Bacterial Taxonomy: The BIG Debate

Erik Munson
Marquette University
Wisconsin Clinical Laboratory Network
Laboratory Technical Advisory Group

The presenter states no conflict of interest and has no financial relationship to disclose relevant to the content of this presentation.

Erik Munson, faculty for this educational event, has received honoraria and travel assistance from Hologic, Incorporated. All of the relevant financial relationships have been mitigated.

OBJECTIVES

- Describe means by which microbial taxonomic updates are officially accepted in the scientific community and how these updates are communicated
- Explain the impact of taxonomic updates on clinical microbiology and affiliated healthcare disciplines
- Discuss controversies/conundrums associated with the implementation of taxonomic updates by the clinical microbiology laboratory

Someone a lot smarter than I am

AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology®

BIOGRAPHICAL FEATURE

Biographical Feature: Franklin P. Koontz, Ph.D., D(ABMM), F(AAM)

"When we're doing these identifications by genetic methods and genomic changes, they say, 'Oh wait a minute. This organism is different than that. While they produce the same disease, they look exactly the same on the plate, they produce the same biochemical reactions, but they're different in [x], so they give it a new name. And eventually everybody in the world is going to have an organism named after him because, you know, the [x] wasn't where it was supposed to be."

J Clin Microbiol. 2020; 58:e01975-19

Yes, there are “novel” problems

HUUUUUUUUUUUUUUUH??

GBE

Comparative Genomics and Pan-Genomics of the Myxococcaceae, including a Description of Five Novel Species: *Myxococcus eversor* sp. nov., *Myxococcus llanfairpwllg-wyngyllgogerychwyrndrobwllllantysiliogogogochensis* sp. nov., *Myxococcus vastator* sp. nov., *Pyxidicoccus caerfyrddi-nensis* sp. nov., and *Pyxidicoccus trucidator* sp. nov.

James Chambers[1,†], Natalie Sparks[1,†], Natashia Sydney[1], Paul G. Livingstone[1,2], Alan R. Cookson[1], and David E. Whitworth [1,*]

INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY

(*IJSEM*)

VALIDATION LIST NO. 201

Oren and Garrity, *Int. J. Syst. Evol. Microbiol.* 2021;71:004943

DOI 10.1099/ijsem.0.004943

MICROBIOLOGY SOCIETY

Valid publication of new names and new combinations effectively published outside the IJSEM

Myxococcus llanfairpwllgwyngyllgogerychwyrndrobwllllantysiliogogogochensis Chambers *et al.* 2021, 1[3,15]	sp. nov.	AM401 (=NBRC 114351=NCCB 100770)	12

atlasobscura.com/places/llanfairpwllgwyngyllgogerychwyrndrobwllllantysiliogogogoch

FLIP-FLOPPING

- *Acinetobacter dijkshoorniae* sp. nov.

  Published in *IJSEM* in 2016
  Designation was found to be synonym of *A. lactucae*
  Reverted to *Acinetobacter lactucae* in 2018

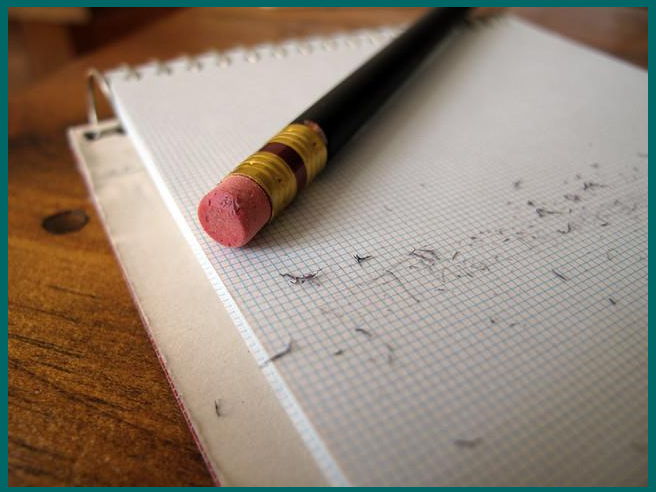
  Int J Syst Evol Microbiol. 2018; 68:131-132

- *Pseudopropionibacterium rubrum* sp. nov.

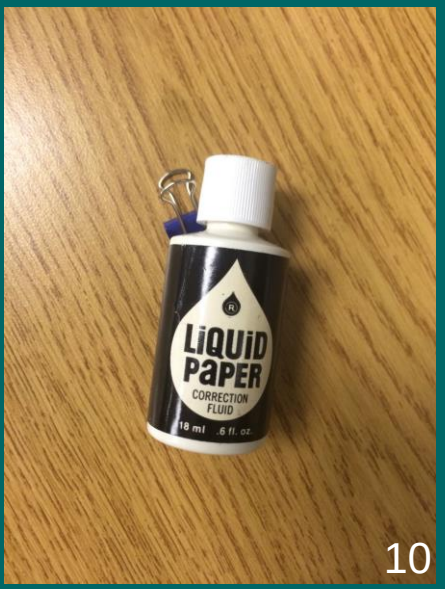
  Effectively described in June 2018
  Accepted by *IJSEM* in September 2018
  Illegitimate designation in August 2019

  Arachnia rubra comb. nov.

  Int J Syst Evol Microbiol. 2019; 69:2612-2615



Yes, there are “revision” problems



International Journal of Systematic and Evolutionary Microbiology (2016), 66, 5575–5599 DOI 10.1099/ijsem.0.001485

Genome-based phylogeny and taxonomy of the '*Enterobacteriales*': proposal for *Enterobacterales* ord. nov. divided into the families *Enterobacteriaceae*, *Erwiniaceae* fam. nov., *Pectobacteriaceae* fam. nov., *Yersiniaceae* fam. nov., *Hafniaceae* fam. nov., *Morganellaceae* fam. nov., and *Budviciaceae* fam. nov.

Enterobacteriaceae

<u>*Enterobacterales*</u>

Enterobacteriaceae
Erwiniaceae fam. nov.
Pectobacteriaceae fam. nov.
Yersiniaceae fam. nov.
Hafniaceae fam. nov.
Morganellaceae fam. nov.
Budviciaceae fam. nov.

LUCKILY…

Table 2A
Enterobacterales
M02 and M07

Table 2A. Zone Diameter and MIC Breakpoints for Enterobacterales

Testing Conditions

Medium: Disk diffusion: MHA
Broth dilution: CAMHB; **iron-depleted CAMHB for cefiderocol (see Appendix I)**[1]
Agar dilution: MHA

Inoculum: Broth culture method or colony suspension, equivalent to a 0.5 McFarland standard

Incubation: 35°C ± 2°C; ambient air
Disk diffusion: 16–18 hours
Dilution methods: 16–20 hours

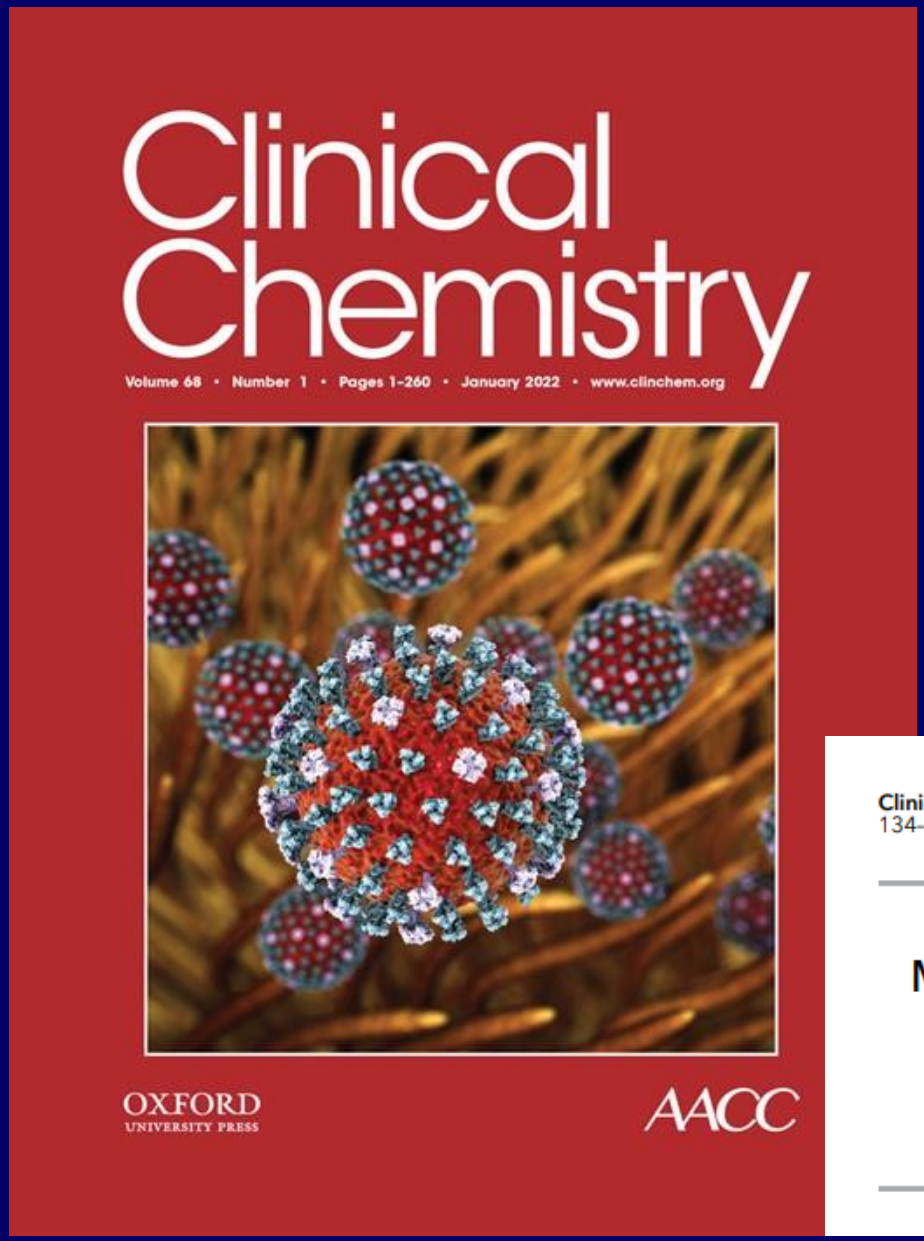
Routine QC Recommendations (see Tables 4A-1 and 5A-1 for acceptable QC ranges)

Escherichia coli ATCC®[a] 25922
Pseudomonas aeruginosa ATCC® 27853 (for carbapenems)
Staphylococcus aureus **ATCC® 25923 (for *Salmonella* enterica ser. Typhi azithromycin disk diffusion testing only; see Table 4A-1)**

Refer to Tables 4A-2 and 5A-2 to select strains for routine QC of β-lactam combination agents.

When a commercial test system is used for susceptibility testing, refer to the manufacturer's instructions for QC test recommendations and QC ranges.

CLSI M100 series



Clinical Chemistry 68:1
134–137 (2022)

Point/Counterpoint

POINT

Microbial Taxonomy: How and Why Name Changes Occur and Their Significance for (Clinical) Microbiology

Radhey S. Gupta*

Clin Chem. 2022; 68:134-137

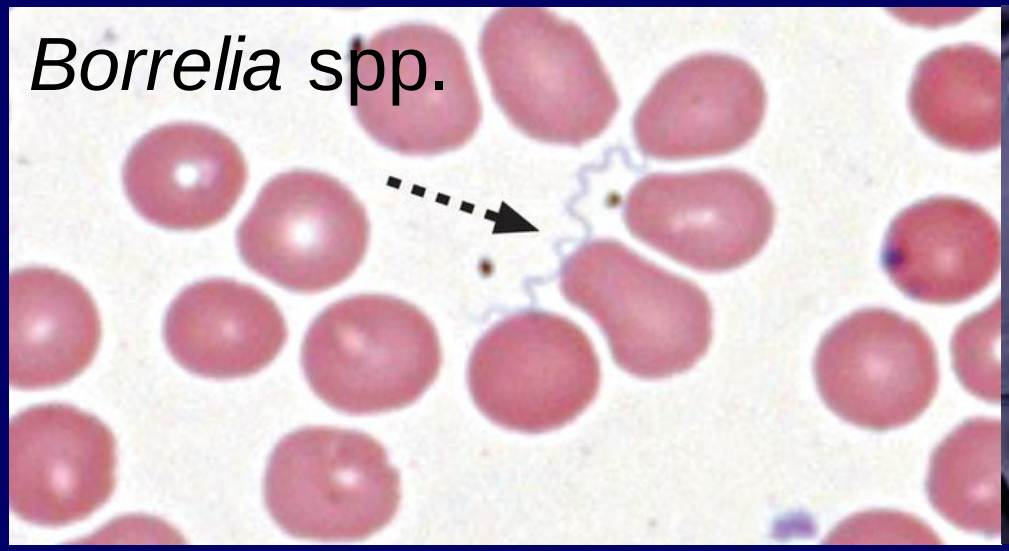
HOW ABOUT THIS ONE?

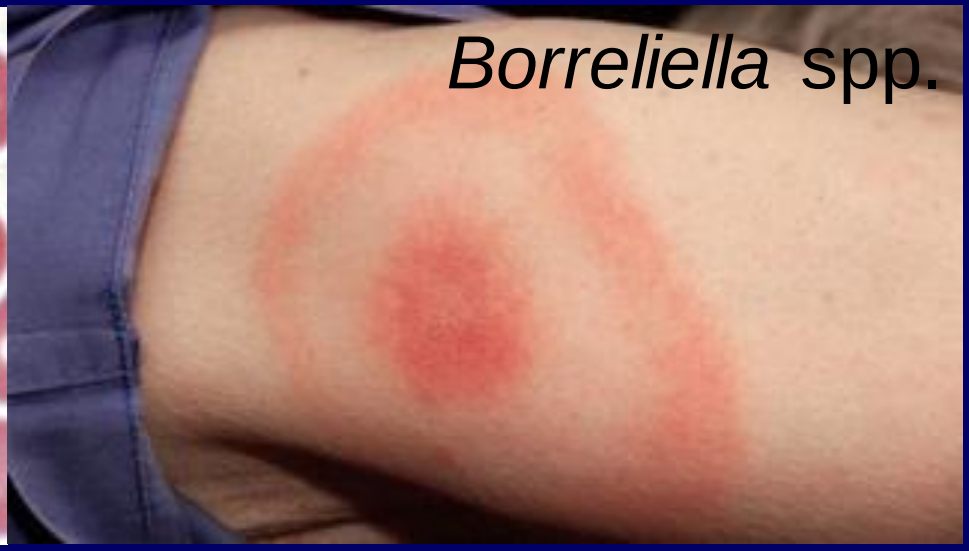
Antonie van Leeuwenhoek (2014) 105:1049–1072
DOI 10.1007/s10482-014-0164-x

ORIGINAL PAPER

A phylogenomic and molecular marker based proposal for the division of the genus *Borrelia* into two genera: the emended genus *Borrelia* containing only the members of the relapsing fever *Borrelia*, and the genus *Borreliella* gen. nov. containing the members of the Lyme disease *Borrelia* (*Borrelia burgdorferi* sensu lato complex)

Mobolaji Adeolu · Radhey S. Gupta





DEBATES IN THE LITERATURE

INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY

LETTER TO THE EDITOR

Margos *et al.*, *Int J Syst Evol Microbiol* 2017;67:1081–1084

DOI 10.1099/ijsem.0.001717

MICROBIOLOGY SOCIETY

There is inadequate evidence to support the division of the genus *Borrelia*

G. Margos,[1,*] D. Marosevic,[1,2] S. Cutler,[3] M. Derdakova,[4] M. Diuk-Wasser,[5] S. Emler,[6] D. Fish,[7] J. Gray,[8,9] K.-P. Hunfeldt,[9,10] B. Jaulhac,[9,11] O. Kahl,[9,12] S. Kovalev,[13] P. Kraiczy,[14] R. S. Lane,[15] R. Lienhard,[16] P. E. Lindgren,[9,17] N. Ogden,[18] K. Ornstein,[9,19] T. Rupprecht,[9,20] I. Schwartz,[21] A. Sing,[1] R. K. Straubinger,[22] F. Strle,[9,23] M. Voordouw,[24] A. Rizzoli,[25] B. Stevenson[26] and V. Fingerle[1,9]

INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY

LETTER TO THE EDITOR

Barbour *et al.*, *Int J Syst Evol Microbiol* 2017;67:2058–2067

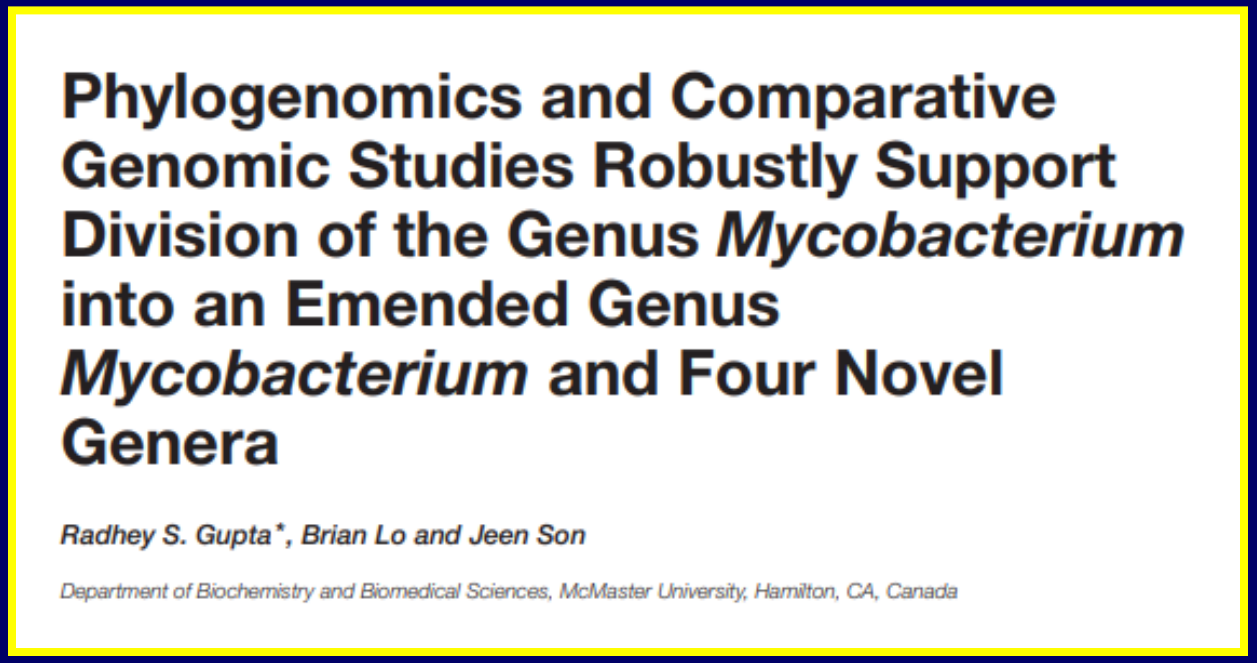
DOI 10.1099/ijsem.0.001815

MICROBIOLOGY SOCIETY

Division of the genus *Borrelia* into two genera (corresponding to Lyme disease and relapsing fever groups) reflects their genetic and phenotypic distinctiveness and will lead to a better understanding of these two groups of microbes (Margos *et al.* (2016) There is inadequate evidence to support the division of the genus *Borrelia*. *Int. J. Syst. Evol. Microbiol.* doi: 10.1099/ijsem.0.001717)

Alan G. Barbour,[1] Mobolaji Adeolu[2] and Radhey S. Gupta[2,*]

HOW ABOUT ANOTHER?



Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus *Mycobacterium* into an Emended Genus *Mycobacterium* and Four Novel Genera

Radhey S. Gupta, Brian Lo and Jeen Son*

Department of Biochemistry and Biomedical Sciences, McMaster University, Hamilton, CA, Canada

Mycolicibacter gen. nov.
Mycolicibacillus gen. nov.
Mycobacteroides gen. nov. (rapid growers)
Mycolicibacterium gen. nov. (rapid growers)

Front Microbiol. 2018; 9:67

REVISIONS TO *Mycobacterium*

- 114 total nomenclature revisions
- 97% accepted by *IJSEM*
- Did not touch: *Mycobacterium tuberculosis*
  Mycobacterium bovis
  Mycobacterium avium
  Mycobacterium leprae
  Mycobacterium kansasii
  Mycobacterium genavense
  Mycobacterium scrofulaceum

Clin Microbiol Newslett. 2020; 42:111-120

DON'T PANIC??

frontiers in Microbiology

ORIGINAL RESEARCH
published: 07 April 2020
doi: 10.3389/fmicb.2020.00468

Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of *Alphaproteobacteria*

Anton Hördt[1], Marina García López[1], Jan P. Meier-Kolthoff[1], Marcel Schleuning[1], Lisa-Maria Weinhold[1,2], Brian J. Tindall[3], Sabine Gronow[3], Nikos C. Kyrpides[4], Tanja Woyke[4] and Markus Göker[1]

Description of *Brucella anthropi* comb. nov.

B. an.thro'pi (Gr. masc. n. *anthropos*, a human being; N.L. gen. n. *anthropi*, of a human being).

Basonym: *Ochrobactrum anthropi* Holmes et al., 1988

The description is as given for *Ochrobactrum anthropi* (Holmes et al., 1988). The type strain is ATCC 49188 = CCUG 24695 = CIP 82.115 = DSMZ 6882 = IFO 15819 = JCM 21032 = LMG 3331 = NBRC 15819 = NCTC 12168.

Brucella anthropi (Holmes *et al.* 1988) Hördt *et al.* 2020, 44[3]	comb. nov. [basonym: *Ochrobactrum anthropi* Holmes *et al.* 1988]	CIP 82.115 (=ATCC 49188=CCUG 24695=DSM 6882=IFO 15819=JCM 21032=LMG 3331=NBRC 15819=NCTC 12168)	32

Front Microbiol. 2020; 11:468; Int J Syst Evol Microbiol. 2020; 70:4043-4049

12/19/2022: Lab Update: Reclassification of Ochrobactrum species into the Brucella genus

Print

Audience: Clinical Laboratories

Level: Laboratory Update

All *Ochrobactrum* species were recently reclassified into the *Brucella* genus to align taxonomical nomenclature with phylogenetic analyses. This change in nomenclature has been reflected in many of the rapid microbial identification systems used in clinical laboratories.

Laboratories should note any bacteria identified as '*Brucella*' on rapid or sequence-based systems and handle all organisms identified as '*Brucella*' species in a class II biosafety cabinet. All bacterial isolates presumptively identified as "*Brucella* species" should be referred to your state public health laboratory for additional testing.

AMERICAN SOCIETY FOR MICROBIOLOGY

Brucella and *Ochrobactrum* Taxonomic Updates for Laboratories

Frequently Asked Questions (FAQ) for Clinical Laboratories

Authors: Rosemary She, Carrie Anglewicz, Kurt Jerke, Ryan Relich, Mark Glazier, Laura Filkins*, Audrey Schuetz*

**Co-corresponding authors*

On behalf of the American Society for Microbiology Clinical and Public Health Microbiology Committee, Laboratory Practices Subcommittee

CONSEQUENCES

- Provider confusion
- Post-exposure prophylaxis
- Which of these are Select Agents (register w/Feds)?
- Packaging/shipping (category A) of Select Agents
- "…unwarranted euthanasia of animals infected with historic members of the *Ochrobactrum* genus…"

J Clin Microbiol. 2023; 61:e0028122

SOME ASSISTS

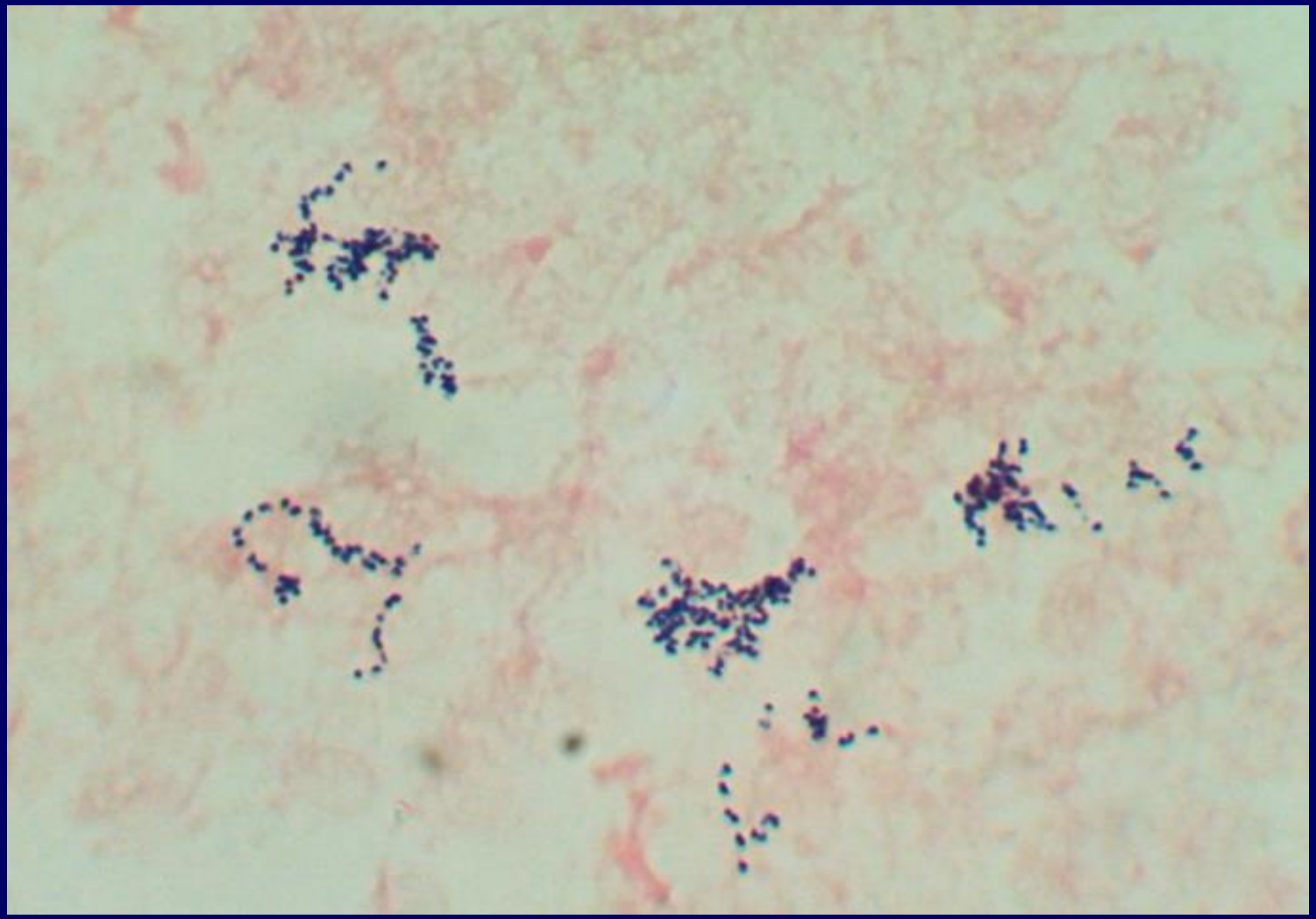
Brucella (*Ochrobactrum*) spp.	Select Agent *Brucella* spp.
Brucella anthropi *Brucella intermedia* 16 others	*Brucella melitensis* *Brucella abortus* (below) *Brucella suis* (below)
Gram-negative bacilli	Gram-negative coccobacilli
Overnight growth	"Two overnight incubations"
Larger colony size on blood, chocolate	Smaller colony size on blood, chocolate
Growth on MacConkey	No growth on MacConkey
Motility (mostly) positive	Motility negative
Urease (mostly) positive	Urease (strongly) positive

ⓘ **Nomenclatural status:** validly published under the ICNP

ⓘ **Taxonomic status:** synonym

Correct name: *Brucella melitensis* (Hughes 1893) Meyer and Shaw 1920 (Approved Lists 1980)

BAR TRIVIA



J Clin Microbiol. 2019; 57:e00381-18

DIRTY DOZEN (out of 76…or 87)

Morganellaceae

- *Morganella* (type genus)
- *Proteus*
- *Providencia*

Yersiniaceae

- *Serratia*
- *Yersinia* (type genus)

Hafniaceae

- *Edwardsiella*

Enterobacteriaceae

- *Citrobacter*
- *Enterobacter*
- *Escherichia* (type genus)
- *Klebsiella*
- *Salmonella*
- *Shigella*

Int J Syst Evol Microbiol. 2016; 66:5575-5599

MORE "PEDAGOGY PRETEND"

- *Aggregatibacter* spp.
- Unifying characteristics of *Enterobacteriaceae*?
- Non-gonococcal urethritis

Original Paper | Published: 20 March 2018

Phylogenetic framework for the phylum Tenericutes based on genome sequence data: proposal for the creation of a new order *Mycoplasmoidales* ord. nov., containing two new families *Mycoplasmoidaceae* fam. nov. and *Metamycoplasmataceae* fam. nov. harbouring *Eperythrozoon*, *Ureaplasma* and five novel genera

Radhey S. Gupta, Sahil Sawnani, Mobolaji Adeolu, Seema Alnajar & Aharon Oren

Antonie van Leeuwenhoek **111**, 1583–1630(2018) | Cite this article

INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY

REQUESTS FOR AN OPINION

Balish *et al.*, *Int J Syst Evol Microbiol* 2019;69:3650–3653

DOI 10.1099/ijsem.0.003632

MICROBIOLOGY SOCIETY

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., *Mycoplasmopsis* gen. nov. [Gupta, Sawnani, Adeolu, Alnajar and Oren 2018] and all proposed species comb. nov. placed therein

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 Spergser,[17] David Taylor-Robinson,[18] Dmitriy Volokhov[19] and Yan Zhao[20]

“unnecessary over-reach verging on taxonomic vandalism”

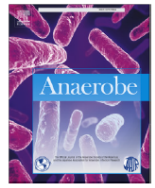
REMEMBER THIS DISASTER?

Anaerobe 40 (2016) 95–99

Contents lists available at ScienceDirect

Anaerobe

journal homepage: www.elsevier.com/locate/anaerobe



Clostridium difficile

Reclassification of *Clostridium difficile* as *Clostridioides difficile* (Hall and O'Toole 1935) Prévot 1938

Paul A. Lawson [a, *], Diane M. Citron [b], Kerin L. Tyrrell [b], Sydney M. Finegold [c, d, e]

International Journal of Systematic and Evolutionary Microbiology (2016), 66, 3761–3764 DOI 10.1099/ijsem.0.001321

Validation List No. 171

List of new names and new combinations previously effectively, but not validly, published

Aharon Oren[1] and George M. Garrity[2]

[1]The Institute of Life Sciences, The Hebrew University of Jerusalem, The Edmond J. Safra Campus, 91904 Jerusalem, Israel

[2]Department of Microbiology & Molecular Genetics, Biomedical Physical Sciences, Michigan State University, East Lansing, MI 48824-4320, USA

Correspondence
Aharon Oren
aharon.oren@mail.huji.ac.il
George M. Garrity
garrity@msu.edu

Name/authors	Proposed as	Nomenclatural type*	Priority†	Reference
Clostridioides Lawson *et al.* 2016, 96	gen. nov.	*Clostridioides difficile*	22	15
Clostridioides difficile (Prévot 1938) Lawson *et al.* 2016, 96	comb. nov. (basonym: *Clostridium difficile* (Hall and O'Toole 1935) Prévot 1938 (Approved Lists 1980)	ATCC 9689 (=DSM 1296)	22	15

WE SORT OF LUCKED OUT ON THIS

- Sequencing of 16S rRNA gene

  rRNA cluster I reserved for genus *Clostridium*
  Clostridium butyricum type species

  Int J Syst Evol Microbiol. 2016; 66:1009-1016

- rRNA cluster IX

  Phylogenetically different than rRNA cluster I
  More similar to *Peptostreptococcaceae*
  Proposed genus *Peptoclostridium*

  Environ Microbiol. 2013; 15:2631-2641

- *Clostridioides* ended up being a “compromise”

Yes, there are benefits

WE (SOME OF US) HAVE TO

CAP checklist standard MIC.11375

incorporate “taxonomic changes that potentially affect the choice of appropriate antimicrobials to report and/or the interpretive breakpoints to use”

PERFORMANCE OF RELEVANT AST

- *Actinobacillus actinomycetemcomitans*

Haemophilus actino…	*Aggregatibacter actino…*
1985	2006
M100	M45
HTM (DD, BMD)	MHB + lysed horse blood (BMD)
9 FQ, 15 cephems	2 FQ, 2 cephems

- *Staphylococcus* spp.

Organism	Phenotypic Methods for Detection of Methicillin (Oxacillin)-Resistant *Staphylococcus* spp.				
	Cefoxitin MIC	Cefoxitin disk diffusion	Oxacillin MIC	Oxacillin disk diffusion	Oxacillin salt agar
S. aureus	Yes (16-20 h)	Yes (16-18 h)	Yes (24 h)	No	Yes (24 h)
S. lugdunensis	Yes (16-20 h)	Yes (16-18 h)	Yes (24 h)	No	No
S. epidermidis	No	Yes (24 h)	Yes (24 h)	Yes (16-18 h)	No
S. pseudintermedius	No	No	Yes (24 h)	Yes (16-18 h)	No
S. schleiferi	No	No	Yes (24 h)	Yes (16-18 h)	No
Staphylococcus spp. (not listed above or not identified to the species level)	No	Yes[a] (24 h)	Yes[a] (24 h)	No	No

Abbreviations: h, hour(s); MIC, minimal inhibitory concentration; MRS, methicillin (oxacillin)-resistant staphylococci; PBP2a, penicillin-binding protein 2a

PATHOGENESIS

- *Elizabethkingia anophelis* sp. nov. (Gambia; 2001)

  Originally isolated from midgut of *Anopheles* spp.
  Neonatal meningitis; thought to require vector
  Identified as *E. meningoseptica* via biochemicals
  Differences in clinical picture (sepsis, meningitis, ↑ mortality) and epidemiology (vertical transmission)
  [As of 2020, *E. anophelis* subsp. *anophelis*]

  Sci Rep. 2016; 6:26045

- *Enterobacter bugandensis* sp. nov. (Tanzania; 2016)

  Most pathogenic *Enterobacter* spp. (*in vitro*)

  Sci Rep. 2018; 8:5392

RESOLVE UNUSUAL PHENOTYPES

- *Corynebacterium belfantii* sp. nov. (France; 2018)
  - Formerly 1 of 4 biovars of *C. diphtheriae*
  - Nitrate reductase-negative
  - Toxin genetic determinant absent
  - Clinical disease encompasses non-specific rhinitis

Int J Syst Evol Microbiol. 2018; 68:3826-3831

- *C. diphtheriae* subsp. *lausannense* subsp. nov.
  - Nitrate reductase-negative
  - Non-toxigenic
  - Lower respiratory tract disease

Front Microbiol. 2018; 9:1743

MICROBIOME CONTRIBUTION

- *Megasphaera massiliensis* sp. nov. (Russia; 2013)

  Originally isolated from feces of HIV-positive male
  In vitro models suggest organism has protective activity versus neuronal cell cytotoxicity

  Front Cell Neurosci. 2019; 13:402

- *Ruthenibacterium lactatiformans* sp. nov. (Russia; 2016)

  Originally isolated from feces of healthy male
  Abundance of this organism found in patients with rheumatoid arthritis

  Genes (Basel) 2019; 10:748

So What?

AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology®

BIOGRAPHICAL FEATURE

Biographical Feature: Franklin P. Koontz, Ph.D., D(ABMM), F(AAM)

"So, I've just gone totally nuts on this stuff and I quit using the genus names. So, I'll call the floor and I tell them they've got a pickettii; they've got a maltophilia; they've got a cepacia. I don't give a genus name anymore because they're confusing the hell out of the doc; he doesn't know what Stenotrophomonas means, but he sure knows what maltophilia means. So, I think we have to stop this rampant name changing. I think it's stupid."

J Clin Microbiol. 2020; 58:e01975-19

HOW FAR DO YOU WANT TO GO??

- *Proteus morganii*

  Int J Syst Bacteriol. 1980; 30:225-420

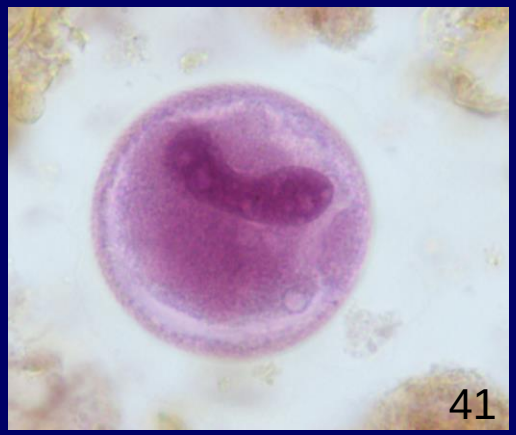
- *Neisseria catarrhalis*

  J Gen Microbiol. 1968; 51:387-392

- *Streptococcus faecalis*

  Int J Syst Bacteriol. 1984; 34:31-34

- *Bacillus coli* (never validly published)



IT GETS EVEN WORSE…

- Nomenclature for prokaryotes introduced in 1700s; utilized botanical rules
- *Staphylococcus aureus* Rosenbach 1884

  Type strain of *S. aureus* (ATCC 12600)

  "Staphylococcus pyogenes aureus" (Rosenbach 1884)
  "Micrococcus aureus" (Zopf 1885)
  "Staphlococcus pyogenes citreus" (Passet 1885)
  "Micrococcus pyogenes" (Lehmann and Neumann 1896)

- Confusing repertoire of ~40,000 names

SYNONYMS

- Homotypic

"Staphylococcus pyogenes aureus", effective name
"Micrococcus aureus", effective name

we'll get to this later

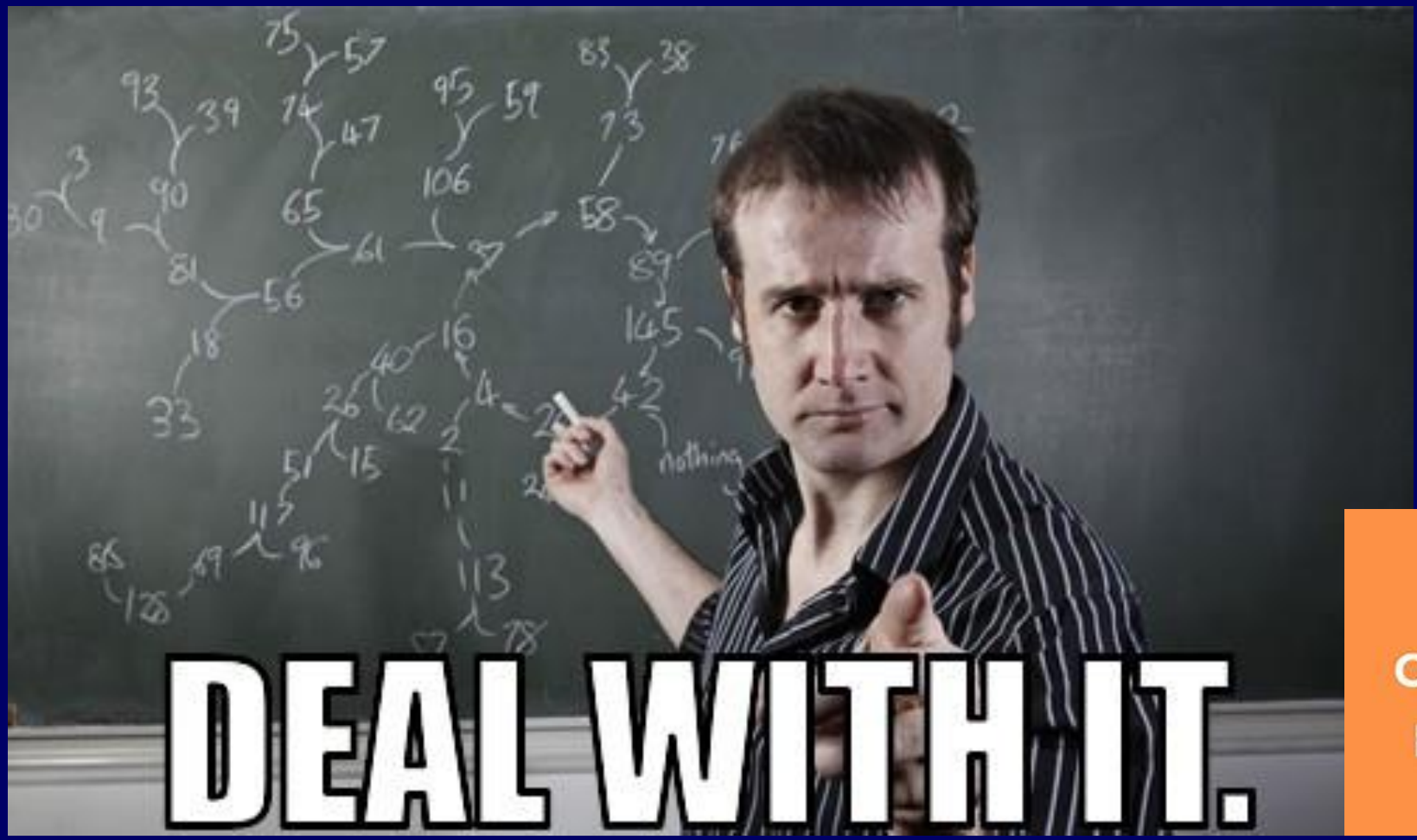
SYNONYMS

- Heterotypic

"Staphlococcus pyogenes citreus", effective name
"Micrococcus pyogenes", effective name

we'll get to this later

Ann Landers Abigail Van Buren

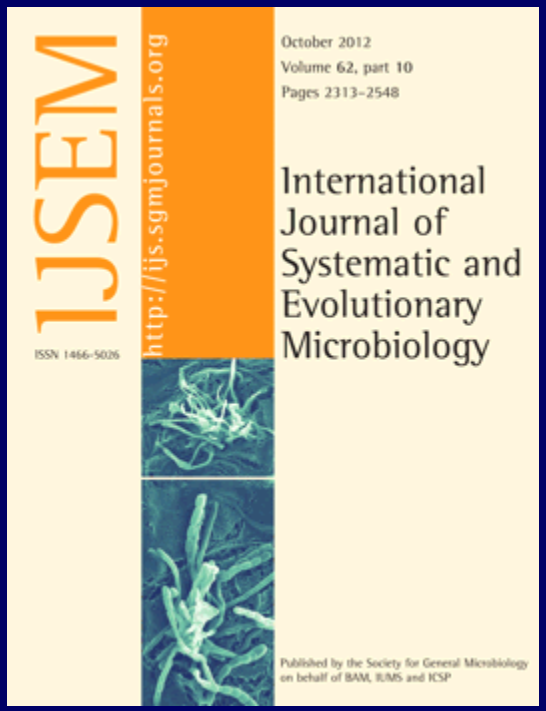


GET OVER IT AND MOVE ON

LAYING DOWN THE LAW

- International Committee on Systematics of Prokaryotes (ICSP)
- THE CODE established in 1975
- Approved Lists of Bacterial Names

  2,300 prokaryotic names
  Reject rest



- All novel nomenclature must be accepted by
  International Journal of Systematic and Evolutionary Microbiology

  International Bulletin of Bacteriological Nomenclature and Taxonomy (1951-1965)
  International Journal of Systematic Bacteriology (1966-1999)

ICSP PERSPECTIVE

- Two General Considerations

  "The progress of bacteriology can be furthered by a precise system of nomenclature accepted by the majority of bacteriologists of all nations."

  "To achieve order in nomenclature, it is essential that scientific names be regulated by internationally-accepted Rules."

- Bacteriologist has responsibility of classifying; ICSP has responsibility of standardizing taxonomy (prescribing naming procedures; assuring correctness)

DISCOVERING YOUR NEW TAXON

- Effective description

  Several recommendations provided in THE CODE
  Minimum standards may vary by genus
  Polyphasic approach to characterization

- Designation of type strain

  Viable isolate deposited in culture collection centers in two nations
  As of January 2018, whole genome sequence of type strain must be deposited in GenBank, with genome accession number included as part of effective description

GIVE IT A NAME

INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY

RESEARCH ARTICLE

Freese *et al.*, *Int. J. Syst. Evol. Microbiol.* 2023;73:006115

DOI 10.1099/ijsem.0.006115

MICROBIOLOGY SOCIETY

OPEN ACCESS

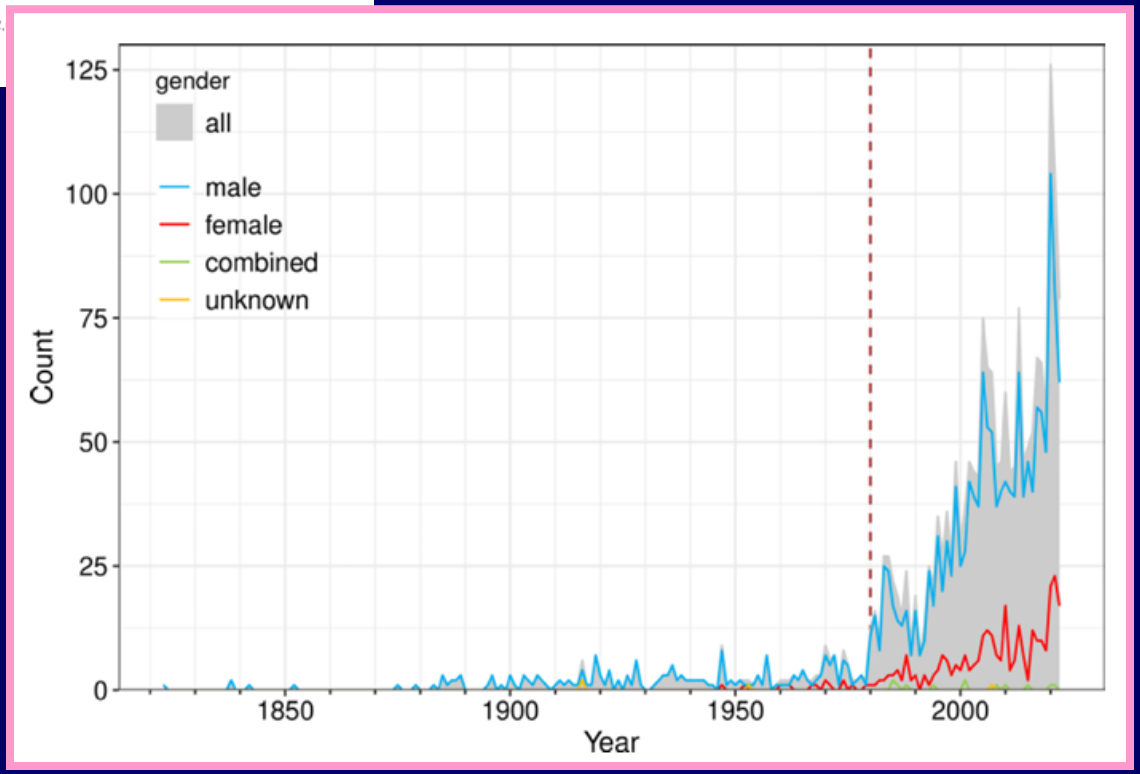
The gender gap in names of prokaryotes honouring persons

Heike M. Freese[1], Lola Giner-Pérez[2,3,4], Aharon Oren[5], Markus Göker[1] and David R. Arahal[2,

2108/23315

1823 . . . 1947

14.8%



Int J Syst Evol Microbiol. 2023; 73:e006115

ACCEPTANCE (DIRECT)

International Journal of Systematic and Evolutionary Microbiology (2012), **62**, 601–607 DOI 10.1099/ijs.0.031658-0

Lactobacillus saniviri sp. nov. and *Lactobacillus senioris* sp. nov., isolated from human faeces

Kaihei Oki, Yuko Kudo and Koichi Watanabe

Yakult Central Institute for Microbiological Research, 1796 Yaho, Kunitachi, Tokyo 186-8650, Japan

Correspondence
Koichi Watanabe
koichi-watanabe@yakult.co.jp

Two Gram-stain-positive strains, YIT 12363^T and YIT 12364^T, were isolated from human faeces. They were rod-shaped, non-motile, asporogenous, facultatively anaerobic and did not exhibit catalase activity. Comparative analyses of 16S rRNA, *pheS* and *rpoA* gene sequences demonstrated that the novel strains were members of the genus *Lactobacillus*. On the basis of 16S rRNA gene sequence similarity, the type strains of *Lactobacillus casei* (95.3 % similarity), *Lactobacillus paracasei* subsp. *paracasei* (95.6 %), *Lactobacillus paracasei* subsp. *tolerans* (95.3 %) and *Lactobacillus rhamnosus* (95.4 %) were the closest neighbours to strain YIT 12363^T. For strain YIT 12364^T, the highest similarity values were observed with the type strains of *Lactobacillus diolivorans*, *Lactobacillus parafarraginis* and *Lactobacillus rapi* (95.8, 96.0 and 96.0 %, respectively). Phenotypic and genotypic features demonstrated that these strains each represent a separate novel species of the genus *Lactobacillus*, and the names *Lactobacillus saniviri* sp. nov. (type strain YIT 12363^T=JCM 17471^T=DSM 24301^T) and *Lactobacillus senioris* sp. nov. (type strain YIT 12364^T=JCM 17472^T=DSM 24302^T), respectively, are proposed.

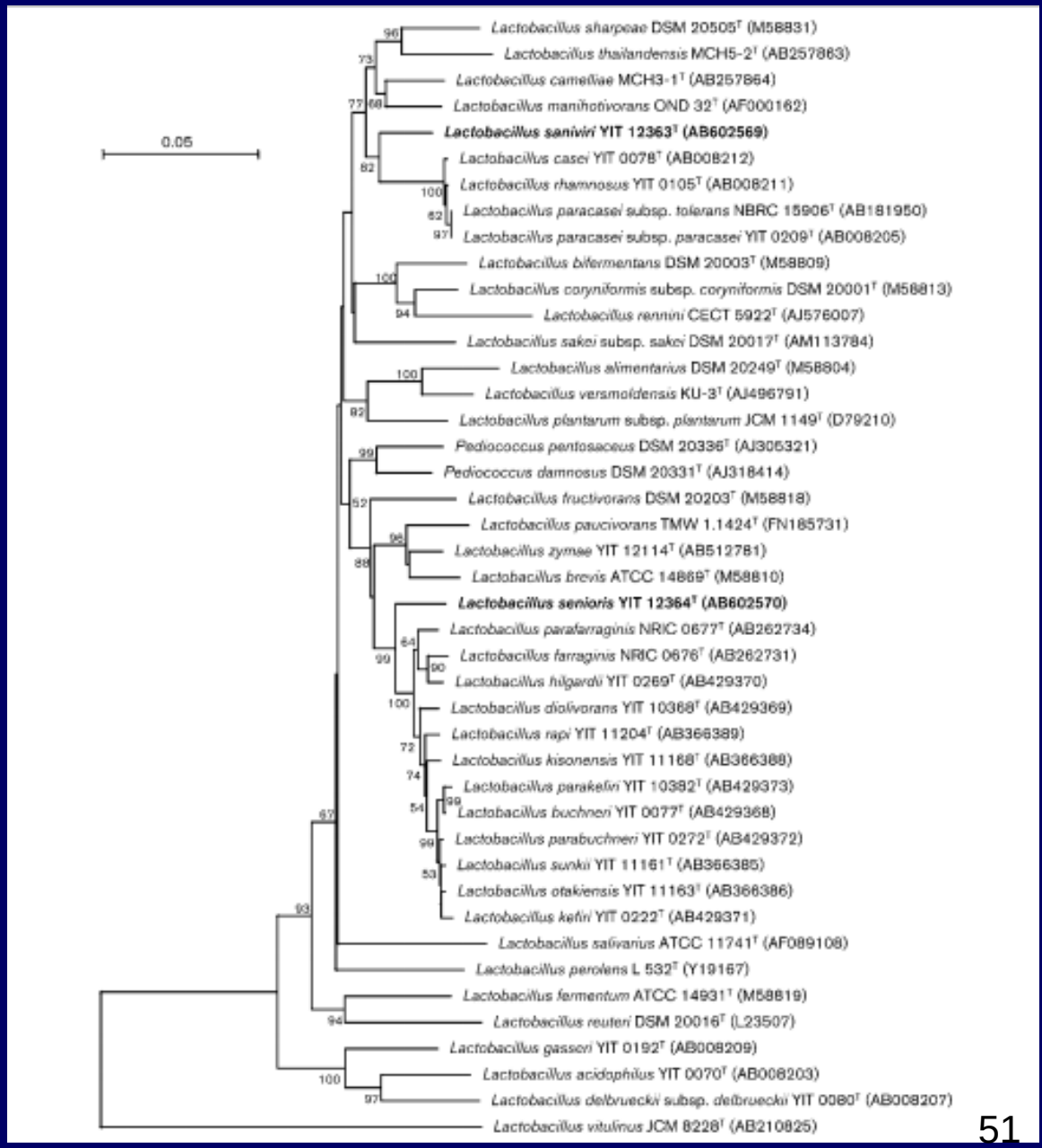
Biochemical

Characteristic	1	2	3
Growth at:			
15 °C	+	−	+
pH 4.0	−	+	+
Tolerance to 5% salt	W	−	−
Ammonia production from arginine	+	+	−
Acid production from:			
Methyl β-D-xylopyranoside	−	+	−
D-Galactose	−	−	W
D-Fructose	+	W	+
Methyl α-D-glucopyranoside	−	+	−
N-Acetylglucosamine	W	−	−
Maltose	−	+	+
Lactose	−	−	W
Melibiose	−	+	+
Sucrose	−	W	+
Melezitose	−	+	+
Raffinose	−	+	+
Turanose	−	+	−
Gluconate	+	W	W
5-Ketogluconate	−	W	W
Optical form of lactic acid	DL	L	DL
Peptidoglycan type	L-Lys–D-Asp	L-Lys–D-Asp	ND
DNA G+C content (mol%)	39.8	41.6	42.0

Chemotaxonomic

Fatty acid	1	2	3	4
Saturated				
$C_{14:0}$	1.16	11.98	–	1.22
$C_{16:0}$	4.1	17.88	2.23	18.2
$C_{16:0}$ 3OH	–	0.36	–	–
$C_{18:0}$	0.82	0.56	1.53	0.59
$C_{18:0}$ 12OH	4.42	4.74	–	–
Unsaturated				
$C_{16:1}\omega5c$	–	0.56	–	–
$C_{16:1}\omega7c$	–	4.63	–	2.28
$C_{18:1}\omega9c$	56.61	30.32	57.22	28.18
$C_{18:1}\omega7c$ DMA	0.71	0.76	0.57	–
$C_{18:2}\omega6,9c$	–	–	1.09	–
Cyclopropane				
C_{19} cyc 9,10	29.29	18.66	34.39	14.9
C_{19} cyc 11,12	–	–	–	5.41
Summed features*				
10	2.3	7.94	2.05	29.22
12	–	0.54	0.93	–
Unknown fatty acid (ECL 18.199)	0.59	1.05	–	–

16S rRNA gene sequencing



Description of *Lactobacillus senioris* sp. nov.

Lactobacillus senioris (se.ni'o.ris. L. gen. n. *senioris* of/from an elderly person, indicating the source of the type strain).

Cells are rod-shaped (0.7 × 1.0–10.0 μm) and occur singly, in pairs or in chains comprising three to four cells. Cells are Gram-stain-positive, non-motile, asporogenous and facultatively anaerobic. Catalase and pseudocatalase are not produced. After anaerobic growth at 37 °C for 72 h, colonies on MRS agar are circular, 1–2 mm in diameter and beige with a smooth or rough surface. In MRS broth, growth occurs at 15 °C but not at 10 °C or 45 °C. Growth does not occur at pH 4.0 or pH 8.5. Growth occurs weakly in the presence of 5 % NaCl but not in the presence of 8 % NaCl. Gas is produced from glucose. Both L- (72 %) and D-lactate (28 %) are produced as the end products from glucose. Ammonia is produced from arginine. Nitrate is not reduced. Acid is produced from L-arabinose, D-ribose, D-xylose, D-glucose, D-fructose, *N*-acetylglucosamine (weakly) and gluconate. Aesculin is not hydrolysed. Dextran is not produced from sucrose. Cells do not contain *meso*-diaminopimelic acid in their cell-wall peptidoglycan. Peptidoglycan structure is of the L-Lys–D-Asp type in the presence of Lys, Glu, Ala and Asp. The major cellular fatty acids are unsaturated fatty acid $C_{18:1}\omega 9c$ and cyclopropane C_{19} cyc 9,10. Phylogenetic analysis of the 16S rRNA gene sequence places the species in the *L. buchneri* group of lactobacilli.

The type strain, YIT 12364^T (=JCM 17472^T=DSM 24302^T), was isolated from faeces of a 100-year-old elderly female person in Okinawa, Japan. The DNA G+C content of the type strain is 41.6 mol%.

Effective description…now valid description

polyphasic characterization
novel species
no synonyms
type strain documented
published in *IJSEM*

(2012: whole genome sequence not required yet)

ACCEPTANCE (ALTERNATE)

- Other journals publish new taxonomy

- Accepted/added by *IJSEM*; validation list

PUBLISH IT--ALTERNATE APPROACH

Antonie van Leeuwenhoek (2014) 106:543–553
DOI 10.1007/s10482-014-0226-0

ORIGINAL PAPER

Nocardia vulneris sp. nov., isolated from wounds of human patients in North America

Brent A. Lasker · Melissa Bell · Hans-Peter Klenk · Cathrin Spröer · Peter Schumann · June M. Brown

Antonie van Leeuwenhoek (2014) 106:543–553

16S rRNA gene sequencing

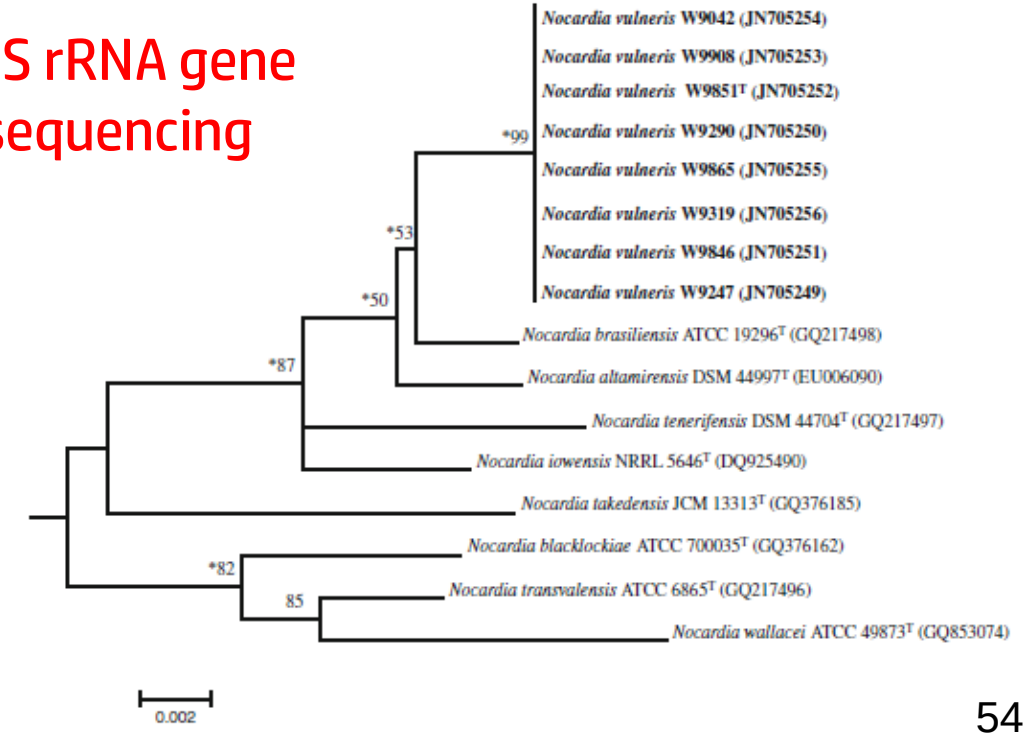


Table 2 Phenotypic properties that distinguish the *N. vulneris* clinical isolates from the type strains of their closest phylogenetically related neighbors

Characteristics	Clinical isolates ($n = 8$)	*N. altamirensis* DSM 44997^T	*N. brasiliensis* ATCC 19296^T	*N. iowensis* DSM 45197^T	*N. tenerifensis* DSM 44704^T
Utilization of:					
Adonitol	−	+	+	+	−
L-arabinose	−	−	+	−	+
D-cellobiose	−7/8	+	−	−	−
Dulcitol	−	−	−	−	+
D-fructose	+	+	+	−	+
D-galactose	+	+	+	−	+
Glycerol	+	−	−	+	+
Lactose	−	−	−	−	−
Maltose	−	+	+	+	+
D-mannitol	+	+	+	−	+
Mannose	+	+	−	+	+
Melibiose	−	+	−	−	−
Raffinose	−6/8	−	−	−	−
Salicin	+	+	+	+	−
D-sorbitol	−	+	−	−	+
Sucrose	−	+	+	+	+
Trehalose	+	+	+	+	−
Growth at 35 °C	+	−	+	+w	+
Growth at 45 °C	−	−	−	+w	+w
Hydrolysis of:					
Adenine (21 days)	+	−	−	−	−
Casein (14 days)	+	−	+	+	−
Hypoxanthine	+	−	−	−	+
Tyrosine	+	−	+	+	−
Urea (Christensen)	+	+	−	+	+
Acetamide (7 days)	−	−	−	+	−
Nitrate reduction (0.2 %)	+	−	−	−	−
Lysis on 5 % rabbit blood agar	+	−	−	−	−
Antimicrobial resistance to[b]:					
Ampicillin (≥32 μg/ml)	S	S	R	R	R
Cefriaxone (≥64 μg/ml)	S	S	R	R	S
Clarithromycin (≥8 μg/ml)	R	I	R	R	I
Ciprofloxacin (≥4 μg/ml)	R	I	R	I	R
Imipenem (≥16 μg/ml)	R	S	R	I	S
Minocycline (≥8 μg/ml)	I	S	I	S	I

Effective description...

polyphasic characterization

novel species

no synonyms

type strain documented

(2014: whole genome sequence not required yet)

Description of *N. vulneris* sp. nov. *N. vulneris* (vul'ne.ris. L. gen. n. *vulneris*, of a wound).

An aerobic, non-motile, Gram-stain positive, weakly acid-fast actinomycete obtained primarily from wound infections. Forms pale orange to tan, molar tooth shaped colonies with abundant aerial and substrate hyphae on HIA with rabbit blood, TSA with sheep blood, Middlebrook and Cohn 7H11 agar with OADC and heart infusion agar. Hemolysis of HIA supplemented with rabbit blood is observed after 7 days at 35 °C but not on TSA supplemented with sheep blood. Utilizes and produces acid from D-fructose, D-galactose, D-glucose, glycerol, i-myo-inositol, D-mannitol, mannose, salicin, and trehalose, but does not utilize adonitol, L-arabinose, D-cellobiose (most strains), dulcitol, i-erythritol, lactose, maltose, melibiose, raffinose (most strains), L-rhamnose, D-sorbitol, sucrose, and D-xylose. Utilizes citrate (most strains) as a sole carbon source but not acetamide as a carbon or nitrogen source. Grows in the presence of lysozyme, reduces nitrate but not nitrite, but has no arylsulfatase activity. Hydrolyses urea, adenine, casein, hypoxanthine, and tyrosine but does not hydrolyse xanthine. Esculin hydrolysis is weakly positive by browning but negative by UV light absorption. Grows at 25 and 35 °C but not 45 °C. Whole-cell hydrolysates contain *meso*-diaminopimelic acid and arabinose and galactose (cell-wall chemotype IV sensu Lechevalier and Lechevalier 1970). MK-8-(H_4)$_{\omega\text{-cyc}}$ and MK-9 are the predominant menaquinones with minor amounts of MK-8 (H_2). Polar lipids are diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol and phosphatidylinositol mannosides. The major fatty acids of the type strain are composed of palmitic acid ($C_{16:0}$), tuberculostearic acid (10-methyl $C_{18:0}$), oleic acid $C_{18:1\ cis9}$ and content of the type strain is 68.4 mol % (68.1 mol % from the 9.4 Mbp draft genome sequence).

The type strain W9851^T (= DSM 45737^T = CCUG 62683^T = NBRC 108936^T) was isolated from a 54-male patient with a leg wound in the state of Illinois. The GenBank accession number of the 16S rRNA gene sequence of the type strain is JN705252 and the accession number for the draft genome sequence is JNFP00000000.

International Journal of Systematic and Evolutionary Microbiology (2015), **65**, 1–4 DOI 10.1099/ijs.0.000008-0

Validation List no. 161

List of new names and new combinations previously effectively, but not validly, published

Aharon Oren[1] and George M. Garrity[2]

[1]The Institute of Life Sciences, The Hebrew University of Jerusalem, The Edmond J. Safra Campus, Givat Ram, 91904 Jerusalem, Israel

[2]Department of Microbiology & Molecular Genetics, Biomedical Physical Sciences, Michigan State University, East Lansing, MI 48824-4320, U.S.A

Correspondence
Aharon Oren
aharon.oren@mail.huji.ac.il
George M. Garrity
garrity@msu.edu

Name/authors	Proposed as	Nomenclatural type*	Priority†	Reference
Nocardia vulneris Lasker *et al.* 2014, 551	sp. nov.	W9851 (=CCUG 62683=DSM 45737=NBRC 108936)	11	14
Paracoccus pacificus Zhang *et al.* 2014, 729	sp. nov.	F14 (=CGMCC 1.12755=LMG 28106=MCCC 1A09947)	18	33
Pedobacter kyungheensis Yang *et al.* 2012, 313	sp. nov.	THG-T17 (=KACC 16221=LMG 26577)	27	32
Photobacterium piscicola Figge *et al.* 2014, 332	sp. nov.	W3 (=LMG 27681=NCCB 100098)****	27	7
Photobacterium sanctipauli Moreira *et al.* 2014, 7##	sp. nov.	A-394 (=CIAM 1982=LMG 27910)	12	21
Rhizobium smilacinae Zhang *et al.* 2014, 721	sp. nov.	PTYR-5 (=CCTCC AB 2013016=LMG 27604)‡‡‡‡	22	34
Roseivivax atlanticus Li *et al.* 2014, 867	sp. nov.	22II-S10s (=LMG 27156=MCCC 1A09150)	5	18
Sphingobacterium pakistanense corrig. Ahmed *et al.* 2014, 330§§§§	sp. nov.	NCCP-246 (=KCTC 23914=LMG 28524) ‖‖‖‖‖‖	35	2
Thiolapillus Nunoura *et al.* 2014, 9 ## ¶¶¶¶	gen. nov.	*Thiolapillus brandeum*	13	26
Thiolapillus brandeum Nunoura *et al.* 2014, 10## ####	sp. nov.	Hiromi 1 (=DSM 23672=JCM 15507)	13	26
Vibrio crosai González-Castillo *et al.* 2014, 462	sp. nov.	CAIM 1437 (=DSM 27145)	9	9
Vibrio madracius Moreira *et al.* 2014, 408	sp. nov.	A-354 (=CBAS 482=LMG 28124)	14	20
Winogradskyella jejuensis Kim & Oh 2012, 891	sp. nov.	CP32 (=JCM 18454=KCTC 23835)	31	12

HOW DO WE FIND OUT ABOUT THIS?

Diagnostic Microbiology and Infectious Disease 83 (2015) 82–88

Contents lists available at ScienceDirect

Diagnostic Microbiology and Infectious Disease

journal homepage: www.elsevier.com/locate/diagmicrobio

Review

Taxonomic update on proposed nomenclature and classification changes for bacteria of medical importance, 2013–2014

J. Michael Janda *

Public Health Laboratory, Department of Public Health, Kern County, Bakersfield, CA 93306-3302

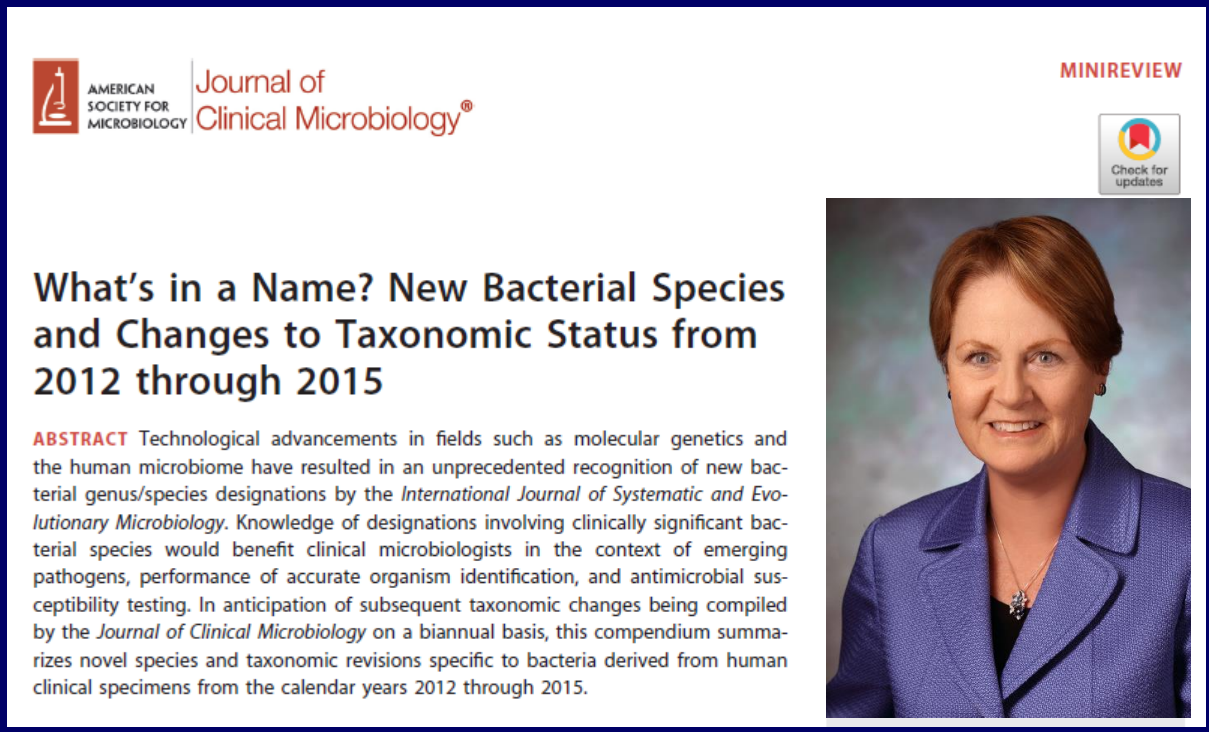
A B S T R A C T

A key aspect of medical, public health, and diagnostic microbiology laboratories is the accurate and rapid reporting and communications regarding infectious agents of clinical significance. Microbial taxonomy in the age of molecular diagnostics and phylogenetics causes changes in this taxonomy at a rapid rate further complicating this process. This review focuses on the description of new species and classification changes proposed over the past 2 years.

KERN COUNTY Public Health Services DEPARTMENT

There have been five (2016, 2017, 2019, 2020)

HOW DO WE FIND OUT ABOUT THIS?



J Clin Microbiol. 2017; 55:24-42

There have been five
(2019, 2021, 2023, 2023)

APPROACHES DIFFER

- *Diagnostic Microbiology and Infectious Disease*

  Scope is bacteriology
  Not all data validated by *IJSEM*
  Novel taxa characterized by 5 strains (or clinical)

- *Journal of Clinical Microbiology*

  Scope expanded to include mycology, virology, parasitology, mycobacteriology, veterinary
  All bacterial taxa validated by *IJSEM*
  Includes all taxa derived from human clinical material
  Later publications have included follow-up

FOLLOW-UP IMPORTANCE

- *Klebsiella michiganensis* sp. nov. (United States; 2012)

  Original isolate from toothbrush holder
  Isolate with KPC-2, NDM-1, NDM-5 recovered from immunocompromised Chinese pt. w/diarrhea

  J Antimicrob Chemother. 2018; 73:536-538

- *Kingella negevensis* sp. nov. (Israel, Switzerland; 2017)

  Original 21 oropharyngeal isolates from healthy kids
  Organism detected from corneal scrapings from a United States patient diagnosed with keratitis

  Am J Trop Med Hyg. 2020; 103:672-674

HELP IS ON THE WAY

CLSI M64
Guideline for Implementation of Taxonomy Nomenclature Changes

Scope

Bacteriology
Mycology

Participants

Clinical (including veterinary)
Industry
Government

Audience

Clinical microbiology
Veterinary microbiology

DISCUSSION TOPICS

- Role for *International Journal of Systematic and Evolutionary Microbiology* WRT bacteriology
- *Journal of Clinical Microbiology* compendia

  An assist for bacteriology revisions/changes
  Time zero for mycology revisions/changes

- Some implementation can be expedited
- Ancillary partner planning; instrument validation
- Roll out/communication (reports, comments)

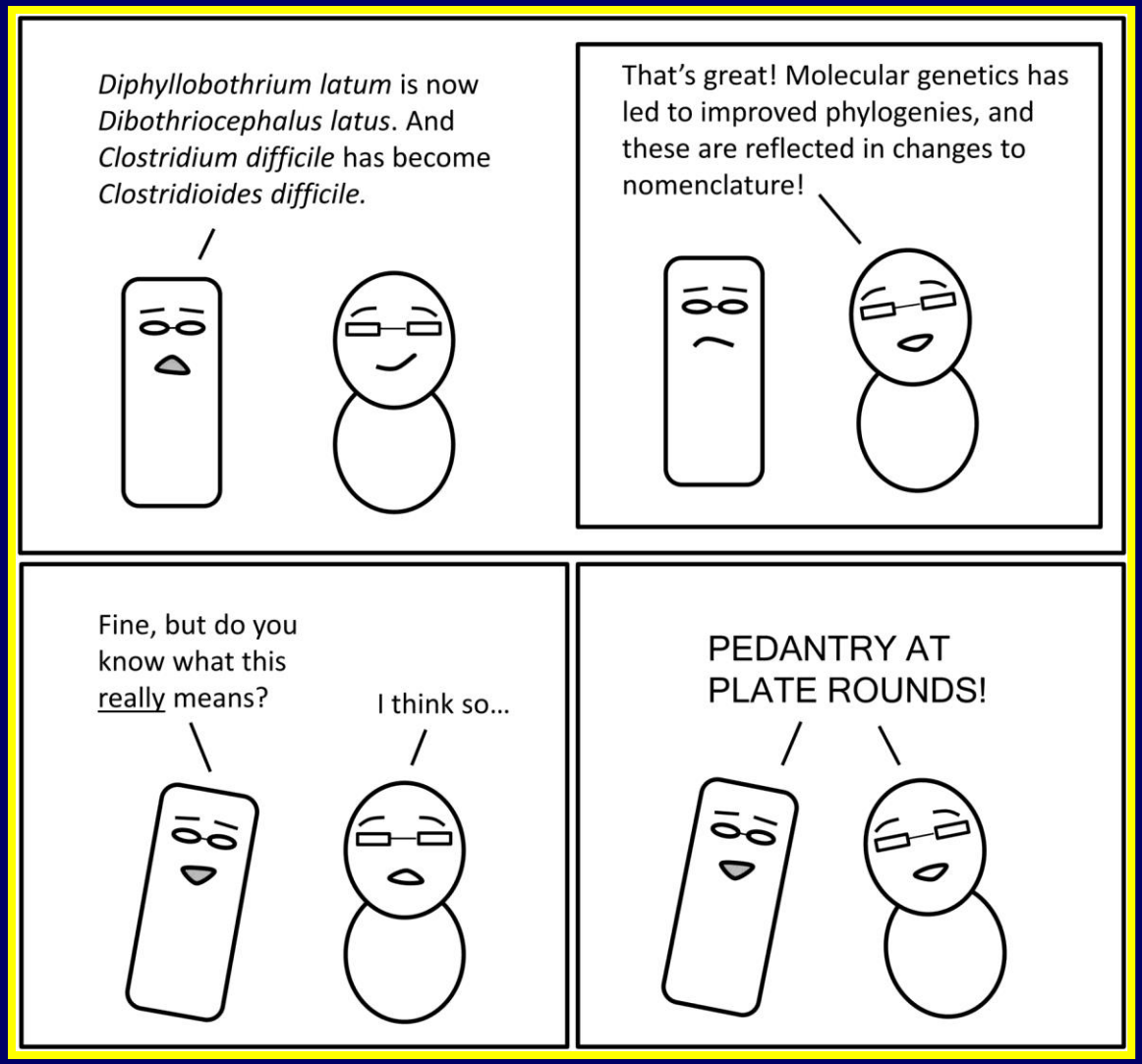
WAIT…WAIT…

- Clinical relevance may not be determined
- Clinicians may become cognizant of changes
- Updating of databases by commercial vendors
- The earlier flip-flopping example
- Daily laboratory operations

  Communication
  Multi-facility laboratory systems
  LIS updates

THANK YOU AND STAY TUNED!!

J Clin Microbiol. 2011; 49:3449



J Clin Microbiol. 2019; 57:e00231-19