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Comparative cryo-electron tomography of pathogenic Lyme disease spirochetes

Mikhail Kudryashev,¹ Marek Cyrklaff,^{1,2} Wolfgang Baumeister,² Markus M. Simon³, Reinhard Wallich⁴ ** and Friedrich Frischknecht¹ *

¹ Department of Parasitology, Hygiene Institute, University of Heidelberg Medical School, Im Neuenheimer Feld 324, 69120 Heidelberg, Germany.

² Department of Molecular Structural Biology, Max Planck Institute for Biochemistry, Am Klopferspitz 18, 82152 Martinsried, Germany.

³ Metschnikoff Laboratory, Max-Planck-Institute for Immunobiology, Stübeweg 51, 79108 Freiburg, Germany.

⁴ Institute for Immunology, University of Heidelberg Medical School, Im Neuenheimer Feld 305, 69120 Heidelberg, Germany.

Correspondence to *E-mail freddy.frischknecht@med.uni-heidelberg.de; Tel. (+49) 6221 566537; Fax (+49) 6221 564643; **E-mail reinhard.wallich@immu.uni-heidelberg.de; Tel. (+49) 6221 564090; Fax (+49) 6221 565611.

ABSTRACT

Spirochetes of the *Borrelia burgdorferi sensu lato* group, the causative agents of Lyme borreliosis, exhibit a complex biology evolved in its zoonotic cycle. Cryo-electron tomography was used to investigate structural features of three species, *B. burgdorferi*, *B. garinii* and *B. afzelii*, known to cause different clinical manifestations in humans. All three organisms revealed an overall similar architecture and showed different numbers of periplasmic flagellar filaments, polar periplasmic void regions, vesicles budding from the outer membrane sheath, which was covered by an amorphous slime layer. The latter was shown to be distinct in its density when comparing the three human-pathogenic Lyme disease spirochetes and *Borrelia hermsii*, a species causing relapsing fever. Tomograms of dividing bacteria revealed vesicles near the site of division and new basal bodies that were attached at each end of newly establishing cytoplasmic cylinder poles, while periplasmic flagellar filaments still passed the impending site of division. Two different kinds of cytoplasmic filaments showed similarities to MreB or FtsZ filaments of other bacteria. The similar and distinct structural features of *Borrelia* and the previously investigated pathogenic and non-pathogenic *Treponema* species emphasize the importance of further studying phylogenetically distant spirochetes.

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