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Nancy Lee
University of Massachusetts Medical School

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Expression of the Integrin Beta 8 Gene (ITGB8) in Epicardial Adipose Tissue is Highly and Directly Correlated with the Degree of Coronary Atherosclerosis

Nancy Lee¹, Sarah Nicoloro², Juerg Straubhaar², Melinda Darrigo², Stanley Tam³, Michael Czech², Timothy Fitzgibbons⁴

¹University of Massachusetts Medical School, Worcester, MA
²University of Massachusetts Medical School, Program in Molecular Medicine, Worcester, MA
³University of Massachusetts Medical School, Department of Medicine, Division of Cardiovascular Medicine, Worcester, MA
⁴University of Massachusetts Medical School, Department of Surgery, Division of Cardiothoracic Surgery, Worcester, MA

Contact: Nancy Lee, nancy.lee@umassmed.edu

Background: In patients with coronary artery disease (CAD), epicardial adipose tissue (EAT) expression of inflammatory genes is high while expression of anti-inflammatory genes is low. We hypothesized that expression of certain genes in EAT would correlate directly with the degree of adjacent CAD. Methods: EAT and paired subcutaneous adipose tissue (SAT) samples were collected from cardiac surgery patients (n=9) with and without CAD. RNA was isolated and hybridized to Affymetrix 1.0 ST chips. Genes differentially expressed in EAT vs. SAT were identified. Probe intensities were correlated with the severity of CAD in each patient using the Gensini score. Results: 35 genes were differentially expressed in EAT at >3.0 fold change (p<0.05). Of these, 14 were correlated with the Gensini score. Expression of ITGB8 had the strongest positive correlation (r=0.94, p<0.01), while TGM2 had the strongest negative correlation (r=-0.80, p<0.01). Importantly, neither of these correlations held true in SAT (Fig. 1). Conclusions: Expression of ITGB8 is directly correlated with CAD severity. ITGB8 has been previously shown to be expressed by fibroblasts and functions to activate TGFβ. TGFβ signaling has also been correlated with advanced atherosclerosis. We speculate that EAT expression of ITGB8 may have pro-inflammatory effects, possibly by activating TGFβ, and stimulating recruitment of dendritic cells or T cells to secondary lymphoid organs in EAT. Whether or not this is the case is a goal of future studies.