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.

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Recently, it has been proposed that strains of *Propionibacterium acnes* from the type III genetic division should be classified as *P. acnes* subsp. *elongatum* subsp. nov., with strains from the type I and II divisions collectively classified as *P. acnes* subsp. *acnes* subsp. nov. Under such a taxonomic re-appraisal, we believe that types I and II should also have their own separate rank of subspecies. In support of this, we describe a polyphasic taxonomic study based on the analysis of publicly available multilocus and whole-genome sequence datasets, alongside a systematic review of previously published phylogenetic, genomic, phenotypic and clinical data. Strains of types I and II form highly distinct clades on the basis of multilocus sequence analysis (MLSA) and whole-genome phylogenetic reconstructions. *In silico* or digital DNA–DNA similarity values also fall within the 70–80 % boundary recommended for bacterial subspecies. Furthermore, we see important differences in genome content, including the presence of an active CRISPR/Cas system in type II strains, but not type I, and evidence for increasing linkage equilibrium within the separate divisions. Key biochemical differences include positive test results for β-haemolytic, neuraminidase and sorbitol fermentation activities with type I strains, but not type II. We now propose that type I strains should be classified as *P. acnes* subsp. *acnes* subsp. nov., and type II as *P. acnes* subsp. *defendens* subsp. nov. The type strain of *P. acnes* subsp. *acnes* subsp. nov. is NCTC 737[T] (=ATCC 6919[T]=JCM 6425[T]=DSM 1897[T]=CCUG 1794[T]), while the type strain of *P. acnes* subsp. *defendens* subsp. nov. is ATCC 11828 (=JCM 6473=CCUG 6369).

Propionibacterium acnes is a Gram-stain-positive anaerobic bacterium and a member of the 'cutaneous' group of human propionibacteria along with *Propionibacterium granulosum*, *Propionibacterium avidum* and '*Propionibacterium humerusii*'.

Although found predominantly on the skin, it can also be isolated from the oral cavity and the genitourinary and gastrointestinal tracts (Patrick & McDowell, 2011). While the bacterium is most noted for its association with the inflammatory skin condition acne vulgaris (Lomholt & Kilian, 2010; McDowell *et al.*, 2012; Fitz-Gibbon *et al.*, 2013), there is now a growing recognition that the spectrum of opportunistic infections and clinical conditions with which it may be associated has been underestimated (Tunney *et al.*, 1999; Cohen *et al.*, 2005; Cavalcanti *et al.*, 2011; Eishi, 2013; Barnard *et al.*, 2016).

In the last 10 years, significant advances in our understanding of this bacterium at the population genetic level have been made using single, multilocus and whole-genome sequence analyses (McDowell *et al.*, 2005, 2008; Lomholt & Kilian, 2010; McDowell *et al.*, 2012; Fitz-Gibbon *et al.*, 2013; Tomida *et al.*, 2013; Scholz *et al.*, 2014). Such work has demonstrated the phylogenetically distinct nature of the originally described serotypes of *P. acnes*, designated types I and II, and identified a third type, designated type III, which displays an ability to form long filamentous cell structures not seen with types I and II (McDowell *et al.*, 2005, 2008). These studies have also identified further phylogenetic subdivisions within the type I clade (IA$_1$, IA$_2$, IB, IC) which differ in genome content, inflammatory potential, association with disease, production of putative virulence determinants and resistance to antibiotics used in the treatment of acne, as well as biochemical and aggregative properties (Valanne *et al.*, 2005; McDowell *et al.*, 2013; Tomida *et al.*, 2013; Johnson *et al.*, 2016; Scholz *et al.*, 2016).

Very recently, Dekio *et al.* (2015) proposed that *P. acnes* type III be reclassified as *P. acnes* subsp. *elongatum* subsp. nov. based on phylogenetic, genomic and phenotypic differences, with strains of type I and II classified as *P. acnes* subsp. *acnes* subsp. nov. (Dekio *et al.*, 2015). In bacterial taxonomy, there are currently no clear guidelines for the establishment of subspecies, and the proposal of such essentially remains at the discretion of the researcher. Nevertheless, the proposal of a novel bacterial subspecies is normally based on consistent phylogenetic differences and phenotypic variations between groups of strains within a species (Brenner *et al.*, 2000). If the major phylogroups of *P. acnes* are now to be reclassified within a subspecies framework, then strains of types I and II also deserve their own taxonomic rank of subspecies. In this paper, we describe a polyphasic taxonomic study based on the analysis of publicly available multilocus sequence and whole-genome datasets, alongside a review of published phylogenetic, genomic, phenotypic and clinical data, to support the reclassification of *P. acnes* types I and II as distinct subspecies. We propose type I as *P. acnes* subsp. *acnes* subsp. nov. as it contains the type strain (ATCC6919[T]), and type II as *P. acnes* subsp. *defendens* subsp. nov. Type III strains remain as *P. acnes* subsp. *elongatum* subsp. nov. (hereafter described as type III) as previously proposed (Dekio *et al.*, 2015).

In 2005, we demonstrated that the *P. acnes* serotypes known as types I and II represented highly distinct phylogenetic groups based on sequence analysis of the *recA* housekeeping gene, as well as the putative haemolysin/ FtsJ-like methyltransferase gene *tly* (McDowell *et al.*, 2005). Application of *recA* typing was also central in the identification of strains representing the type III phylogenetic division (McDowell *et al.*, 2008). Since then, two key multi-locus sequence analysis (MLSA) methods based on eight (MLSA$_8$) and nine protein-encoding genes (MLSA$_9$) have been described for this bacterium, both based on completely different sets of genetic loci (Lomholt & Kilian, 2010; McDowell *et al.*, 2012). With both independent MLSA schemes we find that

types I, II and III form highly distinct clades consistent with the original *recA* and *tly* analysis, and supported by high bootstrap values (Fig. 1). This phylogenetic clustering is also highly congruent with that obtained upon whole-genome analysis of 124 731 SNPs in shared or 'core' regions of 85 *P. acnes* genomes spanning all the major phylogenetic divisions (Fig. S1, available in the online Supplementary Material); the average *P*-distance between each of the types based on core region analysis is 0.444 for types I and II, 0.487 for types I and III, and 0.470 for types II and III (Table 1). Of the core region SNPs, 26 % are unique to type I, with 22 % unique to type II and 24 % unique to type III (Table 1). The genetic distance between types I and II is therefore similar to the distance between type I and type III, and type II and type III. In addition, even though the 16S rRNA gene of *P. acnes* demonstrates a high degree of intra-species sequence identity, the observation of distinct and non-overlapping ribotypes for type I (RT1; RT3; RT4; RT5; RT8; RT16; RT532), type II (RT2; RT6), and type III (RT9) provides further evidence for their different phylogenies (Fitz-Gibbon *et al.*, 2013; Barnard *et al.*, 2016) (Fig. S1).

Alongside phylogenetic analyses, previous whole-genome typing patterns based on methods such as random amplification of polymorphic DNA (RAPD) and non-coding repeat sequences, as well as the analysis of non-core regions, also support types I and II as highly distinct divisions at the genome level (Perry *et al.*, 2003; Tomida *et al.*, 2013; Hauck *et al.*, 2015). While digital or *in silico* DNA–DNA hybridization values (GGDC 2.0 algorithm) between types I, II and III are above the 70 % cut-off value currently used for bacterial species demarcation, thus confirming their membership of the same species, the whole-genome relatedness values are consistent with the proposal that types I and II are also placed in distinct taxonomic ranks in line with that recently proposed for type III (Dekio *et al.*, 2015). Strains representing the different phylogroups within type I (IA$_1$, IA$_2$, IB, IC) share high *in silico* DNA–DNA hybridization values of 91–100 %, but this drops to 74.1–78.5 % when analysed against the type II strains ATCC11828 and JCM18920, and 72.0–72.8 % with the type III strain JCM18909 (Dekio *et al.*, 2015). Strains of type II and III share relatedness values of 72.9–73.2 % (Dekio *et al.*, 2015). These hybridization values between the major divisions are within the 70–80 % similarity boundary recently recommended for bacterial subspecies (Meier-Kolthoff *et al.*, 2014).

Detailed comparative analysis of type I and II whole-genome sequences also reveals some salient differences between the divisions. These include specific genomic inversions and insertions present in type II strains, but not type I, which encode genes related to carbohydrate processing and modification, ABC transporters, nickel import, bacitracin resistance and hypothetical proteins (Fig. S2) (McDowell *et al.*, 2013; Scholz *et al.*, 2016). One of the most striking differences relates to the presence in type II strains of clustered regularly interspaced short palindromic repeats (CRISPR)/Cas locus (Brüggemann *et al.*, 2012b;
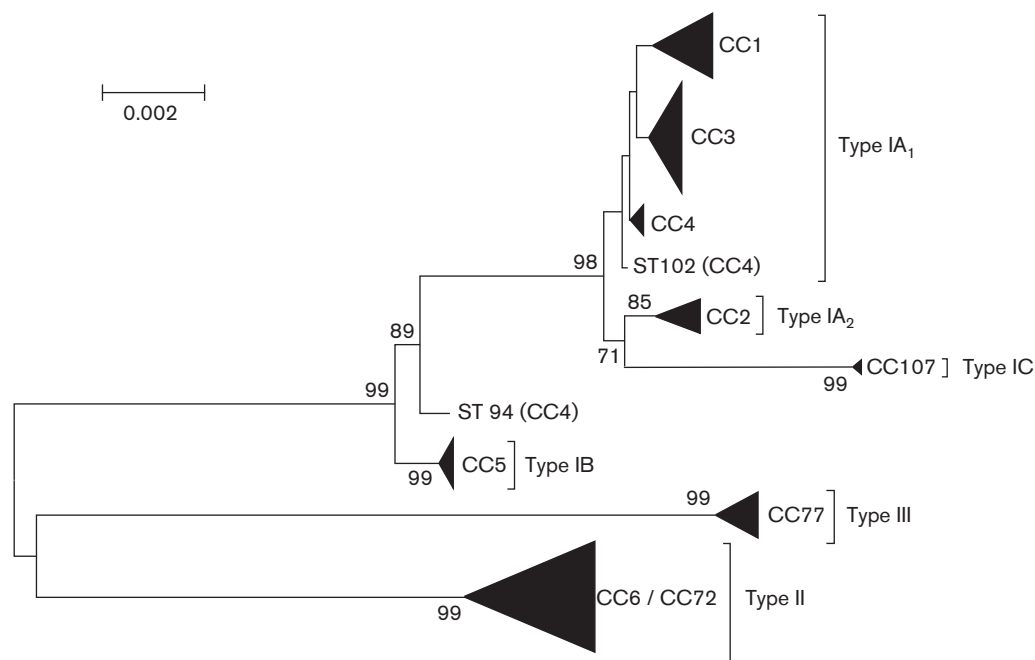
Fig. 1. Minimum evolution phylogenetic tree (MEGA v7.0) (Kumar *et al.*, 2016) of concatenated gene sequences (4253 bp) from all STs currently represented in the MLST$_8$ database (http://pubmlst.org/pacnes/), and covering all major genetic divisions. Sequence input order was randomized, and bootstrapping resampling statistics were performed using 500 data sets. Bootstrap values ($\geq$70 %) are shown on the arms of the tree. Horizontal bar represents genetic distance. CC, Clonal complex.

Fitz-Gibbon *et al.*, 2013). In contrast, type I and type III strains contain CRISPR/Cas gene remnants within their genome, indicating deletion of the locus during the evolutionary history of these phylogroups; the deletions are more extensive in type I strains compared with type III. The deletion of the CRISPR/Cas system in type I and type III strains makes these divisions more susceptible to horizontal gene transfer (HGT) and the acquisition of fitness or virulence traits. The observation of such CRISPR/Cas gene remnants has led to the suggestion that the type I and III divisions may constitute younger subpopulations than type II strains which are descended from a more ancient lineage (Brügge-mann *et al.*, 2012a, b). Since age = ds/(clock rate $\times 2$), where ds is the mean number of synonymous substitutions per site and clock rate is the synonymous molecular clock rate, calculation of the ds values for strains currently representing

the major type I, II and III divisions may give deeper insights into their relative ages. Interestingly, using the Nei–Gojobori method (Jukes–Cantor) (Nei & Gojobori, 1986) in MEGA v7.0 (Kumar *et al.*, 2016), we observed that the ds value for the entire type I division was slightly higher than that for type II based on an initial analysis of concatenated MLSA$_8$ sequence data, while values for type III were lower (Table 1). To investigate this further, we examined the shared core-coding regions of 85 *P. acnes* genomes currently available. Multiple sequence alignments were performed using MUSCLE (Edgar, 2004) and the Jukes–Cantor ds values calculated for each pair of sequences in the alignment using the Nei–Gojobori method as implemented in the Bio-perl package Bio::Align::DNAStatistics (Stajich *et al.*, 2002). As before, the resulting ds values obtained for type I (0.008), type II (0.005) and type III (0.001) revealed higher

Table 1. Genetic characteristics of *P. acnes* phylogroups

Genetic Grouping	P-distance (core SNPs)			ds*	Percentage unique core region SNPs
	Type I	Type II	Type III		
Type I	–	0.444	0.487	0.006±0.001	26
Type II	0.444	–	0.470	0.005±0.001	22
Type III	0.487	0.470	–	0.002±0.001	24
Type I, II, III	–	–	–	0.024±0.003	–

*Based on the analysis of concatenated MLSA$_8$ sequence data using the Nei–Gojobori method (Jukes–Cantor) in MEGA v5.0.

synonymous nucleotide diversity within the large type I clade compared with type II and type III, indicative of an older age. Further studies are therefore required to provide clarity on the series of evolutionary events that have given rise to the emergence and diversity of the current *P. acnes* clades now proposed as subspecies, including the possible diversity-purging effects of periodic selection (Cohan, 2001).

P. acnes has a clonal, epidemic population structure and is in linkage disequilibrium, though rates of HGT within the population as a whole are statistically significant (Lomholt & Kilian, 2010; McDowell *et al.*, 2012, 2013). Previous studies have, however, found that rates of recombination appear to differ throughout the population, and that the association of alleles is less significant when distinct phylogroup populations are considered (McDowell *et al.*, 2012, 2013). In particular, we see a drop in the index of association value (I_A) when strains from the type I and II divisions are considered separately, indicating increasing linkage equilibrium within these distinct clusters (McDowell *et al.*, 2013); this can also be observed on a Neighbour-Net split graph based on $MLST_8$ allelic profile data (Fig. 2). Detailed inspection of $MLSA_8$ datasets also indicates conjugal transfer and replacement of unusually large chromosomal segments in the genome dynamics of the type I clade, particularly between types IA_2 and IB (Lomholt & Kilian, 2010; McDowell *et al.*, 2012, 2013). The idea that rates of genetic interchange are more frequent within, but not between, the major divisions is indicative of increasing sexual isolation which occurs with more genetically divergent organisms (Majewski, 2001). Reduced rates of recombination may also indicate ecological differences since members of the same habitat are more likely to undergo recombination events (sympatric speciation); such population subdivisions can introduce linkage disequilibrium into an analysis if isolates from different niches (Ecotypes) are included (Spratt & Maiden, 1999). Comprehensive analysis of genome differences between the major types does indeed provide potential evidence for distinct environmental challenges within the human host.

Studies by Johnson & Cummins (1972) first revealed types I and II as distinct phenotypes of *P. acnes* based on serological agglutination tests and cell wall sugar analysis; type I strains contain galactose in their cell wall, but this sugar is absent in type II strains which occasionally also contain *meso*-diaminopimelic acid (DAP) (Table 2). The development of more recent monoclonal antibody typing methods for *P. acnes* have further highlighted differences between the cell wall structures of type I and II, as well as type III, based on the expression of unique antigenic determinants, including those in lipoteichoic acid and adhesin proteins (Holland *et al.*, 2010; McDowell *et al.*, 2011; Bae *et al.*, 2014). Differences in cell surface hydrophobicity have also been described for types I and II, and upon growth in liquid media, such as protease peptone yeast (PPY) or brain–heart infusion (BHI) broth, type II strains form a turbid solution

with a slight fine sediment, while strains of type IA and IC can form a large granular sediment or auto-aggregate with a clear solution (Cohen *et al.*, 2005); type IB strains behave as type II with respect to this characteristic. Types I and II can be differentiated from one another and type III upon analysis of bacterial whole-cell proteins by matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) fingerprinting, highlighting further variation at the phenotype level (Nagy *et al.*, 2013; Dekio *et al.*, 2015). Furthermore, differences in the susceptibility of types I and II to bacteriophage infection have also been known for some time (Webster & Cummins, 1978; Liu *et al.*, 2015). The main phylogroups of *P. acnes* share a high degree of similarity with regard to their biochemical phenotype, including traditional tests used to differentiate the bacterium from other 'cutaneous' propionibacteria (Table 2). Notable phylogroup differences, however, include β-haemolytic and neuraminidase activity, as well as sorbitol fermentation, all of which are essentially restricted to the type I division (McDowell *et al.*, 2008; Lomholt & Kilian, 2010; Niazi *et al.*, 2010) (Table 2). The production of lipase also appears to be much lower amongst type II strains versus those from the type I and III divisions (McDowell *et al.*, 2008; Niazi *et al.*, 2010) (Table 2); we have previously described how type II strains have deletions in the TATA box and open reading frame of two candidate lipase genes which may explain this reduced activity (Tomida *et al.*, 2013).

One defining difference between the type I and II phylogroups rests on their association with acne vulgaris. On the basis of both culture and metagenomic analyses, widely disseminated clonal lineages from the type I division have been described in association with acneic skin, but not those from the type II or type III divisions, which appear to be associated more with blood, medical devices and soft tissue infections (Lomholt & Kilian, 2010; McDowell *et al.*, 2011, 2012; Fitz-Gibbon *et al.*, 2013; Rollason *et al.*, 2013). Recently, type III strains have also been linked with the depigmenting skin condition progressive macular hypomelanosis (Petersen *et al.*, 2015, Barnard *et al.*, 2016). Interrogation of the *P. acnes* $MLST_8$ isolate database, which contains information on a large collection of geographically widespread isolates and their clinical sources, reveals a statistically significant enrichment overall for strains from the type I clade in acneic versus healthy skin ($P<0.001$; Fishers exact test, two tailed), while those from the type II clade appear to show no association overall ($P=0.213$; Fishers exact test). More specifically, associations are found between acneic skin and strains from the type IA_1 clonal complexes CC1 (RT1 and RT532) ($P<0.01$; Fishers exact test), CC3 (RT1, RT4 and RT5) ($P=0.043$; Fishers exact test) and CC4 (RT8) ($P=0.021$; Fishers exact test) (Figs 1 and S1). In a previous study, we found that a globally disseminated clonal lineage with the MLST genotype ST6 (Warwick $MLST_7$ scheme analysis) or ST1 ($MLST_8$ analysis) strikingly represented the majority of type IA_1 isolates we analysed from a cohort of patients with acne (McDowell
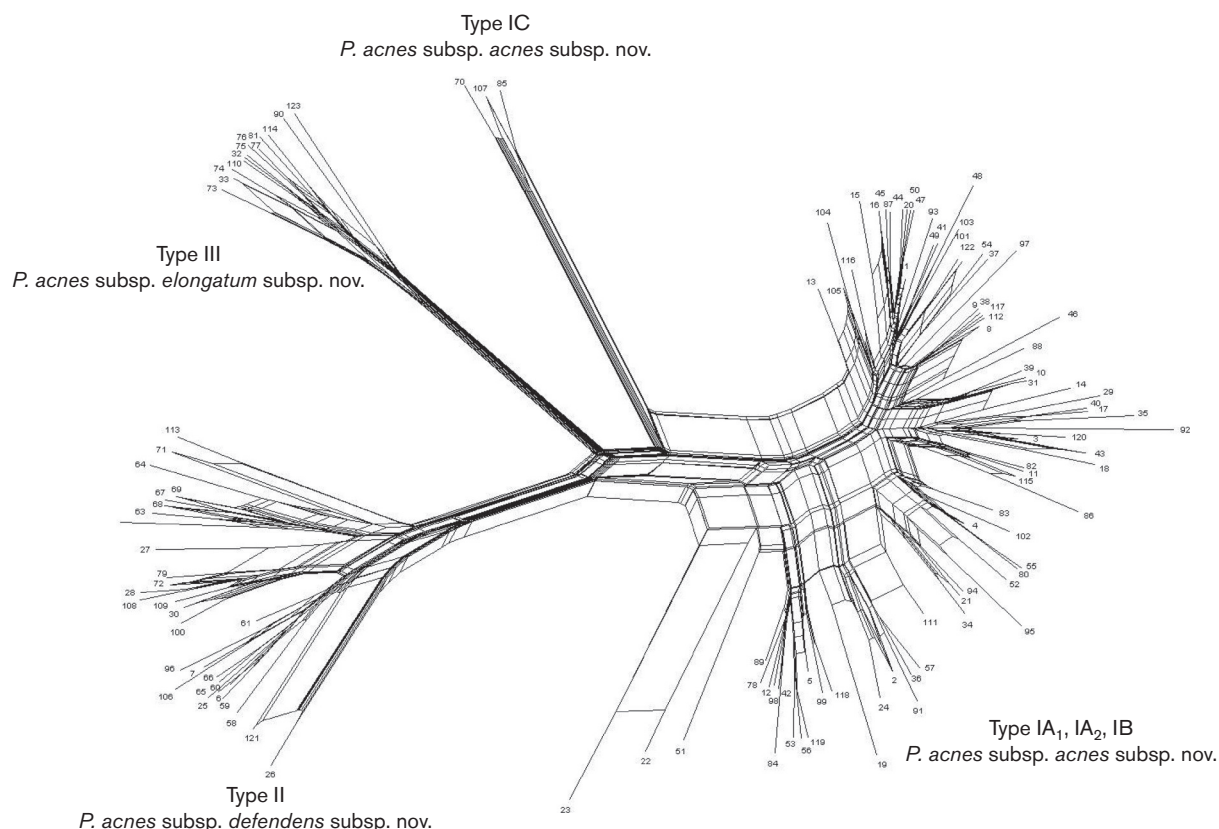
Fig. 2. Neighbour-net split graph (SplitsTree v4.14.4) of allelic profiles from all STs currently represented in the MLST$_8$ database (http://pubmlst.org/pacnes/), and covering all major genetic divisions (Huson & Bryant, 2006). A distance matrix was generated from the allelic profile data and saved in NEXUS format for input to SplitsTree. Parallelogram formations indicative of recombination/ reticulation events are evident within the major type I and II divisions.

et al., 2011). In contrast, specific type II lineages (RT2 and RT6) belonging to CC72 (MLST$_8$) appear to be associated with healthy skin on the basis of metagenomic and culture-based detection (McDowell *et al.*, 2012; Fitz-Gibbon *et al.*, 2013; Johnson *et al.*, 2016). The observation that type II strains, but not those from the type I clade, encode CRISPR/Cas elements may be important in this context, thus preventing the acquisition of genetic loci that may contribute to virulence and acne pathophysiology (Fitz-Gibbon *et al.*, 2013). For example, key type I lineages from CC3 (MLST$_8$; Fig. 1), believed to be associated with acne contain a novel plasmid with a tight adhesion (Tad) locus and two unique genomic islands, known as loci 1 and 2, that contain genes proposed to enhance virulence via increased bacterial adhesion and host immune response (Fitz-Gibbon *et al.*, 2013; Tomida *et al.*, 2013; Kasimatis *et al.*, 2013).

To conclude, we now propose *P. acnes* type I and II as distinct subspecies based on a polyphasic taxonomy approach. The growing number of genomes now becoming available for other propionibacteria will also provide an important opportunity to reexamine the genus and the place of the 'cutaneous' group within it.

Description of *Propionibacterium acnes* subsp. *acnes* subsp. nov.

P. acnes subsp. *acnes* (ac′nes Gr. n. *acme* a point; incorrectly transliterated as N.L. n. *acne* acne; N.L. gen.n. *acnes* of acne). Description based on McDowell *et al.* (2008), Niazi *et al.* (2010), Patrick & McDowell (2011), and Dekio *et al.* (2015).

Four phylogenetically distinct type I groups have been described, known as type IA$_1$, IA$_2$, IB and IC; type IA$_2$, IB and IC represent phylogenetically tight clusters compared with IA$_1$. Cells are Gram-stain-positive, non-motile, non-spore-forming, and anaerobic-to-aerotolerant. Colonies appear as lenticular, minute-to-4.0 mm, white, and can become tan, pink or orange in 3 weeks. Growth is most rapid at 30–37 °C. Surface colonies on blood agar (horse or rabbit) are punctiform-to-0.5 mm, circular, entire-to-pulvinate, translucent-to-opaque, white-to-gray and glistening. The cell shape after anaerobic culture in broth medium ranges from small plump rods to ellipsoids which tend to occur in pairs joined at a slight angle, and the size is approximately 0.4–0.5×0.8–0.9 µm. In defined medium broth culture, type IA and IC strains form a turbid

Table 2. Key phenotypic similarities and differences between type I, II and III strains

+, At least 90 % of isolates are positive; −, at least 90 % of isolates are negative; d+, 40–89 % of isolates are positive; d−, 11–39 % of isolates are positive; ND, not determined.

Characteristic*	Type I	Type II	Type III
Indole production	+	d+	+
Catalase activity	+	+	+
Nitrate reduction	+	+	d+
Gelatin liquefaction	+	+	−
Aesculin hydrolysis	−	−	−
β-Haemolysis (5 days at 37 °C)	d+	−	−
Neuraminidase	d+	−	−
Lipase	d+	d−	d+
L-Pyrrolydonyl arylamidase	d+	d−	−
Pyruvate	d+	+	−
Fermentation of:			
Sorbitol	d+	−	−
Maltose	−	−	−
Sucrose	−	−	−
Glycerol	d+	d+	+
Ribose	d−	d+	−
Cell wall components			
Dermatan sulphate-binding adhesins	d+	−	−
DAP isomer	LL-	LL- (*meso*)	LL-
Amino acids	Ala, Gly, Glu	Ala, Gly, Glu	ND
Sugars	Galactose, Glucose, Mannose	Glucose Mannose	ND

*Key phenotypic characteristics were compiled from data from one or more of the following publications: McDowell *et al.* (2005, 2008, 2011); Lomholt & Kilian (2010); Niazi *et al.* (2010); Patrick & McDowell (2011); Dekio *et al.* (2015).

suspension, while in PPY or BHI broth they form a settled granular sediment with a clear solution. In contrast, type IB strains form a slight fine sediment and turbid solution containing suspended cells. In suitable media with good growth, the final pH is 4.5–5.0. Generally catalase-positive, cultures need to be exposed to air for 1 h before testing. All strains have an absolute requirement for pantothenate, while thiamine, biotin and nicotinamide are stimulatory. Strains are co-haemolytic and variable for β-haemolytic activity and produce a number of extracellular enzymes including ribonuclease, neuraminidase, hyaluronidase, acid phosphatase, lecithinase and lipase. Strains of type IA produce relatively low levels of the putative co-haemolytic Christie–Atkins–Munch–Peterson (CAMP) factor 1, but

type IB strains produce an abundance of this protein. The total quantity of acid (especially the proportion of lactic acid) produced from fermentable carbohydrates is highly variable. Cells ferment glucose, but not sucrose or maltose. Lactate is converted to propionate by most strains but only if the initial oxidation–reduction potential of the medium is sufficiently low, or if the initial growth rate is rapid. Sorbitol fermentation is a variable but defining characteristic of type I strains. Gelatin is hydrolysed, and most strains produce indole and reduce nitrate, but aesculin is not hydrolysed. The major long-chain fatty acid produced in thioglycolate cultures is 13-methyltetradecanoic acid (32–62 %) and iso-$C_{15:0}$ is the predominant cellular fatty acid. Prominent mass ions obtained by MALDI-TOF mass spectrometry are at 3589 and 7179 Da. Peptidoglycan contains alanine, glutamic acid, glycine and LL-DAP. Cell wall sugars are glucose, mannose and galactose. Strains have been isolated from the human skin, oral cavity and genitourinary tract. Type IA_1 and IC strains are associated with acne vulgaris. The DNA G+C content is approximately 60 % based on whole-genome sequencing analysis.

This subspecies is the type subspecies of *P. acnes* and contains the type strain according to Rules 40a and 40b of the Bacteriological Code (Lapage, 1992). The type strain is NCTC 737[T] (=ATCC 6919[T]=JCM 6425[T]=DSM 1897[T]=CCUG 1794[T]), the original type strain of the species, isolated from facial acne in London, 1920 (Genbank accession number NZ_JNHS00000000).

Description of *Propionibacterium acnes* subsp. *defendens* subsp. nov.

P. acnes subsp. *defendens* (de.fen′dens L. part. adj. *defendens*, defending, guarding, protecting; referring to the fact that strains have an active CRISPR/Cas system which guards or controls against foreign mobile genetic elements). Description based on McDowell *et al.* (2008), Niazi *et al.* (2010), Patrick & McDowell (2011), and Dekio *et al.* (2015).

Cells are Gram-stain-positive, non-motile, non-spore forming, and anaerobic-to-aerotolerant. Their cellular and colony morphology is similar to that of type I cells, but they may appear more coccoid and are most similar to previous descriptions of 'Corynebacterium parvum' which is a synonym for *P. acnes*. In defined medium broth culture, strains form a slight fine sediment and turbid solution containing suspended cells. In addition to pantothenate, some strains require haem and vitamin K to grow. Biochemical phenotype is similar to that of type I strains but with some notable differences. Cells are negative for β-haemolysis, and neuraminidase and lipase activity is infrequently found. Abundant levels of CAMP factor 1 are produced; similar to those observed with strains of type IB. Sorbitol fermentation is negative. The predominant cellular fatty acid is iso-$C_{15:0}$ and prominent mass ions obtained by MALDI-TOF mass spectrometry are at 3628 and 7258 Da. Peptidoglycan contains alanine, glutamic acid, glycine, LL-DAP, and

occasionally *meso*-DAP. Cell wall sugars are mannose and glucose, but galactose is not present. Strains have been isolated from the human skin surface, oral cavity and genitourinary tract. Strains are rarely associated with acne vulgaris and some may be associated with skin health and others with opportunistic infection. The DNA G+C content is approximately 60 % based on whole-genome sequencing analysis.

The type strain of *P. acnes* subspecies *defendens* subsp. nov. is ATCC11828 (=JCM 6473=CCUG 6369) isolated from a subcutaneous abscess (Genbank accession number NC_017550).

Description of *Propionibacterium acnes* subsp. *elongatum* subsp. nov.

The description for *P. acnes* subsp. *elongatum* is given in Dekio *et al.* (2015).

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