

A stable home for an equine pathogen: valid publication of the binomial *Prescottella equi* gen. nov., comb. nov., and reclassification of four rhodococcal species into the genus *Prescottella*.

Vartul Sangal¹, Michael Goodfellow², Amanda L. Jones¹ and Iain C. Sutcliffe^{1,*}

Abstract

Opinion 106 of the Judicial Commission has clarified the nomenclature of the taxon variously named *Rhodococcus equi*, '*Prescottella equi*' and *Rhodococcus hoagii*. As a consequence, we present here the genus name *Prescottella* and that of its nomenclatural type species, *Prescottella equi* comb. nov., for valid publication and propose the reclassification of four rhodococcal species as novel combinations in the genus, namely *Prescottella agglutinans* Guo *et al.* 2015 comb. nov., *Prescottella defluvii* Kämpfer *et al.* 2014 comb. nov., *Prescottella soli* Li *et al.* 2015 comb. nov. and *Prescottella subtropica* Lee *et al.* 2019 comb. nov. In addition, we note that a clinical isolate, strain 86–07 (=W8901), likely represents an additional species within the genus *Prescottella*. Nearly a century after the original description of the type strain of the type species as *Corynebacterium equi*, we provide a stable home for *Prescottella equi* and its relatives.

DATA SUMMARY

Supplementary data are available at: <https://doi.org/10.6084/m9.figshare.19688676> [1].

The species originally described by Magnusson in 1923 [2] as *Corynebacterium equi* has had a complicated taxonomic history [3–5], as shown in Table 1, resulting in different authors classifying it as *Rhodococcus equi*, '*Prescottella equi*' and *Rhodococcus hoagii* [6–8]. Arriving at a stable nomenclature for this taxon has been further beset by arcane nomenclatural issues [9, 10] that have been the subject of two Requests for an Opinion submitted to the Judicial Commission [11, 12]. The publication of Judicial Opinion 106 [13] provides nomenclatural clarity as the species epithet *hoagii* in *Corynebacterium hoagii* (Morse 1912) Ebersson 1918 (Approved Lists 1980) and *Rhodococcus hoagii* (Morse 1912) Kämpfer *et al.* 2014 has been placed on the list of *epitheta specifica et subspecifica rejicienda* (i.e. a rejected species epithet, meaning the names *C. hoagii* and *R. hoagii* must not be used).

Our taxonomic opinion is that the species originally described as *C. equi* and later placed in the genus *Rhodococcus* (Table 1) should be classified as the type species of the genus *Prescottella* [7, 14], although the genus name and type species name '*P. equi*' remain only effectively published i.e., lack standing in nomenclature. Additional phylogenomic evidence supporting this classification has been presented [15, 16] although it has been disputed by others [5, 17]. We did not previously apply to validate the name '*Prescottella equi*' because it was not known if the Judicial Commission would determine in favour of the species epithet *equi* or *hoagii*. The publication of Judicial Opinion 106, and the rejection of the epithet *hoagii* in this context, now allows us to formally present the name *Prescottella equi* comb. nov. of the type species of the genus *Prescottella* for valid publication in the *International Journal of Systematic and Evolutionary Microbiology*. Moreover, presentation of a 'protologue' for *Prescottella equi* comb. nov. allows us to rectify oversights in the original proposals [7, 14], in that the basonym and synonyms for this comb. nov. were inadvertently omitted, as highlighted by Tindall [18], although it is noted that at the time

Author affiliations: ¹Faculty of Health and Life Sciences, Northumbria University, Newcastle upon Tyne NE1 8ST, UK; ²School of Natural and Environmental Sciences, University of Newcastle, Newcastle upon Tyne NE1 7RU, UK.

***Correspondence:** Iain C. Sutcliffe, iain.sutcliffe@northumbria.ac.uk

Keywords: *Actinomycetota*; mycolic acids; *Nocardiaceae*; phylogenomics; *Rhodococcus*.

Abbreviations: AAI, average amino acid identity; POCP, percentage of conserved proteins.

Two supplementary data files are available with the online version of this article.

005551 © 2022 The Authors



This is an open-access article distributed under the terms of the Creative Commons Attribution License. This article was made open access via a Publish and Read agreement between the Microbiology Society and the corresponding author's institution.

Table 1. Nomenclature of the species represented by the type strain ATCC 6939^T (=NCTC 1621^T [3]*)

Name and nomenclatural authority	Status
<i>Corynebacterium equi</i> Magnusson 1923 (Approved Lists 1980)	Validly published name. Basonym for <i>Rhodococcus equi</i> and <i>Prescottella equi</i> .
<i>Rhodococcus equi</i> (Magnusson 1923) Goodfellow and Alderson 1977](Approved Lists 1980)	Homotypic synonym. Validly published name.
' <i>Prescottia equi</i> ' (Magnusson 1923) Jones et al. 2013	Homotypic synonym but also an illegitimate name and so cannot be used [7].
' <i>Prescottella equi</i> ' (Magnusson 1923) Jones et al. 2013	Homotypic synonym. Effectively published name, i.e. lacks standing in nomenclature.
<i>Rhodococcus hoagii</i> (Morse 1912) Kämpfer et al. 2014	Validly published but rejected name following issuance of Judicial Commission Opinion 106.

*Additional culture collection deposits of this type strain include ATCC 25729, CCUG 892, CIP 54.72, DSM 20307, HAMB1 2061, IFO 14956, JCM 1311, JCM 3209, LMG 18452, NBRC 101255, NBRC 14956, NRRL B-16538 and VKM Ac-953 [41].

of the original publications in 2013, the wording of Rule 27(2) of the International Code of Nomenclature of Prokaryotes did not formally require basonym/synonyms to be listed.

Subsequent to our proposal that *R. equi* be transferred to the novel genus *Prescottella*, several rhodococcal species have been proposed that show close phylogenetic relationships to *R. equi* which were evident both at the time of their description and in subsequent studies of novel mycolic acid containing taxa. These include *Rhodococcus defluvii* Kämpfer et al. 2014 [8, 19], *Rhodococcus soli* Li et al. 2015 [20], *Rhodococcus agglutinans* Guo et al. 2015 [21] and *Rhodococcus subtropicus* Lee et al.

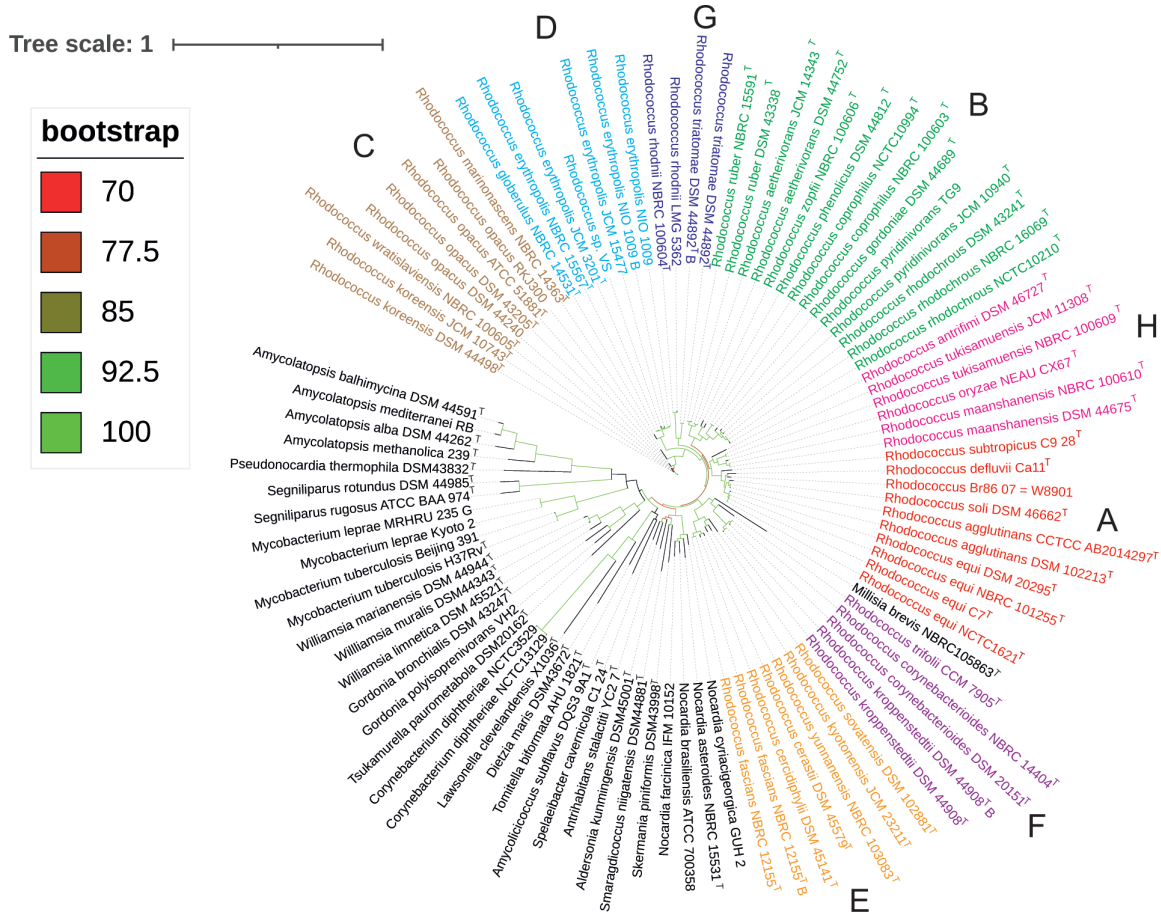


Fig. 1. A maximum-likelihood phylogenetic tree derived from a subset of amino acids from 400 universal proteins. The scale bar shows the normalized fraction of total branch lengths as described by Segata et al. [42]. Rhodococcal genome sequences showing 90% completeness, <5% contamination and <2% ambiguous nucleotides [43] were included in the analyses after annotation by RAST [44].

Table 2. Consensus placement of type strains of rhodococcal species in phylogenomic trees

The phylogenomic trees in the following studies all highlight the close relationships of the species listed to *R. equi* (typically labelled *R. hoagii* reflecting the nomenclature considered appropriate at that time). +, Species clusters with *R. equi*. NI, species not included in the analysis. None of these analyses included *R. soli*.

Reference	<i>R. defluvii</i>	<i>R. agglutinans</i>	<i>R. subtropicus</i>
Kim et al. [45]	+	+	+
Lee and Kim [29]	+	+	+
Kang et al. [46]	+	+	+
Lee et al. [47]	NI	NI	+
Lee et al. [22]	+	+	+

2019 [22]. To explore this further, a phylogenomic tree was generated using IQ-TREE with 100000 bootstrap replicates and SH-like approximate likelihood ratio tests [23] from an alignment created by PhyloPhlAn 3.0 based on 400 universal proteins from genomes of rhodococcal type strains and outgroups [24] (Fig. 1). The tree was visualized using iTOL version 5 [25].

As previously observed [15, 16], this analysis recovered eight well-defined groups of species within *Rhodococcus sensu lato* (Fig. 1, A–H) and confirmed the relationships of the above four species with *R. equi* and with one another. Other phylogenomic data confirming the close relationships of *R. agglutinans*, *R. defluvii* and *R. subtropicus* to *R. equi* are summarized in Table 2. In addition to the phylogenomic evidence presented in Fig. 1, multiple 16S rRNA phylogenetic analyses typically place *R. agglutinans*, *R. defluvii*, *R. soli* and *R. subtropicus* as close relatives of each other and of *R. equi*, although some instability is observed and not all studies include all type strains [8, 16, 20–22, 26–30]. In addition to the five validly published names for species belonging to Group A (*Prescottella*), strain 86–07, originally isolated from a patient with bacteraemia and initially identified as *R. equi* [31], was recovered as a distinct species level lineage. This is consistent with the conclusion of Gulvik et al. [32] that this strain (subsequently renamed W8901) is closely related to but distinct from *R. defluvii*.

To extend the phylogenomic analysis in Fig. 1, average amino acid identity (AAI) values were calculated between the genomes of the type strains of *R. agglutinans*, *R. defluvii*, *R. equi*, *R. soli*, *Rhodococcus* sp. strain 86–07 and *R. subtropicus* (Group A strains in Fig. 1) and other rhodococcal type strains (Supplementary Data file 1) [1] using EzAAI [33]. The AAI data within group A (mean 85.2%, range 81.5–91.8%, calculated using one representative genome for each species) are higher than those between the genomes of group A strains and other rhodococcal genomes (mean 71.6%, range 68.7–74.7%), values which support the separation of the group A strains from other *Rhodococcus* type strains based on the genus threshold of 74–76%

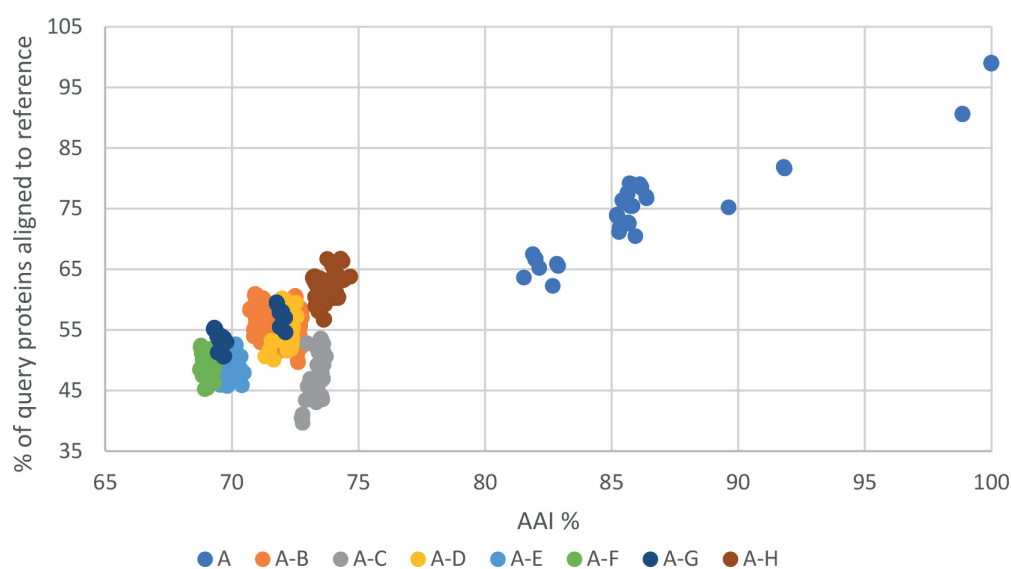


Fig. 2. Pairwise AAI values within *Prescottella* (Group A), and between *Prescottella* and other *Rhodococcus* species groups, plotted in comparison to the proportion of the proteins aligned.

[34, 35]. These data are summarized in Fig. 2, which shows AAI values for Group A strains plotted against the proportion of aligned proteins.

Similarly, percentage of conserved proteins (POCP) analyses, performed using the method of Qin *et al.* [36] (Supplementary Data file 2) [1], confirmed that values within group A (mean 70.6%, range 60.4–79.7%, one representative genome for each species) are higher than those between genomes of group A strains and the other rhodococcal genomes (mean 51.9%, range 38.3–65.3%). Although a 50% threshold for genus delineation was originally proposed [36], it is likely that this figure is overly stringent and should be reappraised, with alternative thresholds in the range 58–66% considered [34, 37–40]. These data clearly show that Group A strains are closely related to each other and well separated from other rhodococcal species groups, notably Group B which contains the type species *Rhodococcus rhodochrous*, which thus represents *Rhodococcus sensu stricto* [15, 16]. AAI values between Group A and Group B were 71.7% (range 70.7–72.8%) and POCP values were 54.3% (range 48.6–59.5%), supporting the conclusion that the Group A and Group B species clusters should be classified as different genera.

Cumulatively, these data show that the original proposal of the genus *Prescottella* [7, 14] is strongly supported by additional genomic analyses. We conclude also that in addition to the type species, *P. equi*, four other species should be reclassified in the genus, namely *Prescottella agglutinans* Guo *et al.* 2015 comb. nov., *Prescottella defluvii* Kämpfer *et al.* 2014 comb. nov., *Prescottella soli* Li *et al.* 2015 comb. nov. and *Prescottella subtropica* Lee *et al.* 2019 comb. nov. Furthermore, we conclude that strain 86–07 (=W8901) most likely represents an additional species within the genus *Prescottella*. Thus, nearly a century after the original description of the type strain of the type species by Magnusson [2], we hope to provide a stable home for *Prescottella equi* gen. nov., comb. nov. and for its relatives.

Description of *Prescottella* gen. nov.

Prescottella (Pres.cot.tel'la. N.L. fem. dim. n. *Prescottella*, named after John Prescott to celebrate his many contributions towards unravelling the pathogenicity of *Rhodococcus equi*).

Aerobic, Gram-positive, non-motile asporogenous cells that exhibit a rod-coccus lifecycle which may show elementary branching. Mesophilic and neutrophilic. Negative for oxidase and positive for catalase activity. Mycolic acids are present. Whole-cell hydrolysates contain *meso*-diaminopimelic acid, arabinose and galactose. The major menaquinones are tetra- and/or dihydrogenated menaquinones with eight isoprene units [MK-8(H₂/H₄)]. The polar lipids include diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol and phosphatidylinositol mannosides. The major fatty acids include C_{16:0} and 10-methyl C_{18:0} (tuberculostearic acid). Members of the genus can be distinguished from those of other genera classified in the family *Nocardiaceae* Castellani and Chalmers 1919 (Approved Lists 1980) based on phylogenomic analyses. The genomic G+C content of members of the genus range from 68.5 to 69.2 mol% and their genomes sizes range from 4.4 to 5.6 Mbp. The type species of the genus is *Prescottella equi* comb. nov.

Description of *Prescottella equi* comb. nov.

Prescottella equi (èqui. L. gen. n. *equi* of the horse).

Basonym: *Corynebacterium equi* Magnusson 1923 (Approved Lists 1980).

Synonyms: see Table 1.

The description is as given for '*Prescottia equi*' in Jones *et al.* [14] and for *Rhodococcus equi* in Goodfellow and Alderson [6]. The G+C content determined from the type strain genome sequence is 68.8% and its approximate size is 5.2 Mbp.

The type strain, C7^T (=ATCC 25729^T=ATCC 6939^T=CCUG 892^T= CIP 54.72^T=DSM 20307^T= HAMBI 2061^T= JCM 1311^T= JCM 3209^T=LMG 18452^T=NBRC 101255^T=NCTC 1621^T=NRRL B-16538^T= VKM Ac-953^T) was isolated from a lung abscess of a foal.

Description of *Prescottella agglutinans* comb. nov.

Prescottella agglutinans (ag.glu'ti.nans. L. part. adj. *agglutinans*, sticking together, agglutinating).

Basonym: *Rhodococcus agglutinans* Guo *et al.* 2015.

The description is as given for *R. agglutinans* in [21]. The G+C content determined from the type strain genome sequence is 69.2mol% and its approximate size is 5.4 Mbp.

The type strain CFH S0262^T (=CCTCC AB2014297^T=KCTC 39118^T) was isolated from a soil sample collected from Cát Bà island in Halong Bay, Vietnam.

Description of *Prescottella defluvii* comb. nov.

Prescottella defluvii (de.flu'vi.i. L. gen. n. *defluvii*, of sewage).

Basonym: *Rhodococcus defluvii* Kämpfer et al. 2014

The description is as given for *Rhodococcus defluvii* in Kämpfer et al. [8]. The G+C content determined from the type strain genome sequence is 68.7% and its approximate size is 5.1 Mbp.

The type strain, Ca11^T (=DSM 45893^T=LMG 27563^T) was isolated from a bioreactor for wastewater treatment in Aachen, Germany.

Description of *Prescottella soli* comb. nov.

Prescottella soli (so'li. L. gen. n. *soli*, of/from the soil).

Basonym: *Rhodococcus soli* Li et al. 2015

The description is as given for *Rhodococcus soli* in Li et al. [20]. The G+C content determined from the type strain genome sequence is 68.5mol% and its approximate size is 5.6 Mbp.

The type strain, DSD51W^T (=KCTC 29259^T=JCM 19627^T=DSM 46662^T=KACC 17838^T), was isolated from a soil sample collected from Kyoto Park, Japan.

Description of *Prescottella subtropica* comb. nov.

Prescottella subtropica (sub.tro'pi.ca. N.L. fem. adj. *subtropica*, subtropical, indicating that the type strain was isolated from a subtropical zone).

Basonym: *Rhodococcus subtropicus* Lee et al. 2019

The description is as given for *Rhodococcus subtropicus* by Lee et al. [22].

The type strain, C9-28^T (=KACC 19823^T=DSM 107559^T), was isolated from soil sampled inside a natural cave on Jeju Island, Republic of Korea.

Funding information

The authors have not received any support for this work from funding agencies.

Acknowledgements

We gratefully acknowledge Felix See-Too (Faculty of Science, University of Malaya, Malaysia) for his assistance in providing the scripts used in calculating the POCP data. We thank the members of the Judicial Commission for their outstanding scholarship in resolving the nomenclatural issues considered in Opinion 106 [12]. We gratefully acknowledge LPSN (<https://lpsn.dsmz.de/>; [41]) as a source for the nomenclatural information compiled in Table 1.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. Sangal V, Goodfellow M, Jones AL, Sutcliffe IC. A stable home for an equine pathogen: valid publication of the binomial *Prescottella equi* gen. nov., comb. nov., and reclassification of four rhodococcal species into the genus *Prescottella*. *Figshare* 2022. DOI: 10.6084/m9.figshare.19688676.
2. Magnusson H. Spezifische infektiöse Ppneumonie beim Ffohlen. Eein neuer Eeitererreger beim Ppferd. *Arch Wiss Prakti Tierheilk* 1923;50:22–38.
3. Sly LI, Mutimer MD, Woolcock JB. Confusing Irregularities in the nomenclature of some *Rhodococcus* species. *Int J Syst Bacteriol* 1983;33:658–659.
4. Goodfellow M. The taxonomic status of *Rhodococcus equi*. *Vet Microbiol* 1987;14:205–209.
5. Vázquez-Boland JA, Meijer WG. The pathogenic actinobacterium *Rhodococcus equi*: what's in a name? *Mol Microbiol* 2019;112:1–15.
6. Goodfellow M, Alderson G. The actinomycete-genus *Rhodococcus*: a home for the "rhodochrous" complex. *J Gen Microbiol* 1977;100:99–122.
7. Jones AL, Sutcliffe IC, Goodfellow M. Proposal to replace the illegitimate genus name *Prescottia* Jones et al. 2013 with the genus name *Prescottella* gen. nov. and to replace the illegitimate combination *Prescottia equi* Jones et al. 2013 with *Prescottella equi* comb. nov. *Antonie van Leeuwenhoek* 2013;103:1405–1407.
8. Kämpfer P, Dott W, Martin K, Glaeser SP. *Rhodococcus defluvii* sp. nov., isolated from wastewater of a bioreactor and formal proposal to reclassify [*Corynebacterium hoagii*] and *Rhodococcus equi* as *Rhodococcus hoagii* comb. nov. *Int J Syst Evol Microbiol* 2014;64:755–761.
9. Tindall BJ. The correct name of the taxon that contains the type strain of *Rhodococcus equi*. *Int J Syst Evol Microbiol* 2014;64:302–308.
10. Goodfellow M, Sangal V, Jones AL, Sutcliffe IC. Charting stormy waters: A commentary on the nomenclature of the equine pathogen variously named *Prescottella equi*, *Rhodococcus equi* and *Rhodococcus hoagii*. *Equine Vet J* 2015;47:508–509.
11. Garrity GM. Conservation of *Rhodococcus equi* (Magnusson 1923) Goodfellow and Alderson 1977 and rejection of *Corynebacterium hoagii* (Morse 1912) Ebersson 1918. *Int J Syst Evol Microbiol* 2014;64:311–312.
12. Vázquez-Boland JA, Scotti M, Meijer WG. Conservation of *Rhodococcus equi* (Magnusson 1923) Goodfellow and Alderson 1977 and rejection of *Rhodococcus hoagii* (Morse 1912) Kämpfer et al. 2014. *Int J Syst Evol Microbiol* 2020;70:3572–3576.
13. Arahall DR, Busse H-J, Bull CT, Christensen H, Chuvochina M, et al. Judicial Opinions 103-111. *Int J Syst Evol Microbiol* 2022;72:005197.
14. Jones AL, Sutcliffe IC, Goodfellow M. *Prescottia equi* gen. nov., comb. nov.: a new home for an old pathogen. *Antonie van Leeuwenhoek* 2013;103:655–671.

15. Sangal V, Goodfellow M, Jones AL, Schwalbe EC, Blom J, et al. Next-generation systematics: an innovative approach to resolve the structure of complex prokaryotic taxa. *Sci Rep* 2016;6:38392.
16. Sangal V, Goodfellow M, Jones AL, Seviour RJ, Sutcliffe IC. Refined systematics of the genus *Rhodococcus* based on whole genome analyses. In: *Biology of Rhodococcus*. Springer Cham, 2019.
17. Anastasi E, MacArthur I, Scotti M, Alvarez S, Giguère S, et al. Pangenome and phylogenomic analysis of the pathogenic actinobacterium *Rhodococcus equi*. *Genome Biol Evol* 2016;8:3140–3148.
18. Tindall BJ. Rule 27 of the International Code of Nomenclature of Prokaryotes: the basonym is not enough. *Int J Syst Evol Microbiol* 2016;66:4897–4899.
19. Sangal V, Jones AL, Goodfellow M, Hoskisson PA, Kämpfer P, et al. Genomic analyses confirm close relatedness between *Rhodococcus defluvii* and *Rhodococcus equi* (*Rhodococcus hoagii*). *Arch Microbiol* 2015;197:113–116.
20. Li S-H, Yu X-Y, Park D-J, Hozzein WN, Kim C-J, et al. *Rhodococcus soli* sp. nov., an actinobacterium isolated from soil using a resuscitative technique. *Antonie van Leeuwenhoek* 2015;107:357–366.
21. Guo Q-Q, Ming H, Meng X-L, Duan Y-Y, Gao R, et al. *Rhodococcus agglutinans* sp. nov., an actinobacterium isolated from a soil sample. *Antonie van Leeuwenhoek* 2015;107:1271–1280.
22. Lee SD, Kim YJ, Kim IS. *Rhodococcus subtropicus* sp. nov., a new actinobacterium isolated from a cave. *Int J Syst Evol Microbiol* 2019;69:3128–3134.
23. Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol* 2015;32:268–274.
24. Asnicar F, Thomas AM, Beghini F, Mengoni C, Manara S, et al. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nat Commun* 2020;11:2500.
25. Letunic I, Bork P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. *Nucleic Acids Res* 2021;49:W293–W296.
26. Nguyen TM, Kim J. *Rhodococcus pedocola* sp. nov. and *Rhodococcus humicola* sp. nov., two antibiotic-producing actinomycetes isolated from soil. *Int J Syst Evol Microbiol* 2016;66:2362–2369.
27. Tánácsics A, Máthé I, Benedek T, Tóth EM, Atasayar E, et al. *Rhodococcus sovatisensis* sp. nov., an actinomycete isolated from the hypersaline and heliothermal Lake Ursu. *Int J Syst Evol Microbiol* 2017;67:190–196.
28. Li C, Cao P, Jiang M, Hou Y, Du C, et al. *Rhodococcus oryzae* sp. nov., a novel actinobacterium isolated from rhizosphere soil of rice (*Oryza sativa* L.). *Int J Syst Evol Microbiol* 2020;70:3300–3308.
29. Lee SD, Kim IS. *Rhodococcus spelaei* sp. nov., isolated from a cave, and proposals that *Rhodococcus biphenylivorans* is a later synonym of *Rhodococcus pyridinivorans*, *Rhodococcus qingshengii* and *Rhodococcus baikonurensis* are later synonyms of *Rhodococcus erythropolis*, and *Rhodococcus percolates* and *Rhodococcus imtechensis* are later synonyms of *Rhodococcus opacus*. *Int J Syst Evol Microbiol* 2021;71:004890.
30. Zhang D, Su Z, Li L, Tang W. *Rhodococcus spongiicola* sp. nov. and *Rhodococcus xishaensis* sp. nov., from marine sponges. *Int J Syst Evol Microbiol* 2021;71:004863.
31. Langer AJ, Feja K, Lasker BA, Hinrikson HP, Morey RE, et al. Investigation of an apparent outbreak of *Rhodococcus equi* bacteremia. *Diagn Microbiol Infect Dis* 2010;67:95–100.
32. Gulvik CA, Batra D, Howard DT, Sheth M, Humrighouse BW, et al. Complete genome sequence of *Rhodococcus* sp. strain W8901, a human clinical specimen, assembled using miseq and minion sequence data. *Microbiol Res Announc* 2021;10:e0061321.
33. Kim D, Park S, Chun J. Introducing EzAAI: a pipeline for high throughput calculations of prokaryotic average amino acid identity. *J Microbiol* 2021;59:476–480.
34. Wirth JS, Whitman WB. Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera *Aestuariaivita*, *Citricella*, *Loktanelia*, *Nautella*, *Pelagibaca*, *Ruegeria*, *Thalassobius*, *Thiobacimonas* and *Tropici-bacter*, and the proposal of six novel genera. *Int J Syst Evol Microbiol* 2018;68:2393–2411.
35. Nicholson AC, Gulvik CA, Whitney AM, Humrighouse BW, Bell ME, et al. Division of the genus *Chryseobacterium*: observation of discontinuities in amino acid identity values, a possible consequence of major extinction events, guides transfer of nine species to the genus *Epilithonimonas*, eleven species to the genus *Kaistella*, and three species to the genus *Halpernia* gen. nov., with description of *Kaistella daneshvariae* sp. nov. and *Epilithonimonas vandammei* sp. nov. derived from clinical specimens. *Int J Syst Evol Microbiol* 2021;70:4432–4450.
36. Qin Q-L, Xie B-B, Zhang X-Y, Chen X-L, Zhou B-C, et al. A proposed genus boundary for the prokaryotes based on genomic insights. *J Bacteriol* 2014;196:2210–2215.
37. Aliyu H, Lebre P, Blom J, Cowan D, De Maayer P. Phylogenomic re-assessment of the thermophilic genus *Geobacillus*. *Syst Appl Microbiol* 2016;39:527–533.
38. Gupta RS. Distinction between *Borrelia* and *Borreliella* is more robustly supported by molecular and phenotypic characteristics than all other neighbouring prokaryotic genera: response to Margos' et al. "The genus *Borrelia* reloaded" (PLoS ONE 13(12): e0208432). *PLoS ONE* 2019;14:e0221397.
39. de la Haba RR, Minegishi H, Kamekura M, Shimane Y, Ventosa A. Phylogenomics of Haloarchaea: the controversy of the genera *Natrinema*-*Haloterrigena*. *Front Microbiol* 2021;12:740909.
40. Xu Z, Masuda Y, Wang X, Ushijima N, Shiratori Y, et al. Genome-Based taxonomic rearrangement of the order geobacterales including the description of *Geomonas azotofigans* sp. nov. and *Geomonas diazotrophica* sp. nov. *Front Microbiol* 2021;12:737531.
41. Parte AC, Sardà Carbasse J, Meier-Kolthoff JP, Reimer LC, Göker M. List of prokaryotic names with standing in nomenclature (LPSN) moves to the DSMZ. *Int J Syst Evol Microbiol* 2020;70:5607–5612.
42. Segata N, Börnigen D, Morgan XC, Huttenhower C. PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. *Nat Commun* 2013;4:2304.
43. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res* 2015;25:1043–1055.
44. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, et al. The RAST Server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 2008;9:75.
45. Kim SM, Lee SD, Koh YS, Kim IS. *Antrihabitans stalagmiti* sp. nov., isolated from a larva cave and a proposal to transfer *Rhodococcus cavernicola* Lee et al. 2020 to a new genus *Spelaeibacter* as *Spelaeibacter cavernicola* gen. nov. comb. nov. *Antonie Van Leeuwenhoek* 2022;115:521–532.
46. Lee SD, Kim IS, Kim YJ, Joung Y. *Rhodococcus cavernicola* sp. nov., isolated from a cave, and *Rhodococcus degradans* is a later heterosynonym of *Rhodococcus qingshengii*. *Int J Syst Evol Microbiol* 2020;70:4409–4415.
47. Kang Y, Chen Y, Zhang Z, Shen H, Zhou W, et al. A case of peritoneal dialysis-associated peritonitis caused by *Rhodococcus kroppenstedtii*. *BMC Infect Dis* 2021;21:565.