

TARGETING THE MYOCARDIAL INFARCTION-SPECIFIC PROTEIN INTERACTION NETWORK USING COMPUTATIONAL ANALYSES

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Myocardial infarction (MI) is a leading cause of death in the United States. Currently, the high mortality rate in MI is partially due to the lack of diagnostic and prognostic biomarkers. Therefore, the purpose of this study was to develop a framework to understand the MI-specific protein interaction network and identify MI-specific biomarkers. Using the Online Mendelian Inheritance in Man (OMIM) database, we selected 73 seed proteins associated with myocardial infarction and expanded these seed proteins to a total of 1341 proteins using public protein interaction databases. We established an MI-specific protein interaction network where each node represented a protein and each edge represented a protein-protein interaction. We also examined the statistical significance of the MI-specific network compared to random networks, and evaluated the importance of the MI-specified proteins with its network properties and research intensity. The established MI-specific protein interaction network had less sub-networks and more links in addition to higher measurements on closeness centrality, clustering coefficient and degree centrality (all $P < 0.05$), suggesting a strong connectivity of hub proteins. In summary, this study established a framework to integrate published data from the literature and provided a promising way to identify biomarkers associated with myocardial infarction.