

The names *Hungateiclostridium* Zhang *et al.* 2018, *Hungateiclostridium thermocellum* (Viljoen *et al.* 1926) Zhang *et al.* 2018, *Hungateiclostridium cellulolyticum* (Patel *et al.* 1980) Zhang *et al.* 2018, *Hungateiclostridium aldrichii* (Yang *et al.* 1990) Zhang *et al.* 2018, *Hungateiclostridium alkallicellulosi* (Zhilina *et al.* 2006) Zhang *et al.* 2018, *Hungateiclostridium clariflavum* (Shiratori *et al.* 2009) Zhang *et al.* 2018, *Hungateiclostridium straminisolvens* (Kato *et al.* 2004) Zhang *et al.* 2018 and *Hungateiclostridium saccincola* (Koeck *et al.* 2016) Zhang *et al.* 2018 contravene Rule 51b of the International Code of Nomenclature of Prokaryotes and require replacement names in the genus *Acetivibrio* Patel *et al.* 1980

B. J. Tindall*

Abstract

A recent publication has created the genus name *Hungateiclostridium* Zhang *et al.* 2018 and the new combinations *Hungateiclostridium cellulolyticum* (Patel *et al.* 1980) Zhang *et al.* 2018, *Hungateiclostridium aldrichii* (Yang *et al.* 1990.) Zhang *et al.* 2018, *Hungateiclostridium alkallicellulosi* (Zhilina *et al.* 2006) Zhang *et al.* 2018, *Hungateiclostridium clariflavum* (Shiratori *et al.* 2009) Zhang *et al.* 2018, *Hungateiclostridium straminisolvens* (Kato *et al.* 2004) Zhang *et al.* 2018 and *Hungateiclostridium saccincola* (Koeck *et al.* 2016) Zhang *et al.* 2018 for names at the rank of species that were previously either included in the genus *Clostridium* Prazmowski 1880, *Acetivibrio* Patel *et al.* 1980 or *Herbivorax* Koeck *et al.* 2016. Rules 23a, 38, 39b, 41a, 42 and 44 have not been followed and an illegitimate name at the rank of genus or illegitimate combinations at the rank of species as defined in Rule 51b(1) and (2) have been created. Another aspect is recognising the fact that an instance of heterotypic synonym has been created between *Acetivibrio* Patel *et al.* 1980, *Herbivorax* Koeck *et al.* 2016 and *Hungateiclostridium* Zhang *et al.* 2018, where the earliest validly published genus name is *Acetivibrio* Patel *et al.* 1980, of which the nomenclatural type is *Acetivibrio cellulolyticus* Patel *et al.* 1980. It follows from Rules 23a, 38, 39a, 39b, 41a, 42 and 44 that the genus name to be used is *Acetivibrio* Patel *et al.* 1980, with new combinations in that genus replacing those published in the genus *Hungateiclostridium* Zhang *et al.* 2018, which together with the genus name are illegitimate according to Rule 51b of the International Code of Nomenclature of Prokaryotes. Additional issues are also addressed with regards to the names *Pseudoclostridium thermosuccinogenes* (Drent *et al.* 1995) Zhang *et al.* 2018, *Pseudoclostridium* Zhang *et al.* 2018 *Oscillospiraceae* Peshkoff 1940 (Approved Lists 1980), *Ruminococcaceae* Rainey 2010, *Eubacteriales* Buchanan 1917 (Approved Lists 1980) and *Clostridiales* Prévot 1953 (Approved Lists 1980)

The taxonomy of the genus *Clostridium* can best be described as reflecting a classification that has been based on a small data set of largely morphological, physiological and biochemical characteristics, which at worst has been

limited to Gram-positive staining, anaerobic, spore-forming rods. Prévot [1] was critical of the taxonomy of the genus and the situation did not improve with the publication of the Approved Lists of Bacterial Names [2], or in the

Author affiliation: Leibniz-Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Inhoffenstraße 7B 38124, Braunschweig, Germany.

***Correspondence:** B. J. Tindall, bti@dsMZ.de

Keyword: *Hungateiclostridium*.

following decades. Even with the publication of the results of an extensive 16S rRNA gene based study by Collins *et al.* [3] changes have been slow to be implemented. While there appears to be general agreement that extensive rearrangements are required that would result in the transfer of many species currently placed in the genus *Clostridium* [4] to other genera, some uncertainty has been caused by proposals to formally recognise *Clostridium* Prazmowski 1880 and *Sarcina* Goodsir 1842 [5] as heterotypic synonyms and to incorrectly interpret the priority of the name *Sarcina* Goodsir 1842 as well as creating illegitimate combinations in the genus *Clostridium* based on the names *Sarcina ventriculi* Goodsir 1842 and *Sarcina maxima* Lindner 1888 [6–8]. A similar issue now arises with the creation of the names *Hungateiclostridium* Zhang *et al.* 2018, *Hungateiclostridium cellulolyticum* (Patel *et al.* 1980) Zhang *et al.* 2018, *Hungateiclostridium aldrichii* (Yang *et al.* 1990.) Zhang *et al.* 2018, *Hungateiclostridium alkalicellulosi* (Zhilina *et al.* 2006) Zhang *et al.* 2018, *Hungateiclostridium clariflavum* (Shiratori *et al.* 2009) Zhang *et al.* 2018, *Hungateiclostridium straminisolvens* (Kato *et al.* 2004) Zhang *et al.* 2018 and *Hungateiclostridium saccincola* (Koeck *et al.* 2016) Zhang *et al.* 2018 [9].

While it is clear that taxonomic revisions relating to validly published names within the genus *Clostridium* are necessary, one must also not forget that the issue is not to just consider validly published names at the rank of species, but also to consider validly published names (at least) at the rank of genus. Zhang *et al.* [9] considered that the names *Clostridium thermocellum* Viljoen *et al.* 1926 (Approved Lists 1980), *Acetivibrio cellulolyticus* Patel *et al.* 1980, *Clostridium aldrichii* Yang *et al.* 1990, *Clostridium alkalicellulosi* Zhilina *et al.* 2006, *Clostridium clariflavum* Shiratori *et al.* 2009, *Clostridium straminisolvens* Kato *et al.* 2004 and *Herbivorax saccincola* Koeck *et al.* 2016 should be included in a genus other than the genus *Clostridium* Prazmowski 1880. In making their proposals, the authors do not mention the fact that as circumscribed the proposed (novel) taxon at the rank of genus included both the nomenclatural type of *Acetivibrio* Patel *et al.* 1980, *Acetivibrio cellulolyticus* Patel *et al.* 1980 and *Herbivorax* Koeck *et al.* 2016, *Herbivorax saccincola* Koeck *et al.* 2016. This creates an instance of heterotypic synonymy between *Acetivibrio* Patel *et al.* 1980 and *Herbivorax* Koeck *et al.* 2016. The nomenclatural type of *Clostridium* Prazmowski 1880 is *Clostridium butyricum* Prazmowski 1880 that was excluded from the circumscription of Zhang *et al.* [9] and was consequently not treated as a heterotypic synonym of *Acetivibrio* Patel *et al.* 1980 and *Herbivorax* Koeck *et al.* 2016. In this instance, the International Code of Nomenclature of Prokaryotes [10] further explains the implementation of Rule 23b under Rules 38, 39a and 39b. In the case of *Acetivibrio* Patel *et al.* 1980 and *Herbivorax* Koeck *et al.* 2016, Rule 38 can be misleading because the wording relates to the ‘unification’ of genera, when in fact emphasis should be put on the role of nomenclatural types (with which a name is permanently attached and determines the application of the name – see Rules 15

and 17) and the recognition of *Acetivibrio* Patel *et al.* 1980 and *Herbivorax* Koeck *et al.* 2016 as heterotypic synonyms, where *Acetivibrio* Patel *et al.* 1980 is the oldest validly published, legitimate genus name. This is further qualified under Rules 42 and 44. The fact that a number of species currently classified as members of the genus *Clostridium* Prazmowski 1880 (Approved Lists 1980) are also considered to be members of the same genus, in this case *Acetivibrio* Patel *et al.* 1980, has no bearing on the selection of the earliest validly published, legitimate genus name or selection of the nomenclatural type of the genus because *Clostridium butyricum* Prazmowski 1880 (Approved Lists 1980), the nomenclatural type of *Clostridium* Prazmowski 1880 (Approved Lists 1980), is excluded and the transfer of the these named *Clostridium* species to another genus is also covered by Rules 41a and 41b [10]. In creating the name *Hungateiclostridium* Zhang *et al.* 2018, the authors do not mention the resulting heterotypic synonymy with *Acetivibrio* Patel *et al.* 1980 and *Herbivorax* Koeck *et al.* 2016 based on their circumscription of the genus. Rule 51b(1) clearly indicates that the creation of the name *Hungateiclostridium* Zhang *et al.* 2018 at the rank of genus that contains the nomenclatural type of *Acetivibrio* Patel *et al.* 1980 (the earliest validly published, legitimate name) creates an illegitimate name at the rank of genus which must be replaced as outlined in Rule 54 of the International Code of Nomenclature of Prokaryotes [10]. Similarly, all combinations in the genus *Hungateiclostridium* Zhang *et al.* 2018 are illegitimate as defined by Rule 51b(2) and must be replaced as outlined in Rule 54. This is the type of nomenclatural problem that Principle 1 of the International Code of Nomenclature of Prokaryotes [10] seeks to avoid.

In dealing with the replacement of names at the rank of species in the genus *Hungateiclostridium* Zhang *et al.* 2018 by the name *Acetivibrio* Patel *et al.* 1980 this also results in an emendation of *Acetivibrio* Patel *et al.* 1980, where specific reference needs to be made to names at the rank of species previously validly published in *Acetivibrio* Patel *et al.* 1980. In the case of *Acetivibrio multivorans* Tanaka *et al.* 1992, this is considered to be a homotypic synonym of *Youngiibacter multivorans* (Tanaka *et al.* 1992) Lawson *et al.* 2014 [11] that is considered here to be the correct name of the taxon. *Acetivibrio ethanoligignens* Robinson and Ritchie 1981 appears not to be a member of the genus *Acetivibrio*, but until such times as an instance of homotypic synonymy is established (ie transferred to another genus) no formal nomenclatural action is required here. *Acetivibrio cellulolyticus* Khan *et al.* 1984 is considered by Murray *et al.* [12] to be a later heterotypic synonym of *Acetivibrio cellulolyticus* Patel *et al.* 1980 and that opinion is followed here:

ACETIVIBRIO PATEL ET AL. 1980 EMEND.

Heterotypic synonym: *Herbivorax* Koeck *et al.* 2016.

Replaced, illegitimate synonym *Hungateiclostridium* Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

The nomenclatural type is *Acetivibrio cellulolyticus* Patel *et al.* 1980. As emended here the following names at the rank of species are included: *Acetivibrio cellulolyticus* Patel *et al.* 1980, *Acetivibrio aldrichii* (Yang *et al.* 1990), *Acetivibrio alkallicellulosi* (Zhilina *et al.* 2006), *Acetivibrio clariflavus* (Shiratori *et al.* 2009), *Acetivibrio ethanolignens* Robinson and Ritchie 1981, *Acetivibrio straminisolvens* (Kato *et al.* 2004), *Acetivibrio saccincola* (Koeck *et al.* 2016) and *Acetivibrio thermocellus* (Viljoen *et al.* 1926).

In the following list of names within the genus *Acetivibrio* Patel *et al.* 1980 only those names are included for which an illegitimate homotypic synonym within the genus *Hungateiclostridium* Zhang *et al.* 2018 was validly published.

ACETIVIBRIO CELLULOLYTICUS PATEL ET AL. 1980

Acetivibrio cellulolyticus (cel.lu.lo.ly'ti.cus. N.L. neut. n. *celulosum* cellulose; Greek masc. adj. *lytikos* capable of loosening, capable of dissolving; N.L. masc. adj. *cellulolyticus* cellulose-dissolving).

Heterotypic synonym: *Acetivibrio cellulosolvens* Khan *et al.* 1984.

Replaced, illegitimate synonym: *Hungateiclostridium cellulolyticum* (Patel *et al.* 1980) Zhang *et al.* 2018.

The nomenclatural type is strain CD2^T (=ATCC 33288^T =DSM 1870^T=LMG 8466^T). Since no name of a new taxon at the rank of species or a new combination has been created, no evidence is required by the International Code of Nomenclature of Prokaryotes as to the continued availability of these deposits, although it should be noted that Zhang *et al.* [9] also cite NRC 2248, despite the fact that this collection has long since closed.

ACETIVIBRIO ALDRICHII (YANG ET AL. 1990) COMB. NOV.

Acetivibrio aldrichii (al.dri'chi.i. N.L. gen. n. *aldrichii* of Aldrich, named after Henry C. Aldrich, University of Florida, Gainesville, for his work on ultrastructural research on strictly anaerobic bacteria).

Basonym: *Clostridium aldrichii* Yang *et al.* 1990.

Replaced, illegitimate synonym: *Hungateiclostridium aldrichii* (Yang *et al.* 1990) Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

Nomenclatural type for which evidence has been presented in conformity with Rule 30(3)(b): strain: P-1^T (=ATCC 49358^T=DSM 6159^T). Zhang *et al.* [9] also cite OGI (now OCM) 112, but it is impossible to tell whether this collection still exists. The original curator, D. R. Boone, passed away in 2005 and evidence of an active collection disappeared from the internet soon after.

ACETIVIBRIO ALKALICELLULOSI (ZHILINA ET AL. 2006) COMB. NOV.

Acetivibrio alkallicellulosi (al.ka.li.cel.lu.lo'si. from the Arabic article *al* the; Arabic n. *qaliy* ashes of the saltwort, soda; N.L. neut. n. *cellulosum* cellulose; N.L. gen. n. *alkalicellulosi* of alkaline cellulose, intended to mean the utilization of cellulose by the bacterium under alkaline conditions).

Basonym: *Clostridium alkallicellulosi* Zhilina *et al.* 2006.

Replaced, illegitimate synonym: *Hungateiclostridium alkallicellulosi* (Zhilina *et al.* 2006) Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

Nomenclatural type for which evidence has been presented in conformity with Rule 30(3)(b): strain Z-7026^T (=DSM 17461^T=VKM B-2349^T).

ACETIVIBRIO CLARIFLAVUS (SHIRATORI ET AL. 2009) COMB. NOV.

Acetivibrio clariflavus (cla.ri fla'vus. L. masc. adj. *clarus* clear, bright, shining, brilliant; L. masc. adj. *flavus* yellow; N. L. masc. adj. *clariflavus*, bright yellow, the colour of the colonies or pigment).

Basonym: *Clostridium clariflavum* Shiratori *et al.* 2009.

Replaced, illegitimate synonym: *Hungateiclostridium clariflavum* (Shiratori *et al.* 2009) Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

Nomenclatural type for which evidence has been presented in conformity with Rule 30(3)(b): strain EBR45^T (=DSM 19732^T=NBRC 101661^T).

ACETIVIBRIO STRAMINISOLVENS (KATO ET AL. 2004) COMB. NOV.

Acetivibrio straminisolvens (stra.mi.ni.sol'vens. L. neut. n. *stramen* straw, litter; L. v. *solvere* to dissolve; N.L. part. adj. *straminisolvens* straw-dissolving).

Basonym: *Clostridium straminisolvens* Kato *et al.* 2004.

Replaced, illegitimate synonym: *Hungateiclostridium straminisolvens* (Kato *et al.* 2004) Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

Nomenclatural type for which evidence has been presented in conformity with Rule 30(3)(b): strain CSK1^T (=DSM 16021^T=JCM 21531^T=NBRC 103399^T). Zhang *et al.* [9] also cite IAM 15070, but this collection was transferred to the JCM in 2007 and then closed. IAM 15070 was accessed to the JCM as JCM 21531.

ACETIVIBRIO SACCINCOLA (KOECK ET AL. 2016) COMB. NOV.

Acetivibrio saccincola (sacc.in'co.la. L. masc. n. *saccus* a bag; L. masc. n. *incola* an inhabitant; N.L. masc. n. *saccincola*

inhabiting a bag, pertaining to isolation of the type strain by accumulation in nylon bags).

Basonym: *Herbivorax saccincola* Koeck *et al.* 2016.

Replaced, illegitimate synonym: *Hungateiclostridium saccincola* (Koeck *et al.* 2016) Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

Nomenclatural type for which evidence has been presented in conformity with Rule 30(3)(b): strain GGR1^T (=DSM 101079^T=CECT 9155^T).

ACETIVIBRIO THERMOCELLUS (VILJOEN ET AL. 1926) COMB. NOV.

Acetivibrio thermocellus (ther.mo.cel'lus. Gr. adj. *thermos* hot; N.L. neut. n. *cellulosum* cellulose; N.L. masc. adj. *thermocellus* a thermophile that digests cellulose).

Basonym: *Clostridium thermocellum* Viljoen *et al.* 1926 (Approved Lists 1980).

Replaced, illegitimate synonym: *Hungateiclostridium thermocellum* (Viljoen *et al.* 1926) Zhang *et al.* 2018.

The description is the same as that given by Zhang *et al.* [9].

Nomenclatural type for which evidence has been presented in conformity with Rule 30(3)(b): DSM 1237^T=JCM 9322^T=LMG 10435^T=NBRC 103400^T.

The family name *Hungateiclostridiaceae* Zhang *et al.* 2018 [9] is also based on a validly published, but illegitimate name (Rule 21a) [10]. Although Rule 21a does not explicitly indicate the fate of a name at the rank of family that is based on a validly published, but illegitimate name at the rank of genus, this would appear to be contrary to the rules of the Code [10] and Rule 23 Note 5 defines such names as being illegitimate. Although illegitimate names may not be used (Rule 51a), Rule 54 does not specifically include Rule 51a under the list of reasons for replacing a name. However, one also has to take into consideration whether the recognition of a new family is justified. The family *Ruminococcaceae* Rainey 2010 [13] was primarily defined based on 'phylogenetic analysis of the 16S rRNA gene' [14] and the family *Hungateiclostridiaceae* is also primarily defined based on the fact that it is a monophyletic group (=clade) to the exclusion of members of the family *Ruminococcaceae*. Zhang *et al.* [9] define the family *Hungateiclostridiaceae* as containing the genera *Thermoclostridium*, *Hungateiclostridium* (here treated as *Acetivibrio*), *Ruminiclostridium*, *Pseudoclostridium*, *Pseudobacteroides*, *Anaerobacterium*, *Ercella*, *Fastidiosipila*, *Mageeibacillus* and *Saccharofermentans*, but the family *Ruminococcaceae* is also defined as containing the genera *Acetivibrio*, *Anaerobacterium* and *Fastidiosipila*, while the names *Pseudobacteroides*, *Ercella*, *Mageeibacillus* and *Saccharofermentans* were not included in the treatment of Rainey [14]. Strictly speaking, the definition of a new family centring on the genera *Thermoclostridium*, *Hungateiclostridium* (here treated as *Acetivibrio*), *Ruminiclostridium*,

Pseudoclostridium, *Pseudobacteroides*, *Anaerobacterium*, *Ercella*, *Fastidiosipila*, *Mageeibacillus* and *Saccharofermentans* would also require an emendation of the family *Ruminococcaceae* Rainey 2010. Zhang *et al.* [9] also include *Monoglobus pectinilyticus* in their 16S rRNA gene sequence based analysis, but not in other sequence-based comparisons perhaps because a genome sequence was not available at the time [15]. Kim *et al.* [16] include *Monoglobus pectinilyticus* in the family *Ruminococcaceae*, while the 16S rRNA gene sequence based comparisons of Zhang *et al.* [9] appear to place this organism in their new family. However, unlike many members of the family *Hungateiclostridiaceae*, this organism is pectinolytic and not cellulolytic making a definition of the family based on cellulolytic activity in addition to monophyly problematic. While taxonomy is a work in progress, Zhang *et al.* [9] do not include *Petroclostridium* in their family *Hungateiclostridiaceae* although there appears to be justification for doing so on the basis of Figs 4 and 5. *Cellulosibacter alkalithermophilus* is also excluded from the family, but is discussed by Zhang *et al.* [9] An additional problem is also the fact that although one can establish the criterion of monophyly as a prerequisite for defining a taxon (ie genus, family, etc) not all monophyletic groups are necessarily currently recognised as taxa. Figures 4 and 5 of Zhang *et al.* [9] would imply that members of the genera *Hungateiclostridium* (here treated as *Acetivibrio*), *Ruminiclostridium*, *Pseudoclostridium* and *Pseudobacteroides* form a monophyletic group to the exclusion of members of the genus *Thermoclostridium*. Similarly, as defined by Zhang *et al.* [9], the combined families *Hungateiclostridiaceae* and *Ruminococcaceae* also constitute a monophyletic group (=clade).

One solution is to refrain from placing the members of the family *Hungateiclostridiaceae* in a separate family and to include them in the family *Ruminococcaceae* and at the same time indicating that the name *Hungateiclostridiaceae* Zhang *et al.* 2018 may not be used. If other authors wish to create a separate family for the evolutionary group treated by Zhang *et al.* [9] as a separate family they may do so, but the wording of the International Code of Nomenclature of Prokaryotes strongly implies that a new name at the rank of family would have to be created [10]. As defined by Rainey [14] the family *Ruminococcaceae* Rainey 2010 includes the genus *Oscillospira* Chatton and Pérard 1913 (Approved Lists 1980), based on its nomenclatural type *Oscillospira guilliermondii* Chatton and Pérard 1913 (Approved Lists 1980). *Oscillospira* Chatton and Pérard 1913 is the nomenclatural type of *Oscillospiraceae* Peshkoff 1940 (Approved Lists 1980). As long as *Oscillospira* Chatton and Pérard 1913 (Approved Lists 1980) is included in the same family as *Ruminococcus* Sijpesteijn 1948, then the family name that has priority is *Oscillospiraceae* Peshkoff 1940 (Approved Lists 1980), also making *Ruminococcaceae* Rainey 2010 an illegitimate name that may not be used and must be replaced (Rules 51a, 51b and 54) [10]. Consequently, it would be appropriate to provide an emendation of *Oscillospiraceae* Peshkoff 1940 (Approved Lists 1980). The status of the name *Ruminococcaceae* Rainey 2010 should also be

recorded in the Notification Lists published in the *International Journal of Systematic and Evolutionary Microbiology*.

EMENDATION OF THE FAMILY *OSCILLOSPIRACEAE* PESHKOFF 1940 (APPROVED LISTS 1980)

Illegitimate synonym: *Ruminococcaceae* Rainey 2010

The properties of the order are those given by Rainey [14] under the family name *Ruminococcaceae* Rainey 2010, which is an illegitimate name, may not be used and is here replaced by the earlier, validly published name *Oscillospiraceae* Peshkoff 1940 (Approved Lists 1980).

The order contains the genera *Acetanaerobacterium*, *Anaerobacterium*, *Acetivibrio*, *Acutalibacter*, *Anaerofilum*, *Anaerotruncus*, *Cellulosibacter*, *Ercella*, *Ethanoligenens*, *Faecalibacterium*, *Fournierella*, *Fastidiosipila*, *Harryflintia*, *Hydrogenoanaerobacterium*, *Mageeibacillus*, *Oscillibacter*, *Oscillospira*, *Paludicola*, *Papillibacter*, *Petroclostridium*, *Pseudobacteroides*, *Ruminococcus*, *Ruthenibacterium*, *Sacharofermentans*, *Sporobacter*, *Subdoligranulum* and *Thermoclostridium*.

In dealing with these taxonomic issues it should also be noted that the nomenclatural type of *Pseudoclostridium thermosuccinogenes* (Drent *et al.* 1995) Zhang *et al.* 2018 [9] is deposited in a single culture collection as DSM 5807. Although this would have been acceptable practice at the time, the basonym *Clostridium thermosuccinogenes* Drent *et al.* 1995 was validly published and in the case of new combinations Rules 27 and 30(3)(b) of the International Code of Nomenclature of Prokaryotes [10] now require the deposit of nomenclatural types in at least two different collections in two different countries as a prerequisite for valid publication of the name. Consequently, the name *Pseudoclostridium thermosuccinogenes* (Drent *et al.* 1995) Zhang *et al.* 2018 is not validly published and has no status under the Code. If the name *Pseudoclostridium thermosuccinogenes* (Drent *et al.* 1995) Zhang *et al.* 2018 is not validly published and has no status under the Code then it also cannot serve as the nomenclatural type of *Pseudoclostridium* Zhang *et al.* 2018. In the absence of a nomenclatural type that must be designated as a prerequisite for valid publication of a name under Rules 16, 27(3) and 29, the name *Pseudoclostridium* Zhang *et al.* 2018 is also not validly published. This information should also be formally recorded in the Notification Lists published in the *International Journal of Systematic and Evolutionary Microbiology*. The problem may be solved by depositing the nomenclatural type of *Pseudoclostridium thermosuccinogenes* (Drent *et al.* 1995) Zhang *et al.* 2018 in (at least) a second culture collection and formally recording this in the pages of the *International Journal of Systematic and Evolutionary Microbiology*, but this is beyond the scope of the present manuscript.

PSEUDOCLOSTRIDIUM THERMOSUCCINOGENES (DRENT *ET AL.* 1995) ZHANG *ET AL.* 2018 IS NOT VALIDLY PUBLISHED

The nomenclatural type of this name is deposited in only one culture collection not at least two as required by Rule 30 3(b), which is a pre-requisite for valid publication of the new combination.

PSEUDOCLOSTRIDIUM ZHANG *ET AL.* 2018 IS NOT VALIDLY PUBLISHED.

The nomenclatural type, *Pseudoclostridium thermosuccinogenes* (Drent *et al.* 1995) Zhang *et al.* 2018 is not validly published and has no status under the Code.

A knock-on effect of the original work of Zhang *et al.* [9] is that in creating a new family with an existing order it would have also been appropriate to emend the order that contained the new family. In their discussion, Zhang *et al.* [9] mention the order *Clostridiales* Prévot 1953 (Approved Lists 1980), although a clear definition of the families contained within that order is not included. Indirectly, Fig. 5 appears to imply that both *Clostridium butyricum* Prazmowski 1880 (Approved Lists 1980), the nomenclatural type of the *Clostridium* Prazmowski 1880 (Approved Lists 1980), and *Eubacterium limnosum* (Eggerth 1935) Prévot 1938 (Approved Lists 1980), the nomenclatural type of *Eubacterium* Prévot 1938 (Approved Lists 1980), are both included in the order *Clostridiales* Prévot 1953 (Approved Lists 1980), of which *Clostridium* Prazmowski 1880 (Approved Lists 1980) is the nomenclatural type. This is, however, problematic because *Eubacterium* Prévot 1938 (Approved Lists 1980) is the nomenclatural type of the order *Eubacteriales* Buchanan 1917 (Approved Lists 1980) and in this case *Eubacteriales* Buchanan 1917 (Approved Lists 1980) has priority over the order name *Clostridiales* Prévot 1953 (Approved Lists 1980). Although Ludwig *et al.* [17] indicate that the use of the order name *Clostridiales* Prévot 1953 (Approved Lists 1980) rather than *Eubacteriales* Buchanan 1917 (Approved Lists 1980) is based on the fact that the genus name *Clostridium* Prazmowski 1880 (Approved Lists 1980) has priority over *Eubacterium* Prévot 1938 (Approved Lists 1980), there appears to be no support for this interpretation in the International Code of Nomenclature of Prokaryotes [10]. Here, an emendation of the order *Eubacteriales* Buchanan 1917 (Approved Lists 1980) would be appropriate when a new family name is created or changes are made to the included families. If the orders *Clostridiales* Prévot 1953 (Approved Lists 1980) and *Eubacteriales* Buchanan 1917 (Approved Lists 1980) were to be treated as distinct taxa then the obvious conclusion would be that the evolutionary group centring on the family *Ruminococcaceae* Rainey 2010 [here treated as the family *Oscillospiraceae* Peshkoff 1940 (Approved Lists 1980)] would have to be transferred to a novel order. In such cases paying attention to the small print in the implementation of the International Code of Prokaryotic Nomenclature [10] can have wide-ranging effects on the way taxa are assigned to the hierarchical

system and the resulting nomenclature and taxonomy. Again it would also be appropriate to indicate in the Notification Lists of the *International Journal of Systematic and Evolutionary Microbiology* that *Eubacteriales* Buchanan 1917 (Approved Lists 1980) and *Clostridiales* Prévot 1953 (Approved Lists 1980) are here treated as synonyms.

EMENDATION OF THE ORDER *EUBACTERIALES* BUCHANAN 1917 (APPROVED LISTS 1980)

Synonym: *Clostridiales* Prévot 1953 (Approved Lists 1980).

The order contains the families *Caldicoprobacteraceae*, *Christensenellaceae*, *Clostridiaceae*, *DeFluviitaleaceae*, *Eubacteriaceae*, *Gracilibacteraceae*, *Heliobacteriaceae*, *Lachnospiraceae*, *Oscillospiraceae*, *Peptococcaceae*, *Peptostreptococcaceae* and *Syntrophomonadaceae*.

Funding information

The author received no specific grant from any funding agency to carry out this work.

Conflict of interest

The author is employed by an organisation that commercially offers both taxonomic services as well as biological material to the scientific community. This may be perceived as a potential conflict of interest.

References

1. Prévot AR. Études de systématique bactérienne. IV Critique de la conception actuelle du genre *Clostridium*. *Ann Inst Pasteur* 1938; 61:72–91.
2. Skerman VBD, McGowan V, Sneath PHA. Approved lists of bacterial names. *Int J Syst Bacteriol* 1980;30:225–420.
3. Collins MD, Lawson PA, Willems A, Cordoba JJ, Fernandez-Garayzabal J *et al*. The phylogeny of the genus *Clostridium*: proposal of five new genera and eleven new species combinations. *Int J Syst Bacteriol* 1994;44:812–826.
4. Cruz-Morales P, Orellana CA, Moutafis G, Moonen G, Rincon G *et al*. Revisiting the evolution and taxonomy of *Clostridia* a phylogenomic update. *Gen Biol Evol* 2019;11:2035–2044.
5. Lawson PA, Rainey FA. Proposal to restrict the genus *Clostridium* Prazmowski to *Clostridium butyricum* and related species. *Int J Syst Evol Microbiol* 2016;66:1009–1016.
6. Tindall BJ. Priority of the genus name *Clostridium* Prazmowski 1880 (Approved Lists 1980) vs *Sarcina* Goodsir 1842 (Approved Lists 1980) and the creation of the illegitimate combinations *Clostridium maximum* (Lindner 1888) Lawson and Rainey 2016 and *Clostridium ventriculi* (Goodsir 1842) Lawson and Rainey 2016 that may not be used. *Int J Syst Evol Microbiol* 2016;66.
7. Bernard K, Burdz T, Wiebe D, Alfa M, Bernier A-M. *Clostridium neonatale* sp. nov. linked to necrotizing enterocolitis in neonates and a clarification of species assignable to the genus *Clostridium* (Prazmowski 1880) emend. Lawson and Rainey 2016. *Int J Syst Evol Microbiol* 2018;68:2416–2423.
8. Bortolotti P, Kipnis E, Faure E, Faure K, Wacrenier A *et al*. *Clostridium ventriculi* bacteremia following acute colonic pseudo-obstruction: a case report. *Anaerobe* 2019;59:32–34.
9. Zhang X, Tu B, Dai L-Rong, Lawson PA, Zheng Z-Zhen *et al*. *Petroclostridium xylanilyticum* gen. nov., sp. nov., a xylan-degrading bacterium isolated from an oilfield, and reclassification of clostridial cluster III members into four novel genera in a new *Hungateclostridiaceae* fam. nov. *Int J Syst Evol Microbiol* 2018;68:3197–3211.
10. Parker CT, Tindall BJ, Garrity GM. International code of nomenclature of prokaryotes (2008 revision). *Int J Syst Evol Microbiol* 2019; 69:S1–111.
11. Lawson PA, Wawrik B, Allen TD, Johnson CN, Marks CR *et al*. *Youngiibacter fragilis* gen. nov., sp. nov., isolated from natural gas production-water and reclassification of *Acetivibrio multivorans* as *Youngiibacter multivorans* comb. nov. *Int J Syst Evol Microbiol* 2014;64:198–205.
12. Murray WD. *Acetivibrio cellulosolvens* is a synonym for *Acetivibrio cellulolyticus*: emendation of the genus *Acetivibrio*. *Int J Syst Bacteriol* 1986;36:314–316.
13. Rainey FA. Family Ruminococcaceae. Validation List no. 132. *Int J Syst Evol Microbiol* 2010;60:469–472.
14. Rainey FA. Family VIII. *Ruminococcaceae*. In: De Vos P, Garrity GM, Jones D, Krieg NR, Ludwig W *et al*. (editors). *Bergey's Manual of Systematic Bacteriology The Firmicutes*, 2nd ed, vol. 3. New York: Springer; 2009. pp. 1016.
15. Kim CC, Healey GR, Kelly WJ, Patchett ML, Jordens Z *et al*. Genomic insights from *Monoglobus pectinilyticus*: a pectin-degrading specialist bacterium in the human colon. *Isme J* 2019;13:1437–1456.
16. Kim CC, Kelly WJ, Patchett ML, Tannock GW, Jordens Z *et al*. *Monoglobus pectinilyticus* gen. nov., sp. nov., a pectinolytic bacterium isolated from human faeces. *Int J Syst Evol Microbiol* 2017; 67:4992–4998.
17. Ludwig W, Schleifer KH, Whitman WB. Revised road map to the phylum firmicutes. In: De Vos P, Garrity GM, Jones D, Krieg NR, Ludwig W *et al*. *Bergey's Manual of Systematic Bacteriology The Firmicutes*, 2nd ed, vol. 3. New York: Springer; 2009. pp. 1–13.

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

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

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