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Editorial · **Open Access** ·

Immune and inflammatory responses in subjects with stable angina and acute myocardial infarction

Lu FANG[1], Anthony M Dart[1,2]

[1]*Baker IDI Heart and Diabetes Institute, Commercial Road, Melbourne, Vic, Australia*
[2]*Department of Cardiovascular Medicine, the Alfred Hospital, Commercial Road, Melbourne, Vic, Australia. E-mail: a.dart@alfred.org.au (Dart AM)*

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Immune and inflammatory responses have been known to play an important role in the initiation, progression and destabilization of atherosclerosis. Chronic inflammatory diseases such as rheumatoid arthritis and probably inflammatory bowel diseases such as Crohn's disease[1] which are associated with systemic inflammation also appear to increase the likelihood of clinically manifest atherosclerotic vascular disease. Acute myocardial infarction (AMI) triggers an intense acute inflammatory response both locally and systemically. However, the differences in systemic immune and inflammatory response between AMI and chronic phase of atherosclerosis are not fully understood.

Two papers in the current issue of the journal by Wang and colleagues have used genome wide gene expression in peripheral leukocytes to examine the differences in several inflammation and immunologic related genes between subjects with and without atherosclerosis and, for those with atherosclerosis between those with and without AMI. In the paper by Yan, *et al*,[2] there was evidence of impaired regulation of T cell activation and proliferation in the AMI group compared with a group of well matched subjects with stable angina (SA), suggesting disregulated immune response in AMI. Given the cross-sectional nature of the study, it is not clear whether any of these changes preceded the acute event. Genes related to mitochondria, electron transport chain, and cellular cation homeostasis were down-regulated, indicating an impaired energy metabolism in leukocytes. In contrast, genes related to inflammatory response, macrophage activation, neutrophil mediated immunity and response to bacterium and DNA damage stimulus were up-regulated in the AMI group compared to the SA group, suggesting an increased inflammatory response and an intense response to tissue damage in AMI. In addition, the up-regulation of positive regulation of the IκB kinase (IKK)/nuclear factor (NF) κB cascade found in the study also indicates the involvement of NFκB signalling pathway in AMI. The enhanced inflammatory response in AMI was further supported by another study by Li, *et al*.[3] who examined gene expression in relation to neutrophils and mononuclear-phagocytes. The authors found up-regulated expression of colony stimulating receptors (GM-CSFR and G-CSFR), chemokines/receptors (monocyte chemoattractant protein-1 (MCP-1), CCR2 (MCP-1 receptor) and CXCR2 (interleukin-8 receptor)) and opsonic receptors on leukocytes in AMI patients when compared to patients with SA. The interactions between these receptors on leukocytes and respective ligands mediate proliferation, differentiation, infiltration and phagocytosis of neutrophils and mononuclear-phagocytes.[4-6] Furthermore, the expression of most of the pattern recognition receptors including toll-like receptors (TLRs), and mannose receptor C (MRC) were also up-regulated in AMI group compared to SA group, suggesting that the increased inflammatory response following AMI is mediated by TLRs and MRC. TLRs activate signalling pathways such as NFκB, and induce expression of inflammatory mediators.[7,8] Whilst these findings are exploratory because of the cross sectional nature of the study they provide systematic analysis of the immune and inflammatory response in AMI. The paper by Li, *et al*.[3] also reported some differences between controls and stable angina patients. However, the interpretation of these findings is hampered by the differences between controls and patients in several characteristic such as age and smoking status and it would be important that these are confirmed with well-matched groups.

In conclusion, AMI is associated with profound changes in genes related to immune response and inflammation on peripheral leukocytes. Future studies are required to identify the key cellular and molecular factors which mediate immune and inflammatory response in AMI.

References

1 Fan F, Galvin A, Fang L, *et al*. Comparison of inflammation, arterial stiffness and traditional cardiovascular risk factors between rheumatoid arthritis and inflammatory bowel disease. *J Inflamm* (*Lond*) 2014; 11: 29.

2 Yan WW, Zhang KS, Duan QL, *et al*. Significantly reduced function of T cells in patients with acute arterial thrombosis. *J Geriatr Cardiol* 2015; 12: 388–394.

3 Li CR, Wang LM, Gong Z, *et al*. Expression characteristics of neutrophil and mononuclear-phagocyte related genes mRNA in the stable angina pectoris and acute myocardial infarction stages of coronary artery disease. *J Geriatr Cardiol* 2015; 12: 380–387.

4 Di Gregoli K, Johnson JL. Role of colony-stimulating factors in atherosclerosis. *Curr Opin Lipidol* 2012; 23: 412–421.

5 Schiff DE, Rae J, Martin TR, *et al*. Increased phagocyte Fc gammaRI expression and improved Fc gamma-receptor-mediated phagocytosis after in vivo recombinant human interferon-gamma treatment of normal human subjects. *Blood* 1997; 90: 3187–3194.

6 Kaikita K, Hayasaki T, Okuma T, *et al*. Targeted deletion of CC chemokine receptor 2 attenuates left ventricular remodeling after experimental myocardial infarction. *Am J Pathol* 2004; 165: 439–447.

7 Krejsek J, Kunes P, Andrys C, *et al*. [Innate immunity, receptors for exogenous and endogenous danger patterns in immunopathogenesis of atherosclerosis—part II: TLR receptors, significance of genetic polymorphism of danger signals receptors]. *Cas Lek Cesk* 2005; 144: 790–794. [Article in Czech].

8 Feng Y, Chao W. Toll-like receptors and myocardial inflammation. *Int J Inflam* 2011: 170352.