(IKK) complex and 24 pathway components in NF-κB signalling pathway. Data-base mining of NF-κB family members and conponnets mRNA expressions are accomplished by querying GEO DataSets profiles under inflammation cytokine stimuli, hypomethylation status, and homocysteine treat. We analysed correlations between gene expression, S-adenosylhomocysteine (SAH), and S-adenosylmethion ine (SAM) levels, and SAM/SAH ratios in 7 mouse tissues.

Results Our results showed that (1) NF-κB family members and pathway components have different expression levels in different tissues, and high expression in mouse, but inactive in human in normal condition; (2) Vascular system has lower response to NF-κB activity; (3) Tissues can be divided into 3 tiers according to essential molecular of NF-κB canonical and non-canonical pathway expression level in normal condition; (4) Canonical pathway is activated immediately after inflammatory cytokine TNF-α, IL-1 stimuli, but non-canonical pathway is up-regulated until 4 h treatment; (5) Lymphotoxin β/LIGHT has no effect on NF-κB family members and components expressions at 4 h; (6) Sca1+ subset endothelial progenitor cells has lower NF-κB family members and components expressions level than Sca1- subset endothelial progenitor cells; (7) Most of NF-κB family members and components expressions are down-regulated by hypomethylation status; (8) Most of NF-κB family members and components expressions are down-regulated by acute homocystein treat in different cell type.

Conclusions These new results provide an insight on the roles of NF-κB family members and components in tissues and cross talk between canonical and non-canonical pathway in different cell type, and its relevance to methylation. Our study is the first to make a model of specific tissue gene expression profiles of NF-κB and regulation of tissue methylation.

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CROSS TALK OF NF-κB CANONICAL AND NON-CANONICAL PATHWAY IN HUMAN AND MOUSE TISSUES

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[1]Xiao Huang, [1]Ren Gong, [2]Xiao-feng Yang, [2]Hong Wang, [1]Xiao-shu Cheng, [2]Xiao Huang. *[1]Department of Cardiology, Second hospital of Nanchang University, Nan Chang, Jiang Xi, China 330006; [2]Department of Pharmacology and Cardiovascular Research Center, Temple University School of Medicine, Philadelphia, PA 19140, USA*

Objectives Nuclear factor-κB (NF-κB) family are critical regulators in immunity, stress responses, apoptosis and differentiation, however, tissue NF-κB metabolism and their relevance to methylation status remain unknown.

Methods We examined gene expression profiles of 5 NF-κB transcription factors, 6 inhibitory IκB proteins (I-κB), 3 IκB kinase