Persistent *Borrelia* Infection in Patients with Ongoing Symptoms of Lyme Disease

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Abstract

Introduction
Lyme disease is a tickborne illness that generates controversy among medical providers and researchers. One of the key topics of debate is the existence of persistent infection with the Lyme spirochete, *Borrelia burgdorferi*, in patients who have been treated with recommended doses of antibiotics yet remain symptomatic. Persistent spirochetal infection despite antibiotic therapy has recently been demonstrated in non-human primates. We present evidence of persistent *Borrelia* infection despite antibiotic therapy in patients with ongoing Lyme disease symptoms.

Materials & Methods
In this pilot study, culture of body fluids and tissues was performed in a randomly selected group of 12 patients with persistent Lyme disease symptoms who had been treated or who were being treated with antibiotics. Cultures were also performed on a group of 10 control subjects without Lyme disease. The cultures were subjected to corroborative microscopic, histopathological and molecular testing for *Borrelia* organisms in four independent laboratories in a blinded manner.

Results
Motile spirochetes identified histopathologically as *Borrelia* were detected in culture specimens, and these spirochetes were genetically identified as *Borrelia burgdorferi* by three distinct polymerase chain reaction (PCR) methods. Spirochetes identified as *Borrelia burgdorferi* were cultured from the blood of seven subjects, from the genital secretions of ten subjects, and from a skin lesion of one subject. Cultures from control subjects without Lyme disease were negative for *Borrelia* using these methods.

Conclusions
Using multiple corroborative detection methods, we showed that patients with persistent Lyme disease symptoms may have ongoing spirochetal infection despite antibiotic treatment, similar to findings in non-human primates. The optimal treatment for persistent *Borrelia* infection remains to be determined.
Introduction

Lyme disease (LD) and similar Lyme-like borrelial infections are caused by members of the *Borrelia burgdorferi* (Bb) sensu lato complex or by members of the *Borrelia* relapsing fever complex such as *B. miyamotoi*, respectively. Following initial infection, *Borrelia* spirochetes can evade host defenses, sequester in immune privileged sites such as joints or the central nervous system, and persist in pleomorphic forms. Tickborne coinfections including *Babesia, Anaplasma, Ehrlichia, Bartonella* and *Rickettsia* may complicate the clinical picture. If LD is not treated early in the course of infection, chronic illness may result and a variety of symptoms may develop. These symptoms include fatigue, musculoskeletal pain, arthritis, cardiac disease and neurological involvement with peripheral neuropathy, meningitis, encephalitis, cranial neuritis and cognitive dysfunction.

Although LD was first recognized in 1975, it remains a controversial illness and the topic of polemic debate. One viewpoint claims that persistent Lyme disease symptoms are related to ongoing spirochetal infection despite antibiotic therapy. This scenario has been demonstrated in animal models including rodents, dogs and horses using various detection methods, and a recent study in non-human primates showing “persistent, intact, metabolically-active *B. burgdorferi* after antibiotic treatment of disseminated infection” offers the strongest support for this pathogenesis. Furthermore, comparable studies have suggested persistent infection after antibiotic therapy as a cause of chronic symptoms in humans. The opposing viewpoint claims that persistent Lyme disease symptoms may be due to spirochetal “debris” without active infection. While a number of studies from Europe and the USA have demonstrated persistence of Bb DNA or antigens in human bodily tissues or fluids, very few studies have demonstrated culture of live *Borrelia* spirochetes, the highest form of evidence for persistent infection in chronic Lyme disease patients.

In this pilot study, we present detailed evidence of persistent *Borrelia* infection despite antibiotic therapy in 12 randomly-selected North American patients with ongoing LD
symptoms. Spirochetal infection was demonstrated by corroborative microscopic, histopathological and molecular detection of live *Borrelia* organisms in cultures of body fluids and tissues from these patients.

**Methods**

**Subject selection**

Subjects included in the study were chosen at random from our North American patient population. All of the LD patients in the study were either clinically diagnosed with LD or had positive Bb serological testing prior to study participation. Serological testing for LD was performed by a Clinical Laboratory Improvement Amendments (CLIA)-certified laboratory (IGeneX Laboratory in Palo Alto, CA), as described in detail elsewhere. Subjects with Morgellons disease (MD) who were seropositive for LD were included in the study (see below). All subjects had been treated with antibiotics prior to the study, and symptomatic patients who remained on antibiotic treatment were included in the study.

**Control selection**

Ten healthy subjects were recruited as controls after informed consent was obtained. These subjects were then tested serologically for LD and those who were negative were accepted as controls. Vaginal or seminal fluids were collected from negative controls and cultured for *Borrelia*, as described below. Culture pellets underwent PCR testing for *Borrelia* in a blinded manner at the University of New Haven and Australian Biologics, as described below. All subjects were adults who gave informed consent to participate in the study. Signed informed consent to collect specimens was obtained in accordance with the ethics approval requirements for sample collection of the Western Institutional Review Board, Puyallup, WA. Approval for anonymous sample testing was also obtained from the Institutional Review Board of the University of New Haven, West Haven, CT. Additional signed informed consent to publish the results was obtained from each subject.
Cultures

To avoid contamination, all cultures were performed under strict aseptic conditions in a laboratory that was free of *Borrelia* reference strains, and cultures of control and patient samples were processed in an identical manner. Inocula were placed in Barbour–Stoner–Kelly H (BSK) complete medium with 6% rabbit serum (Sigma Aldrich, #B8291) containing the following antibiotics: phosphomycin (0.02 mg/ml) (Sigma Aldrich), rifampicin (0.05 mg/ml) (Sigma Aldrich), and amphotericin B (2.5 μg/ml) (Sigma-Aldrich), as described previously. Inocula were prepared as follows:

A. Blood – whole blood (10 ml) was collected by venipuncture and left at room temperature to clot, then centrifuged at low speed to separate red blood cells from sera. The serum supernatants with a small amount of blood cells below the serum layer were collected and were inoculated into the BSK medium.

B. Skin – whole calluses or skin from lesions were removed from MD subjects by scraping with a scalpel blade.

C. Vaginal – vaginal secretions were collected by swabbing inside the vagina with sterile cotton-tipped swabs that were then introduced into the BSK medium.

D. Seminal – semen was self-collected into a sterile vial, then was pipetted into the BSK medium.

Eight ml tubes of inoculated medium were filled to minimize the airspace present, thus providing a microaerobic environment, and incubated at 32°C. Culture fluid was examined by dark-field microscopy for visible spirochetes weekly for up to 4 weeks. Cultures were concentrated by centrifuging the fluid at 15,000 g for 20 minutes, retaining the pellet and discarding the supernatant. For imaging, a small amount of culture pellet was resuspended in 50 μl 0.85% saline solution, washed and centrifuged again. The pellet was mixed with gelatin and then fixed with formalin.

**Dieterle and anti-Bb immunostaining**
Dermatological specimens and/or culture pellets from patients were fixed, sectioned and processed for specialized staining at either McClain Laboratories LLC, Smithtown, NY, or the Department of Biology and Environmental Science, University of New Haven, West Haven, CT, as previously described. Dieterle silver-nitrate staining was performed at McClain Laboratories. Anti-Bb immunostaining was performed at McClain Laboratories or the University of New Haven. In brief, immunostaining was performed using an unconjugated rabbit anti-Bb polyclonal antibody (Abcam ab20950), incubated with an alkaline phosphatase probe (Biocare Medical #UP536L), followed by a chromogen substrate (Biocare Medical #FR805CHC), and counterstained with hematoxylin. Positive and negative controls were prepared for comparison purposes using liver sections from Bb-inoculated and uninfected C3H/HeJ mice followed by Dieterle and immunostaining. Culture pellets from mixed Gram-positive bacteria (Streptococcus and Staphylococcus) and Gram-negative bacteria (Escherichia coli and Klebsiella) were also prepared for comparison purposes as negative controls to exclude cross-reactivity with commonly encountered microorganisms.

Molecular testing

Patient and negative control samples were submitted in a blinded manner to the laboratories performing polymerase chain reaction (PCR) amplification of DNA, as described below.

PCR - University of New Haven

DNA was extracted from culture pellets as previously described. Reactions of blinded samples were performed in triplicate.

*Borrelia* DNA in extracted samples was detected using a published TaqMan assay targeting a 139-bp fragment of the gene encoding the *Borrelia* 16S rRNA, as described previously.
Amplifications were conducted on a CFX96 Real-Time System (Bio-Rad) with cycling of 50°C for 2 minutes, 95°C for 10 minutes, followed by 40 cycles of 95°C for 15 seconds and 60°C for 60 seconds, and fluorescent signals were recorded using CFX96 Real-Time software with the Cq threshold set automatically.

Nested PCR primers for the 16S rRNA, flagellin (Fla), OspC, uvrA and pyrG genes were used as previously described, with a final volume of 50 μl using 10 μl template DNA and final concentrations of 20 mM Tris-HCl (pH 8.4), 50 mM KCl (1X Buffer B, Promega), 2 mM MgCl2, 0.4 mM dNTP mix, 2 μM of each primer, and 2.5 U Taq polymerase (Invitrogen). The first reaction used “outer” primers and the second reaction used “inner” primers, and 1 μl of PCR product from the first reaction was used as template for the second. Cycling was programmed as follows: 94°C for 5 minutes followed by 40 cycles of denaturation at 94°C for 1 minute, annealing for 1 minute, and extension at 72°C for 1 minute, with a final extension step at 72°C for 5 minutes. DNA products were visualized in 1-2% agarose gels.

PCR amplification was followed by Sanger sequencing. PCR products were extracted using the QIAquick Gel Extraction kit (Qiagen) in accordance with the manufacturer’s instructions. Eluates were sequenced in both directions, then were compared by BLAST analysis using the GenBank database (National Center for Biotechnology Information).

**PCR - Australian biologics**

DNA was extracted from culture pellets using the DNeasy Blood and Tissue kit ® (Qiagen) in accordance with the manufacturer’s instructions. Samples were forwarded to Australian Biologics for *Borrelia* DNA and *Treponema denticola/Treponema pallidum* DNA testing. Blinded samples were run in duplicate with positive and negative controls using primers for the *Borrelia* 16S rRNA and rpoC gene targets, as previously described. *Borrelia* DNA was detected by real-time PCR targeting the 16S rRNA gene and/or by endpoint PCR targeting the rpoC gene, as previously described, using the Eco™ Real-Time PCR system with software...
version 3.0.16.0. Thermal profiles were performed with incubation for 2 minutes at 50°C, polymerase activation for 10 minutes at 95°C then PCR cycling for 40 cycles of 10 secs at 95°C dropping to 60°C sustained for 45 secs. The PCR signal magnitude generated (ΔR) was interpreted as either positive or negative as compared to positive and negative controls.

For endpoint PCR, amplicons were visualized on 1-2% agarose gels and extracted from the gels using the QIAquick Gel Extraction kit (Qiagen) in accordance with the manufacturer’s instructions. Sanger sequencing was used for gene analysis, as described previously.59, 67, 68

**PCR – University California Irvine**

The presence of Bb sensu stricto DNA in a set of blinded samples was confirmed by the laboratory of Dr. Alan Barbour (University of California Irvine) by first quantitative PCR,69 and then by sequence of the PCR-amplified 16S-23S intergenic spacer.70 The samples studied included specimens from two of the subjects in this paper, Case 2 and Case 10, as described below.

**Results**

**Subject Histories**

The clinical histories of the 12 study subjects with persistent Lyme disease symptoms (Cases 1-12) are provided below, and the clinical characteristics of the subjects are summarized in Table 1. All subjects had received treatment with 2-4 weeks of antibiotics as recommended by Lyme treatment guidelines endorsed by the Centers for Disease Control and Prevention (CDC).14 Six patients were taking antibiotics at the time of study sampling, as noted in Table 1. None of the controls had received antibiotic therapy.

Case 1.
The subject is a 50-year-old native Canadian woman who resided in an area endemic for LD in eastern Canada. She did not recall an erythema migrans (EM) rash. She developed extreme fatigue and musculoskeletal pain as well as ulcerative skin lesions along with symptoms of formication. Magnification demonstrated filamentous inclusions within the lesions. The subject was seronegative for anti-Bb antibodies excepting two indeterminate IgM bands showing reactivity to the 41 kDa and the 93 kDa proteins, and a weakly positive IgG band showing reactivity to the 41 kDa protein. She was clinically diagnosed with LD by a health care provider in Canada and treated with antibiotics. The subject had discontinued antibiotics three weeks prior to the sampling period, but continued treatment with naturopathic remedies. Despite ongoing treatment with amoxicillin, the subject continues to have persistent symptoms of Lyme disease.

Case 2.

The subject is a 54-year-old Caucasian woman who had a history of outdoor recreational activity in Western Canada including areas in British Columbia that are endemic for LD. She recalled an EM-like rash several years previously, and she did not receive treatment. She developed significant joint pains, muscle aches, headaches, memory loss, fatigue and skin lesions, and she initially tested negative for Lyme disease. She was clinically diagnosed by a Canadian health care provider, and the diagnosis was confirmed later by an American health care provider. She also had positive serological tests for Babesia and Bartonella. She did not have prior knowledge of Morgellons disease, but she did have ulcerative lesions on her face and torso consistent in appearance with the condition. Upon examination with a 50X handheld microscope, filamentous inclusions were observed in her lesions. She has been aggressively treated over the last few years with antibiotic combinations including intravenous ceftriaxone, metronidazole, telithromycin, doxycycline, amoxicillin, ciprofloxacin, tinidazole and atovaquone with little benefit.

Case 3.

The subject is a 63-year-old Caucasian man who had a history of outdoor recreational activity in
endemic areas for Lyme disease, including Europe, Western Canada, and the USA (Connecticut and Rhode Island). Although he recalls tick bites, he did not recall an EM rash. The subject developed musculoskeletal pain and extreme fatigue. His wife (Case 4) had an EM rash and a LD diagnosis that prompted him to get tested for LD. He was seroreactive for anti-Bb antibodies, and DNA was detected in serum using PCR technology. He tested serologically positive for *Babesia microti* and *Anaplasma phagocytophylum*. At the time of sampling he had ongoing treatment with antibiotics, including doxycycline, clarithromycin, cefdinir, clindamycin, tinadazole, atovaquone, clindamycin and hydroxychloroquine. He was symptomatic and taking doxycycline at the time of sampling. His condition has since improved, but he still suffers from musculoskeletal pain.

Case 4.

The subject is a 53-year-old Caucasian woman and the wife of Case 3. She had a history of outdoor recreational activity in Lyme endemic areas of the USA and Canada. She has a history of tick bites and recalled an EM rash after visiting both Connecticut and Rhode Island. Her symptoms included seizures, neuropathy, palpitations and musculoskeletal pain. She had serological testing for Bb and was initially negative, but she became seropositive after taking antibiotics. She also had positive serological testing for *Babesia microti* and *Anaplasma phagocytophylum*. She was symptomatic and taking antibiotics during the time of sample collection. Antibiotics taken included doxycycline, telithromycin, minocycline, clindamycin, clarithromycin, metronidazole, tinidazole, rifampicin, atovaquone, hydroxychloroquine and mefloquine. The subject was taking clarithromycin and cefdinir at the time of sample collection. She is currently asymptomatic.

Case 5.

The subject is a 40-year-old Caucasian woman living in Calgary, Canada, and the partner of case 6. She is a veterinarian and had a history of work exposure to ticks, and she had also travelled to areas endemic for LD in Europe. She did not recall an EM rash. Her symptoms were primarily musculoskeletal and severe headaches. She was seropositive for Bb and *Babesia*, and she had
been treated with the following antibiotics: doxycycline, clarithromycin, metronidazole and atovaquone. She had been taking doxycycline for one month at the time of sample collection.

Case 6.

The subject is a 42-year-old Caucasian man living in Calgary, Canada, and the partner of case 5. He is a veterinarian and had a history of work exposure to ticks. He had also travelled to areas endemic for LD in Europe. He did not recall an EM rash. His symptoms were primarily musculoskeletal, severe headaches, memory loss, vision problems and extreme fatigue. He was seropositive for Bb and Babesia, and he had been treated with the following antibiotics: doxycycline, clarithromycin, metronidazole and atovaquone. He had been taking doxycycline for one month at the time of sample collection.

Case 7.

The subject is a 36-year-old Caucasian woman living in Calgary, Canada. She was bitten by many ticks while working as a tree planter in the mountains, but she does not recall an EM rash. In September 1997 she developed profound fatigue, migratory joint pains, peripheral neuropathy and personality changes consistent with depression. She was seropositive for Bb, and she was eventually treated with intramuscular penicillin, amoxicillin, and minocycline over two years. She remains symptomatic despite antibiotic treatment.

Case 8.

The subject is a 39-year-old Caucasian man residing in Calgary, Canada. He has a history of hiking, camping and other outdoor activities in Alberta and Manitoba, Canada, but no known tick bites or EM rash. He complains of joint pain, low back pain and headaches, and he has been treated for sciatica, depression, insomnia, and anxiety. He also has an extensive history of periodontal disease with recurrent gingival infections, and he has received multiple courses of penicillin and amoxicillin over many years. He had positive serological testing for Lyme disease, and he has not been tested for tickborne coinfections.
Case 9.

The subject is a 71-year-old Caucasian woman living in Ontario, Canada and the partner of Case 10. She was 40 years old when she became ill in 1986 with severe flu-like symptoms, fatigue, severe pelvic pain, blurred vision, rib soreness and night sweats. She did not recall a tick bite or an EM rash. The patient had not knowingly visited a Lyme disease endemic area. She consulted six different physicians over a period of four years before being treated with six weeks of doxycycline for what was diagnosed as pelvic inflammatory disease in 1988, and her symptoms transiently improved. She was clinically diagnosed with Lyme disease in 1990 by a physician in Ontario, as the Ontario government's ELISA test was "negative" for Lyme disease. Over the next 20 years the subject was intermittently treated with doxycycline and her symptoms improved, but never completely resolved, and other symptoms developed such as muscle aches, joint pains, sleep disturbances, bladder and urethral pain, and cognitive impairment. These symptoms waxed and waned over the years. She experienced multiple Jarisch-Herxheimer reactions with repeated doxycycline treatment. The subject's two children were treated for congenital Lyme disease between 1990 and 2004 and are asymptomatic today. In May 2011, the subject was tested by a CLIA-approved laboratory in the USA and was found to be serologically positive for Lyme disease.

Case 10.

The subject is a 72-year-old Caucasian man living in Ontario, Canada and the partner of Case 9. He was 41 years old at the onset of symptoms in 1986 with flu-like muscle aches, joint pains and unrelenting fatigue. He did not recall a tick bite or an EM rash. The subject had not knowingly visited a Lyme disease endemic area. He had consulted 12 different doctors over a period of four years before getting a confirmed diagnosis of Lyme disease, at which point he had developed severe arthritic symptoms, significant neurological symptoms including encephalopathy and dementia with brain magnetic resonance imaging (MRI) showing hyperintense white matter lesions. His antibiotic regimens over 20 years included: tetracycline, amoxicillin plus probenecid, doxycycline, clarithromycin, intravenous ceftriaxone, and
intramuscular benzathine penicillin G. When the subject was on antibiotics he had relief of many symptoms, but he was never completely free of symptoms associated with Lyme disease. He had multiple Jarisch-Herxheimer reactions when new antibiotic regimens were initiated. The two-tiered Lyme disease serology test performed in Canada failed to show positivity for Lyme disease, but the subject subsequently sent blood to a CLIA-approved laboratory in the United States and was found to be seropositive for Lyme disease.

Case 11.

The subject is a 57-year-old Caucasian woman living in Calgary, Canada. She had exposure to ticks while hiking and camping in Canada, but she did not recall an EM rash. She developed musculoskeletal and neuropsychiatric symptoms and was diagnosed with LD after testing serologically positive. She also had positive testing for *Babesia, Ehrlichia* and *Bartonella*. She received intermittent antibiotic therapy with multiple oral, intramuscular and intravenous antibiotics, and her symptoms improved while on antibiotics but relapsed when the antibiotics were discontinued. She remains symptomatic after five years of antibiotic treatment.

Case 12.

The subject is a 46-year-old Caucasian woman living in Alberta, Canada who did not have a history of tick bite or EM rash. She has suffered with skin lesions consistent with Morgellons disease for more than a decade and was diagnosed with Lyme disease in the USA after testing serologically positive for Bb. She has had severe gastrointestinal problems that have necessitated frequent hospitalizations. The gastrointestinal difficulties began after she had gastric bypass surgery. Her intestines form lesions that fuse together, causing blockages. She has been treated aggressively with antibiotics before and after this study by doctors both in the USA and Canada with only minimal benefit. Antibiotic therapy included multiple treatments with intravenous ceftriaxone, doxycycline, clarithromycin and amoxicillin.

Microscopy and Histopathology

Case 1. Whole calluses were submitted for sectioning, Dieterle and anti-Bb immunostaining.
Spirochetes were visible in both Dieterle and anti-Bb immunostains. Blood culture was performed and fluid from the culture demonstrated spherical bodies under darkfield microscopy. Dieterle staining and anti-Bb immunostaining was not performed.

Case 2. Blood culture was performed and fluid from the culture demonstrated spherical bodies under darkfield microscopy. Dieterle staining and anti-Bb immunostains demonstrated spherical bodies. Anti-Bb immunostaining was positive. Vaginal culture was performed and fluid from the culture demonstrated spirochetes and biofilm under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes and biofilm. Skin specimens were not submitted for staining or culture. Repeat blood and vaginal cultures were positive for Borrelia by immunostaining and PCR (see Tables 2-4).

Case 3. Blood culture was performed and fluid from the culture demonstrated spherical bodies and occasional spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostains demonstrated spherical bodies and occasional spirochetes. Anti-Bb immunostaining was positive. Seminal culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes. Repeat blood culture was positive for Borrelia by immunostaining and PCR (see Tables 2-4).

Case 4. Blood culture was performed and fluid from the culture demonstrated spherical bodies and occasional spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostains demonstrated spherical bodies and occasional spirochetes. Anti-Bb immunostaining was positive. Vaginal culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes. Repeat blood culture was positive for Borrelia by immunostaining and PCR (see Tables 2-4).

Case 5. Blood culture was performed and fluid from the culture demonstrated spherical bodies under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spherical bodies. Vaginal culture was performed and fluid from the culture demonstrated
spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes. Repeat blood culture was positive for *Borrelia* by immunostaining and PCR (see Tables 2-4).

Case 6. Blood culture was performed and fluid from the culture demonstrated spherical bodies under darkfield microscopy. Dieterle staining and anti-Bb immunostains demonstrated spherical bodies. Anti-Bb immunostaining was positive. Seminal culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes. Repeat blood culture was positive for *Borrelia* by immunostaining and PCR (see Tables 2-4).

Case 7. Vaginal culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes.

Case 8. Seminal culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes.

Case 9. Vaginal culture was performed and fluid from the culture demonstrated spirochetes, including one that was quite actively motile, under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes.

Case 10. Seminal culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes. Repeat seminal culture was positive for *Borrelia* by immunostaining and PCR (see Tables 2-4).

Case 11. Vaginal culture was performed and fluid from the culture demonstrated spirochetes, including one that was quite actively motile, under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes.
Case 12. Blood culture was performed and fluid from the culture demonstrated spherical bodies under darkfield microscopy. Dieterle staining and anti-Bb immunostains demonstrated spherical bodies. Anti-Bb immunostaining was positive. Skin culture was performed and fluid from the culture demonstrated spirochetes under darkfield microscopy. Dieterle staining and anti-Bb immunostaining demonstrated spirochetes.

The results of darkfield microscopy, Dieterle silver stains and anti-Bb immunostaining from Cases 1-12 are summarized in Table 2. Examples of these spirochete detection methods are shown in Figure 1A-1C.

**Molecular testing**

**PCR Detection of *Borrelia***

PCR detection of *Borrelia* was performed for research purposes only. No data resulting from this study was used diagnostically.

Samples (whole dermatological calluses, blood culture, vaginal cultures, and seminal cultures) from the study patients were submitted for PCR detection and sequencing of *Borrelia* DNA at both the University of New Haven, CT, and Australian Biologics, Sydney, Australia in a blinded manner. *Borrelia* DNA was detected by at least one laboratory for all 12 patients, and amplicon sequences consistent with Bb DNA were obtained for 10/12 patients. Blinded negative cultures from healthy, seronegative subjects along with the blinded suspected positive cultures from LD patients were sent to University of New Haven and Australian Biologics. All negative controls were PCR-negative for *Borrelia* strains.

Australian Biologics performed PCR for the detection of *Treponema denticola* and *Treponema pallidum* on all study samples and blinded controls. Treponemal DNA was not detected in any samples. For Cases #2 and #10, additional PCR and sequencing on genital cultures was performed at the University of California, Irvine, in the laboratory of Dr. Alan Barbour. In these samples, *Borrelia* DNA was detected with qPCR and then confirmed as Bb sensu stricto by sequence of the 16S-23S intergenic spacer.
Positive PCR results are summarized in Table 3, and positive sequencing results are summarized in Table 4. PCR sequences and BLAST analyses are shown in Supplemental Figure 1.

Discussion

In this pilot study, we cultured live *Borrelia* organisms from 12 antibiotic-treated subjects with persistent Lyme disease symptoms, thus showing that viable spirochetes can be found in LD patients despite antibiotic therapy. Half of these subjects were taking antibiotics at the time of sampling. Patient cultures showed *Borrelia* spiral forms and spherical bodies, as described in other publications.\(^7,^{59,66}\) We demonstrated the presence of *Borrelia* infection in cultures from these patients using corroborative microscopy, histopathology and PCR techniques, and we obtained sequences for amplicons from 10/12 patients. Repeat cultures of blood, semen and vaginal secretions were positive for Bb by microscopy, histopathology and PCR in six patients tested by four different laboratories. Cultures from healthy *Borrelia*-seronegative controls were consistently negative, making the possibility of *Borrelia* contamination in LD patient samples extremely unlikely.

Persistent *Borrelia* infection may result in part from the wide variety of tissues and fluids that support spirochetal growth.\(^{16-37}\) The tissues susceptible to *Borrelia* infection include fibroblasts, skin, synovial tissue, ligaments, cardiac tissue, glial cells, neurons, endothelial cells, lymphoid tissue and hepatic tissue.\(^5,^{48,59,71-81}\) The pleotropic nature of *Borrelia* infection may allow the spirochete to evade the host immune system and antibiotic therapy, as outlined below.

The role of cysts and biofilms in persistent *Borrelia* infection is controversial.\(^{10,82,83}\) Ongoing Lyme disease symptoms may arise from spirochetes hidden in biofilms or surviving as cell wall-deficient cysts (L-forms), by intracellular *Borrelia* sequestration or by sequestration within privileged sites where antibiotics do not attain therapeutic levels.\(^{13,37,84-86}\) Regardless of the mechanism by which *Borrelia* spirochetes persist in tissues, persistent *Borrelia* infection requires treatment, and options at present are limited and controversial.\(^{10,13,83}\) The controversy is fueled by disagreement over viability of the spirochetes, as described below.
Although there is evidence of post-treatment *Borrelia* infection in animals and humans, some researchers speculate that *Borrelia* antigens and DNA detected in studies are merely spirochetal “debris.” Wormser et al. offered an “amber” hypothesis as a possible explanation for persistent symptoms, namely that persistent Lyme arthritis is caused by non-viable spirochetes enmeshed in joints within host-derived fibrinous or collagenous matrices. Bockenstedt et al. proposed that the inflammation seen in mice described in their study following antibiotic treatment was caused by *Borrelia* DNA and proteins representing non-infectious spirochetal “debris” deposited in tissues.

In contrast, those who support the idea that active infection is responsible for persisting Lyme disease symptoms propose that there are various protective mechanisms providing spirochetal resistance or tolerance to antibiotics including intracellular invasion, biofilm formation, cell-wall deficient L-forms, cysts, and the formation of persister cells. Furthermore the “amber” and “debris” hypotheses of symptom persistence are difficult to support because *Borrelia* DNA is rapidly cleared from murine tissues after prompt antibiotic treatment, and the DNA of non-viable spirochetes is cleared from mouse tissue within several hours. The present study confirms the presence of live *Borrelia* spirochetes in patients who had been treated with antibiotics for persistent Lyme disease symptoms.

Recent studies have focused on “persister cells” and “sleeper cells” as spirochetal agents of persistence in Lyme disease. The concept involves organisms that are tolerant to antibiotics and can downregulate their metabolic needs via a “stringent response” to survive in a hostile environment, only to reemerge when the environment becomes more favorable. A similar mechanism of persistent infection has been described in *E. coli, Mycobacteria* and *Salmonella*. The survival of metabolically tolerant spirochetes in privileged sites would explain our findings of viable *Borrelia* in antibiotic-treated patients once the antibiotics are withdrawn and culture conditions are optimized. The factors that influence viability of “persister cells” and “sleeper cells” in patients with persistent Lyme disease symptoms merit further study.
Three of our study subjects had a controversial skin condition commonly called Morgellons disease (MD). The distinguishing feature of this skin condition is the presence of white, black, or brightly colored filaments that lie under, are embedded in, or project from skin lesions (see Figure 1D). While some medical practitioners erroneously consider MD to be a purely delusional disorder, MD appears to be a *Borrelia* filamentous dermatitis. MD patients exhibit symptoms that resemble those of Lyme disease, such as fatigue, joint pain, and neuropathy, and the skin condition has been shown to be associated with *Borrelia* infection. Spirochetes from different *Borrelia* species have been detected in MD patient specimens. We obtained positive *Borrelia* cultures from all three of our MD subjects.

The mechanism of MD filament evolution has not been resolved, but as collagen and keratin filaments arise from proliferative keratinocytes and fibroblasts in human epithelial tissue, we speculate that *Borrelia* infection alters keratin and collagen gene regulation. *Borrelia* bacteria can invade fibroblasts and keratinocytes where they survive and replicate intracellularly. As shown by in vitro studies, *Borrelia* spirochetes can be isolated from keratinocyte and fibroblast monolayers despite treatment with antibiotics. Persistent refractory infection in MD patients may therefore result in part from sequestration of live *Borrelia* spirochetes within keratinocytes and fibroblasts.

*Borrelia* spirochetes have been detected in vaginal and seminal secretions. We cultured *Borrelia* spirochetes in genital secretions from 10 of our study subjects who had taken or were currently taking antibiotic therapy. Bb is a complex organism that is related to the spirochetal agent of syphilis, and therefore may have similar infectious capabilities. As outlined above, *Borrelia* spirochetes penetrate tissues, can form cystic structures, hide in biofilms, become intracellular, and sequester in privileged sites (brain, eye and synovium). These specialized abilities of the *Borrelia* spirochete suggest that the genital tract could harbor infection. The vagina and the seminal vesicles are privileged sites, and that may explain why the organism can persist in the genital tract despite antimicrobial therapy in a manner similar to syphilis, chlamydia, human immunodeficiency virus (HIV), Ebola and Zika virus.

In summary, in this pilot study we demonstrated persistent infection despite antibiotic therapy.
in 12 North American patients with ongoing symptoms of LD. Cultures were positive in all 12
patients in our study, indicating that the *Borrelia* spirochetes were replicating and therefore
alive. The spirochetes were genetically identified as Bb in a blinded fashion using PCR and gene
sequencing in three separate laboratories. In contrast, cultures from control subjects without
Lyme disease were negative for *Borrelia* spirochetes. Our findings provide evidence that
persistent infection rather than spirochetal “debris” was at least in part responsible for ongoing
symptoms in these cases of Lyme disease, and the results mirror recent observations in a non-
human primate model of treated Lyme disease.\textsuperscript{37} Larger clinical studies using corroborative
techniques are needed to confirm the findings in this pilot study.

**Acknowledgements**

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for giving permission to publish his results. We are grateful to our patients and control subjects
for providing samples for the study.

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manuscript.

**Conflicts of Interest:**

The authors have no conflicts of interest to declare.
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Supporting Information Legends

Figure 1
A: Darkfield microscopy of culture fluid from Case 7 showing live spirochetes. Magnification 1000x.
B: Dieterle silver stain of culture fluid from Case 10 showing live spirochetes. Magnification 1000x.
C: Borrelia immunostain of culture fluid from Case 9 showing live spirochetes. Magnification 1000x.
D. Typical dermal filaments from patient with Morgellons disease. Magnification 100x.

Table 1: Clinical Characteristics of Study Patients. EM, erythema migrans; MD, Morgellons disease; MS, musculoskeletal; F, fatigue; N, neurological; Bab, Babesia microti or Babesia duncani; Bart, Bartonella henselae; Ana, Anaplasma phagocytophilum; Ehr, Ehrlichia chafeensis. Abx, on antibiotics at time of testing.

Table 2: Summary of Microscopy Results from Patient Culture Samples. N/A, not available

Table 3: Summary of PCR Results from Patient Culture Samples. *Sequenced; RT, real time PCR; N, nested PCR; E, endpoint PCR; N/A not available; (+/-) One specimen was positive for Bb DNA, one specimen was negative (different collection dates).

Table 4: Summary of BLAST Sequence Analysis of Patient PCR Samples. F, forward sequence; R, reverse sequence. UNH, University of New Haven; AB, Australian Biologics; UCI, University of California Irvine.

Supplemental Figure 1: PCR Sequences and BLAST Analyses from Individual Patient Cultures. UNH, University of New Haven; AB, Australian Biologics; UCI, University of California Irvine.
Table 1. Patient Clinical Characteristics

<table>
<thead>
<tr>
<th>Case #</th>
<th>Age/ Gender</th>
<th>EM Rash</th>
<th>Sx</th>
<th>MD Lesions</th>
<th>LD Seroreactivity</th>
<th>Co-infections</th>
<th>Abx</th>
</tr>
</thead>
<tbody>
<tr>
<td>Case 1</td>
<td>50F</td>
<td>No</td>
<td>MS, F</td>
<td>Yes</td>
<td>Negative</td>
<td>Unknown</td>
<td>Yes</td>
</tr>
<tr>
<td>Case 2</td>
<td>54F</td>
<td>Yes</td>
<td>MS, F</td>
<td>Yes</td>
<td>Negative</td>
<td>Bab, Bart</td>
<td>No</td>
</tr>
<tr>
<td>Case 3</td>
<td>63M</td>
<td>No</td>
<td>MS, F</td>
<td>No</td>
<td>Positive</td>
<td>Bab, Ana</td>
<td>Yes</td>
</tr>
<tr>
<td>Case 4</td>
<td>53F</td>
<td>Yes</td>
<td>MS, F</td>
<td>No</td>
<td>Negative, seroconverting to positive</td>
<td>Bab, Ana</td>
<td>Yes</td>
</tr>
<tr>
<td>Case 5</td>
<td>40F</td>
<td>No</td>
<td>MS, N</td>
<td>No</td>
<td>Positive</td>
<td>Bab</td>
<td>Yes</td>
</tr>
<tr>
<td>Case 6</td>
<td>42M</td>
<td>No</td>
<td>MS, N</td>
<td>No</td>
<td>Positive</td>
<td>None</td>
<td>Yes</td>
</tr>
<tr>
<td>Case 7</td>
<td>36F</td>
<td>No</td>
<td>MS, N</td>
<td>No</td>
<td>Positive</td>
<td>None</td>
<td>Yes</td>
</tr>
<tr>
<td>Case 8</td>
<td>39M</td>
<td>No</td>
<td>MS, N</td>
<td>No</td>
<td>Positive</td>
<td>Unknown</td>
<td>No</td>
</tr>
<tr>
<td>Case 9</td>
<td>71F</td>
<td>No</td>
<td>MS, F, N</td>
<td>No</td>
<td>Positive</td>
<td>None</td>
<td>No</td>
</tr>
<tr>
<td>Case 10</td>
<td>72M</td>
<td>No</td>
<td>MS, F, N</td>
<td>No</td>
<td>Positive</td>
<td>None</td>
<td>No</td>
</tr>
<tr>
<td>Case 11</td>
<td>57F</td>
<td>No</td>
<td>MS</td>
<td>No</td>
<td>Positive</td>
<td>Bab, Ehr, Bart</td>
<td>No</td>
</tr>
<tr>
<td>Case 12</td>
<td>46F</td>
<td>No</td>
<td>MS</td>
<td>Yes</td>
<td>Positive</td>
<td>Bab</td>
<td>No</td>
</tr>
</tbody>
</table>

EM, erythema migrans; MD, Morgellons disease; MS, musculoskeletal; F, fatigue; N, neurological; Bab, Babesia microti or Babesia duncanii; Bart, Bartonella henselae; Ana, Anaplasma phagocytophilum; Ehr, Ehrlichia chafeensis. Abx, on antibiotics at time of testing.
Table 2: Microscopy of Patient Samples

<table>
<thead>
<tr>
<th>Case #</th>
<th>Sample type</th>
<th>Darkfield</th>
<th>Dieterle</th>
<th>Bb immunostain</th>
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<tbody>
<tr>
<td>Case 1</td>
<td>whole callus</td>
<td>N/A</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td></td>
<td>blood culture</td>
<td>spirochetes</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>Case 2</td>
<td>blood culture</td>
<td>spherules</td>
<td>spherules</td>
<td>positive, spherules</td>
</tr>
<tr>
<td></td>
<td>vaginal culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes, biofilm</td>
</tr>
<tr>
<td>Case 3</td>
<td>blood culture</td>
<td>spirochetes/spherules</td>
<td>spirochetes/spherules</td>
<td>positive spirochetes/spherules</td>
</tr>
<tr>
<td></td>
<td>seminal culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 4</td>
<td>blood culture</td>
<td>spirochetes/spherules</td>
<td>spirochetes/spherules</td>
<td>positive spirochetes/spherules</td>
</tr>
<tr>
<td></td>
<td>vaginal culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 5</td>
<td>blood culture</td>
<td>spherules</td>
<td>spherules</td>
<td>positive, spherules</td>
</tr>
<tr>
<td></td>
<td>vaginal culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 6</td>
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<td>spherules</td>
<td>spherules</td>
<td>positive, spherules</td>
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<tr>
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<td>seminal culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 7</td>
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<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 8</td>
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<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 9</td>
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<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 10</td>
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<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 11</td>
<td>vaginal culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
<tr>
<td>Case 12</td>
<td>blood culture</td>
<td>spherules</td>
<td>spherules</td>
<td>positive, spherules</td>
</tr>
<tr>
<td></td>
<td>skin culture</td>
<td>spirochetes</td>
<td>spirochetes</td>
<td>positive, spirochetes</td>
</tr>
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Table 3: PCR Analysis of Patient Culture Samples

<table>
<thead>
<tr>
<th>Case #</th>
<th>Sample type</th>
<th>University of New Haven</th>
<th>Australian Biologics</th>
<th>UC – Irvine</th>
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<tbody>
<tr>
<td>1</td>
<td>whole callus</td>
<td>16S rRNA (N), pyrG (N)<em>, fla (N)</em></td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>blood culture</td>
<td>pyrG (N), fla (N)*</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>2</td>
<td>blood culture</td>
<td>16S rRNA (N)</td>
<td>16S rRNA (RT), rpoC (E)*</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>vaginal culture</td>
<td>pyrG (N)*, fla (N)</td>
<td>16S rRNA(RT)*</td>
<td>qPCR 16S-23S intergenic spacer</td>
</tr>
<tr>
<td>3</td>
<td>blood culture</td>
<td>16S rRNA (N)*</td>
<td>16S rRNA(RT)</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>seminal culture</td>
<td>16S rRNA (RT), 16S rRNA (N)*, fla (N)</td>
<td>16S rRNA(RT), rpoC (E)*</td>
<td>N/A</td>
</tr>
<tr>
<td>4</td>
<td>blood culture</td>
<td>16S rRNA (N), pyrG (N)</td>
<td>16S rRNA(RT), rpoC (E)*</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>vaginal culture</td>
<td>16S rRNA (RT), 16S rRNA (N), pyrG (N), fla (N)</td>
<td>16S rRNA(RT), rpoC (E)*</td>
<td>N/A</td>
</tr>
<tr>
<td>5</td>
<td>blood culture</td>
<td>16S rRNA (RT), 16S rRNA (N), pyrG (N)</td>
<td>16S rRNA(RT)</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>vaginal culture</td>
<td>16S rRNA (N)</td>
<td>16S rRNA(RT), rpoC (E)*</td>
<td>N/A</td>
</tr>
<tr>
<td>6</td>
<td>blood culture</td>
<td>16S rRNA (RT), 16S rRNA (N), pyrG (N)</td>
<td>16S rRNA(RT)</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>seminal culture</td>
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<td>16S rRNA(NT)</td>
<td>N/A</td>
</tr>
<tr>
<td>7</td>
<td>vaginal culture</td>
<td>16S rRNA (N)*</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>8</td>
<td>seminal culture</td>
<td>16S rRNA (N)*</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>9</td>
<td>vaginal culture</td>
<td>pyrG (N)</td>
<td>16S rRNA(NT)</td>
<td>N/A</td>
</tr>
<tr>
<td>10</td>
<td>seminal culture</td>
<td>pyrG (N)</td>
<td>16S rRNA(NT)</td>
<td>(+/-) qPCR16S-23S intergenic spacer</td>
</tr>
<tr>
<td>11</td>
<td>vaginal culture</td>
<td>16S rRNA (N)</td>
<td>16S rRNA(NT), rpoC (E)*</td>
<td>N/A</td>
</tr>
<tr>
<td>12</td>
<td>whole callus</td>
<td>uvrA (N)*</td>
<td>N/A</td>
<td>N/A</td>
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<tr>
<td></td>
<td>blood culture</td>
<td>pyrG</td>
<td>16S rRNA(NT)</td>
<td>N/A</td>
</tr>
</tbody>
</table>

* Sequenced; RT, real time PCR; N, nested PCR; E, endpoint PCR; N/A not available; (+/-) One specimen was positive for Bb DNA, one specimen was negative (different collection dates)
Table 4: BLAST Sequence Analysis of Patient PCR Samples

<table>
<thead>
<tr>
<th>Case #</th>
<th>Culture specimen</th>
<th>Sequence</th>
<th>Length</th>
<th>E-value</th>
<th>BLAST match</th>
<th>LAB</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>callus</td>
<td>pyrG</td>
<td>680</td>
<td>0.0</td>
<td>100%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>callus</td>
<td>fla</td>
<td>367</td>
<td>2e-172</td>
<td>100%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>blood</td>
<td>fla F</td>
<td>364</td>
<td>2e-176</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>blood</td>
<td>fla R</td>
<td>367</td>
<td>2e-172</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td>2</td>
<td>vaginal</td>
<td>pyrG F</td>
<td>656</td>
<td>0.0</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>vaginal</td>
<td>pyrG R</td>
<td>659</td>
<td>0.0</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>vaginal</td>
<td>rpoC</td>
<td>79</td>
<td>4e-32</td>
<td>100%</td>
<td>AB</td>
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<tr>
<td></td>
<td>vaginal</td>
<td>16S-23S Intergenic spacer</td>
<td>474</td>
<td>0.0</td>
<td>100%</td>
<td>UCI</td>
</tr>
<tr>
<td>3</td>
<td>blood</td>
<td>16S rRNA F</td>
<td>415</td>
<td>0.0</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>blood</td>
<td>16S rRNA R</td>
<td>415</td>
<td>0.0</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td></td>
<td>seminal</td>
<td>16S rRNA</td>
<td>388</td>
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<td>99%</td>
<td>UNH</td>
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<tr>
<td></td>
<td>blood 1 month Abx</td>
<td>rpoC</td>
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<td>96%</td>
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<td>100%</td>
<td>AB</td>
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<td>99%</td>
<td>UNH</td>
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<td>seminal</td>
<td>16S rRNA</td>
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<td>100%</td>
<td>UNH</td>
</tr>
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<td>seminal</td>
<td>16S-23S Intergenic spacer</td>
<td>474</td>
<td>0.0</td>
<td>99%</td>
<td>UCI</td>
</tr>
<tr>
<td>10</td>
<td>vaginal</td>
<td>rpoC</td>
<td>156</td>
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<td>100%</td>
<td>AB</td>
</tr>
<tr>
<td>11</td>
<td>callus</td>
<td>uvrA F</td>
<td>653</td>
<td>0.0</td>
<td>99%</td>
<td>UNH</td>
</tr>
<tr>
<td>12</td>
<td>callus</td>
<td>uvrA R</td>
<td>651</td>
<td>0.0</td>
<td>99%</td>
<td>UNH</td>
</tr>
</tbody>
</table>

F, forward sequence; R, reverse sequence; Bbss, B. burgdorferi sensu stricto; Abx, antibiotics
Supplemental Figure 1

SEQUENCES FROM UNIVERSITY OF NEW HAVEN

Sequences for Case #1 UNH

Whole callus
pyrG

NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGGAGTGGTAATATTTCTTTTATTCATTTAACATATGTGCCAAGTCCAGCTGGAATTAATGAGCACAAATCTAAACCTACTCACAAAGTGT
TAAAAACCTAAAAACACAGCTGTTTTCCCCGATTTAATTATTTGCTAGAAGTTACGACATTTCTATT
ATTGACAAATGTGGATGGTTTCTACTATTTATGAAATTCTATATCTTTTTATAACGAGGAGTTG
ACATGAGATTTAAGCTCTAAGTAAAATATTTAAGGTTATTCACAAATTGAGAGCCTTTTC
AAAGCTTTGAGAGTTTAAAAATCAATTITTTTTATGCTATAAATAACTTAATTTGCT
ATTGTGTTAATAATGCTGAACTTGTGACTTTATGCAATTAGAGAGCCTTTTGGTTC
ATTGTGCAAGCCATTTGGATTTGACTTAAATAGACATTATTTAATTAGTTGAGGAGCTTTTGGAG
ATGGGACGTCAGCTTTAATTGAGAGCTTTTGGAGGAGCTTTTGGAGATTTGNCTCGNNN

Length 680 bp, BLAST 100% identity with Bbss, e value 0

Whole callus
Fla

NNNNNNNNNNNNNNNNNNNNNNNNCGAAATTAATGAGTTGGCTGATCAAGCTCAATATAACACCAATGCACATGTATCACAACAAAATCTCTCTCAAAATGTAAGAACA
GCTGAAAGACCTTGGAATGCAAGTCTGCAAATAACACCCAGCTACCTTCAGGTCT
CAAGCGTTTGGGACTTTAAGAGAGTTGCTGTTGGAGCAAAACAGAGATGAAAGCTATTGCTGT
AATATTTATGCAGCTATTGTGCAAATCTTTTCTCTGGTGAGGGAGCTCAAACTGCTCAGGCTGC
ACCGGTTCAAGGCAGGTTGCTCACAGGAAGAGGAGCTGCAACAGCCAGCACTTGCACAGCAC
CTTCA

Length 367 bp, BLAST 100% identity with Bbss, e value 2e-172

Blood culture
Fla

Forward
NNNNNNNNNNNNNNNNNNNNNNNNCANCAACNACAGCAGAAATTAATAGAATTTGCTGATCAAGACTC
AATATACCAATGCAATGTATCTTACAAACAAATCTCTCTCAAAATGTAAGAACAGCTG
AAAGCTTGGGGAATGCAAGCTGCAAAATAACACCCAGCTACCTTCAGGTCTCAGG
CGTCTTTGGAATAGGTTGCTGGACAAAACAGAGATGAAAGCTATTGCTGAAAATA
TTATGTGCAAGTTGCAAAATCTCTGCTGAGGGGCTCAAAACTCTGCAGGCTGCA
ACCGTTCAAGGAGGGTTGCTCACAGGAAGGAGGAGCTCAACAGGACGCACTCTGACAGC
CTTCA
Length 364 bp, BLAST 99% identity with Bbss, e value 2e-176

**Reverse**

NNNNNNNNNNNNNNNNNNNNACTNNNNNNNNCGGAATATAGAATTTGCTGATCAA
GCTCAATATACCAATGCACATGTATCAAACAAATCTGCTTCTCAAAAAATGTAAGAAACA
GCTGAAAGAGCTTGGGATGCAAGCTGCAAAAAATTTACCAACACCACAGCAGCTTTCAGCTCT
CAAGCGTCTGGAGACTTTAAGAGTTCATGTGGAGCAAAACAAAGTAGAAGCATTGCTGTA
AATATTATATGCGACTAACATGTTGCAATATTTCTTCTGTTGAGGGAGCTCAACAGCCACCT
GACCTCA

Length 367 bp, BLAST 100% identity with Bbss, e value 2e-172

**Sequences for Case #2 UNH**

**Vaginal culture**

**pyrG**

**Forward**

ATAGCCATAATTTTACCTCTNTATCTTTTGGCTCTCAAAGGCGCCAGAAACAAATATGCGT
CAAACCTTCTTTAAACAGCTCTCTATTTAAACATTGAAATCAAATTAAGTGCTTTTTAAATAG
CAAATCCCAATGGCGTCAACATGAACAAAAAGCTCTCTCTAATTTTCTTGCATGAAACATTAC
TCTGTCGATATTGGTTCCTGTAATACTTGGCATAATATGTGAACCTGTTTAAAAAGTATATG
GCGATTTTACAAAGCTCTTAAGGCTCTGCTTATATAAAAAGATATAGGAATTTCTTTCAATA
TAGAAGGCCTAAATCTCATGTACACCCCTTTTATAAAAAGATTGGAATTTCATAAATA
GTAGAAACATCAACATTGGCTCAATAATAGTGCTCTCAACATGGCAAAAACATTGCCACT
TTTTCTCTGATTTGGTTCCTGTAATACTTTGGAACCTTCTAGCATAATATTAAATTTTGCG
AACAAATACTCTTGAATTTAAACACCTTTTGTTGAGTAGTTTAGATTCTTTGCTCATTATT
CCAGCTGGAGCTTTGCAATGTTTTGCTATGTTGAGAGCACTTCTATTATTGACAATGTTGATGT
TTTATGAAATTCCTATATATTTTATAAGGCTAGTTTAAGTATXAGGCTTCCTAAGTT
AAATATTAAAGGTGTGATCAAAAATAAGAAGAGCTTTTCAAGCTTTGAGGATATAAAATC
TAATTTTTTGTGCATAAAAAAAAAATTTAATATTGCTATTGGTGAATAATAGCTGAACCTTG
ATGATTTTATGCACTCAATTAAGAAGCTTTTGGTTTCTGATGTCGACAAAACTTTGGAATTTG
CTTTAAATTTTCTCTTACTGTCTCAATAAAAATAAAATTTTTTACATAT99% B31 sequence, it
has one nucleotide difference

Length 656 bp, BLAST 99% identity with Bbss, e value 0

**Reverse**

GATTGGGAGTGGTAAATTTTTTTTTTTTATCATATGTTGCAAAGTCTGGAATTT
AATGAGCACAACATCTAACAACCTCTCACAACAAAGGTGTATTTAAAACCCTTTAATAAAAACAGCAGTATT
TTCCCGGATTTAATATTGCTAGAAAGTCTCAACAAGTATTGACAACCAAACATCGAGAAA
AATACGGAATTTTGCACATTGAGGAGCTCTTCTATAATTGGACAAATGTGTGATTCTCTACTA
TTATGAAATTTCTTATATTTTTATAAGGCGTTTAGATGTTTAAGCTCTAAGTT
AAATATTAAAGGTGTGATCAAAAATAAGAAGAGCTTTTCAAGCTTTGAGGATATAAAATC
TAATTTTTTGTGCATAAAAAAAAAATTTAATATTGCTATTGGTGAATAATAGCTGAACCTTG
ATGATTTTATGCACTCAATTAAGAAGCTTTTGGTTTCTGATGTCGACAAAACTTTGGAATTTG
CTTTAAATTTTCTCTTACTGTCTCAATAAAAATAAAATTTTTTACATAT99% B31 sequence, it
has one nucleotide difference

Length 659 bp, BLAST 99% identity with Bbss, e value 0
Sequences for Case #3 UNH

Blood culture
16S rRNA

Forward
NNNNNNNNNNNNNNNNNNGGAGATCTAAGCAGTGGCGAACGGGTAGT
AACCCTGCTGGAAGGATGTCAAGTTAATAATGATGTACGTTATACCCTG
AATAAGGCTAGTTAATTGTAATAGTGGAAAGGAAAGCCTTTAAAGCTTG
TTGTAGATGAGTCTGCGTCTTATTAGCTAGTTGGTAGGGTAAAGCCTAC
CAAGGCAATGATAAGTAACCGGCCTGAGAGGGTGACGGTCACACTG
GAACTGAGATACGCTTACCTGCACACTGGAATGATTTGCTACTATCC
CCTTGACTTGTCAAGTTAAGACGAGCACTACGCAAAGCTTTAAAGCTT
CTTTTGTAGGA
Length 415 bp, BLAST 99% identity with Bbss, e value 0

Reverse
NNNNNNNNNNNNNNNNNNNNNTCTTCNNNCCNGGAGGTTAACAAGCAGT
GGCACCTGGAAGGATGTCAAGTTAATAATGATGTACGTTATACCCTG
AATAAGGCTAGTTAATTGTAATAGTGGAAAGGAAAGCCTTTAAAGCTTG
TTGTAGATGAGTCTGCGTCTTATTAGCTAGTTGGTAGGGTAAAGCCTAC
CAAGGCAATGATAAGTAACCGGCCTGAGAGGGTGACGGTCACACTG
GAACTGAGATACGCTTACCTGCACACTGGAATGATTTGCTACTATCC
CCTTGACTTGTCAAGTTAAGACGAGCACTACGCAAAGCTTTAAAGCTT
CTTTTGTAGGA
Length 415 bp, BLAST 100% identity with Bbss, e value 0

Seminal culture
16S rRNA

GTAGCATACTACATTCCAGGCGAACGGGTAGTGAACGCGTGGATGTACTTATC
ACTATAGATGATTGAGTAATAACCCGAAATAAGGCTAGTTAAATTGTTAAT
GGGAAAGCCTTTTAAGCCTGCTTTGAGTAGTGGACTGCTGCTCTTTATAGCT
AGTTGATAGTTGCGTAGCTGGAATGATTTGCTACTATCCCTGCAGGAA
GGAAGCTGACGGAGCACTACGCTGGAAGGATGATTTGCTACTATCCCTG
TTATAGGARGAATAAGCTTTTGATAGGA
Length 388 bp, BLAST 99% identity with Bbss, e value 0

Sequences for Case #7 UNH

Vaginal culture
16S rRNA

NNNNNNNNNNNNNNNNNNNNNCGCAGGAGGCTGTGGAAGGATGTACGTAC
CTAGTTAATAAGGCTAGTTAATAACCCGAAATAAGGCTAGTTAAATTGTT
AATTTGATGAAAGGAGCCTTTTAAAGCTTGCTTTGAGTAGTGGACTGCTG
CTTTATAGCTAGGA

Length 43 bp, BLAST 99% identity with Bbss, e value 0
TTGGTAGGGTAAATGCCTACCAAGGCAATGATAAGTAACCGGCCTGAGAGGGTGAACGG
TCACACTGGAAGCTGAGATAAGGGTGACGCCGTCAGCTCGTGAATGAGGAAGAGTCGAAAGATGG
AAAATTCTTTTATATTGAAGAATAGCCTTTTGTAGGA

Length 396 bp, BLAST 99% identity with Bbss, e value 0

**Sequences for Case #8 UNH**

**Seminal culture**

16S rRNA

AGCTTTGTAGGACCTGGCTTAGAACCTAAGCGCTGGCAGGTGCGTTAAGCAGATAGGAATAAA
GCTTTGTAGGACCTGGCTTAGAACCTAAGCGCTGGCAGGTGCGTTAAGCAGATAGGAATAAG
GCTTTGTAGGACCTGGCTTAGAACCTAAGCGCTGGCAGGTGCGTTAAGCAGATAGGAATAAGC
GCTTTGTAGGACCTGGCTTAGAACCTAAGCGCTGGCAGGTGCGTT

Length 221 bp, BLAST 100% identity with Bbss, e value 7e-10

**Sequences for Case #12 UNH**

**Whole callus**

uvrA

Forward

CNNNNNNNNNNNNNNNANNNNNTATCGTATGCCTATCTCTGTGGCAGGCTAGCTACGCTAT
TAGGCTTGCTACTCAATAGGATACGTACGCTTTCCGTTAGTTATTTAGTTTTGAGCCATGACA
AGTATTTGCTCCTCATAAGAGATAATGAAAAATTAATCTCCTACTCTCTTGAATATTTAAA
ATCTTGGAATATCGTAAATTGTTGTTAGACATGAGCACAAGCTTTGGCTACTCGGGACTA
TATTATTGATATGGGCTCTGGCTGGAATTCTCTGAGGGAATAGGGGCAAAAGCTCGGTGCTGCTA
AGTATTGGTCTTCATCAAAGAGATAATGAAAAATTAATCTCTACTCTTAAATCTGAGGAATAAGC
GCTTGTTAGAATATTTTAAATATAGACTAATGATCCCTTTGAGTTTTTACCGTAA
AAAATAGATTTCCGTAAGTCTACGAGTAAACACTTTACTTATCGAGGTTGATATCCAGCTC
TGATAGTAGATAGAAGAGCTTATGAAATGAAAAATTTTGAGTTGGCAGAAGATATTTTGGGTAT
GAAAAATCGTAAAATATTATCTAATAAAATACAGTACTAGTATCGCTTTGGGAGTTTTTACCGTAA
AAACAGGTGTGTCTCAGGGCTAGGAAAAAGCATCTTTACTCTAAGCAGGTTGATATCCAGCTC
TGATAGTAGATAGAAGAGCTTATGAAATGAAAAATTTTGAGTTGGCAGAAGATATTTTGGGTAT
GAAAAATCGTAAAATATTATCTAATAAAATACAGTACTAGTATCGCTTTGGGAGTTTTTACCGTAA

Length 653 bp, BLAST 99% identity with Bbss, e value 0
SEQUENCES FROM AUSTRALIAN BIOLOGICS

Sequences for Case #2 AB

Vaginal culture
rpoC
GGAGATGTTGTAAAGCAGGAGATGCTCTCGGATGGCTGATGAGATGATATCTGATTTTA
AATATAAGAAAGGCAACATCAATAANANTTTTNNGCN
Length 651 bp, BLAST 99% identity with Bbss, e value 0

Sequences for Case #3 AB

Blood culture
rpoC
TAAAGGGTACTTCAGCCTTTTACGCTTTTGAGATGACTCCCACCTAAAATTCAAGCAG
GGGATTCTACATCTACTAAGCCTTTTACCTTTTTACCTTTGAATTGAA
Length 103 bp, BLAST 96% identity with Bbss, e value 0.11

Seminal culture, 1 month on abx
rpoC
ATTTTCATGCCGATGTATCCATGCTATCTCTGCTTTGTTACACTCTCCTACATCAAACAA
GATTCTTTGCTGGAATATAATGTTTCTGTTCAACCAACCATGTTCTCTCAAAATATTAAT
AAGCCTTTTACCTTTGAATTGAA
Length 146 bp, BLAST 100% identity with Bbss, e value 9e-57

Seminal culture, 4 months on abx
rpoC
TTAAGAGGCAGCAGCAGCTGTATGAGCTGGAATACATAAGTGTATATTCCAGCTGAAA
ACATCTTTTCAGTTAGAGACGAGATGTTGTAAGAACGGAGATATGCTTTGATGGTAG
AATAATCCATGATGCTTGAATTTTAGGGGA
Length 158 bp, BLAST 98% identity with Bbss, e value 3e-52

Sequences for Case #4 AB

Vaginal culture
rpoC

TGCTTTTACACATCTCCGTCTCTAACCACAAAAAGATGTGTTCGCTGGAATATAATGCTTA
TGTTCAACCCCCATACCTCATCTAAAAATATTATAAAGCCTTTTTACCTTTTTGAAATTGG

Length 118bp, BLAST 99% identity with Bbss, e value 1e-51

Sequences for Case #5 AB

Vaginal culture
rpoC

TCCAGCTGGAAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAAGCAGGAG
ATATGCTTTGTGATGGTAGAATTAATCCTATGATGTGCTTGAAATTTTAGGTGG

Length 109 bp, BLAST 99% identity with Bbss, e value 6e-47

Sequences for Case #11 AB

Vaginal culture
rpoC

TATGGTAATGATCATGTGTATGAGGTAGGACGGTGACGATGTTGTCTTTTTAG
GTGGCAAGGTGGGATGCTTGATGTTTTTGGGAAAAGCAGGAATATGGTCTTT
GTGATGTTAGAATAATCCTCATGATGTGCTTGAAATTTTAGGTGGGA

Length 156 Bp, BLAST 100% identity with Bbss, e value 1e-25

SEQUENCES FROM UNIVERSITY OF CALIFORNIA, IRVINE

Sequences for Case #2 UCI

16S-23S Intergenic spacer
Vaginal culture

ATGCCTTTCATCACATTGTCTTCGCTTICTTGTACTAGCCATTTGTACTGTCTGTGACGCCAGGACATA
AGGGCATATGATTGGAGCTACATCCACCTCTCCGACTTGCTATCCAGCAGTCTTTATCGAGTCCACCACAT
TACATGTGCTTCATACAGATAACAGGTTTGGCTGTCTTGGCGGACTTTACCCCAACACCTCAGCAGGAAGGTGA
CGACCAACATAGCAGACCTGTATATAGACCCAAAACGGAGAATATTATCTCTAACTATATATTATATGTGCAA
GCCCCGCTATTGCTGTGATCAGGAAATTAAAACCATGCTCACCACCCGCCGCTTGGCGGCCCCTGCAATTCC
TTTGAGTTTCACTCTTGAGGACATACTCCTCCACCACGGGAGCACAACCTAAACAGCAGCTGTACTTTATAGTT
AACACCAAGGTGCTAGTTAGCCAC

Length 474bp, BLAST 100% identity with Bbss, e value 0
Sequences for Case #10 UCI

16S-23S Intergenic spacer
Seminal culture

ATGCCTTTGCTTCACATCACTGTTTGCCTTCCGCTTTGTACAGGCCATTGTAGACAGCTGTGT
AGCCAGGACATAAGGGCCATGATGATTTGACGTCATCCTCACCCTTACCTCCGGACTTACAC
CGGCAGTCTTTATCTGAGTCCCAACCATTACATGCTGTAACAGATAAACACGCTTTGCGCT
CGTTGCGGGACTTAAACCAACACCTCACAGCACGAGCTGACGACAACCATGCAGCACCTG
TATATAGACCCCCAAAACGGGGATAATTATCTCTACTATATATATATATTATGTCAAGCCCTG
GTAAGGTTCTCGGCTATCCTGAATTAAACCACATGCTCCACCCTGGACTGCGGGCCCCCG
TCAATTCCCTTGGATTTACTCTTTGCGGGCATACTCCCAAGGCGCAGCACAATTACACGTTA
GCCTCGGTTACTAATTATAGTTAAACACCAAGTTGCATCGTTACAGC

Length 474bp, BLAST 99% identity with Bbss, e value 0