AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology®

COMMENTARY

If You're Not Confused, You're Not Paying Attention: *Ochrobactrum* Is Not *Brucella*

Edgardo Moreno,[a] Earl A. Middlebrook,[b] Pamela Altamirano-Silva,[c] Sascha Al Dahouk,[d] George F. Araj,[e] Vilma Arce-Gorvel,[f] Ángela Arenas-Gamboa,[g] Javier Ariza,[h] Elías Barquero-Calvo,[a] Giorgio Battelli,[i] Wilson J. Bertu,[j] José María Blasco,[k] Mile Bosilkovski,[l] Simeon Cadmus,[m] Clayton C. Caswell,[n] Jean Celli,[o] Carlos Chacón-Díaz,[c] Esteban Chaves-Olarte,[c] Diego J. Comerci,[p] Raquel Conde-Álvarez,[q,r] Elizabeth Cook,[s] Silvio Cravero,[t] Maryam Dadar,[u] Xavier De Boelle,[v] Fabrizio De Massis,[w] Ramón Díaz,[r] Gabriela I. Escobar,[x] Luis Fernández-Lago,[y] Thomas A. Ficht,[z] Jeffrey T. Foster,[aa] Bruno Garin-Bastuji,[bb] Jacques Godfroid,[cc] Jean-Pierre Gorvel,[f] Leyla Güler,[dd] Sevil Erdenliğ-Gürbilek,[ee] Amayel M. Gusi,[j] Caterina Guzmán-Verri,[a] Jiang Hai,[ff] Gabriela Hernández-Mora,[gg] Maite Iriarte,[q,r] Nestor R. Jacob,[hh] Anne Keriel,[ii] Maamar Khames,[jj] Stephan Köhler,[kk] Jean-Jacques Letesson,[v] Maite Loperena-Barber,[r] Ignacio López-Goñi,[r] John McGiven,[ll,mm] Falk Melzer,[nn] Ricardo Mora-Cartin,[oo] Jacob Moran-Gilad,[pp] Pilar M. Muñoz,[k] Heinrich Neubauer,[nn] David O'Callaghan,[ii] Reuben Ocholi,[qq] Ángel Oñate,[rr] Piyush Pandey,[ss] Georgios Pappas,[tt] J. Tony Pembroke,[uu] Martin Roop,[vv] Nazaret Ruiz-Villalonos,[a] Michael P. Ryan,[ww] Suzana P. Salcedo,[eee] Miriam Salvador-Bescós,[q,r] Félix J. Sangari,[xx] Renato de Lima Santos,[yy] Aristarchos Seimenis,[zz] Gary Splitter,[aaa] Marcela Suárez-Esquivel,[a] Darem Tabbaa,[bbb] Marcos David Trangoni,[t] Renee M. Tsolis,[ccc] Nieves Vizcaíno,[y] Gamal Wareth,[nn] Susan C. Welburn,[ddd] Adrian Whatmore,[ll,mm] Amaia Zúñiga-Ripa,[q,r] Ignacio Moriyón[q,r]

[a]Programa de Investigación en Enfermedades Tropicales, Escuela de Medicina Veterinaria, Universidad Nacional, Heredia, Costa Rica
[b]Genomics and Bioanalytics, Los Alamos National Laboratory, Los Alamos, New Mexico, USA
[c]Centro de Investigación en Enfermedades Tropicales, Universidad de Costa Rica, San José, Costa Rica
[d]Department of Environmental Hygiene, German Environment Agency, Berlin, Germany
[e]Department of Pathology and Laboratory Medicine, American University of Beirut Medical Center, Beirut, Lebanon
[f]Centre d'Immunologie de Marseille-Luminy, Aix-Marseille Université, CNRS, INSERM, Marseille, France
[g]Department of Veterinary Pathobiology, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas, USA
[h]Infectious Disease Department, Hospital Universitario de Bellvitge, Universidad de Barcelona, Barcelona, Spain
[i]Department of Medical Veterinary Sciences, University of Bologna, Bologna, Italy
[j]Brucellosis Research Laboratory, Bacterial Research Division, National Veterinary Research Institute, Vom, Nigeria
[k]Departamento de Ciencia Animal, Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain
[l]University Hospital for Infectious Diseases and Febrile Conditions, Medical Faculty, Saints Cyril and Methodius University, Skopje, Republic of North Macedonia
[m]Centre for Control and Prevention of Zoonoses, Faculty of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria
[n]Center for One Health Research, Virginia-Maryland College of Veterinary Medicine, Blacksburg, Virginia, USA
[o]Larner College of Medicine at the University of Vermont, Department of Microbiology and Molecular Genetics, Burlington, Vermont, USA
[p]Instituto de Investigaciones Biotecnológicas Dr. Rodolfo A. Ugalde, Universidad Nacional de San Martín, Buenos Aires, Argentina
[q]Instituto de Investigación Sanitaria de Navarra (IdisNa), Pamplona, Spain
[r]Departamento de Microbiología y Parasitología, Universidad de Navarra, Pamplona, Spain
[s]International Livestock Research Institute, Nairobi, Kenya
[t]Centro de Investigación en Ciencias Veterinarias y Agropecuarias, Instituto Nacional de Tecnología Agropecuaria, Hurlingham, Argentina
[u]Razi Vaccine and Serum Research Institute, Agricultural Research, Education, and Extension Organization, Karaj, Iran
[v]Research Unit in Biology of Microorganisms, Namur Research Institute for Life Sciences, University of Namur, Namur, Belgium
[w]Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, Teramo, Italy
[x]Laboratorio de Brucelosis, Laboratorio Nacional de Referencia, INEI-ANLIS Dr. Carlos G. Malbrán, Buenos Aires, Argentina
[y]Departamento de Microbiología y Genética, Universidad de Salamanca, Salamanca, Spain
[z]Texas A&M University, Veterinary Pathobiology, College Station, Texas, USA
[aa]Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, Arizona, USA
[bb]French Agency for Food, Environmental, and Occupational Health and Safety, Maisons-Alfort, France
[cc]Department of Arctic and Marine Biology, Faculty of Biosciences, Fisheries, and Economics, University of Tromsø-The Arctic University of Norway, Tromsø, Norway

Editor Alexander J. McAdam, Boston Children's Hospital

Address correspondence to Ignacio Moriyón, imoriyon@unav.es.

The authors declare no conflict of interest.

[This article was published on 3 July 2023 with a byline that lacked Suzana P. Salcedo. The byline was updated in the current version, posted on 14 July 2023.]

The views expressed in this article do not necessarily reflect the views of the journal or of ASM.

Published 3 July 2023

[dd]MG Veterinary Diagnostic Laboratory, Meram, Konya, Turkey
[ee]Harran University, Faculty of Veterinary Medicine, Microbiology Department, Şanlıurfa, Şanlıurfa, Turkey
[ff]State Key Laboratory for Infectious Disease Prevention and Control, National Institute for Communicable Disease Control and Prevention, Beijing, People's Republic of China
[gg]Servicio Nacional de Salud Animal, Ministerio de Agricultura y Ganadería, Heredia, Costa Rica
[hh]Hospital Argerich, Department of Infectious Diseases, Buenos Aires, Argentina
[ii]Centre National de Référence des Brucella, U1047, University of Montpellier/INSERM, CHU de Nîmes, Nimes, France
[jj]University of Medea, Faculty of Sciences, Department of Biology, Medea, Algeria
[kk]Institut de Recherche en Infectiologie de Montpellier, CNRS, University of Montpellier, Montpellier, France
[ll]WOAH Reference Laboratory for Brucellosis, Animal and Plant Health Agency, Weybridge, United Kingdom
[mm]FAO Reference Centre for Brucellosis, Department of Bacteriology, Animal and Plant Health Agency, Weybridge, United Kingdom
[nn]Friedrich Loeffler Institut, Institute of Bacterial Infections and Zoonoses, Jena, Germany
[oo]Section of Rheumatology, Department of Medicine, The University of Chicago, Chicago, Illinois, USA
[pp]Microbiology, Advanced Genomics, and Infection Control Applications Laboratory, Department of Health Systems Management, School of Public Health, Faculty of Health Sciences, Ben-Gurion University of the Negev, Beer-Sheva, Israel
[qq]Bacteriology, Parasitology, and Virology Department, National Veterinary Research Institute, Vom, Nigeria
[rr]Laboratory of Molecular Immunology, Department of Microbiology, Faculty of Biological Sciences, Universidad de Concepción, Concepción, Chile
[ss]Department of Microbiology, Assam University, Silchar, Assam, India
[tt]Institute of Continuing Medical Education of Ioannina, Ioannina, Greece
[uu]School of Natural Sciences and Bernal Institute, University of Limerick, Limerick, Ireland
[vv]Department of Microbiology and Immunology, East Carolina University School of Medicine, Greenville, North Carolina, USA
[ww]Department of Applied Science, Technological University of the Shanno, Limerick, Ireland
[xx]Instituto de Biomedicina y Biotecnología de Cantabria, Consejo Superior de Investigaciones Científicas, Universidad de Cantabria, Santander, Spain
[yy]Departamento de Clínica e Cirurgia Veterinárias, Escola de Veterinária, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil
[zz]Mediterranean Zoonoses Control Centre, World Health Organization, Athens, Greece
[aaa]School of Veterinary Medicine, University of Wisconsin-Madison, Madison, Wisconsin, USA
[bbb]Department of Veterinary Public Health, Faculty of Veterinary Medicine, Hama University, Hama, Syria
[ccc]Department of Medical Microbiology and Immunology, School of Medicine, University of California, Davis, Davis, California, USA
[ddd]Division of Infection and Pathway Medicine, Centre for Infectious Diseases, School of Biomedical Sciences, College of Medicine and Veterinary Medicine, The University of Edinburgh, Edinburgh, United Kingdom
[eee]Department of Pathobiological Sciences, University of Wisconsin-Madison, Madison, Wisconsin, USA

ABSTRACT Bacteria of the genus *Brucella* are facultative intracellular parasites that cause brucellosis, a severe animal and human disease. Recently, a group of taxonomists merged the brucellae with the primarily free-living, phylogenetically related *Ochrobactrum* spp. in the genus *Brucella*. This change, founded only on global genomic analysis and the fortuitous isolation of some opportunistic *Ochrobactrum* spp. from medically compromised patients, has been automatically included in culture collections and databases. We argue that clinical and environmental microbiologists should not accept this nomenclature, and we advise against its use because (i) it was presented without in-depth phylogenetic analyses and did not consider alternative taxonomic solutions; (ii) it was launched without the input of experts in brucellosis or *Ochrobactrum*; (iii) it applies a non-consensus genus concept that disregards taxonomically relevant differences in structure, physiology, population structure, core-pangenome assemblies, genome structure, genomic traits, clinical features, treatment, prevention, diagnosis, genus description rules, and, above all, pathogenicity; and (iv) placing these two bacterial groups in the same genus creates risks for veterinarians, medical doctors, clinical laboratories, health authorities, and legislators who deal with brucellosis, a disease that is particularly relevant in low- and middle-income countries. Based on all this information, we urge microbiologists, bacterial collections, genomic databases, journals, and public health boards to keep the *Brucella* and *Ochrobactrum* genera separate to avoid further bewilderment and harm.

KEYWORDS *Brucella*, *Ochrobactrum*

Names of infectious diseases and their etiological agents are relevant because they describe the properties of these entities and thus are essential medical and veterinary terminologies. For example, tuberculosis, brucellosis, tetanus, and gonorrhea are terms that

TABLE 1 Concerns arising from the *Ochrobactrum/Brucella* cladistics presented in reference 1

Concern	Comment
Phylogeny based on evolutionary abstraction	The authors extol the utility of alignment supermatrices of core genomes for inferring trees of closely related species, but they infer a tree based on BLASTp distance neighbor joining with minimum evolution refinement for all alphaproteobacteria and then, with this tree, revise the closely related *Brucella/Ochrobactrum*, whose core genomes are easily alignable.
Phylogenetics without context	The omission and addition of sequences commonly change tree topologies. Leaving out samples that are not type strains will likely necessitate further revisions to correct misleading topologies or to account for yet-to-be type strain placements.
The proposed "*Brucella*" is polyphyletic at conception	All brucellae (core and not core) are consistently recovered as monophyletic; however, *Ochrobactrum* is commonly rendered polyphyletic by *Brucella* but also *Pseudochrobactrum*, *Falsochrobactrum*, and *Paenochrobactrum*, as shown in the authors' own rRNA tree and the works they cite.
Omission of alternative taxonomy fixes	Renaming the *Ochrobactrum thiophenivorans* clade to another genus resolves the polyphyly presented by the authors, keeping *Brucella* and the *Ochrobactrum anthropi/intermedium* clade monophyletic. This resolution is supported by Leclercq et al. (19) and the GTDB (https://gtdb.ecogenomic.org) and leaves the type species of *Ochrobactrum* (*Ochrobactrum anthropi*) and *Brucella* (*Brucella melitensis*) within their respective genera.

have been unequivocally linked to particular bacterial pathogens for over one century. For those who understand their meaning, these names are not vague concepts but rather precise medical conditions that require treatment and prevention. While cephalosporins are recommended to combat *Neisseria gonorrhoeae*, the causative agent of gonorrhea, this antibiotic does not cure tuberculosis or brucellosis caused by *Mycobacterium* or *Brucella* organisms, respectively. Similarly, vaccines that prevent a specific infection do not protect against other bacterial diseases.

In this context, the need for different prevention and treatment strategies exemplifies the profound differences among pathogens and their biological diversity. For medical practitioners and veterinarians, using names molded by scientific interactions with microorganisms for over one century is not a professional onomatomania but a triumph in understanding complex processes and a serious responsibility. For this reason, introducing or modifying nomenclatures should be done with the cooperation of experts and consensus on the subject. Otherwise, there is a risk of causing confusion and damage rather than clarity and benefit.

Particularly problematic has been a publication by bacterial taxonomists who included *Ochrobactrum* within the genus *Brucella* (1), a nomenclature recently examined in the *Journal of Clinical Microbiology*, albeit not without warning (2). As widely known, the brucellae are dangerous intracellular pathogens of animals and humans, while *Ochrobactrum* organisms are free-living organisms associated with soil and plants. Those taxonomists justified such merging based on a two-dimensional genomic analysis (chiefly, the level of sequence divergence) and applied a cladistic rather than systematic evolutionary "concept" of the genus (see reference 3 for a discussion). However, only the latter aligns with the polyphasic taxonomy recommended in authoritative prokaryotic taxonomy manuals, because it includes both genomic analyses and biologically significant traits (4). Consistent with their perspective on genus definition, those taxonomists attempted to minimize the differences by arguing that these phylogenetically related bacteria are not markedly separated because they merely belong to two different "risk groups" and "*Ochrobactrum* species are also known from clinical specimens" (1).

Aside from the lack of appropriate in-depth phylogenetic analyses (Table 1) and discussions of other phylogenetic hypotheses and alternative taxonomic solutions (all without the necessary *Brucella/Ochrobactrum* expert input), the proposal was refuted on the basis of relevant characteristics (3). These characteristics include divergent lifestyles and differences in structure, metabolism, physiology, population structure, core-pangenome assemblies, genome structure, genomic traits, clinical features, treatment, diagnosis, and, above all, pathogenicity and risk groups (Table 2), arguments taxonomically more relevant than a limited phylogenetic analysis alone. These differences make unfeasible a biologically meaningful

TABLE 2 Comparison between the *Brucella* and *Ochrobactrum* genera[a]

Divergent property	Finding for: *Brucella*	*Ochrobactrum*
Genome size (Mb)	3.1–3.4	4.7–8.3
Pangenome type (no. of genes)	Closed (~11,000)	Open (>74,000)
No. of genes in core genome	~1,000	~75
DNA-DNA hybridization (%)	~20–30[b]	
No. of RNA genes	54	78–85
Presence of IS*711* insertion sequences	In all species and strains	Absent
No. and type of plasmids	None	Variable (up to 6) and conjugative
Phylogeny	Monophyletic	Polyphyletic
No. of lysogenic phages	None	>4 (present in at least in some species)
Lateral gene transfer	Absent	Present
Speciation type	Allopatric	Sympatric
Overall cell envelope properties	Permeable to hydrophobic probes and resistant to polycationic peptides	Impermeable to hydrophobic probes and sensitive to polycationic peptides (*O. anthropi* and *O. intermedium*)
No. of transport reactions	~47	~111
Metabolic redundancy	Low	High
No. of metabolic pathways	254 (35 unique for the genus)	313 (94 unique for the genus)
Removal of toxic metals	No	Yes (species/strains)
Degradation of phenolic compounds, petroleum wastes, and xenobiotics	No	Yes (species/strains)
Capable of root nodulation	No	Yes (species/strains)
Lifestyle	Pathogen	Saprophyte
Natural habitat	Intracellular	Soil and root plant surfaces
Transmission to humans	Host-host interaction/animal products	Mostly iatrogenic[b]
Virulence	Finely tuned	Fortuitous/opportunistic[b]
Virulence mechanisms	Escape from the immune response/deviation of intracellular trafficking	No true virulence mechanisms (virulence depends on the host's immune status)
Type IV secretion system	Required for intracellular trafficking and lifestyle	Devoted to plasmid conjugation with a different origin
Infection dynamics	Long-lasting infection and low proinflammatory response	Acute proinflammatory/pyogenic; self-limiting in immunocompetent hosts[b]
Animal disease	Globally distributed and prioritized in many countries (20); about 1.25 billion and 1.9 billion susceptible cattle and small ruminants, respectively, in nonindustrialized countries (with endemic disease)[c]	Not reported as agents of contagious disease
Human health	Present in at least 101 countries worldwide (in 2018) and hugely underreported (21); based on fragmentary (but valid) seroprevalence studies, the annual number of cases may be in the range of 330,000–19,000,000 cases (22)	A total of 288 cases published between 1998 and 2020 (9)
Diagnosis	Well-standardized serological methods	No serological tests are available or necessary
Treatment	WHO-recommended long bitherapy in uncomplicated cases (doxycycline and streptomycin or doxycycline and rifampin)	Depending on antibiotic resistance, short-term broad-spectrum intravenous monotherapy with β-lactams, such as imipenem-cilastatin or cefepime, or oral therapy with co-trimoxazole or ciprofloxacin (9)
Acquired antibiotic resistance	Not reported for doxycycline and streptomycin, including isolates from relapse cases; reported rifampicin resistance in a few strains, possibly due to *in vitro* overestimation (23), and very rarely confirmed by *ropB* mutations (24)	Plasmid-encoded resistance to different families of antibiotics, such as β-lactams (penicillins and cephalosporins, with emerging cases of carbapenem resistance) (9)

(Continued on next page)

TABLE 2 (Continued)

Divergent property	Finding for:	
	Brucella	*Ochrobactrum*
Vaccine	Available (for domestic ruminants) and critically important to control disease	Not available or recommended
WHO/OIE/FAO recommendations/ regulations	Detailed, as follows: (i) humans: diagnosis, treatment, and prophylaxis; (ii) animals: diagnostic procedures/protocols (with emphasis on prescribed tests for international trade) and vaccination	None
WHO biosafety risk group (human disease)	RG3 (high individual risk and low community risk)	RG1 (no or low individual and community risk)

[a]Data extracted from reference 3 (copyright owned by the authors).
[b]Compared with the *O. anthropi*/*O. intermedium* group, the closest phylogenetic relatives of *Brucella* species (6).
[c]Figures were calculated by totaling FAOSTAT population data for 2013 for the European Union, North America, Australia, and New Zealand (industrialized countries) and subtracting this value from the world sheep and goat population (https://www.fao.org/faostat/es/#data [accessed 6 June 2023]).

description of the expanded *Brucella* genus, as shown by the fact that the description of the new *Brucella* species was given only by citing the original *Ochrobactrum* species publication, with no attempt to justify or explain the adequacy for the genus amendment in the current *Bergey's Manual of Systematics of Archaea and Bacteria* (5). Obviously, no *Ochrobactrum* strain is represented to any extent by *Brucella melitensis*, the type species that exemplifies the genus in this authoritative taxonomy manual (5).

The differences are even more evident for clinicians and workers in infectious diseases. While some free-living *Ochrobactrum* strains occasionally display opportunistic pathogen behavior in medically compromised patients, the brucellae do not multiply in the open environment; they are highly contagious intracellular pathogens endowed with an array of peculiar virulence adaptations, causing a long-lasting syndrome known as brucellosis (3, 6–8). In contrast, the few opportunistic *Ochrobactrum* strains are extracellular, inducing inflammatory disorders like those caused by other opportunistic bacteria, and lack true virulence factor genes (9–11). Thus, the diagnosis, anamnesis, prevention, epidemiology, and treatment of such infections depart from those of brucellosis. Moreover, *Ochrobactrum* species show broad antibiotic resistance encoded in the genome and plasmids. In contrast, *Brucella* organisms rarely develop antibiotic resistance, because of their lifestyle, lack of plasmids, and absence of contemporary recombination (Table 2). There are excellent serological tests for diagnosis of the most prevalent *Brucella* infections, while no serological tools are currently available for *Ochrobactrum* infections. Similarly, brucellosis in domestic ruminants can be controlled with vaccines, but such vaccines are not available or recommended to prevent *Ochrobactrum* infections. The list goes on (3). Illustrative of the unnecessary and serious confusion created, She et al. (12), on behalf of the ASM Clinical and Public Health Microbiology Committee, Laboratory Practices Subcommittee, recently elaborated a list of all known (thus far) *Ochrobactrum* "*Brucella* species," warning about the problems in the identification of the "true" brucellae when using some matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) approaches, nucleic acid detection methods, and automated phenotypic method databases. Examination of the simple tests provided to distinguish these obviously different bacteria also illustrates the uncertain basis of this merger.

Lumping these two bacterial groups into the same genus is unreasonable and unsafe, affecting the mainstream of science and creating risks for patients, veterinarians, medical doctors, laboratory workers, health authorities, and legislators who deal with brucellosis, which are particularly grave in low- and middle-income countries. *Brucella* and brucellosis have specific meanings depicted in textbooks, databases, and technical manuals regardless of the *Brucella* species since they produce the same syndrome, differing in virulence and host preference (6–8). Similarly, the widely different characteristics of opportunistic *Ochrobactrum* infections have been established (9–11).

It is difficult to know why the new taxonomic tag has appeared rapidly in influential databases, bacteriological collections, and online sources, including Wikipedia. Indeed, the proposed genus is in the List of Prokaryotic Names with Standing in Nomenclature (https://lpsn.dsmz.de/genus/brucella), and its easy accessibility could explain this fast spread. However, microbiologists (and institutions and databases) not familiar with the intricacies of the International Code of Nomenclature of Prokaryotes (13) are probably not aware that such a list is just a record of validly published names, i.e., those that appear in peer-reviewed journals and are then periodically listed in the *International Journal of Systematic and Evolutionary Microbiology* (in this case, in reference 14). Therefore, the names in the list are not official names endorsed by the International Committee on Systematics of Prokaryotes but a taxonomic "opinion" (*stricto sensu*) and not a scientific truth. In specific cases, these validly published names lack the support of working groups of experts in a bacterial group; significantly, the merging of *Ochrobactrum* and *Brucella* was launched without the input of brucellosis or *Ochrobactrum* specialists. What is probably not evident is that former names like *Ochrobactrum* remain validly published when an updated list with a new proposal appears, so that their preferential use is a choice open to acceptance by the interested parties.

Since the Swedish naturalist Linnaeus pioneered taxonomic work, taxonomy has provided names for living organisms, while phylogeny explores evolutionary histories. However, constructing phylogenies is one thing and formulating sets of codes for recovering information from a taxonomic scheme is quite another. Accordingly, taxonomy should be exercised as a responsible consensual understanding among the experts and parties interested in a bacterial group, especially when dealing with dangerous pathogens, and not routinely derived from quantitative phylogenetic information.

Names are not neutral, because they enclose information. As illustrated in Shakespeare's plot when Juliet Capulet asks Romeo Montague to disown his family name: "It's only your name which is my enemy. You are who you are, even if you weren't a Montague. What is a Montague? It's not a hand, nor a foot, nor an arm, nor a face, nor any other concrete part of the body. Oh, be some other name! What's in a name?" (15) And yet, because of their names, both lovers died in a cruel plot. This drama is not the story of star-crossed lovers but a tragedy of names shaping the destiny of two characters whose appellations represent an ancient quarrel impossible of reconciliation. Similarly, taxonomic names may have serious consequences if not adjusted to the realm of facts in microbiology, as in other fields (16). Therefore, taxonomy should be a system from which meaningful information is retrievable, not a perplexing arrangement of names disconnected from reality. What valuable information can be retrieved from names of soil bacteria such as "*Brucella ciceri*" (*Ochrobactrum ciceri*) or "*Brucella anthropi*" (*Ochrobactrum anthropi*)? Are chickpeas carrying "*B. ciceri*" risky for transmitting brucellosis, and should they be treated as vectors of pathogenic risk group 3 agents? Is environmental "*B. anthropi*" a pathogen with a preference for humans, as *Brucella ceti* is for dolphins and *Brucella canis* is for dogs? The most salient issue is how to deal with confusion without adding to it.

These issues are becoming increasingly relevant in clinical microbiology. Not surprisingly, the *Ochrobactrum-Brucella* case is not unique; similar unilateral rearrangements of nomenclature affecting other pathogens have followed and preceded. As expected, some have warned that similarly confusing new nomenclatures should be ignored (17, 18). Similarly, we advise using the *Ochrobactrum* and *Brucella* nomenclature, which, as stressed above, remains valid. The stewards of information, such as bacterial collections, genomic databases, encyclopedias, journals, reviewers, editorial boards, and scientists, must take into account these considerations in the process of reviewing, writing, and accepting unvindicated nomenclature proposals, acknowledging that *Ochrobactrum* is not *Brucella* and chickpeas are not cows.

REFERENCES

1. Hördt A, López MG, Meier-Kolthoff JP, Schleuning M, Weinhold L-MM, Tindall BJ, Gronow S, Kyrpides NC, Woyke T, Göker M. 2020. Analysis of 1,000+ type-strain genomes substantially improves taxonomic classification of *Alphaproteobacteria*. Front Microbiol 11:468. https://doi.org/10.3389/fmicb.2020.00468.
2. Munson E, Carroll KC. 2023. Update on accepted novel bacterial isolates derived from human clinical specimens and taxonomic revisions published in 2020 and 2021. J Clin Microbiol 61:e00282-22. https://doi.org/10.1128/jcm.00282-22.
3. Moreno E, Blasco JM, Letesson JJ, Gorvel JP, Moriyón I. 2022. Pathogenicity and its implications in taxonomy: the *Brucella* and *Ochrobactrum* case. Pathogens 11:377. https://doi.org/10.3390/pathogens11030377.
4. Gillis M, Vandamme P, De-Vos P, Swings J. 2015. Polyphasic taxonomy: theory and practice of classification, p 43–48. *In* Castenholz RW, Garrity GM (ed), Bergey's manual of systematic bacteriology. Springer, New York, NY.
5. Scholz HC, Banai M, Cloeckaert A, Kämpfer P, Whatmore AM. 2018. *Brucella*. *In* Trujillo ME, Dedysh S, DeVos P, Hedlund B, Kämpfer P, Rainey FA, Whitman WB (ed), Bergey's manual of systematics of archaea and bacteria. John Wiley & Sons, Inc., New York, NY. https://doi.org/10.1002/9781118960608.gbm00807.pub2.
6. Roop RM, Barton IS, Hopersberger D, Martin DW. 2021. Uncovering the hidden credentials of *Brucella* virulence. Microbiol Mol Biol Rev 85:e00021-19. https://doi.org/10.1128/MMBR.00021-19.
7. Corbel MJ, Alton GG, Banai M, Díaz R, Dranovskaia BA, Elberg SS, Garin-Bastuji B, Kolar J, Mantovani A, Mousa AM, Moriyón I, Nicoletti P, Seimenis A, Young EJ. 2006. Brucellosis in humans and animals. World Health Organization, Geneva, Switzerland.
8. Moreno E. 2021. The one hundred year journey of the genus *Brucella* (Meyer and Shaw 1920). FEMS Microb Rev 45:fuaa045. https://doi.org/10.1093/femsre/fuaa045.
9. Ryan MP, Pembroke JT. 2020. The genus *Ochrobactrum* as major opportunistic pathogens. Microorganisms 8:1797. https://doi.org/10.3390/microorganisms8111797.
10. Barquero-Calvo E, Conde-Álvarez R, Chacón-Díaz C, Quesada-Lobo L, Martirosyan A, Guzmán-Verri C, Iriarte M, Manček-Keber M, Jerala R, Gorvel J-P, Moriyón I, Moreno E, Chaves-Olarte E. 2009. The differential interaction of *Brucella* and *Ochrobactrum* with innate immunity reveals traits related to the evolution of stealthy pathogens. PLoS One 4:e5893. https://doi.org/10.1371/journal.pone.0005893.
11. Holmes B, Popoff M, Kiredjian M, Kersters K. 1988. *Ochrobactrum anthropi* gen. nov., sp. nov. from human clinical specimens and previously known as group Vd. Int J Syst Bacteriol 38:406–416. https://doi.org/10.1099/00207713-38-4-406.
12. She R, Anglewicz C, Jerke K, Relich R, Glazier M, Filkins L, Schuetz A. 2023. *Brucella* and *Ochrobactrum* taxonomic updates for laboratories: frequently asked questions (FAQ) for clinical laboratories. ASM Press, Washington, DC. https://asm.org/Guideline/Brucella-and-Ochrobactrum-Taxonomic-Updates-for-La. Accessed 15 May 2023.
13. Parker CT, Tindall BJ, Garrity GM. 2019. International Code of Nomenclature of Prokaryotes. Int J Syst Evol Microbiol 69:S1–S111. https://doi.org/10.1099/ijsem.0.000778.
14. Oren A, Garrity G. 2020. List of new names and new combinations previously effectively, but not validly, published. Int J Syst Evol Microbiol 70:4043–4049. https://doi.org/10.1099/ijsem.0.004244.

15. Shakespeare W. 1597. Romeo and Juliet. Act 2, Scene 2. Full scene modern English. My Shakespeare. https://myshakespeare.com/romeo-and-juliet/act-2-scene-2-full-scene-modern-english. Accessed 26 June 2023.
16. Garnett ST, Christidis L. 2017. Taxonomy anarchy hampers conservation. Nature 546:25–27. https://doi.org/10.1038/546025a.
17. Tortoli E, Brown-Elliott BA, Chalmers JD, Cirillo DM, Daley CL, Emler S, Floto RA, Garcia MJ, Hoefsloot W, Koh WJ, Lange C, Loebinger M, Maurer FP, Morimoto K, Niemann S, Richter E, Turenne CY, Vasireddy R, Vasireddy S, Wagner D, Wallace RJJ, Wengenack N, van Ingen J. 2019. Same meat, different gravy: ignore the new names of mycobacteria. Eur Respir J 54:1900795. https://doi.org/10.1183/13993003.00795-2019.
18. Lancet Infectious Diseases. 2019. C. difficile: a rose by any other name. Lancet Infect Dis 19:449. https://doi.org/10.1016/S1473-3099(19)30177-X.
19. Leclercq SO, Cloeckaert A, Zygmunt MS. 2020. Taxonomic organization of the family *Brucellaceae* based on a phylogenomic approach. Front Microbiol 10:3083. https://doi.org/10.3389/fmicb.2019.03083.
20. Centers for Disease Control and Prevention, National Center for Emerging and Zoonotic Infectious Diseases. 2023. Completed OHZDP workshops. https://www.cdc.gov/onehealth/what-we-do/zoonotic-disease-prioritization/completed-workshops.html. Accessed 10 April 2023.
21. Laine CG, Scott HM, Arenas-Gamboa Á. 2022. Human brucellosis: widespread information deficiency hinders an understanding of global disease frequency. PLoS Negl Trop Dis 16:e0010404. https://doi.org/10.1371/journal.pntd.0010404.
22. Kirk MD, Pires SM, Black RE, Caipo M, Crump JA, Devleesschauwer B, Döpfer D, Fazil A, Fischer-Walker CL, Hald T, Hall AJ, Keddy KH, Lake RJ, Lanata CF, Torgerson PR, Havelaar AH, Angulo FJ. 2015. World Health Organization estimates of the global and regional disease burden of 22 foodborne bacterial, protozoal, and viral diseases, 2010: a data synthesis. PLoS Med 12:e1001921. https://doi.org/10.1371/journal.pmed.1001921.
23. Johansen TB, Scheffer L, Jensen VK, Bohlin J, Feruglio SL. 2018. Whole-genome sequencing and antimicrobial resistance in *Brucella melitensis* from a Norwegian perspective. Sci Rep 8:8538. https://doi.org/10.1038/s41598-018-26906-3.
24. Ma HR, Xu HJ, Wang X, Bu ZY, Yao T, Zheng ZR, Sun Y, Ji X, Liu J. 2023. Molecular characterization and antimicrobial susceptibility of human *Brucella* in northeast China. Front Microbiol 14:1137932. https://doi.org/10.3389/fmicb.2023.1137932.