

PROTEOMICS AND METABOLOMICS OF HUMAN ATHEROSCLEROTIC ARTERIES

Fernando Vivanco

Fundación Jiménez Díaz

In the last years vascular proteomics has experienced an impressive development and the majority of the proteomic techniques have been applied to study the atherosclerotic lesions. Among the multiple types of samples that can be studied (tissue, cells, circulating cells, etc.) to gain insight on the atherothrombotic process, we have chosen the analysis of secretomes of human arteries, including coronary, mammary and radial arteries. The rationale for this selection is because, most probably, the secretome is the best source for the identification of potential novel biomarkers of atherosclerosis. Thus, we have analysed the secretome of human arteries using a novel protocol that avoids contaminant plasma proteins and permits the identification of the true secreted proteins. A comparative analysis of the secretomes from human coronary, mammary and radial arteries will be presented. In a further step, validation of the arterial origin of the proteins was performed, incubating arterial sections with isotopically labelled amino acids.

The SIMS-TOF analysis of human carotid arteries, in a group of diabetes type 2 patients, showing the distribution of several lipids within the artery wall, and their involvement in the inflammatory process, will be also presented.