

Lyme Disease in Humans

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Abstract

Lyme disease (Lyme borreliosis) is a tick-borne, zoonosis of adults and children caused by genospecies of the *Borrelia burgdorferi* sensu lato complex. The ailment, widespread throughout the Northern Hemisphere, continues to increase globally due to multiple environmental factors, coupled with increased incursion of humans into habitats that harbor the spirochete. *B. burgdorferi* sensu lato is transmitted by ticks from the *Ixodes ricinus* complex. In North America, *B. burgdorferi* causes nearly all infections; in Europe, *B. afzelii* and *B. garinii* are most associated with human disease. The spirochete's unusual fragmented genome encodes a plethora of differentially expressed outer surface lipoproteins that play a seminal role in the bacterium's ability to sustain itself within its enzootic cycle and cause disease when transmitted to its incidental human host. Tissue damage and symptomatology (i.e., clinical manifestations) result from the inflammatory response elicited by the bacterium and its constituents. The deposition of spirochetes into human dermal tissue generates a local inflammatory response that manifests as erythema migrans (EM), the hallmark skin lesion. If treated appropriately and early, the prognosis is excellent. However, in untreated patients, the disease may present with a wide range of clinical manifestations, most commonly involving the central nervous system, joints, or heart. A small percentage (~10%) of patients may go on to develop a poorly defined fibromyalgia-like illness, post-treatment Lyme disease (PTLD) unresponsive to prolonged antimicrobial therapy. Below we integrate current knowledge regarding the ecologic, epidemiologic, microbiologic, and immunologic facets of Lyme disease into a conceptual framework that

sheds light on the disorder that healthcare providers encounter.

Introduction

Lyme disease is the prototype of an emerging infectious disease (Steere et al., 2004; Paules et al., 2018). The isolation of its etiologic agent, *Borrelia burgdorferi*, from humans in 1983 (Benach et al., 1983; Steere et al., 1983a; Barbour and Benach, 2019) capped an intensive hunt for a pathogen that just a short time before had been cultured from a black legged (deer) tick (Burgdorfer et al., 1982), initially named *Ixodes dammini* (Spielman et al., 1979) but subsequently found to belong to a species, *I. scapularis*, whose range had been expanding in the U.S. since it was first recognized since the 1920s (Burgdorfer and Gage, 1986; Eisen and Eisen, 2018). Critical to the chain of events that led to the discovery of the Lyme disease spirochete was the observation that many patients involved in an outbreak of oligoarthritis in Southeastern Connecticut also had a skin rash, erythema chronicum migrans (ECM; now erythema migrans, EM) (Steere et al., 1977a; Steere et al., 1977b), previously associated in Europe with the bite of the sheep tick *Ixodes ricinus* (Afzelius, 1910; Lipschütz, 1913; Afzelius, 1921; Lipschütz, 1923). The isolation of *B. burgdorferi* (Benach et al., 1983; Steere et al., 1983a; Barbour and Benach, 2019) sparked an explosive increase in our knowledge of the bacterium, the disease it causes, and the enzootic cycle that sustains and creates risk to humans who intrude upon it. We now know that Lyme disease (Lyme borreliosis) is the most prevalent tick-borne illness in the Palearctic region of the Northern Hemisphere and that its incidence continues to increase globally due to myriad

demographic and environmental factors, including climate change (Mead, 2015; Ostfeld and Brunner, 2015; Schotthoefer and Frost, 2015; Semenza and Suk, 2018; Sharareh et al., 2019). Although the clinical manifestations of Lyme disease continue to be a source of considerable controversy, it is generally accepted that a relatively small number of syndromes dominate the clinical picture and that the vast majority of patients present with treatment-responsive acute illness (Steere et al., 2016; Stanek and Strle, 2018). Serologic surveys conducted in high prevalence areas indicate that asymptomatic infection also is relatively common (Hanrahan et al., 1984; Steere et al., 2003; Wilhelmsson et al., 2016; Carlsson et al., 2018); thus, despite the bacterium's notorious reputation, benign outcomes often occur. The genomic sequence of *B. burgdorferi* revealed that the spirochete lacks genes encoding known toxigenic molecules as well as the secretory apparatus required to deliver them to the extracellular milieu it inhabits within its mammalian host (Fraser et al., 1997; Casjens et al., 2000). Whereas reservoir hosts are unaffected by lifelong infection with Lyme disease spirochetes (Oliver et al., 2003; Hersh et al., 2014) due to a poorly understood form of immunologic tolerance (Barbour, 2017), infected humans often mount local and systemic inflammatory responses that make them ill (Steere et al., 2016; Stanek and Strle, 2018). From this perspective, one can regard clinical Lyme disease in humans as an evolutionary "mismatch" between pathogen and the intolerant immune system of its incidental host. Beyond this reductionist view, however, we still have only a limited understanding of the microbial factors, pathogenic mechanisms, and immunologic responses that determine outcomes following the adventitious encounter of humans with this zoonotic microorganism.

Over the years, a number of excellent clinical reviews of Lyme disease have been published in journals and textbooks, and there is no need to reiterate all of this information herein (Radolf and Samuels, 2021; Stanek et al., 2012; Steere et al., 2016; Stanek and Strle, 2018). In addition, medical societies in both the United States and Europe have issued comprehensive guidelines for the diagnosis and management of this infection (Wormser et al., 2006; Halperin et al., 2007; Eldin et al., 2019). Rather, the primary objective of this review is to integrate current knowledge regarding the ecologic, epidemiologic, microbiologic, and immunologic facets of Lyme disease into a conceptual framework that sheds light

on the disorder practitioners see and manage. As will be seen, many of the principal factors that determine the level of risk for populations and individuals lie outside the sphere of human activity. Since our goal is to develop a mechanistic picture of the human disorder, we intend to rely as much as possible upon data obtained from human studies; extrapolation from *in vitro* and animal models is necessary, indeed, unavoidable, given the constraints of human experimentation. At the same time, this review attempts to grapple with a vexing but fundamental issue—the extent to which infection in humans deviates from the infectious process in nature and that observed in experimental animal models.

Historical overview

The history of what we now call Lyme disease, dating back to the early part of the twentieth century, is instructive for contemporary understanding (Burgdorfer, 1986, 1993). However, the discoveries that ushered in our current understanding of the illness began in 1981, when Willy Burgdorfer, Jorge Benach and Alan Barbour identified a new *Borrelia* species from ticks collected on eastern Long Island (Burgdorfer et al., 1982; Barbour and Benach, 2019). As Burgdorfer (Burgdorfer, 1993) and, most recently, Barbour and Benach (Barbour and Benach, 2019) note in their colorful first-hand accounts, the finding was serendipitous and well illustrates Louis Pasteur's famous dictum that "chance favors only the prepared mind". Burgdorfer and Benach were seeking a vector to explain an outbreak of Rocky Mountain spotted fever on Eastern Long Island but stumbled across spirochetes when they dissected midguts from *Ixodes scapularis* ticks, recently recognized as the vector for *Babesia microti* (Spielman et al., 1979). Burgdorfer was aware that a possible spirochetal etiology for Lyme disease had been "in the air" since the late 1940s. Two other strokes of fortune contributed to the discovery: Benach possessed a bank of sera from convalescent Lyme disease patients, while Barbour, at the time studying relapsing fever at the Rocky Mountain Laboratory, had developed an improved medium for cultivation of *Borrelia*. They found that antibodies in the sera of Lyme disease patients reacted intensely with spirochetes in dissected tick midguts and spirochetes isolated from tick midguts using Barbour's newly formulated (BSKII) medium (Burgdorfer et al., 1982). Within a year, groups separately led by Benach and Allen Steere isolated spirochetes from blood, skin, and cerebrospinal fluid (CSF), thereby establishing it as the etiologic agent (Burgdorfer et al., 1982;

Burgdorfer, 1986). Using DNA-DNA hybridization, two groups (Hyde and Johnson, 1984; Schmid et al., 1984) subsequently showed that the spirochete was a new species of *Borrelia*, subsequently named *B. burgdorferi* (Johnson et al., 1984).

It soon became apparent that a variety of clinical syndromes described in the European medical literature were, in fact, manifestations of a tick-transmitted disorder caused by members of what eventually came to be known as the *B. burgdorferi* sensu lato complex (Belfaiza et al., 1993; Wang et al., 1999a; Cutler et al., 2017). EM, the classic skin lesion associated with this infectious disease, was first described by Afzelius, a Swedish dermatologist, in 1910 (Afzelius, 1910). Afzelius also correctly hypothesized that EM resulted from the tick-borne transmission to humans of a zoonotic pathogen (Afzelius, 1921); in 1921, Lipschütz identified *Ixodes ricinus* as the vector (Lipschütz, 1923). By the beginning of World War II, European investigators knew that EM was associated with several neurologic and dermatologic disorders and with musculoskeletal complaints (Garin, 1922; Bannwarth, 1941, 1944). After the war, Lenhoff (Lenhoff, 1948), a Swedish pathologist, described what he believed were spirochetes in biopsies of EM lesions, while Hollström (Hollstrom, 1951) demonstrated that penicillin was effective for its treatment.

In 1970, Rudolph J. Scrimanti, a Wisconsin dermatologist, reported the first case of Lyme disease acquired in the United States. The patient, by serendipity a physician, was bitten by a tick above his right iliac crest while grouse hunting in North Central Wisconsin. Three months later, he presented with an enormous EM rash extending from his right mid-chest to mid-back, encircling his right axilla and iliac crest, accompanied by hyperesthesia of the T12 and L1 dermatomes. Fortunately, Scrimanti knew of this “curious condition” from the European literature and of its responsiveness to penicillin; incredibly, the patient was symptom-free within 48 h of receiving what by today’s standards is considered a miniscule dose (1.2 MU) of intramuscular benzathine penicillin G. In 1976, Mast and Burrows (Mast and Burrows, 1976) reported the first cluster of cases from Southeastern Connecticut. Soon afterwards, Yale rheumatologists Allen Steere and Steven Malawista began investigating cases of arthritis in patients, many of whom were children, in and around Old Lyme, Connecticut. Mothers of afflicted children, skeptical of the diagnosis of juvenile rheumatoid

arthritis made by local physicians, had informed the State Health Department about the outbreak and called it to the attention of Steere and Malawista. In their initial reports, they called the mysterious ailment Lyme arthritis (Steere et al., 1977a; Steere et al., 1977b). However, with the realization that most arthritis patients previously had EM and that non-arthritic manifestations (heart block, facial nerve palsy and/or meningitis) were associated with the rash, they subsequently changed the name to “Lyme disease” (Steere and Malawista, 1979). Shortly thereafter, they “closed the loop” by correlating cases of Lyme disease with the distribution of *I. scapularis* in the Northeast and *I. pacificus* in California and Oregon (Steere and Malawista, 1979). Of note, European authorities prefer Lyme borreliosis because, in their view, U.S. patients diagnosed with Lyme disease do not always have a disorder with a clear-cut infectious etiology (Stanek and Strle, 2018). Detailed narratives of the medical sleuthing that led to the discovery of *B. burgdorferi* can be found in Radolf and Samuels (2021), in Edlow’s entertaining book *Bull’s Eye, Unraveling the Medical Mystery of Lyme Disease* (Edlow, 2003), and in the gripping narrative recently published by Barbour and Benach (2019).

Epidemiology

Please see Radolf and Samuels (2021) for a complete discussion of the epidemiology of Lyme disease. Lyme disease became a notifiable condition in the U.S. in 1991. Since 2008, a confirmed case has been defined as either (i) EM in a person with possible or known tick exposure in an endemic area or laboratory evidence of infection (almost always serological) or (ii) at least one recognized clinical manifestation other than EM along with confirmatory laboratory evidence (Schwartz et al., 2017). From 2008 to 2015, 208,834 confirmed cases were reported to the CDC with the highest number (29,959) in 2009 (Figure 1) (Schwartz et al., 2017). During this period, Lyme disease accounted for 82% of all tick-borne diseases and 63% of all vector-borne disease reported in the US, making it by far the most prevalent vector-borne illness in the United States and *Ixodes scapularis* the most important vector (Hamer et al., 2010; Mead, 2015; Rosenberg et al., 2018). Nationwide studies of health insurance claims (Nelson et al., 2015) and commercial laboratory diagnostic tests (Hinckley et al., 2014) suggest that underreporting is common and that the actual number of cases is closer to 300,000 per year (*i.e.*, about tenfold higher than reported). Fourteen states,

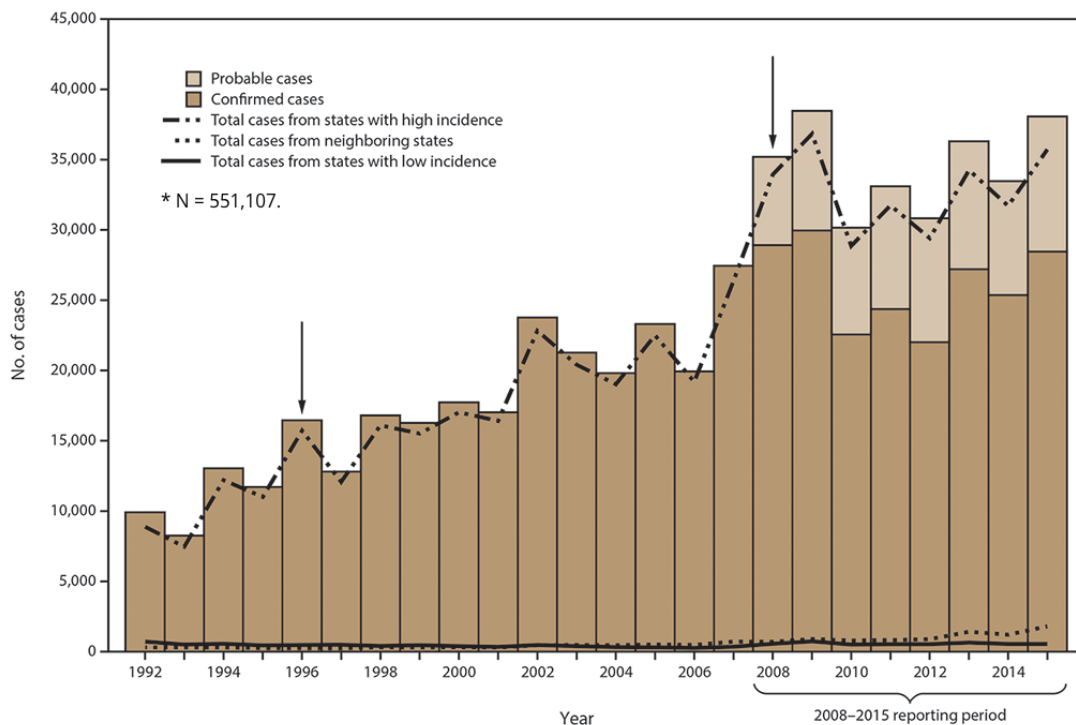


Figure 1. Number of confirmed and probable Lyme disease cases in the United States, 1992-2015. Arrows indicate notable changes in case definitions. The case definition was revised in 1996 to recommend a two-step testing method and in 2008 to increase specificity of laboratory evidence of infection and to include provision for report of probable cases (reproduced from Schwartz *et al.*, 2017).

all located in the Northeast, mid-Atlantic, and upper Midwest (Connecticut, Delaware, Maine, Maryland, Massachusetts, Minnesota, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island, Vermont, Virginia, and Wisconsin), accounted for 95.7% of confirmed cases; Delaware, Connecticut, and Vermont had the highest incidences (~65-69 cases per 100,000 population) (Figure 2) (Schwartz *et al.*, 2017). For all years, confirmed and probable cases peaked during the first week in July, consistent with nymphs being the principal stage for transmission. The age distribution was bimodal, with peaks between 5-9 years and 50-55 years, a slight male predominance (56%), and whites representing the overwhelming majority (~90%) of cases (Schwartz *et al.*, 2017). EM was the most common clinical manifestation, accounting for nearly three-fourths (72.2%) of patients, and carditis least

common (1.5%); 27.5% had arthritis and 12.5% had a neurologic manifestation. Serologic surveys in the U.S. and Europe have revealed substantial rates of asymptomatic or subclinical infections among persons living in endemic areas (Hanrahan *et al.*, 1984; Steere *et al.*, 2003; Wilhelmsson *et al.*, 2016; Carlsson *et al.*, 2018). Not surprisingly, risk is proportional to time spent outdoors, whether recreationally or occupationally, in or near tick-infested woods and vegetation (Hengge *et al.*, 2003; Finch *et al.*, 2014).

The last three decades have witnessed not only an impressive increase in the incidence of Lyme disease in North America but also a relentless expansion of its geographic range. Although historically associated with incursion into deciduous forests (Dennis and Hayes, 2002), Lyme disease now poses a threat to

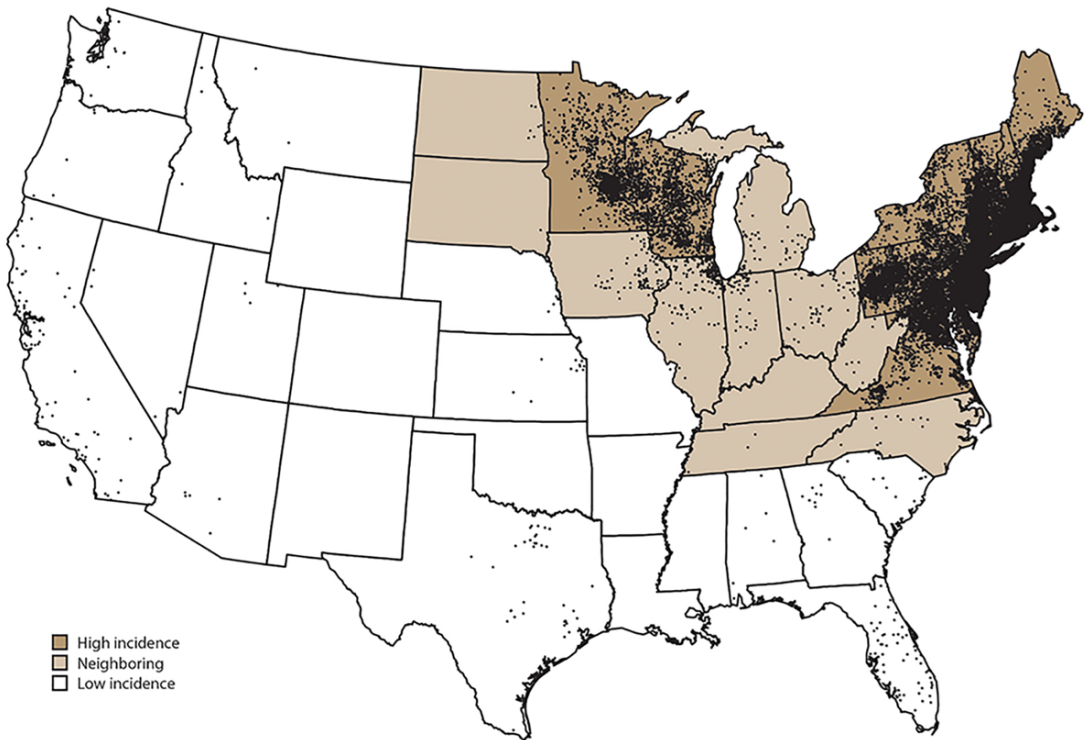


Figure 2. Average annual number of confirmed Lyme disease cases by county of residence in the United States, 2008-2015. Each dot represents one confirmed case (reproduced from Schwartz *et al.*, 2017).

urban dwellers, as evidenced by cases acquired in New York City (VanAcker *et al.*, 2019) and identification of *B. burgdorferi*-infected ticks in Chicago (Hamer *et al.*, 2012). Moreover, the disease has expanded beyond the confines of the continental United States. It has emerged as a health threat in Southern Canada (Ogden *et al.*, 2009; Gasmi *et al.*, 2019), where the number of reported cases increased from 144 in 2005 to more than 2000 in 2017, and multiple surveys have reported identification of *B. burgdorferi*-infected *I. scapularis* ticks (Bouchard *et al.*, 2015; Gasmi *et al.*, 2016; Ogden *et al.*, 2019). Although improved reporting and increased awareness are likely contributory factors (Orloski *et al.*, 1998; Aenishaenslin *et al.*, 2016), there is a strong consensus among entomologists that these epidemiologic trends reflect the collective impact of environmental drivers that increase the likelihood of human encounters with infected ticks

(Eisen *et al.*, 2016; Stone *et al.*, 2017). Among the most important of these are (i) climate-mediated expansion of tick habitats (Ostfeld and Brunner, 2015; Dumic and Severini, 2018), (ii) dispersal of infected *I. scapularis* by migratory birds (Olsen *et al.*, 1995; Brinkerhoff *et al.*, 2011; Hasle *et al.*, 2011), (iii) increased densities of vertebrate reservoirs and deer populations upon which *I. scapularis* feed and mate as lands cleared for agriculture become reforested (Eisen and Eisen, 2018), and (iv) the increased risk of transmission associated with decreased biodiversity in endemic areas (LoGiudice *et al.*, 2003; Granter *et al.*, 2014; Ruyts *et al.*, 2016). In short, one cannot divorce environmental factors fueling the proliferation of *B. burgdorferi* *sensu lato* in the wild (Gern, 2008) from their cumulative effects on human populations (Schwartz *et al.*, 2017; Rosenberg *et al.*, 2018).

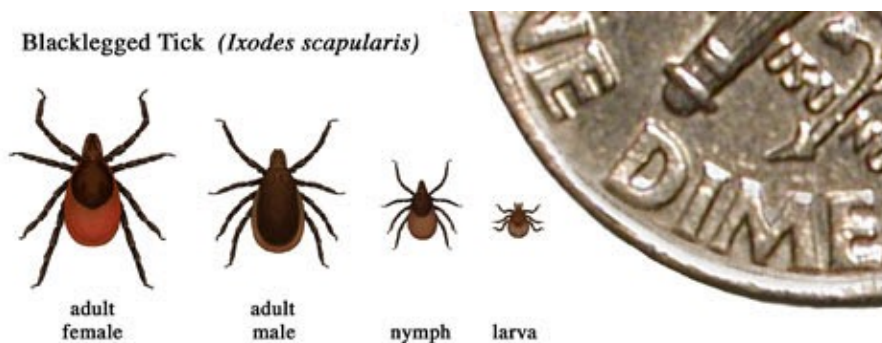


Figure 3. *Ixodes scapularis* stages.

Lyme disease also is the most prevalent vector-borne illness in Europe, where it is widely, though nonuniformly, distributed (Hubalek, 2009; Rizzoli et al., 2011; Sykes and Makiello, 2017). Remarkably, Lyme disease is not a mandatory notifiable disease in many European countries, complicating country by country comparison of epidemiologic data (van den Wijngaard et al., 2017). Although methods used to acquire surveillance and laboratory data vary greatly (van den Wijngaard et al., 2017), an estimated 85,000 cases occur each year throughout Europe (Sykes and Makiello, 2017). In Europe, as in the U.S., new cases peak in the summer months of June through August (Hubalek, 2009), and underreporting is believed to be common (van den Wijngaard et al., 2017). In Northern Europe, disease rates are highest in the Baltic states and Southern Sweden; in Central Europe, highest incidences are in Austria and Slovenia (Hubalek, 2009; Rizzoli et al., 2011; Sykes and Makiello, 2017). At the southern limits of the disease range (e.g., Italy and the Balkans), incidence decreases rapidly from north to south (Hubalek, 2009). Disease rates across the Continent parallel the densities of *I. ricinus* ticks affected with the pathogenic species most frequently detected in patients, *B. afzelii* and *B. garinii* (Coipan et al., 2016; Strnad et al., 2017; Estrada-Pena et al., 2018). Lyme disease rates are increasing in Europe for the same reasons as in North America—increased awareness (Smith and Takkinen, 2006), coupled with increasing distribution and abundance of *I. ricinus* due to the same environmental drivers, with climate change probably a major culprit (Medlock et al., 2013; Semenza and Suk, 2018).

Ecology

Although ticks capable of vectoring Lyme disease spirochetes often take their blood meals from humans, humans are not required for perpetuation of either ticks or spirochetes in nature. Humans are incidental, presumably “dead-end,” hosts that become infected when their lifestyles or activities intersect with habitats harboring spirochetes (Gern, 2009; Radolf et al., 2012; Eisen and Eisen, 2018). Only ticks belonging to the hard tick genus *Ixodes* are vector competent, that is, capable of acquiring and transmitting spirochetes (Lane et al., 1991; Gern, 2009; Eisen and Eisen, 2018). *B. burgdorferi* sensu lato is transmitted mainly by ticks of the *Ixodes ricinus* complex (Burgdorfer et al., 1991; Piesman and Gern, 2004) (also see Radolf and Samuels, 2021), *I. scapularis* in the Northeastern and Upper Midwestern United States; *I. pacificus* on the Pacific Coast; *I. ricinus* in Europe, Western Asia, and North Africa; and *I. persulcatus* in Eastern Europe and Asia (Gern, 2009; Mannelli et al., 2012; Franke et al., 2013). *Ixodes* ticks have a two-year life cycle with four life stages: egg, larva, nymph and adult (Figure 3). Ticks are born uninfected. Larvae acquire the spirochete by feeding on an infected reservoir host, and, after molting to the nymphal stage, transmit the pathogen when they feed on an uninfected reservoir or incidental host (Figure 4) (Gern, 2009; Radolf et al., 2012; Eisen and Eisen, 2018). The dependence of *B. burgdorferi* sensu lato on efficient transstadial transmission for long-term survival is an important distinction from relapsing fever spirochetes, which can be maintained within their argasid vectors by vertical or transovarial transmission (Barbour and Hayes, 1986; Rollend et al., 2013) (also see Radolf and Samuels, 2021).

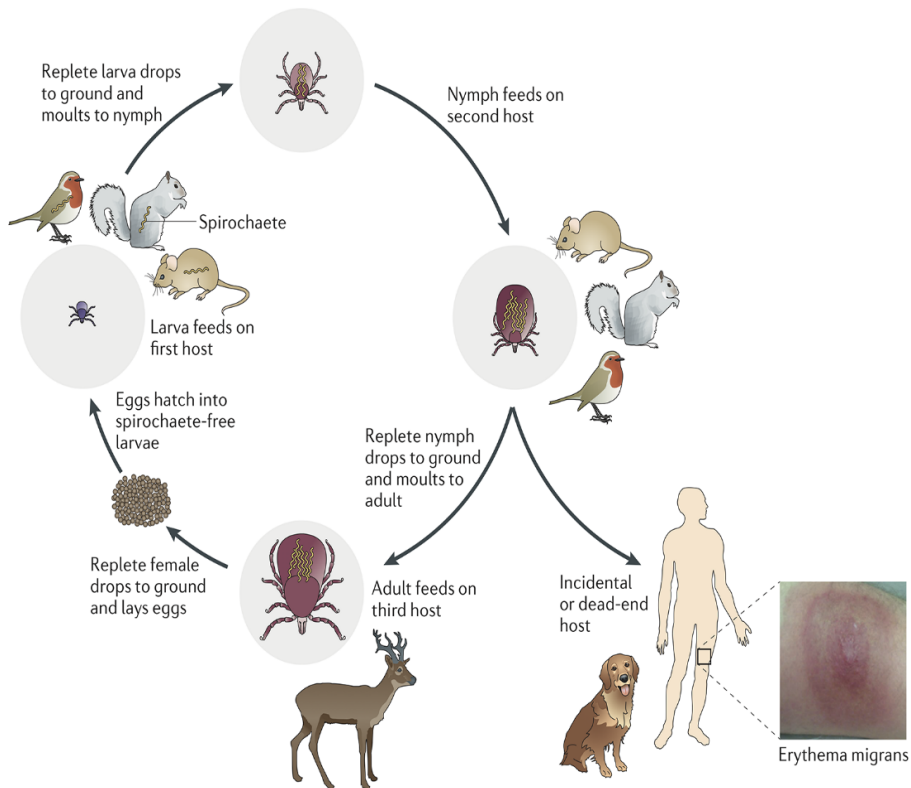


Figure 4. The enzootic cycle of *Borrelia burgdorferi*. *Ixodes* ticks undergo a three-stage life cycle (larva, nymph and adult, with one blood meal per stage). Larval ticks acquire spirochetes by feeding on an infected reservoir animal, and the bacterium is retained during the subsequent stages. Transmission of spirochetes to a competent reservoir host by a feeding nymph perpetuates the enzootic cycle for the next generation of larval ticks. Adult ticks are not important for maintenance of *B. burgdorferi* in the wild; however, deer are important for maintenance of the tick population because adult ticks mate on them. Nymphs are responsible for the vast majority of spirochete transmission to humans, generally considered dead-end hosts, as are dogs. (Reprinted with permission from Radolf et al. 2012.)

Nymphal ticks are responsible for the majority of human infections (Piesman et al., 1987a; Falco et al., 1996; Dennis and Hayes, 2002). In addition to having high infection rates, nymphs quest during the summer months when humans are most likely to be outdoors and, because of their small size (approximately that of a poppy seed), are difficult to detect on body surfaces, clothing, and pets (Dennis and Hayes, 2002). Not surprisingly, the risk of infection for humans correlates with infection rates in vectors and reservoir hosts as well as tick density (Mather et al., 1996; Stafford et al., 1998; Falco et al., 1999; Pepin et al., 2012).

Immature ticks (larvae and nymphs) have a broad host range, including rodents, insectivores, birds, lagomorphs, and ungulates (LoGiudice et al., 2003; Ogden et al., 2008). Besides explaining how humans acquire infection, the aggressive feeding behaviors of these non-nidicolous (openly host-seeking) generalists enhance the opportunities for transmission of spirochetes amongst infection-competent vertebrates, linkage of ecological niches, and expansion of the geographic range of the disease (Kurtenbach et al., 2006). Although adult stage ticks have a twofold greater prevalence of infection than

nymphs (Schwartz et al., 1997), they are much less important as vectors of human disease because adult males do not feed, and adult females usually feed on large reservoir-incompetent animals, typically white-tailed deer (Anderson, 1988; Kurtenbach et al., 2006). Furthermore, adults quest in late autumn through early spring when humans are less apt to encounter them and more apt to be wearing protective clothing (Falco et al., 1999; Dennis and Hayes, 2002). The western black-legged tick, *Ixodes pacificus*, is the primary vector of Lyme disease on the Pacific Coast (Campagna et al., 1983; Lane et al., 2007). Because *I. pacificus* larvae and nymphs preferentially feed on *B. burgdorferi*-refractory lizards (Lane and Loye, 1989; Lane and Quistad, 1998), infection rates in *I. pacificus* ticks are low (Lane et al., 2013; Rose et al., 2019), with a corresponding decrease in regional prevalence of human disease. Natural transmission cycles exist in non-endemic regions of the United States but are of lesser importance for humans because they involve reservoir hosts in remote geographic areas, less vector-competent *Ixodes* species, tick species with narrow host ranges that tend not to bite humans, and/or *Borrelia* species with limited infectivity for humans (Maupin et al., 1994; Dolan et al., 1997; Norris et al., 1999; Oliver et al., 2003; Franke et al., 2013).

Animals are reservoir competent if they become infected following the bite of an infected tick and can re-transmit the pathogen to a naïve vector (Mather et al., 1989; Hanincova et al., 2006; Brunner et al., 2008). In the case of Lyme disease, infection in a reservoir host must be of long enough duration to serve as a blood meal source for more than one tick life stage. As eloquently stated by Barbour (Barbour, 2017), what this (i.e., reservoir competence) “effectively means is usually a combination of resistance to and tolerance of infection in reservoir hosts of long-standing.” *Peromyscus leucopus*, the white-footed mouse, which thrives in habitats ranging from pristine forest to degraded woodlots, is a principal reservoir in the Northeast and North Central United States (Donahue et al., 1987; LoGiudice et al., 2003; Barbour, 2017). Once infected with *B. burgdorferi*, *P. leucopus* can remain infected for life without end-organ pathology (i.e., inflammatory response) or decreased longevity (Moody et al., 1994; Oliver et al., 2003; Schwanz et al., 2011; Voordouw et al., 2015) – dual indicators of a high degree of tolerance. Despite *B. burgdorferi*’s reputation as a “generalist” pathogen (Hanincova et

al., 2006), not all *I. scapularis* blood meal hosts are equally competent reservoirs; moreover, evidence exists that tick hosts other than *P. leucopus* (e.g., shrews and chipmunks) can contribute to the maintenance of enzootic cycles in endemic areas (LoGiudice et al., 2003; Kurtenbach et al., 2006; Brisson et al., 2008; Franke et al., 2013). The degree of biodiversity in a given locale, more specifically, the relative proportions of competent and incompetent species, is a major determinant of the transmission risk for humans (LoGiudice et al., 2003; Granter et al., 2014; Ruyts et al., 2016). As noted earlier, in recent years, there has been growing appreciation of passerine birds as both reservoir hosts and vehicles for dissemination of infected ticks (Richter et al., 2000; Hasle et al., 2011; Norte et al., 2013). *I. ricinus*, the sheep tick, is the principal vector for Lyme disease spirochetes isolated from European patients (Gern, 2009). This tick is widely distributed throughout Europe with a range extending from Ireland to the Urals and from Southern Sweden to North Africa (McCoy et al., 2013; Cull et al., 2018; Estrada-Pena et al., 2018). The spatial prevalence of spirochete-infected *I. ricinus* ticks differs considerably and can be quite patchy even in areas with high overall densities (Estrada-Pena et al., 2018). According to a recent meta-analysis (Strnad et al., 2017), the highest rate of infected ticks was found in Central Europe and the lowest in the British Isles. *B. afzelii* and *B. garinii*, the genospecies most frequently associated with disease in European patients (Staneek and Strle, 2018), are the most commonly identified in questing *I. ricinus* nymphs (Rauter and Hartung, 2005; Estrada-Pena et al., 2018). The vector ecology of Lyme disease in Europe is even more complicated than in North America because of the greater diversity of European *Borrelia* populations (discussed below) and differences in reservoir host preferences (Gern, 2009; Mannelli et al., 2012; Franke et al., 2013). Small mammals, ground-foraging birds, and reptiles are common hosts for the larval and nymphal stages of *I. ricinus*, while adults (females) feed mostly on large mammals such as ungulates; both immature and adult stages will attach to humans (Gern, 2002). Only a small number of the more than 300 vertebrates serving as blood meal hosts for questing *I. ricinus* ticks are reservoir competent (Gern, 2009; Mannelli et al., 2012). Whereas both rodents and birds can serve as reservoirs for *B. burgdorferi* (Kurtenbach et al., 2006), *B. afzelii* depends mainly on rodents (mice and voles), while *B. garinii* depends on birds (Comstedt et al., 2011; Mannelli et al., 2012). Thus, *I.*

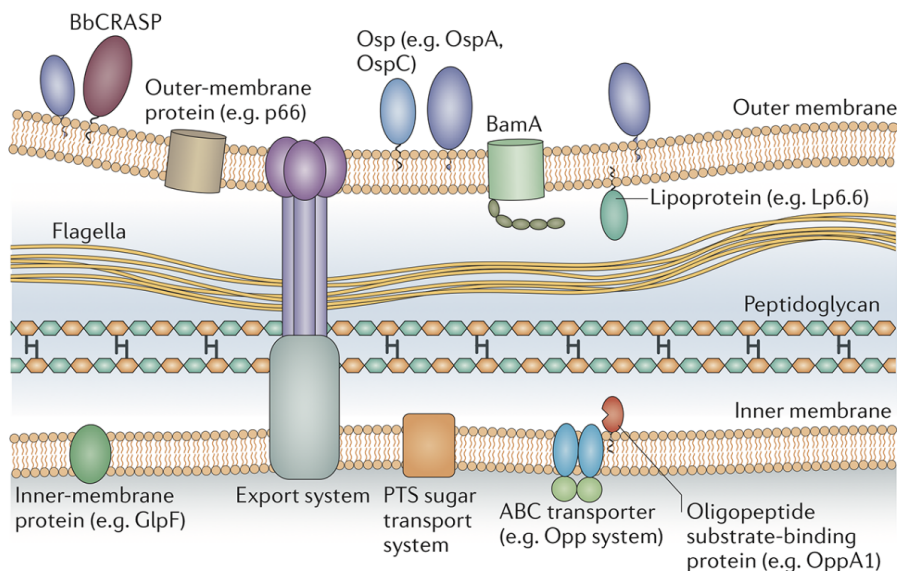


Figure 5. The borrelial cell envelope. The outer membrane contains outer-surface lipoproteins (Osps) in high density and β -barrel outer-membrane-spanning proteins such as BamA in low density. The inner membrane is rich in integral membrane proteins, many of which are transporters. BbCRASP, complement regulator-acquiring surface protein; OppA1, oligopeptide permease A1; PTS, phosphotransferase system. Reprinted with permission from Radolf et al. 2012.

ricinus can be likened to a “mixing vessel” for different *Borrelia* strains and species, with host associations driven by the filtering effect of spirochete selectivity for particular vertebrates, rather than adaptation of the bacterium to a vector with narrow feeding preferences (Margos et al., 2011). Two additional tick species, *I. hexagonus* and *I. uriae*, maintain the spirochete in transmission cycles separate from those of *I. ricinus*. *I. hexagonus* has a more restricted host range than *I. ricinus*, feeding primarily on carnivores, such as foxes and mustelids, occasionally on lagomorphs, and rarely birds (Gern, 2002). Transmission cycles involving *I. uriae*, a seabird specialist that feeds on a range of avian marine species, have been implicated in global dispersal of *B. garinii* (Olsen et al., 1993; Olsen et al., 1995; Comstedt et al., 2011; Munro et al., 2019).

The spirochete

The spirochete-host interface - the outer membrane
Like all spirochetes (Holt, 1978), *B. burgdorferi* is a diderm consisting of an outer membrane (OM) that surrounds the periplasmic space, the peptidoglycan, the cytoplasmic membrane, and the protoplasmic

cylinder (Figure 5) (Barbour and Hayes, 1986; Charon et al., 2009). The organelles of motility, the flagella, are contained entirely within the periplasmic compartment (Charon et al., 2012). In addition to propagating a planar wave that enables the spirochete to penetrate collagen matrices in connective tissue and endothelial junctions (Norman et al., 2008; Charon et al., 2012; Harman et al., 2012; Harman et al., 2013), the flagellar filaments also serve a cytoskeletal function (Charon et al., 2012). As they wind around the protoplasmic cylinder, they push against the elastic peptidoglycan sacculus, bending it to create the cell's distinctive flat-wave morphology (Motaleb et al., 2000; Charon et al., 2009) (also see Radolf and Samuels, 2021).

The *B. burgdorferi* OM comprises the host-pathogen interface in all milieus through which the spirochete transits or in which it takes up final residence; it is not surprising, therefore, that this structure has attracted great interest over the years (Barbour and Hayes, 1986; Kenedy et al., 2012; Radolf et al., 2012; Zuckert, 2019) (also see Radolf and Samuels, 2021). Because of its double-membrane architecture, *B.*

burgdorferi often has been likened to Gram-negative bacteria. This analogy is inaccurate from the standpoints of phylogenetics (Paster et al., 1991; Daubin et al., 2002), ultrastructure (Radolf et al., 2012; Zuckert, 2019), composition (LaRocca et al., 2010; Radolf et al., 2012; LaRocca et al., 2013), and genomics (Fraser et al., 1997; Casjens et al., 2000; Stewart et al., 2005; Qiu and Martin, 2014). The OM of Gram-negative bacteria is an asymmetric bilayer composed of glycerophospholipids in the inner leaflet and the highly inflammatory glycolipid lipopolysaccharide (LPS) in the outer (Konovalova et al., 2017). Early reports that *B. burgdorferi* contains LPS (Beck et al., 1985; Habicht et al., 1986) were disproved, initially by chemical and immunological analysis (Takayama et al., 1987; Radolf et al., 1991), and subsequently by genomic sequencing (Fraser et al., 1997). The absence of LPS has important clinical ramifications inasmuch as spirochetemic Lyme disease patients rarely, if ever, manifest sepsis-like pathophysiology comparable to that seen in patients with Gram-negative bacteremia (Wormser et al., 2005; Wormser, 2006). Consequently, the presence of a sepsis syndrome in a Lyme disease patient should prompt a search for co-infections, such as babesiosis and anaplasmosis, also transmitted by ixodid ticks (Sanchez et al., 2016).

The OM of *B. burgdorferi* differs in other important respects from its Gram-negative counterparts: (i) It is much more easily damaged during routine laboratory manipulations (e.g., centrifugation and resuspension) and is far more susceptible to detergent solubilization (Brusca et al., 1991; Cox et al., 1996). (ii) It contains a much lower density of proteins with membrane-spanning domains, as assessed by freeze-fracture electron microscopy (Walker et al., 1991; Radolf et al., 1994). (iii) Although proteins with porin-like properties and function have been identified in the *B. burgdorferi* OM (Pinne et al., 2004; Pinne et al., 2007; Barcena-Uribarri et al., 2013; Kenedy et al., 2014), the bacterium does not contain orthologs for well-characterized Gram-negative porins (Fraser et al., 1997; Nikaido, 2003; Kenedy et al., 2016). (iv) The spirochete, however, does contain orthologs for TolC and the other components of an ATP-dependent efflux pump shown to contribute to the bacterium's inherent antimicrobial resistance (Bunikis et al., 2008). (v) Though lacking LPS, *B. burgdorferi* OM contains three abundant (comprising 50-60% of total lipids), immunogenic, but non-inflammatory, lower molecular weight glycolipids – cholesteryl- β -D-galactopyranoside, cholesteryl 6-O-acyl- β -D-

galactopyranoside, and mono- α -galactosyl-diacylglycerol (Wheeler et al., 1993; Norgard et al., 1996; Ben-Menachem et al., 2003; Kinjo et al., 2006; Schroder et al., 2008; Huang et al., 2016). The cholesterol glycolipids spontaneously phase partition from the other lipids, forming lipid rafts or microdomains into which segregates a subset of outer surface lipoproteins (LaRocca et al., 2010; Toledo et al., 2014; Huang et al., 2016). Surprisingly, *B. burgdorferi* contains an ortholog for LptD, the outer membrane protein in Gram-negative bacteria that inserts newly exported LPS into the outer membrane (Botos et al., 2016); it is tempting to speculate that *Borrelia* appropriated the Gram-negative LPS transport pathway to serve its own needs – localization of glycolipids to the OM. (vi) Arguably, the most notable difference is the number and variety of lipoproteins that adorn the borrelial surface (Kenedy et al., 2012; Radolf et al., 2012; Dowdell et al., 2017). In Gram-negative microorganisms, lipoproteins typically are anchored to the inner leaflet of the outer membrane or the periplasmic leaflet of the cytoplasmic membrane and not exported to the bacterial surface (Zuckert, 2014; Konovalova et al., 2017). Although the tertiary structures of borrelial outer surface lipoproteins differ considerably (Li et al., 1997; Eicken et al., 2001; Kumaran et al., 2001; Eicken et al., 2002; Brangulis et al., 2018), their membrane topologies are identical. They are soluble polypeptides tethered to the external leaflet of the outer membrane by N-terminal lipids (Jones et al., 1995). This topological configuration presumably enables *Borrelia* to differentially express the enormous number of surface structures needed to sustain its dual-host lifestyle and helps explain its ability to infect a wide variety of vertebrate hosts (Wywiał et al., 2009; Radolf et al., 2012; Brisson et al., 2013; Brissette and Gaultney, 2014; Caine and Coburn, 2016; Tufts et al., 2019).

Differential gene expression – tick transmission and back again

Because animals syringe-inoculated with *in vitro*-cultivated organisms develop manifestations indistinguishable from animals inoculated with ticks (Barthold et al., 2010), the arthropod phases of the bacterial life cycle might be considered irrelevant to pathogenesis. However, in the real world, Lyme disease spirochetes are transmitted by ticks and, therefore, the tick-mammal interface must be regarded as the starting point for the infectious process (Tilly et al., 2008; de Silva et al., 2009; Radolf et al., 2012; Steere et al., 2016) (also see

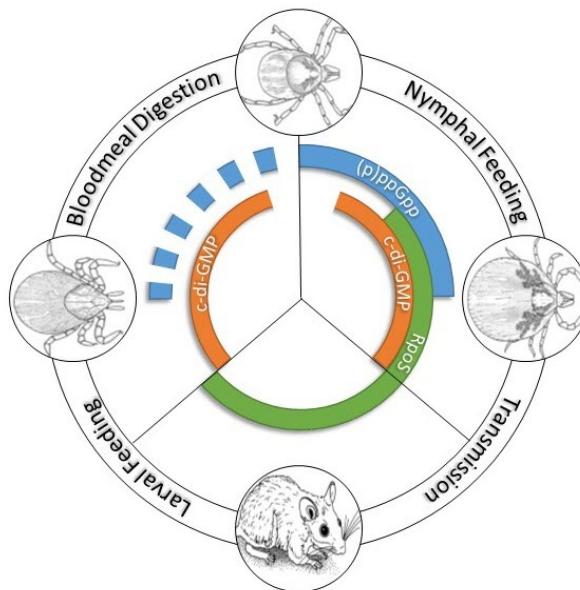


Figure 6. *B. burgdorferi* gene regulatory programs throughout the enzootic cycle. The second messengers (p)ppGpp and cyclic di-GMP regulate gene expression during the tick phases of the cycle. RpoS transcribes genes required for transmission (nymphal blood meal) and infection of the vertebrate reservoir. RpoS is OFF in unfed ticks and feeding larvae. (Figure courtesy of Dr. Ashley Groshong).

Radolf and Samuels, 2021). Indeed, there is now overwhelming evidence that spirochetes in feeding ticks undergo complex alterations in their transcriptional and protein profiles that are not reproduced by *in vitro* culture conditions (Cugini et al., 2003; Iyer et al., 2015; Caimano et al., 2016; Stevenson and Seshu, 2018). Collectively, these changes enable the spirochete to adapt physiologically to the feeding midgut environment (He et al., 2011; Pappas et al., 2011; Dunham-Ems et al., 2012; Caimano et al., 2015; Bontemps-Gallo et al., 2016; Caimano et al., 2016), while, at the same time, preparing it for challenges looming during the mammalian phase (Grimm et al., 2004; Fisher et al., 2005; Dunham-Ems et al., 2012). They also promote binding to the bacterial surface of serum proteins that exploit mammalian proteolytic systems to facilitate dissemination from tick to mammal (Hu et al., 1995; Coleman et al., 1997; Onder et al., 2012) and protect against complement-mediated lysis (Kraiczy, 2016b; Zhi et al., 2018; Xie et al., 2019). The obligatory time course for this programmatic sequence explains why spirochetes are infrequently transmitted to mice (Piesman et al., 1987b; Ohnishi et al., 2001;

Dunham-Ems et al., 2009) or humans (Berger et al., 1995; Falco et al., 1996; Sood et al., 1997; Nadelman et al., 2001) when ticks are attached for less than 48 h. It is critical for physicians to be aware of this time frame because it establishes the window of opportunity for antimicrobial prophylaxis (Nadelman et al., 2001; Wormser, 2006) and can be used to provide re-assurance to individuals who removed recently attached ticks that their risk of infection is low.

Our understanding (albeit still rather limited) of the genetic regulatory mechanisms that control the infectious process (Figure 6) dates back to the seminal discovery by Schwan and co-workers (Schwan et al., 1995) that OspC, an outer surface lipoprotein *B. burgdorferi* requires to establish mammalian infection (Grimm et al., 2004; Tilly et al., 2006; Dunham-Ems et al., 2012), is upregulated within the nymphal midgut during the blood meal. They also noted that this phenomenon can be mimicked by shifting from ambient to mammalian body temperature during *in vitro* cultivation. The Norgard group's description of the RpoN/RpoS

master regulatory pathway in a series of landmark papers (Hubner et al., 2001; Yang et al., 2003; Ouyang et al., 2009) provided mechanistic insight into these observations. Following a temperature shift *in vitro*, or at the outset of the nymphal blood meal in nature (Caimano et al., 2007), the spirochete's alternative sigma factor RpoN works in concert with the response regulator Rrp2 and the Fur/PerR ortholog, BosR, to transcribe *rpoS*, the downstream "effector" sigma factor (for a complete discussion see Radolf and Samuels, 2021). Although RpoS was shown originally to transcribe just *ospC* and the *dbpA* gene encoding decorin-binding protein A (DbpA), another virulence determinant (Guo et al., 1995; Hagman et al., 1998; Fischer et al., 2003), we now know that the RpoS regulon encompasses approximately 10% of the *B. burgdorferi* genome, and includes many genes of unknown function (Caimano et al., 2007; Caimano et al., 2019). In *Escherichia coli*, activation of RpoS induces a complex, coordinated adaptive response involving a large cohort of genes that enables the bacterium to resist abiotic, physiological and environmental stresses (Chiang and Schellhorn, 2010; Hengge, 2011). The *B. burgdorferi* RpoS regulon, in contrast, contains only a handful of genes with discernible roles in physiology and stress responses (Caimano et al., 2007; Caimano et al., 2019). Organisms lacking RpoS are avirulent by tick- as well as needle-inoculation (Caimano et al., 2004; Fisher et al., 2005; Hyde et al., 2009; Ouyang et al., 2009; Xu et al., 2010; Dunham-Ems et al., 2012), implying that the RpoN/RpoS pathway regulates genes that promote dissemination within the tick as well as genes that function within the mammal. In contrast to the RpoS regulon in mammals, the cohort of genes controlled by the RpoN/RpoS pathway within feeding ticks is poorly defined. Gilmore's group has identified two RpoS-dependent genes, *bba64* and *bba66*, required for tick transmission (Gilmore et al., 2010; Patton et al., 2013).

Following inoculation into the dermis of its naïve vertebrate host, the spirochete must solidify its foothold at the bite site via a poorly understood program for differential gene expression with multiple regulatory layers designated by the umbrella term "mammalian host adaptation" (Barthold et al., 1995; Montgomery et al., 1996; Akins et al., 1998) (see Radolf and Samuels, 2021). One involves turning OFF pathways that enable spirochetes to survive the many noxious aspects of the blood meal (Bontemps-Gallo et al., 2016); principal among these is the Hk1/

Rrp1 two-component system that signals via the pleiotropic effector molecule cyclic-di-GMP (Hengge, 2009; He et al., 2011; Kostick et al., 2011; Caimano et al., 2015). Whether the absence of a tick-specific environmental signal or the appearance of a new mammalian host-derived cue(s) turns OFF synthesis of c-di-GMP by the diguanylate cyclase Rrp1 remains a matter of conjecture. The RpoN/RpoS pathway plays two critical, inter-dependent roles in mammalian host adaptation. First, it represses σ^{70} -dependent tick-phase genes (Caimano et al., 2005; Caimano et al., 2007; Caimano et al., 2019), the midgut colonization factor OspA (de Silva et al., 1996; Pal et al., 2004a; Yang et al., 2004) being the prototype. This so-called "gatekeeper" repressor function of RpoS appears to work in tandem with the loss of c-di-GMP signaling to terminate expression of tick-phase genes (Caimano et al., 2019). For reasons that have yet to be determined, not all tick-phase genes (e.g., *ospA* and *lp6.6*) repressed by RpoS are upregulated by c-di-GMP. Although it is often stated that downregulation of OspA occurs within the tick in response to the blood meal (Pal et al., 2004a; Tilly et al., 2008; Caine et al., 2017), multiple lines of evidence argue that it is delayed until spirochetes reach the mammal (Belperron and Bockenstedt, 2001; Ohnishi et al., 2001; Mulay et al., 2009; Adams et al., 2017; Caimano et al., 2019). In other words, the reciprocal relationship between the expression of OspA and OspC is a mammalian host phase, not tick phase, phenomenon (Montgomery et al., 1996). RpoS-mediated downregulation of OspA and other immunogenic tick-phase lipoproteins explains why infection fails to generate antibodies against them (Gern et al., 1993; Golde et al., 1993; Brunet et al., 1995; Piesman et al., 1997; Vaz et al., 2001).

As noted already, the RpoN/RpoS pathway also upregulates expression of gene products required for infectivity. Of these, the lipoproteins OspC, DbpA/B, and BBK32 are by far the most extensively explored (Radolf et al., 2012; Groshong and Blevins, 2014; Caine and Coburn, 2016). The X-ray crystal structure of OspC, solved independently by two groups nearly twenty years ago, revealed an elongated, α -helical homodimer with putative ligand-binding sites at the distal "crown" of the dimer and at the interface between two opposing helices of the monomers (Eicken et al., 2001; Kumaran et al., 2001; Earnhart et al., 2010). The relationship(s) between this structure and OspC's reported biological functions remains enigmatic. Along with directly recruiting the immunosuppressive tick salivary protein SALP15 to

the bacterial surface (Anguita et al., 2002; Ramamoorthi et al., 2005; Hovius et al., 2008a), OspC interferes with innate clearance mechanisms (Stewart et al., 2006), putatively preventing phagocytosis by macrophages (Carrasco et al., 2015), and serves as a surface receptor for plasminogen (Lagal et al., 2006; Onder et al., 2012) and complement inhibitors (Caine et al., 2017) (see Radolf and Samuels, 2021). DbpA and B are adhesins for decorin, heparan, dermatan sulfate, heparan sulfate, and glycosaminoglycans (GAGs) (Guo et al., 1998; Brown et al., 2001; Fischer et al., 2003; Pikas et al., 2003; Morgan and Wang, 2013). BBK32 is an adhesin, binding fibronectin and GAGs (Probert et al., 2001; Seshu et al., 2006; Moriarty et al., 2012; Lin et al., 2015), and an inhibitor of the classical complement pathway (Garcia et al., 2016; Xie et al., 2019). Whereas OspC functions primarily or exclusively at the bite site and is downregulated several weeks after infection due to the immune pressure exerted by the appearance of OspC antibodies (Liang et al., 2002; Tilly et al., 2006), DbpA/B and BBK32 function “downstream”, facilitating hematogenous dissemination and spirochete tropisms for heart and joints (Brown et al., 2001; Norman et al., 2008; Weening et al., 2008; Hyde et al., 2011; Moriarty et al., 2012; Fortune et al., 2014; Lin et al., 2014; Caine and Coburn, 2015; Lin et al., 2015; Ebady et al., 2016). Elegant studies by Moriarty’s group (Moriarty et al., 2012) revealed that BBK32 exerts its fibronectin and GAG binding activities in a sequential manner. Tethering to fibronectin on the endovascular surface recruits spirochetes from the circulating blood compartment, while binding to GAGs stabilizes interactions with endothelial cells, setting the stage for transmigration between endothelial cells (Szczepanski et al., 1990; Coleman et al., 1995). DbpA/B and BBK32 are just two elements of *B. burgdorferi*’s complicated adhesin story. Lyme disease spirochetes express a bewildering array of surface molecules with redundant ligand-binding activities; whether they work cooperatively or preferentially depending on the milieu and host infected is simply not understood (Caine and Coburn, 2016). This wide assortment of adhesins may help to determine the range of vertebrate hosts, including humans, that a borrelial species and, even strains within a species, can parasitize (Tufts et al., 2019).

Correct expression of adhesins in time and space is just one facet of the pathogenic process. Spirochetes deploy an arsenal to persist long enough in the

reservoir to transit back to the vector when opportunity “knocks” in the form of a larva taking a blood meal. Such “persistence functionalities” include (i) directed motility to locate and penetrate dermal blood vessels following deposition and negotiate endovascular and tissue barriers at metastatic sites, all in response to chemotactic signals not even remotely understood (Charon et al., 2012; Motaleb et al., 2015; Hyde, 2017); (ii) expression of the proper combination of outer and inner membrane transporters to appropriate the huge spectrum of nutrients “generously” supplied by the vertebrate host to support the bacterium’s extremely limited biosynthetic capacity (Fraser et al., 1997; Gherardini et al., 2010; Corona and Schwartz, 2015); (iii) adjustment of central metabolism to take maximal advantage of the nutrients available within the various micro-environments in which it takes up residence (Corona and Schwartz, 2015; Iyer et al., 2015; Groshong et al., 2017), all while fending off innate and subsequently adaptive defenses, particularly complement (Kraiczky, 2016b; Tracy and Baumgarth, 2017) and antibodies (Norris, 2014; Stone and Brissette, 2017), as an “exposed” parasite within the extracellular milieu (Radolf et al., 2012). (Please see Radolf and Samuels, 2021, for comprehensive reviews of motility/chemotaxis, virulence, and immune evasion mechanisms.)

Upon larval acquisition, the RpoN/RpoS pathway rapidly shuts OFF, the HK1/Rrp1 pathway rapidly turns ON, and expression of tick-phase genes resumes, enabling successful colonization of the vector (Donahue et al., 1987; Yang et al., 2004; Caimano et al., 2015; Iyer et al., 2015; Caimano et al., 2019). How often do spirochetes execute this complex maneuver in humans? Although there is no question that Lyme disease spirochetes can persist in untreated humans and give rise to disease manifestations well after inoculation (Steere et al., 2016; Stanek and Strle, 2018), there are no reliable data as to whether persistence in humans is a common or rare occurrence. Are humans dead-end hosts because they are incompetent reservoirs or poorly accessible targets of opportunity for larvae? The biology underlying this question has clinical relevance. The technique called xenodiagnosis – allowing naïve larvae to feed on subjects to assess infection status (Telford et al., 2014) – is being used to determine whether individuals who remain symptomatic following treatment for Lyme disease (see below) harbor spirochete “persisters” (Marques et al., 2014). The rationale for xenodiagnosis as a

diagnostic tool becomes cloudy if untreated individuals cannot infect ticks (Bockenstedt and Radolf, 2014).

Phylogenetic diversity and human disease

Taxonomy and disease

Borrelia species fall into two major phyletic clusters, each with considerable heterogeneity (Bunikis et al., 2004; Cutler et al., 2017; Stone et al., 2017). One contains the relapsing fever spirochetes. With the notable exceptions of the louse-borne agent of endemic relapsing fever, *B. recurrentis*, and the *I. ricinus* complex-borne *B. miyamotoi*, relapsing fever spirochetes are transmitted by soft-bodied, argasid ticks (see Radolf and Samuels, 2021). The other cluster contains the agents of Lyme disease. The recognition by the early 1990s that multiple *Borrelia* species cause Lyme disease led to the designation of this cluster as the *Borrelia burgdorferi* sensu lato complex and the original isolate as *B. burgdorferi* sensu stricto (herein *B. burgdorferi*). Presently, the sensu lato complex comprises at least 20 proposed or confirmed species worldwide, nine of which have been found to cause human disease: *B. burgdorferi*, *B. afzelii*, *B. garinii*, *B. bavariensis*, *B. spielmanii*, *B. lusitanae*, *B. bissetii*, *B. valaisiana*, and *B. mayonii* (Belfaiza et al., 1993; Wang et al., 1999a; Schotthoefler and Frost, 2015; Pritt et al., 2016; Cutler et al., 2017). However, the great majority of human Lyme disease cases are due to four pathogenic species, namely *B. burgdorferi* sensu stricto, *B. afzelii*, and *B. garinii* and the closely related *B. bavariensis*. Other species have been detected in specimens from only a few patients or, in single cases, which raises questions regarding their importance in the pathogenesis of human disease. In contrast to the United States, Lyme borreliosis in Europe is caused predominantly by *B. afzelii*, *B. garinii*, *B. bavariensis* (formerly *B. garinii* OspA type 4) and only rarely by *B. burgdorferi* (Stanek and Strle, 2018). As noted earlier, *B. afzelii* depends mainly on rodents as reservoir hosts, while *B. garinii* (as well as *B. bavariensis*) preferentially parasitizes birds (Comstedt et al., 2011; Mannelli et al., 2012). *In vitro* susceptibility to rodent versus avian complement has been invoked to explain these differences (Kraiczy, 2016b).

B. burgdorferi was thought to be the sole genospecies in the United States until 1995 when Marconi and associates (Marconi et al., 1995) isolated *B. andersonii* from cottontail rabbits and *I. dentatus* ticks. Subsequently, it became evident that

enzootic cycles exist involving non-sensu stricto species and “specialist” ixodid ticks with strong, selective host preferences and little or no proclivity to bite humans. Perhaps the best characterized of these is *B. bissetii* (Bissett and Hill, 1987), transmitted by *I. pacificus*, *I. affinis* and *I. spinipalpis* and recovered and/or detected by PCR throughout the United States in ticks and a variety of vertebrates (Postic et al., 1998; Picken and Picken, 2000; Piesman, 2002; Oliver et al., 2003; Margos et al., 2016) and, in rare instances, humans (Picken et al., 1996; Girard et al., 2011; Golovchenko et al., 2016; Rudenko et al., 2016). Molecular evidence for infection of humans by *B. americana* and *B. andersonii*, particularly in Southern states, also has been reported (Clark et al., 2014). Moreover, *B. mayonii* was recently isolated from a few human specimens in upper midwestern U.S. (Pritt et al., 2016). However, in the United States, *B. burgdorferi* remains the primary agent of disease.

Recently, an already confusing taxonomic situation has become controversial. A comparative genomic search for molecular signatures to distinguish relapsing fever from Lyme disease spirochetes spawned a proposal that the two clusters be placed into separate genera (Adeolu and Gupta, 2014). The genus *Borrelia* would contain just the agents of relapsing fever, along with *B. miyamotoi*, while a new genus, *Borrelliella*, would contain the agents of Lyme disease. The phylogenetic significance of these differences, and whether they justify the division, has been hotly debated (Barbour et al., 2017; Margos et al., 2017b; Margos et al., 2018; Estrada-Pena and Cabezas-Cruz, 2019). Opponents of this reclassification argue that it entails risks to public health and patient safety (Stevenson et al., 2019).

Comparison of *B. burgdorferi* sensu lato genospecies in United States and Europe

The most obvious clues that microbial genetics may be responsible for the differences in human disease have come from studies of the clinical presentation of Lyme borreliosis caused by different *Borrelia* genospecies and subspecies: in North America (*B. burgdorferi*) or Europe (namely *B. afzelii*, *B. garinii*, and *B. bavariensis*). With all four species, the first sign of infection is usually an expanding EM skin lesion (Nadelman et al., 1996; Strle et al., 1996; Steere, 2001). However, compared with *B. afzelii* or *B. garinii* infection in Europe, EM caused by *B. burgdorferi* in the U.S. is associated with a greater number of symptoms and more frequent hemato-

genous dissemination (Strle et al., 1999; Carlsson et al., 2003; Logar et al., 2004; Wormser et al., 2005; Wormser, 2006; Jones et al., 2008; Cerar et al., 2016). More pronounced differences are observed with later manifestations of disease that demonstrate *B. burgdorferi* is considerably more arthritogenic than *B. afzelii*, which usually remains localized to the skin, or *B. garinii* and *B. bavariensis*, which are predominantly associated with neurologic complications (van Dam et al., 1993; Balmelli and Piffaretti, 1995; Coipan et al., 2016; Jahfari et al., 2017; Gallais et al., 2018; Stanek and Strle, 2018; Grillon et al., 2019). An appreciation of these regional differences may help clinicians with the diagnosis and treatment of Lyme disease specific to a region. Differences in clinical presentation in North America and Europe also are observed by comparing patients infected on the two continents by *B. burgdorferi*. Infection with *B. burgdorferi* in the U.S. is associated with more symptomatic early infection compared to that in Europe, which resembles the milder infection seen with *B. afzelii* and *B. garinii*. Moreover, European *B. burgdorferi* strains appear to be more neurotropic than *B. burgdorferi* genotypes from North America and are associated with certain clinical manifestations, such as acrodermatitis chronica atrophicans, seldomly, if ever, found in the U.S. (Jungnick et al., 2015). These findings raise the intriguing possibility that strains in a region accrue similar characteristics by sharing genetic information; if so, then the feeding nymphal tick, where actively replicating strains can encounter each other, is the likely venue for such exchange.

Intraspecies genotypes are associated with distinct clinical phenotypes

B. burgdorferi can be divided into three genotypes, 16S-23S rRNA intergenic spacer types 1-3 (RST1-3), based on restriction fragment length polymorphisms of the 16S-23S rRNA intergenic spacer (IGS) (Wang et al., 1999a). OspC typing divides *B. burgdorferi* strains into ~30 genotypes (Liveris et al., 1999; Wang et al., 1999a; Wormser et al., 1999; Wang et al., 2001; Wang et al., 2002; Jones et al., 2006; Wormser et al., 2008a; Hanincova et al., 2013). The high degree of sequence variability among *ospC* genes is believed to reflect the selection of allelic variants by immunologic pressure exerted during infection of vertebrates (Wang et al., 1999b; Barbour and Travinsky, 2010; Baum et al., 2013). Individual vertebrate species serve as reservoir hosts for only a subset of OspC genotypes (Brisson and Dykhuizen, 2004; Hanincova et al., 2013; Vuong et al., 2014). A

similar situation pertains to humans – only a subset of *ospC* genotypes circulating in ticks cause human disease (Seinost et al., 1999; Dykhuizen et al., 2008; Wormser et al., 2008a; Hanincova et al., 2013). These results imply that the tick serves as an incubator for *ospC* diversity, while the vertebrates upon which infected ticks feed exert a “filtering” effect, selecting for OspCs that “match” putative ligands in the blood meal host.

OspC and RST typing systems have been particularly useful in stratifying *B. burgdorferi* strains according to clinical presentation of disease (Liveris et al., 1999; Seinost et al., 1999; Wang et al., 1999a; Wormser et al., 1999; Bunikis et al., 2004; Alghaferi et al., 2005; Jones et al., 2006; Hanincova et al., 2008; Wormser et al., 2008a; Hanincova et al., 2013). All three RST types and 24 (of over 30) OspC types of *B. burgdorferi* have been recovered from patients with Lyme disease (Liveris et al., 1999; Wang et al., 1999a; Jones et al., 2006; Wormser et al., 2008b; Jones et al., 2009; Barbour and Travinsky, 2010). More recently, multilocus sequence typing (MLST) studies have been used to further sub-stratify the strains and provide additional insights into human infection that ultimately will require comparative genomics strategies to elucidate (Jungnick et al., 2015). According to the *Borrelia* MLST Database (<https://pubmlst.org/borrelia/>), >900 MLST sequence types have been identified, of which 220 are associated with disease in humans. Use of multiple typing systems together presumably can provide more information for clinical correlations than either system alone.

Several studies have now demonstrated differential pathogenicity among various genotypes within *B. burgdorferi* (Seinost et al., 1999; Wormser et al., 1999; Wang et al., 2001; Wang et al., 2002; Jones et al., 2006; Wormser et al., 2008b; Jones et al., 2009; Strle et al., 2011b). As a generalization, RST1 genotypes contain *ospC* alleles associated with invasive disease, whereas RST3 genotypes contain predominantly noninvasive *ospC* alleles (Hanincova et al., 2008; Wormser et al., 2008a). For example, RST1 strains are more often detectable in blood in mice and humans (Wormser et al., 1999; Wang et al., 2001; Wang et al., 2002; Jones et al., 2006; Dykhuizen et al., 2008), suggesting that they disseminate more readily and/or reach higher numbers in blood. Moreover, RST1 OspC type A strains are associated with more symptomatic early infection in patients with EM, and they more frequently cause antibiotic-refractory Lyme arthritis

than other strains (Jones et al., 2009; Strle et al., 2011b). The greater disease severity and propensity for dissemination of RST1 vs RST3 genotypes was corroborated experimentally in the murine model (Wang et al., 2001; Wang et al., 2002). The data also suggest that RST1 strains are likely a contributing factor in the prevalence and severity of Lyme disease in the Northeastern U.S. (Derdakova et al., 2004; Margos et al., 2008; Hoen et al., 2009). In the mouse model, RST1 OspC type A strains have higher transmission efficiency from mice to ticks than other strains (Derdakova et al., 2004). In addition, they appear to be a recently evolved clonal lineage that may be an important factor in the emergence of the Lyme disease in the northeastern U.S. (Margos et al., 2008; Qiu et al., 2008; Hoen et al., 2009).

Like *B. burgdorferi*, only certain subsets of *B. afzelii* or *B. garinii* ospC types could be linked to human infection. Of the 14 ospC groups in *B. afzelii*, nine were found in human isolates and only two associated with invasive disease. Gallais et al. (Gallais et al., 2018) as well as Coipan et al. (Coipan et al., 2016) found a small number of *B. afzelii* sequence types associated with localized or disseminated infection. Similarly, only nine of the 22 ospC groups identified in *B. garinii* were isolated from humans, and four contained all invasive isolates. In a PCR-based comparison of tick and EM *B. afzelii* strains, Tijssen-Klasen et al. (Tijssen-Klasen et al., 2013) also found a correlation between specific IGS and ospC haplotypes in the patient samples. These results were extended by MLST analyses that indicated that only a small number of *B. afzelii* sequence types associated with localized or disseminated infection (Derdakova et al., 2004; Margos et al., 2008; Qiu et al., 2008; Hoen et al., 2009; Gallais et al., 2018).

Plasmid-encoded variable lipoproteins and host specificity

The *B. burgdorferi* genome encodes over 120 lipoproteins (Setubal et al., 2006), the large majority of which make their way to the spirochete's surface at some point during the enzootic cycle via a poorly understood secretory pathway (Kenedy et al., 2012; Dowdell et al., 2017; Zuckert, 2019); many exhibit high degrees of sequence polymorphisms presumably driven by adaptive pressures exerted by vertebrates (Roberts et al., 1998; Wywiał et al., 2009; Haven et al., 2011; Casjens et al., 2012; Brisson et al., 2013; Mongodin et al., 2013). Among these sequence variable lipoproteins are the lp56-encoded

DbpA/B paralogs; the cp32-encoded OspE/OspF/Elp, Mlp, and RevA paralogous families; and the PFam54 paralogs, many, but not all, encoded on lp54. In addition to sequence variability at specific loci, for some of these families, the mix of paralogs varies between strains (Wywiał et al., 2009; Brisson et al., 2013; Caimano et al., 2019). Importantly, variants of proteins within a family can differ functionally. For example, isogenic *B. burgdorferi* mutants expressing strain-specific DbpA variants exhibit pronounced differences in binding to GAGs and cultured kidney epithelial cells (Benoit et al., 2011) and marked differences in tissue tropisms in the murine model (Lin et al., 2014). Despite the high degree of structural similarity among Pfam54 paralogs, only one, BBA68 (CspA), binds complement inhibitory factors (Wywiał et al., 2009; Brangulis et al., 2019). Although a challenging hypothesis to test experimentally, it is now widely believed that variability in the repertoires of these host-interactive Osps is a principal determinant of differential infectivity for vertebrate species, including humans (Tufts et al., 2019). As noted above, work with OspC establishes a paradigm for this line of thinking. Another, pioneered by Kurtenbach (Kurtenbach et al., 1998; Kurtenbach et al., 2002), is that serum resistance/susceptibility determines host-range; this appealing concept has prompted investigation of an ever expanding array of complement inhibitory proteins (Garcia et al., 2016; Krawczyk, 2016a, b; Caine et al., 2017; Marcinkiewicz et al., 2019; Tufts et al., 2019; Xie et al., 2019). One can integrate these paradigms by positing that dissemination and long-term survival of *B. burgdorferi* in a particular host requires an "appropriate" combination of early survival/host adaptation Osps (e.g., OspC and anticomplementary lipoproteins) and adhesins/invasins that function during later stages of infection. It then follows that (i) whether an inoculated strain has the correct assortment of Osps to cause local or systemic human disease is a chance event and (ii) variations in Osp repertoires may give rise to different clinical manifestations. It is even conceivable that some clinical manifestations without known counterparts in nature (e.g., neuroborreliosis) are the inadvertent consequence of adaptive changes at loci functionally downstream of OspC.

Novel sequencing approaches to characterize *Borrelia* genetic diversity and its impact on phenotypic heterogeneity

Recent advances in sequencing technologies raise the possibility that deep genetic characterization of

clinical isolates may elucidate strain- and species-specific differences that promote virulence, immunogenicity, organ tropism, or persistent infection. Second-generation technologies, particularly those commercialized by Illumina, excel at “resequencing” and can produce very high-quality genomic sequences. However, the sequence reads are relatively short (36-250 bases) and cannot resolve longer genomic fragments or areas with extensive diversity. Thus, while short read approaches have been used with success to study the genome sequence of *B. burgdorferi* chromosome and conserved plasmids cp26 and lp54 (Castillo-Ramirez et al., 2016; Margos et al., 2017a; Tyler et al., 2018), they are poorly suited to the study of the less-conserved plasmids. Recently, technologies that produce longer reads have been introduced by Oxford Nanopore Technologies (ONT) and Pacific Biosciences. These methods can generate much longer sequence reads, albeit at lower sequence quality, making them unsuitable for assembly in the absence of additional high-accuracy sequence (Bashir et al., 2012; Antipov et al., 2016; Wick et al., 2017). However, the combination of these short- and long-read sequencing approaches is poised to open the full landscape of *B. burgdorferi* genomic analyses for clinical correlations. Early successes include demonstration of the utility of long-read approaches for obtaining finished sequence of plasmids (Kingry et al., 2016; Margos et al., 2017a; Jabbari et al., 2018) and a detailed study, carried out by Chaconas and colleagues, of the mutation rate and switching kinetics at the *vlsE* locus (Verhey et al., 2018).

Infection of humans

The bite site

The seminal event in the natural history of Lyme disease is, of course, the deposition of spirochetes into the skin when an infected tick, usually a nymph, feeds on a human instead of a vertebrate in the wild. Although spirochetes undergo dramatic expansion (≥ 300 -fold) within the midgut during the blood meal, only a remarkably small number manage to complete the journey from tick to vertebrate (De Silva and Fikrig, 1995; Coleman et al., 1997; Dunham-Ems et al., 2009). Along the way, they encounter myriad anatomical, biochemical, and immunological barriers that passively and actively reduce their numbers (Pal et al., 2004b; Fisher et al., 2005; Bontemps-Gallo et al., 2016; Sonenshine and Macaluso, 2017; Shaw et al., 2018). qPCR and immunofluorescence analysis yielded values of approximately 20 spirochetes per salivary gland at peak infectivity (Ohnishi et al., 2001;

Piesman et al., 2001). While this number is well below published ID₅₀ values determined using *in vitro*-cultivated organisms (Sadziene et al., 1993; Xu et al., 1996), it must be remembered, per above, that spirochetes delivered by ticks undergo dramatic transcriptomic and proteomic changes during feeding (Cugini et al., 2003; Pal and Fikrig, 2003; Drecktrah et al., 2015; Iyer et al., 2015; Caimano et al., 2016; Bernard et al., 2018; Stevenson and Seshu, 2018) in addition to exploiting the battery of pharmacologic, hemostatic, anticomplementary, and immuno-suppressive factors in the tick salivary cocktail (“saliva-assisted transmission”) (Hovius, 2009; Chmelar et al., 2016; Simo et al., 2017; Nuttall, 2019) (also see Radolf and Samuels, 2021). In recent years, tick salivary proteins that contribute to pathogen transmission have been identified (Fikrig and Narasimhan, 2006; Hovius et al., 2008b; Murfin and Fikrig, 2017; Simo et al., 2017). Of these, the multi-functional Salp15 has been the most extensively studied. In addition to inhibiting activation of naïve CD4⁺ T cells by binding to CD4 (Anguita et al., 2002; Tomas-Cortazar et al., 2017) and dendritic cells through interactions with DC-SIGN (Hovius et al., 2008a), Salp15 binds to OspC on spirochetes within saliva, protecting against antibody-mediated killing (Ramamoorthi et al., 2005). Even so, the spirochetes that do complete the journey from midgut to dermis initially have a precarious existence. In mice, dissemination does not occur if the inoculation site is excised within the first several days of tick detachment (Shih et al., 1992). Moreover, spirochetes inoculated into skin are antigenically heterogeneous and do not appear to have a uniform ability to establish infection (Ohnishi et al., 2001). At some point, they overcome the local bottleneck to colonization of their new mammalian host and dissemination (Troy et al., 2013; Rego et al., 2014). The importance of the RpoN/RpoS-regulated genes (Figure 6) and anti-complementary surface lipoproteins for early survival in the mammal was discussed above (also see Radolf and Samuels, 2021).

With their foothold established, spirochetes begin to replicate and migrate outwards along the plane of the skin and downward towards the dermal microvasculature (Figure 7) (Skare et al., 2016; Hyde, 2017). In *ex vivo* gelatin matrices that mimic the extracellular collagenous matrix spirochetes traverse *in vivo* (Zambrano et al., 2004; Dunham-Ems et al., 2009), the pathogen moves at a rapid clip, ~4 microns per second (Harman et al., 2012), far

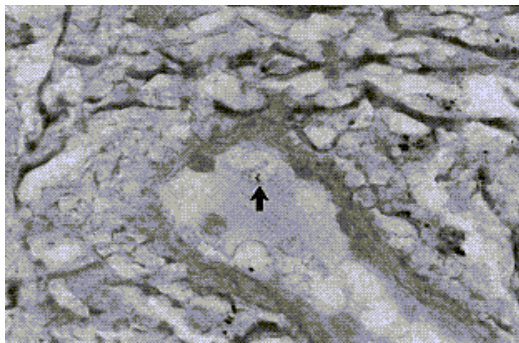


Figure 7. Silver stained biopsy from an erythema migrans lesion showing a spirochete that has penetrated a dermal venule. (Reproduced with permission from Duray, 1989b).

faster than pursuing phagocytes (Vig and Wolgemuth, 2014). Motility, however, is not uniform; spirochetes transition between a variety of motility states determined by transient adhesions, although the specific adhesins involved have yet to be identified (Harman et al., 2012). Presumably, these movements, along with PAMPs shed by live and dead organisms, trigger local danger signals that result in the accumulation of resident innate immune cells, primarily macrophages and dendritic cells, as well as the recruitment of circulating immune cells with skin-homing capacity (Mulleger et al., 2000; Salazar et al., 2003; Petzke and Schwartz, 2015; Marques et al., 2017). The ensuing inflammatory response gives rise to the hallmark skin lesion, erythema migrans (EM) (Wormser, 2006; Nadelman, 2015; Stanek and Strle, 2018). Eventually, organisms reach densities easily detected by culture, PCR (Nowakowski et al., 2001; Aguero-Rosenfeld et al., 2005; Ruzic-Sabljic and Cerar, 2017), and even histopathology (Duray, 1989b). Not surprisingly, detection of spirochetes by culture or PCR correlates with lesion size (Stupica et al., 2015). The rate of expansion of EM lesions (~20 cm² per day) is thought to reflect the speed at which spirochetes migrating away from the bite site are trailed by the local inflammatory response (Dandache and Nadelman, 2008). Along these lines, a mathematical model predicted that the rates of bacterial replication and dissemination within the dermis are the primary determinants of the rate of EM progression (Vig and Wolgemuth, 2014). A cardinal difference between Lyme disease in humans and mice is that the latter do not develop EM (Barthold, 1996); in other words,

development of EM can be considered an indication of the lack of local tolerance of humans to the presence of *B. burgdorferi*. Like humans, tick or needle-inoculated non-human primates develop EM (Philipp et al., 1993; Pachner et al., 2001; Embers et al., 2017), as do rabbits (Wheeler et al., 1989; Foley et al., 1995), another non-reservoir host species.

Asymptomatic infection

Clinical manifestations are not an inevitable outcome of tick inoculation with *B. burgdorferi*. As noted previously, seroepidemiologic studies in Lyme disease endemic areas have shown that substantial proportions of persons with antibodies to *B. burgdorferi* are asymptomatic. In Europe, asymptomatic or subclinical infection may be as common as clinically apparent disease, whereas in the U.S. only a small subset of infected patients are asymptomatic (Hanrahan et al., 1984; Steere et al., 2003; Wilhelmsson et al., 2016; Carlsson et al., 2018). In the OspA vaccine trial, 30 of the 269 patients who met the criteria for Lyme disease were classified as having asymptomatic IgG seroconversion to *B. burgdorferi* (Steere et al., 1998). Upon subsequent investigation, 14 of these individuals were found to have had symptoms and/or a rash compatible with EM that was not appreciated during their participation in the study. Eight patients, however, were truly asymptomatic and went untreated. Surprisingly, only one of these eight individuals developed a late complication – arthritis (Steere et al., 2003). Wormser and co-workers (Wormser et al., 2001b) proposed that some asymptomatic infections may be attributed to non-invasive strains. This is another way of stating that at least some uneventful outcomes reflect the general non-permissiveness of humans as hosts for Lyme disease spirochetes. Unfortunately, methodologies to distinguish patients who have cleared “benign” asymptomatic infection from those who may be persistently infected and at risk for subsequent late complications do not exist. The management of asymptomatic persons found to be seroreactive for Lyme disease is an important unresolved issue for practitioners in endemic areas (Wormser et al., 2006). A comparison with syphilis, caused by *Treponema pallidum*, a spirochete that has evolved to persist in humans, is instructive: It is well recognized that patients with latent syphilitic infection are at risk of recrudescence, and, therefore, must be treated (Radolf et al., 2019).

Hematogenous dissemination and organ system invasion

That spirochetes disseminate hematogenously during early infection has been known since *B. burgdorferi* was first isolated in the early 1980s (Benach et al., 1983; Steere et al., 1983a). Wormser and colleagues (Wormser et al., 2001a) showed that spirochetemia occurs in approximately 40% of patients with EM but that the extremely low spirochete concentrations in blood (estimated to be ~1 bacterium per 10 ml) necessitate culturing large volumes of plasma (Wormser et al., 2001a) (also see Radolf and Samuels, 2021). The low spirochete burdens in blood during early Lyme disease also explains why PCR analysis of blood, a volume-limited technique, has poor diagnostic yield (Aguero-Rosenfeld et al., 2005; Lohr et al., 2018). Since untreated patients cannot be followed prospectively, it is not known whether spirochetemia occurs constantly at low levels or at varying levels intermittently. In a large retrospective review of spirochetemic EM patients evaluated using the large-volume culture technique, hematogenous dissemination was not associated with duration or size of EM (Wormser et al., 2005); these results are in accord with data that borrelial genotypic factors are the predominant determinants of whether invasive infection occurs. Approximately 20% of EM patients have secondary EM-like skin lesions, a clinical indicator of hematogenous dissemination analogous to the rash of secondary syphilis (Wormser et al., 2005). Interestingly, blood cultures were positive in only five of 26 patients with extracutaneous manifestations of Lyme disease, four of whom had concomitant erythema migrans (Nowakowski et al., 2009); these results suggest that spirochetemia occurs predominantly during early infection. Even though spirochetemia may be difficult to detect, the high proportion of constitutional symptoms strongly points to the systemic nature of Lyme disease even when it appears microbiologically localized (Wormser, 2006; Steere et al., 2016). The discovery of metabolic (Molins et al., 2017) and proteomic (Zhou et al., 2020) signatures in the blood of early Lyme disease patients further indicates the systemic nature of earlier illness regardless of whether clinical signs of dissemination are present.

Little is known about the mechanisms by which circulating spirochetes recognize and invade target organs. Studies with cultured human umbilical vein endothelial cells have shown that organisms rapidly attach to vascular endothelium and negotiate their way through intercellular junctions (transmigration),

subsequently attaching to subendothelial matrix components (Comstock and Thomas, 1989; Szczepanski et al., 1990). Real-time intravital confocal microscopy revealed that transmigration through capillaries and post-capillary venules *in vivo* is a multi-step process engaged in by only a small percentage of GFP-expressing spirochetes introduced intravenously into mice (Moriarty et al., 2008; Norman et al., 2008). The role of the adhesin BBK32 in trans-endothelial migration was described above.

Aside from skin, the heart, joints, and nervous system are the most affected metastatic sites (see below). How frequently do blood-borne spirochetes gain access to these organ systems? Unlike with experimental animal models, obtaining precise values for the incidence rates of disseminated manifestations of Lyme disease in humans is a major challenge. For example, while some authorities cite incidence rates for carditis as high as 10% (Scheffold et al., 2015), these values are almost certainly overestimates, perhaps reflecting the era when early Lyme disease often went unrecognized and, therefore, untreated. Based on surveillance data obtained from 2001-2010, the CDC determined that cardiac involvement occurs in approximately 1% of reported cases (Forrester et al., 2014). On the other hand, cardiac involvement occurs in diverse strains of laboratory mice and in most inoculated animals (Barthold et al., 1990) (also see Radolf and Samuels, 2021). Thus, the comparatively low percentage of carditis in humans suggests that *B. burgdorferi* does not have as strong a tropism for human cardiac tissue. This conclusion is supported by studies with rhesus macaques that found that carditis was absent or mild unless animals were immunosuppressed (Philipp et al., 1993; Cadavid et al., 2004).

In an early report describing 12 U.S. patients with acute disseminated Lyme disease, six with acute cranial neuritis, three with multiple EM, and three with both cranial neuritis and multiple EM, eight patients had spirochetal DNA in their cerebrospinal fluid (CSF) detectable by PCR (Luft et al., 1992). More recent, large European studies involving patients infected with neurotropic *Borrelia* genospecies indicate that these findings greatly overestimated the incidence of CNS invasion during early Lyme disease. During a 5.5-year period, Strle and colleagues (Ogrinc et al., 2013) found neurologic symptoms in only 161 of 2751 (6%) patients with erythema migrans; of these, only 31 (19%) had CSF

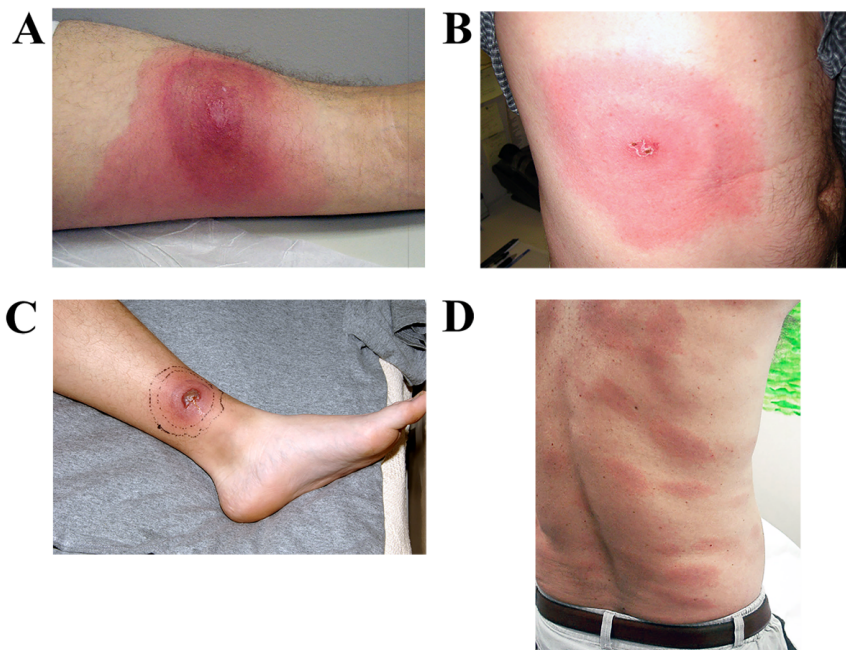


Figure 8. Erythema migrans (EM) lesions: (A) Diffuse EM expanding centripetally over the right quadriceps. (B) EM lesion on the right torso forming a classic “bulls-eye” pattern; note the central eschar (the tick bite site). (C) Ulcerated necrotic and EM lesion. Black lines demarcate area of receding erythema following antibiotic therapy. (D) Multiple EM lesions of disseminated early Lyme disease over the posterior trunk and lower back.

abnormalities, and spirochetes were isolated from only 6 of 127 untreated individuals (Ogrinc et al., 2013). In a subsequent study, they isolated spirochetes from only 12 of 177 persons with Bannwarth Syndrome (15%) (Ogrinc et al., 2016). These latter results bear out Halperin’s contention that neurologic complications in Lyme disease often result from inflammation of blood vessels supplying nerve roots and peripheral nerves as opposed to penetration of the blood-brain barrier and/or invasion of brain parenchyma (Halperin, 2008).

Clinical Manifestations

Early studies divided Lyme disease into three distinct stages analogous to those of syphilis (Steere, 2001): Stage 1, erythema migrans; Stage 2, neurologic or cardiac involvement, and Stage 3, arthritis. This staging system is still in use today (Steere et al., 2016). It is particularly important for caregivers on the front lines to think in terms of localized infection, EM, and early and late consequences of dissemination

(Trayes et al., 2018; Schoen, 2020). However, only a minority of untreated patients develops all clinical manifestations, although in some patients signs of early and disseminated Lyme disease are present at the same time.

Skin

Numerous clinical series have established that EM is the most common manifestation of *B. burgdorferi* infection in the United States and Europe (Berglund et al., 1995; Steere and Sikand, 2003; Wormser et al., 2006; Enkelmann et al., 2018; Stanek and Strle, 2018). Most patients presenting with this rash have primary EM, the lesion that develops at the site of tick inoculation, typically within 7 to 14 days after detachment. Primary EM can be located anywhere but in adults occurs most commonly below the waist. In North American studies, only 14-32% of individuals presenting with EM recall a tick bite. To distinguish EM from the transient and more localized inflammatory reactions that often develop following

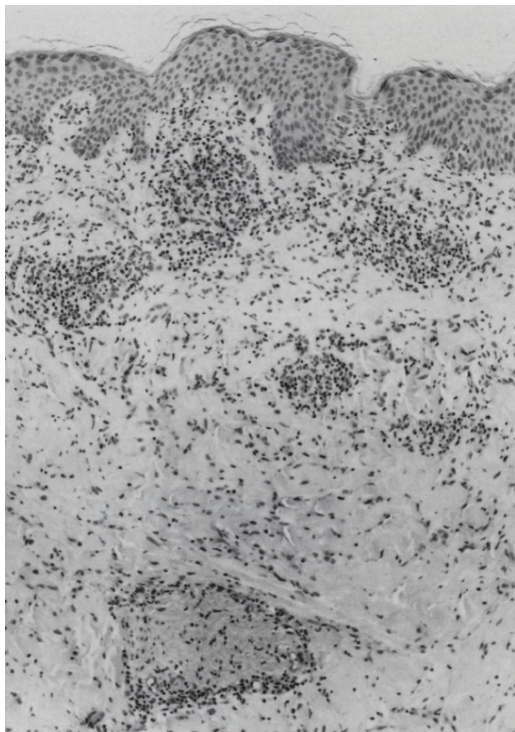


Figure 9. Biopsy taken from the center of an EM lesion showing a superficial and deep perivascular and interstitial infiltrate of lymphocytes and histiocytes. H&E, x 100 (Reprinted with permission from de Koning et al.)

an insect bite, the Centers for Disease Control and Prevention designated 5 cm as the minimum lesion diameter required for clinical diagnosis (Figure 8). While this size criterion improves the specificity of clinical diagnosis, it must be emphasized that *bona fide* EM lesions can be less than 5 cm, particularly when detected shortly after tick detachment. EM is traditionally described as an expanding, annular, erythematous skin lesion with central clearing, the so-called classic “bull’s eye rash” (Steere, 2001). Central clearing, however, is not as characteristic as was once thought: two large North American studies found only 37% (Nadelman et al., 1996) and 9% (Smith et al., 2002) of patients had central clearing. Central clearing appears to be more common in Europe, where most cases are due to *B. afzelii* and have a longer duration prior to treatment (Strle et al., 1999; Dandache and Nadelman, 2008). EM-associated systemic illness can vary from none to

moderate constitutional symptoms consisting of arthralgia, malaise, fatigue, headache, and low-grade fever and chills (Berglund et al., 1995; Wormser et al., 2006; Dandache and Nadelman, 2008; Stanek and Strle, 2018). Studies of EM patients have reported a difference in the incidence of extracutaneous manifestations in America and Europe. Less than 50% of European patients have extracutaneous manifestations as opposed to more than 75% of patients in the United States (Strle et al., 1999; Dandache and Nadelman, 2008). Regional lymphadenopathy is the most common physical finding associated with EM in both Europe and North America. Differences in EM and associated symptoms caused by *B. garinii* and *B. afzelii* also have been noted (Logar et al., 2004; Strle et al., 2011a). Patients with *B. garinii* had shorter incubation periods, faster evolution of their EM, and more symptomatic lesions (burning, itching, and pain) as well as modestly increased systemic symptomatology.

The most common histological pattern of EM is a superficial and deep dermal infiltrate consisting mostly of lymphocytes, but also containing neutrophils, macrophages, and plasma cells, often in a perivascular distribution (Figure 9) (Duray, 1989b; de Koning, 1993). Over the years, efforts to dissect this cellular response have been predicated on the assumption that it plays a pivotal role in determining the outcome of infection, possibly helping to initiate the ill-defined, treatment-recalcitrant symptomatic state known as post-treatment Lyme disease syndrome (PTLDS) (Crowder et al., 2014; Weitzner et al., 2015; Bouquet et al., 2016) (also see Radolf and Samuels, 2021). Using an epidermal blister fluid suction technique to extract dermal cells for immunophenotypic analysis by flow cytometry, Salazar and co-workers (Salazar et al., 2003) showed that EM infiltrates contain diverse cellular elements derived from both the innate and adaptive arms of the immune system, including plasmacytoid dendritic cells and memory-effector T cells. Greater than 80% of lesional T cells expressed CCR5 and/or CXR3, suggesting a strongly polarized Th1 response, confirmed by high levels of IFN- γ in the blister (interstitial) fluids. Th1 polarization of skin-recruited, antigen-sensitized T cells was supported by Glickstein et al (Glickstein et al., 2003), who found IFN- γ to be the predominant cytokine produced by peripheral blood leukocytes from culture-confirmed EM incubated with borrelial lysates, and by Jones et al. (Jones et al., 2008), who found high levels of



Figure 10. Borrelial lymphocytoma. Image shows a firm, indolent swelling of the left nipple of an eight-year-old boy with prior history of a tick bite and serological evidence of Lyme disease. Photograph courtesy of Ulrich Heininger, University Children's Hospital, Basel, Switzerland.

transcripts for IFN- γ and Th1-associated chemokines in RNAs extracted from EM lesions. The latter study also was noteworthy for its comparison of the chemokine and cytokine mRNA profiles of EM lesions from European and U.S. patients infected with *B. afzelii* and *B. burgdorferi*, respectively. Consistent with the generally milder course of EM in Europe (Strle et al., 1999; Dandache and Nadelman, 2008), they found that lesions from U.S. patients had significantly higher mRNA levels for chemokines associated with macrophage activation and Th1 cell recruitment. Similarly, studies in serum from EM patients, or in macrophage cell cultures stimulated with *Borrelia* isolates from these patients, demonstrated that infection with U.S. *B. burgdorferi* strains elicits higher levels of cytokines and chemokines associated with innate and Th1 adaptive responses than European *B. afzelii* or *B. garinii* strains (Strle et al., 2009).

A recent comparative microarray analysis of mRNAs extracted from 18 EM biopsies and 27 controls has provided an unprecedented global assessment of the transcriptional response elicited by *B. burgdorferi* infection of human skin (Marques et al., 2017). CXCL9, CXCL10, and CXCL11, chemokines strongly implicated in early and late Lyme disease pathogenesis (Lepej et al., 2005; Mullegger et al., 2007; Shin et al., 2010), were the most highly induced genes. Interferon signaling was the top activated pathway, followed by pathways for pattern recognition receptors of bacteria and viruses and DC maturation. Based upon this comprehensive dataset, Marques et al. (Marques et al., 2017) proposed a model for the immunopathogenesis of cutaneous *B.*

burgdorferi infection that explains the genesis and amplification of the local inflammatory response along with a novel mechanism spirochetes deploy for evading it. Briefly, TLR-mediated activation of local and recruited phagocytes upon ingestion and degradation of spirochetes elicits numerous inflammatory mediators, including Th1-polarizing chemokines. Production of IFN- γ by T cells and type I IFNs by macrophages and plasmacytoid dendritic cells bolsters phagocytosis and elicits myriad interferon-responsive genes; the latter include genes encoding enzymes involved in tryptophan catabolism. The authors hypothesized that spirochetes exploit the inhibition of T cell priming and enhanced development of FoxP3⁺ Tregs resulting from tryptophan depletion.

In Europe, but not North America, Lyme disease is associated with two additional dermatologic disorders: borrelial lymphocytoma (BL) and acrodermatitis chronica atrophicans (ACA) (Steere et al., 2016; Stanek and Strle, 2018). BL may occur concurrently with EM or a few days before or up to several weeks after EM (Strle et al., 1992; Brehmer-Andersson et al., 1998; Glatz et al., 2015; Maraspin et al., 2016), generally manifesting as solitary, bluish-red nodule on the ear lobe or the nipple area (Figure 10) (Strle et al., 1992; Colli et al., 2004). Histopathologically, BL is characterized by a dense polyclonal lymphocytic infiltrate in the dermis or subcutaneous tissue; differentiation from lymphoma is usually not very difficult since lymphocytic infiltration in BL is polyclonal, while in lymphoma it is oligoclonal or monoclonal (Colli et al., 2004). Maraspin et al. (Maraspin et al., 2016) reported an isolation rate of one in three from BL tissue and that *B. afzelii* is the main causative agent; of 13 typed strains, 11 were *B. afzelii*, one was *B. garinii*, and one was *B. bissettii*. Although systemic symptoms are rarely associated with lymphocytoma, most patients report mild symptoms localized to the site of the lesion.

ACA is an extremely late manifestation, typically developing months to years after the onset of untreated infection (Brehmer-Andersson et al., 1998; Brandt et al., 2015). Occurring throughout Northern, Central, and Eastern Europe, ACA is associated primarily with *B. afzelii* infection. Initially the skin lesions are distinguished by inflammation and edema. With time, the lesions become increasingly atrophic. ACA typically involves the distal extensor part of extremities and, less commonly the trunk,

sparing the face. Polyneuropathy, small joint arthritis with subluxation, arthritis of the large joints, and periosteal thickening of the bones may occur in the same extremity as ACA.

Lyme neuroborreliosis

The neurologic manifestations of Lyme disease, often referred to as Lyme neuroborreliosis, reflect the capacity of *B. burgdorferi* sensu lato to invade diverse targets within the peripheral and central nervous system and to cause neurological complications weeks to months after infection (Halperin, 2003; Koedel et al., 2015; Halperin, 2018; Garcia-Monco and Benach, 2019). Early nervous system involvement is usually manifested by the involvement of cranial and/or peripheral nerves or nerve roots typically associated with lymphocytic meningitis. Classical Bannwarth syndrome (BS) is defined as meningoradiculoneuritis; cranial neuritis may be or may not be present (Halperin, 2015; Ogrinc et al., 2016; Shah et al., 2018; Garcia-Monco and Benach, 2019). BS is the most typical manifestation of Lyme neuroborreliosis in adult European populations (Ogrinc et al., 2016); although rare in the U.S., a cluster of five cases recently was reported from the upper Midwest (Shah et al., 2018). Currently, peripheral facial palsy and an isolated aseptic (viral-like) meningitis picture are the most common early neurologic manifestation in the U.S. (Garcia-Monco and Benach, 2019). Initial studies of North American patients with untreated EM found that approximately 15% developed meningitis or cranial neuritis within the first three months after presentation (Steere et al., 1983b; Halperin et al., 1989). It is now believed that early neurologic involvement is much more common in Europe than in the United States, reflecting the prevalence of neurotropic strains of *B. garinii* (Koedel et al., 2015; Steere et al., 2016; Stanek and Strle, 2018).

Although late disseminated *B. burgdorferi* infection has been linked to a variety of nervous system disorders over the years, the neurologic entities now generally accepted as causally associated with late Lyme disease – encephalomyelitis, encephalopathy, and axonal polyneuropathy (Logigian et al., 1990; Logigian and Steere, 1992; Wormser et al., 2006) – are quite rare. As documented in the 2006 IDSA Lyme disease guidelines (Wormser et al., 2006), only one case of encephalomyelitis, nine patients with peripheral neuropathy and seven patients with encephalopathy were seen by the panel members in the 5 years preceding their publication. Peripheral

nerve involvement in late Lyme disease is an axonopathy that may be distributed symmetrically or asymmetrically, and in some cases, resemble polyneuritis multiplex (Halperin et al., 1990; Logigian et al., 1990). Patients with this entity complain of paresthesias and hyperesthesias and have abnormal nerve conduction. In Europe, peripheral neuropathy may be found in association with ACA but rarely, if ever, occurs in patients without ACA or other Lyme disease manifestations (Kristoferitsch et al., 1988; Mygland et al., 2006). Halperin (Halperin, 2008) has voiced considerable skepticism that Lyme disease is a significant cause of stroke.

Not surprisingly, the inflammatory mechanisms underlying CNS neuroborreliosis are complex, involving both innate and adaptive immune systems. Building upon their *in vivo* work with the primate model, Philipp and co-workers (Ramesh et al., 2003; Bernardino et al., 2008; Ramesh et al., 2008) demonstrated in an elegant series of studies that spirochetes induce profound proinflammatory and apoptotic changes in rhesus macaque glial cells and astrocytes and, most recently, isolated brain slices, that involve diverse chemokines, cytokines, and TLR-mediated signals. Analysis of cerebrospinal fluids from neuroborreliosis patients has identified borreliacidal antigen-specific CD4⁺ T cells, CD8⁺ T cells, and B cells (Cepok et al., 2003; Jacobsen et al., 2003; Rupprecht et al., 2005; Lunemann et al., 2007), as well as unusual subsets of dendritic cells (Pashenkov et al., 2001). Collectively, these results underscore how greatly CNS infection by Lyme disease spirochetes differs from meningitis caused by pyogenic bacteria.

Lyme carditis

As with all forms of disseminated Lyme disease, the incidence of symptomatic cardiac involvement in the United States appears to have decreased dramatically and is now considered to be approximately 1% (Forrester et al., 2014). Available evidence indicates that carditis does not occur if early Lyme disease patients without cardiac manifestations are appropriately treated (Robinson et al., 2015). When first described, concurrent EM and other forms of early Lyme disease was the rule (van der Linde, 1991); in recent years, however, one-half or less of patients present with concurrent EM (Forrester and Mead, 2014; Marcos et al., 2019). In their recent review, Forrester and Mead (Forrester and Mead, 2014) noted a striking male predominance (84%), a finding supported by a retrospective chart review

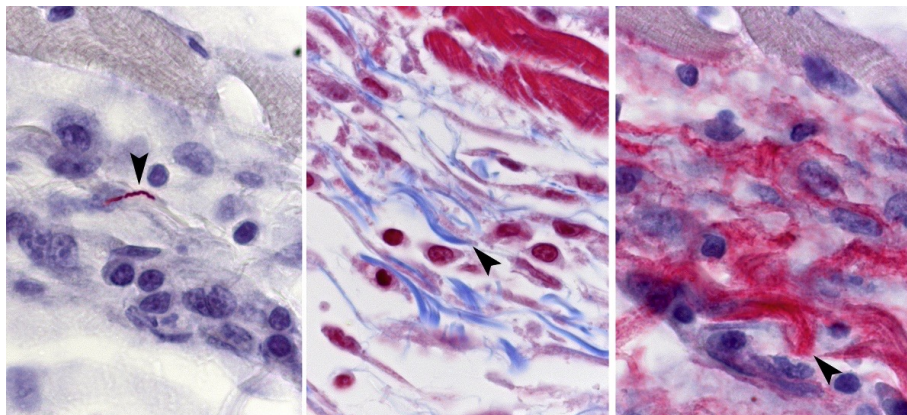


Figure 11. Localization of spirochetes (left panel, immunohistochemistry, arrowhead) with collagen (middle panel, blue, trichrome, arrowhead) and decorin (right panel, red, immunohistochemistry) in the myocardium of a patient with fatal myocarditis. (Reproduced with permission from Muehlenbachs et al., 2016).

conducted at Stony Brook, Long Island (Marcos et al., 2019).

The principal manifestation of Lyme carditis is atrioventricular block proximal to the bundle of His, which can fluctuate and progress rapidly (typically within hours, occasionally within minutes) (Fish et al., 2008; Robinson et al., 2015). Other forms of conduction system disease, such as atrial fibrillation (Zainal et al., 2019) and sick sinus syndrome (Gazendam et al., 2020), also have been reported. Although diffuse myocardial involvement has been seen in cases that have come to autopsy (Duray, 1989a; Tavora et al., 2008; Muehlenbachs et al., 2016), clinically apparent acute myocarditis is uncommon (Robinson et al., 2015). Valvular heart disease also occurs but is extremely rare, with only a handful of microbiologically confirmed cases reported (Nikolić et al., 2020). Two PCR-confirmed cases occurred in the United States (Paim et al., 2018; Haddad et al., 2019), while one European case was attributed to *B. bissettii* (Rudenko et al., 2008). Early European studies reported an etiologic association between Lyme disease and chronic dilated cardiomyopathy, but these have not subsequently been reproduced on either side of the Atlantic (Robinson et al., 2015). Even without therapy, Lyme carditis may be self-limited (Steere et al., 1980). With appropriate therapy, the prognosis is excellent, with a

medium time of 6 days to improvement or restoration of normal sinus rhythm.

With only 11 cases in the literature, sudden death is an extremely rare, though, tragically, now well-recognized outcome of Lyme carditis (Marx et al., 2019). In 2013, the CDC called attention to the potential for Lyme disease to cause cardiac fatalities when it reported three cases occurring from November, 2012 to July, 2013 in young individuals (26 to 38 years) from Connecticut, Massachusetts, and New Hampshire (Centers for Disease and Prevention, 2013). Muehlenbachs et al. (Muehlenbachs et al., 2016) evaluated autopsy tissue samples from these, plus two additional cases, by light microscopy, immunohistochemistry (IHC), and PCR. Pancarditis with a characteristic “road map” distribution of infiltrates consisting of lymphocytes (T cell predominant but also B cells), histiocytes, and plasma cells were seen in all five. The conduction system was specifically evaluated in two cases; the presence of severe inflammation in the sinoatrial and AV nodes, including intense necrotizing inflammation of the AV node in one, led them to speculate that involvement of the conduction system caused the deaths. However, arrhythmias also seem likely in some. In all five, spirochetes were widely detected by Warthin-Starry silver stain, IHC, and PCR and co-localized with collagen and decorin (Figure 11). The ease of detecting spirochetes in heart samples



Figure 12. Lyme arthritis manifested as left knee swelling in a young adult. Clinically there was no redness, few constitutional symptoms, and little pain. The patient recovered after a 4-week course of oral antibiotics. Photograph courtesy of Dr. Jeffrey Thompson, Connecticut Children's Medical Center.

contrasted with the paucity of bacteria detected by IHC and PCR in numerous other organs, indicating that in these patients *B. burgdorferi* clearly possessed a tropism for cardiac tissue.

Lyme arthritis

Arthritis is the most common and serious rheumatologic consequence of spirochetal infection and dissemination. Although Lyme arthritis was once believed to be a North American phenomenon because of the defining epidemic in the 1970s (Steere et al., 1977b) and the paucity of reports of tick-related arthritis in the European literature of the day (Stanek and Strle, 2018), this entity also occurs in European patients without a clear genospecies predominance (Herzer, 1993; Steere, 1997; Haugeberg et al., 2014; Enkelmann et al., 2018). The incubation period for joint involvement can vary from days to years, usually 3 to 6 months, from the time of infection (Steere et al., 1987; Herzer, 1991), and it is presumed that spirochetes typically invade joints well before the onset of arthritic symptoms (Bockenstedt and Wormser, 2014). In some patients, episodes of periarticular pain may precede frank arthritis by weeks to months (Stanek and Strle, 2018). The presence of high-titer antibodies to multiple *B. burgdorferi* antigens in the sera of Lyme arthritis

patients (Akin et al., 1999; Wormser et al., 2006) is consistent with the concept of a period of quiescence within the joint prior to the development of clinically evident arthritis (Bockenstedt and Wormser, 2014).

Lyme arthritis is a monoarticular or oligoarticular large joint arthritis characterized by episodes of inflammation with swelling, large effusions and surprisingly little pain (Arvikar and Steere, 2015). The knee is the most commonly affected joint, but other large or small joints, such as the ankle, shoulder, elbow or wrist, may be affected (Figure 12); exclusive involvement of small joints is unusual (Arvikar and Steere, 2015; Stanek and Strle, 2018). In the original study defining the arthritic complications of Lyme disease, prior to use of antibiotics for treatment of the infection, 34 of 55 patients who presented with EM went on to develop arthritis (Steere et al., 1987). Twenty-eight of the 34 patients experienced intermittent arthritis with the episodes of joint swelling lasting from a few days to several months before spontaneously resolving. Over time, the interval between episodes gradually increased before the arthritis spontaneously remitted. Six patients, however, had a year or more of unremitting arthritis. According to a more recent report by the CDC, of ~150,000 newly reported cases of Lyme disease in the U.S. (reported on from 1992-2006) up to 30% present as Lyme arthritis. In contrast, in Europe, the percentage of *B. burgdorferi*-infected individuals who develop arthritis is less than 10% (Enkelmann et al., 2018; Stanek and Strle, 2018). Synovial biopsy of untreated Lyme arthritis shows synovial hypertrophy with vascular proliferation, a mixed infiltrate including T cells, B cells, and follicular dendritic cells (Steere et al., 1979; Duray and Steere, 1986). Consistent with findings in tissue, joint fluid in Lyme arthritis patients contains markedly elevated levels of cytokines and chemokines associated with innate and adaptive immune responses, with particularly high levels of IFN γ -inducible chemokines CXCL9 and CXCL10. The levels of these mediators are nominally lower in serum supporting the idea that these immune responses are occurring locally in joints (Jones et al., 2008; Strle et al., 2017). In addition to inflammatory mediators, matrix-degrading enzymes such as matrix metalloproteinases (MMPs), which degrade both collagen and proteoglycans (Murphy and Nagase, 2008), are believed to contribute to the erosion of cartilage and bone. MMPs have been detected by zymography in the synovial fluids of Lyme arthritis patients (Hu et al., 2001), and in *ex vivo* experiments, *B. burgdorferi* elicits their production by cartilage

explants (Lin et al., 2001), chondrocytes (Behera et al., 2004) and monocytes (Gebbia et al., 2004).

The pathogenesis of Lyme arthritis is enigmatic from several standpoints. Though undoubtedly arising from hematogenous dissemination of spirochetes into joints or periarticular tissues, with only two documented exceptions (Snydman et al., 1986; Schmidli et al., 1988), efforts to recover live spirochetes from synovial fluid as a rule have been unsuccessful. In 1994, Nocton and co-workers (Nocton et al., 1994) made two seminal observations: (i) *B. burgdorferi* DNA can be detected in synovial fluids from the large majority (75 of 88) of Lyme arthritis patients and (ii) PCR-positive patients usually respond well to antimicrobial therapy. In PCR-positive patients, resolution of arthritis with antibiotics confirms that spirochete-elicited inflammation drives the arthritic process (Bockenstedt and Wormser, 2014). However, where the spirochetes producing the DNA are hiding in these individuals and what triggers the inflammation after a presumptive period of quiescence remain mysteries (Bockenstedt and Wormser, 2014). The murine model offers some help with the first conundrum. In mice, spirochetes do not infect the joint spaces per se but are visualized in collagen-rich, periarticular structures (Barthold et al., 1991; Bockenstedt and Wormser, 2014).

Although Lyme arthritis usually resolves following appropriate antibiotic therapy, some patients (estimated to be ~10%) have a persistent proliferative synovitis, characterized by synovial hyperplasia, vascular damage, intense inflammation, and fibrosis, termed post-infectious, antibiotic-refractory Lyme arthritis (Steere and Angelis, 2006; Chan and Pollock, 2015). Patients diagnosed with this entity are strongly seropositive but usually lack a PCR signal for *B. burgdorferi* DNA in joints (Wormser et al., 2006; Li et al., 2011). The central mechanistic question is how spirochetes initiate a localized, dysregulated inflammatory process that persists after they have been eradicated (Singh and Girschick, 2004; Shin et al., 2007; Shen et al., 2010; Strle et al., 2012). The increased prevalence of certain HLA alleles that are also associated with rheumatoid arthritis (Steere et al., 1990) spawned the hypothesis that antibiotic-refractory Lyme arthritis is a form of infection-induced autoimmunity caused by molecular mimicry (Klempner and Huber, 1999; Bolz and Weis, 2004). Subsequent studies identified a sequence in OspA as the molecular mimic for a sequence in hLFA-1 (Gross et al., 1998; Chen et al., 1999) and

reported that the HLA-DR alleles overrepresented in antibiotic-refractory arthritis patients bind the OspA mimotope (Steere et al., 2006). The public health consequences of these publications were enormous since OspA was the antigenic component of the Lyme disease vaccine released at approximately the same time (Sigal et al., 1998; Steere et al., 1998). Unsubstantiated concerns about autoimmunity due to vaccination with OspA contributed to the commercial failure of the vaccine and its withdrawal from the market (Plotkin, 2011; Willyard, 2014). In subsequent publications, Steere's group backed away from the association of persistent synovitis with T cell reactivity to either OspA or LFA-1 (Kannian et al., 2007; Drouin et al., 2013). However, in support of the concept of spirochete-induced autoimmunity, the Steere group has now identified four novel self-antigens, ECGF, ApoB-100, Annexin A2, and MMP10, which are targets of T and B cell responses in patients with refractory Lyme arthritis (Drouin et al., 2013; Pianta et al., 2015; Crowley et al., 2016; Arvikar et al., 2017; Strle et al., 2017; Steere, 2020).

Although the etiology remains unclear, much has been learned in recent years about the dysregulated inflammatory processes that underlie post-infectious Lyme arthritis (Steere, 2020). For example, patients with a particular single nucleotide polymorphism in TLR1, particularly those who are infected with *B. burgdorferi* RST1 strains, appear to be predisposed to excessive Th1-associated inflammation (Strle et al., 2012). Compared with antibiotic-responsive Lyme arthritis patients, persons with post-infectious arthritis had lower levels of CD4⁺CD25⁺ regulatory T cells in their synovial fluids and their regulatory T cells were less effective at downregulating Th1 effector responses (Vudattu et al., 2013). High throughput RNA sequencing revealed a robust IFN γ response in synovium that correlates inversely with expression of genes involved in tissue repair and drives differentiation of fibroblast-like synoviocytes into immune effector cells that are thought to amplify and perpetuate these dysregulated Th1 responses (Lochhead et al., 2019a; Lochhead et al., 2019b). An alternative, or perhaps complementary, mechanism for persistent inflammation based on innate immunity recently has been proposed. Jutras *et al.* (Jutras et al., 2019) reported that *B. burgdorferi* cannot recycle peptidoglycan and sheds peptidoglycan fragments (muropeptides) into its environment. They postulated that peptidoglycan fragments shed into synovial fluid prior to the eradication of bacteria causes chronic activation of NOD2-dependent arthritogenic

pathways. Thus, the infection with certain *Borrelia* strains in genetically predisposed individuals appears to set the stage for dysregulated immune responses with particularly high levels of IFN γ that promote synovial hypertrophy, inhibit tissue repair, and are permissive to the development of autoreactive T and B cell responses in joints. Microbial remnants such as peptidoglycan, which can persist in the absence of active spirochete infection, may further perpetuate these responses.

Lyme Disease in Children

As noted earlier, Lyme disease began as an affliction of children (Steere et al., 1977b) and it continues so to this day. The clinical manifestations of Lyme disease in children, as in adults, mainly involve the skin, central nervous system, joints, and heart (Feder, 2008; Sood, 2015). The primary EM lesion in children is most commonly found on the head and neck (26%), arms or legs (25%), or lower back (24%) (Salazar et al., 1993; Gerber et al., 1996). Awareness of EM in the head and neck is important because such lesions can be hidden by the hairline. Less frequently lesions can be found over the abdomen (9%), the axilla (8%), the groin (5%), or the chest (3%) (Gerber et al., 1996). Most single EM lesions in children are uniformly erythematous; however, they also can have central erythema or clearing and, in rare instances, painful central ulcerations (Figure 8C). Children also may present with constitutional symptoms, including fever (24%), fatigue (58%), headache (42%) and arthralgias (33%) (Gerber et al., 1996). The presence of multiple EMs has been documented in up to 40% of children (Gerber et al., 1996; Arnez et al., 2003) and most have associated fever (45%), fatigue (80%), and headache (70%). Similar to adults with Lyme disease, ~20% of children may present with constitutional symptoms as the only manifestation (Feder et al., 1993; Gerber et al., 1996). Practitioners in endemic areas need to have a high index of suspicion to avoid missing the diagnosis in such children.

Of course, arthritis also may be the presenting manifestation of Lyme disease in children (Steere et al., 1977b; Szer et al., 1991). As in adults, the incubation period is highly variable with a mean of about 4 months (Szer et al., 1991). In contrast to the early era, most children who present with Lyme arthritis today do not have a history of EM. In these children, the rash was either unseen, or perhaps they never had it at all. Lyme arthritis in children usually involves single large joints, most commonly the knee

(Gerber et al., 1998). However, series describing monoarticular arthritis of the hips and elbows in children have appeared of late (Cruz et al., 2017; Gendelberg and Hennrikus, 2018). Fever occurs in 25-50% of children with Lyme arthritis, as opposed to adults who are usually afebrile. Joint fluid obtained from these children may have large numbers of leukocytes ($> 50,000$ cells/mm³) with a predominance of neutrophils. If not suspected, the disease can be mistaken for septic arthritis caused by pyogenic bacteria (e.g., *Staphylococcus aureus*). A recent series comparing Lyme arthritis of the hip to septic arthritis emphasized that the former is more likely to occur in children who are afebrile and without leukocytosis (Cruz et al., 2017). If treated appropriately, the prognosis is excellent and with rare exceptions a full recovery is the outcome. Antibiotic-refractory Lyme arthritis is unusual in children (Daikh et al., 2013; Sood, 2015).

Lyme disease in children also may present with neurologic manifestations (Cook et al., 1997; Eppes et al., 1999; Sood, 2015). Most children with neuroborreliosis do not provide a history of EM. The most common neurologic presentations in children include facial nerve palsy and lymphocytic meningitis (Cook et al., 1997; Eppes et al., 1999; Sood, 2015). Children with Lyme meningitis also may have increased intracranial pressure, and some have optic neuritis and papilledema (Kan et al., 1998); increased intracranial pressure may occur in the absence of meningitis (Kan et al., 1998; Sood, 2006). Though rare, BS should be considered in children in Europe or who have traveled to Europe who present with characteristic radicular pain (Sood, 2015). The CSF pleocytosis is predominantly lymphocytic; in one study, a CSF containing 10% or more neutrophils had a negative predictive value of 99% for Lyme disease compared to viral meningitis (Shah et al., 2005). More severe neurologic manifestations, such as myelitis and severe encephalitis, are exceedingly rare in young children. Though rare, Lyme carditis may also occur in children (Bolourchi et al., 2019). When it occurs, the most common manifestation in children is transient high-grade AV block (Silver et al., 2007). Less commonly, children may present in heart failure because of myocarditis. The prognosis of both neurologic and cardiac Lyme disease in children is excellent following appropriate therapy (Wormser et al., 2006).

Maternal-fetal transmission of *B. burgdorferi* has never been definitively documented, and epidemi-

ologic investigations have failed to establish an association between infection and adverse outcomes of pregnancy (Strobino et al., 1993; Gerber and Zolneraitis, 1994; Sood, 2015).

Reinfection

Recurrent episodes of Lyme disease can theoretically be due to either relapse or reinfection (Nadelman and Wormser, 2007). For EM to be due to relapse, the lesion must occur at the same site as the original infection and within a relatively short time interval. Reinfection is defined as EM occurring at a site distant from the initial lesion, often with a punctum or eschar indicative of a recent tick bite, months to years after the initial treated episode. Evidence for the relapse scenario is scant. Two groups have reported their inability to re-isolate spirochetes from the site of EM following therapy, although administration of antibiotics at the time of re-culture confounds interpretation of these data (Berger et al., 1992; Nadelman et al., 1993). In contrast, longitudinal studies conducted in highly endemic areas, Westchester, NY and Block Island, RI, found that up to 20% of patients treated for EM met criteria for reinfection (Nowakowski et al., 2003; Krause et al., 2006). An impressive report provided compelling molecular evidence based on *ospC* genotyping of isolates from 17 patients with 22 paired episodes of EM that recurrences are caused by different *B. burgdorferi* strains (Nadelman and Wormser, 2013). Using statistical modeling, this group subsequently argued that elicitation of durable strain-specific immunity explains why patients were reinfected with different strains (Khatchikian et al., 2014). Without serological data, however, this hypothesis remains unproven, and there is evidence from the mouse model that protective immunity following tick inoculation wanes within a year (Piesman et al., 1997). Furthermore, Barthold and Bockenstedt (Barthold and Bockenstedt, 1993) showed that levels of antibodies capable of conferring passive protection fall off much more rapidly than antibodies detected by ELISA with whole cell lysates. The implication of this finding is that high reactivity in serodiagnostic tests may not be an accurate indicator of immune status. One also must remember that a substantial percentage of persons with EM do not have detectable antibodies, even after treatment (Wormser, 2006). Such individuals will be susceptible to reinfection within a relatively short time if they live in an endemic area or frequently engage in high-risk activities.

Serologic response

The need for accurate serologic tests for diagnosis of Lyme disease has been a major driving force behind efforts to elucidate the humoral response to the spirochete. Consequently, the antibody response to *B. burgdorferi* *sensu lato* has been extensively dissected over the years with increasingly sophisticated methodologies in order to identify borrelial polypeptides that are not only highly immunogenic in a large percentage of patients but also specific for *B. burgdorferi* (Craft et al., 1986; Dressler et al., 1993; Engstrom et al., 1995; Aguero-Rosenfeld et al., 2005; Nowalk et al., 2006; Lohr et al., 2018) (also see Radolf and Samuels, 2021). This combination has not been easy to find. Cross-reactivity between *B. burgdorferi* FlaB, the major flagellar sheath protein, and flagellar antigens of commensal bacteria is the primary reason why this polypeptide, which induces a robust antibody response early in infection (Dressler et al., 1993), fell out of favor as a diagnostic antigen (Aguero-Rosenfeld et al., 2005; Lohr et al., 2018). OspC also induces a strong antibody response during early infection (Fung et al., 1994), consistent with the murine studies demonstrating its critical role for the establishment of infection following tick inoculation, but immunodominant epitopes of OspC proteins from different isolates are extremely heterogeneous (Lohr et al., 2018). A number of other borrelial proteins, many, but not all, lipoproteins, are strong immunogens but are hypervariable, expressed relatively late in the course of disease, and/or recognized by an insufficient percentage of patients (Aguero-Rosenfeld et al., 2005; Wilske et al., 2007; Lohr et al., 2018). Ironically, the antigenically variable VlsE protein, which in the murine model facilitates evasion of antibody responses, has a region with a conserved epitope that is highly immunogenic in early as well as late Lyme disease patients and has been exploited for improved serodiagnosis in Europe as well as North America (Liang et al., 1999) (Liang et al., 1999; Wormser et al., 2013; Lohr et al., 2018; Stanek and Strle, 2018; Zannoli et al., 2020).

Because approximately one-half of patients with EM do not mount detectable antibody responses to the pathogen, lack of seroreactivity cannot be used to rule out the diagnosis of EM (Wormser et al., 2006; Dandache and Nadelman, 2008). There is evidence that serodiagnostic sensitivity is improved by employing borrelial antigens known to be expressed *in vivo* during early infection (Brandt et al., 2019). Seroreactivity increases substantially following

therapy for EM (Vaz et al., 2001; Dandache and Nadelman, 2008), indicating that killing of organisms causes liberation of spirochetal antigens and enhances processing for antibody production. Most untreated patients have detectable antibodies within a month of infection. Accordingly, clinical manifestations caused by the dissemination of spirochetes, are for the most part, accompanied by seroreactivity (Wormser et al., 2006; Lohr et al., 2018; Stanek and Strle, 2018). The flip side of this coin is that IgG antibodies can be present for life and, therefore, cannot be used by themselves as indicators of active infection. While assays using whole cell lysates are less affected by strain variability and the heterogeneity in patient responses than those using single antigens, they can yield false-positives due to the presence of cross-reactive, background antibodies. This problem has been circumvented by the development of the two-tiered testing algorithm in which immunoblotting is used to confirm serologic reactivity by ELISA (Aguero-Rosenfeld et al., 2005; Wormser et al., 2006; Lohr et al., 2018; Stanek and Strle, 2018). The success of the two-tiered approach rests upon the implementation of strict criteria for the interpretation of immunoblots based on reactivity with a small subset of borrelial polypeptides defined by their SDS-PAGE mobilities (*i.e.*, apparent molecular masses) (Dressler et al., 1993). It is noteworthy, considering the T cell reactivity studies discussed below, that reactivity with OspA is not a criterion for immunoblot reactivity.

The general picture that has emerged over the years is that IgG and IgM antibodies to the spirochete develop slowly and are directed against an increasingly diverse array of proteins as infection progresses (Craft et al., 1986; Dressler et al., 1993; Lohr et al., 2018). The earliest responses are to flagellin B (FlaB), OspC (25 kDa) and BmpA (39 kDa) with responses to a number of additional antigens, such as VlsE, fibronectin-binding protein (BBK32), and decorin-binding protein A (DbpA), developing as *B. burgdorferi* disseminates (Bacon et al., 2003; Aguero-Rosenfeld et al., 2005; Wilske et al., 2007; Lohr et al., 2018). This temporal pattern is consistent with the notion that the bacterium draws upon an expanding repertoire of differentially expressed proteins once within its vertebrate host, including the phased expression of paralogous surface-exposed lipoproteins (Caimano et al., 2019). Carroll and co-workers (Nowalk et al., 2006) completed an extensive proteomics-based survey of murine and

human antibody responses to *B. burgdorferi* proteins, concluding that the contours of the two antibody profiles share many similarities during early infection.

What role, if any, do antibodies play in control of the disease process in humans? This question is far more difficult to answer for humans than in mice because humans cannot be followed serially without treatment and they cannot be passively immunized prior to experimental infection. The presence of intense and diverse antibody responses in patients with late manifestations of disease (Steere, 2001) is clear-cut evidence that, as in mice, spirochetes can persist despite high titers of circulating antibodies (see below). Nevertheless, there is *in vitro* evidence that the antibodies produced during human infection have bactericidal activity (Pavia et al., 1997; Callister et al., 2002) and can passively protect animals against inoculation with *in vitro* cultivated spirochetes (Fikrig et al., 1994). Robinson and coworkers (Blum et al., 2018) dramatically advanced this notion using single-cell paired-chain and bulk heavy-chain antibody repertoire sequencing to investigate circulating B cell responses during early Lyme disease. They demonstrated expanded memory B cell and plasmablast populations that produce antibodies with specificities for several *B. burgdorferi* antigens (*e.g.*, VlsE, DbpA, DbpB, and OspC) and that recombinant mAbs recognizing several of these inhibit spirochete growth *in vitro*. They also noted that robust plasmablast responses encoding *B. burgdorferi*-inhibitory antibodies were associated with more rapid disease resolution. As stated earlier, infection with less invasive borrelial strains has been proposed as one explanation for the high prevalence of asymptomatic *B. burgdorferi* infection in endemic areas (Wormser et al., 2001b). The capacity of humoral responses to contain and even eliminate spirochetes provides a second, non-mutually exclusive explanation, which also is in accord with the idea that humans lack reservoir-competence for the bacterium (Bockenstedt and Radolf, 2014).

Chronic Lyme disease and post-treatment Lyme disease syndrome

Please see the comprehensive discussion by Marques and Hu in Radolf and Samuels (2021). At one time, the term “chronic Lyme disease” (CLD) referred to late stage manifestations of untreated *B. burgdorferi* *sensu lato* infection, such as encephalomyelitis, encephalo-pathy, neuropathy, arthritis, and ACA (Koedel et al., 2015). Over the years, however, this term has come to denote

persons with chronic, subjective complaints (e.g., neurocognitive syndromes, mood disorders, fibromyalgia-type symptoms, and chronic fatigue), in the absence of a documented history of Lyme disease or objective physical or laboratory evidence of infection, who some practitioners maintain are afflicted by treatment-recalcitrant Lyme disease spirochetes (Cameron et al., 2004; Feder et al., 2007; Marques, 2008; Baker, 2010; Stricker and Johnson, 2014; Lantos, 2015). Few “mainstream” authorities believe there is convincing evidence for persistent infection (or any infection, for that matter) in these individuals (Feder et al., 2007; Koedel et al., 2015; Baker and Wormser, 2017; Shapiro et al., 2017). Clinicians who routinely diagnose CLD contend that the conventional laboratory tests mainstream practitioners rely upon are notoriously unreliable (Cameron et al., 2004; Stricker and Johnson, 2014). To further support their position, these self-designated “Lyme literate” physicians and their staunch supporters in advocacy groups cite myriad studies purporting to show that during chronic infection *B. burgdorferi* assumes unusual morphologies (variously termed “L forms”, “round bodies”, “L forms”, etc.) and/or metabolic states resistant to standard treatment regimens (Stricker and Johnson, 2011; Lantos, 2015; Sharma et al., 2015; Timmaraju et al., 2015; Feng et al., 2016b; Baker and Wormser, 2017). Even so, the pathophysiologic rationale is difficult to grasp (Halperin, 2008; Baker and Wormser, 2017). As noted by Halperin, for spirochetes to persist and cause disease without provoking discernable inflammation or an immunologic response manifested by detectable serum antibodies, *B. burgdorferi* would have to differ from virtually every other known chronic, systemic bacterial pathogen. The outcome of this questionable line of thinking is prolonged antimicrobial therapy of uninfected (though truly unwell) individuals, sometimes involving unusual regimens and agents of unproven efficacy for Lyme disease (Feder et al., 2007; Lantos et al., 2015). The potential dangers of these treatment regimens have been well documented (Lantos, 2015). While historically a North American phenomenon (Barbour and Fish, 1993), CLD appears to be gaining traction in Europe and, understandably, generating increasing concern among European investigators (Koedel et al., 2015; Gentilini and Bricaire, 2019; Peri et al., 2019).

Almost 30 years ago, clinicians began to report that some Lyme disease patients have persistent

nonspecific symptoms after receiving an adequate course of therapy (Dinerman and Steere, 1992; Asch et al., 1994; Shadick et al., 1994). In its 2006 guidelines, the Infectious Diseases Society of America created a working definition for this entity, now called “post-treatment Lyme disease syndrome” or PTLDS: clinical symptoms persisting at least six months after treatment for Lyme disease in persons who lack objective evidence of treatment failure, reinfection, or relapse (Wormser et al., 2006; Aucott, 2015; Lantos, 2015; Strle and Strle, 2020). PTLDS differs from CLD in one particularly important respect – patients with PTLDS have unequivocal documentation for appropriately treated Lyme disease. PTLDS occurs in only a small percentage of treated patients. As noted by Lantos in an excellent review (Lantos, 2015), only 222 (3.8%) of 5846 patients screened to participate in clinical trials for PTLDS had credible evidence for past Lyme disease, while less than 10% of patients in ten prospective studies of EM and early disseminated Lyme disease described persistent symptoms such as myalgias or fatigue 9 or more months following treatment. Fortunately, multiple longitudinal studies in the U.S. and Europe report that functional impairment by PTLDS diminishes over time (Cerar et al., 2010; Wormser et al., 2015; Stupica et al., 2018a; Stupica et al., 2018b; Wormser et al., 2020).

As with CLD, the central questions surrounding PTLDS are the underlying mechanism(s) of persistent symptomatology and whether extended antimicrobial therapy, or indeed any antimicrobial treatment in addition to that initially administered, is beneficial (DeLong et al., 2012; Fallon et al., 2012; Klempner et al., 2013). Convincing evidence for *Borrelia* infection in PTLDS patients has not been obtained using PCR, culture, or xenodiagnosis of blood and/or spinal fluid (Klempner et al., 2001; Fallon et al., 2008; Marques et al., 2014). In the absence of direct microbiologic evidence, response to extended therapy has come to be regarded as an alternative means of addressing the persistence question (Klempner et al., 2013). Five double-blind, placebo-controlled treatment trials in the U.S. and Europe have failed to demonstrate lasting benefit for extended therapy (Klempner et al., 2001; Kaplan et al., 2003; Krupp et al., 2003; Fallon et al., 2008; Berende et al., 2016). “Lyme literate” skeptics reject these results on methodologic grounds (DeLong et al., 2012; Fallon et al., 2012; Klempner et al., 2013), also pointing to the evidence, per above, that spirochetes *in vivo* become “persisters” refractory to

conventionally used agents (Stricker and Johnson, 2011; Sharma et al., 2015; Timmaraju et al., 2015; Feng et al., 2016b). Proponents of the persister theory were heartened by a highly publicized study maintaining, based on scant data for recovery of viable organisms, that spirochetes persisted in treated rhesus macaques (Embers et al., 2012). Agents that purportedly kill persister spirochetes *in vitro* have been identified (Sharma et al., 2015; Theophilus et al., 2015; Feng et al., 2016a; Feng et al., 2016c), while one group has reported that the combination of daptomycin plus doxycycline eradicated persister (aggregated, stationary phase) organisms from mice, whereas doxycycline plus ceftriaxone did not (Feng et al., 2019). One can safely predict that at some time in the future clinical trials of regimens believed capable of eliminating persister forms will be done.

In the absence of compelling evidence for bacterial persistence, other investigators lean towards the notion that spirochetes initiate an inflammatory process that is not turned off once the organisms have been eradicated. Using intravital microscopy in mice, Bockenstedt *et al.* (Bockenstedt et al., 2012) showed that *B. burgdorferi* antigens, but not infectious spirochetes, remain adjacent to cartilage for extended periods after antibiotic treatment; they proposed that this residual debris is the cause of ongoing inflammation. Investigations in humans also provide some, but not entirely consistent, support for a post-infectious inflammatory process. Strle *et al.* (Strle et al., 2014) reported that high IL-23 levels at presentation with early Lyme disease correlated with development of persistent symptoms, while Aucott *et al.* (Aucott et al., 2016) found elevated levels of the T cell chemokine CCL19 in PTLDS patients. Wormser's group found that PTLDS patients have significantly higher C-reactive protein (CRP) levels than treated patients who become asymptomatic (Uhde et al., 2016) or persons with chronic fatigue/fibromyalgia (Uhde et al., 2018). RNA-seq analysis of early Lyme disease patients revealed a differential gene expression signature that continued for at least six months post-treatment in symptomatic, but not asymptomatic, treated individuals (Bouquet et al., 2016). In contrast, another group recently reported that transcriptional signatures associated with early disseminated Lyme disease normalized within six months of antibiotic treatment (Petzke et al., 2020). And so it goes....

Future Directions

Lyme disease is now regarded as one of the first in a series of explosive infectious disease phenomena that gave rise to the contemporary concept of emerging infectious diseases - the notion that the infectious agents that impact human welfare are dynamic and strongly influenced by factors both within and outside the normal sphere of human activity. In fact, since the first description of the disease, we have come to appreciate the global dimensions of the threat to human health posed by *B. burgdorferi* sensu lato and its arthropod vectors. Over the years, the notoriety and novelty of the disease have attracted the attention of numerous investigators; as this article and other reviews (see Radolf and Samuels, 2021) attest, our knowledge of the disorder, its etiologic agent, and the natural world that shape them has expanded at a meteoric pace. So, what remains to be done from the perspective of disease in humans? Vaccine development is an obvious answer, although pharmaceutical companies have shown at best muted enthusiasm for the development of second-generation vaccines after the commercial failure and precipitous withdrawal of the first-generation vaccine based on OspA. Clearly, alternative prophylactic strategies that focus on preventing enzootic transmission and spread of the pathogen warrant great emphasis. But the major thrust needs to be in the realms of cellular and molecular pathogenesis.

While genetic and bioinformatics breakthroughs undoubtedly will be made, the ultimate question is how to interpret this information in the context of human disease. As any syphilologist will affirm, Lyme disease researchers are blessed not only with a cultivatable organism but an excellent and extremely versatile animal model whose full potential has not yet been realized. However, to quote a now clichéd maxim, "humans are not mice", and extrapolation is always fraught with danger. Nor are all the major features of human disease recapitulated by the murine model. As examples one need only point to erythema migrans and central nervous system complications, both of which underscore the existence of unique interactions between the spirochete and human cells. With the exception of AIDS, and, perhaps, COVID-19 most recently, no infectious disease presents a stronger paradigm for translational research. With the advent of systems biology and related genomics-based technologies, investigators need to build upon findings made with surrogate systems rather than regarding them as

ends in themselves. The stakes are high, judging by the intensity of the Lyme disease wars currently being waged on the medical and legal fronts (see Radolf and Samuels, 2021). We not only need to understand how *B. burgdorferi* accomplishes its parasitic strategy once introduced into humans, but also how the outcomes of this interaction differ from those seen in experimental systems and how engagement of the human immune system by the bacterium appears to leave debilitating footprints after its progress has been arrested.

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