

# Identification of evolutionary conserved DNA sequence and corresponding S21 ribosomal protein region for diagnostic purposes of all *Borrelia* spirochetes

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**It is still under investigation, whether all *Borrelia* sp. causing Lyme borreliosis and other diseases are already identified and properly classified as human pathogens. For this reason, it is of great importance to develop a diagnostic ELISA test that detects all *Borrelia* sp. The aim of this study was to identify conserved DNA and protein regions present in all currently known *Borrelia* sp. In experimental studies 31 available *Borrelia* sp. genomes were aligned and screened for the presence of evolutionary conserved regions. As a result of bioinformatics analysis, one evolutionally conserved DNA region encoding a core fragment of the S21 ribosomal protein was identified. Both a couple of genus-specific PCR primers and the S21 protein B-cell epitope were designed for prospective diagnostic purposes.**

**Keywords:** *Borrelia* sp., Lyme disease, diagnostic

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**Abbreviations:** ELISA, Enzyme-Linked Immunosorbent Assay; IgG, Immunoglobulin G; PCR, Polymerase Chain Reaction; PDB, Protein Data Bank

## INTRODUCTION

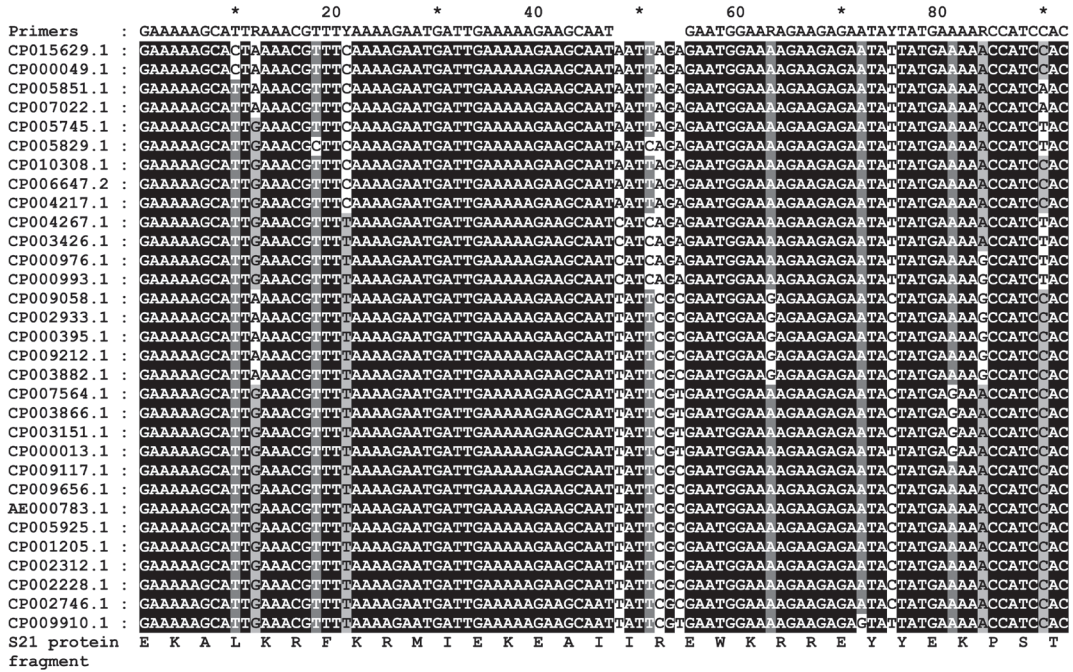
It is still under investigation if all the *Borrelia* species causing Lyme borreliosis and other diseases (Barstad *et al.*, 2018; Cutler *et al.*, 2016; Jahfari *et al.*, 2017; Stanek & Reiter, 2011), mainly around the N hemisphere, are fully identified and properly classified as human pathogens (Schneider *et al.*, 2008; Rudenko *et al.*, 2008). In the summer, people visiting the woodlands are exposed to the attack of ticks that can be vectors of virulent *Borrelia* sp. From a diagnostic point of view, the high genetic diversity of *Borrelia* sp. makes it difficult to detect specifically those species that are responsible for the development of the disease. Therefore, it is not easy to make progress in the field of accurate medical treatment of infected people and epidemiological studies. In the present study, conserved DNA sequences and the corresponding S21 ribosomal protein region were identified and found to be common to all *Borrelia* sp. deposited at the Gene Banks in NCBI (National Center for Biotechnology Information) and DDBJ (DNA Databank of Japan). Identification of all *Borrelia* sp. at a time can help in the detection of a rare pathogenic strain that cannot be identified using currently available tests specific to *Borrelia* sp. sensu lato and *Borrelia* sp. sensu stricto (Jahfari *et al.*, 2017). In the *16SrDNA* gene it is possible to identify conserved regions shared by all *Borrelia* sp. (Parola *et al.*, 2011; Ni

*et al.*, 2014). However, greater variability within the *flaB* gene requires optimization of DNA amplification conditions if genus-specific primers are used (Wodecka *et al.*, 2010). The conserved region of S21 gene discovered in our study can therefore be used as an alternative target in the diagnostics of *Borrelia* sp. by PCR, but mainly, as an additional test to exclude false positive results obtained for the *16SrDNA* or *flaB* genes, in the case of contamination of the samples by previous amplicons. However, we recommend the use of PCR-based tests to detect *Borrelia* sp. directly from ticks, rather than from clinical samples.

The immunological assays available commercially and assays developed in many laboratories worldwide have a widely divergent sensitivity and specificity (Kodym *et al.*, 2018). They are based on native whole-cell antigens, purified antigens (flagellar components), or whole-cell antigens combined with recombinant antigens. Furthermore, the vast majority of borrelial proteins are cross-reactive (Reed, 2002). The complexity of the antigenic composition among *Borrelia* genospecies and differential expression of proteins in the host and vector (temporal and spatial antigenic variability) has posed challenges for the serodiagnosis of borreliosis. This variability impedes the development of a single immunodiagnostic assay for all major *Borrelia* genospecies. The optimal combination of the most specific epitopes in the form of recombinant chimeric proteins could increase the discrimination abilities of serodiagnostic tests. In the present study we also designed a chimeric antigen for the specific detection of *Borrelia* sp.

## MATERIALS AND METHODS

In this study, 31 complete *Borrelia* sp. genomes were aligned using MAFFT v. 7.271 software (Kato *et al.*, 2002), and a DNA fragment encoding the most conserved protein within the entire *Borrelia* sp. proteome, S21, was identified. The conserved amino-acid sequence of the S21 protein was then compared with all protein sequences deposited at the Proteins Data Bank of Japan. Next, we used RaptorX Structure Prediction server (<http://raptorx.uchicago.edu/>) to predict the 3D structure of the whole S21 ribosomal protein and its conserved fragment (Figs. 3A and 3B, respectively). The 5MMJ PDB protein structure from the small subunit of the chloroplast *Spinacia oleracea* ribosome was selected by the RaptorX online software as a template (Bieri *et al.*, 2017) after comparison with all available 3D protein structures from Protein Data Bank (PDB) (Källberg *et al.*, 2012). B-cell epitopes present within the whole S21



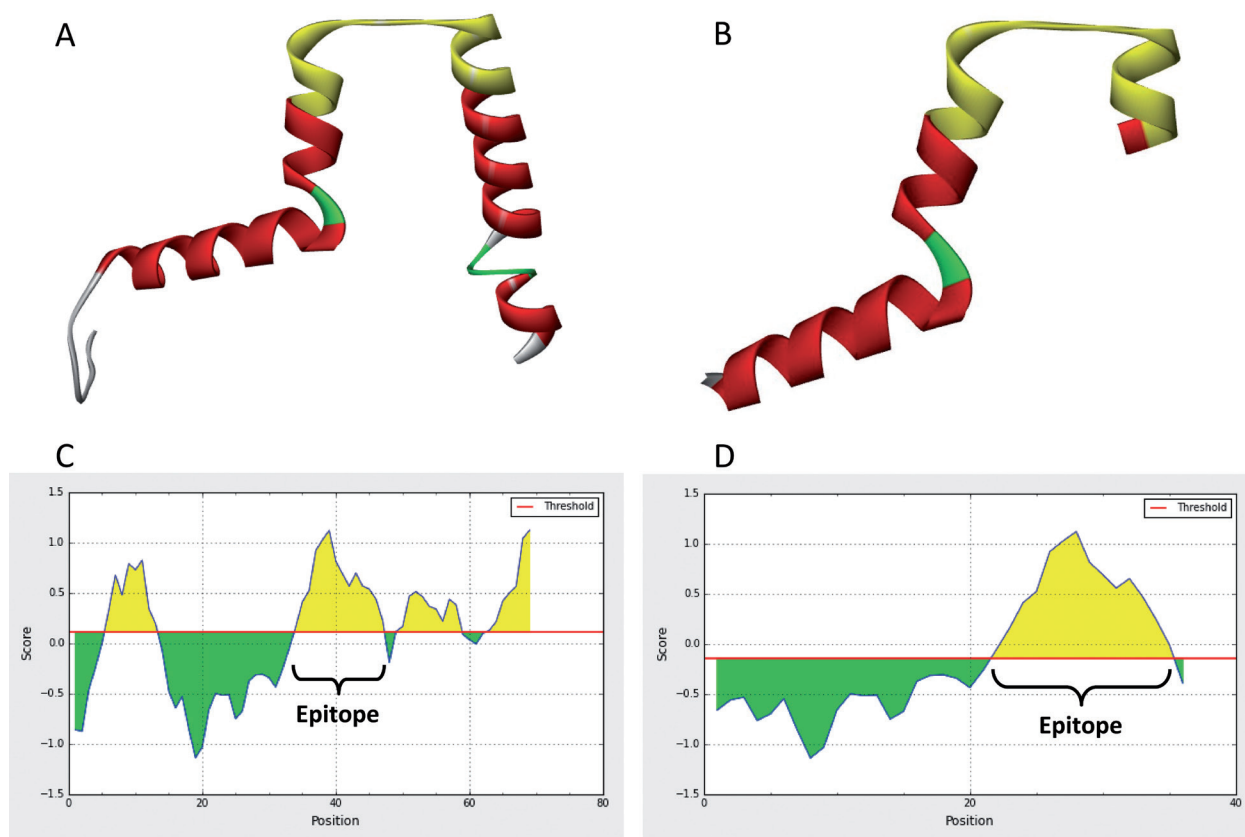
Bor\_spF 5' GAAAAGCATTAAACCGTTTAAAAGAAATGATTGAAAAGAAGCAAT  
 Bor\_spR 5' GTGGATGGYTTTTTCATARTATTCCTCTTCTYTTCCATTTC

Figure 1. Multiple sequence alignment of the S21 ribosomal protein gene fragment for 31 genomic sequences deposited at the National Centre for Biotechnology Information (NCBI). Bor\_spF and Bor\_spR are the degenerated primer sequences selected for PCR detection of all *Borrelia* sp.

>A0A0E1U9C3 *Borrelia burgdorferi* 64b, S21 ribosomal protein  
 MVTVTVDKNELEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVKEKAFKRKQAKKVRKLRKQKTNR  
 The most conserved protein region in *Borrelia* sp.

| UniProt Accession number | Species name                  | Amino-acid sequence of conserved region |
|--------------------------|-------------------------------|---|
| A0A0A7UV08               | <i>Borrelia chilonensis</i>   | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| G0AL63                   | <i>Borrelia bissettii</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| D6RX98                   | <i>Borrelia valaisiana</i>    | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A1L6VPK9               | <i>Borrelia mayonii</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| C0APY9                   | <i>Borrelia spielmanii</i>    | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A0E1U9C3               | <i>Borrelia burgdorferi</i>   | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| C0APG6                   | <i>Borrelia finlandensis</i>  | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| B7XSS9                   | <i>Borrelia garinii</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A1L8ZCR4               | <i>Borrelia bissettii</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| B7J1I4                   | <i>Borrelia burgdorferi</i>   | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| O51271                   | <i>Borrelia burgdorferi</i>   | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| Q662A9                   | <i>Borrelia bavariciensis</i> | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| Q0SNQ5                   | <i>Borrelia afzelii</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A1G4PL64               | <i>Borrelia japonica</i>      | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| I0FC33                   | <i>Borrelia crocidurae</i>    | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A142JBW0               | <i>Borrelia hermsii</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| W5SZF6                   | <i>Borrelia coriaceae</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| W5SHF8                   | <i>Borrelia crocidurae</i>    | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| W5SMU4                   | <i>Borrelia anserina</i>      | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| B5RR73                   | <i>Borrelia recurrentis</i>   | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| B2RZW7                   | <i>Borrelia hermsii</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| B5RL82                   | <i>Borrelia duttonii</i>      | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| W5SDG3                   | <i>Borrelia miyamotoi</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A1D8TDL4               | <i>Borrelia miyamotoi</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A172XAR9               | <i>Borrelia turicatae</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A0A0E1C180               | <i>Borrelia hermsii</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| A1QZ52                   | <i>Borrelia turicatae</i>     | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| W6TIG2                   | <i>Borrelia parkeri</i>       | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |
| W5SR45                   | <i>Borrelia duttonii</i>      | LEKALKRFRKRMIEKEAIIREWKRREYEEKPSTIRVK   |

Figure 2. Multiple sequence alignment of the S21 protein fragment of 29 *Borrelia/Borrelia* sp. amino acid sequences deposited in the Protein Bank of Japan. Highlighted in grey is the conserved region characteristic for ribosomal S21 protein of *Borrelia/Borrelia* sp. The predicted B-cell epitope is distinguished on a black background.



**Figure 3. The structure of ribosomal S21 protein of *Borrelia burgdorferi* 64b obtained using homology modelling.**

(A) – the entire amino-acid sequence of the S21 protein; (B) – the conserved region within S21 proteins from *Borrelia/Borrelia* sp.; (C) – predicted B-cell epitope within the whole S21 ribosomal protein; (D) – predicted B-cell epitope within the conserved region of the S21 ribosomal protein of *Borrelia/Borrelia* sp.

ribosomal protein and the S21 conserved protein motif were predicted using B Cell Epitope Prediction Tools (<http://tools.immuneepitope.org/main/bcell/>), (Larsen *et al.*, 2006).

## RESULTS AND DISCUSSION

Multiple alignments of *Borrelia* sp. genomes allowed for the selection of the most conserved DNA protein coding region (Fig. 1). The identified DNA region was used to design slightly degenerate PCR primers: Bor\_spF and Bor\_spR specific to all *Borrelia* sp. Translation of the selected DNA region revealed, irrespective of point mutations in the DNA sequences from different genomes, an identical amino-acid chain among all of the analyzed *Borrelia* sp, suggesting that this core part of the ribosomal S21 protein is evolutionary conserved. All amino-acid sequences with 100% similarity identified using BLAST server at DDBJ belonged to the genus *Borrelia/Borrelia* (Fig. 2). The conserved part of S21 ribosomal protein may potentially serve as an intracellular antigen, indicating active human infection caused by all of the *Borrelia* spirochetes on the basis of ribosomal metabolism. The structure prediction analysis confirmed a similar 3D-conformation for both the entire S21 protein and for the conserved region only (Figs. 3A and 3B, respectively). Therefore, based on bioinformatics analysis, we can speculate that it will be possible to immunize animals for the production of specific antibodies using the S21 protein conserved region. Because the selected S21 protein fragment has a molecular weight below 5kDa, it may

act as a hapten that is capable of inducing an immune response and recognizing specific antibodies only when attached to a large carrier such as a protein or assembled into one chimeric protein with other fragments of various antigens. This is why we suggest combining two genus-specific protein fragments, the S21 conserved peptide (Fig. 2) and, for example, a part of the FlaB protein: QIRGLSQASRNTSKAINFIQTTEGNL. Successful application of chimeric proteins, assembled using molecular biology techniques, in immunological assays for the diagnosis of viral, bacterial and parasitic diseases has already been demonstrated (Alcaro *et al.*, 2003; Holec-Gąsior *et al.*, 2012a, Holec-Gąsior *et al.*, 2012b; Drapala *et al.*, 2014; Ferra *et al.*, 2015). To date, only a few studies have shown the reactivity of this kind of proteins with specific IgG antibodies from human sera of individuals with Lyme borreliosis (Gomes-Solecki *et al.*, 2000; Schreterova *et al.*, 2017). However, chimeric proteins are a new generation of recombinant products which have the potential to replace the native antigen (e.i. crude fractions of sonicated cells of microorganisms). Furthermore, the construction of recombinant chimeras containing genes from several genospecies can allow generating one protein that confers antigenicity to multiple strains. In addition, the use of pure chimeric proteins as diagnostic antigens provides greater flexibility in adapting the test to different assay formats. Thus, the S21-FlaB fusion peptide proposed in this study appears to be a very promising antigen. The core region of the S21 protein contains the B-cell epitope (Figs. 3C and 3D), whereas FlaB, the major endoflagellar filament protein (Motaleb *et al.*,



2000), acts as an antigen targeting the initial antibody response of the host (Aguero-Rosenfeld *et al.*, 1993). The advantage of the chimeric antigen designed in this study is 100% specificity to all *Borrelia* sp. and the presence of two different antigens.

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### LITERATURE

- Aguero-Rosenfeld ME, Nowakowski J, McKenna DF, Carbonaro CA, Wormser GP (1993) Serodiagnosis in early Lyme disease. *J Clin Microbiol* **31**: 3090–3095
- Alcaro MC, Peroni E, Rovero P, Papini AM (2003) Synthetic peptides in the diagnosis of HIV infection. *Curr Protein Pept Sci* **4**: 285–290
- Barstad B, Quarsten H, Tveitnes D, Noraas S, Ask IS, Saeed M, Bosse F, Vigemyr G, Huber I, Øymar K (2018) Direct molecular detection and genotyping of *Borrelia burgdorferi* sensu lato in cerebrospinal fluid of children with Lyme neuroborreliosis. *J Clin Microbiol* **56**: pii: e01868-17. doi: 10.1128/JCM.01868-17
- Bieri P, Leibundgut M, Saurer M, Boehringer D, Ban N (2017) The complete structure of the chloroplast 70S ribosome in complex with translation factor pY. *EMBO J* **36**: 475–486. doi: 10.15252/embj.201695959
- Cutler SJ, Ruzic-Sabljić E, Potkonjak A (2017) Emerging borreliae - Expanding beyond Lyme borreliosis. *Mol Cell Probes* **31**: 22–27. doi: 10.1016/j.mcp.2016.08.003
- Drapala D, Holec-Gąsior L, Kur J (2015) New recombinant chimeric antigens, P35-MAG1, MIC1-ROP1, and MAG1-ROP1, for the serodiagnosis of human toxoplasmosis. *Diagn Microbiol Infect Dis* **82**: 34–39
- Ferra B, Holec-Gąsior L, Kur J (2015) A new *Toxoplasma gondii* chimeric antigen containing fragments of SAG2, GRA1, and ROP1 proteins-impact of immunodominant sequences size on its diagnostic usefulness. *Parasitol Res* **114**: 3291–3299. doi: 10.1007/s00436-015-4552-6
- Gomes-Solecki MJ, Dunn JJ, Luft BJ, Castillo J, Dykhuizen DE, Yang X, Glass JD, Dattwyler RJ (2000) Recombinant chimeric *Borrelia* proteins for diagnosis of Lyme disease. *J Clin Microbiol* **38**: 2530–2535
- Holec-Gąsior L, Ferra B, Drapala D, Lautenbach D, Kur J (2012a) A new MIC1-MAG1 recombinant chimeric antigen can be used instead of the *Toxoplasma gondii* lysate antigen in serodiagnosis of human toxoplasmosis. *Clin Vaccine Immunol* **19**: 57–63
- Holec-Gąsior L, Ferra B, Drapala D (2012b) MIC1-MAG1-SAG1 chimeric protein, a most effective antigen for detection of human toxoplasmosis. *Clin Vaccine Immunol* **19**: 1977–1979
- Jahfari S, Krawczyk A, Coipan EC, Fonville M, Hovius JW, Sprong H, Takumi K (2017) Enzootic origins for clinical manifestations of Lyme borreliosis. *Infect Genet Evol* **49**: 48–54. doi: 10.1016/j.meegid.2016.12.030
- Katoh K, Misawa K, Kuma K, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Res* **15**: 3059–3066
- Källberg M, Wang H, Wang S, Peng J, Wang Z, Lu H, Xu J (2012) Template-based protein structure modeling using the RaptorX web server. *Nat Protoc* **7**: 1511–1522. doi:10.1038/nprot.2012.085
- Kodym P, Kurzová Z, Berenová D, Pícha D, Smíšková D, Moravcová L, Malý M (2018) Serological diagnostics of Lyme borreliosis: comparison of universal and *Borrelia* species-specific tests based on whole-cell and recombinant antigens. *J Clin Microbiol* **56**: pii: e00601-18. doi: 10.1128/JCM.00601-18
- Larsen JE, Lund O, Nielsen M (2006) Improved method for predicting linear B-cell epitopes. *Immunome Res* **2**: 2. doi:10.1186/1745-7580-2-2
- Motaleb MA, Corum L, Bono JL, Elias AF, Rosa P, Samuels DS, Charon NW (2000) *Borrelia burgdorferi* periplasmic flagella have both skeletal and motility functions. *Proc Natl Acad Sci USA* **97**: 10899–10904. doi: 10.1073/pnas.200221797
- Ni XB, Jia N, Jiang BG, Sun T, Zheng YC, Huo QB, Liu K, Ma L, Zhao QM, Yang H, Wang X, Jiang JF, Cao WC (2014) Lyme borreliosis caused by diverse genospecies of *Borrelia burgdorferi* sensu lato in northeastern China. *Clin Microbiol Infect* **20**: 808–814. doi: 10.1111/1469-0691.12532
- Parola P, Diatta G, Socolovschi C, Mediannikov O, Tall A, Bassene H, Trape JF, Raoult D (2011) Tick-borne relapsing fever borreliosis, rural Senegal. *Emerg Infect Dis* **17**: 883–885. doi: 10.3201/eid1705.100573
- Reed KD (2002) Laboratory testing for Lyme disease: Possibilities and practicalities. *J Clin Microbiol* **40**: 319–324
- Rudenko N, Golovchenko M, Růžek D, Piskunova N, Mallátová N, Grubhoffer L (2008) Detection of *Borrelia bissettii* in cardiac valve tissue of a patient with endocarditis and aortic valve stenosis in the Czech Republic. *J Clin Microbiol* **46**: 3540–3543. doi:10.1128/JCM.01032-08
- Schneider BS, Schriefer ME, Dietrich G, Dolan MC, Morshed MG, Zeidner NS (2008) *Borrelia bissettii* isolates induce pathology in a murine model of disease. *Vector-Borne Zoonotic Dis* **8**: 623–633. doi:10.1089/vbz.2007.0251
- Schreterova E, Bhide M, Potocnakova L, Borszekova Pulzova L (2017) Design, construction and evaluation of multi-epitope antigens for diagnosis of Lyme disease. *Ann Agric Environ Med* **24**: 696–701
- Stanek G, Reiter M (2011) The expanding Lyme *Borrelia* complex - clinical significance of genomic species. *Clin Microbiol Infect* **17**: 487–493. doi:10.1111/j.1469-0691.2011.03492.x
- Wodecka B, Leońska A, Skotarczak B. (2010) A comparative analysis of molecular markers for the detection and identification of *Borrelia* spirochaetes in *Ixodes ricinus*. *J Med Microbiol* **59**: 309–314. doi: 10.1099/jmm.0.013508-0