Proteomic analysis of THP-1 cells exposed to dyslipidemic and atherosclerotic serums

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INTRODUCTION

Atherosclerosis is caused by lipids accumulation in arteries and vessels, leading to the development of atheroma plaques. During the process, different cell types suffer alterations that makes them to accumulate in the arterial intima. A key player in the atheroma plaque formation are foam cells, macrophages that internalize modified cholesterol, such as the oxidized LDL. Recent studies are focused on the study of THP-1 cell line to analyze the macrophages role and behaviour in atherosclerotic environment.

In this study, a label free quantitative (LFQ) proteomic analysis has been performed, with the objective of finding biomarkers and signaling and metabolic pathways that are altered in THP-1 cells, after being exposed to different serum of dyslipidemic, dyslipidemic with complications (+) and atherosclerotic patients.



DIFFERENTIAL EXPRESSION ANALYSIS

EXPLORATORY ANALYSIS AND DATA CLUSTERING













Figure 1. Heatmap of some differential proteins and PLS-DA graphic (RStudio). Venn diagram and upsetplot that show which proteins are differentially expressed for different comparisons (amica).

🔵 Downregulated 🛛 🛑 Upregulated

Figure 2. Volcano plots diagrams (Rstudio) representing the differential protein expression in THP-1 after the incubation with the serum. Differences were considered significant when p-value < 0.05 and log2 (Fold-Change) > 0.5 / < -0.5

FUNCTIONAL ENRICHMENT ANALYSIS





DLP+_913

DLP+_763

25

2222

Figure 3. Differential proteins network from AT vs DLP+ comparison (STRING), enriched functions selection from AT vs DLP+ contrast, with their respective -log (p-values) (Enrichr), and violin plot representation of a differential protein.

Preliminary results display 5580 identified proteins, and show different expression patterns in THP-1 cells in response to the incubation with the serum from different patients. Some processes obtained in functional analysis were associated with lipids metabolism, apoptosis, immune response and macrophages markers.