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In-silico analysis of HAND class transcription factor during cardiac hypertrophy

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The present study investigated HAND (Heart and neural crest derivatives) is a basic helix-loop-helix (bhlh) transcription factor essential for normal cardiac and extra-embryonic development. In spite of their high evolutionarily conserved genetic function, expressions of these factors differ subtly across species. Cardiac hypertrophy demonstrated HAND1 (ehand) downregulated corresponding to cardiomyopathy and HAND2 (dhand) expressed in atria. The downregulation expression observed in human cardiomyopathy reflects a permissive role. Cardiomyocytes (cardiac myocytes) reinitiate fetal gene program and initiate adaptive physiological changes, which allow heart to compensate. Therefore,

a great deal of research is required for identification of HAND gene and their specific bhlh domain. The genomic complement of bhlh transcription factor is an essential component for identification of the specific gene. Our investigation suggested that the number of HAND gene and their bhlh domain in genome. The conserved bhlh domain, motifs, phylogeny, chromosome location and gene expression analysis demonstrated HAND gene is responsible for cardiac development. In this study, we performed bioinformatics and computational techniques together information on HAND transcription factor in mammals.

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