Identification of lncRNA-Mediated ceRNA Network Reveals Potential Biomarkers for Early Stage Acute Myocardial Infarction

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ABSTRACT Acute myocardial infarction (AMI) is a leading cause of. Hence, in this study, the researchers aimed to identify long non-coding RNA (lncRNA) biomarkers for early stage AMI based on lncRNA-mediated competitive endogenous RNA (ceRNA) network (LMCN). Seed lncRNAs were selected from the LMCN through network topological centrality analysis. Subsequently, a sub-LMCN was extracted from LMCN based on Biclique algorithm. Ultimately, Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analyses were conducted on nodes in the sub-LMCN. Researchers found 45 lncRNAs, 1,756 mRNAs and 2,323 ceRNA interactions in the LMCN, of which 9 seed lncRNAs were obtained. A sub-LMCN with 22 lncRNAs, 341 mRNAs, and 811 ceRNA interactions were extracted. A total of 12 GO terms and 6 pathways were denoted as functional genes of early stage AMI. The seed lncRNAs and their functional genes might be potential biomarkers for early stage AMI treatment.