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Identification of altered pathways in hypertrophic cardiomyopathy based on combined data of protein-protein interactions and molecular pathways

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ABSTRACT. The purpose of our study was to identify molecular pathways altered during the pathogenesis of hypertrophic cardiomyopathy (HCM) based on data from the STRING protein-protein interaction (PPI) database and the REACTOME pathway database. Identification of differentially expressed genes (DEGs) was carried out, followed by construction of a targeted network and selection of hub genes in this network. PPI pairs in each pathway were extracted, and altered pathways were identified when the said pathway differed from common interactions within the targeted network with a P value of less than 0.05. These altered pathways were further validated based on enrichment of hub genes in pathways within the targeted network. Through this method, we identified 1085 DEGs. The DEGs were inputted into the STRING database, and the resulting targeted network was composed of 3631 interactions. Based on the selection criteria, 30 significantly changed pathways were screened in total. Among

these, the top five pathways were found to be involved in immune modulation, signal transduction, hemostasis, and G protein-coupled receptor signaling. Similarly, enrichment in hub gene interactions was also found in members within the altered pathways, including those involved in the innate immune system, the immune system, and signal transduction pathways. These altered pathways are important for understanding the underlying mechanisms of HCM, and can be used for clinical application of treatments in the future.

Key words: Hypertrophic cardiomyopathy; Targeted network; Molecular pathway; Protein-protein interaction

