

PROTEOMIC ANALYSIS OF SERA FROM RHEUMATOID ARTHRITIS B6 WT AND CD38KO MICE BY USING PROTEOMINER FRACTIONATION AND TWO-DIMENSIONAL DIFFERENCE GEL ELECTROPHORESIS (DIGE)

A. Rosal-Vela⁽¹⁾, *J. Postigo*⁽²⁾, *S. García-Rodríguez*⁽¹⁾, *E. Zumaquero*⁽¹⁾, *M.V. Longobardo*⁽¹⁾, *A. Lario*⁽¹⁾, *P. Navarro*⁽¹⁾, *R. Merino*⁽³⁾, *J. Merino*⁽²⁾, *M. Zubiaur*⁽¹⁾, *J. Sancho*⁽¹⁾.

⁽¹⁾ Instituto de Parasitología y Biomedicina "López-Neyra", CSIC, ⁽²⁾ Facultad de Medicina, Universidad de Cantabria, ⁽³⁾ Instituto de Biomedicina y Biotecnología de Cantabria, CSIC.

Rheumatoid arthritis (RA) is a systemic, chronic, autoimmune disease that affects joints producing inflammation and destruction of the articular cartilage. Combination of the collagen-induced arthritis (CIA) model and knock-out mice can increase the understanding of pathogenesis of RA. Proteominer[®] changes the dynamic range of the serum proteome reducing high abundant proteins in serum such as albumin, IgG, transferrin, etc., and increases the concentration of low abundant proteins, which can help to identify low abundant proteins as potential biomarkers, or proteins involved in the case of study.

Proteomic analysis of sera from CIA B6 wt and CD38ko mice by using ProteoMiner fractionation and 2-D DIGE.

Serum samples from wt and CD38ko mice affected and non-affected with the disease were applied to Proteominer[®] Small-Capacity kit (BioRad). DIGE experimental design and labeling procedure was performed following manufacturer's instructions (GE Healthcare). First dimension of 2-D gels were run on Protein IEF Cell and second dimension on Criterion Dodeca Cell (BioRad). Gels were scanned with the Amersham Typhoon Imager 9410 and gel images were analyzed using Amersham DeCyder 6.0 software. SYPRO Ruby stained gel spots were excised, trypsin-digested and proteins were identified by mass spectrometry.

About 300 spots were detected. Among them, 25 proteins had different expression profile between wt and CD38ko mice affected with RA. Some proteins such as ceruloplasmin, Complement C4B, ficolin, Complement factor H, and IgG were significantly over-expressed in wt mice (>1.5 fold), while transferrin or transthyretin were significantly over-expressed in CD38ko mice.

Most of the differentially expressed proteins identified in the sera of RA+ B6 wt versus RA+ CD38ko mice are involved in inflammatory processes, and they belong to the group of medium and low abundant proteins in sera. Some of them could be indicative of the relatively mild pathological process found in RA+ CD38ko mice.