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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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1 **Title:** Recommended rejection of the names *Malacoplasma* gen. nov., *Mesomycoplasma* gen.

2 nov., Metamycoplasma gen. nov., Metamycoplasmataceae fam. nov., Mycoplasmoidaceae fam.

3 nov., *Mycoplasmoidales* ord. nov., *Mycoplasmoides* gen. nov., *Mycoplasmopsis* gen. nov.

4 [Gupta, Sawnani, Adeolu, Alnajar and Oren 2018] and all proposed species comb. nov. placed

- 5 therein. Request for an Opinion.
- 6

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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

38 Since its inception, the International Code of Nomenclature of Prokaryotes ("the Code") [1] has 39 emphasized the importance of type material as a reference to be used when considering the 40 identity of specimens. Nomenclatural types permanently bear the name of the taxon. The 41 names that are to be used must conform to the Code's rules regarding valid publication, 42 legitimacy, and priority of publication to ensure that each taxon bears only one correct name 43 [Code Principle 8, "Each order or taxon of a lower rank with a given circumscription, position, 44 and rank can bear only one correct name, i.e., the earliest that is in accordance with the Rules 45 of this Code."] The correct name also requires a given circumscription, which is an indication of 46 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 47 48 potential and ecology of the strains in the taxon [2,3].

49

50 Competing systems of nomenclature are not new for genus *Mycoplasma* and related members 51 of the orders Mycoplasmatales and Entomoplasmatales [4]. The determinative characteristics 52 used over the past century to circumscribe about 200 of those species lead to significant 53 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 54 55 nomenclatural type of genus Mycoplasma, hence family Mycoplasmataceae, order 56 Mycoplasmatales, and class Mollicutes. In a 16S rRNA gene sequence-based framework, M. 57 mycoides subsp. mycoides and a few closely related Mycoplasma species and subspecies 58 constituting the "mycoides cluster" sit amid other genera correctly placed in family 59 Entomoplasmataceae of order Entomoplasmatales. The historical basis for this anomaly is well-60 understood but it has been impractical to resolve [4,5]. Most recently, Gupta et al. [6,7] 61 attempted to address it through retrospective searches for signature core genomic indels, 62 signature amino acid sequences, or concatenated amino acid sequences of selected members 63 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.

67

68 The International Committee on Systematics of Prokaryotes' (ICSP) Subcommittee on the 69 taxonomy of *Mollicutes* reviewed the work of Gupta et al. [6] during its 2018 meeting [10]. The 70 core genome sequence-based taxonomic framework was viewed as being entirely consistent 71 with the existing polyphasic taxonomy of *Mollicutes* and a significant vindication of many 72 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 73 74 refined to accommodate multiple genomes per species, additional taxa, and the well-recognized 75 critical role that horizontal gene transfer has played in the evolution of many members of the 76 class. However, the consensus opinion of the Subcommittee members is that the proposed 77 nomenclatural revisions [6,7] are at the present time an unnecessary over-reach verging on 78 taxonomic vandalism. It is highly doubtful the nomenclature proposed will ever be adopted, 79 either on practical grounds involving the names of major pathogens currently regulated in 80 medicine and agriculture by international laws, or by the community of specialists based on one 81 or more of the following eight essential points in nomenclature as emphasized in the Code.

82 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 83 84 very first Principle ("Aim at stability of names.") both stress the great importance of preserving 85 validly established names. Gupta et al. [6,7] rename about 40 extant species in various genera 86 and introduce 11 new taxa to accommodate them throughout various levels in the hierarchy of 87 Mollicutes. Because the original names would retain standing in nomenclature such that either 88 name could be used [6], the changes would destabilize the nomenclature for microbiologists 89 and regulatory agencies who actually use these names to refer to living organisms for practical

90 purposes. This retreat toward the past, when some species of *Mycoplasma* had as many as five 91 different names [5], can be expected to further isolate theoretical systematists from applied 92 microbiologists. In addition, because the proposed scheme of nomenclature depends in part on 93 genomic differences as minor as a single indel, and only a single genome sequence was 94 analyzed for each of these rapidly-evolving species, frequent nomenclatural amendments may 95 be necessary to maintain monophyly as has already been experienced by Gupta et al. [7].

96 Avoid or reject the use of names which may cause error or confusion. The next essential 97 point of the Code's first Principle is, "Avoid or reject the use of names which may cause error or 98 confusion." Further, in Chapter 3 the Code's Rule 56a(5) states, "A name may be placed on [the 99 list of rejected names (nomina rejicienda)] for various reasons, including the following... A 100 perilous name (nomen periculosum), i.e. a name whose application is likely to lead to 101 accidents endangering health or life or both or of serious economic consequences." Many of the 102 proposed comb. nov. names [6] refer to species that are very important in medicine or 103 agriculture. Examples include Mycoplasma ("Mycoplasmoides") genitalium, Mycoplasma 104 ("Metamycoplasma") hominis, Mycoplasma ("Mycoplasmoides") pneumoniae, Mycoplasma 105 ("Mycoplasmopsis") agalactiae, Mycoplasma ("Mycoplasmopsis") bovis, Mycoplasma 106 ("Mycoplasmoides") gallisepticum, Mycoplasma ("Mesomycoplasma") hyopneumoniae, and 107 Mycoplasma ("Mycoplasmopsis") synoviae. Avian and bovine mycoplasmosis are World 108 Organisation for Animal Health (Office International des Epizooties; "OIE")-listed notifiable 109 diseases (http://www.oie.int/animal-health-in-the-world/oie-listed-diseases-2019/) and are also 110 notifiable in many states in the US. The risk of confusion between *Mycoplasma*, 111 Mesomycoplasma, Metamycoplasma, Mycoplasmopsis, and Malacoplasma seems very high. 112 Medical errors and confusion with respect to diagnosis, treatment, and prevention and control of 113 diseases that endanger life or health of humans and animals, and to the application of 114 international laws that govern transportation, import/export, and guarantine of microorganisms 115 or infected individuals, with potential serious economic consequences, are highly likely to result

116 from attempts to replace the well-established and universally recognized name *Mycoplasma*.

117 Mesomycoplasma, Metamycoplasma, Mycoplasmopsis, and Malacoplasma are nomina

118 *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.

<u>The purpose of giving a name to a taxon is not to indicate the history of the taxon.</u> 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.

132 The name of a taxon should not be changed without sufficient reason. Principle 9 of the 133 Code states, "The name of a taxon should not be changed without sufficient reason based 134 either on further taxonomic studies or on the necessity of giving up a nomenclature that is 135 contrary to the Rules of this Code." Nothing about the extant nomenclature is contrary to the 136 Code. The Subcommittee does not dispute that the nomenclatural changes proposed are based 137 on new studies, but the majority of members are united in judgment that the findings are clearly 138 not sufficient to justify those changes for any other than cladistic purposes, which are far 139 outweighed by more important practical reasons to avoid nomenclatural destabilization and the 140 risk of errors and confusion that the new names introduce. On balance, this contravenes 141 Principle 9.

<u>Avoid names that are very long or difficult to pronounce.</u> 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.

146 A name is not validly published if it was proposed in anticipation of the future acceptance 147 of a particular circumscription. The Code's Rule 28b states, "A name or epithet is not validly 148 published in the following circumstances... (2) It was merely proposed in anticipation of the 149 future acceptance of the taxon concerned or the acceptance of a particular circumscription, 150 position, or rank for the taxon which is being named or in anticipation of the future discovery of 151 some hypothetical taxon." Despite their presence on Validation Lists [8,9] serious doubt remains 152 among the community of specialists represented by the Subcommittee regarding acceptability of 153 the circumscriptions given by Gupta et al. [6,7]. As stated above, the analyses remain to be 154 independently replicated, and there is serious concern that frequent nomenclatural amendments 155 may be necessary as the approach to circumscription is refined to include multiple genomes 156 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

162 circumscription."

163

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*

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

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