et al. Why we continue to use the name *Propionibacterium acnes*. *Br J Dermatol* 2018;179:1227.
 14. Nouioui I, Carro L, García-López M, Meier-Kolthoff JP, Woyke T et al. Genome-Based taxonomic classification of the phylum *Actinobacteria*. *Front Microbiol* 2018;9:2007.
 15. Oren A, Garrity GM. List of new names and new combinations previously effectively, but not validly, published. *Int J Syst Evol Microbiol* 2018;68:3379–3393.
 16. Meier-Kolthoff JP, Hahnke RL, Petersen J, Scheuner C, Michael V et al. Complete genome sequence of DSM 30083^T, the type strain (U5/41^T) of *Escherichia coli*, and a proposal for delineating subspecies in microbial taxonomy. *Stand Genomic Sci* 2014;9:2.
 17. Nagy E, Urbán E, Becker S, Kostrzewa M, Vörös A et al. MALDI-TOF MS fingerprinting facilitates rapid discrimination of phylotypes I, II and III of *Propionibacterium acnes*. *Anaerobe* 2013;20:20–26.
 18. McDowell A. Over a decade of *recA* and *tly* gene sequence typing of the skin bacterium *Propionibacterium acnes*: what have we learnt? *Microorganisms* 2018;6:1.
 19. Petersen RL, Scholz CF, Jensen A, Brüggemann H, Lomholt HB. *Propionibacterium acnes* phylogenetic type III is associated with progressive macular hypomelanosis. *Eur J Microbiol Immunol* 2017;7:37–45.
 20. Barnard E, Liu J, Yankova E, Cavalcanti SM, Magalhães M et al. Strains of the *Propionibacterium acnes* type III lineage are associated with the skin condition progressive macular hypomelanosis. *Sci Rep* 2016;6:3196.

Five reasons to publish your next article with a Microbiology Society journal

1. The Microbiology Society is a not-for-profit organization.
2. We offer fast and rigorous peer review – average time to first decision is 4–6 weeks.
3. Our journals have a global readership with subscriptions held in research institutions around the world.
4. 80% of our authors rate our submission process as 'excellent' or 'very good'.
5. Your article will be published on an interactive journal platform with advanced metrics.

Find out more and submit your article at microbiologyresearch.org.