INTERNATIONAL JOURNAL OF
SYSTEMATIC AND EVOLUTIONARY
MICROBIOLOGY

ICSP MINUTES
Mousavi and Young, *Int. J. Syst. Evol. Microbiol.* 2022;72:005453
DOI 10.1099/ijsem.0.005453

MICROBIOLOGY SOCIETY

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International Committee on Systematics of Prokaryotes, Subcommittee on the taxonomy of Rhizobia and Agrobacteria, minutes of the annual meeting by videoconference, 5 July 2021, followed by online discussion until 31 December 2021

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Abstract

Minutes of the closed meeting of the International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Rhizobia and Agrobacteria held by videoconference, 5 July 2021, followed by online discussion until 31 December 2021, and list of recent species.

MEETING BY VIDEOCONFERENCE

Minute 1. Call to order

The annual Subcommittee meeting by videoconference was called to order by Peter Young, Subcommittee Chairperson, at 11.00 UTC on 5 July 2021.

Minute 2. Record of attendance

Present (18): J. Peter W. Young (University of York, UK, Chairperson), Seyed Abdollah Mousavi (University of Turku, and University of Helsinki, Finland, Secretary), Julie Ardley (Murdoch University, Perth, Australia), Philippe de Lajudie (IRD, Montpellier, France), Bertrand Eardly (Penn State Berks College, Reading, PA, USA), Nemanja Kuzmanović (Julius Kühn-Institut, Braunschweig, Germany), Florent Lassalle (Imperial College, St Mary's Hospital, London, UK), Kristina Lindström (University of Helsinki, Finland), Esperanza Martinez-Romero (UNAM, Cuernavaca, Mor., Mexico), Xavier Nesme (INRA, University of Lyon I, Villeurbanne, France), Alvaro Peix (Institute of Natural Resources and Agrobiology, Salamanca, Spain), Joanna Puławska (Research Institute of Horticulture, Skierniewice, Poland), Emma T. Steenkamp (University of Pretoria, South Africa), Tomasz Stępkowski (University of Life Sciences, Warsaw, Poland), Chang-Fu Tian (China Agricultural University, Beijing, PR China), Gehong Wei (Northwest A and F University, Yangling, Shaanxi, PR China), Anne Willems (University of Gent, Belgium) and Jerri Edson Zilli (Embrapa Agrobiologia, Seropédica, Rio de Janeiro, Brazil).

Apologies for absence (2): Lionel Moulin (IRD, Montpellier, France) and Ridha Mhamdi (Centre de Biotechnologie de Borj-Cédria, Hammam-lif, Tunisia).

Minute 3. Publication of previous minutes

The minutes of our previous meeting (2020) have been published [1].

Minute 4. New members

The Subcommittee decided to encourage new members to join in order to face new challenges, to cover more items, and technical and geographical concerns. Three names were suggested and the secretary agreed to contact them.

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Keywords: agrobacteria; International Subcommittee on Taxonomy; rhizobia.

Abbreviations: ANI, average nucleotide identity; cpAAI, core-proteome average amino acid identity; dDDH, digital DNA–DNA hybridization; LPSN, List of Prokaryotic Names with Standing in Nomenclature; LTP, All Species Living Tree Project.

Minute 5. Following up the progress in resolutions (minutes 5.1 and 5.2) of the previous (2020) meeting

As decided in our two past meetings, some members edited information on rhizobia and agrobacteria on Wikipedia pages. Wikipedia is an open resource, which is accessible to everybody. It seems that the taxonomic information on many of the Wikipedia pages have been updated in connection with the List of Prokaryotic names with Standing in Nomenclature (LPSN; www.bacterio.net/). Thus, the members were encouraged to improve and add more biological information on Wikipedia pages (rather than only the taxonomic changes, which are updated by the LPSN regularly). The Subcommittee blog (https://taxonomyagrorhizo.blogspot.com/) does not necessarily reflect the official decisions made by our Subcommittee. Therefore, the members are encouraged to use the blog as an unofficial public outlet to write their opinions and comments, and to increase interactions and visibility of our recommendations.

Minute 6. New species and genera, since the last meeting

The LPSN provides valuable and up to dated taxonomic information; however, it seems that the LPSN is not necessarily linked to genomic sequences for all taxa. We thus, decided to carry on maintaining the list of new species and genera that were published since our last meeting (Table 1).

Minute 7. Nagoya protocol

The Brazilian member (Jerri Zilli) mentioned that they had promising meetings and negotiations with authorities of the ministry of environment of Brazil. Since last year, the Ministry of Environment has improved the rules for accessibility of bacterial strains regarding the Nagoya Protocol. In the case of India, the strains isolated from India are not sufficiently accessible to describe a new species. However, some researchers are in discussion with the government in India about making the rules acceptable, which might enable researchers to validate names of new species isolated from India in future.

Minute 8. Recent information on LTP database

The new version of All-Species Living Tree Project (LTP) has been recently released [2] (https://imedea.uib-csic.es/mmg/ltp/). The LTP database contains the 16S rRNA gene sequences of all type strains with validly published names until December 2020, as well as all sequences of new species not yet listed in the notification lists of the *International Journal of Systematic and Evolutionary Microbiology*, but published in this journal. The new release has three major features: (i) an improved alignment; (ii) new reconstructions of the global phylogeny of the classified species; and (iii) a list of taxa that need to be evaluated. The LTP aims to regularly update the validly published nomenclatural classification changes and new taxa proposals. The LTP is a very useful database since it can show the phylogenetic position of all validated rhizobial and agrobacterial species names, although we note that related species do not always have distinct 16S rRNA gene sequences [3–5]

Minute 9. Recent relevant publications in taxonomy

9.1. We discussed the recent paper by Velázquez *et al.* [6], in which the authors pointed out that strain ATCC 4720^T is the authentic type strain of *Agrobacterium tumefaciens*. The authors noted that the strains NCIB 9042^T and ATCC 4720^T were recorded as the original type strains of *Agrobacterium radiobacter* and *A. tumefaciens,* respectively. Nevertheless, in the list of the valid names of bacteria complied by Skerman *et al.* [7], the strains ATCC 19358^T and ATCC 23308^T were reported as the types strain of *A. radiobacter* and *A. tumefaciens*, respectively. In the case of *A. radiobacter*, this did not create a problem, since both cultures represented the same strain, just from different culture collections. However, this misnaming caused serious taxonomic problems for *A. tumefaciens* since the strain ATCC 23308^T showed 87% DNA–DNA relatedness with *A. radiobacter* IAM 12048^T in a study by Sawada *et al.* [8]. Based on this result, Sawada *et al.* [8] proposed the rejection of the name *A. tumefaciens* since *A. radiobacter* has priority according to Rule 38 of the Bacteriological Code. During the last decades, several researchers used the 'wrong' strain ATCC 23308^T (B6^T=CFBP 2413^T=HAMBI 1811^T=ICMP 5856^T=LMG 187^T=NCPPB 2437^T) as the type strain of *A. tumefaciens* [9, 10]. For instance, Mousavi *et al.* [10] proposed that *A. tumefaciens* was placed in a monophyletic clade with *A. radiobacter*. Therefore, they proposed that *A. tumefaciens* is no longer a valid species name since it was described after *A. radiobacter*. Based on the results of the average nucleotide identity based on BLAST (ANIb) and digital DNA–DNA hybridization (dDDH) performed by Velázquez *et al.* [6], the ANIb and dDDH values between *A. tumefaciens* ATCC 4720^T and *A. radiobacter* NCIB 9042^T were 86.5 and 31.3%, respectively. This clearly shows that strain ATCC 4720^T belongs to a different species rather than *A. radiobacter*. Therefore, the authors requested the Judicial Commission to issue an opinion correcting the type strain of *A. tumefaciens* from ATCC 23308^T to ATCC 4720^T, and have been waiting for the decision of the Judicial Commission. We discussed this issue, and members were in favour of the proposal of retaining *A. tumefaciens* as a valid species name, with ATCC 4720^T as the type strain.

9.2. The main results of a recent manuscript [11] were presented by two members of our Subcommittee (Nemanja Kuzmanović and Florent Lassalle). In this study, the authors performed a phylogenomic study of 94 strains of the family *Rhizobiaceae*. Based on the results of a phylogeny based on 170 nonrecombinant loci (using a pairwise core-proteome average amino acid identity (cpAAI) threshold of approximately 86%), the genus name *Sinorhizobium* should be retained as a valid genus name that encompasses 17 species. Moreover, the authors proposed delineation of a new genus name *Xaviernesmea* gen. nov. for the former species *Rhizobium*

Table 1. Novel taxa described since the last meeting of the Subcommittee

The names indicated in inverted commas have been proposed in effective publications, but have not yet been validated by publication in the *International Journal of Systematic and Evolutionary Microbiology* (have not been included in a validation list).

Species and nomenclatural type strain	Origin	Type strain genome NCBI assembly accession	Symbiotic/ pathogenic genes	Plant tests	Reference
Agrobacterium					
Agrobacterium leguminum MOPV5^{T} (=CECT 30096^{T}=LMG 31779^{T})	Root nodules of *Phaseolus vulgaris*, Spain	GCF_015704895.1			[23]
Agrobacterium tomkonis IIF1SW-B^{T} (=LMG 32164^{T}=NRRL B-65602^{T})	Surface of observation dome, International Space Station	GCF_020215515.1		Tum−	[24]
Burkholderia					
Burkholderia guangdongensis DHOM02^{T} (=KCTC 42625^{T}=LMG 28843^{T})	Forest soil, PR China	GCF_013403875.1			[25]
'*Burkholderia mayonis*' BDU6^{T} (=LMG 29941 ^{T}=ASM152374v2 ^{T})	Soil sample, Australia	GCF_001523745.2			[26]
'*Burkholderia perseverans*' CBAS 719 ^{T} (=LMG 31557 ^{T}=INN12^{T})	Leaf litter samples, Brazil	NA			[27]
'*Burkholderia savannae*' MSMB266^{T} (=TSD-82^{T}=LMG 29940^{T})	Soil sample, Australia	GCF_001524445.2			[26]
Bradyrhizobium					
Bradyrhizobium acaciae 10BB^{T} (SARCC 730^{T}=LMG 31409^{T})	*Acacia dealbata, South Africa*	GCF_020889785.1	*nodA*	Nod+	[28]
Bradyrhizobium agreste CNPSo 4010^{T} (=WSM 4802^{T}=LMG 31645^{T})	root nodules of *Glycine clandestina*, Australia	GCF_016031625.1	*nodC*	Nod+	[29]
Bradyrhizobium altum Pear77^{T} (SARCC 754^{T}=LMG 31407^{T})	*Pearsonia obovata, South Africa*	GCF_020889705.1	*nodA*	Nod+	[28]
Bradyrhizobium glycinis CNPSo 4016^{T} (=WSM 4801^{T}=LMG 31649 ^{T})	Root nodules of *Glycine tabacina*, Australia	GCF_016031655.1	*nodC*	Nod+	[29]
Bradyrhizobium diversitatis CNPSo 4019 ^{T} (=WSM4799^{T}=LMG 31650^{T})	Root nodules of *Glycine max*, Australia	GCF_016031635.1	*nodC*	Nod+	[29]
Bradyrhizobium oropedii Pear76^{T} (SARCC 731^{T}=LMG 31408^{T})	*Pearsonia obovata*, South Africa	GCF_020889685.1	*nodA*	Nod+	[28]
Bradyrhizobium quebecense 66S1MB^{T} (=LMG 31547^{T}=HAMBI 3720^{T})	Root nodules of soybean, Canada	GCF_013373795.3	*nodC, nifH*	Nod+	[30]
Bradyrhizobium septentrionale 1S1^{T} (=LMG 29930^{T}=HAMBI 3676^{T})	Root nodules of soybean, Canada	GCF_011516645.4	*nodC, nifH*	Nod+	[30]
Ciceribacter					
Ciceribacter daejeonensis comb. nov. L61^{T} (=KCTC 12121^{T}=IAM 15042^{T})		GCF_014280875.1			[31]
'*Ciceribacter ferrooxidans*' F8825^{T} (=CCTCC AB 2018196^{T}=KCTC 62948^{T})	Fe(II)-rich sediment, PR China	GCF_004137355.1			[32]
Ciceribacter selenitireducens comb. nov. B1^{T} (=ATCC BAA-1503^{T}=LMG 24075^{T})		GCF_000518785.1			[31]
Ciceribacter naphthalenivorans comb. nov. TSY03b^{T} (=KCTC 23252^{T}=NBRC 107585^{T})		GCF_007992095.1			[31]
Cupriavidus					
'*Cupriavidus cauae*' MKL-01^{T}	Human blood sample, Republic of Korea	GCF_008632125.1			[33]
'*Cupriavidus neocaledonicus*' STM 6070^{T}	*Mimosa pudica* nodules, New Caledonia	GCF_000372525.1	*nodA*, *nifH*		[34]
Devosia					
Devosia aurantiaca H239^{T} (=KACC 21662^{T}=JCM 33930^{T})	Soil, Republic of Korea	GCF_011058215.1			[35]

Continued

Table 1. Continued

Species and nomenclatural type strain	Origin	Type strain genome NCBI assembly accession	Symbiotic/ pathogenic genes	Plant tests	Reference
Devosia beringensis S02^{T} (=JCM 33772^{T}=CCTCC AB 2019343^{T})	Surface sediment, Bering Sea	GCF_014926585.1			[36]
Devosia equisanguinis M6-77^{T} (=CIP 111628^{T}=LMG 30659^{T})	Horse blood, Germany	GCF_900631955.1			[37]
Devosiafa ecipullorum CC-YST696^{T} (=BCRC 81284^{T}=JCM 34167^{T})	Chicken manure, Taiwan	GCF_015158295.1			[38]
'*Devosia oryziradicis*' G19^{T} (KCTC 82688^{T}=NBRC 114842^{T})	Rhizosphere of rice, Republic of Korea	GCF_016698645.1			[39]
'*Devosia rhizoryzae*' LEGU1^{T} (=KCTC 82712^{T}=NBRC 114485^{T})	Rhizosphere of rice, Republic of Korea	GCF_016698665.1			[39]
Mesorhizobium					
Mesorhizobium comanense 3P27G6^{T} (=DSM 110654^{T}=CECT 30067^{T})	Thermal water basin, Italy	GCF_005503535.1	*nodEFLNT, nifPSUV*		[40]
Mesorhizobium microcysteis MaA-C15^{T} (=KACC 21226^{T}=JCM 33503^{T})	Xenic culture of *Microcystis aeruginosa,* Republic of Korea	GCF_008180155.1	–		[41]
'*Mesorhizobium neociceri*' CCANP35^{T} (=CECT 9773^{T}=LMG 31150^{T})	Nodules of *Cicer canariense*, Spain	GCF_013520985.1	*nodC, nifH*	Nod+	[42]
'*Mesorhizobium xinjiangense*' lm94^{T} (=KCTC 72863^{T}=CCTCC AB2019377^{T})	Rhizosphere soil of *Alhagi sparsifolia,* PR China	GCF_009749525.1			[43]
Methylobacterium					
Methylobacterium ajmalii IF7SW-B2^{T} (=NRRL B-65601^{T}=LMG 32165^{T})	International Space Station	GCF_016613415.1			[44]
'*Methylobacterium radiodurans*' 17Sr1-43 ^{T} (=KCTC 52906 ^{T}=NBRC 112875^{T})	Soil sample, Republic of Korea	GCF_003173735.1			[45]
Methylobacterium segetis 17J42-1^{T} (=KCTC 62267^{T}=JCM 33059^{T})	Soil sample, Republic of Korea	GCF_004348265.1			[46]
Microvirga					
'*Microvirga alba*' BT350^{T} (=KCTC 72385^{T}=NBRC 114848^{T})	Soil, Republic of Korea	GCF_015694465.1			[47]
'*Microvirga antarctica*' 3D7^{T} (=CGMCC 1.13821^{T}=KCTC 72465^{T})	Soil, Antarctica	GCF_017921815.1			[48]
'*Microvirga mediterraneensis*' Marseille-Q2068^{T}	Human skin, France	GCF_013520865.1			[49]
'*Microvirga pudoricolor*' BT291^{T} (=KCTC 72368^{T}=NBRC 114845^{T})	Soil, Republic of Korea	GCF_016892705.1			[47]
Neorhizobium					
'Neorhizobium lilium' 24NR^{T} (=ACCC 61588^{T}=JCM 33731^{T})	*Lilium pumilum* bulbs, PR China	GCF_004053875.1	*nodACD-, nifH-*		[50]
Neorhizobium tomejilense T17_20^{T} (=LMG 30623^{T}=CECT 9621^{T})	Dryland agricultural soil, Spain	GCF_002968845.1			[51]
Pararhizobium					
'Pararhizobium mangrovi' BGMRC 6574^{T} (=KCTC 72636^{T}=CGMCC 1.16783^{T})	*Aegiceras corniculatum* stem, PR China	GCF_006516965.1			[52]
Paraburkholderia					
Paraburkholderia acidicola G-6302^{T} (=ATCC 31363^{T}=BCRC 13035^{T})	Soil, Japan	GCF_002362315.1			[53]
Paraburkholderia acidiphila 7Q-K02^{T} (=KCTC 62472^{T}=LMG 29209^{T})	Forest soil, PR China	GCF_009789655.1			[25]
Paraburkholderia acidisoli DHF22^{T} (=GDMCC 1.1448^{T}=LMG 30262^{T})	Forest soil, PR China	GCF_009789675.1			[25]

Continued

Table 1. Continued

Species and nomenclatural type strain	Origin	Type strain genome NCBI assembly accession	Symbiotic/ pathogenic genes	Plant tests	Reference
Paraburkholderia antibiotica G-4-1-8^{T} (=KACC 21617^{T}=NBRC 114603^{T})	Forest soil, Republic of Korea	GCF_012927125.1			[54]
Paraburkholderia dioscoreae Msb3^{T} (=LMG 31881^{T}=DSM 111632^{T}).	Leaves of *Dioscorea bulbifera*	GCF_902459535.1			[55]
Paraburkholderia domus with LMG 31832^{T} (=CECT 30334^{T})	Forest soil, Belgium	GCF_905220705.1			[56]
Paraburkholderia guartelaensis CNPSo 3008^{T} (=U13000^{T}=G29.01^{T})	Nodules of *Mimosa gymnas*, Brazil	GCF_004353905.1	*nodC*	Nod+	[57]
Paraburkholderia haematera LMG 31837^{T} (=CECT 30336^{T})	Forest soil, Belgium	GCF_905220975.1			[56]
Paraburkholderia lacunae S27^{T} (=KACC 19714^{T}=JCM 32721^{T})	Soil, Republic of Korea	GCF_003353175.1			[58]
Paraburkholderia nemoris LMG 31836^{T} (=CECT 30335^{T})	Forest soil, Belgium	GCF_905221015.1			[56]
Paraburkholderia polaris RP-4-7^{T} (=KACC 2162^{T}=NBRC 114605^{T})	Soil, Norway	GCF_012927345.1			[54]
Paraburkholderia ultramafica comb. nov. STM10279^{T} (=CIP110886^{T}=LMG 28614^{T})		GCF_902859915.1			[25]
***Peteryoungia* gen. nov.**					[31]
Peteryoungia ipomoeae comb. nov. shin9-1^{T} (=LMG 27163^{T}=KCTC 32148^{T})		GCF_004912165.1			[31]
Peteryoungia desertarenae ADMK78^{T} (=MCC 3400^{T}=KACC 21383^{T})	Desert sand, India	GCF_005860795.2	–		[31]
Peteryoungia rosettiformans comb. nov. W3^{T} (=CCM 7583^{T}=MTCC 9454^{T})		GCF_004912135.1			[31]
Peteryoungia wuzhouensis comb. nov. W44^{T} (GDMCC 1.1257^{T}=KCTC 62194^{T})		GCF_003205195.1			[31]
Peteryoungia rhizophila comb. nov. 7209-2^{T} (=CGMCC 1.15691^{T}=DSM 103161^{T})		GCF_004912145.1			[31]
Rhizobium					
Rhizobium changzhiense WYCCWR 11279^{T} (=HAMBI 3709^{T}=LMG 31534^{T})	Root nodules of *Vicia sativa*, PR China	GCF_013087625.1	*nodC*		[59]
'*Rhizobium flavescens*' FML-4^{T} (=CCTCC AB 2019354^{T}=KCTC 62839^{T})	Chlorothalonil-contaminated soil, PR China	GCF_011319365.1	*nodA, nifH*	Nod-	[60]
'*Rhizobium rhizolycopersici* " DBTS2^{T} (= CICC 24887^{T}=ACCC61707 ^{T})	Rhizosphere of tomato, PR China	GCF_013378445.1	*nod-,nif-*	Nod-	[61]

oryzae, which had an uncertain phylogenetic position in previous studies [10, 12]. The authors created 14 new species combination in the family *Rhizobiaceae*, and proposed delineation of two new genera for some of the current members of the genera *Neorhizobium* and *Rhizobium*. Interestingly, the authors of this work also proposed that a threshold of cpAAI >86% could be used to separate the genera of the family *Rhizobiaceae*. The delineation of a new subgenus instead of a new genus was discussed in our meeting. Even though subgenus is an acceptable and official taxonomic level in classification of prokaryotes, most of the members thought that using subgenus might cause unnecessary complexities in the taxonomy of agrobacteria and rhizobia. However, we cannot forbid researchers to propose a subgenus.

Minute 10. Adjournment of videoconference

The meeting by videoconference was adjourned at 12:53 UTC on 5 July 2021. As usual, it was decided to continue the meeting and discussion online until 31 December 2021.

ONLINE CONTINUATION OF MEETING

Minute 11. New members

Three scientists were later contacted by the Subcommittee secretary. George Colin diCenzi (Queen's University, Canada) and Praveen Rahi (National Centre for Cell Science, India) were further elected as regular members, and contributed in the online discussion to prepare the present minutes.

Minute 12. Reclassification of *Ochrobactrum Lupini* as *Brucella Anthropi*

In 2005, *Ochrobactrum lupin*i was described based on a polyphasic study including phenotypic, chemotaxonomic, and molecular features (16S and 23S rRNA) of the strains isolated from *Lupinus albus* [13]. However, a new study based on multiple genome ANI approaches, dDDH and phylogenetic analysis by Volpiano *et al*. [14] showed that similarity between the type strains *Ochrobactrum anthropi* ATCC 49188^T, *O. lupini* LUP21^T (97.55% ANIb, 98.25% ANIm, 97.99% gANI, 97.94% OrthoANI and 83.9% dDDH) exceeds the usual species delineation threshold. Thus, the authors proposed that *O. lupini* should be considered a later heterotypic synonym of *O. anthropi*. More recently, Hördt *et al*. [15] have proposed the amalgamation of the entire genus *Ochrobactrum* into *Brucella*. They described both *Brucella anthropi* and *B. lupini*, but we consider that *B. lupini* is a later heterotypic synonym of *B. anthropi* in light of the evidence provided by Volpiano *et al*. [14].

Minute 13. *Rhizobium fabae* is a synonym of *Rhizobium pisi* and *Rhizobium azibense* is a synonym of *Rhizobium gallicum*

A recent paper [16] presented genomic distance metrics among a large number of type strains in the *Rhizobiales*. Particularly relevant to our remit are their proposals that *R. fabae* [17] should be considered as a later heterotypic synonym of *R. pisi* [18], and that *R. azibense* [19] should be considered as a later heterotypic synonym of *R. gallicum* [20]. We support both these proposals.

Minute 14. Proposal for revising the ICNP rules

Recently, Rahi [21] published an opinion on the vexed subject of the Nagoya Protocol and access to type strain cultures. In this paper, he proposed "the problems imposed by policies designed to increase accessibility to genetic resources could be resolved by revising the ICNP rules to accommodate the many researchers working in countries that are signatories of the Convention on Biological Diversity and the Nagoya Protocol. This could be achieved by redefining 'restriction-free access' in Rule 30 [4] of the Code and by keeping regulated access to cultures under international legislation, like the Convention on Biological Diversity, the Nagoya Protocol and quarantine laws, free from restriction". The Subcommittee has not yet discussed this publication, although the issue is one that it has considered previously.

Minute 15. Resignation and thanks

Dr. Philippe de Lajudie, Prof. Kristina Lindström and Prof. Xavier Nesme announced their resignation from the Subcommittee because of retirement. The Subcommittee expressed their warm thanks to Philippe de Lajudie for taking his commitment as Secretary seriously as well as his long and active years of membership with appreciated contributions. The Subcommittee expressed their sincere appreciations to Prof. Kristina Lindström for her excellent professional contributions to the Subcommittee for such a long time, and particularly during all the years when she was Secretary and worked hard to keep the Subcommittee members active. The Subcommittee extended sincere gratitude to Prof. Xavier Nesme for his contributions and thoughtful ideas while a member of the Subcommittee. The Subcommittee also remembers with gratitude Prof. Wenxin Chen (1926–2021, China Agricultural University), who was a member of the Subcommittee until 2015, and of course she and her laboratory have made huge contributions to taxonomy of rhizobia over very many years, describing a large number of new species.

Minute 16. Membership status

Article 6 of the Statutes of the ICSP details rules on the organization and missions of subcommittees and specifies membership rules [22]. The members of our Subcommittee are listed as below:

Regular members (those who are members of a society affiliated to the *International Union of Microbiological Societies* and therefore have voting rights in the administrative workings of the Subcommittee): J. Peter W. Young (Microbiology Society), George Colin diCenzi (Canadian Society of Microbiologists), Bertrand Eardly (American Society for Microbiology), Florent Lassalle (Microbiology Society), Esperanza Martinez-Romero (Asociación Mexicana de Microbiologia), Alvaro Peix (Spanish Society for Microbiology), Praveen Rahi (Bergey's International Society for Microbial Systematics), Emma T. Steenkamp (South African Society for Microbiology, SASM), Chang-Fu Tian (Chinese Society for Microbiology), Gehong Wei (Chinese Society for Microbiology), Anne Willems (Microbiology Society, Belgian Society for Microbiology), Jerri Edson Zilli (Brazilian Society of Microbiology)

Co-opted members: Julie Ardley, Nemanja Kuzmanović, Ridha Mhamdi, Lionel Moulin, Seyed Abdollah Mousavi, Joanna Puławska, Tomasz Stępkowski, Pablo Vinuesa

Minute 15. Closing

The online phase of this meeting was closed on 31 December 2021.

The authors received no specific grant from any funding agency.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. **de Lajudie P, Mousavi SA, Young JPW**. International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Rhizobia and Agrobacteria. Minutes of the closed meeting by videoconference, 6 July 2020. *Int J Syst Evol Microbiol* 2021;71:004784.
2. **Ludwig W, Viver T, Westram R, Francisco Gago J, Bustos-Caparros E, *et al***. Release LTP_12_2020, featuring a new ARB alignment and improved 16S rRNA tree for prokaryotic type strains. *Syst Appl Microbiol* 2021;44:126218.
3. **Martens M, Delaere M, Coopman R, De Vos P, Gillis M, *et al***. Multilocus sequence analysis of *Ensifer* and related taxa. *Int J Syst Evol Microbiol* 2007;57:489–503.
4. **Young JPW, Moeskjær S, Afonin A, Rahi P, Maluk M, *et al***. Defining the *Rhizobium leguminosarum* species complex. *Genes* 2021;12:111.
5. **Mousavi SA, Gao Y, Penttinen P, Frostegård Å, Paulin L, *et al***. Using amplicon sequencing of *rpoB* for identification of inoculant rhizobia from peanut nodules. *Lett Appl Microbiol* 2022;74:204–211.
6. **Velázquez E, Flores-Félix JD, Sánchez-Juanes F, Igual JM, Peix Á**. Strain ATCC 4720^T is the authentic type strain of *Agrobacterium tumefaciens*, which is not a later heterotypic synonym of *Agrobacterium radiobacter*. *Int J Syst Evol Microbiol* 2020;70:5172–5176.
7. **Sneath PHA, McGowan V, Skerman VBD**. Approved lists of bacterial names. *Int J Syst Evol Microbiol* 1980;30:225–420.
8. **Sawada H, Ieki H, Oyaizu H, Matsumoto S**. Proposal for rejection of *Agrobacterium tumefaciens* and revised descriptions for the genus *Agrobacterium* and for *Agrobacterium radiobacter* and *Agrobacterium rhizogenes*. *Int J Syst Bacteriol* 1993;43:694–702.
9. **Lindström K, Young JPW**. International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of *Agrobacterium* and *Rhizobium*: minutes of the meeting, 7 September 2010, Geneva, Switzerland. *Int J Syst Evol Microbiol* 2011;61:3089–3093.
10. **Mousavi SA, Willems A, Nesme X, de Lajudie P, Lindström K**. Revised phylogeny of *Rhizobiaceae*: proposal of the delineation of *Pararhizobium* gen. nov., and 13 new species combinations. *Syst Appl Microbiol* 2015;38:84–90.
11. **Kuzmanović N, Fagorzi C, Mengoni A, Lassalle F, diCenzo GC**. Taxonomy of *Rhizobiaceae* revisited: proposal of a new framework for genus delimitation. *Int J Syst Evol Microbiol* 2022;72:005243.
12. **Mousavi SA, Österman J, Wahlberg N, Nesme X, Lavire C, *et al***. Phylogeny of the *Rhizobium-Allorhizobium-Agrobacterium* clade supports the delineation of *Neorhizobium* gen. nov. *Syst Appl Microbiol* 2014;37:208–215.
13. **Trujillo ME, Willems A, Abril A, Planchuelo A-M, Rivas R, *et al***. Nodulation of *Lupinus albus* by strains of *Ochrobactrum lupini* sp. nov. *Appl Environ Microbiol* 2005;71:1318–1327.
14. **Gazolla Volpiano C, Hayashi Sant'Anna F, Ambrosini A, Brito Lisboa B, Kayser Vargas L, *et al***. Reclassification of *Ochrobactrum lupini* as a later heterotypic synonym of *Ochrobactrum anthropi* based on whole-genome sequence analysis. *Int J Syst Evol Microbiol* 2019;69:2312–2314.
15. **Hördt A, López MG, Meier-Kolthoff JP, Schleuning M, Weinhold LM, *et al***. Analysis of 1,000+ type-strain genomes substantially improves taxonomic classification of *Alphaproteobacteria Front Microbiol* 2020;11:468.
16. **Volpiano CG, Sant'Anna FH, Ambrosini A, São José JF, Beneduzi A, *et al***. Genomic metrics applied to rrhizobiales (hhyphomicrobiales): species reclassification, identification of unauthentic genomes and false type strains. *Front Microbiol* 2021;12:614957.
17. **Tian CF, Wang ET, Wu LJ, Han TX, Chen WF, *et al***. *Rhizobium fabae* sp. nov., a bacterium that nodulates *Vicia faba*. *Int J Syst Evol Microbiol* 2008;58:2871–2875.
18. **Ramírez-Bahena MH, García-Fraile P, Peix A, Valverde A, Rivas R, *et al***. Revision of the taxonomic status of the species *Rhizobium leguminosarum* (Frank 1879) Frank 1889AL, *Rhizobium phaseoli* Dangeard 1926AL and *Rhizobium trifolii* Dangeard 1926AL. *R. trifolii* is a later synonym of *R. leguminosarum*. Reclassification of the strain *R. leguminosarum* DSM 30132 (=NCIMB 11478) as *Rhizobium pisi* sp. nov. *Int J Syst Evol Microbiol* 2008;58:2484–2490.
19. **Mnasri B, Liu TY, Saidi S, Chen WF, Chen WX, *et al***. *Rhizobium azibense* sp. nov., a nitrogen fixing bacterium isolated from root-nodules of *Phaseolus vulgaris*. *Int J Syst Evol Microbiol* 2014;64:1501–1506.
20. **Amarger N, Macheret V, Laguerre G**. *Rhizobium gallicum* sp. nov. and *Rhizobium giardinii* sp. nov., from *Phaseolus vulgaris* nodules. *Int J Syst Evol Microbiol* 1997;47:996–1006.
21. **Rahi P**. Regulating access can restrict participation in reporting new species and taxa. *Nat Microbiol* 2021;6:1469–1470.
22. **Whitman WB, Bull CT, Busse H-J, Fournier P-E, Oren A, *et al***. Request for revision of the statutes of the international committee on systematics of prokaryotes. *Int J Syst Evol Microbiol* 2019;69:584–593.
23. **Castellano-Hinojosa A, Correa-Galeote D, Ramírez-Bahena M-H, Tortosa G, González-López J, *et al***. *Agrobacterium leguminum* sp. nov., isolated from nodules of *Phaseolus vulgaris* in Spain. *Int J Syst Evol Microbiol* 2021;71:005120.
24. **Singh NK, Lavire C, Nesme J, Vial L, Nesme X, *et al***. Comparative genomics of novel *Agrobacterium* G3 strains isolated from the international space station and description of *Agrobacterium tomkonis* sp. nov. *Front Microbiol* 2021;12:3369.
25. **Gao Z, Zhang Q, Lv Y, Wang Y, Zhao B**. *Paraburkholderia acidiphila* sp. nov., *Paraburkholderia acidisoli* sp. nov. and *Burkholderia guangdongensis* sp. nov., isolated from forest soil, and reclassification of *Burkholderia ultramafica* as *Paraburkholderia ultramafica* comb. nov. *Int J Syst Evol Microbiol* 2021;71:004690.
26. **Hall CM, Baker AL, Sahl JW, Mayo M, Scholz HC, *et al***. Expanding the *Burkholderia pseudomallei* complex with the addition of two novel species: *Burkholderia mayonis* sp. nov. and *Burkholderia savannae* sp. nov. *Appl Environ Microbiol* 2021;88:e01583-21.
27. **Andrade JP, de Souza HG, Ferreira LC, Cnockaert M, De Canck E, *et al***. *Burkholderia perseverans* sp. nov., a bacterium isolated from the Restinga ecosystem, is a producer of volatile and diffusible compounds that inhibit plant pathogens. *Braz J Microbiol* 2021;52:2145–2152.
28. **Avontuur JR, Palmer M, Beukes CW, Chan WY, Tasiya T, *et al***. *Bradyrhizobium altum* sp. nov., *Bradyrhizobium oropedii* sp. nov. and *Bradyrhizobium acaciae* sp. nov. from South Africa show locally restricted and pantropical *nodA* phylogeographic patterns. *Mol Phylogenet Evol* 2022;167:107338.
29. **Klepa MS, Ferraz Helene LC, O'Hara G, Hungria M**. *Bradyrhizobium agreste* sp. nov., *Bradyrhizobium glycinis* sp. nov. and *Bradyrhizobium diversitatis* sp. nov., isolated from a biodiversity hotspot of the genus *Glycine* in Western Australia. *Int J Syst Evol Microbiol* 2021;71:004742.

30. **Bromfield ESP, Cloutier S**. *Bradyrhizobium septentrionale* sp. nov. (sv. septentrionale) and *Bradyrhizobium quebecense* sp. nov. (sv. septentrionale) associated with legumes native to Canada possess rearranged symbiosis genes and numerous insertion sequences. *Int J Syst Evol Microbiol* 2021;71:004831.
31. **Rahi P, Khairnar M, Hagir A, Narayan A, Jain KR,** ***et al***. *Peteryoungia* gen. nov. with four new species combinations and description of *Peteryoungia desertarenae* sp. nov., and taxonomic revision of the genus *Ciceribacter* based on phylogenomics of *Rhizobiaceae*. *Arch Microbiol* 2021;203:3591–3604.
32. **Deng T, Qian Y, Chen X, Yang X, Guo J,** ***et al***. *Ciceribacter ferrooxidans* sp. nov., a nitrate-reducing Fe(II)-oxidizing bacterium isolated from ferrous ion-rich sediment. *J Microbiol* 2020;58:350–356.
33. **Kweon OJ, Ruan W, Khan SA, Lim YK, Kim HR,** ***et al***. *Cupriavidus cauae* sp. nov., isolated from blood of an immunocompromised patient. *Int J Syst Evol Microbiol* 2021;71:004759.
34. **Klonowska A, Moulin L, Ardley JK, Braun F, Gollagher MM,** ***et al***. Novel heavy metal resistance gene clusters are present in the genome of *Cupriavidus neocaledonicus* STM 6070, a new species of *Mimosa pudica* microsymbiont isolated from heavy-metal-rich mining site soil. *BMC Genomics* 2020;21:1–18.
35. **Khan SA, Kim HM, Chun BH, Jeon CO**. *Devosia aurantiaca* sp. nov., isolated from mountain soil and proposal of *Albitalea* gen. nov. to replace the illegitimate prokaryotic genus name *Geomonas* Khan et al. 2020. *Curr Microbiol* 2021;78:2548–2555.
36. **Zhang Y-X, Yu Y, Luo W, Zeng Y-X, Du Z-J,** ***et al***. *Devosia beringensis* sp. nov., isolated from surface sediment of the Bering Sea. *Int J Syst Evol Microbiol* 2021;71:004995.
37. **Kämpfer P, Busse H-J, Clermont D, Criscuolo A, Glaeser SP**. *Devosia equisanguinis* sp. nov., isolated from horse blood. *Int J Syst Evol Microbiol* 2021;71:005090.
38. **Lin S-Y, Tsai C-F, Hameed A, Tang Y-S, Young C-C**. Description of *Devosia faecipullorum* sp. nov., harboring antibiotic-and toxic compound-resistace genes, isolated from poultry manure. *Int J Syst Evol Microbiol* 2021;71:004901.
39. **Chhetri G, Kim I, Kang M, Kim J, So Y,** ***et al***. *Devosia rhizoryzae* sp. nov., and *Devosia oryziradicis* sp. nov., novel plant growth promoting members of the genus *Devosia*, isolated from the rhizosphere of rice plants. *J Microbiol* 2022;60:1–10.
40. **Pedron R, Luchi E, Albiac MA, Di Cagno R, Catorci D,** ***et al***. *Mesorhizobium comanense* sp. nov., isolated from groundwater. *Int J Syst Evol Microbiol* 2021;71:005131.
41. **Jung J, Seo YL, Kim KR, Park HY, Jeon CO**. *Mesorhizobium microcysteis* sp. nov., isolated from a culture of *Microcystis aeruginosa*. *Int J Syst Evol Microbiol* 2021;71:004847.
42. **León-Barrios M, Flores-Félix J-D, Pérez-Yépez J, Ramirez-Bahena M-H, Pulido-Suárez L,** ***et al***. Definition of the novel symbiovar canariense within *Mesorhizobium neociceri* sp. nov., a new species of genus *Mesorhizobium* nodulating *Cicer canariense* in the "Caldera de Taburiente" National Park (La Palma, Canary Islands). *Syst Appl Microbiol* 2021;44:126237.
43. **Meng D, Liu Y-L, Zhang J-J, Gu P-F, Fan X-Y,** ***et al***. *Mesorhizobium xinjiangense* sp. nov., isolated from rhizosphere soil of *Alhagi sparsifolia*. *Arch Microbiol* 2021;204:1–6.
44. **Bijlani S, Singh NK, Eedara VVR, Podile AR, Mason CE,** ***et al***. *Methylobacterium ajmalii* sp. nov., isolated from the International Space Station. *Front Microbiol* 2021;12:534.
45. **Maeng S, Kim D-U, Lim S, Lee B-H, Lee K-E,** ***et al***. *Methylobacterium radiodurans* sp. nov., a novel radiation-resistant *Methylobacterium*. *Arch Microbiol* 2021;203:3435–3442.
46. **Ten LN, Li W, Elderiny NS, Kim MK, Lee S-Y,** ***et al***. *Methylobacterium segetis* sp. nov., a novel member of the family *Methylobacteriaceae* isolated from soil on Jeju Island. *Arch Microbiol* 2020;202:747–754.
47. **Oh H, Kim MK, Srinivasan S**. *Microvirga pudoricolor* sp. nov., and *Microvirga alba* sp. nov., isolated from soil in South Korea. *Arch Microbiol* 2021;203:6071–6077.
48. **Zhu L, Ping W, Zhang S, Chen Y, Zhang Y,** ***et al***. Description and genome analysis of *Microvirga antarctica* sp. nov., a novel pink-pigmented psychrotolerant bacterium isolated from Antarctic soil. *Antonie van Leeuwenhoek* 2021;114:2219–2228.
49. **Boxberger M, Ben Khedher M, Magnien S, Cassir N, La Scola B**. Draft genome and description of *Microvirga mediterraneensis* strain Marseille-Q2068T sp. nov., a new bacterium isolated from human healthy skin. *New Microbes New Infect* 2021;40:100839.
50. **Liu L, Shi S, Liang L, Xu L, Chi M,** ***et al***. *Neorhizobium lilium* sp. nov., an endophytic bacterium isolated from *Lilium pumilum* bulbs in Hebei province. *Arch Microbiol* 2020;202:609–616.
51. **Soenens A, Gomila M, Imperial J**. *Neorhizobium tomejilense* sp. nov., first non-symbiotic *Neorhizobium* species isolated from a dryland agricultural soil in southern Spain. *Syst Appl Microbiol* 2019;42:128–134.
52. **Li M, Liu Y, Liu K, Luo S, Yi X,** ***et al***. *Pararhizobium mangrovi* sp. nov., isolated from *Aegiceras corniculatum* stem. *Curr Microbiol* 2021;78:2828–2837.
53. **Rudra B, Gupta RS**. Phylogenomic and comparative genomic analyses of species of the family *Pseudomonadaceae*: proposals for the genera *Halopseudomonas* gen. nov. and *Atopomonas* gen. nov., merger of the genus *Oblitimonas* with the genus *Thiopseudomonas*, and transfer of some misclassified species of the genus *Pseudomonas* into other genera. *Int J Syst Evol Microbiol* 2021;71:005011.
54. **Dahal RH, Kim J, Chaudhary DK, Kim D-U, Kim J**. Description of antibiotic-producing novel bacteria *Paraburkholderia antibiotica* sp. nov. and *Paraburkholderia polaris* sp. nov. *Int J Syst Evol Microbiol* 2021;71:005060.
55. **Herpell JB, Vanwijnsberghe S, Peeters C, Schindler F, Fragner L,** ***et al***. Paraburkholderia dioscoreae sp. nov., a novel plant associated growth promotor. *Int J Syst Evol Microbiol* 2021;71:004969.
56. **Vanwijnsberghe S, Peeters C, De Ridder E, Dumolin C, Wieme AD,** ***et al***. Genomic aromatic compound degradation potential of novel *Paraburkholderia* species: *Paraburkholderia domus* sp. nov., *Paraburkholderia haematera* sp. nov. and *Paraburkholderia nemoris* sp. nov. *Int J Mol Sci*2021;22:7003.
57. **Paulitsch F, Dall'Agnol RF, Delamuta JRM, Ribeiro RA, da Silva Batista JS,** ***et al***. *Paraburkholderia guartelaensis* sp. nov., a nitrogen-fixing species isolated from nodules of Mimosa gymnas in an ecotone considered as a hotspot of biodiversity in Brazil. *Arch Microbiol* 2019;201:1435–1446.
58. **Feng T, Jeong SE, Lim JJ, Hyun S, Jeon CO**. *Paraburkholderia lacunae* sp. nov., isolated from soil near an artificial pond. *J Microbiol* 2019;57:232–237.
59. **Zhang J, Peng S, Andrews M, Liu C, Shang Y,** ***et al***. *Rhizobium changzhiense* sp. nov., isolated from effective nodules of *Vicia sativa* L. in North China. *Int J Syst Evol Microbiol* 2019;71:004724.
60. **Su X-J, Liu G-P, Zhang L, Zhou X-Y, Qiao W-J,** ***et al***. *Rhizobium flavescens* sp. nov., isolated from a chlorothalonil-contaminated soil. *Curr Microbiol* 2021;78:2165–2172.
61. **Thin KK, He S-W, Wang X, Wang Y, Rong M,** ***et al***. *Rhizobium rhizolycopersici* sp. nov., isolated from the rhizosphere soil of tomato plants in China. *Curr Microbiol* 2021;78:830–836.