# Microbial Taxonomy Revision:
## Enough is Enough!...Or Is It?

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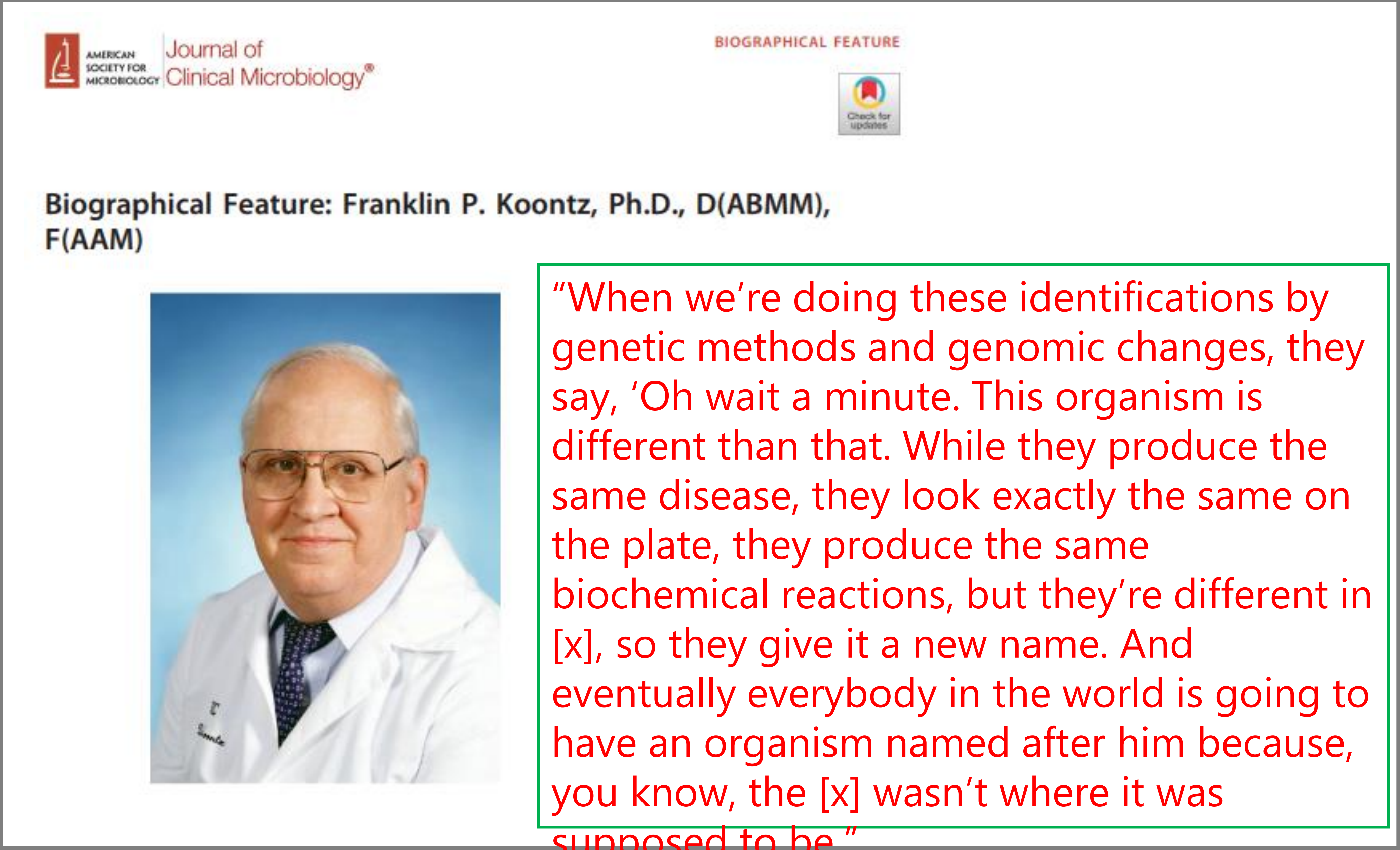
Laboratory Technical Advisory Group

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

Someone a lot smarter than I am



AMERICAN SOCIETY FOR MICROBIOLOGY Journal of Clinical Microbiology®

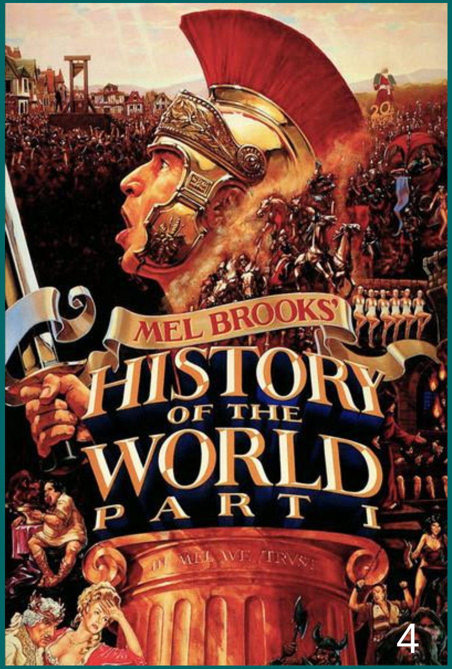
BIOGRAPHICAL FEATURE

# 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. 58:e01975-19

# 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

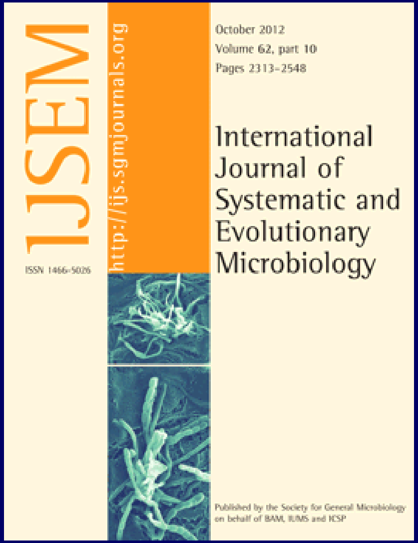
# WE’VE GOTTA CLEAN THIS UP

- 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

# LAYING DOWN THE LAW

- Approved Lists of Bacterial Names

  January 1980
  2,300 prokaryotic names
  Reject rest



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Systematic and
Evolutionary
Microbiology

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

- 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)

# Discovering your novel taxon

# DISCOVERING YOUR NEW TAXON

- Effective description
  - Several recommendations provided in THE CODE
  - Minimum standards may vary by genus
  - Polyphasic approach to characterization (next slide)
- 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

# POLYPHASIC CHARACTERIZATION

- Phenotypic
    - Cultivation conditions (medium, incubation, duration)
    - Classical observations (colony morphology, Gram, catalase, oxidase, motility, biochemical tubes)
    - Chemotaxonomic markers (fatty acid, isoprenoid)
    - MALDI-TOF MS contribution

*Number of characteristics must be sufficiently high to distinguish new species from related species; recommend 5 strains (including type)*

# POLYPHASIC CHARACTERIZATION

- Phenotypic

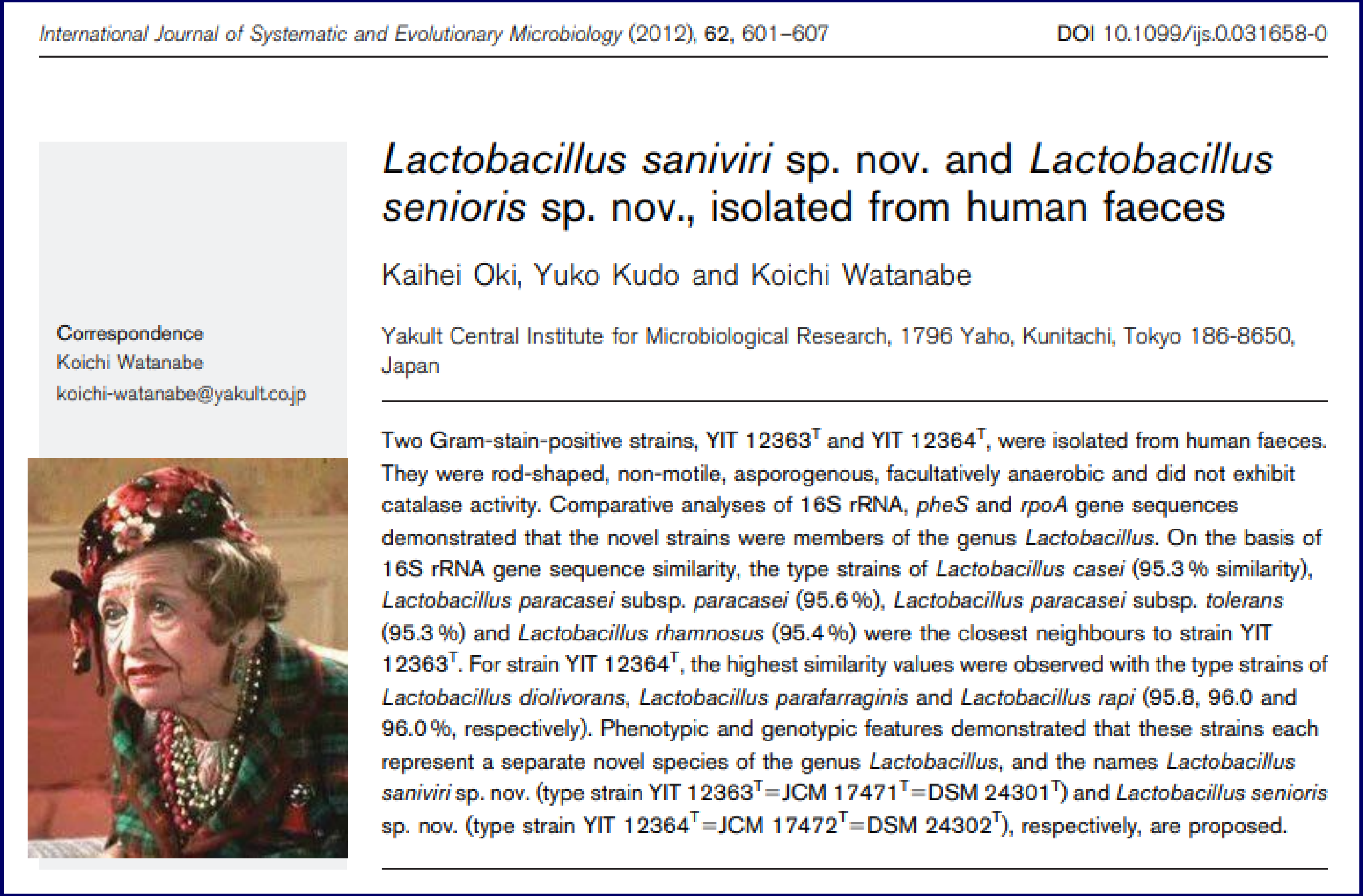
- Genotypic
  - % G + C content
  - DNA-DNA hybridization
  - 16S rRNA (98.8% threshold) and housekeeping gene sequence analysis
  - Phylogenetic tree presentation

# POLYPHASIC CHARACTERIZATION

- Phenotypic
- Genotypic
- Whole genome sequencing

  96% average nucleotide identity (90% coverage)
  Can vary (*S. maltophilia* 88.5%; *M. tuberculosis* 98.8%)

# 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

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

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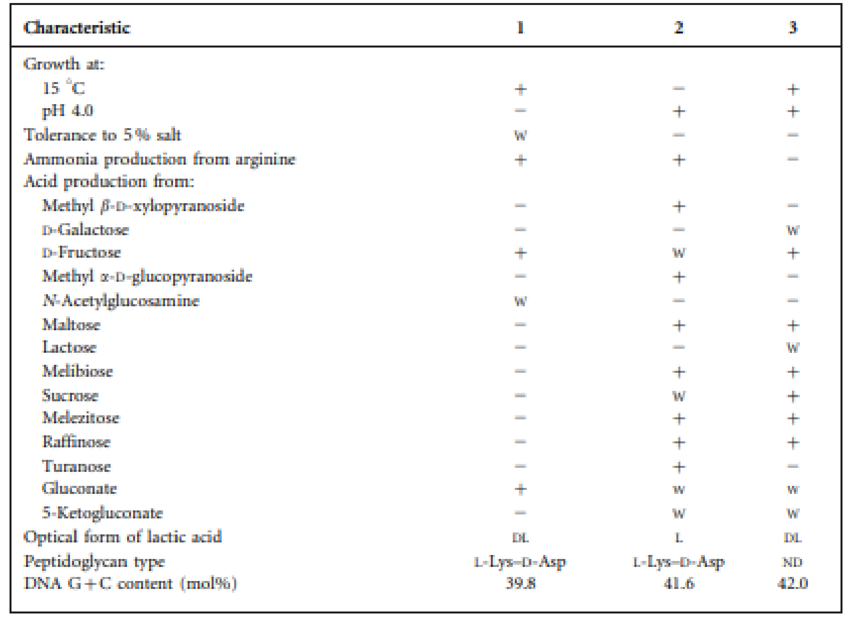
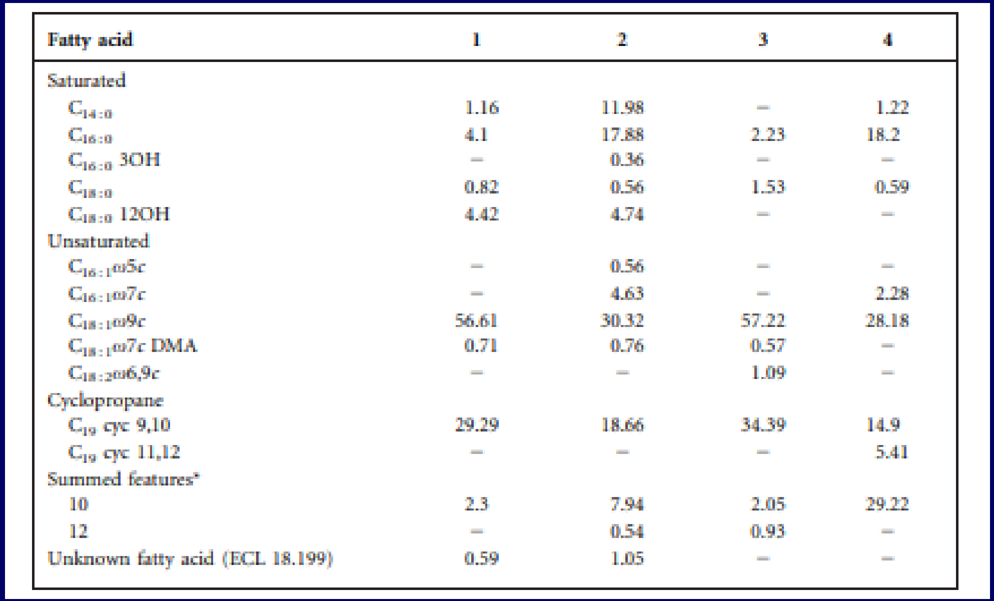
Two Gram-stain-positive strains, YIT 12363$^T$ and YIT 12364$^T$, were isolated from human faeces. They were rod-shaped, non-motile, asporogenous, facultatively anaerobic and did not exhibit catalase activity. Comparative analyses of 16S rRNA, *pheS* and *rpoA* gene sequences demonstrated that the novel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



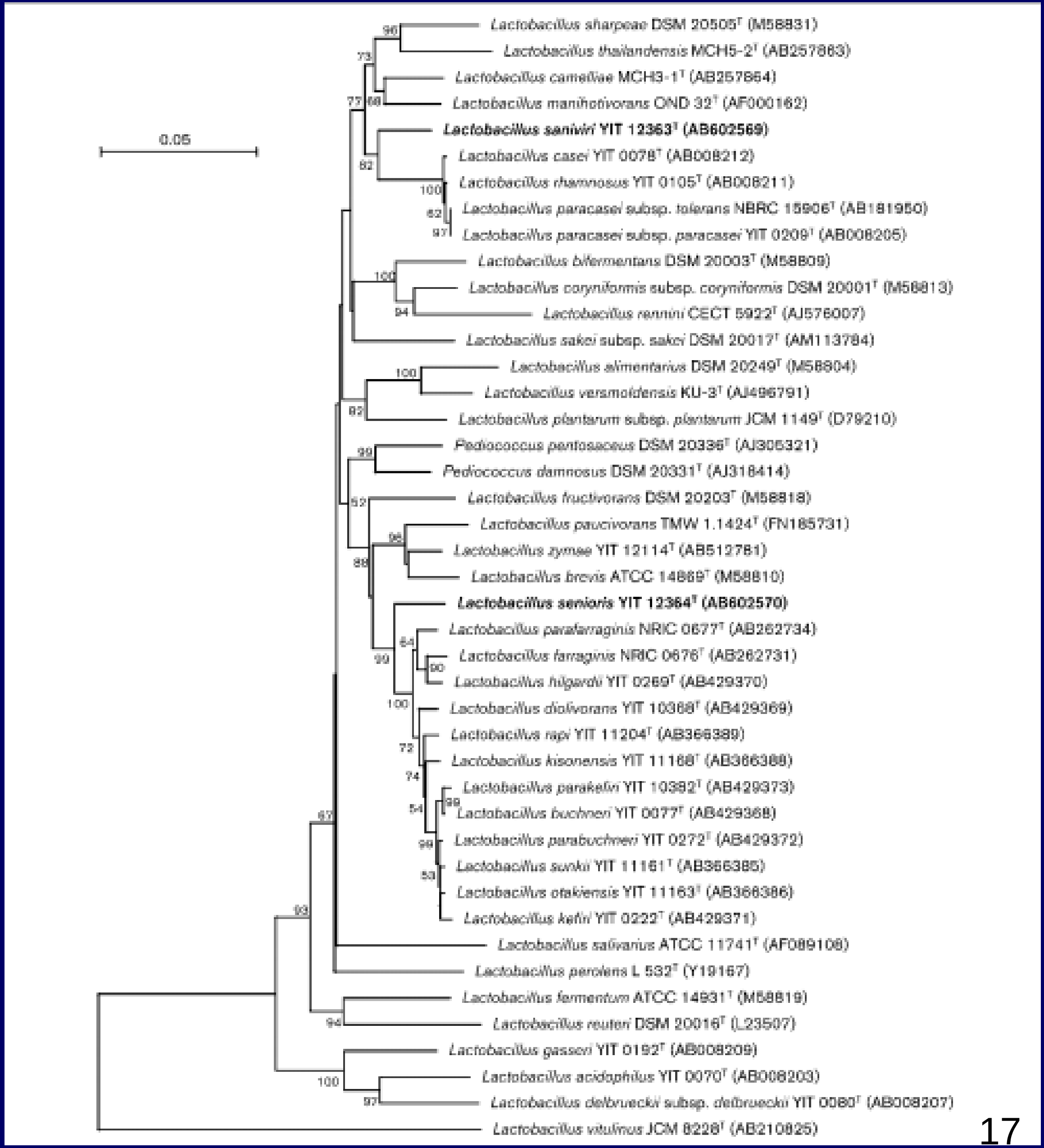
| Characteristic | 1 | 2 | 3 |
|---|---|---|---|
| Growth at: | | | |
| 15 °C | + | − | + |
| pH 4.0 | − | + | + |
| Tolerance to 5 % salt | w | − | − |
| Ammonia production from arginine | + | + | − |
| Acid production from: | | | |
| Methyl β-D-xylopyranoside | − | + | − |
| D-Galactose | − | − | w |
| 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 |

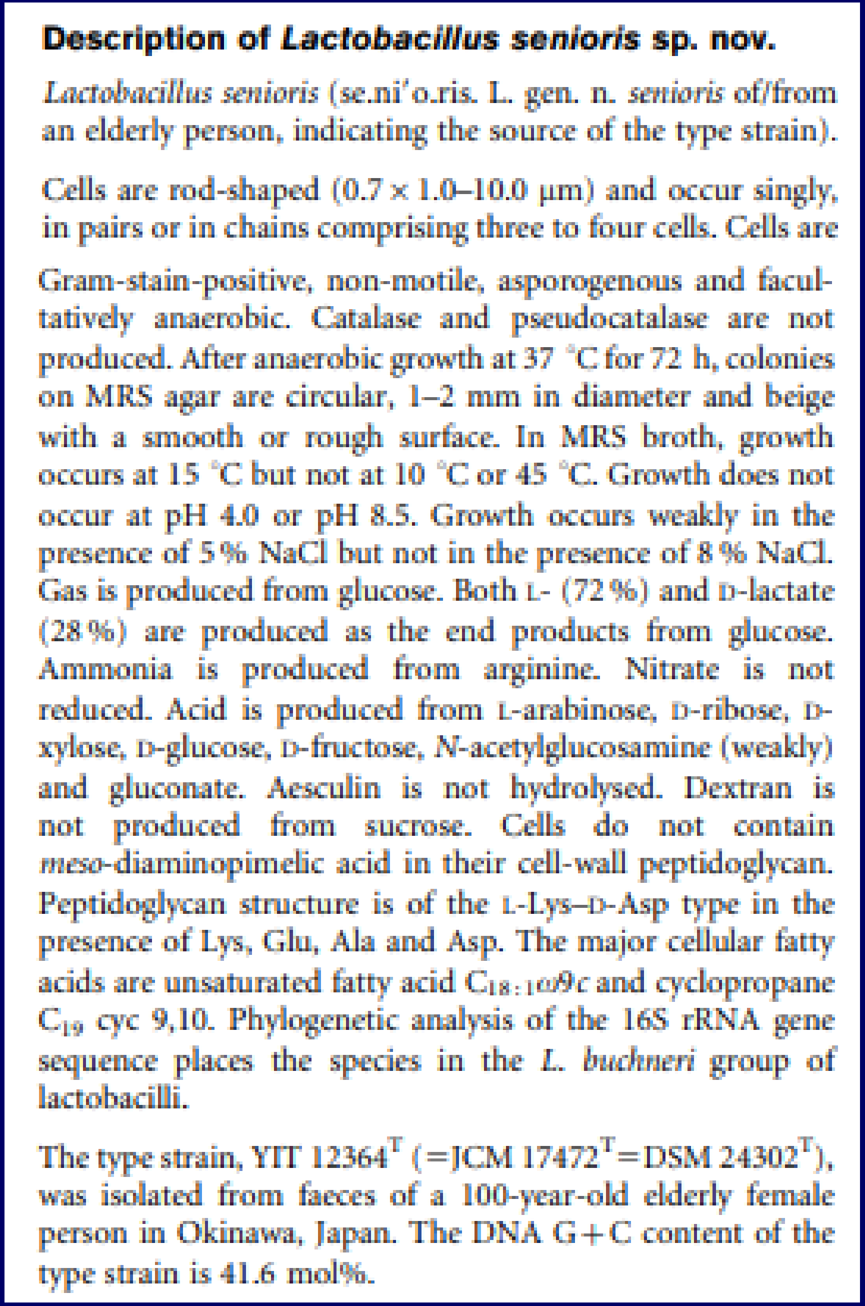
# Chemotaxonomic



| 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 $C_{18:1}\omega9c$ 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

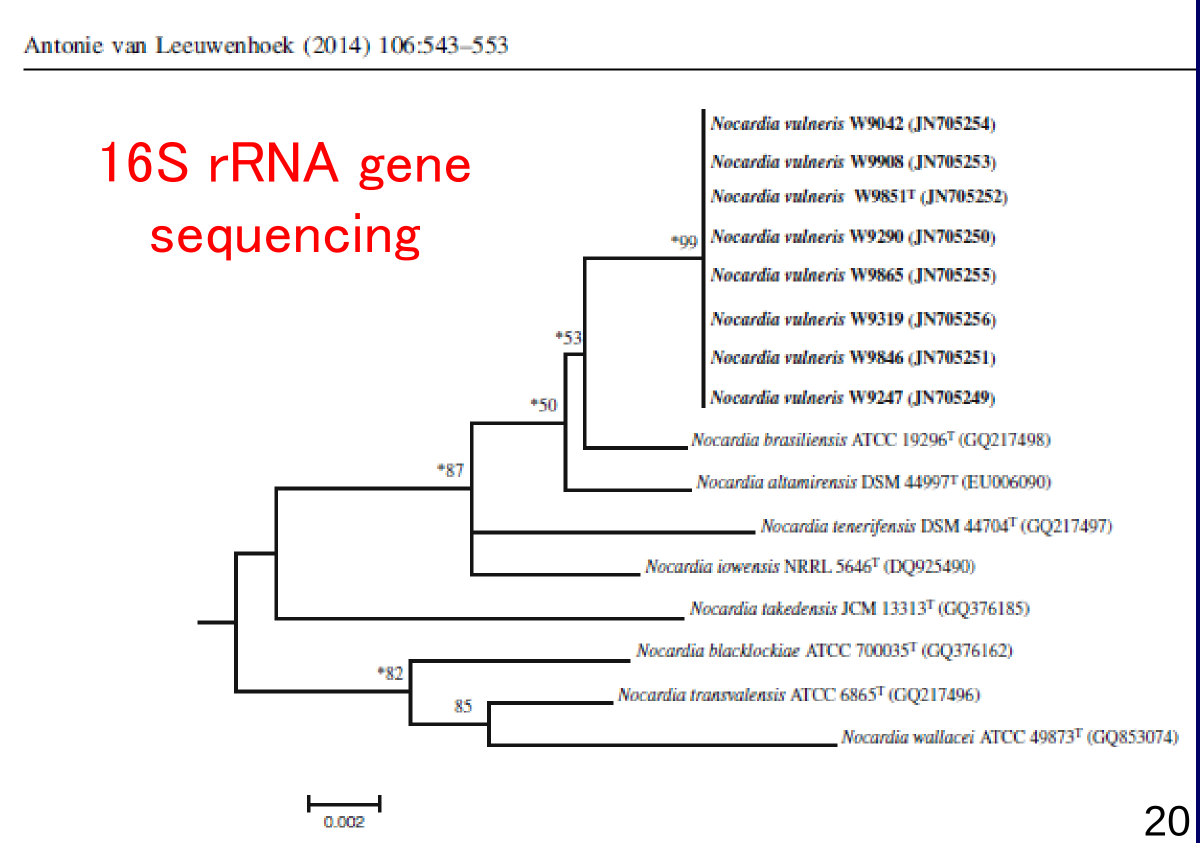
# PUBLISH IT--ALTERNATE APPROACH

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

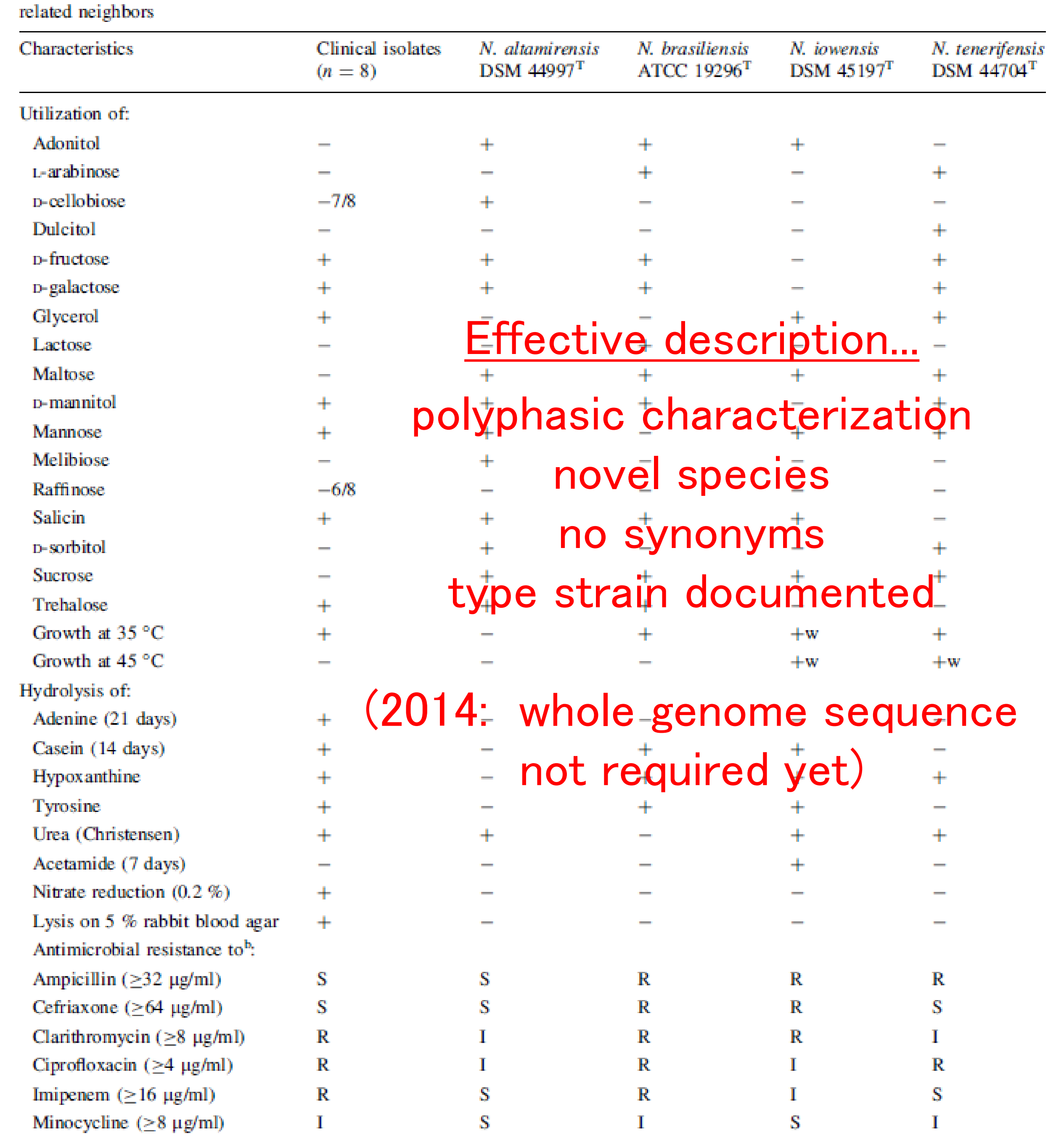


**Table 2** Phenotypic properties that distinguish the *N. vulneris* clinical isolates from the type strains of their closest phylogenetically related neighbors

| 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…

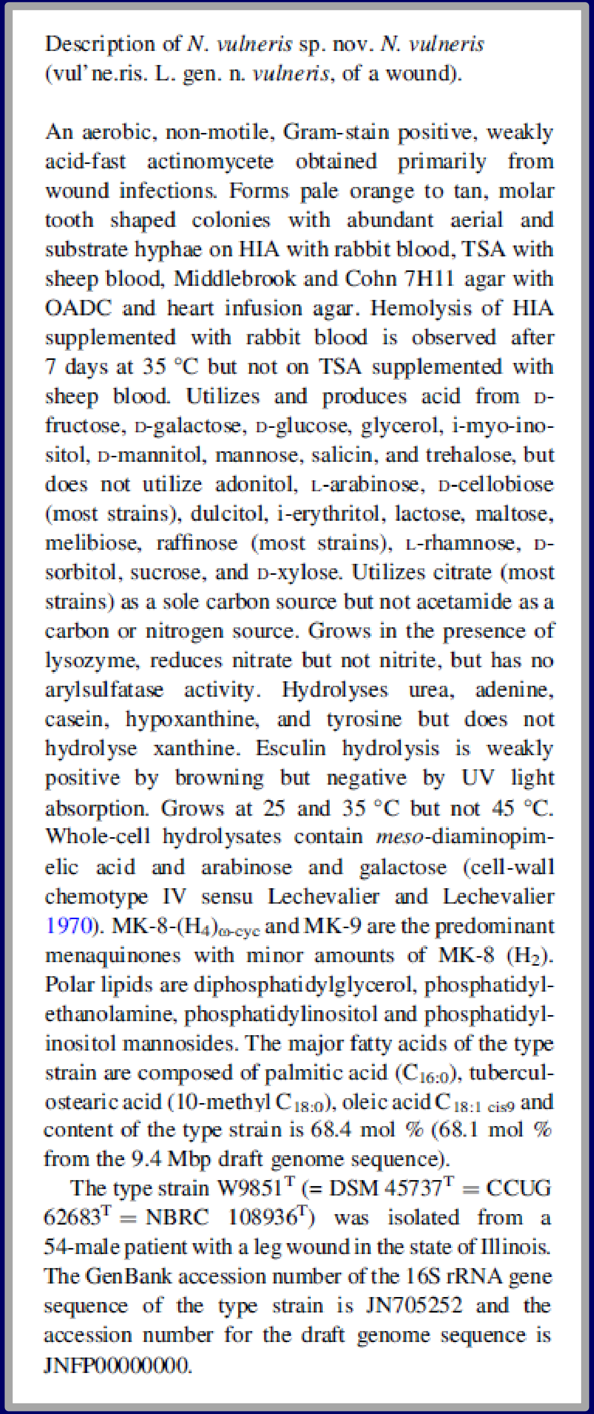
polyphasic characterization

novel species

no synonyms

type strain documented

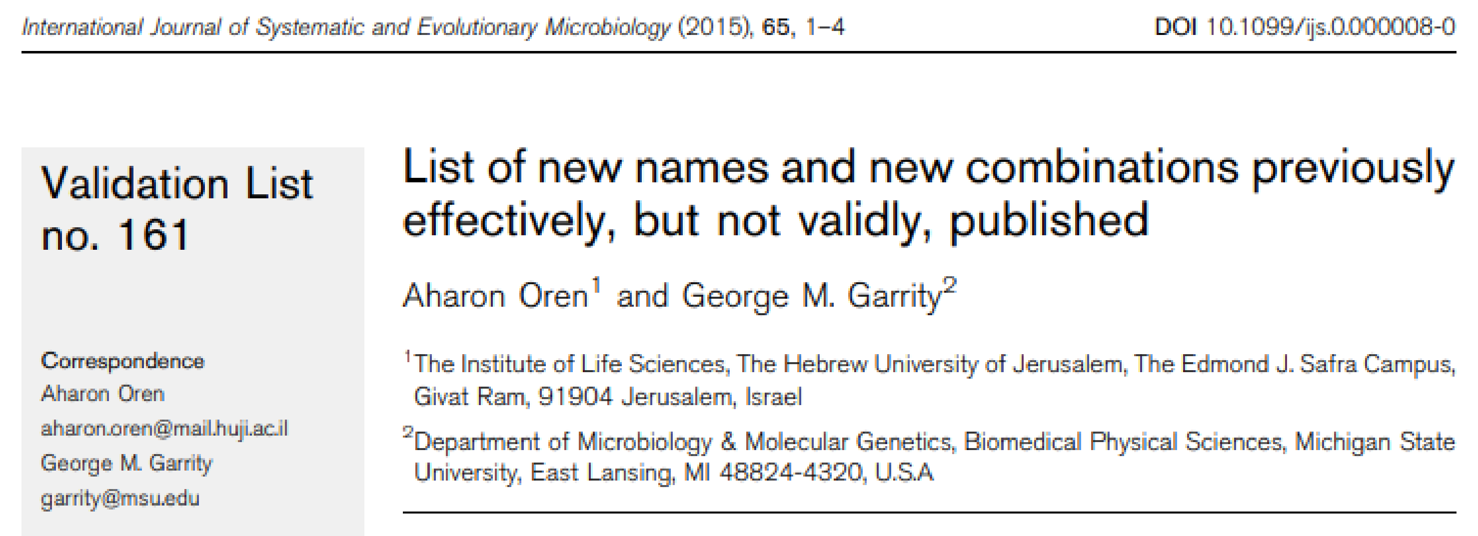
(2014: whole genome sequence
not required yet)



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

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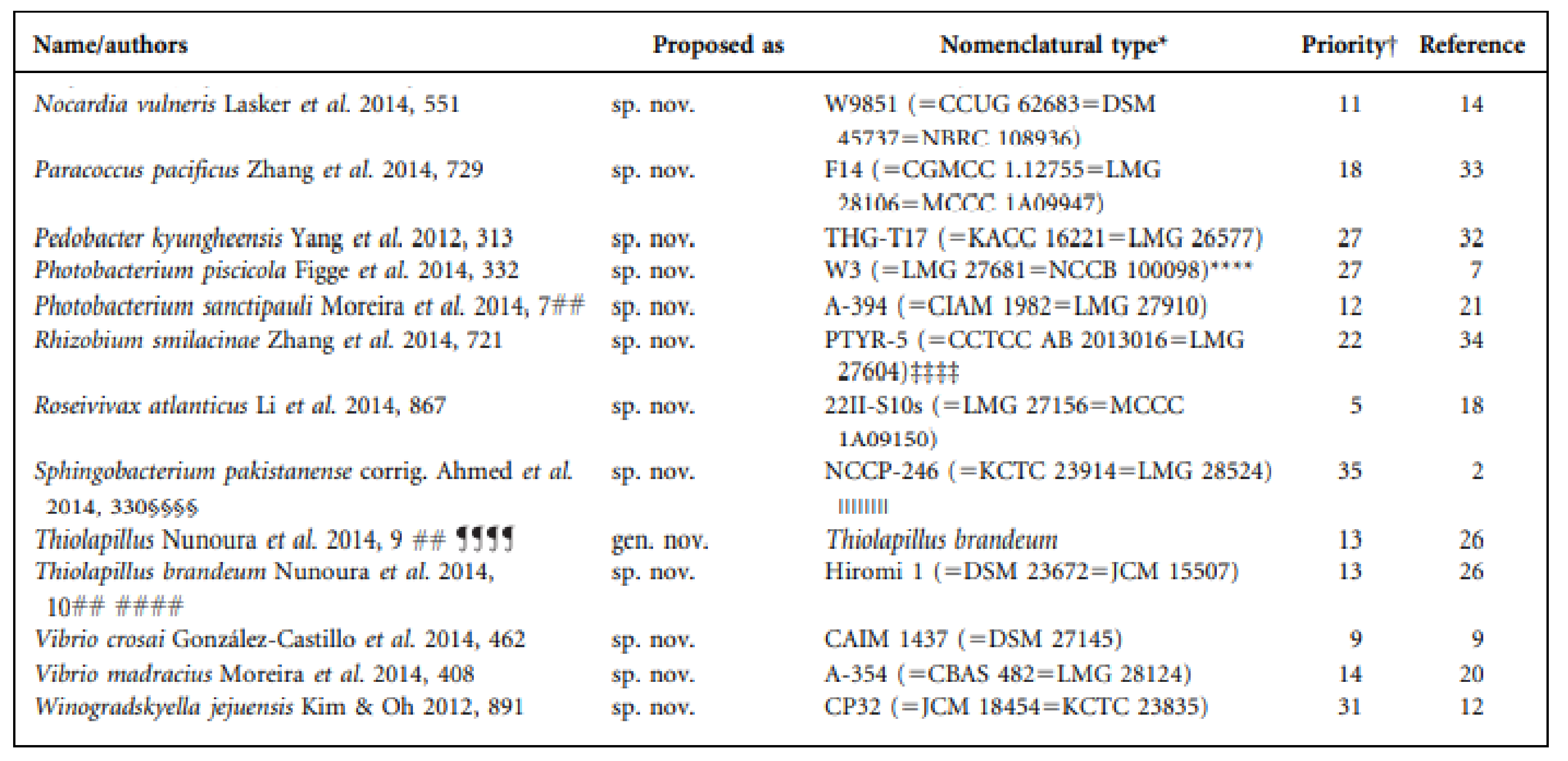
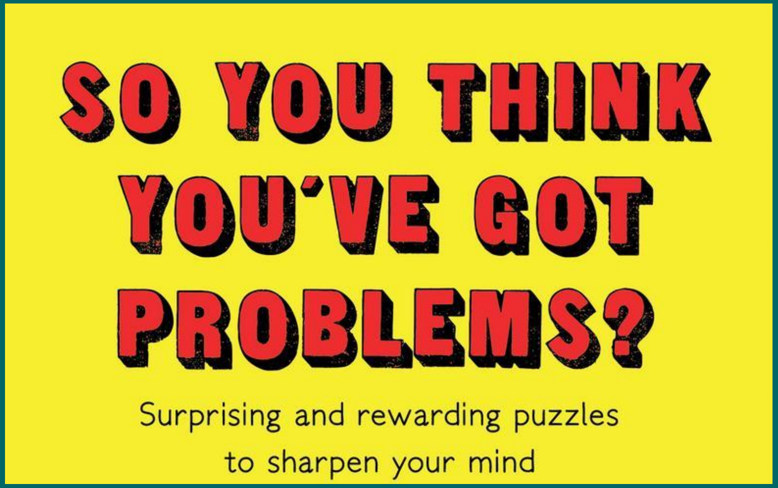


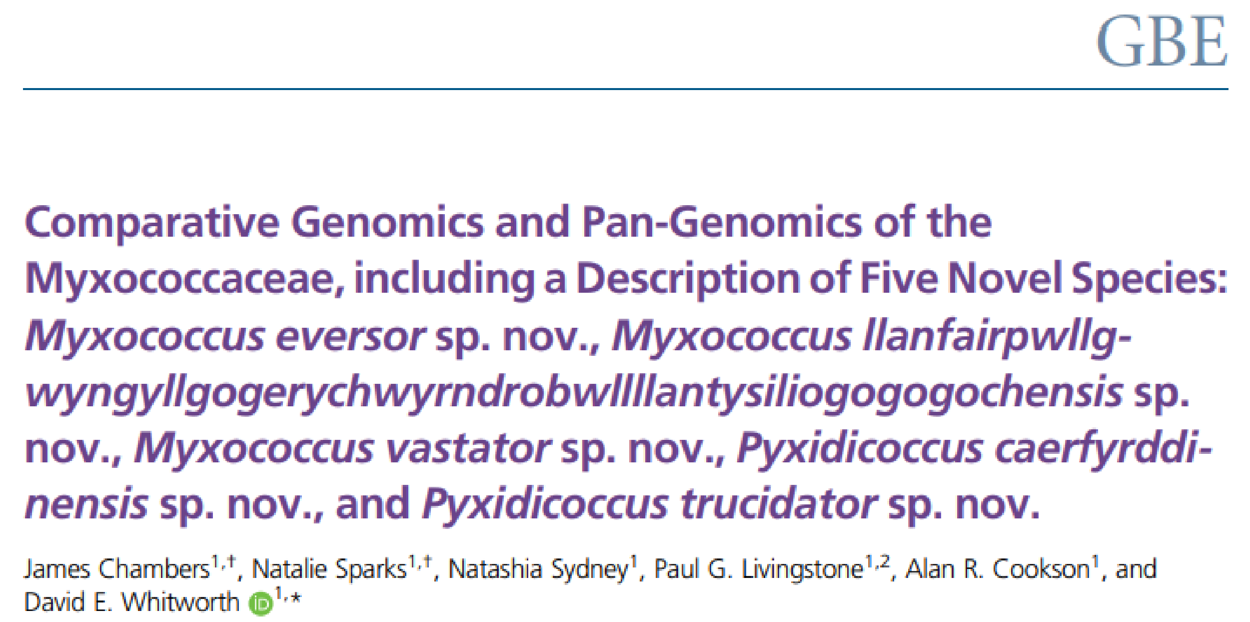
| Name/authors | Proposed as | Nomenclatural type* | Priority† | Reference |
|---|---|---|---|---|
| *Nocardia vulneris* Lasker *et al.* 2014, 551 | sp. nov. | W9851 (=CCUG 62683=DSM 45737=NBRC 108936) | 11 | 14 |
| *Paracoccus pacificus* Zhang *et al.* 2014, 729 | sp. nov. | F14 (=CGMCC 1.12755=LMG 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 |


SO YOU THINK YOU'VE GOT PROBLEMS?

Surprising and rewarding puzzles
to sharpen your mind

# Yes, there are "novel" problems

# HUUUUUUUUUUUUUUH??



GBE

## Comparative Genomics and Pan-Genomics of the Myxococcaceae, including a Description of Five Novel Species: *Myxococcus eversor* sp. nov., *Myxococcus llanfairpwllgwyngyllgogerychwyrndrobwllllantysiliogogogochensis* sp. nov., *Myxococcus vastator* sp. nov., *Pyxidicoccus caerfyrddinensis* 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**

MICROBIOLOGY SOCIETY

**VALIDATION LIST NO. 201**

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

DOI 10.1099/ijsem.0.004943

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

| | | | | |
|---|---|---|---|---|
| *Myxococcus llanfairpwllgwyngyllgogerychwyrndrobwllllantysiliogogogochensis*<br>Chambers *et al.* 2021, 1 | sp. nov. | AM401 (=NBRC 114351=NCCB 100770) | 12 | [31] |

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

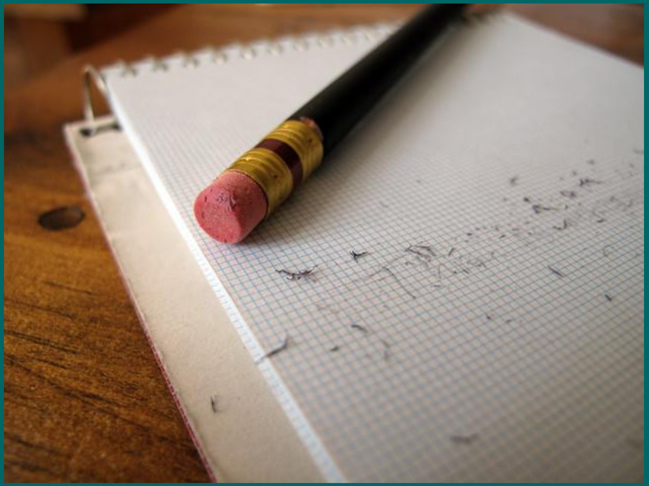
    Int J Syst Evol Microbiol. 2018; 68:131-132

- *Pseudopropionibacterium rubrum* sp. nov.

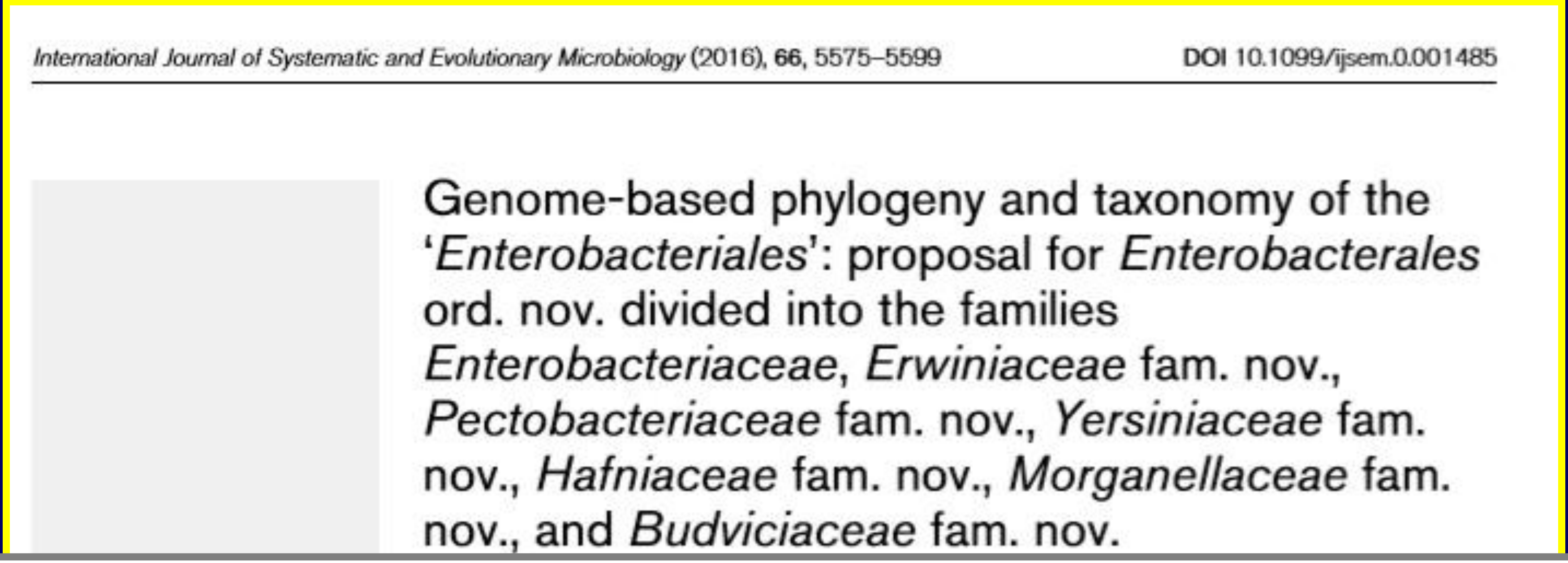
    Effectively described in June 2018
    Accepted by *IJSEM* in September 2018
    Illegitimate designation in August 2019

    *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*

*Enterobacterales*

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

# LUCKILY…

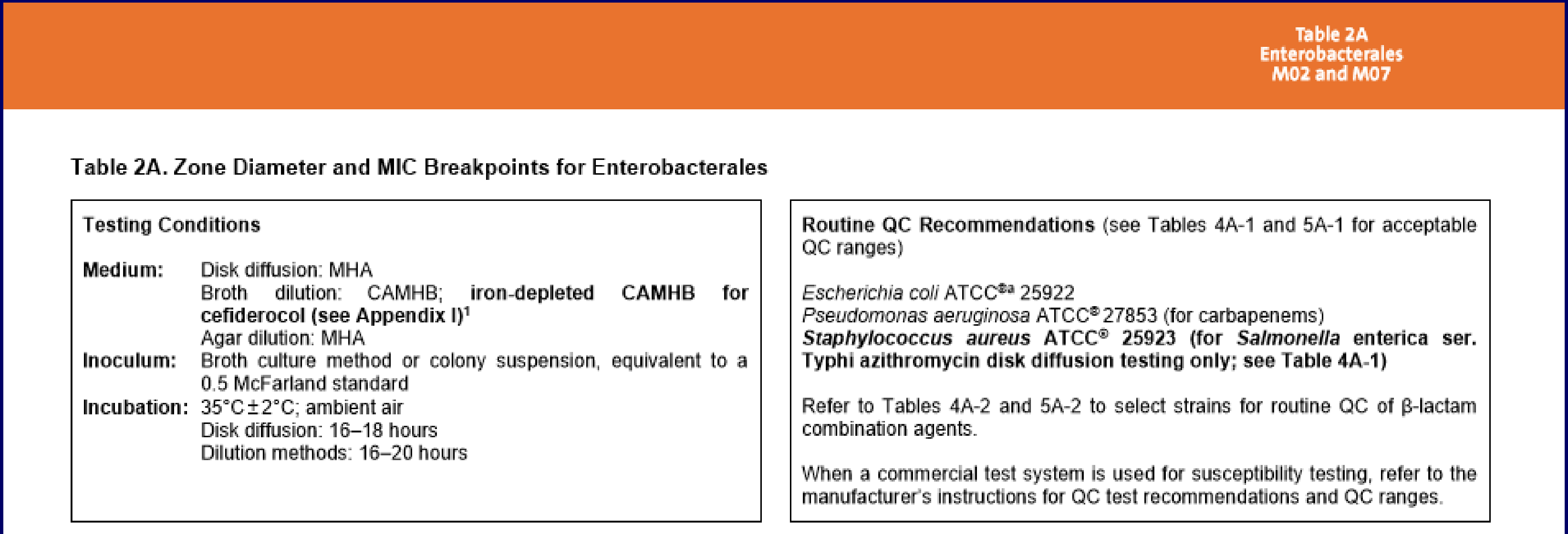


**Table 2A**
**Enterobacterales**
**M02 and M07**

**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

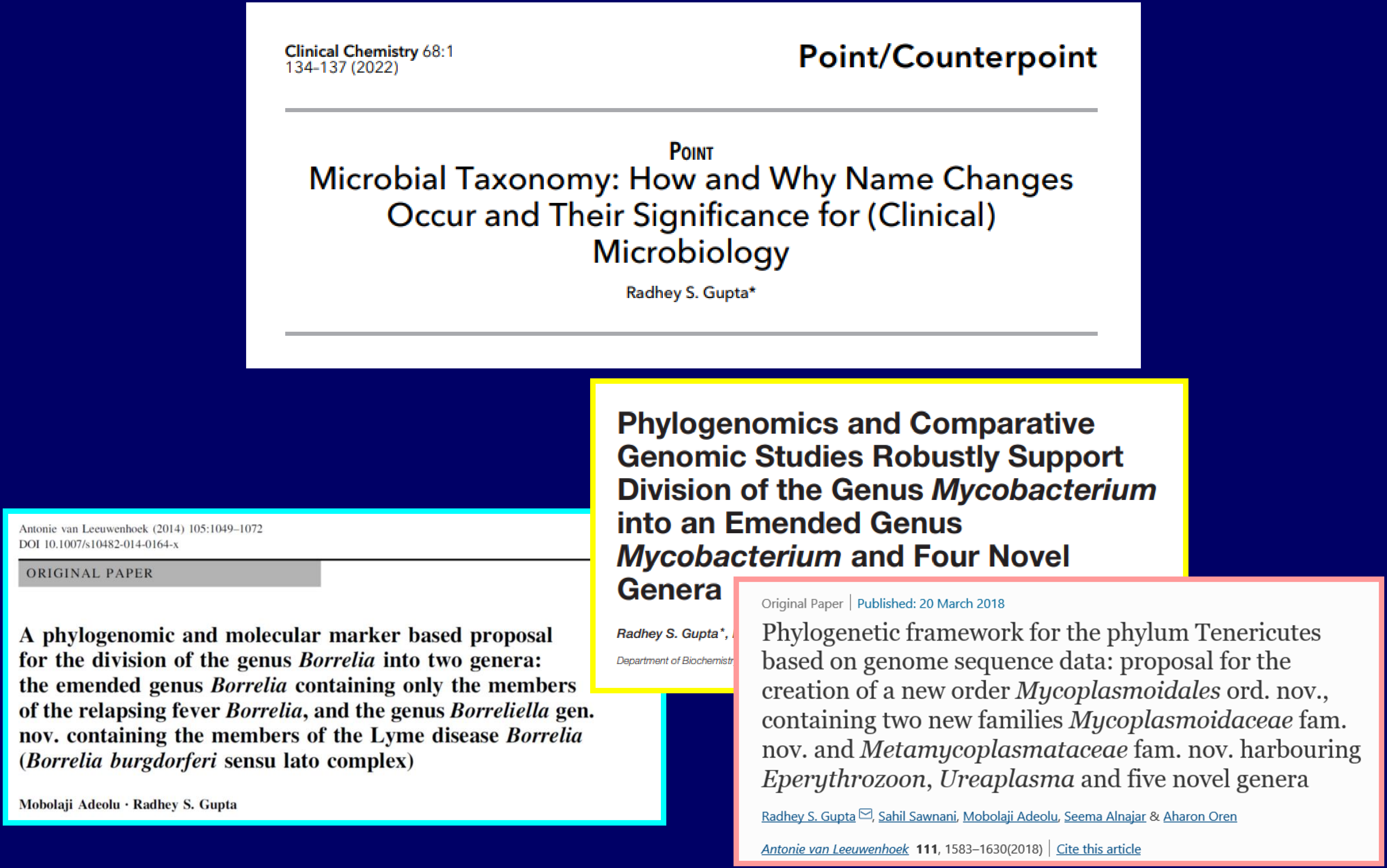
**Routine QC Recommendations** (see Tables 4A-1 and 5A-1 for acceptable QC ranges)

*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*

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

*Radhey S. Gupta*,*

*Department of Biochemistr*

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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**

---

Original Paper | Published: 20 March 2018

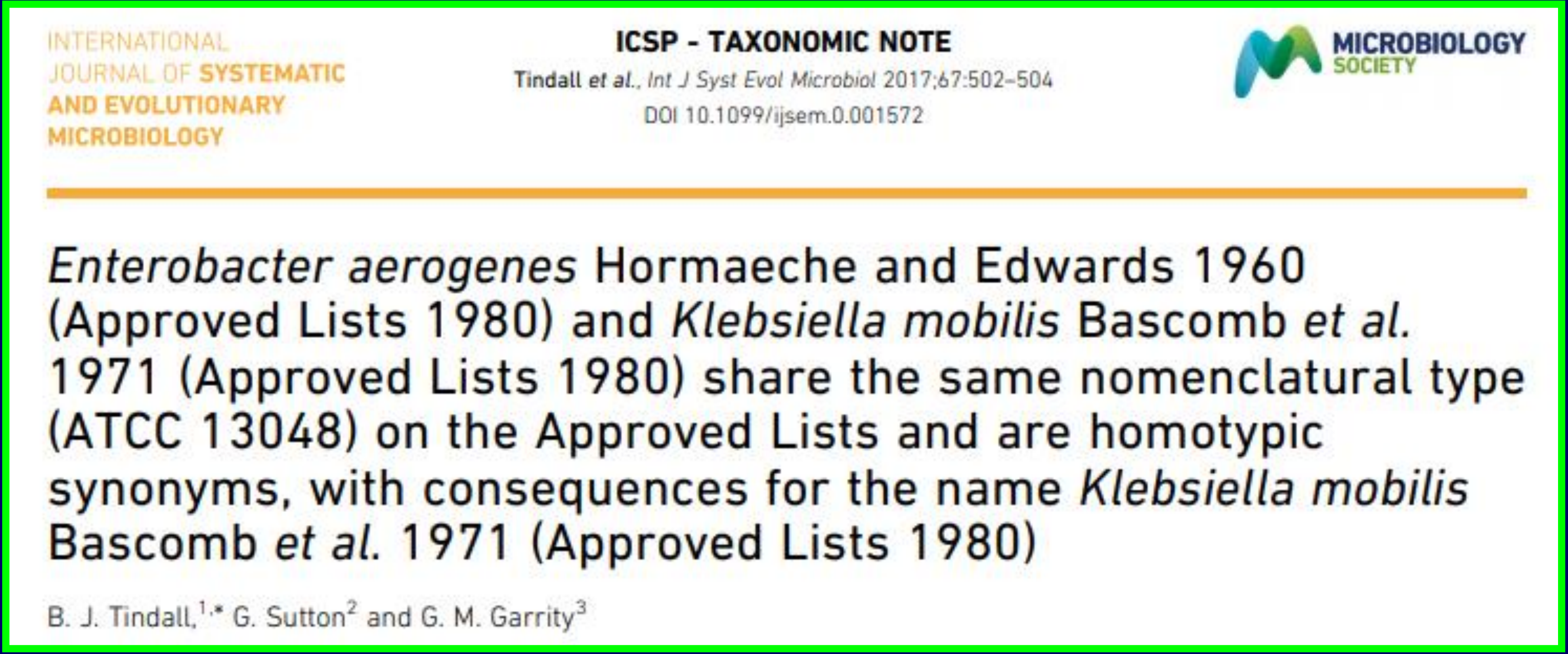
Phylogenetic framework for the phylum Tenericutes based on genome sequence data: proposal for the creation of a new order *Mycoplasmoidales* ord. nov., containing two new families *Mycoplasmoidaceae* fam. nov. and *Metamycoplasmataceae* fam. nov. harbouring *Eperythrozoon*, *Ureaplasma* and five novel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

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

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

Clin Chem. 2022; 68:134-137

# 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)

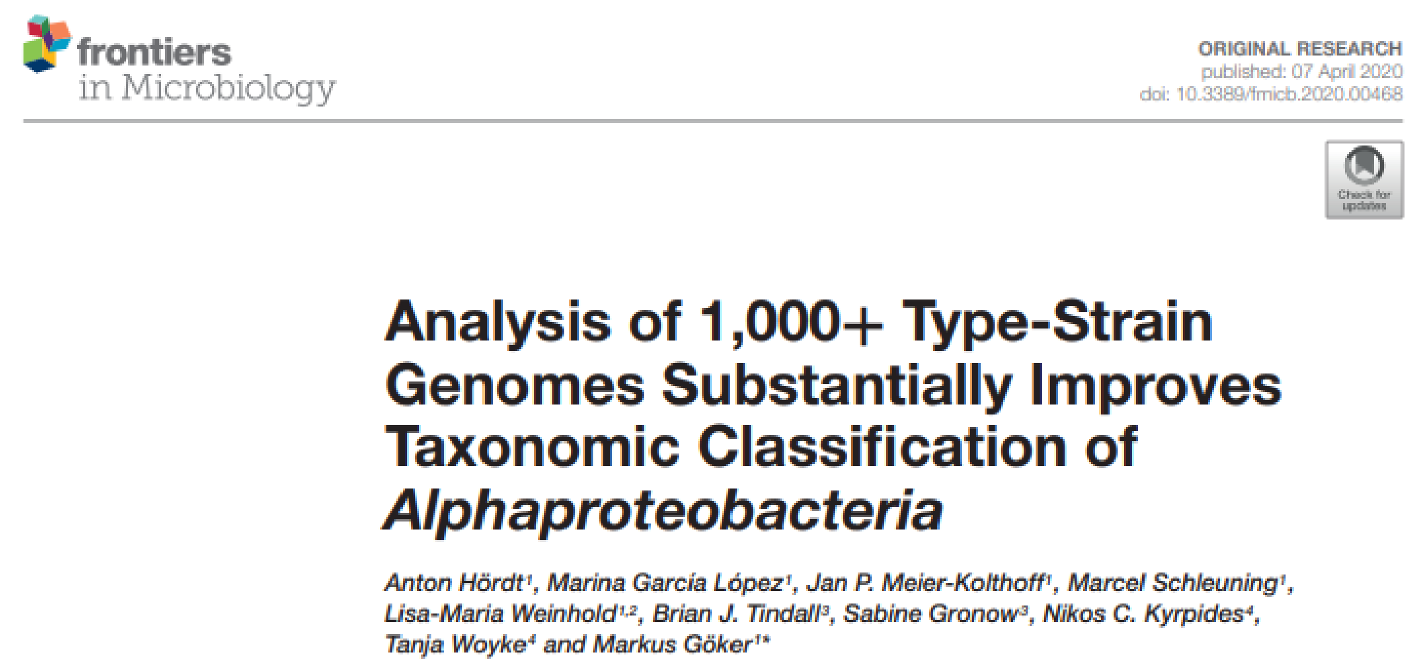
B. J. Tindall,[1,*] G. Sutton[2] and G. M. Garrity[3]

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

| **Antimicrobial Agent** | **Percentage Susceptible** | | |
|---|---|---|---|
| | *K. pneumoniae* | *K. aerogenes* | *E. cloacae* complex |
| ampicillin-sulbactam | 81 | 0 | 0 |
| piperacillin-tazobactam | 92 | 81 | 76 |
| cefazolin† | 91 | 0 | 0 |
| cefuroxime | 85 | 0 | 0 |
| ceftazidime | 93 | 82 | 74 |
| ceftriaxone | 91 | 81 | 70 |
| cefepime | 96 | 97 | 96 |
| aztreonam | 92 | 84 | 75 |
| meropenem | 99 | 99 | 99 |
| gentamicin | 96 | 99 | 95 |
| ciprofloxacin | 89 | 95 | 93 |
| trimethoprim-sulfamethoxazole | 90 | 97 | 93 |
| nitrofurantoin | 34 | 11 | 36 |

† CLSI M100 urine breakpoints

# DON'T PANIC??



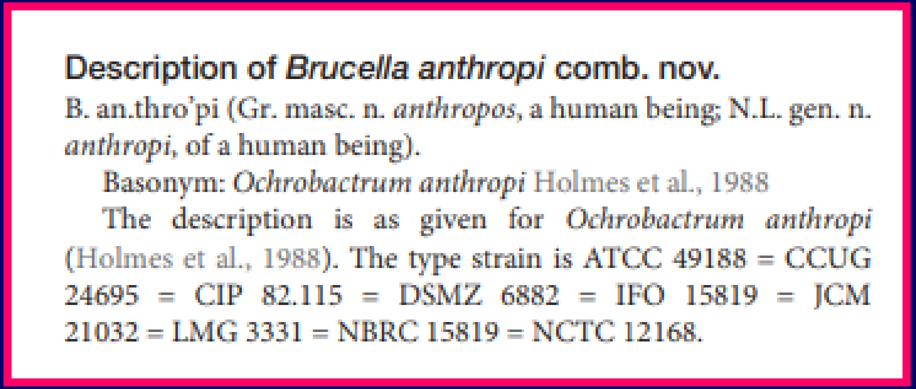
frontiers in Microbiology

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

Check for updates

## 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.

Front Microbiol. 2020; 11:468

# **DIRTY DOZEN** (out of 75)

*Morganellaceae*

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

*Yersiniaceae*

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

*Hafniaceae*

- *Edwardsiella*

*Enterobacteriaceae*

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

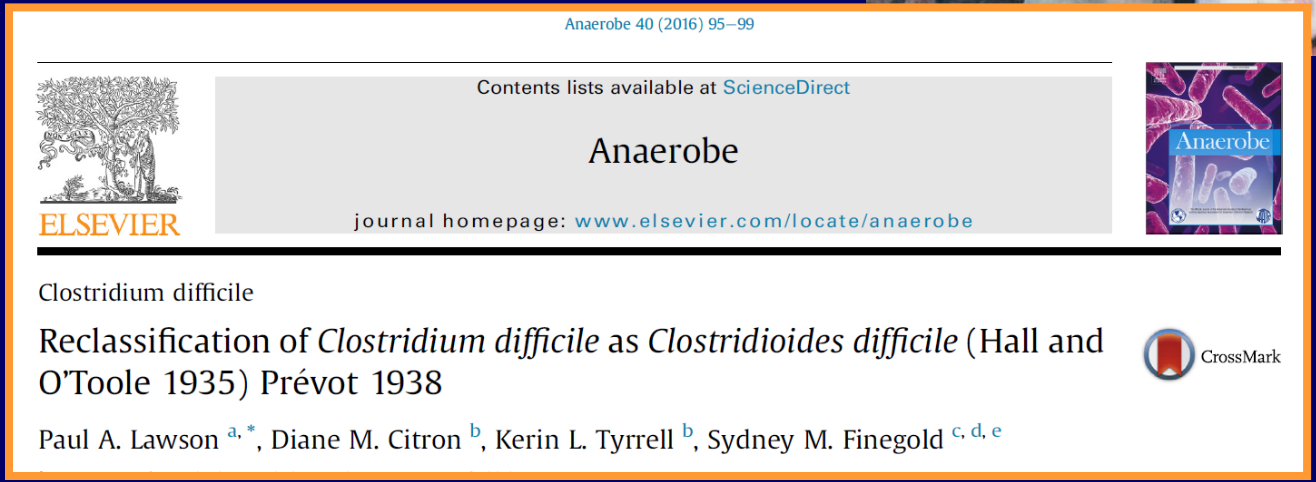
Int J Syst Evol Microbiol. 2016; 66:5575-5599

# NAME THAT *Enterobacterales*

tility Indole MIO (Ornithine) Citrate Urea Phenylalanine

# MORE “PEDAGOGY PRETEND”

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


Anaerobe 40 (2016) 95–99

Contents lists available at ScienceDirect

Anaerobe

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

ELSEVIER

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]

# 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”

COLLEGE of AMERICAN PATHOLOGISTS

# PERFORMANCE OF RELEVANT AST


3rd Edition

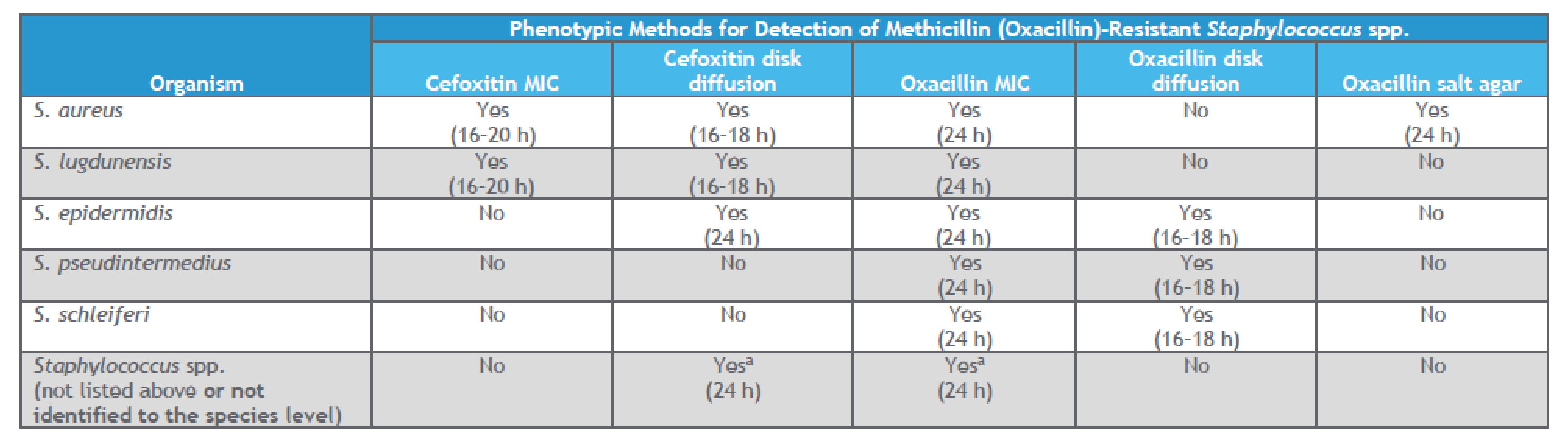
M45

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

- *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<br>(16-20 h) | Yes<br>(16-18 h) | Yes<br>(24 h) | No | Yes<br>(24 h) |
| *S. lugdunensis* | Yes<br>(16-20 h) | Yes<br>(16-18 h) | Yes<br>(24 h) | No | No |
| *S. epidermidis* | No | Yes<br>(24 h) | Yes<br>(24 h) | Yes<br>(16-18 h) | No |
| *S. pseudintermedius* | No | No | Yes<br>(24 h) | Yes<br>(16-18 h) | No |
| *S. schleiferi* | No | No | Yes<br>(24 h) | Yes<br>(16-18 h) | No |
| *Staphylococcus* spp.<br>(not listed above or not identified to the species level) | No | Yes[a]<br>(24 h) | Yes[a]<br>(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
  Hong Kong research revealed differences in clinical picture (sepsis, pneumonia, meningitis; ↑ mortality) and epidemiology (vertical transmission)

  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

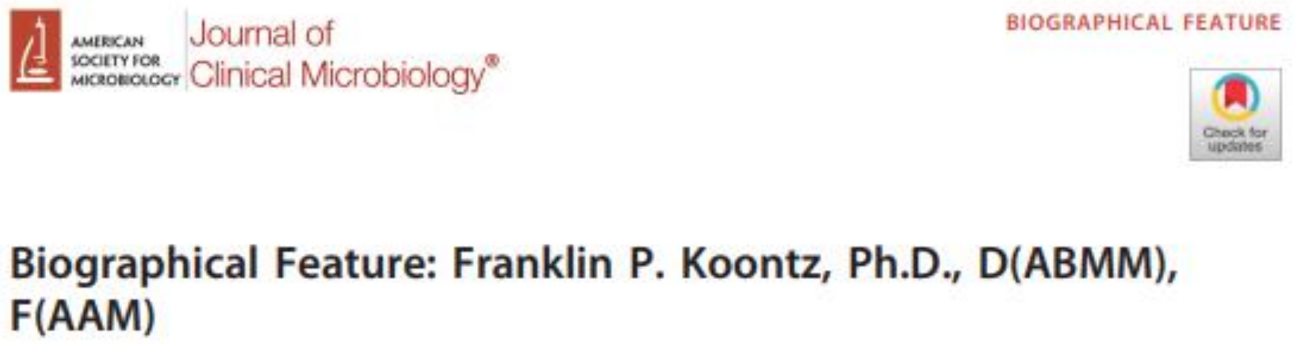
  Front Cell Neurosci. 2019; 13:402

- *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. 58:e01975-19

# HOW FAR DO YOU WANT TO GO??

- *Proteus morganii*

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

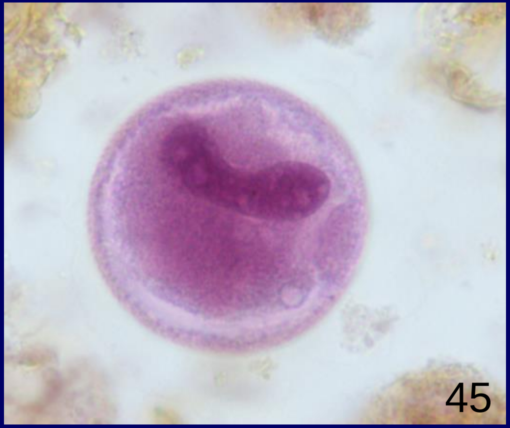
- *Neisseria catarrhalis*

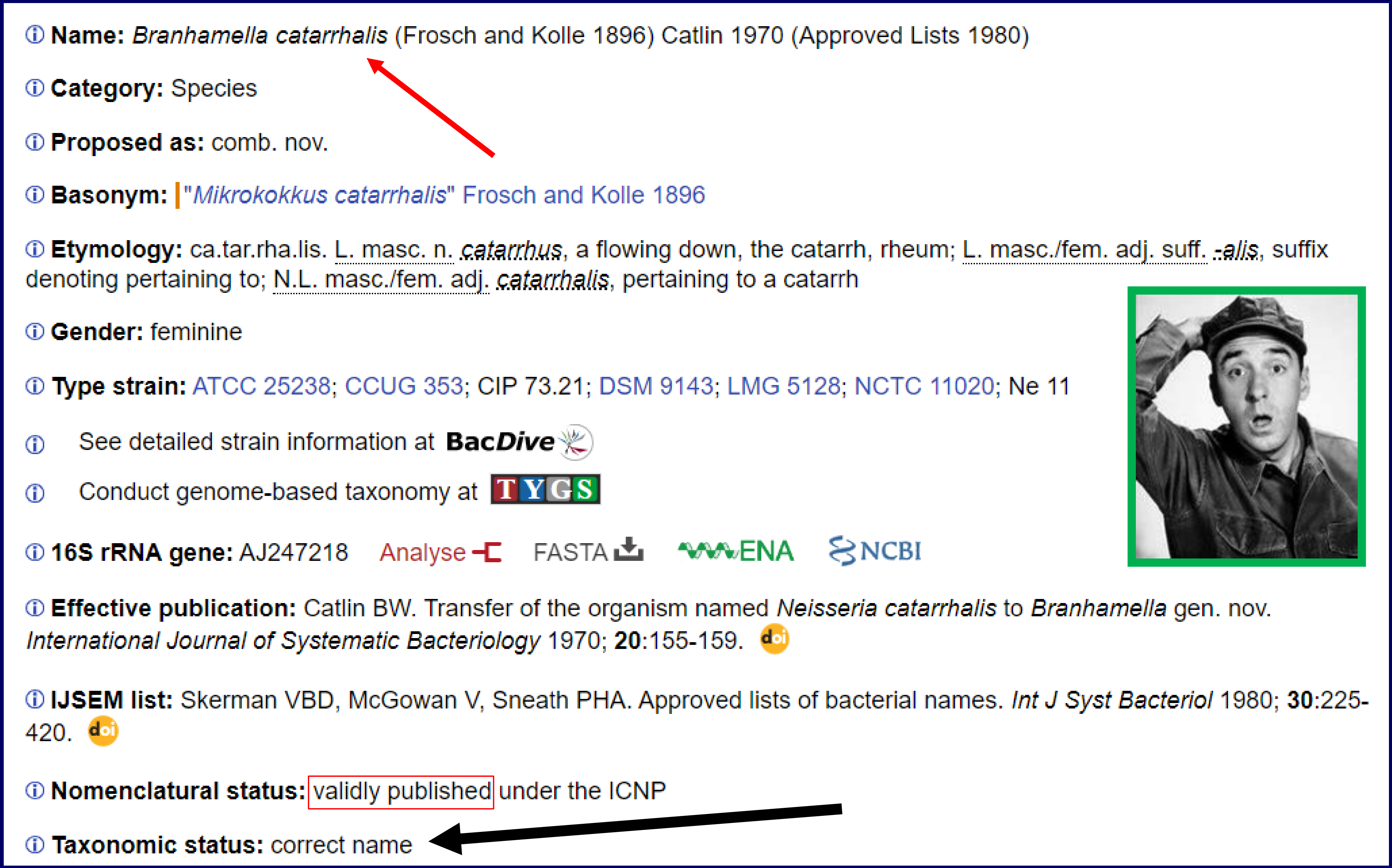
  Int J Syst Bacteriol. 1970; 20:155-159

- *Streptococcus faecalis*

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

- *Bacillus coli* (never validly published)





**Name:** *Branhamella catarrhalis* (Frosch and Kolle 1896) Catlin 1970 (Approved Lists 1980)

**Category:** Species

**Proposed as:** comb. nov.

**Basonym:** "*Mikrokokkus catarrhalis*" Frosch and Kolle 1896

**Etymology:** ca.tar.rha.lis. L. masc. n. *catarrhus*, a flowing down, the catarrh, rheum; L. masc./fem. adj. suff. *-alis*, suffix denoting pertaining to; N.L. masc./fem. adj. *catarrhalis*, pertaining to a catarrh

**Gender:** feminine

**Type strain:** ATCC 25238; CCUG 353; CIP 73.21; DSM 9143; LMG 5128; NCTC 11020; Ne 11

See detailed strain information at **BacDive**

Conduct genome-based taxonomy at **TYGS**

**16S rRNA gene:** AJ247218 Analyse FASTA ENA NCBI

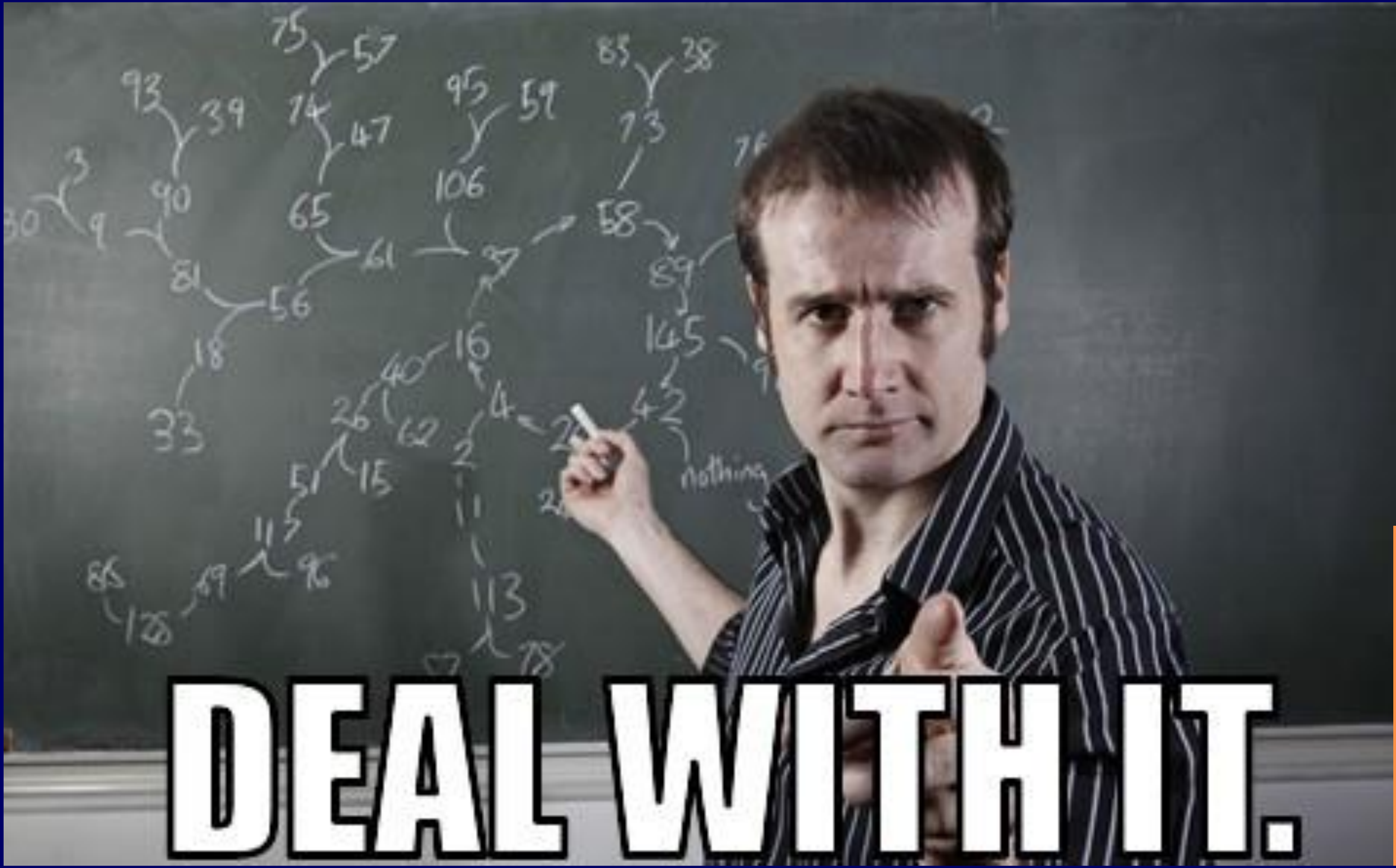
**Effective publication:** Catlin BW. Transfer of the organism named *Neisseria catarrhalis* to *Branhamella* gen. nov. *International Journal of Systematic Bacteriology* 1970; **20**:155-159. doi

**IJSEM list:** Skerman VBD, McGowan V, Sneath PHA. Approved lists of bacterial names. *Int J Syst Bacteriol* 1980; **30**:225-420. doi

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

**Taxonomic status:** correct name

lpsn.dsmz.de/species (www.bacterio.net)


DEAL WITH IT.


GET
OVER IT
AND
MOVE
ON

# 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

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?

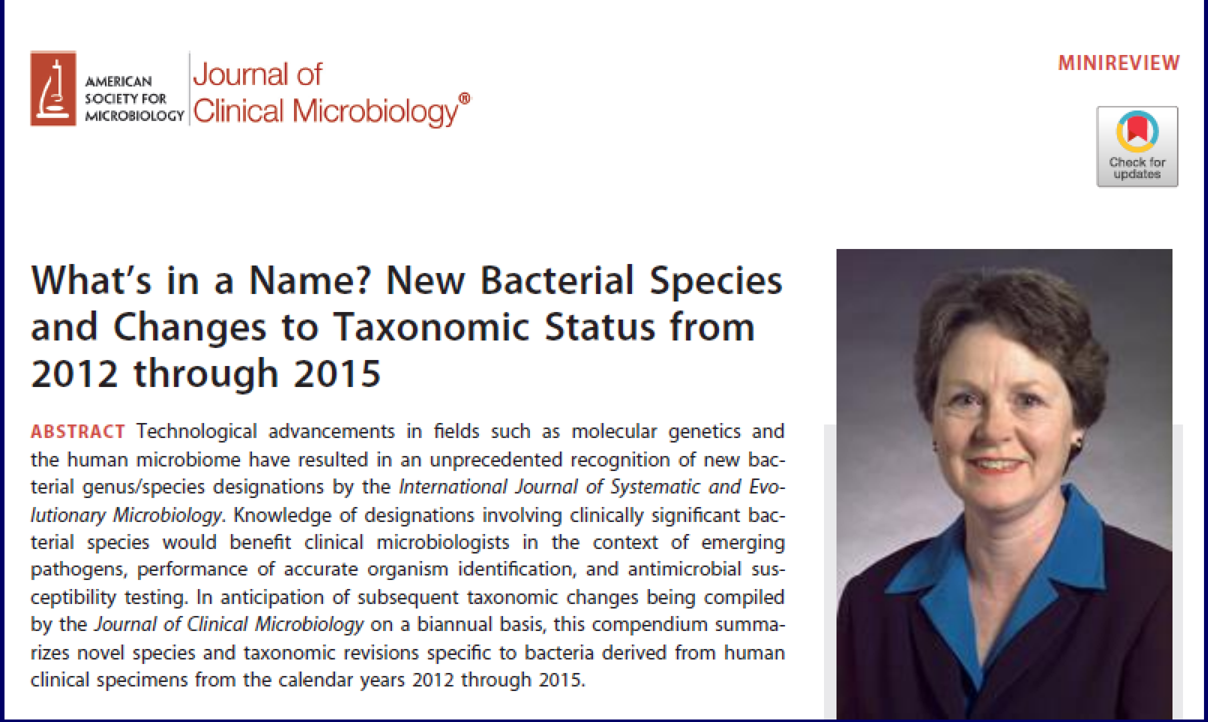
JOURNAL OF
Clinical
Microbiology

JCM

Photo quiz (see page 3113)

Published Monthly by the
American Society
for Microbiology

SEPTEMBER 2011, VOLUME 49, NUMBER 9



AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology®

MINIREVIEW

## 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. 2017; 55:24-42

There will soon be four
(2019, 2021, 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
    (spoiler alert → veterinary!!!!)
    All bacterial taxa validated by *IJSEM*
    Includes all taxa derived from human clinical material
    Later publications have included follow-up

# HELP MAY BE ON THE WAY

CLINICAL AND
LABORATORY
STANDARDS
INSTITUTE®

M64 (Document Development Committee)
Guideline for Implementation of Taxonomy
Nomenclature Changes

### Scope

Bacteriology
Mycology

### Participants

Clinical (including veterinary)
Industry
Government

### Audience

Clinical microbiology
Veterinary microbiology

# DISCUSSION TOPICS

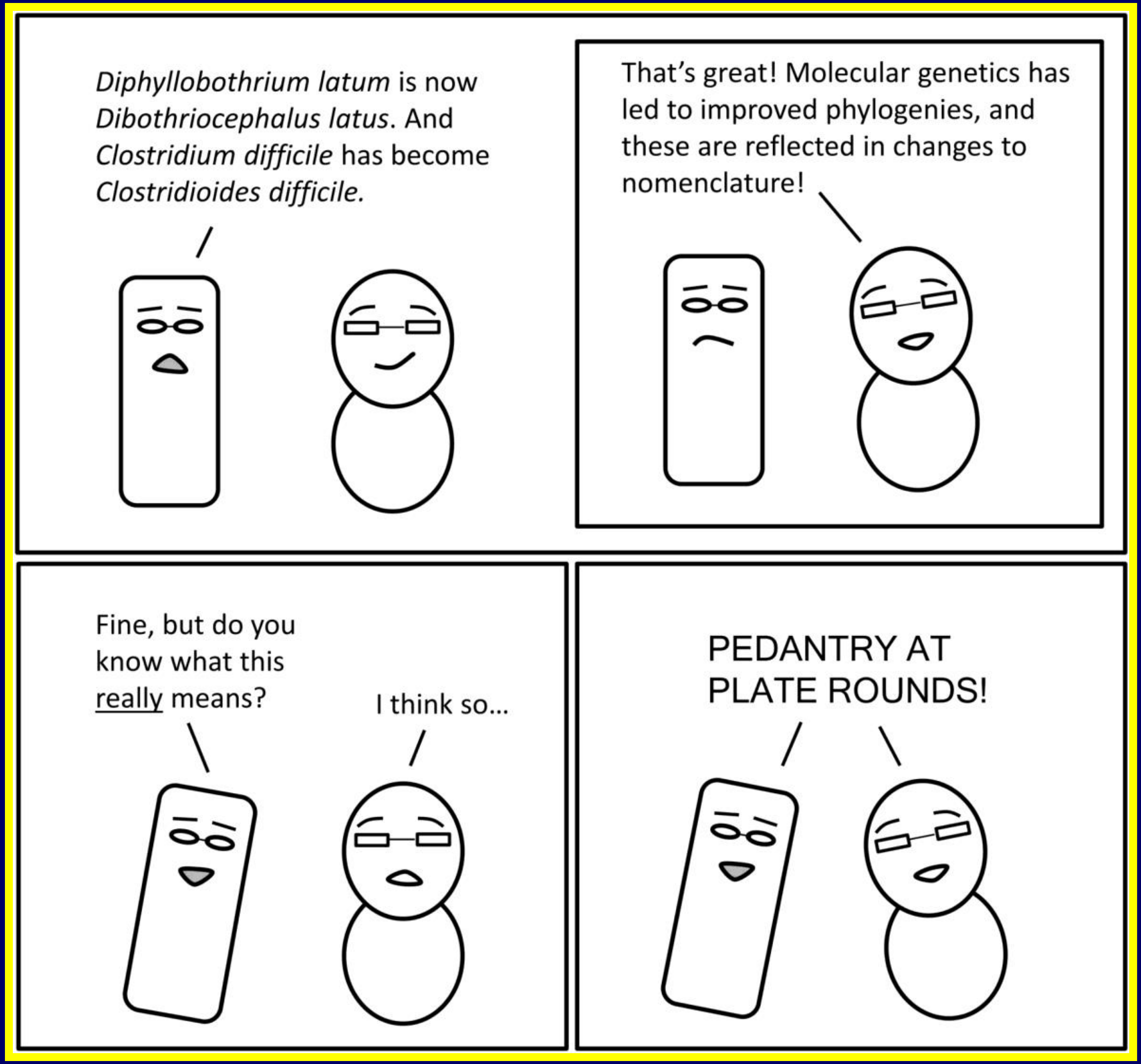
- Role for *International Journal of Systematic and Evolutionary Microbiology* WRT bacteriology
- *Journal of Clinical Microbiology* compendia
    - An assist for bacteriology revisions/changes
    - Time zero for mycology revisions/changes
- Some implementation can be expedited
- Ancillary partner planning; 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