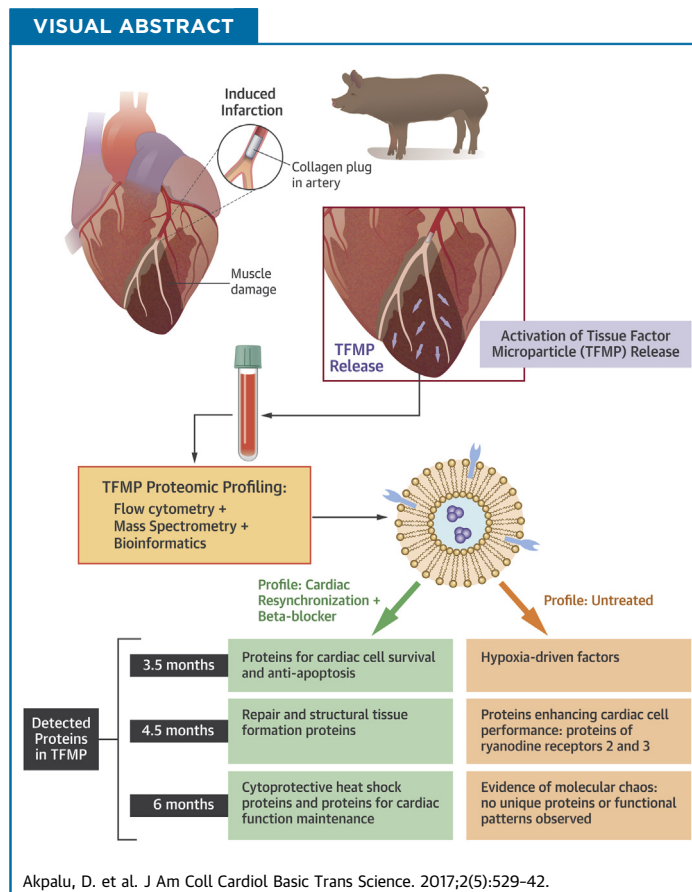


PRECLINICAL RESEARCH

Matrix Signaling Subsequent to a Myocardial Infarction

A Proteomic Profile of Tissue Factor Microparticles

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HIGHLIGHTS

- The occurrence of an MI activates production of TFMPs.
- We induced an MI in Yucatan miniswine and collected plasma samples over a 6-month period post-MI.
- Experimental groups consisted of infarcted but untreated animals and infarcted animals treated with CRT plus β -blocker.
- Using proteomic profiling, we confirm the heterogeneity of TFMP protein content with respect to physiological status of the host temporally.
- Spatially, the contents of the TFMPs provided information about multiple entities supplemental to what we obtained from assessing a set of 8 currently used cardiac biomarkers.
- The results from this study support recommending TFMP protein content profiling be used prospectively as a viable investigative methodology for chronic ischemic cardiomyopathy to help improve our understanding of β -adrenergic receptor signaling after an MI.

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ABBREVIATIONS AND ACRONYMS

ADRB1	= β 1-adrenergic receptor
ADRB2	= β 2-adrenergic receptor
AR	= adrenergic receptor
ARRB1	= β 1-arrestin
BB	= β -blocker
cAMP	= cyclic adenosine monophosphate
CRT	= cardiac resynchronization therapy
EDV	= end-diastolic volume
EF	= ejection fraction
ELISA	= enzyme-linked immunosorbent assay
ESV	= end-systolic volume
FACS	= fluorescence-activated cell sorting
GRK	= G-protein receptor kinase
HSP	= heat shock protein
HUVEC	= human umbilical vein endothelial cell
LVAd MV	= left ventricular area around the mitral valve at diastole
LVAs MV	= left ventricular area around the mitral valve at systole
LVAd PM	= left ventricular area around the papillary muscle at diastole
LVAs PM	= left ventricular area around the papillary muscle at systole
MI	= myocardial infarction
MP	= microparticle
PCR	= polymerase chain reaction
TF	= tissue factor
TFMP	= tissue factor-bearing microparticle
TnT	= troponin T

SUMMARY

This study investigated the release and proteomic profile of tissue factor microparticles (TFMPs) prospectively (up to 6 months) following a myocardial infarction (MI) in a chronic porcine model to establish their utility in tracking cellular level activities that predict physiologic outcomes. Our animal groups ($n = 6$ to 8 each) consisted of control, noninfarcted (negative control); infarcted only (positive control); and infarcted animals treated with cardiac resynchronization therapy (CRT) and a β -blocker (BB) (metoprolol succinate). The authors found different protein profiles in TFMPs between the control, infarcted only group, and the CRT + BB treated group with predictive impact on the outward phenotype of pathological remodeling after an MI within and between groups. This novel approach of monitoring cellular level activities by profiling the content of TFMPs has the potential of addressing a shortfall of the current crop of cardiac biomarkers, which is the inability to capture composite molecular changes associated with chronic maladaptive signaling in a spatial and temporal manner. (J Am Coll Cardiol Basic Trans Science 2017;2:529–42) © 2017 Published by Elsevier on behalf of American College of Cardiology Foundation. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Advances in diagnosis and management of myocardial infarction (MI) have accounted for a decrease in acute mortality from MI (1,2). Much, however, remains to be understood about the cellular and molecular mechanisms of MI longitudinally beyond the initial few days and weeks.

Progressive chronic heart failure and the reduction in cardiac output after an MI cause the activation of neurohormonal responses and perturbation in long-term adrenergic signaling, which leads to changes in the sympathetic nervous system (3). β -adrenergic receptor (AR) activation, in addition to increasing acute cardiac performance, initiates multiple signaling cascades simultaneously through G-protein receptor kinases (GRKs) and β -arrestin-mediated pathways. With an adaptive upregulation of GRK2, there is a concordant increase in heart failure phenotype, in part mediated by the depletion of β -AR-mediated inotropic reserve (4–6). Additionally, chronic activation of the sympathetic nervous system leads to pathological remodeling, necrosis, and apoptosis (7). Two

important aspects in the treatment of chronic heart failure with pathological remodeling include the use of β -blockers (BBs) and cardiac resynchronization therapy (CRT) (4–6). Together these interventions improve

symptoms and enhance left ventricular function while slowing down the progression of maladaptive remodeling and improving morbidity and mortality in appropriately selected patients (4–6).

Previous investigations revealed an elevation of microparticle (MP) levels in patients with cardiovascular diseases, specifically those with acute coronary syndromes (8–11). MPs are small vesicles released from the plasma membrane of cells such as platelets, leukocytes, erythrocytes, endothelial cells, and muscle cells; they contain cell surface proteins along with cytoplasmic components of their cells of origin (8,9,12–15). MPs produced as a result of human atherosclerotic plaque formation possess tissue factor (TF) activity along with an outer membrane composed of phosphatidylserine for prohemostatic activity (8,9,11,12,16,17). In patients with various forms of cardiovascular disease, circulating MPs cause endothelial cell dysfunction (9,11,12,16,18–20) and act as a key driver of atherosclerosis (9,12,13,15,21). In addition to ensuring hemostasis, TF plays a cell signaling role by promoting pleiotropic inflammatory responses. Hitherto, the reports of the elevation of tissue factor (TF) microparticles (MPs) in patients have been of quantitative observations, with no studies describing the protein content of TFMPs over the long term. This study investigated the release and proteomic profile of TFMPs prospectively after an MI in a chronic porcine model.

The majority of the current models of post-MI signaling are in smaller animal models with limited

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