

## CHARACTERIZATION OF INDIVIDUALIZED PROTEOMIC PROFILES IN ST-SEGMENT ELEVATION AND NON ST-SEGMENT ELEVATION ACUTE CORONARY SYNDROME

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**INTRODUCTION:** Acute Coronary Syndrome (ACS) is one of the main causes of morbidity and mortality in developed countries. Despite the research advances in recent years, ACS prevention and treatment strategies still suffer from significant limitations therefore new theoretical and technical approaches are required. The application of proteomics to ACS research constitutes an invaluable tool for the searching of new disease mechanisms, novel biomarkers and therapeutic targets, as well as to increase our understanding of the origin and development of this syndrome. In this work, we focused in the establishment of an individualized proteomic profile in non ST-segment elevation ACS (NSTEMI-ACS) and ST-segment elevation ACS (STEMI-ACS) using two-dimensional difference gel electrophoresis (2D-DIGE) and mass spectrometry (MALDI-TOF/TOF).

**MATERIAL AND METHODS:** EDTA plasma samples of 20 patients with NSTEMI-ACS, 20 patients with STEMI-ACS and 20 healthy controls recruited from the cardiology service of Hospital Virgen de la Salud were collected for this study. 2D-DIGE experiments were carefully designed for STEMI-ACS vs healthy controls (n=6) and for NSTEMI-ACS vs healthy controls (n=5). Previously, all plasma samples were depleted using a Multi Affinity Removal column (MARS Hu-14, Agilent Technologies). Selected reaction monitoring (SRM) and immunoblotting were used for the validation process.

**RESULTS:** 2-D Differential analysis revealed 24 differentially expressed spots in plasma of NSTEMI-ACS patients (12 upregulated, 12 downregulated) and 47 in STEMI-ACS (13 upregulated, 34 downregulated). The identification step is currently being completed and several of the identified proteins have already been validated.

**CONCLUSIONS:** Our proteomic 2D-DIGE experiments demonstrate that STEMI-ACS and NSTEMI-ACS can be defined by different and individualized proteomic profiles. These results could illuminate the understanding of changes implicated in the atherosclerotic process in both cases. We also expect to identify interesting proteins, which could be used as novel potential biomarkers for the prognosis and/or treatment of ACS in clinical practice.