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Identification and Integrative Analysis of Novel Genes with Cardiac Expression in Mouse

Chunghee Cho

Department of Life Science, Gwangju Institute of Science and Technology, Gwangju 500-712

The functions of the cardiovascular system depend on the heart. This muscular organ beats about 100,000 times each day. Subtle changes in genes expressed in cardiac muscle can cause serious heart disease. Comprehensive understanding of molecular and physiological events occurring in cardiac muscle requires identification and characterization of unknown genes as well as known genes expressed in this tissue. One of the inclusive approaches to discover novel genes expressed in a given cell or tissue is to analyze a database with cell- or tissue-specific transcriptomes. Such database is UniGene which provides information on gene-oriented clusters and tissue types of gene expression. Furthermore, UniGene database combined with other computational bioinformatics databases provides a great deal of information for predicting the tissue specificity of gene expression, genomic nature, and structure and function of novel gene products. Of thirteen mouse heart libraries deposited in UniGene database at the NCBI (available on the World Wide Web at www.ncbi.nlm.nih.gov), we focused on the adult mouse cardiac muscle library (Library 8901), consisting of 827 UniGene entries. Our classification of these gene entries revealed that 671 entries are known genes (previously named or assigned with potential functions) and the other 156 entries are potentially novel genes (unnamed genes with unknown or unassigned function). Thus, our study has been directed to these novel gene candidates previously unexplored. Our initial investigation was to determine whether these candidates are genuine novel genes with significant and evident expression in cardiac muscle, employing various expression analysis methods. Based on the authenticity of the candidates, we obtained comprehensive information about the novel genes at the gene and protein levels. This includes various *in vitro* and *in silico* analyses. Collectively, the full exploitation of the novel genes with cardiac expression will provide a new basis for studies to uncover molecular mechanisms underlying cardiac system.