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Transcriptome network analysis of potential candidate genes for heart failure

J. Chen[1,2], H.Y. Wang[1,2] and C.Y. Zeng[1,2]

[1]Department of Cardiology, Daping Hospital,
Third Military Medical University Cardiology, Chongqing, China
[2]Chongqing Institute of Cardiology, Chongqing, China

Corresponding author: C.Y. Zeng
E-mail: chunyuzeng@hotmail.com

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ABSTRACT. The purpose of this study was to examine the hypothesis that a transcriptome network can be developed through a set of transcription factors regulated by the expression of various genes induced by dilated cardiomyopathy can be identified and modulated to respond to heart failure. We searched for significant pathways related to dilated cardiomyopathy using the GSE4172 microarray data to identify potential genes related to heart failure. We mapped differentially expressed genes to pathways and constructed a regulation network to investigate the regulatory relationships between transcription factors and pathways. Some transcription factors and target genes in the networks have been clearly linked to heart failure in previous studies. We also found new transcription factors and target genes, such as CCAAT/enhancer-binding protein delta and JunB, responsible for inflammatory cardiomyopathy. Transcriptome network analysis was useful in the identification of candidate genes in heart failure. This method is well suited for microarray data and therefore is proposed as a powerful tool in the search for new pathways related to disease.

Key words: Transcriptome network; Candidate genes; Heart failure

