Microbial Taxonomy Updates:

What are They and Why Should We Care?

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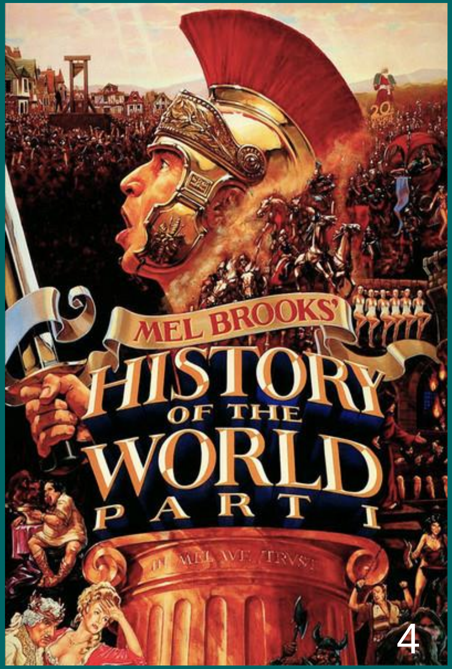
Laboratory Technical Advisory Group

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

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

A History Lesson



FIRST ATTEMPTS

- 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

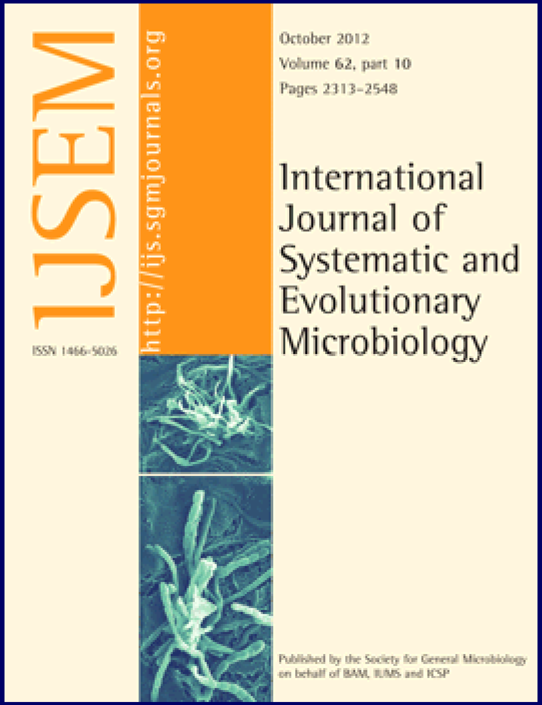
Ann Landers Abigail Van Buren

WE'VE GOTTA CLEAN THIS UP

- International Committee on Systematics of Prokaryotes (ICSP)

- First Congress for Bacteriology Plenary Session established contemporary approaches (1973)
- *International Code of Nomenclature of Bacteria* (THE CODE) published in 1975

REFORMS


IJSEM

http://ijs.sgmjournals.org

ISSN 1466-5026

October 2012
Volume 62, part 10
Pages 2313–2548

International Journal of Systematic and Evolutionary Microbiology

Published by the Society for General Microbiology on behalf of BAM, IUMS and ICSP

- Approved Lists of Bacterial Names
  - January 1980
  - 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)
- Valid nomenclature types were required to be “designated” (i.e., deposit type strains)

MOST RECENT CODE UPDATE IN 2019

- 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)

Identification of New Taxa

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

PHENOTYPIC CHARACTERIZATION

- Number of characteristics must be sufficiently high to distinguish new species from related species; recommend 5 strains (including type strain)
- Cultivation conditions (medium, incubation, duration)
- Classical observations
  - Gram morphology, arrangement
  - Motility, oxidase, catalase
  - Colony morphology
  - Carbohydrates
- Chemotaxonomic markers
  - Cellular fatty acid typing
  - Peptidoglycan typing
  - Isoprenoid classes
  - Mycolates
- MALDI-TOF MS contribution

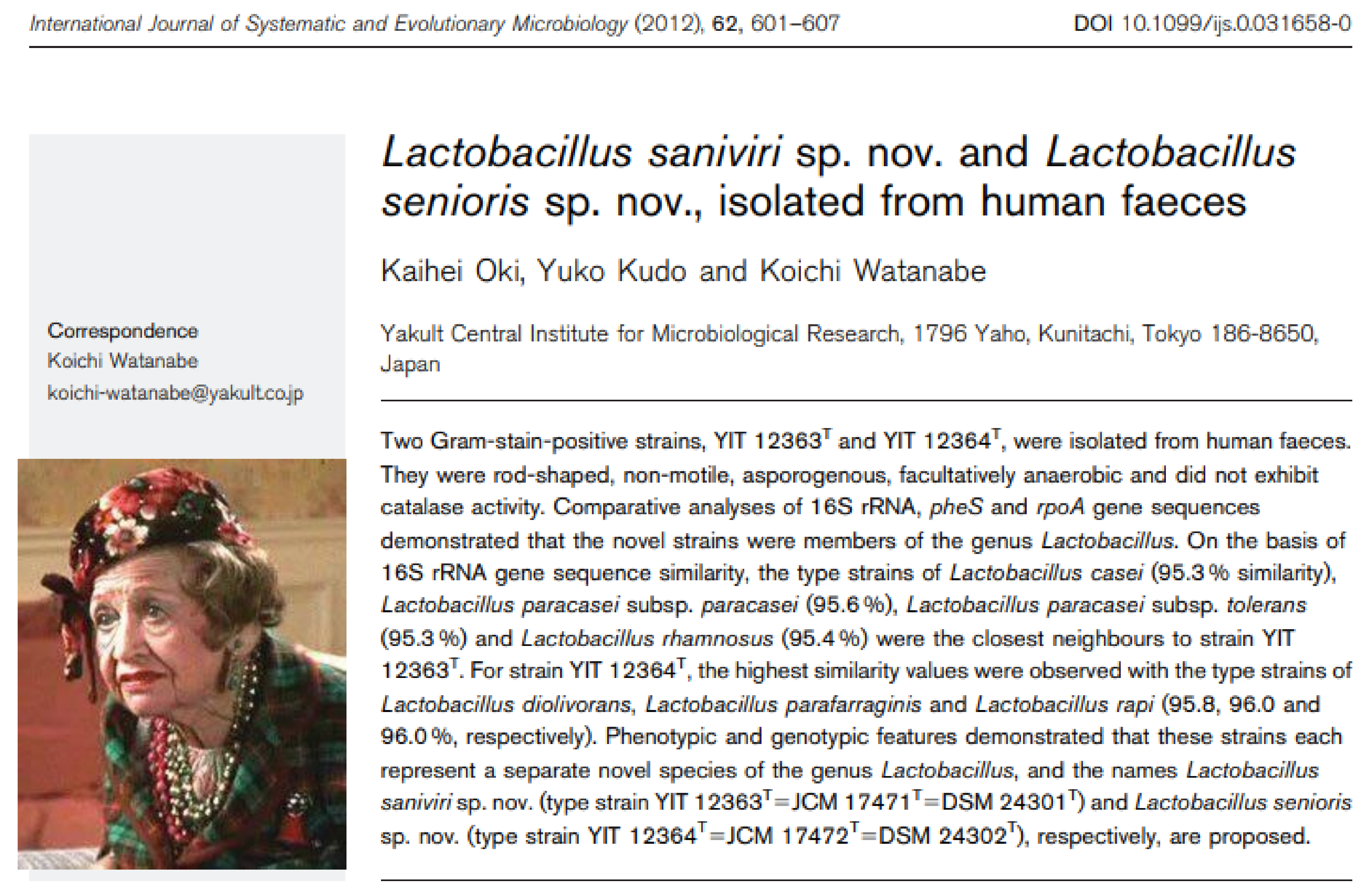
GENOTYPIC CHARACTERIZATION

- % G + C content
- DNA-DNA hybridization (70% threshold)
- Gene sequence analysis
    - 16S rRNA gene is molecular modality of choice
    - Occasionally supplemented by housekeeping genes
        - *rpoB*, *secA1*, *pheS*
    - Present findings with phylogenetic tree
- 98.8% 16S rRNA threshold; can vary with genus

WHOLE GENOME SEQUENCING

- Interpretation predicated on:
  - High-quality genomes with minimal contamination
  - Zero or small number of contigs
  - Adequate depth of coverage; algorithm for analysis
- Analytical parameters
  - Tetranucleotide frequency average
  - Average amino acid identity
  - Average nucleotide identity (ANI)
- 96% ANI (over 90% coverage) threshold; can vary
  - 98.8% for *Mycobacterium tuberculosis*
  - 88.5% for *Stenotrophomonas maltophilia*

PUBLISH IT--DIRECT APPROACH



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

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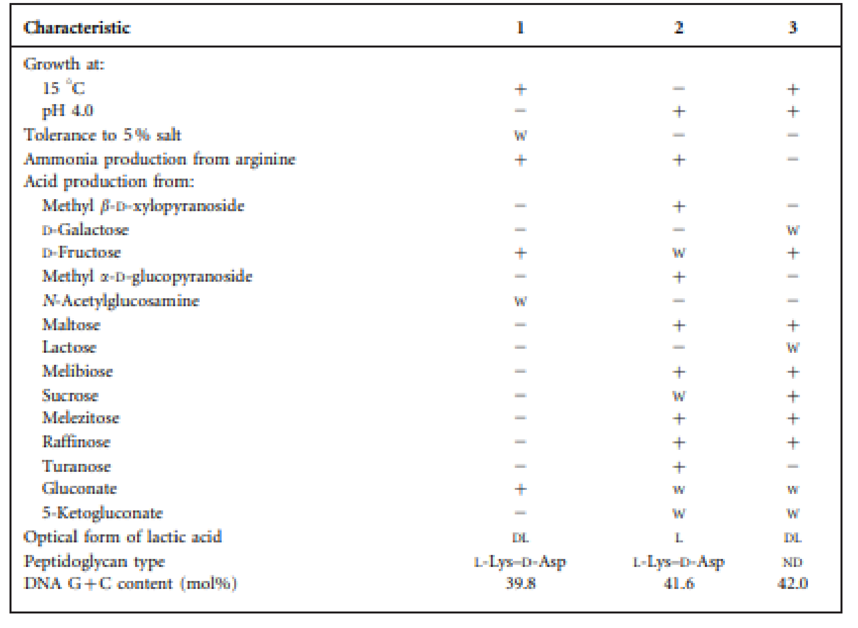
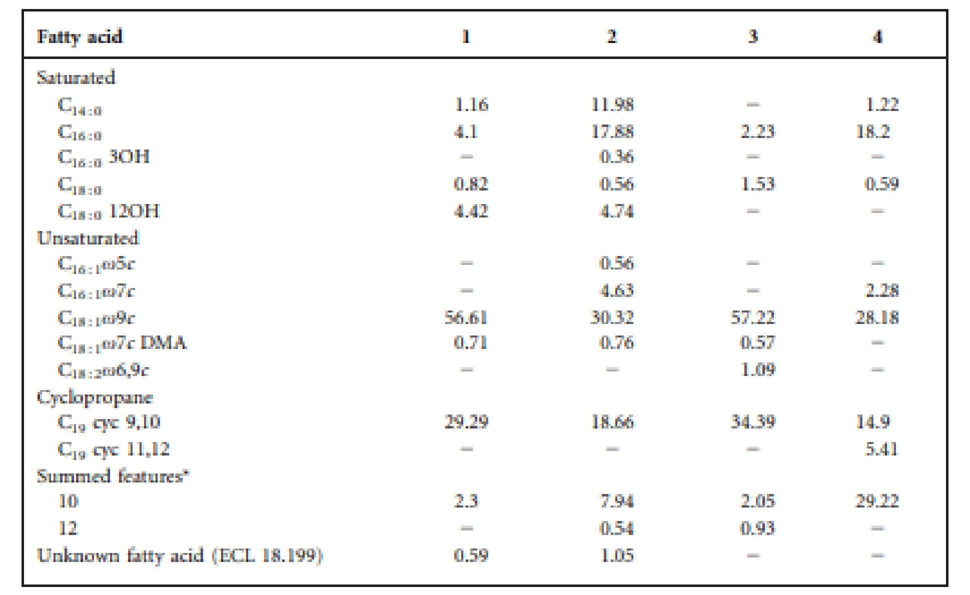
Two Gram-stain-positive strains, YIT 12363^T and YIT 12364^T, were isolated from human faeces. They were rod-shaped, non-motile, asporogenous, facultatively anaerobic and did not exhibit catalase activity. Comparative analyses of 16S rRNA, *pheS* and *rpoA* gene sequences demonstrated that the novel 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



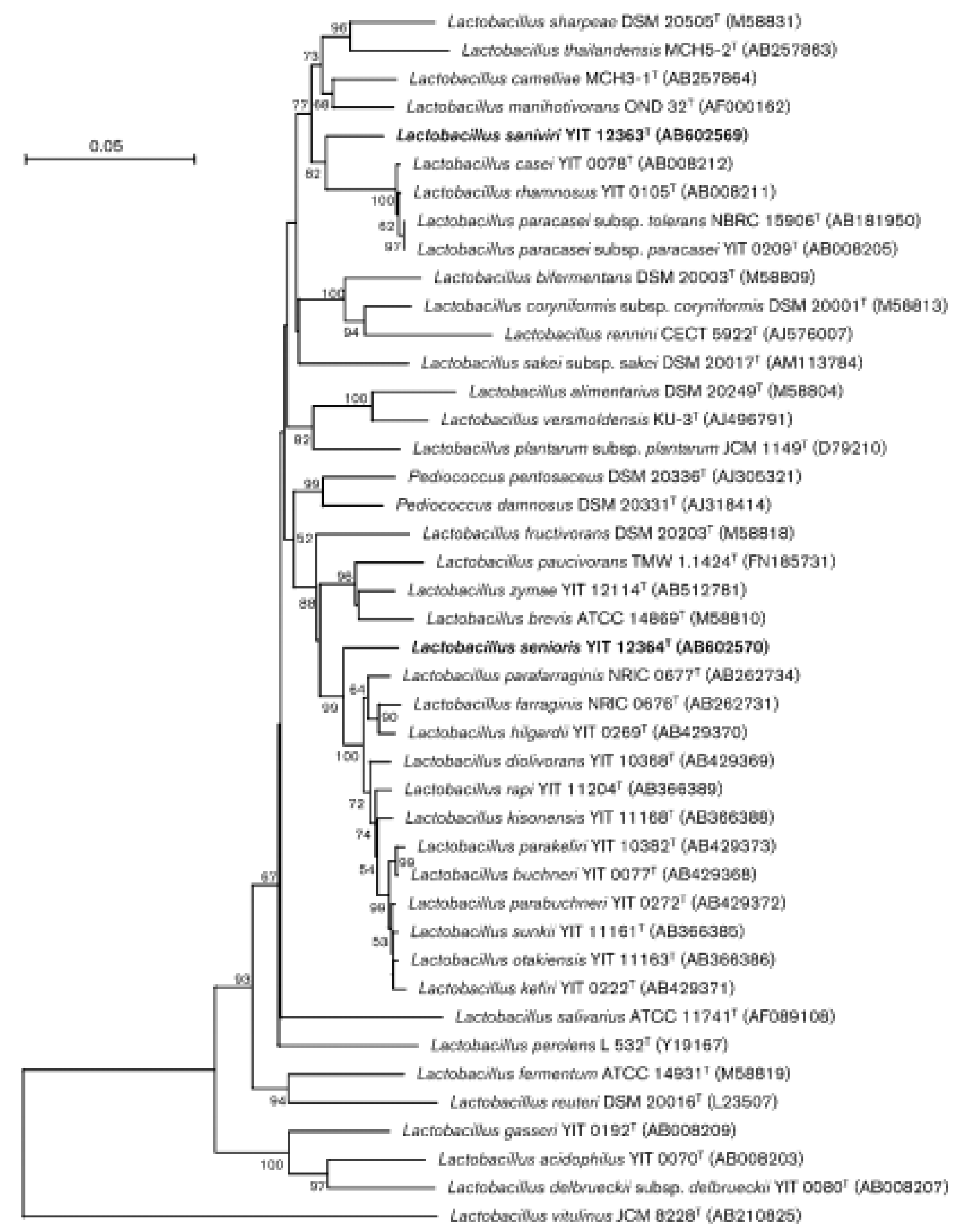
Characteristic	1	2	3
Growth at:			
15 °C	+	−	+
pH 4.0	−	+	+
Tolerance to 5% salt	w	−	−
Ammonia production from arginine	+	+	−
Acid production from:			
Methyl β-D-xylopyranoside	−	+	−
D-Galactose	−	−	w
D-Fructose	+	w	+
Methyl α-D-glucopyranoside	−	+	−
N-Acetylglucosamine	w	−	−
Maltose	−	+	+
Lactose	−	−	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

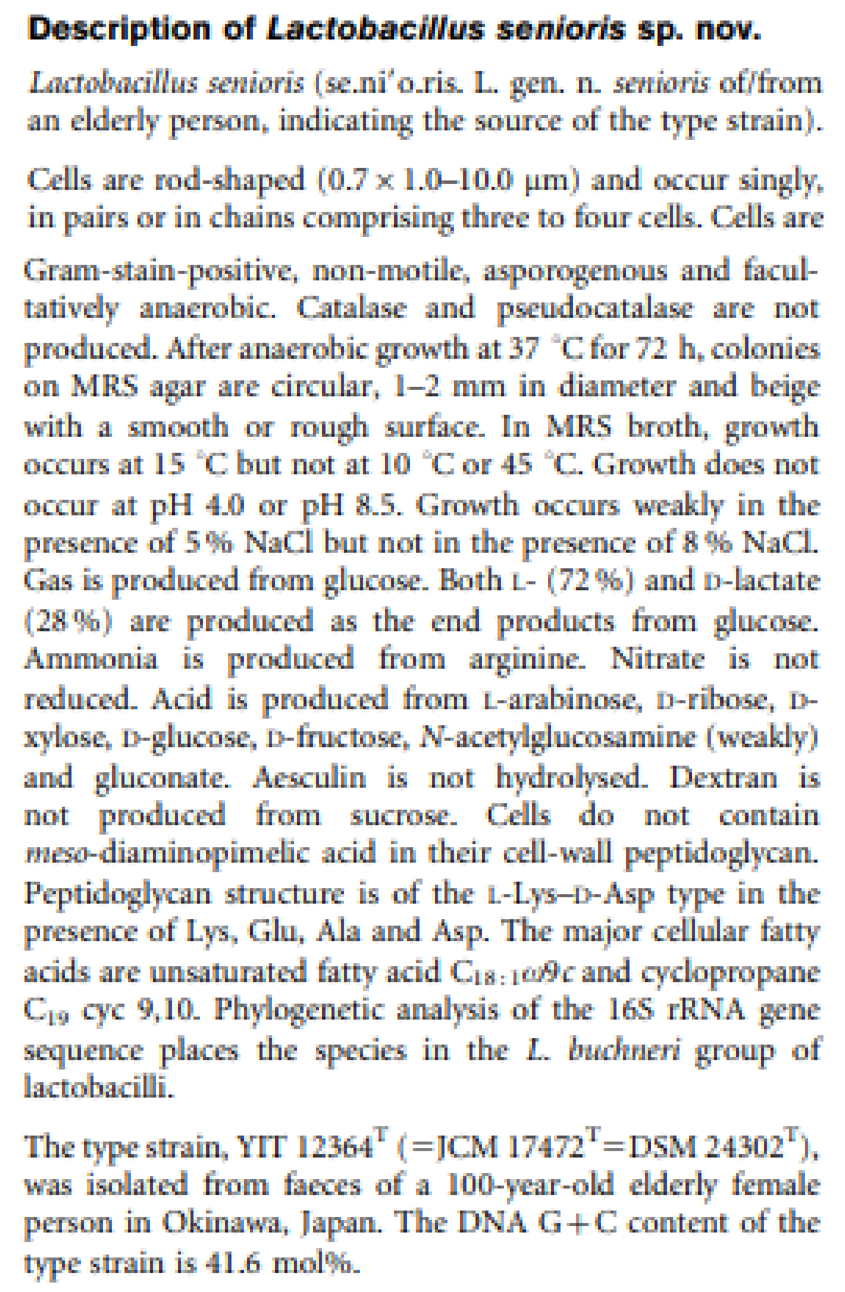
Chemotaxonomic



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)

PUBLISH IT--ALTERNATE APPROACH

- 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

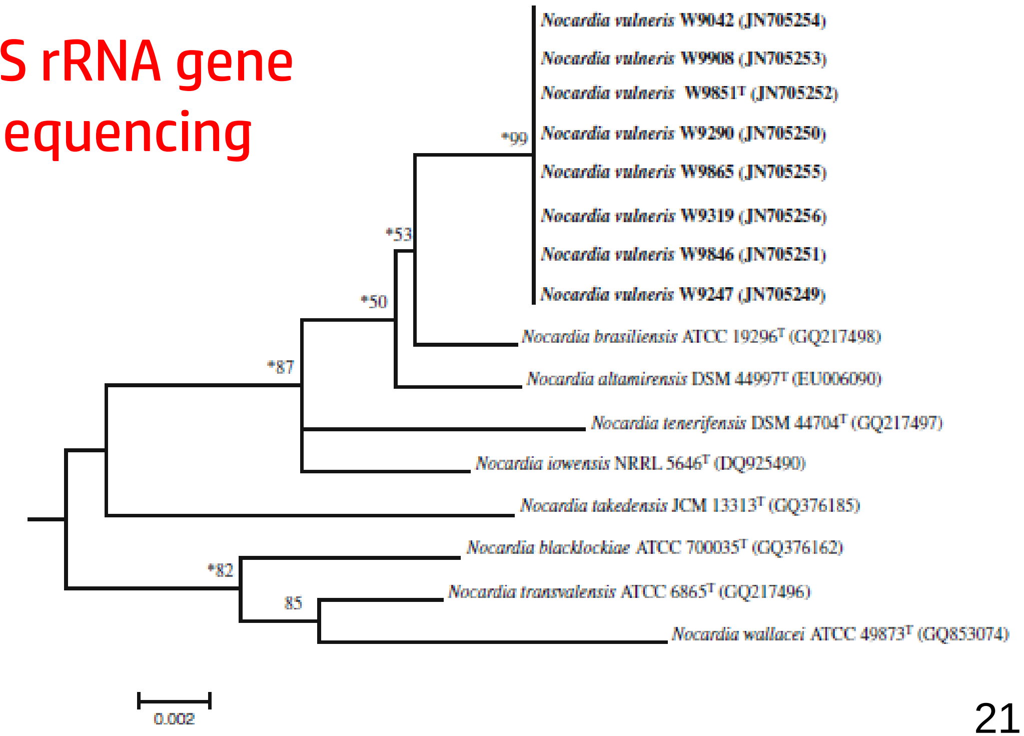
ORIGINAL PAPER

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



Effective description…

polyphasic characterization
novel species
no synonyms
type strain documented

(2014: whole genome sequence
not required yet)

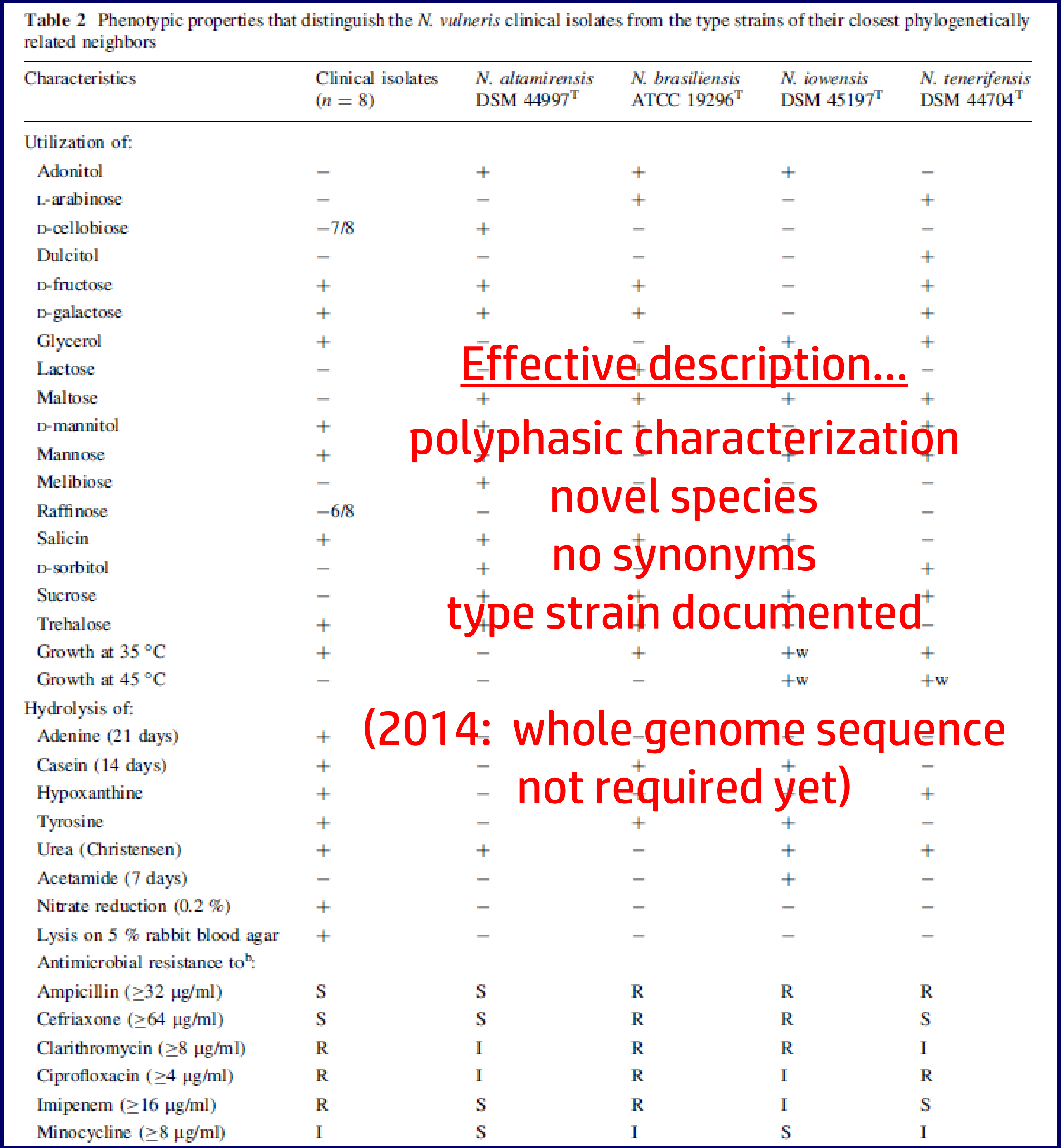
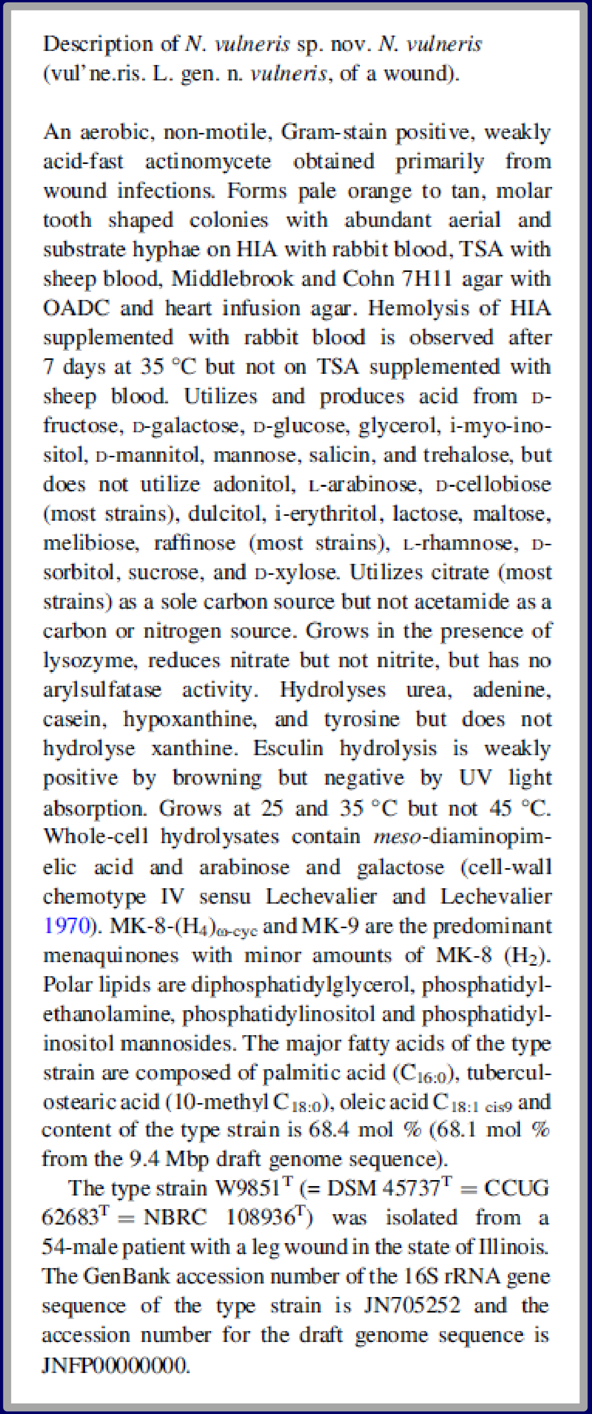


Table 2 Phenotypic properties that distinguish the *N. vulneris* clinical isolates from the type strains of their closest phylogenetically related neighbors

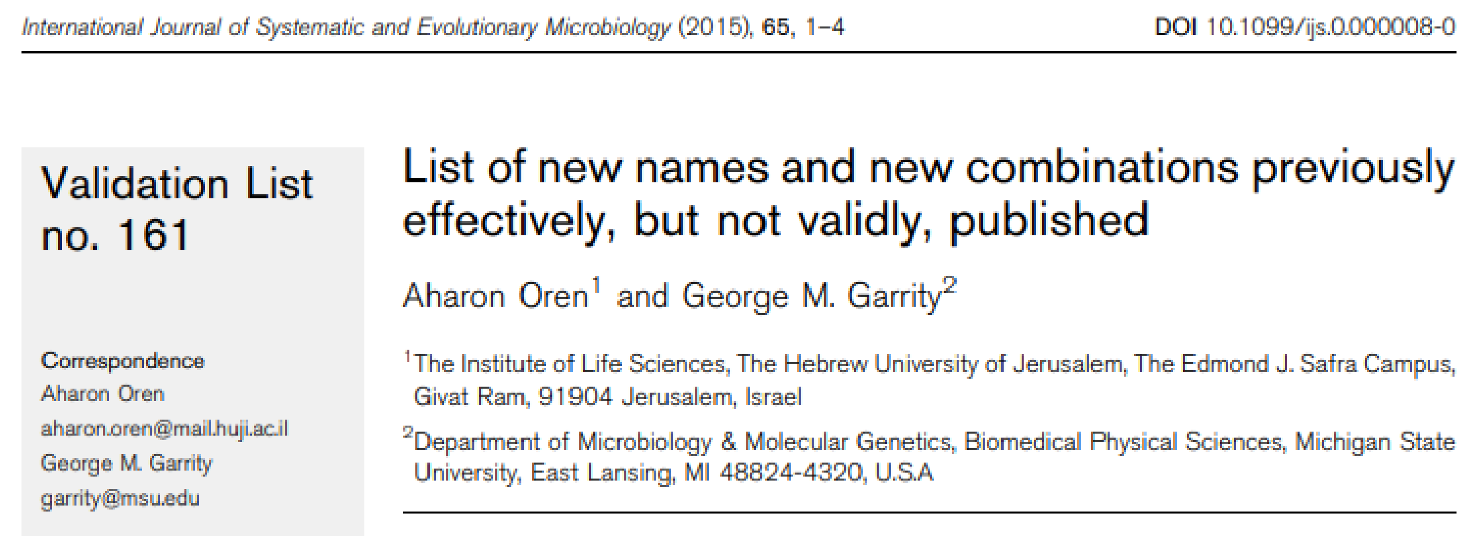
Characteristics	Clinical isolates ($n = 8$)	*N. altamirensis* DSM 44997^{T}	*N. brasiliensis* ATCC 19296^{T}	*N. iowensis* DSM 45197^{T}	*N. tenerifensis* DSM 44704^{T}
Utilization of:					
Adonitol	−	+	+	+	−
L-arabinose	−	−	+	−	+
D-cellobiose	−7/8	+	−	−	−
Dulcitol	−	−	−	−	+
D-fructose	+	+	+	−	+
D-galactose	+	+	+	−	+
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



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

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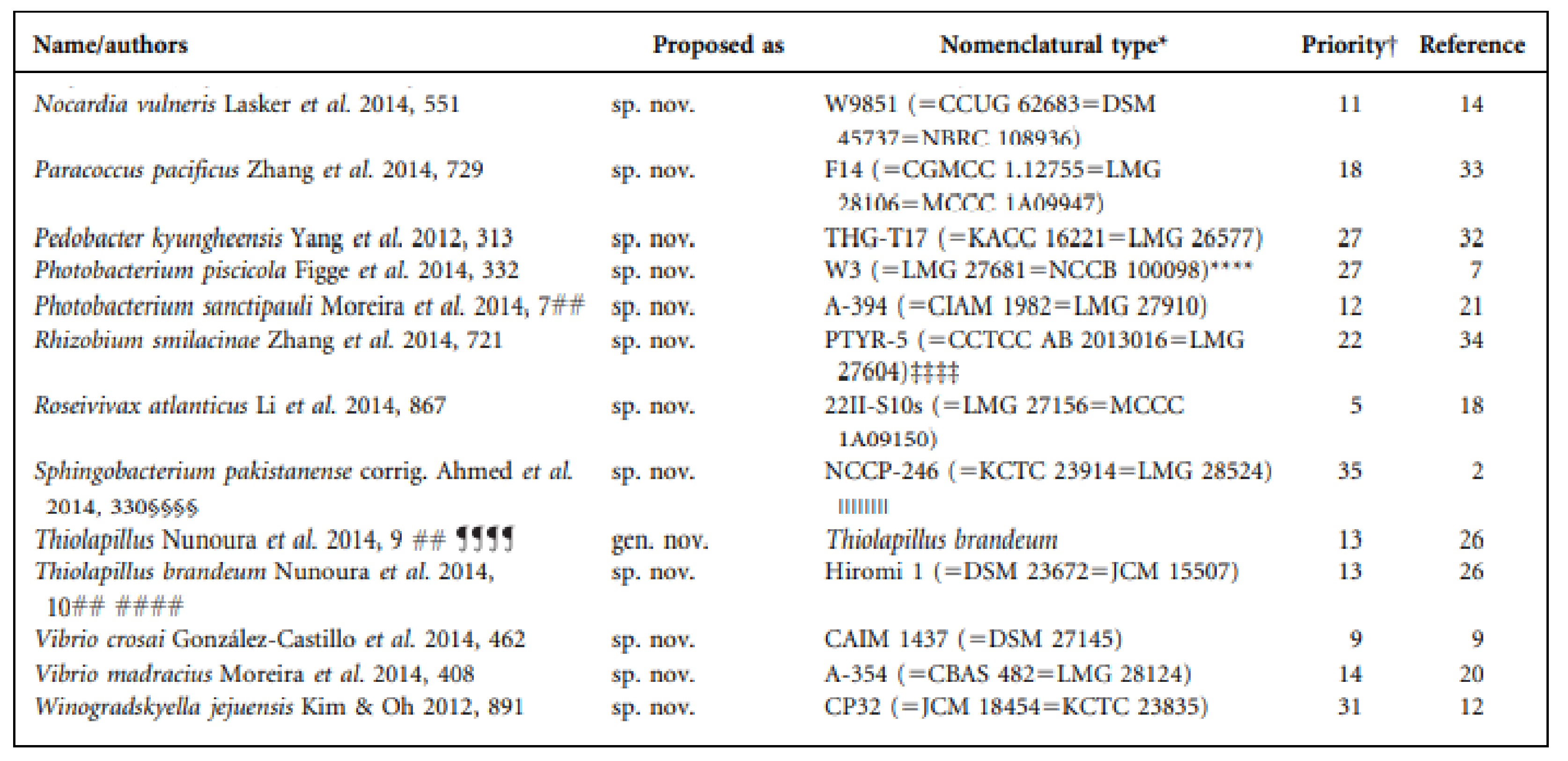


Name/authors	**Proposed as**	**Nomenclatural type***	**Priority†**	**Reference**
Nocardia vulneris Lasker *et al.* 2014, 551	sp. nov.	W9851 (=CCUG 62683=DSM 45737=NBRC 108936)	11	14
Paracoccus pacificus Zhang *et al.* 2014, 729	sp. nov.	F14 (=CGMCC 1.12755=LMG 28106=MCCC 1A09947)	18	33
Pedobacter kyungheensis 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?

ELSEVIER
ISSN 0732-8893

LATEST IMPACT FACTOR 2.528

VOLUME 81
NUMBER 1
JANUARY 2015

Diagnostic Microbiology & Infectious Disease

www.dmidjournal.com

Included in this issue . . .

Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* from 4 Cuban hospitals
Osney Leiva Peláez et al.

Real-world performance of a microarray-based rapid diagnostic for Gram-positive bloodstream infections and potential utility for antimicrobial stewardship
Samuel L. Aitken et al.

Comparison of the Vitek MS and Bruker Microflex LT MALDI-TOF MS platforms for routine identification of commonly isolated bacteria and yeast in the clinical microbiology laboratory
Eszter Deak et al.

Emergence of serogroup 15 *Streptococcus pneumoniae* of diverse genetic backgrounds following the introduction of pneumococcal conjugate vaccines in Hong Kong
Veranja Liyanapathirana et al.

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

ELSEVIER

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

ABSTRACT

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 now been five (2016, 2017, 2019, 2020)

HOW DO WE FIND OUT ABOUT THIS?

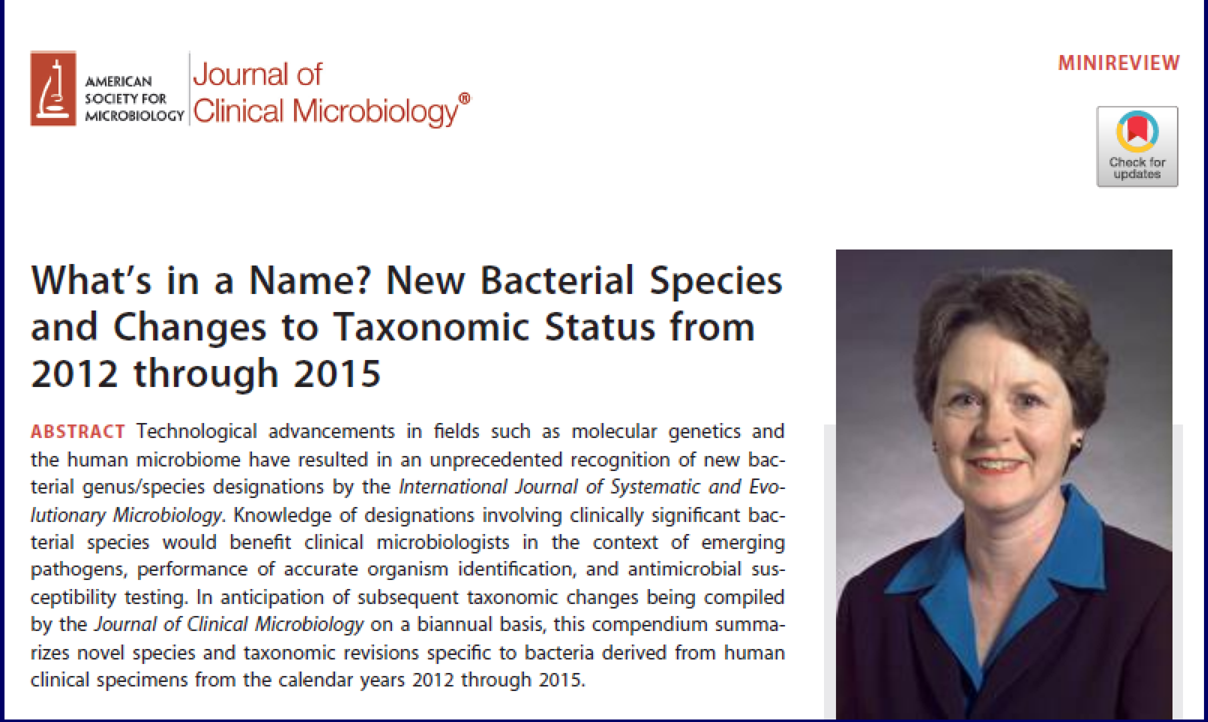
JOURNAL OF
Clinical
Microbiology

JCM

Published Monthly by the
American Society
for Microbiology

Photo quiz (see page 3113)

SEPTEMBER 2011, VOLUME 49, NUMBER 9



AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology®

MINIREVIEW

Check for updates

What's in a Name? New Bacterial Species and Changes to Taxonomic Status from 2012 through 2015

ABSTRACT Technological advancements in fields such as molecular genetics and the human microbiome have resulted in an unprecedented recognition of new bacterial genus/species designations by the *International Journal of Systematic and Evolutionary Microbiology*. Knowledge of designations involving clinically significant bacterial species would benefit clinical microbiologists in the context of emerging pathogens, performance of accurate organism identification, and antimicrobial susceptibility testing. In anticipation of subsequent taxonomic changes being compiled by the *Journal of Clinical Microbiology* on a biannual basis, this compendium summarizes novel species and taxonomic revisions specific to bacteria derived from human clinical specimens from the calendar years 2012 through 2015.

J. Clin. Microbiol. **55:** 24-42; 2017

There will soon be three
(2019, 2021)

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
  - All 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. **73:** 536-538; 2018

- *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. **103:** 672-674; 2020

Changes (i.e., Revisions)

WHY SHOULD WE CARE? #1

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”

COLLEGE of AMERICAN
PATHOLOGISTS

WHY SHOULD WE CARE? #2

- *Actinobacillus actinomycetemcomitans*


3rd Edition

M45

Methods for Antimicrobial Dilution and Disk Susceptibility Testing of Infrequently Isolated or Fastidious Bacteria

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

- *Plesiomonas* spp. moved from M45 to M100 (why?)
- M100 throw-away categories?

  Streptococcus viridans group
  Other non-*Enterobacterales*

WHY SHOULD WE CARE? #3

- *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
  Hong Kong research revealed differences in clinical picture (sepsis, pneumonia, meningitis; ↑ mortality) and epidemiology (vertical transmission)

  Sci. Rep. **6:** 26045; 2016

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

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

  Sci. Rep. **8:** 5392; 2018

WHY SHOULD WE CARE? #4

- *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. **68:** 3826-3831; 2018

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

Front. Microbiol. **9:** 1743; 2018

WHY SHOULD WE CARE? #5

- *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

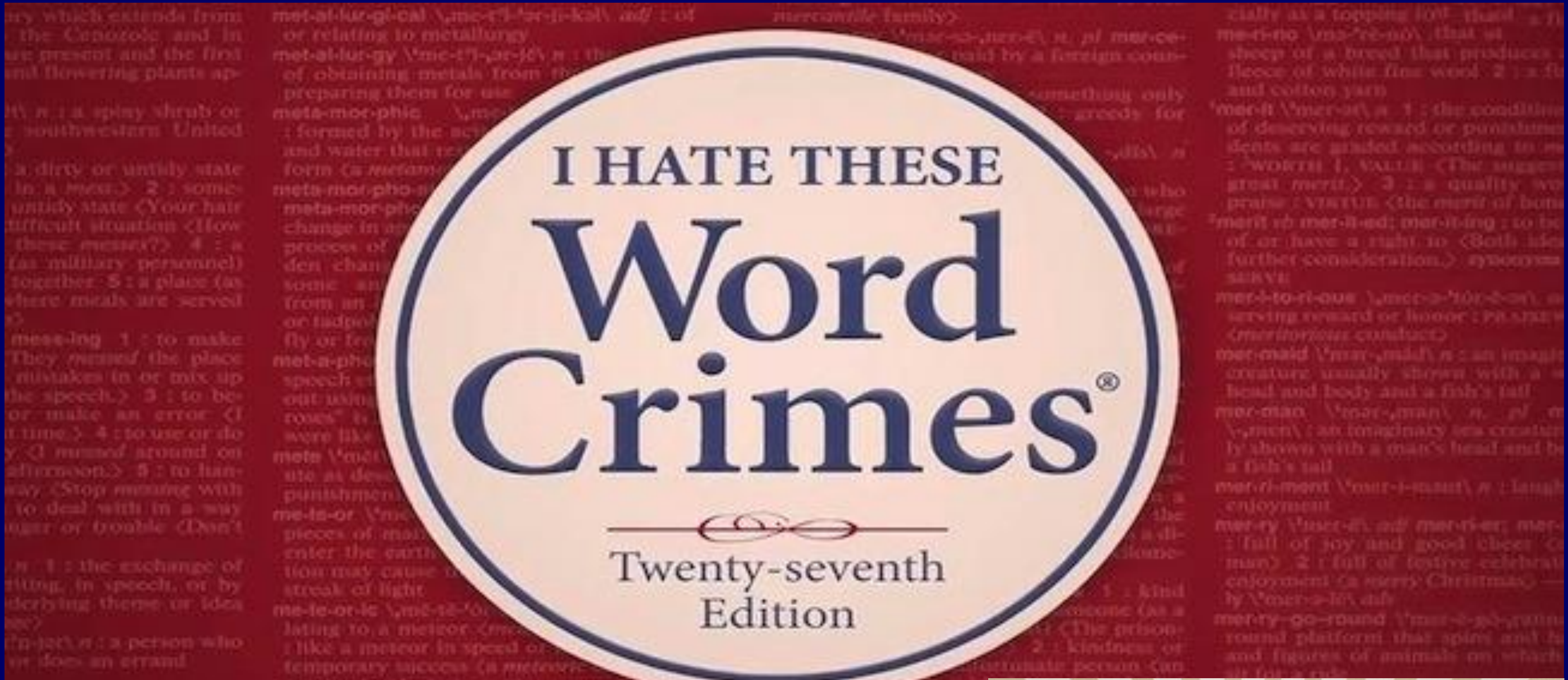
  Front. Cell Neurosci. **13:** 402; 2019

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

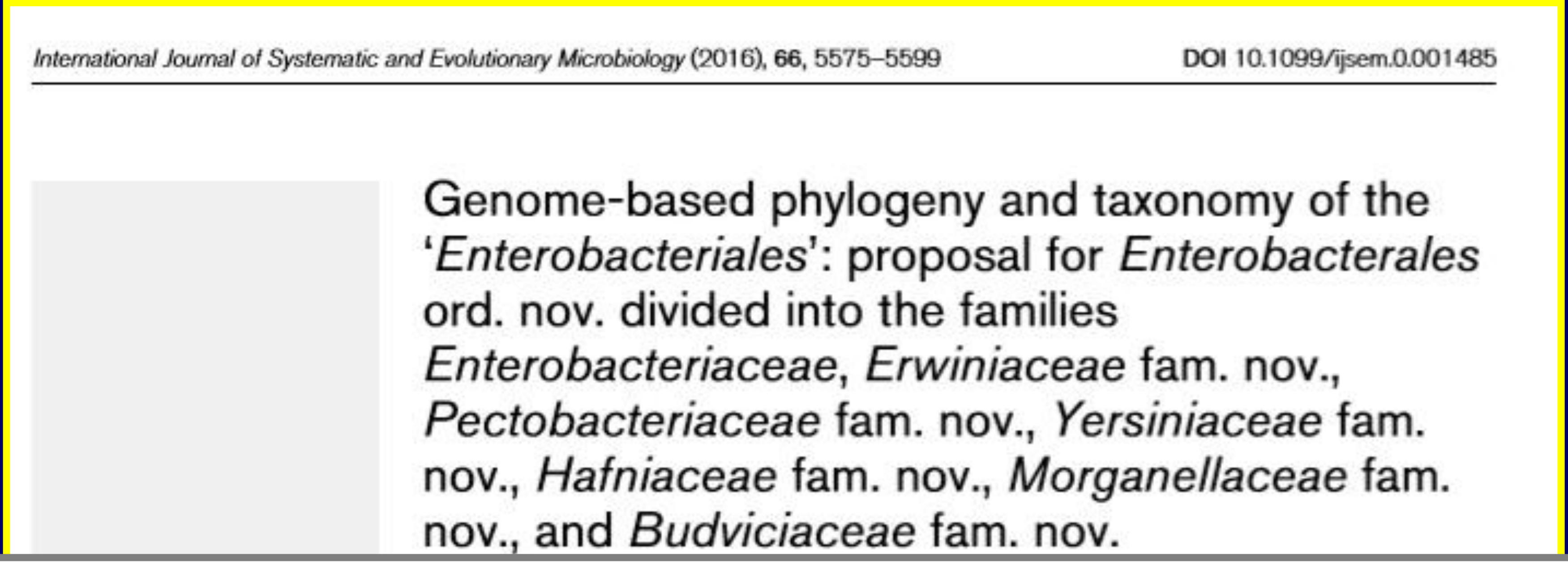
  Originally isolated from feces of healthy male

  Abundance of this organism found in patients with rheumatoid arthritis

  Genes (Basel) **10:** 748; 2019



Okay, now here's the deal
I'll try to educate ya
Gonna familiarize
You with the nomenclature
You'll learn the definitions
Of nouns and prepositions
Literacy's your mission



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

Enterobacterales

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

DIRTY DOZEN (out of ~70)

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. **66:** 5575-5599; 2016

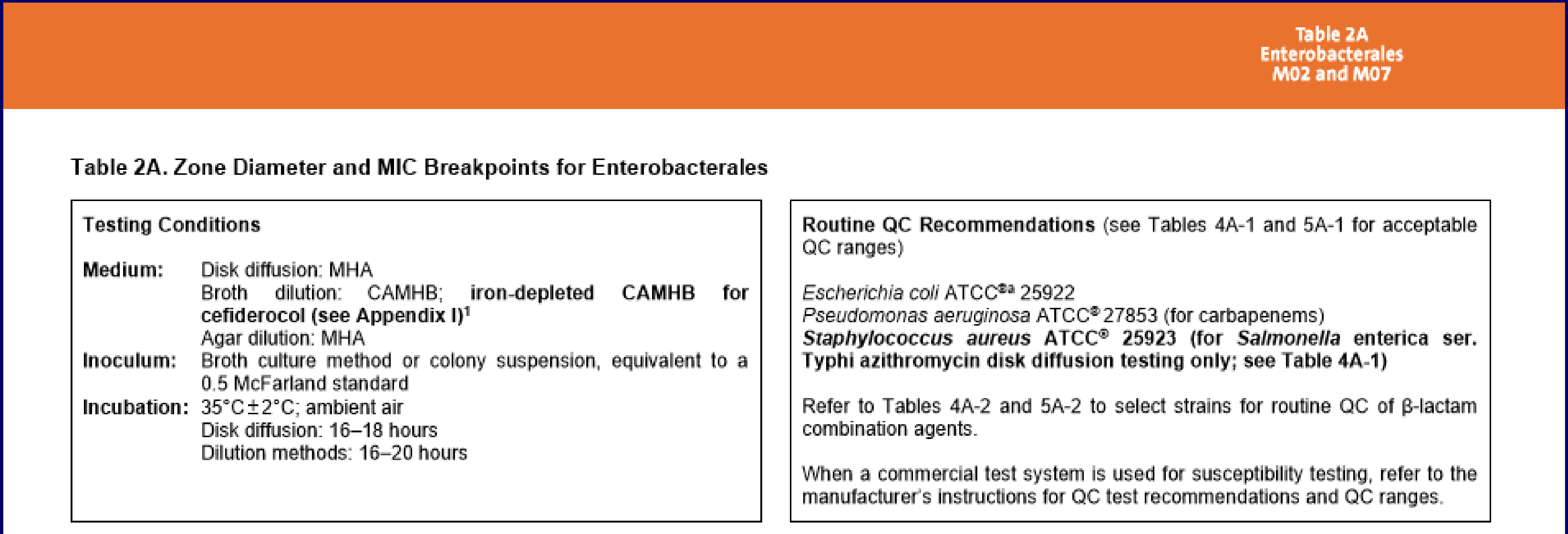


Table 2A
Enterobacterales
M02 and M07

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

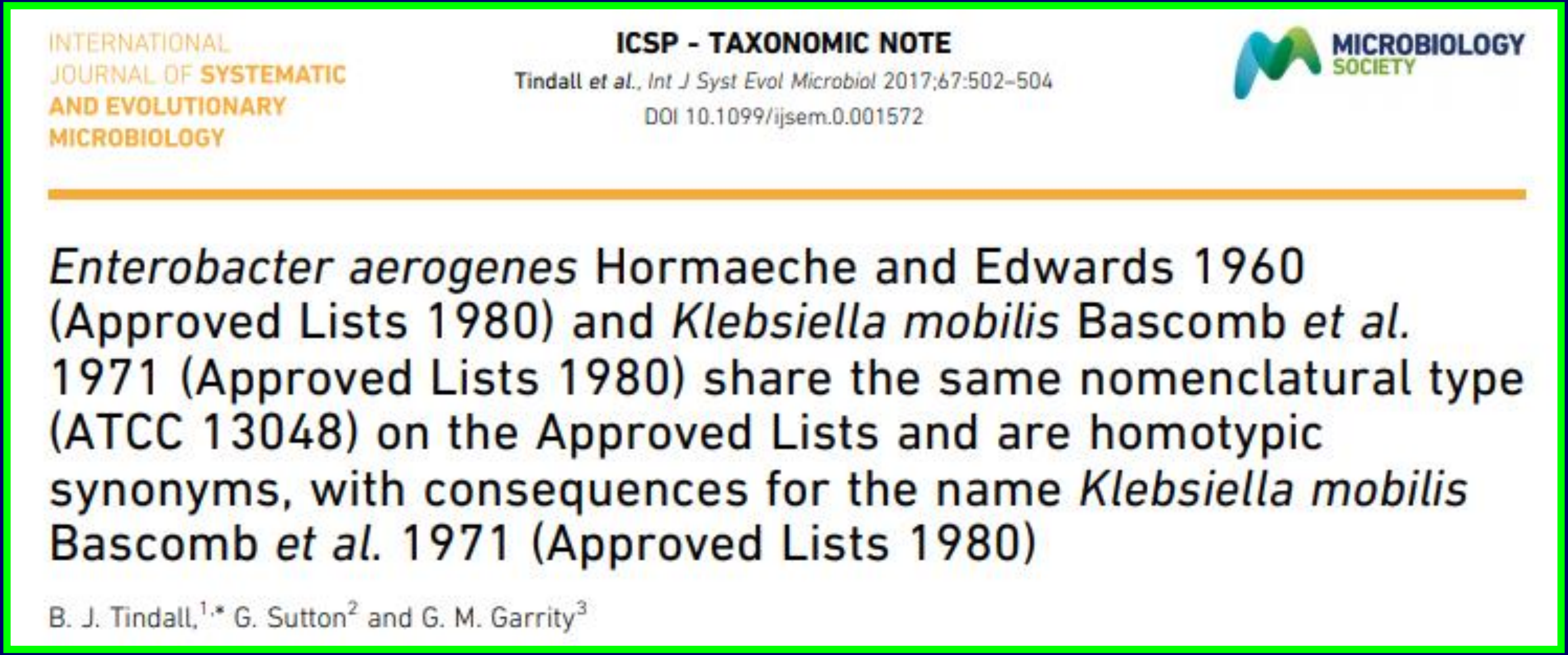
Routine QC Recommendations (see Tables 4A-1 and 5A-1 for acceptable QC ranges)

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.

SAME ORDER



INTERNATIONAL JOURNAL OF **SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY**

ICSP - TAXONOMIC NOTE

Tindall *et al., Int J Syst Evol Microbiol* 2017;67:502–504

DOI 10.1099/ijsem.0.001572

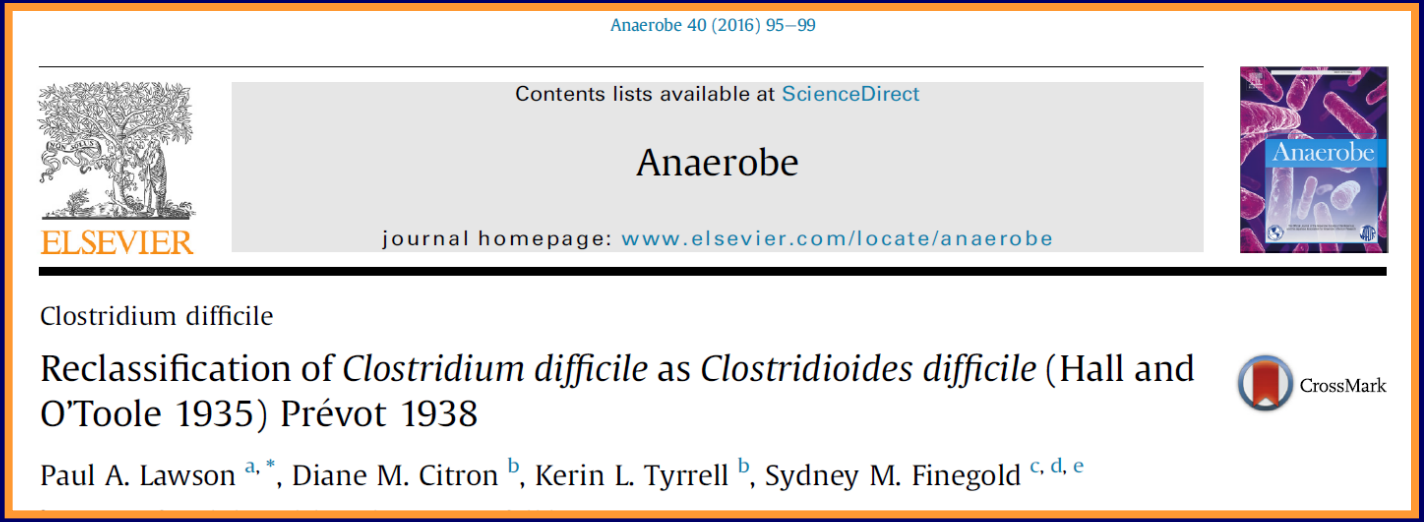
MICROBIOLOGY SOCIETY

Enterobacter aerogenes Hormaeche and Edwards 1960 (Approved Lists 1980) and *Klebsiella mobilis* Bascomb *et al.* 1971 (Approved Lists 1980) share the same nomenclatural type (ATCC 13048) on the Approved Lists and are homotypic synonyms, with consequences for the name *Klebsiella mobilis* Bascomb *et al.* 1971 (Approved Lists 1980)

B. J. Tindall,[1,*] G. Sutton[2] and G. M. Garrity[3]

- *Klebsiella aerogenes* originally “linked” to taxon *Klebsiella mobilis*; *K. mobilis* declared illegitimate
- Empiric susceptibility consequences

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

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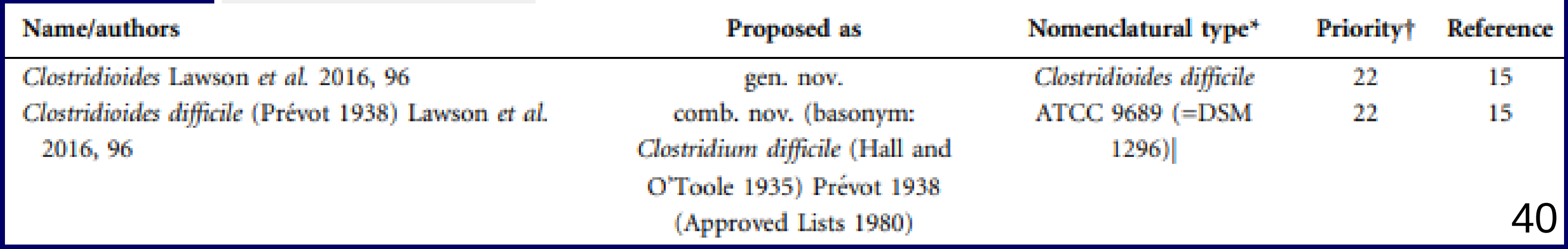
Aharon Oren
aharon.oren@mail.huji.ac.il
George M. Garrity
garrity@msu.edu



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. **66:** 1009-1016; 2016

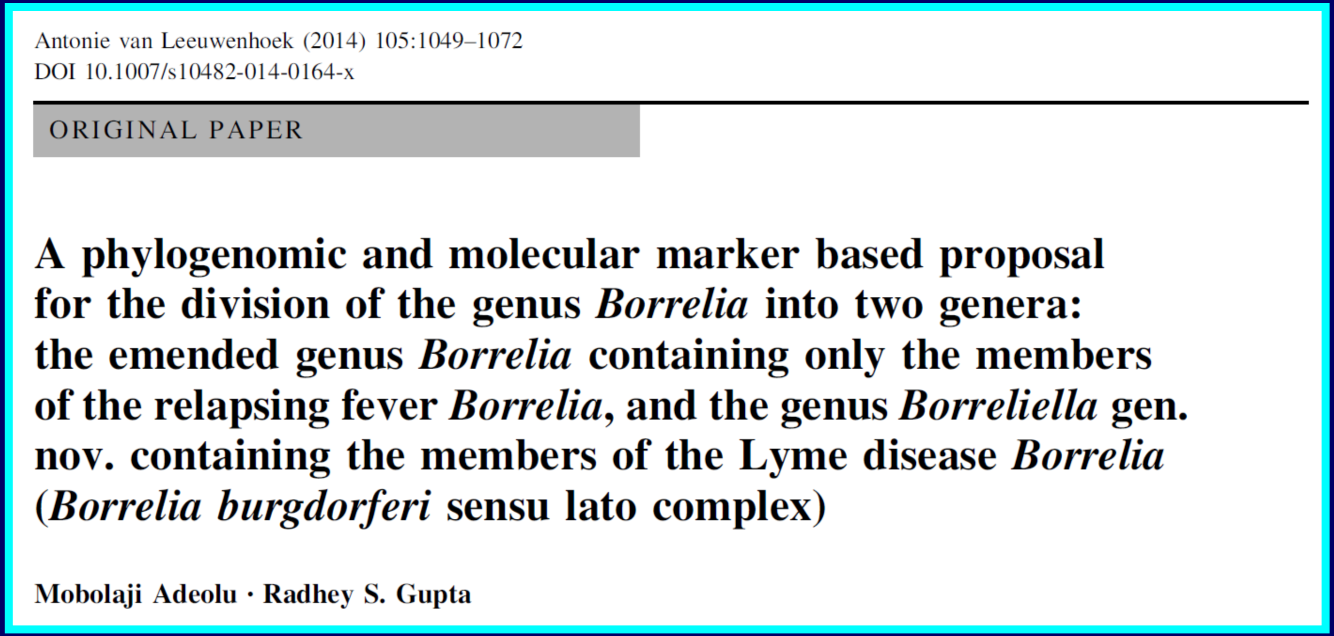
- rRNA cluster IX

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

  Environ. Microbiol. **15:** 2631-2641; 2013

- *Clostridioides* ended up being a “compromise”

HOW ABOUT THIS ONE?

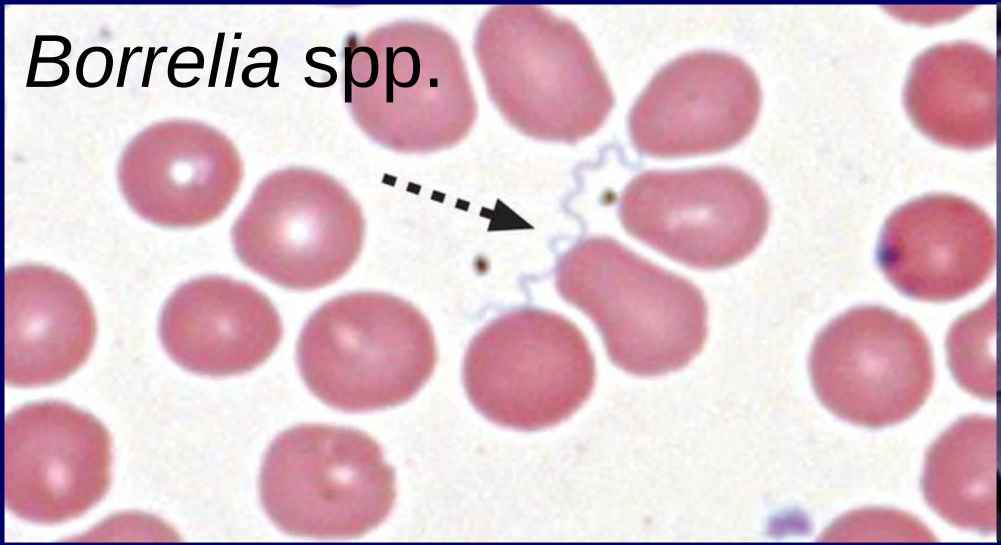


Antonie van Leeuwenhoek (2014) 105:1049–1072
DOI 10.1007/s10482-014-0164-x

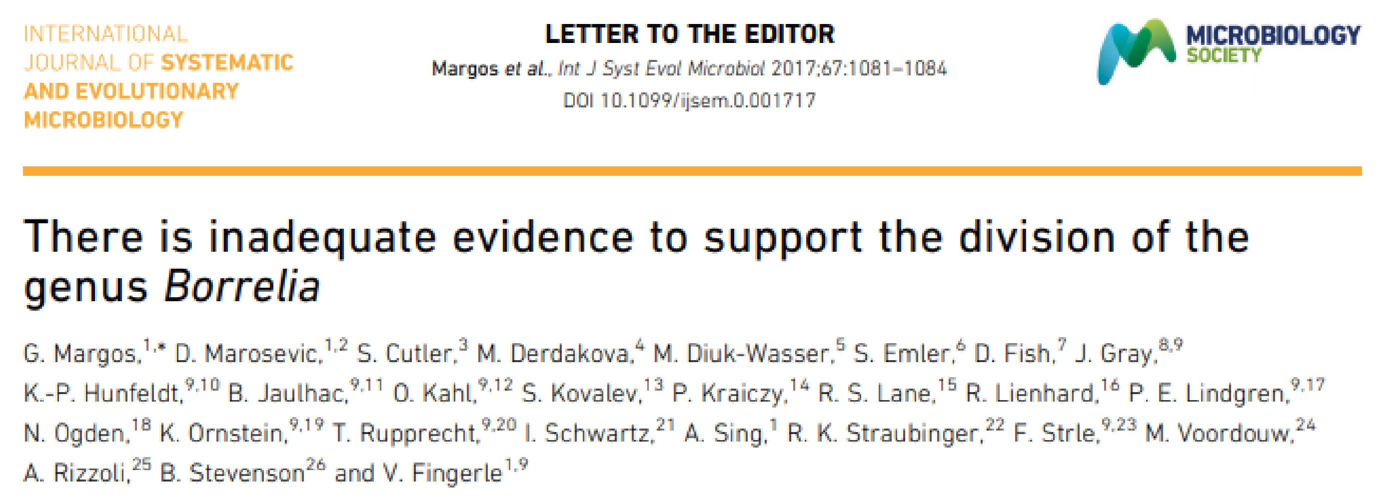
ORIGINAL PAPER

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
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AND EVOLUTIONARY
MICROBIOLOGY

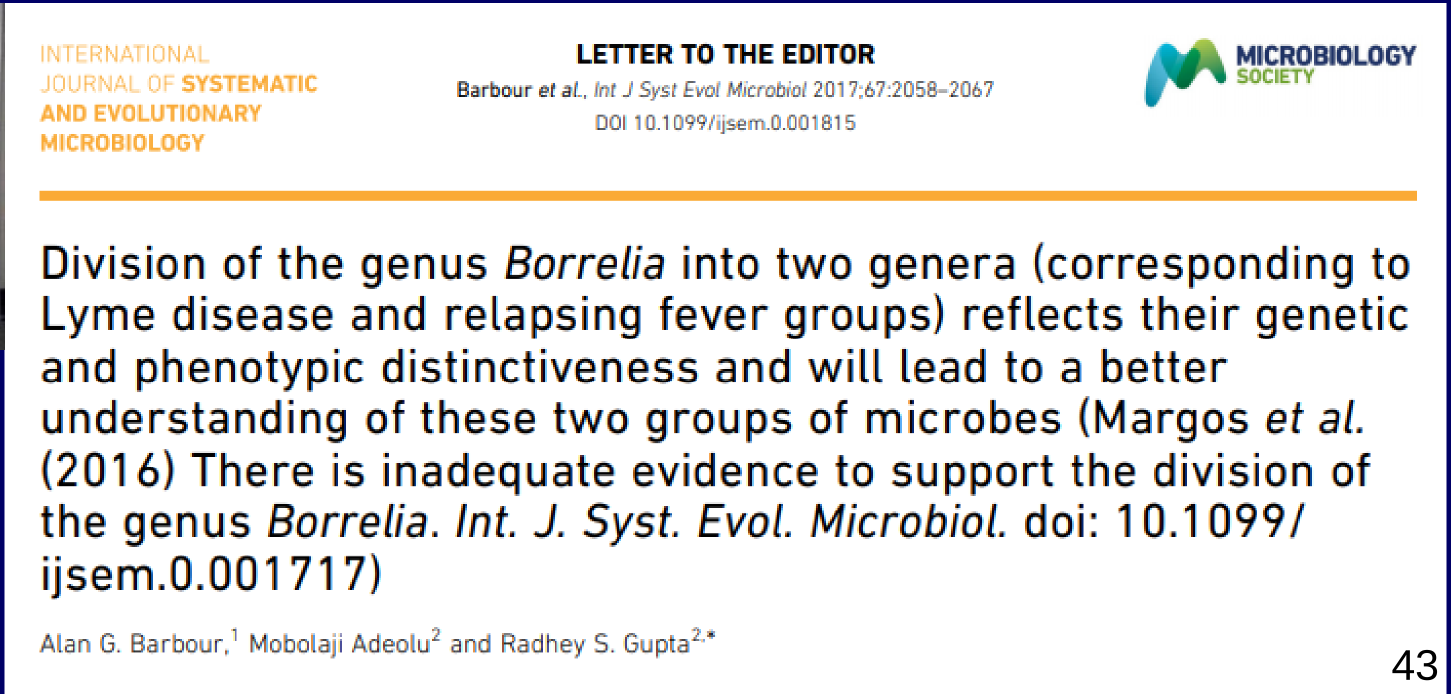
LETTER TO THE EDITOR

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

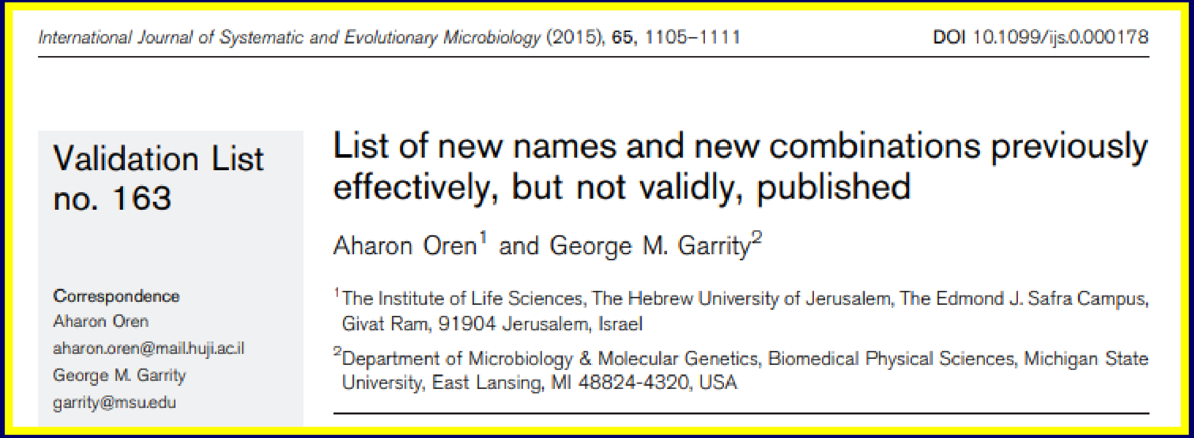
Barbour *et al.*, *Int J Syst Evol Microbiol* 2017;67:2058–2067
DOI 10.1099/ijsem.0.001815

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,*]

SEVERAL HAVE BEEN ACCEPTED



International Journal of Systematic and Evolutionary Microbiology (2015), **65**, 1105–1111 **DOI** 10.1099/ijs.0.000178

Validation List no. 163

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, USA

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

Borreliella bavariensis comb. nov.
Borreliella burgdorferi comb. nov.
Borreliella carolinensis comb. nov.
Borreliella garinii comb. nov.
Borreliella japonica comb. nov.
Borreliella kurtenbachii comb. nov.
Borreliella sinica comb. nov.
Borreliella spielmanii comb. nov.

INTERNATIONAL JOURNAL OF **SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY**

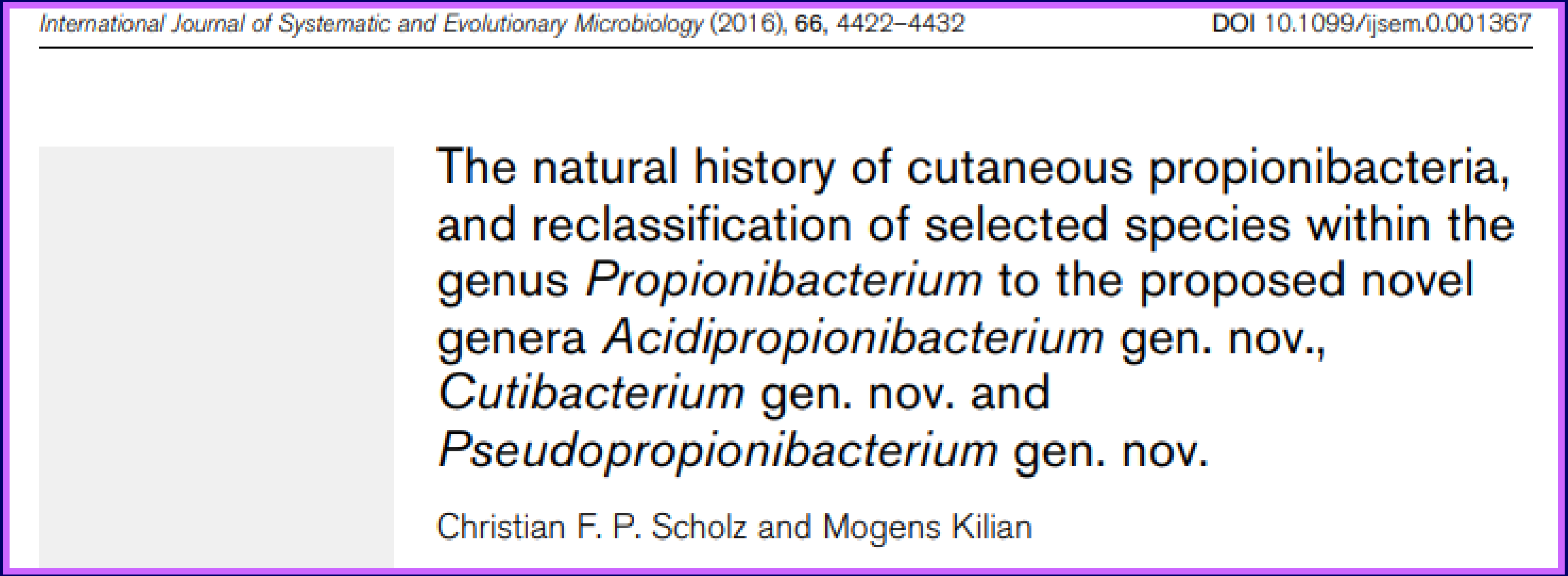
VALIDATION LIST NO. 182
Oren and Garrity, *Int J Syst Evol Microbiol* 2018;68:2130–2133
DOI 10.1099/ijsem.0.002831

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

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

Borreliella afzelii comb. nov.
Borreliella americana comb. nov.
Borreliella valaisiana comb. nov.

ANOTHER GRAM-POSITIVE ROD



International Journal of Systematic and Evolutionary Microbiology (2016), **66**, 4422–4432 **DOI** 10.1099/ijsem.0.001367

The natural history of cutaneous propionibacteria, and reclassification of selected species within the genus *Propionibacterium* to the proposed novel genera *Acidipropionibacterium* gen. nov., *Cutibacterium* gen. nov. and *Pseudopropionibacterium* gen. nov.

Christian F. P. Scholz and Mogens Kilian

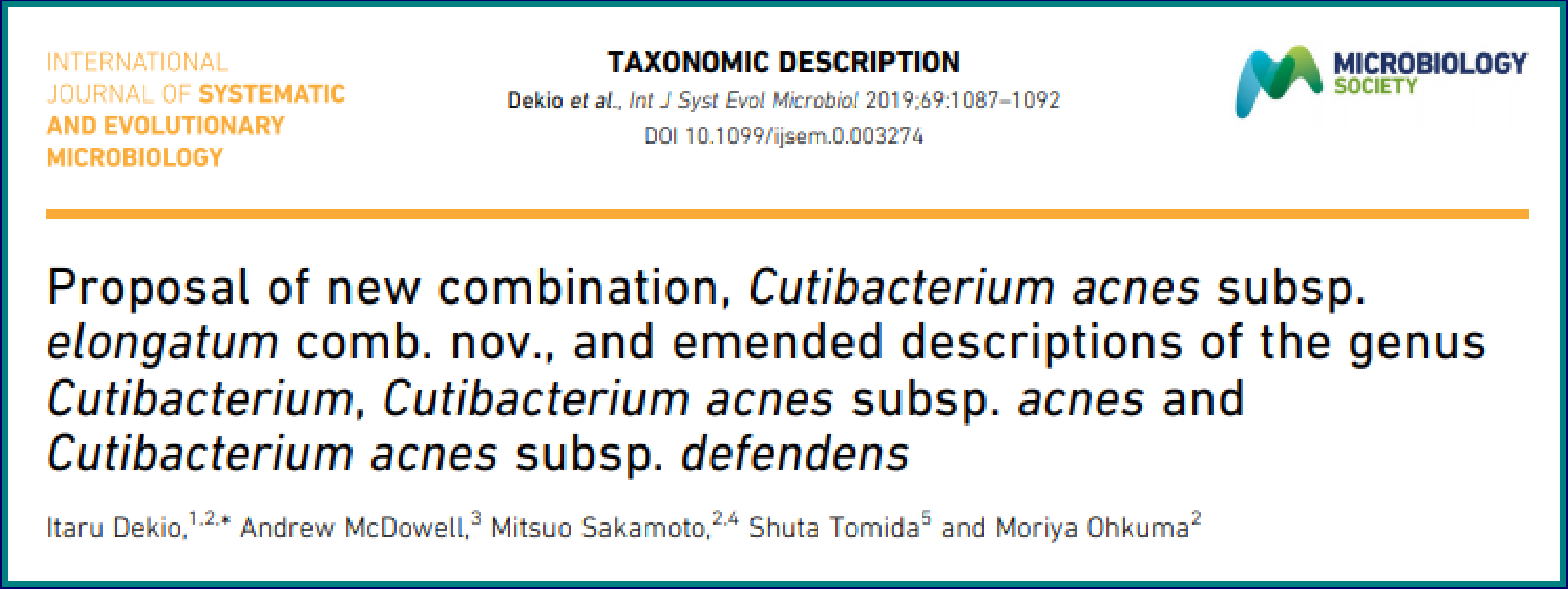
6 *Acidipropionibacterium* spp.

3 *Cutibacterium* spp. (including *Cutibacterium acnes* comb. nov)

Pseudopropionibacterium propionicum comb. nov.

Propionibacterium spp.

MORE *Cutibacterium* spp.



INTERNATIONAL
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MICROBIOLOGY

TAXONOMIC DESCRIPTION

Dekio *et al.*, *Int J Syst Evol Microbiol* 2019;69:1087–1092
DOI 10.1099/ijsem.0.003274

Proposal of new combination, *Cutibacterium acnes* subsp. *elongatum* comb. nov., and emended descriptions of the genus *Cutibacterium*, *Cutibacterium acnes* subsp. *acnes* and *Cutibacterium acnes* subsp. *defendens*

Itaru Dekio,[1,2,*] Andrew McDowell,[3] Mitsuo Sakamoto,[2,4] Shuta Tomida[5] and Moriya Ohkuma[2]

Cutibacterium acnes subsp. *acnes*
Cutibacterium acnes subsp. *elongatum* comb. nov.
Cutibacterium acnes subsp. *defendens*

Big Ones for 2021

NOVEL SPECIES TO KEEP AN EYE ON

- Gram-positive cocci (n = 6)

  Four new species of *Macrococcus* spp.
  Staphylococcus cornubiensis sp. nov. is fourth member of
  Staphylococcus intermedius group

- Gram-positive bacilli (n = 7)

  Two new species of *Tsukamurella* spp.
  Corynebacterium fournieri sp. nov.
  Corynebacterium belfantii sp. nov.
  Corynebacterium diphtheriae subsp. *diphtheriae* subsp. nov.
  subsp. *lausannense* subsp. nov.

J. Clin. Microbiol. **59:** e01309-20; 2021

NOVEL SPECIES TO KEEP AN EYE ON

- Gram-negative bacilli (n = 23)

  Eight new species of *Enterobacteriacae*
  Two new species of *Morganellaceae*
  Yersinia kristensenii subsp. *rochesterensis* subsp. nov.
  Pandorea fibrosis sp. nov. from CF respiratory secretions
  Elizabethkingia occulta sp. nov.
  Three new species of *Gardnerella* spp.
  Campylobacter armoricus sp. nov. (also French shellfish)

- Spirochetes (n = 1)

  Leptospira venezuelensis sp. nov.

J. Clin. Microbiol. **59:** e01309-20; 2021

NOVEL SPECIES TO KEEP AN EYE ON

- Anaerobic Gram-positive bacteria (n = 25)

Clostridium neonatale sp. nov.

Outbreak of neonatal necrotizing enterocolitis
Originally identified as *Clostridium clostridioforme*

Bacterial vaginosis	*Murdochiella vaginalis* sp. nov. *Collinsella vaginalis* sp. nov.

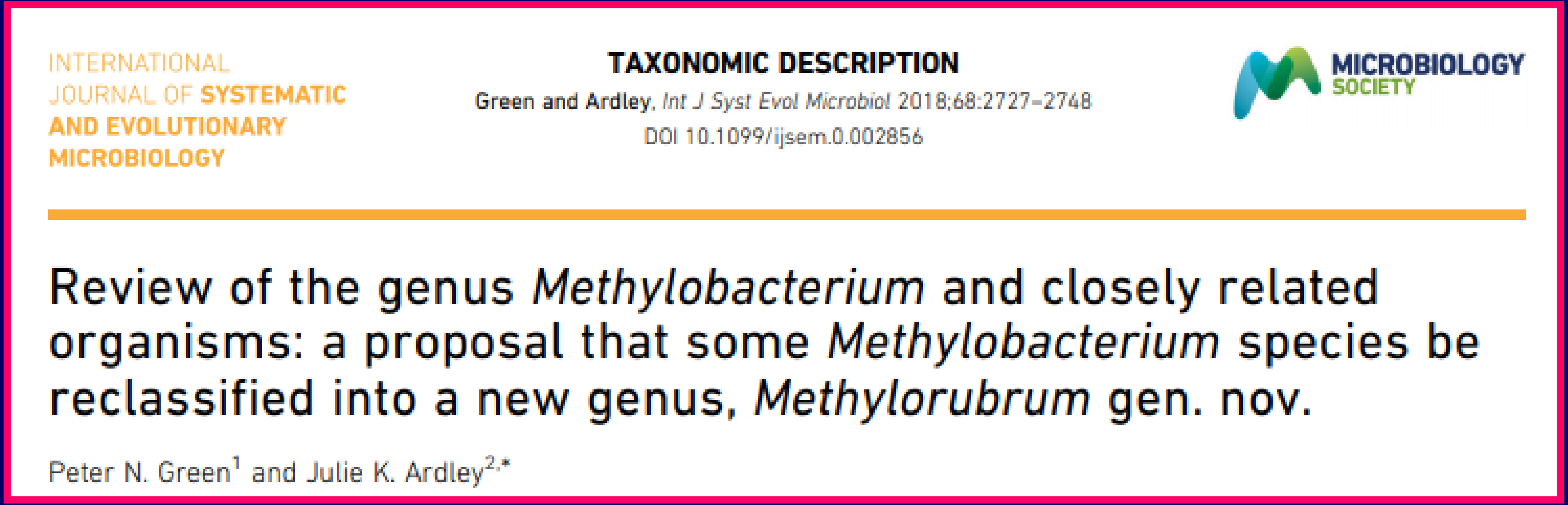
- Anaerobic Gram-negative bacteria (n = 12)

Gram-negative cocci	*Veillonella infantium* sp. nov. *Libanicoccus massiliensis* sp. nov. *Sutterella megalosphaeroides* sp. nov.

Three new *Prevotella* spp.; two new *Parabacteroides* spp.

J. Clin. Microbiol. **59:** e01309-20; 2021

REVISIONS TO *Methylobacterium*



INTERNATIONAL
JOURNAL OF **SYSTEMATIC
AND EVOLUTIONARY
MICROBIOLOGY**

TAXONOMIC DESCRIPTION
Green and Ardley, *Int J Syst Evol Microbiol* 2018;68:2727–2748
DOI 10.1099/ijsem.0.002856

MICROBIOLOGY
SOCIETY

Review of the genus *Methylobacterium* and closely related organisms: a proposal that some *Methylobacterium* species be reclassified into a new genus, *Methylorubrum* gen. nov.

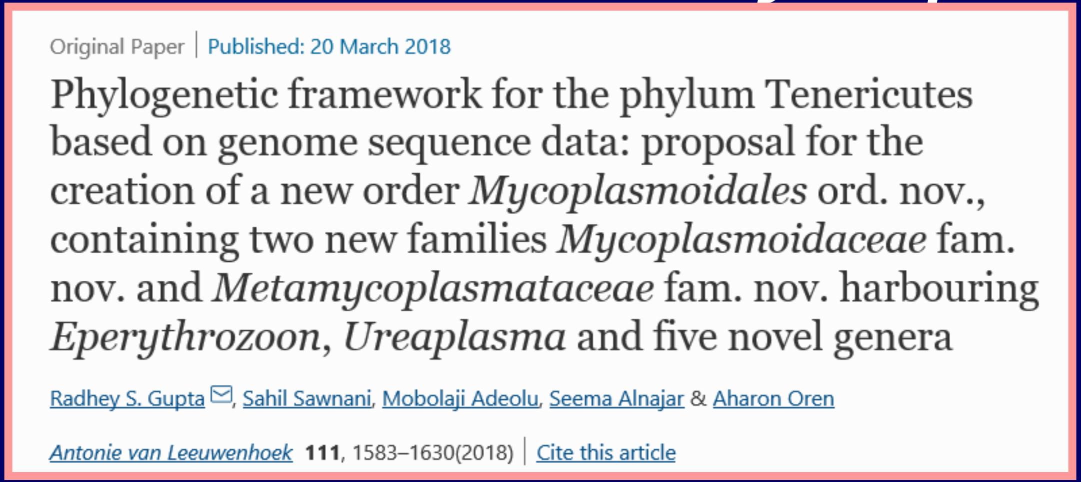
Peter N. Green[1] and Julie K. Ardley[2,*]

- Eleven species move to *Methylorubrum* gen. nov.

Methylorubrum extorquens comb. nov.
Methylorubrum aminovorans comb. nov.
Methylorubrum thiocyanatum comb. nov.
Methylorubrum rhodesianum comb. nov.
M. zatmanii comb. nov.
M. podarium comb. nov.

- Over 30 species stay in *Methylobacterium*

REVISIONS TO *Mycoplasma*



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

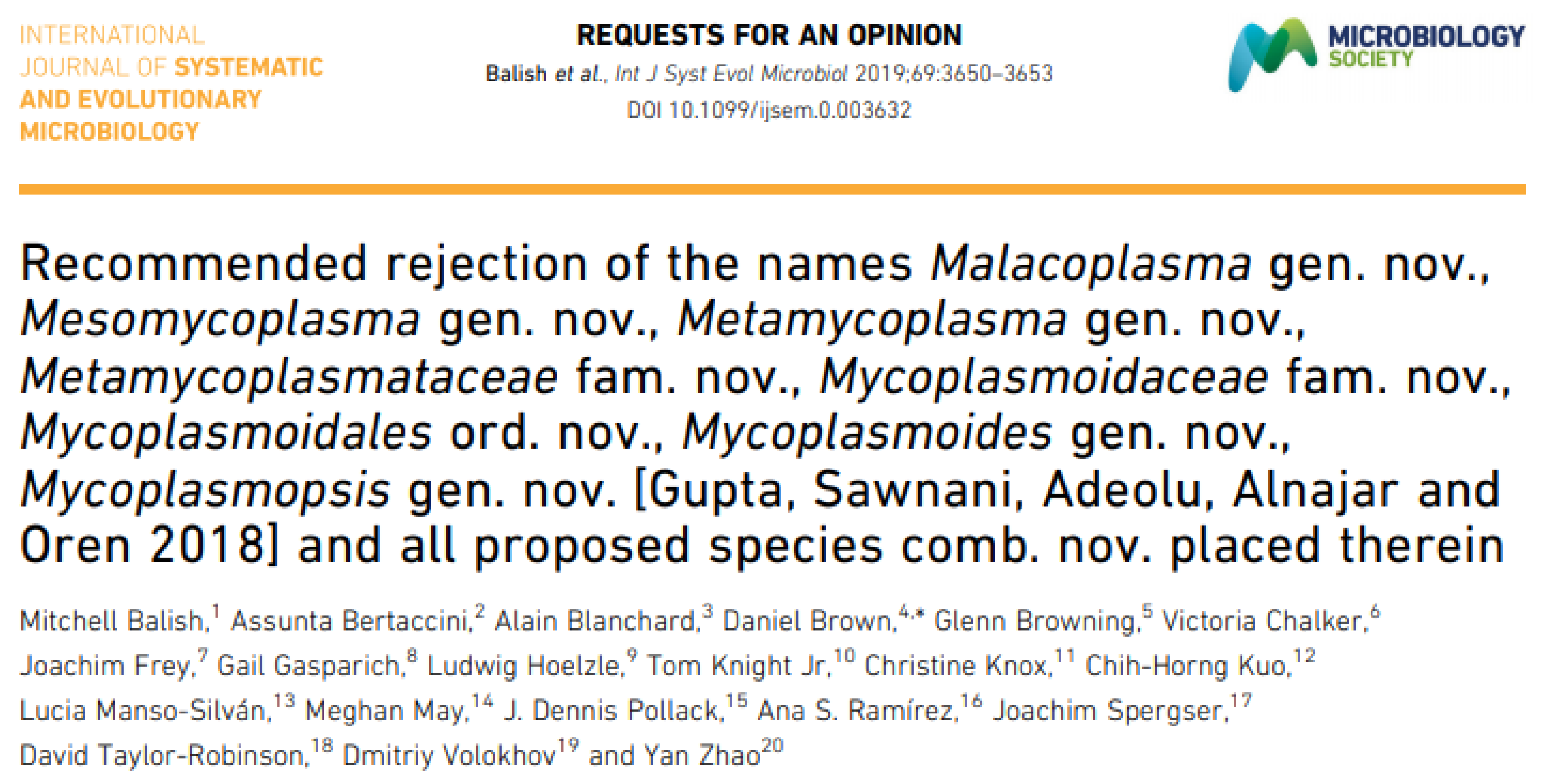
Radhey S. Gupta, Sahil Sawnani, Mobolaji Adeolu, Seema Alnajar & Aharon Oren

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

- 105 total nomenclature revisions
- Five novel genera

Malacoplasma gen. nov.
Mesomycoplasma gen. nov.
Metamycoplasma gen. nov. (*Metamycoplasma hominis*)
Mycoplasmoides gen. nov. (*Mycoplasmoides genitalium, pneumoniae*)
Mycoplasmopsis gen. nov.

Antonie Van Leeuwenhoek **111:** 1583-1630; 2018



INTERNATIONAL
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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

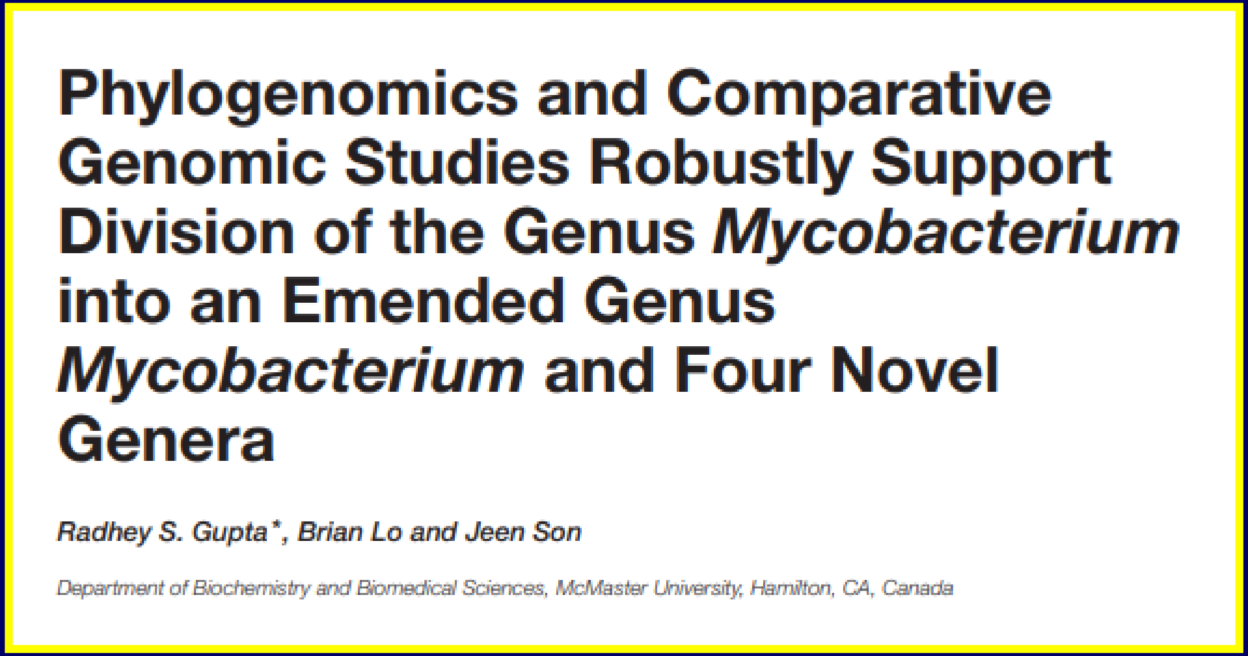
MICROBIOLOGY
SOCIETY

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”

REVISIONS TO *Mycobacterium*



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

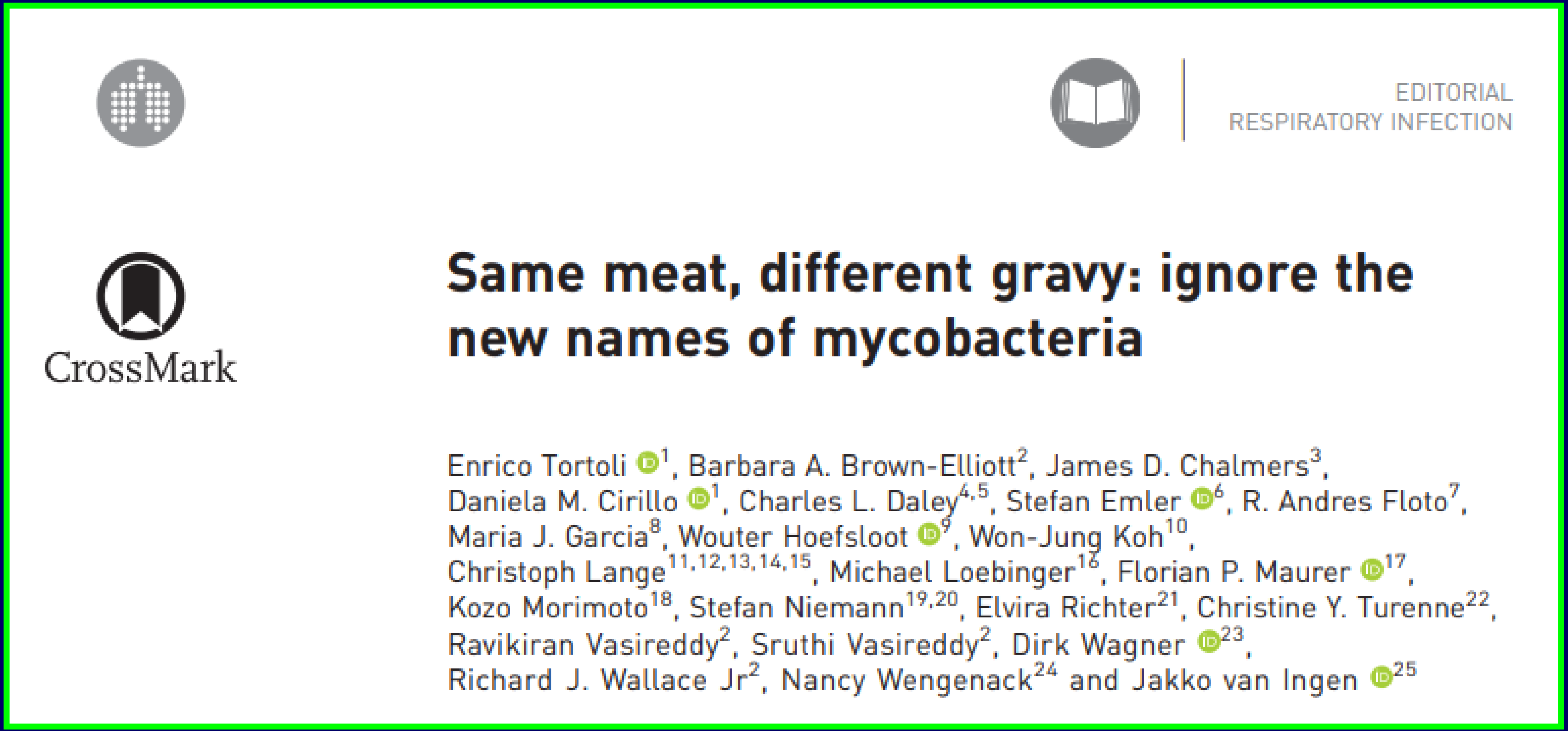
Mycolicibacter gen. nov.
Mycolicibacillus gen. nov.
Mycobacteroides gen. nov. (rapid growers)
Mycolicibacterium gen. nov. (rapid growers)

Front. Microbiol. **9:** 67; 2018

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. **42:** 111-120; 2020



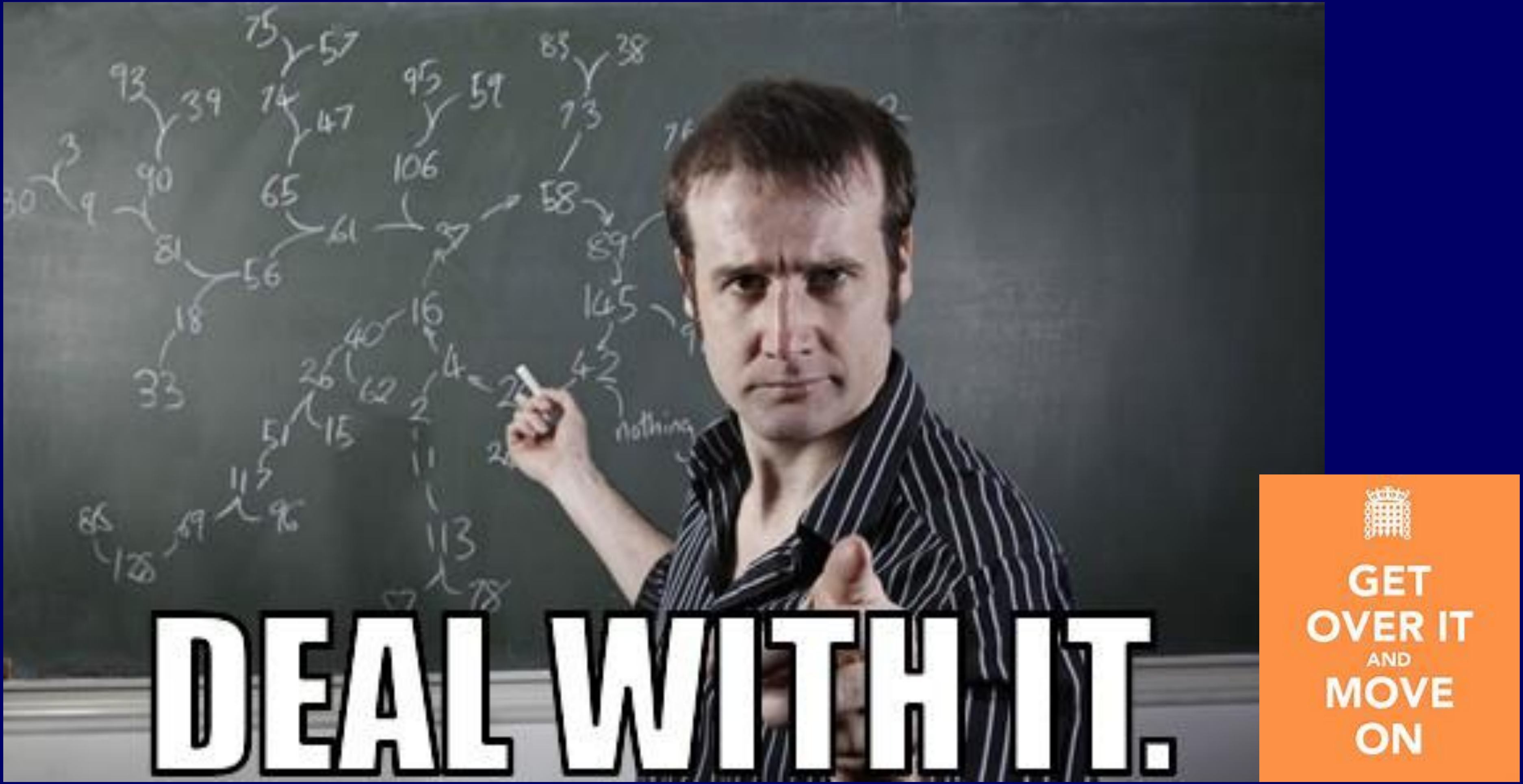
EDITORIAL
RESPIRATORY INFECTION

Same meat, different gravy: ignore the new names of mycobacteria

Enrico Tortoli[1], Barbara A. Brown-Elliott[2], James D. Chalmers[3], Daniela M. Cirillo[1], Charles L. Daley[4,5], Stefan Emler[6], R. Andres Floto[7], Maria J. Garcia[8], Wouter Hoefsloot[9], Won-Jung Koh[10], Christoph Lange[11,12,13,14,15], Michael Loebinger[16], Florian P. Maurer[17], Kozo Morimoto[18], Stefan Niemann[19,20], Elvira Richter[21], Christine Y. Turenne[22], Ravikiran Vasireddy[2], Sruthi Vasireddy[2], Dirk Wagner[23], Richard J. Wallace Jr[2], Nancy Wengenack[24] and Jakko van Ingen[25]

Eur. Respir. J. **54:** 1900795; 2019

So What?


DEAL WITH IT.
GET OVER IT AND MOVE ON

WAIT…WAIT…

- Clinical relevance may not be determined
- Clinicians may become cognizant of changes
- Updating of databases by commercial vendors
- Utilization of databases (interfaces) by users
- Daily laboratory operations
  - Communication
  - Multi-facility laboratory systems
  - LIS updates

TIMING

- *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. **68:** 131-132; 2018

- *Pseudopropionibacterium rubrum* sp. nov.

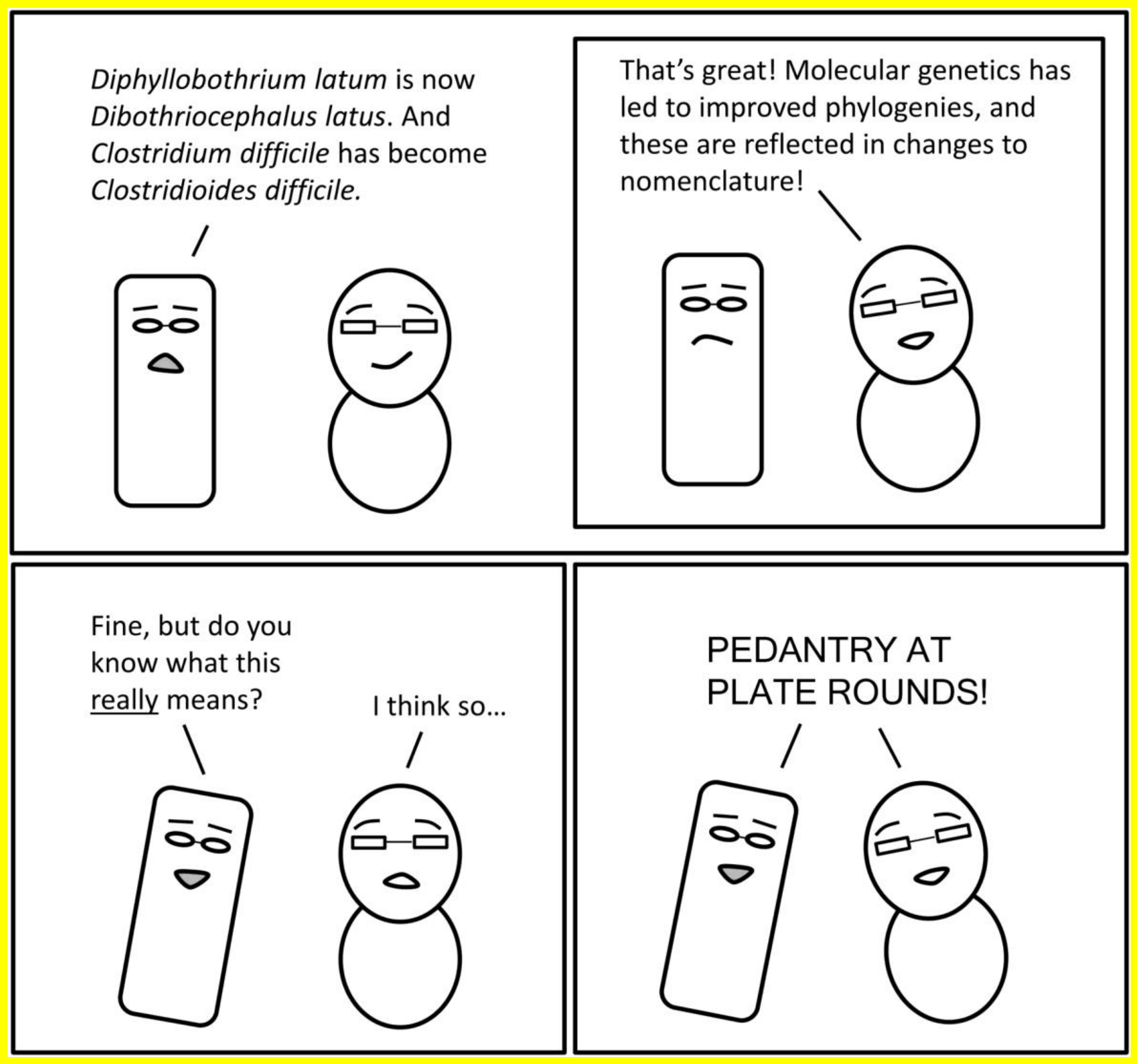
  Effectively described in June 2018
  Accepted by IJSEM in September 2018
  Illegitimate designation in August 2019

  Arachnia rubra comb. nov.

  IJSEM. **69:** 2612-2615; 2019

CLINICAL AND LABORATORY STANDARDS INSTITUTE®

J. Clin. Microbiol. **49:** 3449; 2011



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Thank you for your attention.
Have a good (better) 2021.