Comparative RNA profile analysis of idiopathic dilated cardiomyopathy and ischemic cardiomyopathy


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ABSTRACT. Previous research has focused on revealing the functions of each individual gene and/or pathway in idiopathic dilated cardiomyopathy (DCM) or ischemic cardiomyopathy (IC). However, the common or specific pathways of the initiation and processes of DCM and IC are still unclear. Here, we attempted to uncover the critical genes and potential molecular networks that play important roles in DCM and IC progression commonly or specifically. The transcriptional profiles from normal and DCM or IC patient samples were analyzed and compared using bioinformatic methods. Initially, the normal and DCM or IC sample data were processed and the most notable differentially expressed genes (DEGs) from DCM or IC were identified. By comparing the DEGs from DCM with those from IC, the DCM- and IC-specific DEGs were identified. The gene ontology and Kyoto Encyclopedia of Genes and Genomes pathway analyses indicated the significance of multiple biological processes as well as signaling pathways that affect heart function and DCM or IC progression. Protein-protein interaction network analysis identified the relationships between different genes, and some important genes such as MYC and FN1 were found to be hubs, which master each individual module of DCM-specific and IC-specific DEGs, respectively. We discovered commonalities and differences
of gene expression profiles and molecular pathways between different cardiomyopathies. The gene discovery and molecular signature analysis in this study could offer insights into disease mechanisms and also identify markers useful for diagnostic, prognostic, and therapeutic purposes.

Key words: Idiopathic dilated cardiomyopathy; Ischemic cardiomyopathy; Transcriptional profiles; Molecular network