



ICP 2022 DUBLIN

International Association
for Paratuberculosis

ABSTRACT BOOK

ICP 2022

15th International Association
for Paratuberculosis

12 -16 June 2022 | Dublin Castle

[@paratb2022](#)



An Roinn Talmhaíochta,
Bia agus Mara
Department of Agriculture,
Food and the Marine



International Association
for Paratuberculosis

Proteomic analysis of sera from Holstein Friesian cows with different pathological forms of bovine paratuberculosis (PTB)

Miss ALEJANDRA ISABEL Navarro Leon¹, Dr. Marta Muñoz¹, Miss Natalia Iglesias¹, Miss Cristina Blanco Vázquez¹, Dr. Ana Balseiro², Dr. Fernando J. Corrales³, Dr. Sergio Ciordia³, Dr. Fátima Raquel Milhano³, Dr. Rosa Casais¹

¹Center for Animal Biotechnology, Servicio Regional de Investigación y Desarrollo Agroalimentario (SERIDA), 33394, Gijón, Spain, ²Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León; Instituto de Ganadería de Montaña (IGM, CSIC-ULE), Finca Marzanas, Grulleros, 24346, León, Spain, ³Functional Proteomics Laboratory, National Center for Biotechnology, Consejo Superior de Investigaciones Científicas (CSIC), , Spain

The lack of sensitive diagnostic methods able to detect *Mycobacterium avium* subspecies paratuberculosis (MAP) subclinical infected animals is an obstacle for PTB control. Sera collected from naturally infected Holstein Friesian cows with different pathological forms of PTB and negative control animals with no lesions detected (n=4, each group) were analyzed using TMT-6plex quantitative proteomics to identify and quantify peptides/proteins differentially expressed (DE) between groups. Three comparisons were performed: focal versus (vs.) control, diffuse vs. control, and focal vs. diffuse. One (focal vs. control), eight (diffuse vs. control) and four (focal vs. diffuse) DE bovine proteins (q-value \leq 0.05) were identified. Alpha-1-acid glycoprotein (ORM1) was found to be upregulated in animals with focal and diffuse lesions vs. control animals, while Bovine Fetuin-B, Vitamin D-binding protein, and Complement component C6 were found exclusively upregulated in animals with diffuse lesions. Upregulation of Lipopolysaccharide-binding protein and Serpin domain-containing protein was found in animals with focal lesions vs. animals with diffuse lesions. In addition to the above-mentioned DE proteins, other proteins (q-value > 0.05 and p-value < 1- π 0) likely to be involved in relevant biological processes were analyzed with the Ingenuity Pathway Analysis (IPA) software tool. These proteins are involved in different biological processes such as humoral immune response, inflammatory response, and organismal injury and abnormalities. Considering the fold change, cellular localization, and biological function, eight of these DE proteins included in the resulting IPA networks were selected for further validation by specific Western Blot analysis and ELISA, using a set of serum samples from 127 animals with different pathological forms of PTB and 138 control animals from PTB-free farms. In this study, we obtained the serum proteomic profiles of animals with different pathological forms of MAP infection, which contributes to a better understanding of the pathogenesis of PTB and could provide new potential diagnostic biomarkers for PTB.