

PROTEOMIC ANALYSIS OF INTIMAL LAYER FROM HUMAN CORONARY ATHEROTHROMBOTIC ARTERIES

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Introduction: The study of coronary artery atherothrombosis is of relevance nowadays as it is one of the leading causes of mortality in developed world. Early detection of the pathology could prevent in most cases complications derived from coronary obstruction due to atherome plaque rupture. Proteomic differential expression analysis of human atherosclerotic coronary arteries versus healthy arteries could highlight diagnostic and prognostic biomarkers of coronary artery disease (CAD). Complete artery tissue proteomic studies involve analysis of many cell types at a time which may show different proteomic profiles at different locations in the vessel. Atherosclerotic process initiates at the intima so that proteomic analysis of this layer independently of the media and adventitia is mandatory in the search for early diagnosis biomarkers of CAD.

Methods: Intimal layer from 12 human specimens of coronary with atherome plaque and radial (control) biopsies from coronary bypass surgery and atherosclerotic and healthy coronary necropsies was isolated by laser microdissection and pressure catapulting (LMPC). Combination of LMPC with saturation labelling DIGE allowed us to perform 2-DE based differential protein abundance analysis with less than 5 µg of intimal protein subproteome.

Results: 30 spots showed significant variation in atherothrombotic arteries in comparison to healthy arteries. Identification of those spots is carried out on a 4800 MALDI-TOF/TOF Analyzer (Applied Biosystems).