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Sommario/riassunto	The interplay between host and pathogen is a complex co-evolutionary battle of surveillance and evasion. The pathogen continuously develops mechanisms to subvert the immune response in order to establish infection while the immune system responds with novel mechanisms of detection. Because the majority of Lyme disease pathology is due to an over-exuberant immune response, much research in Borrelia burgdorferi pathogenesis has been devoted to understanding the mammalian host response to the bacterium. Immunological studies continue to be an active area of research employing emerging techniques, such as intra-vital imaging. These studies have furthered our understanding of inflammatory processes during long-term infection and provided some surprising insights, such as the continued presence of bacterial products after clearance. The field of Lyme disease has long debated the etiology of long-term inflammation and recent studies in the murine host have shed light on relevant cell types and inflammatory mediators that participate in the pathology of Lyme arthritis. Live imaging and bioluminescent studies have allowed for a novel view of the bacterial life cycle, including the tick mid-gut, tick-to-mammal transmission and dissemination throughout a mouse. A

number of tick and bacterial proteins have been shown to participate in the completion of the enzootic cycle. Novel mechanisms of gene regulation are continuously being identified. However, B. burgdorferi lacks many traditional virulence factors, such as toxins or specialized secretion systems. Many genes in the B. burgdorferi genome have no known homolog in other bacteria. Therefore, studies focusing on host-pathogen interactions have therefore been limited by an incomplete understanding of the repertoire of bacterial virulence factors. Questions such as how the pathogen causes disease, colonizes the tick and evades host immune-surveillance have been difficult to address. Genetic studies involving single gene deletions have identified a number of important bacterial proteins, but a large-scale genomics approach to identify virulence factors has not been attempted until recently. The generation of a site-directed mutagenesis library is an important step towards a detailed analysis of the B. burgdorferi genome and pathogenome. Using this library, high-throughput genomic studies, utilizing techniques such as massively parallel sequencing have been promising and could be used to identify novel virulence determinants of disease in the mammalian host or persistence in the tick vector. Continued research on this unique pathogen and its specific interaction with host and vector may have far reaching consequences and provide insights for diverse disciplines including ecology, infectious disease, and immunology. Here, several reviews will discuss the most recent advances and future studies to be undertaken in the field of B. burgdorferi biology.