# International Symposium on Tick-Borne Pathogens and Disease

## ITPD 2019 Vienna, Austria
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Under the auspices of the Austrian Society for Hygiene, Microbiology and Preventive Medicine (ÖGHMP)

**Organisers**

ÖGHMP and ESGBOR

**Venue**

Parkhotel Schönbrunn, Vienna, Austria

# Preliminary Programme

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Österreichische Gesellschaft für Hygiene, Mikrobiologie und Präventivmedizin

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and

ESCMID

**ESGBOR**
ESCMID Study Group for Lyme Borreliosis

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**AZ Med.Info**
Contact: Lisa Thek, Natalie Ubl
Phone: +43 1 531 16-74 or -75
Fax: +43 1 531 16-61
E-mail: azmedinfo@media.co.at

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MAW Exhibition Management
Contact: Kerstin Hamata
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P77 **Subtypes of Borrelia burgdorferi sensu lato strains from Serbia characterized by pulsed-field gel electrophoresis after MluI restriction of genomic DNA**

Sanja Ćakić 1, Tjaša Cerar-Kišek 2, Gorana Veinović1, Darko Mihaljica 1, Ratko Sukara 1, Eva Ružić-Sabljić 2 Snežana Tomanović1

1Group for Medical Entomology, Centre of Excellence for Food and Vector Borne Zoonoses, Institute for Medical Research, University of Belgrade, Belgrade, Serbia, 2Laboratory for Diagnostics of Borreliosis and Leptospirosis, Institute for Microbiology and Immunology, Faculty of Medicine, University of Ljubljana, Ljubljana, Slovenia

The geographic distribution of *Borrelia burgdorferi* sensu lato species in Europe exhibits dynamic spatial and temporal variations. The observation that genetically divergent strains within the same *Borrelia* species show different tendencies for haematogenous dissemination after tick bite gave rise to the notion of different pathogenicity of strains. The aim of this study was subtype delineation of *B. burgdorferi* sensu lato strains isolated from unfed *Ixodes ricinus* ticks from different eco-geographical regions in Serbia. It has been shown that pulsed-field gel electrophoresis after *Mlu*I restriction of the genomic DNA (*Mlu*I Large Restriction Fragment patterns- MluI-LRFP) represents a highly specific and reproducible method for *Borrelia* genotypization. Results of the present study are based on 28 local strains previously classified into four species: *B. afzelii* (n=14), *B. garinii* (n=6), *B. valaisiana* (n=2), *B. lusitaniae* (n=8). Using MluI-LRFP, we were able to delineate all *Borrelia* species included in the study. Each of the 4 examined *Borrelia* species displayed unique MluI-LRFPs that enabled straightforward separation of strains into particular species, and also subtypes of strains within species. Among analyzed strains following MluI-LRFP subtypes were recognized: *B. afzelii* - Mla1 (13/14, 92.8%) and Mla2 (1/14, 7.2%), *B. garinii* - Mlg1 (1/6, 16.7%) and Mlg2 (5/6, 83.3%), *B. valaisiana* - Mlv1 and Mlv2, *B. lusitaniae* - Mll2 (2/8, 25%), Mll3 (2/8, 25%), Mll4 (2/8, 25%), Mll5 (2/8, 25%). The subtypes of *B. lusitaniae* (Mll3, Mll4, and Mll5) identified in the present analysis have not been reported previously. Considering the presence of different subtypes of pathogenic species, *B. afzelii*, *B. garinii*, and two species with a potential pathogenic risk, i.e. *B. lusitaniae* and *B. valaisiana*, we conclude that Serbia represents an area with a high risk for Lyme borreliosis (LB). Genotyping of local strains will greatly improve understanding of LB in Serbia.