Immune escape strategies of *Borrelia burgdorferi*, the causative agent of Lyme disease

*Borrelia burgdorferi* sensu stricto, *B. afzelii*, *B. garinii*, *B. spielmanii*, and *B. bavariensis* all of which belong to the *B. burgdorferi* sensu lato-complex are the causative agents of Lyme disease or Lyme borreliosis in Europe. This multi-faceted disorder is the most commonly reported vector-borne infectious disease in Germany. Transmission of the highly motile, spiral-shaped bacteria to humans and vertebrate hosts occurs primarily through the bite of infected *Ixodes* spp. ticks. For prolonged survival in diverse environments such as arthropod vectors and vertebrate hosts, *Borrelia* have developed elegant and indispensable strategies to persistently infect and survive in the vector or diverse reservoir hosts (Fig. 1).

![Fig. 1: Immune escape strategies of *Borrelia burgdorferi*](image)

One particular strategy of spirochetes to efficiently overcome the innate immune system of their hosts involve natural resistance to complement-mediated killing. Previously, we have demonstrated that serum-resistant *Borrelia* express up to five distinct complement regulator-acquiring surface proteins or CRASPs to hijack immune regulators factor H, factor H-like protein 1 (FHL-1), and the factor H-related protein 1 (CFHR-1) from plasma for controlling complement activation on the bacterial surface thereby escaping from complement-mediated killing. In addition, we identified and characterized a number of CRASPs derived from serum-resistant *B. burgdorferi, B. afzelii* as well as *B. spielmanii* isolates on the molecular level (Fig. 2).
Fig. 2: CRASP proteins of distinct Borrelia species

Our current research focus is on the analysis of protein-protein interactions of borrelian outer surface lipoproteins with members of the factor H protein family and other human plasma proteins, e.g. plasminogen. Further analyses include studies on (i) the interaction of Borreliae with components of the extracellular matrix, (ii) serum susceptibility of other borrelian species with unknown human pathogenic potential, and (iii) the relevance of the species-specific resistance to complement-mediated killing by animal sera.

Combined, these studies are aimed at revealing more information on the pathogenesis of Lyme disease spirochetes and their different immune evasion mechanisms and may possibly lead to new therapeutic, diagnostic and preventative strategies for this common vector-borne zooanthroposisis.

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