Platelet gene expression profile in acute myocardial infarction

Cecilia Carubbi[1], Elena Masselli[1], Guidantonio Malagoli Tagliazucchi[2], Prisco Mirandola[1], Giulia Pozzi[1], Diego Ardissino[2], Giuliana Gobbi[1] and Marco Vitale[1]

[1] Department of Medicine and Surgery – University of Parma, 43126 Parma, Italy.
[2] Division of Cardiology - Azienda Ospedaliero Universitaria di Parma, 43126 Parma, Italy.

Acute myocardial infarction is a sudden event that is fatal in around one-third of patients. It is primarily due to coronary atherosclerotic plaque rupture with subsequent platelet (PLT) activation/aggregation and thrombus formation. PLTs have a key role in the genesis and progression of atherosclerosis and in thrombus formation[1]. PLTs are anucleated cells which retain mRNA from their megakaryocyte precursor, therefore PLT mRNA is unique in representing a nearly fixed transcriptome[2].

We tested the hypothesis that platelet transcriptome acts as a fingerprint indicating the development of a future myocardial infarction, with the final goal of identifying a specific STEMI gene-signature, able to discriminate patients with acute event from healthy donors (HD) and from patients affected by stable coronary artery disease (sCAD), the phenotypically closest clinical condition to STEMI.

Peripheral blood samples (50mL) were collected in Na-citrate tubes from 20 myocardial infarction patients (MI), 20 sCAD and 20 HD. Highly purified platelets were obtained by leukocyte depletion as previously described[3]. Platelet RNA extraction were performed by TRIzolTM reagent according to the manufacturer's protocol. Gene expression profile was analyzed using an Affymetrix GeneChip system (Cancer Genomics and Bioinformatics Laboratory Facility, Kimmel Cancer Center, Jefferson University. Philadelphia, US).

The exploratory analysis of PLT transcriptome confirmed differences in gene expression between STEMI, sCAD and HD. Hence, the common differentially expressed genes (DEGs) derived from the STEMI vs sCAD and STEMI vs HD comparisons were obtained and tested by k-nearest neighbor classification and bootstrap. A set of 17 STEMI-related DEGs was identified, showing good sensitivity and specificity for the discrimination of STEMI patients.

Overall, we described a STEMI-specific gene expression patterns, suggesting that PLT transcriptome allows to characterize a powerful fingerprint of STEMI theoretically able to predict a future acute event.

References

[1] Furie B, Furie BC. (2008) Mechanisms of thrombus formation. N Engl J Med. 28;359(9):938-49.
[2] Healy AM, et al. (2006) Platelet expression profiling and clinical validation of myeloid-related protein-14 as a novel determinant of cardiovascular events. Circulation 16;113(19):2278-84.
[3] Carubbi C et al. (2012) Protein kinase C ε expression in platelets from patients with acute myocardial infarction.Plosone 7(10):e46409.