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Recommended rejection of the names *Malacoplasma* gen. nov., *Mesomycoplasma* gen. 1 nov., *Metamycoplasma* gen. nov., *Metamycoplasmataceae* fam. nov., *Mycoplasmoidaceae* fam. 2 nov., *Mycoplasmoidales* ord. nov., *Mycoplasmoides* gen. nov., *Mycoplasmopsis* gen. nov. 3 [Gupta, Sawnani,

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Title: Recommended rejection of the names *Malacoplasma* gen. nov., *Mesomycoplasma* gen. nov., *Metamycoplasma* gen. nov., *Metamycoplasmataceae* fam. nov., *Mycoplasmoidaceae* fam. nov., *Mycoplasmoidales* ord. nov., *Mycoplasmoides* gen. nov., *Mycoplasmaopsis* gen. nov. [Gupta, Sawnani, Adeolu, Alnajar and Oren 2018] and all proposed species comb. nov. placed therein. Request for an Opinion.

Author names: Mitchell Balish,¹ Assunta Bertaccini,² Alain Blanchard,³ Daniel Brown,⁴ Glenn Browning,⁵ Victoria Chalker,⁶ Joachim Frey,⁷ Gail Gasparich,⁸ Ludwig Hoelzle,⁹ Tom Knight, Jr.,¹⁰ Christine Knox,¹¹ Chih-Horng Kuo,¹² Lucia Manso-Silván,¹³ Meghan May,¹⁴ J. Dennis Pollack,¹⁵ Ana S. Ramírez,¹⁶ Joachim Spargser,¹⁷ David Taylor-Robinson,¹⁸ Dmitriy Volokhov,¹⁹ Yan Zhao²⁰

¹ Miami University, Oxford, Ohio, USA; ² *Alma Mater Studiorum* - Università di Bologna, Bologna, Italy; ³ Université de Bordeaux, Bordeaux, France; ⁴ University of Florida, Gainesville, Florida, USA; ⁵ University of Melbourne, Melbourne, Australia; ⁶ Public Health England, London, England, UK; ⁷ Universität Bern, Bern, Switzerland; ⁸ Salem State University, Salem, Massachusetts, USA; ⁹ Universität Hohenheim, Stuttgart, Germany; ¹⁰ Ginkgo Bioworks Inc., Boston, Massachusetts, USA; ¹¹ Queensland University of Technology, Brisbane, Australia; ¹² Academia Sinica, Taipei, Taiwan; ¹³ UMR ASTRE, Montpellier, France; ¹⁴ University of New England, Biddeford, Maine, USA; ¹⁵ The Ohio State University, Columbus, Ohio, USA; ¹⁶ Universidad de Las Palmas de Gran Canaria, Spain; ¹⁷ Veterinärmedizinische Universität Wien, Vienna, Austria; ¹⁸ Imperial College London, London, England, UK; ¹⁹ US FDA, Silver Spring, Maryland, USA; ²⁰ USDA-ARS, Beltsville, Maryland, USA

Correspondence: Daniel R. Brown (drbrown@ufl.edu)

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28

29 **Abstract:** The consensus of the members of the International Committee on Systematics of
30 Prokaryotes' Subcommittee on the taxonomy of *Mollicutes* is that recently proposed sweeping
31 changes to nomenclature of members of the *Mycoplasmatales*, specifically involving
32 introduction of the names *Malacoplasma* gen. nov., *Mesomycoplasma* gen. nov.,
33 *Metamycoplasma* gen. nov., *Metamycoplasmataceae* fam. nov., *Mycoplasmoidaceae* fam. nov.,
34 *Mycoplasmoidales* ord. nov., *Mycoplasmoides* gen. nov., *Mycoplasmopsis* gen. nov., and all
35 proposed species or subspecies comb. nov. placed therein, should be rejected because they
36 violate one or more essential points of the International Code of Nomenclature of Prokaryotes.
37

Since its inception, the International Code of Nomenclature of Prokaryotes ("the Code") [1] has emphasized the importance of type material as a reference to be used when considering the identity of specimens. Nomenclatural types permanently bear the name of the taxon. The names that are to be used must conform to the Code's rules regarding valid publication, legitimacy, and priority of publication to ensure that each taxon bears only one correct name [Code Principle 8, "Each order or taxon of a lower rank with a given circumscription, position, and rank can bear only one correct name, i.e., the earliest that is in accordance with the Rules of this Code."] The correct name also requires a given circumscription, which is an indication of the limits of the taxon [Code Principle 8, *Note 2 (i)*, "By circumscription is meant an indication of the limits of a taxon..."]. Such circumscription is reasonably expected to reflect the phenotypic potential and ecology of the strains in the taxon [2,3].

Competing systems of nomenclature are not new for genus *Mycoplasma* and related members of the orders *Mycoplasmatales* and *Entomoplasmatales* [4]. The determinative characteristics used over the past century to circumscribe about 200 of those species lead to significant paraphyly and polyphyly in later 16S rRNA gene sequence-based systematics [5]. The most striking example is the situation of *Mycoplasma mycoides* subsp. *mycoides* strain PG-1^T, the nomenclatural type of genus *Mycoplasma*, hence family *Mycoplasmataceae*, order *Mycoplasmatales*, and class *Mollicutes*. In a 16S rRNA gene sequence-based framework, *M. mycoides* subsp. *mycoides* and a few closely related *Mycoplasma* species and subspecies constituting the "mycoides cluster" sit amid other genera correctly placed in family *Entomoplasmataceae* of order *Entomoplasmatales*. The historical basis for this anomaly is well-understood but it has been impractical to resolve [4,5]. Most recently, Gupta et al. [6,7] attempted to address it through retrospective searches for signature core genomic indels, signature amino acid sequences, or concatenated amino acid sequences of selected members of the class *Mollicutes* that might justify the sweeping nomenclatural revisions necessary to

attain comprehensive monophyly within these orders. Eight of the new names proposed subsequently appeared on Validation Lists in IJSEM [8,9] and so became subject to Request for an Opinion.

The International Committee on Systematics of Prokaryotes' (ICSP) Subcommittee on the taxonomy of *Mollicutes* reviewed the work of Gupta et al. [6] during its 2018 meeting [10]. The core genome sequence-based taxonomic framework was viewed as being entirely consistent with the existing polyphasic taxonomy of *Mollicutes* and a significant vindication of many decades of work by mycoplasmologists. It showed how a whole genome-based taxonomy of *Mollicutes* may be achievable eventually if the approach can be independently replicated and refined to accommodate multiple genomes per species, additional taxa, and the well-recognized critical role that horizontal gene transfer has played in the evolution of many members of the class. However, the consensus opinion of the Subcommittee members is that the proposed nomenclatural revisions [6,7] are at the present time an unnecessary over-reach verging on taxonomic vandalism. It is highly doubtful the nomenclature proposed will ever be adopted, either on practical grounds involving the names of major pathogens currently regulated in medicine and agriculture by international laws, or by the community of specialists based on one or more of the following eight essential points in nomenclature as emphasized in the Code.

Aim at stability of names. The Preface ("While the Code regulates nomenclature, one of its main goals is to maintain stability in names...") and the primary essential point of the Code's very first Principle ("Aim at stability of names.") both stress the great importance of preserving validly established names. Gupta et al. [6,7] rename about 40 extant species in various genera and introduce 11 new taxa to accommodate them throughout various levels in the hierarchy of *Mollicutes*. Because the original names would retain standing in nomenclature such that either name could be used [6], the changes would destabilize the nomenclature for microbiologists and regulatory agencies who actually use these names to refer to living organisms for practical

purposes. This retreat toward the past, when some species of *Mycoplasma* had as many as five different names [5], can be expected to further isolate theoretical systematists from applied microbiologists. In addition, because the proposed scheme of nomenclature depends in part on genomic differences as minor as a single indel, and only a single genome sequence was analyzed for each of these rapidly-evolving species, frequent nomenclatural amendments may be necessary to maintain monophyly as has already been experienced by Gupta et al. [7].

Avoid or reject the use of names which may cause error or confusion. The next essential point of the Code's first Principle is, "Avoid or reject the use of names which may cause error or confusion." Further, in Chapter 3 the Code's Rule 56a(5) states, "A name may be placed on [the list of rejected names (*nomina rejicienda*)] for various reasons, including the following... A **perilous name** (*nomen periculosum*), i.e. a name whose application is likely to lead to accidents endangering health or life or both or of serious economic consequences." Many of the proposed comb. nov. names [6] refer to species that are very important in medicine or agriculture. Examples include *Mycoplasma* ("*Mycoplasmoides*") *genitalium*, *Mycoplasma* ("*Metamycoplasma*") *hominis*, *Mycoplasma* ("*Mycoplasmoides*") *pneumoniae*, *Mycoplasma* ("*Mycoplasmopsis*") *agalactiae*, *Mycoplasma* ("*Mycoplasmopsis*") *bovis*, *Mycoplasma* ("*Mycoplasmoides*") *gallisepticum*, *Mycoplasma* ("*Mesomycoplasma*") *hyopneumoniae*, and *Mycoplasma* ("*Mycoplasmopsis*") *synoviae*. Avian and bovine mycoplasmosis are World Organisation for Animal Health (Office International des Epizooties; "OIE")-listed notifiable diseases (<http://www.oie.int/animal-health-in-the-world/oie-listed-diseases-2019/>) and are also notifiable in many states in the US. The risk of confusion between *Mycoplasma*, *Mesomycoplasma*, *Metamycoplasma*, *Mycoplasmopsis*, and *Malacoplasma* seems very high. Medical errors and confusion with respect to diagnosis, treatment, and prevention and control of diseases that endanger life or health of humans and animals, and to the application of international laws that govern transportation, import/export, and quarantine of microorganisms or infected individuals, with potential serious economic consequences, are highly likely to result

from attempts to replace the well-established and universally recognized name *Mycoplasma*.
Mesomycoplasma, *Metamycoplasma*, *Mycoplasma*opsis, and *Malacoplasma* are *nomina*
periculosa that will detract from understanding also by the non-scientific public.

Avoid the useless creation of names. According to Principle 1 of the Code it is also
essential to "Avoid the useless creation of names." The proposed names [6] provide no benefit
to the large majority of basic and applied microbiologists or regulatory agencies who are most
concerned with the phenotypic potential or ecology of the strains. Only the smallest minority of
specialists, cladists who pursue monophyly in all things, may have use for them. On balance,
this contravenes Principle 1.

The purpose of giving a name to a taxon is not to indicate the history of the taxon.
According to Principle 4 of the Code, "The primary purpose of giving a name to a taxon is to
supply a means of referring to it rather than to indicate the characters or the history of the
taxon." The principal goal of the nomenclatural revisions proposed [6,7] was to attain
comprehensive monophyly within the *Mycoplasmatales* and *Entomoplasmatales*. To achieve
this, numerous comb. nov. were created with no purpose other than to signify a presumed
history of descent from a common ancestor. This contravenes Principle 4.

The name of a taxon should not be changed without sufficient reason. Principle 9 of the
Code states, "The name of a taxon should not be changed without sufficient reason based
either on further taxonomic studies or on the necessity of giving up a nomenclature that is
contrary to the Rules of this Code." Nothing about the extant nomenclature is contrary to the
Code. The Subcommittee does not dispute that the nomenclatural changes proposed are based
on new studies, but the majority of members are united in judgment that the findings are clearly
not sufficient to justify those changes for any other than cladistic purposes, which are far
outweighed by more important practical reasons to avoid nomenclatural destabilization and the
risk of errors and confusion that the new names introduce. On balance, this contravenes
Principle 9.

Avoid names that are very long or difficult to pronounce. The primary advice of Chapter 3, Recommendation 6 of the Code is, "Avoid names or epithets that are very long or difficult to pronounce." *Metamycoplasmataceae* and *Mycoplasmoidaceae* are long names and awkward to pronounce.

A name is not validly published if it was proposed in anticipation of the future acceptance of a particular circumscription. The Code's Rule 28b states, "A name or epithet is not validly published in the following circumstances... (2) It was merely proposed in anticipation of the future acceptance of the taxon concerned or the acceptance of a particular circumscription, position, or rank for the taxon which is being named or in anticipation of the future discovery of some hypothetical taxon." Despite their presence on Validation Lists [8,9] serious doubt remains among the community of specialists represented by the Subcommittee regarding acceptability of the circumscriptions given by Gupta et al. [6,7]. As stated above, the analyses remain to be independently replicated, and there is serious concern that frequent nomenclatural amendments may be necessary as the approach to circumscription is refined to include multiple genomes within species, additional taxa, etc.

A change in the name of a taxon is not warranted by an alteration of the diagnostic characters or of the circumscription. The renaming proposed [6,7] is based entirely on selected diagnostic characters of the genomes (indels, coding sequences, etc.) that are used to alter the extant circumscriptions. This plainly contravenes Rule 37b of the Code, "A change in the name of a taxon is not warranted by an alteration of the diagnostic characters or of the circumscription."

For these reasons, as anticipated only to a limited extent by Gupta et al. ("...the possibility exists that in the future Requests for an Opinion will be submitted to the Judicial Commission of the International Committee on Systematics of Prokaryotes, proposing to place some of the new names on the list of *nomina rejicienda*..." [6]) the Subcommittee on taxonomy of *Mollicutes*

respectfully recommends that the Judicial Commission of the ICSP should promptly issue an Opinion rejecting the proposed names *Malacoplasma* gen. nov., *Mesomycoplasma* gen. nov., *Metamycoplasma* gen. nov., *Metamycoplasmataceae* fam. nov., *Mycoplasmoidaceae* fam. nov., *Mycoplasmoidales* ord. nov., *Mycoplasmoides* gen. nov., *Mycoplasmaopsis* gen. nov., and all proposed species or subspecies comb. nov. included therein [6,7]. Failure to do so can be expected to exacerbate the divide between systematists and applied microbiologists, and the larger community's general disinterest in adherence to the Code.

Author Statements

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