

# Rejection of the name *Borrelia* and all proposed species comb. nov. placed therein

Gabriele Margos<sup>1,2,\*</sup>, Santiago Castillo-Ramirez<sup>3</sup>, Sally Cutler<sup>2,4</sup>, Ram B. Dessau<sup>2,5</sup>, Randi Eikeland<sup>2,6</sup>, Agustin Estrada-Peña<sup>7</sup>, Alexander Gofton<sup>8</sup>, Lucía Graña-Miraglia<sup>3</sup>, Klaus-Peter Hunfeld<sup>2,9</sup>, Andreas Krause<sup>10</sup>, Reto Lienhard<sup>11</sup>, Per-Eric Lindgren<sup>2,12</sup>, Charlotte Oskam<sup>13</sup>, Ivo Rudolf<sup>14</sup>, Ira Schwartz<sup>15</sup>, Andreas Sing<sup>1</sup>, Brian Stevenson<sup>16</sup>, Gary P. Wormser<sup>17</sup> and Volker Fingerle<sup>1,2</sup>

## Abstract

Rejection (*nomen rejiciendum*) of the name *Borrelia* and all new combinations therein is being requested on grounds of risk to human health and patient safety (Principle 1, subprinciple 2 and Rule 56a) and violation to aim for stability of names, to avoid useless creation of names (Principle 1, subprinciple 1 and 3) and that names should not be changed without sufficient reason (Principle 9 of the International Code of Nomenclature of Prokaryotes).

## INTRODUCTION

The genus *Borrelia*, initially described by Swellengrebel 1907, was divided by Adeolu and Gupta [1] into two genera, one retaining the name *Borrelia* (comprising largely species associated with tick-borne relapsing fever illnesses), the other named *Borrelia* gen. nov. containing species of the *Borrelia burgdorferi* sensu lato species complex (which cause Lyme borreliosis). Subsequent work has shown that the genus separation was based on insufficient data and the drawn conclusions are only supported by a subset of species of the genus *Borrelia* [2–5]. Following publication of the genus separation the names of eight out of 20 species were validated in Validation List 163 [6]. In a later list [7] three further species were re-named. As this will generate confusion amongst medical practitioners and health professionals, it may seriously affect human health and welfare.

## Risks to human health and patient safety

Lyme borreliosis (also called Lyme disease) is the most common arthropod-borne bacterial disease of humans in North America and Europe affecting an estimated 300 000 people each year in the USA, and, according to health insurance data, over 200 000 cases of Lyme borreliosis occur every year in Germany alone [8–14].

Symptoms of Lyme borreliosis can vary widely among patients and may include characteristic skin lesions, arthritis, meningitis, radiculoneuritis, facial nerve paralysis, ocular involvement and atrioventricular nodal block [10, 15–20]. Notably, symptoms caused by some relapsing fever species, e.g. *B. miyamotoi*, may resemble that of Lyme borreliosis [21, 22]. Failure to treat this infection during the early stages can result in later severe clinical manifestations that may be more difficult to treat, such as Lyme arthritis and acrodermatitis

**Author affiliations:** <sup>1</sup>Bavarian Health and Food Safety Authority, National Reference Center for *Borrelia*, Oberschleissheim, Germany; <sup>2</sup>Members of the ESCMID Study Group for Lyme Borreliosis (ESGBOR, [www.escmid.org/esgbor](http://www.escmid.org/esgbor)); <sup>3</sup>Programa de Genómica Evolutiva, Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México, CP 62210, Cuernavaca, Morelos, México; <sup>4</sup>School of Health, Sport and Bioscience, University of East London, London E15 4LZ, UK; <sup>5</sup>Department of Clinical Microbiology, Slagelse Hospital, Denmark; <sup>6</sup>Norwegian Advisory Unit for Tick Borne Diseases, Sørlandet Hospital, Norway; <sup>7</sup>Department of Animal Pathology, Faculty of Veterinary Medicine, 50013 Zaragoza, Spain; <sup>8</sup>Australian National Insect Collection CSIRO, Black Mountain, Acton, ACT, 2901, Australia; <sup>9</sup>Zentralinstitut für Labormedizin, Mikrobiologie & Krankenhaushygiene, Krankenhaus Nordwest, Akademisches Lehrkrankenhaus der Johann Wolfgang Goethe-Universität, Frankfurt am Main, Germany; <sup>10</sup>Abteilung Rheumatologie und Klinische Immunologie, Immanuel Krankenhaus Berlin, Berlin, Germany; <sup>11</sup>Microbiologiste FAMH, Laboratoire *Borrelia* (CNRT/ NRZK Spiez), La Chaux-de-Fonds, Switzerland; <sup>12</sup>Department of Biomedical and Clinical Sciences (BKV), Division of Inflammation and Infection (II), Linköping University, Sweden; <sup>13</sup>Vector & Waterborne Pathogens Research Group, College of Science, Health, Engineering and Education, Murdoch University, Murdoch, 6150, Australia; <sup>14</sup>Institute of Vertebrate Biology, v.v.i., Academy of Sciences of the Czech Republic, CZ-691 42 Valtice, Czech Republic; <sup>15</sup>Department of Microbiology and Immunology, New York Medical College, Valhalla, NY, USA; <sup>16</sup>Department of Microbiology, Immunology and Molecular Genetics and Department of Entomology, University of Kentucky, Lexington, Kentucky, 40502, USA; <sup>17</sup>Division of Infectious Diseases, New York Medical College, Valhalla, NY, USA.

\*Correspondence: Gabriele Margos, [gabriele.margos@igl.bayern.de](mailto:gabriele.margos@igl.bayern.de)

**Keywords:** *Borrelia*; Lyme disease; nomenclature.

**Abbreviations:** CSI, conserved signature indel; CSP, conserved signature protein; LB, Lyme borreliosis; RF, relapsing fever.

A supplementary figure is available with the online version of this article.

chronica atrophicans. A missed or delayed diagnosis of Lyme carditis might even contribute to patient mortality [10, 15, 17, 23–25]. Due to considerations of human health and welfare, we respectfully ask the Judicial Commission to reject *Borrelia* and all new combinations contained in it as *nomina periculosa* (as per Rule 56a of the International Code of Nomenclature of Prokaryotes) [26]. Following this guidance, we described safety concerns pertaining to changing the genus name of Lyme borreliosis-causing spirochetes [27]:

1. The names ‘Lyme borreliosis’ and ‘*Borrelia*’ are thoroughly intertwined in medical literature. It is imperative that physicians and other care givers receive prompt and accurate information when diagnosing and treating patients. New information on treatment recommendations or diagnostic tests is frequently published. From discovery onward, all publications on Lyme borreliosis describe the causative bacteria as members of the genus *Borrelia*. Only the paper on renaming the genus [1], and few others, even mention the word ‘*Borrelia*’ (22 times used as author keyword since 2012–2019 compared with 1255 times for *Borrelia* as per scopus search 20/12/2019).

2. Throughout the world, countless databases store diagnostic and treatment information. Search algorithms are usually based on keyword matches in order to retrieve the requested information. Thus, a search for *Borrelia* will be likely to fail to identify information that uses the name *Borrelia*, and vice versa. There is significant potential that such a failure could lead to diagnostic confusion and sub-optimal patient treatment, increasing the potential of poor outcomes for patients. Overcoming this problem would require replacement of every database and/or access program throughout the world, which is not a practical solution. The possible risk to human health far outweighs any benefit of the proposed bacterial species name change.

3. In some countries, payment for the delivery of diagnostic testing services and clinical care to patients is highly dependent upon the use of standardized, precise disease codes and procedural codes (e.g. ICD-10, CPT in the USA). Such coding in hospitals, clinics, health care systems and insurance companies is indeed based on the terminology ‘*Borrelia*’. Inconsistencies in coding and related descriptors in computer systems, along with debates about whether *Borrelia burgdorferi* is the same causative agent as *Borrelia burgdorferi*, present genuine risks of confusion, denial of claims and delay in proper insurance coverage. Consequently, access to diagnosis and treatment may be compromised, which could endanger the patient’s health.

4. Government regulations vary around the world. Similarly, health insurance coverages and procedures vary extensively. A diagnostic test or treatment regimen with approved use for treating infections by *Borrelia burgdorferi* sensu lato may not automatically be accepted for *Borrelia burgdorferi*. In such cases, a patient may be denied treatment or misdiagnosed. Again, this risk to human health needs to be of primary concern.

5. Lyme borreliosis is an occupational and public risk in many countries for persons using forested or grassy areas for work (e.g. forestry) or recreation. Public health interventions including education materials rely heavily on the terminology *Borrelia* to properly inform the public and industry stakeholders about this pathogen, the risk of infection, and how to limit exposure. Specific diagnosis and treatment are often covered by professional insurance programs; debates about *Borrelia* as being the same as *Borrelia* have the potential to delay proper insurance coverage and, consequently, diagnosis and treatment. This endangers the patient’s health and – in consequence – further employment.

### Violation of Principle 1, subprinciples 1 and 3, and Principle 9 of the International Code of Nomenclature of Prokaryotes

Although the International Code of Nomenclature of Prokaryotes (ICNP) is concerned mainly with taxonomical nomenclature, it is difficult to completely separate this from other taxonomical disciplines such as classification and characterization. The preface of the latest edition of the Code holds that ‘While the Code does not attempt to interfere with the process of classification it does lay down clear rules that stipulate that taxa must be distinguishable, that types must be properly designated and (where appropriate) authentic strains must be made available without restriction, and that data on which descriptions are based must be included. The Code provides the critical links between nomenclature, classification and characterization.....’, we would like to raise some critical issues regarding the separation of the genus *Borrelia* affecting its nomenclatural changes.

6. The genus *Borrelia* emend [3] currently comprises 43 named species (LPSN bacterio.net) including 21 species within the relapsing fever-associated group (RF), 21 species within the Lyme borreliosis-associated group (LB), and one species (*Borrelia turcica*) within the novel reptile-associated group. However, there is a wide diversity of borreliae not represented by official named species [28–35]. Some of these novel species of the genus *Borrelia* phylogenetically cluster within previously characterized borreliae lineages such as *Candidatus Borrelia texasensis*, *Candidatus Borrelia kalaharica*, and *Borrelia* sp. from Tanzania in the argasid-transmitted RF clade, and *B. chilensis* in the Ixodes-transmitted LB clade [28, 29, 32, 33]. However, more significant is the extensive diversity of members of the genus *Borrelia* being described from metastriate ticks that form deeply branching unique monophyletic lineages within the genus. Such species include *Candidatus Borrelia tachyglyssi* from echidnas [34], several novel species from Testudines [30], lizards [36–38], and snakes [39], and two putative species associated with *Haemaphysalis* spp. and Asian deer [35] (Fig S1 in online version).

The proposal by Adeolu and Gupta [1] to split the genus *Borrelia* into two, *Borrelia* (relapsing-fever group spirochetes) and a novel genus *Borrelia* [Lyme borreliosis (LB) group spirochetes] [1] left out all of the metastriate-transmitted

**Table 1.** *Borrelia* – key features of clades (Table from <https://doi.org/10.1016/j.ttbdis.2019.101335>)

Clade	<i>Borrelia burgdorferi sensu lato</i>	Relapsing fever group of spirochetes	Reptile- and echidna-associated spirochetes
<b>Morphology*</b>	Motile spirochaetal bacteria, helically shaped with tapered ends; diderm membrane architecture (outer surface membrane, periplasmic space, peptidoglycan-cytoplasmic membrane); periplasmic flagella ( $n=4-14$ ); 0.2–0.3 $\mu\text{m}$ diameter 10–30 $\mu\text{m}$ in length	Motile spirochaetal bacteria, helically shaped with tapered ends; diderm membrane architecture (outer surface membrane, periplasmic space, peptidoglycan-cytoplasmic membrane); periplasmic flagella ( $n=8-20$ ); 0.2–0.5 $\mu\text{m}$ diameter 10–40 $\mu\text{m}$ in length	Motile spirochaetal bacteria, helically shaped with tapered ends; periplasmic flagella ( $n=10$ ); 0.2–0.3 $\mu\text{m}$ diameter 10–25 $\mu\text{m}$ in length
<b>Genomic features*</b>	Fragmented genome, linear chromosome, plasmids (5–70 kb) Size 1.5 Mb DNA G+C content 28 %; common ancestry of plasmids cp26 (all LB) and lpB ( <i>B. miyamotoi</i> )	Fragmented genome, linear chromosome, plasmids (5–165 kb), Size 1.5 Mb DNA G+C content 27–30 %; common ancestry of plasmids cp26 (all LB) and lpB ( <i>B. miyamotoi</i> )	Fragmented genome, linear chromosome, plasmids (30–130 kb) Size 1.5 Mb DNA G+C content 30%
<b>Vector species</b>	Hard ticks of genus <i>Ixodes</i>	Hard ticks of genera <i>Ixodes</i> , <i>Rhipicephalus</i> , <i>Amblyomma</i> , <i>Haemaphysalis</i> Soft ticks of genera <i>Ornithodoros</i> , <i>Argas</i> ; Body louse <i>Pediculus humanus</i> ;†	Hard ticks of genera <i>Hyalomma</i> , <i>Amblyomma</i> , <i>Ixodes</i> , <i>Bothriocroton</i>
<b>Pathogenicity profile*</b>	Commonly tissue pathogens, transient blood phase except in <i>B. mayonii</i> (blood densities up to $10^5-10^6$ cells $\text{ml}^{-1}$ ).	Commonly found in blood before/ during febrile periods but colonize also tissue. For many unknown. <i>B. duttonii</i> is well known to cross the placenta causing peri-natal mortality; <i>B. miyamotoi</i> infection may resemble Lyme (neuro)borreliosis.	Unknown
<b>Transovarial transmission</b>	Rare, shown for <i>B. afzelii</i> §	Common	Unknown

\*Information is available only for a subset of species, not for all species.

†The louse may not be considered a proper vector because transmission occurs when the louse is crushed and gut contents are smeared into the skin.

§[45].

species of the genus species, the inclusion of which significantly alter our understanding of borreliae evolution.

7. The authors described conserved signature indels (CSIs) and conserved signature proteins (CSPs) that could be used to distinguish between the LB *Borrelia* and the RF *Borrelia* groups. The description of the new genera indicated that only these genetic markers are able to distinguish the two genera while there is overlap in morphology [e.g. helical cells, 0.2–0.3  $\mu\text{m}$  in width, 3–180  $\mu\text{m}$  in length (the latter being a mistake as cells of both groups are usually 10–30  $\mu\text{m}$  in length)], phenotypic traits (e.g. motility via periplasmic flagella, microaerophily, vector-transmission) and genomic DNA G+C content (26–32 mol%) of the two groups. As we have previously pointed out, it is uncontested that differences in CSI and CSP exist between the clades of LB and RF species [3], however there are similarities and overlaps in traits that need to be taken into consideration when studying taxonomy (Table 1). Apart from a common morphology that is shared by spirochaetal bacteria (with some variations within groups, e.g. number of flagella, number and regularity of spirals), a similar genome structure, similar DNA G+C content, a further common property of species within the genus *Borrelia*

is that they are, with one exception, maintained in natural transmission cycles by ticks as vectors. Thus, it is our view that the renaming is based on selected genomic characters, i.e. on CSIs and CSPs in only two of the clades contributing to the genus *Borrelia*. In a third clade of species (e.g. *B. turcica* and *Candidatus B. taylori* which have been subsumed under RF species by [40]), 17–20 % of these characters do not follow the predicted pattern of having RF-specific CSIs but have a signature of LB CSIs. In our opinion this disregards principle 1 subprinciple 3 of the Code ('Avoid the useless creation of names') and principle 9 (The name of a taxon should not be changed without sufficient reason...) and is in conflict with the statement in the preface (...it [the Code] does lay down clear rules that stipulate that taxa must be distinguishable...).

8. Following division of the genus *Borrelia* into two separate genera, 14 out of 20 species were renamed in the new genus *Borrelia* [1] and 11 validated in IJSEM [6, 7]. We would like to highlight that in 2018 and 2019, two independent studies evaluated a justification of the genus separation [2, 3]. The first study sequenced the genomes of species 'intermittent' between the RF clade and the LB clade, a reptile-associated and a newly described echidna-associated species [3, 41].

Data based on the percentage of conserved proteins (POCP) [42] and on clustering of CSIs indicated that all groups should remain within a single genus [3]. Independently, using a phyloproteomics approach the second study concluded that the separation of RF and LB group spirochetes was not supported by their data [2]. A recent review that included a phylogenetic analysis of near full length 16S rRNA sequences of all reported species of the genus *Borrelia* revealed that many strains and species need to be evaluated before judgment is justified on the genus as a whole [5] (see Fig. S1, available in the online version of this article).

Given the situation outline above, the proposed changes in taxonomy of the genus *Borrelia*, i.e. the creation of two different genera is a violation of principle 1, subprinciples 1 and 3 of the Code as the proposed changes are premature, i.e. based on insufficient data, which does not support stability of names (violation of subprinciple 1) and uselessly creates new names (subprinciple 3). The latest publication by Gupta [40] on taxonomy of the genus *Borrelia* reiterates results of earlier studies and thus violates principle 9 of the Code which states that ‘The name of a taxon should not be changed without sufficient reason based either on further taxonomic studies or on the necessity of giving up a nomenclature that is contrary to the Rules of this Code.’

Moreover, there is also confusion amongst the scientific community as a result of splitting the genus *Borrelia* into two. Most notably, researchers have experienced frustration during the submission of sequence data to online databases, such as the NCBI sequence database GenBank [43], whereby sequences have been incorrectly renamed post-submission as *Borrelia*. For example, despite the original submission as *Candidatus Borrelia taylori* and supporting evidence that it does not cluster within the LB species clade, it was renamed as *Candidatus Borrelia taylori*. The name has since been reverted to the genus *Borrelia*, however, the genus *Borrelia* remains as a synonym within the sequence metadata (e.g. GenBank Accession CP025785 and KY586964) [34, 41].

The genus *Borrelia* is currently validated in its original form [44] and other analyses such as proteomics, analyses of phenotypic and ecological data are consistent with this view [5]. For this and the reasons outlined above we would like to ask the Judicial Commission to support the rejection of the name *Borrelia* and all combinations therein.

#### Funding information

The National Reference Center for *Borrelia* was supported by the Robert Koch-Institute, Berlin, Germany.

#### Acknowledgements

At the business meeting of ESGBOR, Amsterdam 2019 it was discussed that the genus ‘*Borrelia*’ is the preferred terminology.

#### Author contributions

G.M., V.F., B.S., A.G., C.O., A.E-P., S.C., I.S., G.W. conceptualization S.C-R., I.R. resources All authors reviewed and edited the ms

#### Conflicts of interest

The author(s) declare that there are no conflicts of interest.

#### References

1. Adeolu M, Gupta RS. 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 *Borrelia* gen. nov. containing the members of the Lyme disease *Borrelia* (*Borrelia burgdorferi* sensu lato complex). *Antonie van Leeuwenhoek* 2014;105:1049–1072.
2. Estrada-Peña A, Cabezas-Cruz A. Phyloproteomic and functional analyses do not support a split in the genus *Borrelia* (phylum Spirochaetes). *BMC Evol Biol* 2019;19:54.
3. Margos G, Gofton A, Wibberg D, Dangel A, Marosevic D et al. The genus *Borrelia* reloaded. *PLoS One* 2018;13:e0208432.
4. Margos G, Marosevic D, Cutler S, Derdakova M, Diuk-Wasser M et al. There is inadequate evidence to support the division of the genus *Borrelia*. *Int J Syst Evol Microbiol* 2017;67:1081–1084.
5. Margos G, Fingerle V, Cutler S, Gofton A, Stevenson B et al. Controversies in bacterial taxonomy: the example of the genus *Borrelia*. *Ticks Tick Borne Dis* 2020;11:101335.
6. Oren A, Garrity GM. List of new names and new combinations previously effectively, but not validly, published. *Int J Syst Evol Microbiol* 2015;65:1105–1111.
7. Oren A, Garrity GM. List of new names and new combinations previously effectively, but not validly, published. *Int J Syst Evol Microbiol* 2018;68:2130–2133.
8. Schwartz AM, Hinckley AF, Mead PS, Hook SA, Kugeler KJ. Surveillance for Lyme Disease - United States, 2008–2015. *MMWR Surveill Summ* 2017;66:1–12.
9. Stanek G, Strle F. Lyme borreliosis: a European perspective on diagnosis and clinical management. *Curr Opin Infect Dis* 2009;22:450–454.
10. Steere AC, disease L. Lyme disease. *N Engl J Med* 2001;345:115–125.
11. Sykes RA, Makiello P. An estimate of Lyme borreliosis incidence in Western Europe. *J Public Health* 2017;39:74–81.
12. Müller I, Freitag MH, Poggensee G, Scharnetzky E, Straube E et al. Evaluating frequency, diagnostic quality, and cost of Lyme borreliosis testing in Germany: a retrospective model analysis. *Clin Dev Immunol* 2012;2012:1–13.
13. Nelson CA, Saha S, Kugeler KJ, Delorey MJ, Shankar MB et al. Incidence of Clinician-Diagnosed Lyme disease, United States, 2005–2010. *Emerg Infect Dis* 2015;21:1625–1631.
14. Radolf JD, Caimano MJ, Stevenson B, Hu LT, . Of ticks, mice and men: understanding the dual-host lifestyle of Lyme disease spirochaetes. *Nat Rev Microbiol* 2012;10:87–99.
15. Stanek G, Strle F. Lyme borreliosis. *The Lancet* 2003;362:1639–1647.
16. Pinto DS. Cardiac manifestations of Lyme disease. *Med Clin North Am* 2002;86:285–296.
17. Forrester JD, Mead P. Third-degree heart block associated with Lyme carditis: review of published cases. *Clin Infect Dis* 2014;59:996–1000.
18. Hegerova LT, Olson TC. The ticking heart: a case and review of acute Lyme cardiac complications. *Minn Med* 2014;97:42.
19. Kuchynka P, Palecek T, Havranek S, Vitkova I, Nemecek E et al. Recent-onset dilated cardiomyopathy associated with *Borrelia burgdorferi* infection. *Herz* 2015;40:892–897.
20. Robinson ML, Kobayashi T, Higgins Y, Calkins H, Melia MT. Lyme carditis. *Infect Dis Clin North Am* 2015;29:255–268.
21. Boden K, Lobenstein S, Hermann B, Margos G, Fingerle V. *Borrelia miyamotoi*-associated neuroborreliosis in immunocompromised person. *Emerg Infect Dis* 2016;22:1617–1620.
22. Telford SR, Goethert HK, Molloy PJ, Berardi VP, Chowdri HR et al. *Borrelia miyamotoi* disease: neither Lyme disease nor relapsing fever. *Clin Lab Med* 2015;35:867–882.
23. Koene R, Boulware DR, Kemperman M, Konety SH, Groth M et al. Acute heart failure from Lyme carditis. *Circ Heart Fail* 2012;5:e24–26.



24. Shenthar J, Shetty SB, Krishnamurthy D. Diagnosis not to be missed: Lyme carditis, rare but reversible cause of complete atrio-ventricular block. *Indian Heart J* 2014;66:723–726.
25. Yoon EC, Vail E, Kleinman G, Lento PA, Li S *et al.* Lyme disease: a case report of a 17-year-old male with fatal Lyme carditis. *Cardio-vasc Pathol* 2015;24:317–321.
26. Parker CT, Tindall BJ, Garrity GM. International Code of Nomenclature of prokaryotes. *Int J Syst Evol Microbiol* 2019;69:S1–S111.
27. Stevenson B, Fingerle V, Wormser GP, Margos G. Public health and patient safety concerns merit retention of Lyme borreliosis-associated spirochetes within the genus *Borrelia*, and rejection of the genus novum *Borrelia*. *Ticks Tick Borne Dis* 2019;10:1–4.
28. Mitani H, Talbert A, Fukunaga M. New world relapsing fever *Borrelia* found in *Ornithodoros porcinus* ticks in central Tanzania. *Microbiol Immunol* 2004;48:501–505.
29. Lin T, Gao L, Seyfang A, Oliver JH. 'Candidatus *Borrelia* texasensis', from the American dog tick *Dermacentor variabilis*. *Int J Syst Evol Microbiol* 2005;55:685–693.
30. Takano A, Fujita H, Kadosaka T, Konnai S, Tajima T *et al.* Characterization of reptile-associated *Borrelia* sp. in the vector tick, *Amblyomma geoemydae*, and its association with Lyme disease and relapsing fever *Borrelia* spp. *Environ Microbiol Rep* 2011;3:632–637.
31. Fedorova N, Kleinjan JE, James D, Hui LT, Peeters H *et al.* Remarkable diversity of tick or mammalian-associated *Borrelia* in the metropolitan San Francisco Bay area, California. *Ticks Tick Borne Dis* 2014;5:951–961.
32. Ivanova LB, Tomova A, González-Acuña D, Murúa R, Moreno CX *et al.* *Borrelia chilensis*, a new member of the *Borrelia burgdorferi* sensu lato complex that extends the range of this genospecies in the southern hemisphere. *Environ Microbiol* 2014;16:1069–1080.
33. Fingerle V, Pritsch M, Wächtler M, Margos G, Ruske S *et al.* "Candidatus *Borrelia* kalaharica" detected from a febrile traveller returning to Germany from vacation in Southern Africa. *PLoS Negl Trop Dis* 2016;10:e0004559.
34. Loh S-M, Gillett A, Ryan U, Irwin P, Oskam C. Molecular characterization of 'Candidatus *Borrelia* tachyglossi' (family *Spirochaetaceae*) in echidna ticks, *Bothriocroton concolor*. *Int J Syst Evol Microbiol* 2017;67:1075–1080.
35. Kumagai Y, Sato K, Taylor KR, Zamoto-Niikura A, Imaoka K *et al.* A relapsing fever group *Borrelia* sp. is widely distributed among wild deer in Japan. *Ticks Tick Borne Dis* 2018;9:465–470.
36. Panetta JL, Šíma R, Calvani NED, Hajdušek O, Chandra S *et al.* Reptile-associated *Borrelia* species in the goanna tick (*Bothriocroton undatum*) from Sydney, Australia. *Parasit Vectors* 2017;10:616.
37. Kaenkan W, Nooma W, Chelong I-A, Baimai V, Trinachartvanit W *et al.* Reptile-associated *Borrelia* spp. in *Amblyomma* ticks, Thailand. *Ticks Tick Borne Dis* 2020;11:101315.
38. Takano A, Kuwata R, Shimoda H, Hadi UK *et al.* Detection and isolation of tick-borne bacteria (*Anaplasma* spp., *Rickettsia* spp., and *Borrelia* spp.) in *Amblyomma varanense* ticks on lizard (*Varanus salvator*). *Microbiol Immunol* 2019;63:328–333.
39. Takano A, Goka K, Une Y, Shimada Y, Fujita H *et al.* Isolation and characterization of a novel *Borrelia* group of tick-borne borreliae from imported reptiles and their associated ticks. *Environ Microbiol* 2010;12:134–146.
40. Gupta RS. Distinction between *Borrelia* and *Borrelia* is more robustly supported by molecular and phenotypic characteristics than all other neighbouring prokaryotic genera: Response to Margos' *et al.* "The genus *Borrelia* reloaded" (PLoS ONE 13(12): e0208432). *PLoS One* 2019;14:e0221397.
41. Gofton AW, Margos G, Fingerle V, Hepner S, Loh S-M *et al.* Genome-wide analysis of *Borrelia turcica* and 'Candidatus *Borrelia* tachyglossi' shows relapsing fever-like genomes with unique genomic links to Lyme disease *Borrelia*. *Infection, Genetics and Evolution* 2018;66:72–81.
42. Qin Q-L, Xie B-B, Zhang X-Y, Chen X-L, Zhou B-C *et al.* A proposed genus boundary for the prokaryotes based on genomic insights. *J Bacteriol* 2014;196:2210–2215.
43. Benson DA, Cavanaugh M, Clark K, Karsch-Mizrachi I, Lipman DJ *et al.* Genbank. *Nucleic Acids Res* 2013;41:D36–D42.
44. Oren A, Garrity GM. Notification that new names of prokaryotes, new combinations, and new taxonomic opinions have appeared in volume 69, part 5 of the IJSEM. *Int J Syst Evol Microbiol* 2019;69:2177–2178.
45. van Duijvendijk G, Coipan C, Wagemakers A, Fonville M, Ersöz J *et al.* Larvae of *Ixodes ricinus* transmit *Borrelia afzelii* and *B. miyamotoi* to vertebrate hosts. *Parasit Vectors* 2016;9:97.

### Five reasons to publish your next article with a Microbiology Society journal

1. The Microbiology Society is a not-for-profit organization.
2. We offer fast and rigorous peer review – average time to first decision is 4–6 weeks.
3. Our journals have a global readership with subscriptions held in research institutions around the world.
4. 80% of our authors rate our submission process as 'excellent' or 'very good'.
5. Your article will be published on an interactive journal platform with advanced metrics.

Find out more and submit your article at [microbiologyresearch.org](https://microbiologyresearch.org).