Division of the genus *Borrelia* into two genera (corresponding to Lyme disease and relapsing fever groups) reflects their genetic and phenotypic distinctiveness and will lead to a better understanding of these two groups of microbes (Margos et al. (2016) There is inadequate evidence to support the division of the genus *Borrelia. Int. J. Syst. Evol. Microbiol*. doi: 10.1099/ijsem.0.001817)

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This rebuttal Letter responds to a Letter in *IJSEM* by Margos et al. challenging division of the genus *Borrelia* into two genera. We discuss here point-by-point the issues raised by Margos et al. and show that much of their criticism is unfounded and in several cases based on misreading of the presented results. We summarize here the extensive evidence based on genomic, genetic and phenotypic properties showing that the members of the family *Borreliaceae* (containing mainly the genus *Borrelia*) comprise two distinct and cohesive groups of microbes, differing in diseases they cause and other phenotypes. Prior to the proposed division, *Borrelia* species causing Lyme disease (LD) were already functionally treated as a distinct group, referred to as ' *B. burgdorferi sensu lato* ' to distinguish them from the other cluster of *Borrelia* species, which includes all known species causing relapsing fever (RF). With the more explicit division of *Borreliaceae* species into two genus-level groups, which are distinguishable from each other based on numerous unique genetic and molecular characteristics, attention can now be focused on the biological significance of different molecular characteristics differentiating the two groups. The clear distinction of the LD and the RF groups of microbes based on numerous highly reliable markers, which are expected to be present even in uncharacterized members of these two groups, should aid in the improved diagnosis as well as treatment of these two diseases, which is hindered by the conflation of a common name for agents causing two different types of diseases.

The members of the family *Borreliaceae* include species that are the causative agents of Lyme disease (LD) and others that are the agents of tick- and louse-borne relapsing fever (RF) [1–3]. Recent phylogenetic and comparative analyses of protein sequences from *Borreliaceae* genomes have provided compelling evidence that the *Borreliaceae* species in fact comprise two genetically distinct groups and that they can be reliably distinguished based on numerous independent molecular characteristics [4]. Based on these phylogenetic/genomic studies, as well as supporting phenotypic characteristics, Adeolu and Gupta [4] proposed the division of the genus *Borrelia* into two genera. In that proposal an emended genus *Borrelia* retained all the species known to cause the clinically and epidemiologically distinctive disorder of RF, while all agents of LD, as well as closely related species not known to cause human disease, were placed into a new genus, *Borreliella* [4]. This latter group has been widely referred to as ' *Borrelia burgdorferi sensu lato* ', which has functioned as a short-hand for distinguishing this increasingly numerous but cohesive group from all other *Borrelia* species. Although the family *Borreliaceae* also contains the species *Cristispira pectinis* with a validly published name [5, 6], there is no cultured isolate or sequence information available for this species. Thus, for all practical purposes, the family *Borreliaceae* originally comprised only a single genus, *Borrelia*, which is now split into two genera, reflecting the long-standing recognition of two groups within it, i.e. ' *B. burgdorferi sensu lato* ' (also termed the 'Lyme disease group of spirochetes' or 'Lyme disease *Borrelia*') and the RF clade.

Margos et al. [7] in a Letter to the Editor in the *IJSEM* criticized the splitting of the family *Borreliaceae* into two genera on three major grounds. (i) The evidence based on genomic characteristics distinguishing the two proposed groups was

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**Abbreviations:** AA1, average amino acid identity; ANI, average nucleotide identity; CSI, conserved signature insertion/deletion; CSP, conserved signature protein; LD, Lyme disease; RF, relapsing fever.
preliminary. (ii) Some Borreliaaceae species do not adhere to the typical phenotypic patterns of the LD and RF groups, thus blurring the distinction between the groups of disease agents. (iii) This division would have various ‘adverse consequences’. While recognizing that a name change for a medically important microbe is never to be taken lightly, we respectfully disagree with the conclusions of Margos et al. [7] and discuss point-by-point the issues raised in their letter. We show that much of the criticism of splitting the family Borreliaaceae into two genera is unfounded.

GENOMIC EVIDENCE FOR THE COHESIVENESS OF THE FAMILY BORRELIAACEAE AND FOR THE PRESENCE OF TWO DISTINCT GROUPS WITHIN THIS FAMILY

The phylogram presented in Fig. 1 of Borreliaaceae species for which there are genome sequences summarizes and updates the evidence for two cohesive groups/genera within the family. The tree is based on concatenated sequences of 762 proteins comprising the core proteins in the genomes of Borreliaaceae species. The tree is very similar in topology and branch support to the earlier tree that was based on 25 conserved proteins from fewer species [4]. As can be seen, the Borreliaaceae species form two distinct clades, which are resolved with high (~100%) statistical support, corresponding to the RF and the LD group of species. Although all Borreliaaceae species studied to date have similar G+C nucleotide contents of ~29 mol% for their chromosomes, five B. burgdorferi sensu lato species had significantly higher CG dinucleotide contents for a given G+C content than eight RF group species, including B. miyamotoi and B. anserina [2].

Fig. 1 also summarizes and maps the different molecular markers that were identified previously [4], namely conserved signature insertions/deletions (CSIs) and conserved signature proteins (CSPs), which are either specifically characteristic of all Borreliaaceae species or uniquely characteristic of one or the other of the two observed clades. Margos et al. [7] in their critique did not acknowledge the greater than 100 molecular markers that were described for the family Borreliaaceae and they also overlooked 38 other described CSIs (table 4 of Adeolu and Gupta’s article [4]), which distinguish the LD and the RF groups of Borreliaaceae species.

A gauge of the utility of a categorization protocol is whether the distinguishing criteria (i.e. the ‘rules’) hold as new organisms are characterized and then become candidates for taxonomic classification. Since the publication of the paper describing the proposed split of the genus Borrelia, genome sequences for five additional Borreliaaceae species (namely B. coriaceae, B. finlandensis, B. japonica, B. mayonii and B. chilenensis) became available. B. coriaceae groups with the RF clade, and the other four species group in the LD clade (Fig. 1). We examined the distribution (i.e. presence/absence) of different described molecular markers in these species. Significantly, all of the described CSIs and CSPs specific for the family Borreliaaceae as a whole are present in all five of these species. Likewise, all of the CSIs and CSPs for the RF group are present in B. coriaceae, but they are lacking in B. finlandensis, B. japonica, B. mayonii and B. chilenensis. The complementary pattern is observed for the distribution of molecular markers that are specific for the LD group of Borreliaaceae species. Sequence information for one representative updated CSI each for the LD and RF group of species is presented in Fig. 2. Based on these results, the described molecular markers are not only specific for the two groups of Borreliaaceae species, but they continue to exhibit a high degree of predictable ability to be found in any novel species belonging or related to these groups.

Margos et al. [7] also criticised the Adeolu and Gupta [4] article for excluding information for a newly described but relatively uncharacterized group of Borreliaaceae species that use reptiles as reservoir hosts. However, this reading of the article is incorrect. The 16S rRNA phylogram (Fig. 2) in the Adeolu and Gupta [4] article in fact includes B. turcica, which constitutes the species from this group with a validly published name and its position was indicated to be indeterminate based on the presented results. However, in the phylogenetic tree presented by Margos et al. [7], which includes B. turcica and other related reptile-associated strains of Borreliaaceae without taxonomic standing, these species/stains exhibit the same pattern of branching as described by Takano et al. [8], which was acknowledged by Adeolu and Gupta [4]. It should be noted, however, that in other recent studies [9, 10], the position of the reptile-associated Borrelia species with respect to its branching position was found to be variable. Thus, further studies based on whole genome data are needed to clarify the position of B. turcica and the ‘reptile group’ of strains.

But let us prospectively consider how more sequence information, as it becomes available, for this newly identified group of Borreliaaceae spirochetes (or, for that manner, any novel species related to this family) might affect the proposed division for this family. Any novel species belonging to the family Borreliaaceae could exhibit one of the three branching patterns noted below. The distribution patterns of the described signatures for three possible branching patterns involving a novel species can be predicted as follows:

(1) The species branches either within the LD group or as an outgroup of this clade. In this case, it is predicted that the sequenced strain (as seen for B. finlandensis, B. japonica, B. mayonii and B. chilenensis) will contain either some or all of the signatures specific for the LD group, but generally none for the RF group, indicating that the strain is related to the LD group of species. The addition of B. finlandensis, B. japonica, B. mayonii and B. chilenensis are examples of this branching pattern (Fig. 1).

(2) The novel species/strain branches either within the RF group or as an outgroup of this clade, and such a strain (as seen with B. coriaceae) is expected to contain either some or all of the signatures for the RF clade, but generally none for the LD group. The
addition of *B. coriaceae* is an example of this branching pattern (Fig. 1).

(3) The sequenced species/strain forms an outgroup of both the LD and RF groups of species in phylogenetic trees. While harbouring at least some of the signatures for the family *Borreliaceae* it does not contain any of the signatures specific for the LD or the RF clades. In this case, further comparative genomic studies on this group of species/strains need be carried out to identify molecular markers specific for this clade. Depending upon the other genetic and phenotypic characteristics of these species/strains, consideration that they may form a separate genus within the family *Borreliaceae* would be warranted.

Based upon the distribution pattern of the described signatures in any novel species, it should be possible to establish, in all cases, whether the newly described species is a part of the described LD or RF groups, or, alternatively, it forms a clade that is distinct from these two groups. Thus, in contrast to the assertion of Margos et al. [7] that, as novel *Borreliaceae* species are discovered, the distinction between the two groups will become increasingly blurred, we predict that the molecular markers described here will prove instrumental in unambiguously establishing the relationship of newly identified species to either the RF or the LD groups of species and that this can provide insights into the biology of these organisms. The notion that there is a smooth continuum of species out there – with all possible permutations in current existence, waiting only to be discovered – does not reflect the general experience of evolutionary biology.

Margos et al. [7] also questioned the signature value of a few of the CSPs, because they are lacking in an isolated species.
However, the loss of a gene in a particular species, which is otherwise uniquely shared by all other members of the group, does not significantly diminish its value as a signature or diagnostic characteristic for the group. Additionally, they also critiqued the Adeolu and Gupta [4] article on the grounds that a number of CSPs that distinguish between the two groups of Borreliae are of unknown function at the time of annotation and, for that reason, are of limited utility as useful signatures. However, this contention appears to reflect a misunderstanding of the earlier work on CSPs for other LD clade Borrelia (11/11) RF clade Borrelia (0/11) Other Bacteria

Fig. 2. Updated information for conserved signature indels in (a) glucose-6-phosphate isomerase and (b) GTP binding protein which are specific for the LD and RF clades. Sequence information for the following five species (namely B. coriaceae, B. finlandensis, B. japonica, B. mayonii and B. chilensis), which have become available since the Adeolu and Gupta [4] publication, has been added to the sequence alignments and the novel species are found to contain the CSIs specific for the LD or the RF clade as predicted. The numbers in parentheses indicate the number of species from a given group in which the described CSI is found over the total number of species from the group for which sequence information was available.

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groups of prokaryotes, including Alphaproteobacteria, Actinobacteria, the PVC superphylum, Halobacteria and Chlamydiae [11–15]. Most of these CSPs were of unknown function at the time they were first characterized, although further studies have shown them to be highly reliable molecular markers for these groups, and biochemical studies on them are leading to discovery of novel and important functions that were hitherto unrecognized [16–20]. Thus, not knowing the function of a conserved protein that is uniquely shared by a given group of species should not be a cause for criticism. Rather, it should be recognized as an opportunity and a challenge, as indicated below, to understand its function and why it is uniquely present in one group of organisms but not another [21].

Margos et al. [7] present a figure showing high synteny between the chromosomes of B. burgdorferi and both an example from the LD group and an example from the RF group (a similar analysis had earlier been published by one of us [2]). However, this was principally a demonstration of conservation of gene order and indirect evidence of the rarity of chromosome rearrangements, such as inversions and large duplications, in these taxa. This is plausibly attributable to the absence or rarity of insertion sequences, transposable elements or lysogenic phages in the chromosome or, alternatively, to imposed constraints from the linear organization of their chromosomes [22]. Moreover, the analysis by Margos et al. [7] excludes the multiple plasmids that are present in different Borreliaeae species and that make up approximately one-third of the overall genetic content. One of the distinguishing features of the RF group of species, including B. anserina (GenBank accession number CP014325), is the presence of large linear plasmids (megaplasmid) of 90–190 kb, which have limited synteny and similarity with any single plasmid of an LD group species [23]. The chromosomal and megaplasmids in the RF clade appear to be co-evolving [2].

More informative than chromosome gene order for inferring evolutionary relationships are genome-wide pairwise comparisons of genes and proteins that species have in common. Adeolu and Gupta [4] previously reported pairwise comparisons of the genomic average nucleotide identity (ANI) values between species from the RF group and those in the LD group. ANI is a widely accepted criterion for determining the genomic relatedness of species at species and genus levels [24–26]. The ANI analysis showed that the species from the RF clade are distinct from those in the LD clade and the differences in ANI values between the two groups support their placement into two distinct genera [4]. In Fig. 3, we present here an average amino acid identity (AAI) matrix for all Borreliaeae species for which genomes have been sequenced and are publicly available. The Borreliaeae species again form two distinct groups, corresponding to the two proposed genera.

In conclusion, all the different lines of evidence based on genome sequence data strongly support the existence of two distinct and cohesive groups within the family Borreliaeae.

PHENOTYPIC TRAITS DISTINGUISHING THE RF GROUP AND THE LD GROUP OF SPIROCHETES

Here, we review the informative phenotypic traits of ‘Borrelia burgdorferi sensu lato’, which either singly or in combination serve to distinguish this clade from the original members of the genus Borrelia (i.e. the RF clade), which mostly comprise the several different species that cause RF but also include the long-recognized agents of avian spirochetasis (B. anserina) and bovine borreliosis (B. theileri), as well as the more recently described disease agents, such as B. miyamotoi. Margos et al. [7] contend that the genus Borrelia prior to the proposed split was ‘cohesive’ due to their ‘shared spirochaetal morphology’ and ‘common vector-borne style’, but then list exceptions to this broad statement.

An obvious difference between the two clades, and one of undoubted medical and public health relevance, is that one cluster includes all the known species that cause LD and the other cluster includes all the known species that cause RF [1–3]. The differences in the diseases that occur in humans have their counterparts in natural and experimental infections in mammalian hosts [3, 27–30]. In comparison with infections by the RF group of species (including B. anserina and B. miyamotoi), infections caused by LD group species tend to be chronic and with higher persistent densities of spirochetes in tissues rather than the blood [31–33]. During RF in humans and experimental animal models, spirochetes in unconcentrated blood are usually detectable by light microscopy of thin blood smears. In fact, this is still the most common method for laboratory diagnosis of RF [34, 35].

The newly described LD agent B. mayonii was reported to reach higher densities in the blood of infected patients than was observed during infections with B. burgdorferi [36], but Pritt et al.’s estimated cell densities for B. mayonii in the blood of 10^4–10^5 per millilitre are at least two orders of magnitude lower than what is commonly observed during RF in humans and in animal models. Moreover, contrary to the reported findings in some human cases, B. mayonii spirochetes were not detected by Dolan et al. [37] in the blood of experimentally infected mice while they persistently had spirochetes in skin tissue and remained infectious for ticks. This pattern of few or no spirochetes in the blood while they persist in the tissues fits the phenotypes of other LD species. In our opinion, Margos et al.’s [7] statement that ‘B. mayonii produced high spirochetal blood densities, akin to that seen following infection with species of the RF group’ is not an accurate interpretation of the literature. Contrary to Margos et al.’s [7] assertion the symptomology (sic) that differentiates (human infection from) RF spirochaetes from (human infection from) the LB group of spirochaetes has not been further ‘blurred’.

Two vector-related traits that stand out for differentiating between the two groups of spirochetes are the location of the spirochetes in an unfed tick at the time that the blood
meal commences [38, 39] and the maintenance of the spirochete in nature by transovarial transmission [40–42].

The vectors for the RF group of species represent a variety of arthropods, including the body louse, argasid (or soft) ticks and the two major types, prostriate and metastriate, of ixodid (or hard) ticks [3, 41, 43]. Except for the particular case of B. recurrentis, which is not transmitted by its louse vector through saliva [39], all the other RF group species that have been investigated to this point are disseminated from the midgut to the salivary glands before the subsequent moult and the next blood meal. This is of medical and ecological importance, because it means transmission of the pathogen to the host can begin soon after feeding begins. These include species that are transmitted by either argasid, prostriate or metastriate ticks: B. duttonii in Ornithodoros moubata [44], B. anserina in Argas species [45], B. theileri in Rhipicephalus (Boophilus) microplus [46], B. crocidurae in Ornithodoros species [47], B. hermsii in Ornithodoros hermsi [48], B. turicatae in Ornithodoros turicata [49, 50] and B. miyamotoi in Ixodes scapularis (personal communication, Linda Bockenstedt, Yale University). We note that this characteristic of the RF clade holds even for Borrelia species transmitted by hard ticks, which are slow-feeding in contrast to the rapid-feeding soft ticks, such as Ornithodoros and Argas species.

This characteristic contrasts with the findings for B. burgdorferi sensu lato, for which the only known competent vectors are certain species of the prostriate genus Ixodes. In their consensus summary of a workshop on the relationship between the pathogen and its arthropod vector, Burgdorfer et al. [51] wrote that ‘… the Lyme disease spirochete in its Ixodes vectors remains in the midgut, where it aggregates near the microvillar brush border and in the intercellular spaces of the gut epithelium’. Subsequent studies have confirmed this (reviewed in [38, 39]). Previous reports of dissemination of an LD agent in unfed ticks were before B. miyamotoi was discovered and may have been misidentification of B. miyamotoi as B. burgdorferi or other LD agent by non-specific stains or cross-reactive polyclonal antisera.

Most species in the RF group feature transovarial transmission in their tick vectors; this phenomenon has not been
documented in any member of *B. burgdorferi sensu lato* to date [40–42]. Transovarial transmission has been shown for RF group species transmitted by hard ticks as well as soft ticks. These include *B. theileri* in the metastriate tick *R. microplus* [46], *B. miyamotoi* in the prostriate *I. scapularis* [52] and *B. lonestari* in the metastriate *Amblyomma americanum* [53]. Older reports of transovarial transmission of *B. burgdorferi sensu lato* in *Ixodes* species ticks are attributable to misidentification of *B. miyamotoi* for an LD species [42]. Transovarial maintenance is of medical and ecological importance, because it confers the capacity for larval ticks to transmit the pathogen to humans and other vertebrates.

We end this survey with a consideration of morphological differences that were observed between the 'Lyme disease spirochetes' and other *Borrelia* species. In their 1984 paper Schmid et al. [54] noted that 'the Lyme disease spirochetes differ from *Borrelia* spp. morphologically'. Johnson et al. [55] and Hovind-Hougen [56] distinguished between the new spirochetes and known *Borrelia* species in the number of insertion points for flagella they had at their ends. While ultrastructural morphology is infrequently used at present in descriptions of bacteria, a literature review reveals that even as additional species were added to the *B. burgdorferi sensu lato* cluster, the original observation of comparatively fewer flagella in 'Lyme disease spirochetes' than in other *Borrelia* species has generally held up. The most commonly reported values for flagella at one end of cells of *B. burgdorferi sensu lato* are 7–8, within a range of 4–12, for the following species: *B. burgdorferi* [3, 57–60]; *B. afzelii* and *B. garinii* [58–60]; *B. sinica* [61]; and *B. japonica* [62].

Except for *B. anserina*, which was reported to have 7–8 flagella at an end [59], all other examples of RF group species that have been adequately examined by ultrastructural criteria have had an estimated 15–30 flagella at one end. These include *B. recurrentis* [57, 59], *B. hermsii* [63, 64], *B. microti* [59, 65] and *B. persica* [66]. *B. recurrentis* was reported to have eight flagella at each end, but the insertion points are not well visualized in the figure that was provided [67].

In conclusion, the phenotypic differences between the RF and LD clades, including the diseases that members cause, and the ecological and medical significances of these differences are greater than are claimed by Margos et al. [7].

### POSSIBLE ADVERSE CONSEQUENCES OF THE RECLASSIFICATION OF MEMBERS OF THE FAMILY **BORRELIACEAE**

Margos et al. [7] write of ‘adverse consequences of splitting the genus *Borrelia*. There is only limited space in this venue to address these undocumented assertions. Suffice it to say that there are counter-arguments about the ‘adverse consequences’ of continued dependence on *Borrelia burgdorferi sensu lato* as a genus proxy for an expanding group of species, only a few of which are truly associated with human disease.

But we first anticipate another potential criticism: allusion to the attempted split of the medically important genus *Chlamydia* into two genera, *Chlamydia* and *Chlamydiophila* [68], as an argument against splitting *Borreliaceae* species. However, the analogy between the taxonomic circumstances for these two sets of pathogens can be taken only so far. The evidence in favour of this split of *Chlamydia* was comparatively weak [69]. The two proposed genera exhibit a high level of similarity in their 16S rRNA gene sequences and no consistent phenotypic differences [70, 71].

In another, more recent example of name change for a medically important organism, the species *Clostridium difficile* was transferred to a new genus, *Clostridioides*, based primarily on its branching in a separate clade in the 16S rRNA tree and some protein trees from that corresponding to the type species of the genus, *Clostridium butyricum* [72, 73]. The only other molecular evidence used in support of the reclassification of *C. difficile* was a number of CSIs that Gupta and Gao [74] previously described for the ‘*Clostridium sensu stricto*’ clade that were absent in *C. difficile*.

In comparison with the *Chlamydia* and *Clostridium* proposals, the case for the existence of two cohesive groups within the genus *Borrelia* is much stronger. From the presented evidence, it is clear that the members of the family *Borreliaceae* comprise two distinct groups differing from each other in numerous genetic and genomic characteristics, phenotypic characteristics, and in the diseases they cause in humans and other animals. As stated above, prior to the proposal for the split, the genus *Borrelia* was functionally treated as two different groups, with the LD group pervasively referred to as *’B. burgdorferi sensu lato’* or ‘Lyme disease *Borrelia*’ to distinguish those species from the RF agents and other *Borrelia* species [1, 2, 75]. Thus, the proposal for splitting the family *Borreliaceae* into two groups only formalizes the existence of two de facto cohesive groups within this family, which were already widely recognized [1, 2, 75].

Before addressing specific concerns, we also highlight some benefits of a clarification of phylogenetic relationships for better understanding the microbiology and ecology of these pathogens. Extensive work on these sequence-based characteristic markers on other groups of prokaryotes have shown that these markers possess a high degree of predictive ability to be identified in other group members, for which no sequence information may be available at the time (reviewed in [76, 77]). With the more explicit division of the *Borreliaceae* species into two genus-level groups, attention can be focused on unique genetic and molecular characteristics that differentiate the two groups of microbes [78]; the described characteristics in other groups of bacteria have been found to play important and generally essential roles [79]. For *Borreliaceae* species, some of the CSIs that distinguish between the RF and LD groups are in proteins, such as the flagellar motor switch protein FliM, chemotaxis proteins CheY and CheW, and cell shape-determining protein MreB [4], that
may be determinants of the aforementioned morphological differences between Borreliaeae species.

Margos et al. [7] write that ‘splitting the genus does not provide any assistance as far as clinical evaluation is concerned’ and further that ‘it does not help end user communities including in clinical medical practice, public health, or those studying the ecology of the bacteria’. They more provocatively write that this ‘division complicates an already complicated situation which will serve only to lead to further confusion among scientists, clinicians, public health authorities and the general public.’ These claims are not developed or documented in the Letter. Many journal readers, especially the majority who are not specialists in the field of LD, may be mystified about what the ‘complicated situation’ is. One could reasonably make the counter-argument that timely diagnosis and treatment of RF, a Neglected Tropical Disease (http://journals.plos.org/plosntds) and an infection with a higher mortality rate than LD [35], is hindered by the ‘confusion’ from the plethora of Borrelia species names and the mistaken assumption that if it is a ‘Borrelia’, it means LD.

That said, we acknowledge the argument for retaining the genus Borrelia for the LD group of species, if for no other reason than the most commonly known species in the genus is B. burgdorferi. However, B. anserina is the type species of the genus Borrelia and is part of the RF clade (Fig. 1). Hence, according to the rules governing the description of any new genus, the genus name Borrelia must be retained for the RF clade [1, 80, 81]. The splitting of a genus into subgenera is also avoided in prokaryotic systematics and none appear to have been proposed for over 35 years. Thus, the only option available was to place the LD group of Borreliaeae species into a new genus to indicate their distinctness from the RF group of species. The similarity of the name Borreliella to the original name of the genus Borrelia makes it unlikely that the species with the new names (e.g. Borreliella burgdorferi) could be confused with an unrelated species. We note that it remains ‘B. burgdorferi’ in abbreviation for the scientific and medical literature and as a stand-alone complete name (as in ‘E. coli’) in news media and for the general public. Furthermore, the name Borreliaeae for the family allows researchers, clinicians and epidemiologists working in the LD area to continue using the term ‘borreliosis’, e.g. ‘lyme borreliosis’ and ‘neuroborreliosis’, to describe the disease and its manifestations.

Finally, we recognize the inconvenience and disruptions that for a while follow a taxonomic name change in a medically important group of microbes, but ultimately medical progress and public health advancement are best served by openness to scientific findings. Thus, the division of Borreliaeae species into two distinct genera, which reflects the underlying genetic and phenotypic diversity of this group, should prove greatly advantageous for progress of biomedical and ecological studies on these microbes in the long run.

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Conflicts of interest
The authors declare that there are no conflicts of interest.

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