

DIFFERENT GENE EXPRESSION MODULATION IS THE MAJOR EFFECT DUE TO SHEAR STRESS AND STENT APPLICATION IN HUVECS MODEL: PRELIMINARY RESULTS

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Aim: Although it is known that disturbed shear stress may cause endothelial damage, the mechanism by which a stent procedure may affect the endothelium is not yet fully clarify. We present the preliminary data on gene expression analysis of human endothelial cells in a laminar flow bioreactor (LFB) system submitted to different physical (flow changes) and/or mechanical (stent application) stimuli.

Methods: HUVECs are submitted to low and physiological (1 and 10 dyne/cm²) shear stress in absence (AS) or presence (PS) of stent positioning in a LFB system for 24 hours. Gene expression profile was assessed using Affymetrix platform after total RNA extraction. Different expressed genes were identified based on one-way ANOVA analysis with p values of < 0.01 and a fold changed > 3 in modulus. Low shear stress was compared with physiological one in AS and PS conditions.

Results: We identified two major gene clusters: cluster 1 includes twenty six genes commonly expressed in both 1AS versus 10AS and 1PS versus 10PS comparison; cluster 2 includes 78 genes found in 1PS versus 10PS condition only. The first cluster involves several mediators of inflammatory and apoptotic response while the second one different regulators of cell cycle, lipid metabolism and cytoskeleton organization.

Conclusions: Our preliminary results show that low shear stress together with stent procedure are the experimental conditions that mainly modulate the highest number of genes in human endothelial model. Those genes belong to pathways specifically involved in the endothelial dysfunction.

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