



24th Annual Congress

ESVCP 2022 ECVCP

European Society of Veterinary Clinical Pathology
College

Belgrade, Serbia | October 5-8, 2022

Programme Proceedings &



www.esvcp-belgrade.rs



oral presentations

CANINE BABESIOSIS THROUGH THE EYES OF PROTEOMICS AND METABOLOMICS

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The research of canine babesiosis (CB), a common vector-borne disease, is reminiscent of a never-ending story with the continual intricacies regarding epidemiology, molecular pathogenesis, natural course, translational aspects, etc. Proteomics and metabolomics are the rapid-evolving, powerful “-omic” disciplines focused on the deciphering (patho)biological pathways. The lecture brings a glance into the proteomics and metabolomics contribution to the comprehensive understanding of CB. Most of the studies addressed CB caused by *Babesia canis*. In adjunction to the gene expression analysis, the proteomic approach added new pieces to the puzzle of the host-parasite interaction: the proteins involved in invasion, virulence, and escaping the immune mechanisms. The proteomic studies using serum also provided valuable details for the perception of the systemic response during CB, involving inflammation, hemolysis, hemostatic alterations, dyslipidemia, protein modifications, etc. The combined application of the three metabolomic approaches in serum pinpointed the alterations in the metabolism of amino acids, small peptides, polyamines, and several classes of lipids. Also, the analyses of the urinary proteome indicated several pathways whose interplay forms the basis for acute kidney injury, one of the most frequent CB complications.



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The metabolic study yielded further phenotypic details for urine, including changes in the metabolism of amino and fatty acids, and in the urea cycle. The advanced achievements in the field of CB proteomics and metabolomics will “shed the light” on the currently hidden pathophysiology mechanisms and pave the way for the high-volume clinical validation of the discovered biomarkers.

Keywords: *Canine babesiosis, proteomics, metabolomics, serum, urine*

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