

Level: 200 Bioinformatics.

Paper Name: Expression profiling and bioinformatics analysis of circulating microRNAs in patients with acute myocardial infarction.

Abstract:

ST-segment elevation myocardial infarction (STEMI), non-ST-segment elevation myocardial infarction (NSTEMI), and acute coronary syndrome (ACS) are clinical syndromes characterised by rupture or invasion of coronary atherosclerotic plaques secondary to total or partial occlusive thrombosis (NSTEMI), and angina pectoris (UA). Acute myocardial infarction (AMI) refers to both STEMI and NSTEMI (AMI).

The most severe form of coronary atherosclerotic heart disease is acute myocardial infarction. Rapid onset, rapid development, and high mortality are all features of this disease. The incidence of AMI has risen year after year in some countries. The pathogenesis of cardiovascular disease is not well understood at this time.

AMI mortality can be greatly reduced with prompt, accurate diagnosis and early reperfusion therapy. Creatine kinase isoenzyme (CK-MB) and troponin cTnI are currently used as biomarkers for the diagnosis of AMI (cTnI). For the diagnosis of AMI, cTnI is considered the gold standard. Finding more sensitive and specific, more focused AMI diagnostic markers in time windows is critical. MicroRNAs (miRNAs) have been found to play a significant role in disease development and can be used as biomarkers in studies. miRNAs have been identified as a biomarker for AMI and its associated.

miRNA is a type of noncoding RNA with a length of 18-22 bp that regulates the expression of many genes in the body. They are soluble therefore have the ability to diagnose diseases that are linked to them. miRNAs are actively secreted from living cells under stimulation or released into biological fluids. We performed a case-control analysis in a hospital. We used high-throughput sequencing technology to detect miRNA in all of the participants in this study. The role of miRNA in AMI, as well as the relationship between miRNA and the incidence and trend of AMI.

INTRODUCTION

The most serious form of coronary atherosclerotic heart disease is acute myocardial infarction (AMI). miRNA is a type of endogenous noncoding small molecule RNA that plays a key role in the development of certain diseases.

RNA sequencing was used to compare the miRNA expression profiles of 16 patients with AMI to six non-AMI controls.

A total of 181 differentially expressed miRNAs in AMI patients were identified when compared to the miRNA expression profiles of non-AMI controls, with 96 upregulated miRNAs and 85 downregulated miRNAs. The qRT-PCR findings of differentially expressed miRNAs were consistent with the results of highthroughput sequencing. The qRT-PCR findings of differentially expressed miRNAs were consistent with the results of highthroughput sequencing. GO study predicted 19 841 target genes for these 181 differentially expressed miRNAs. Twenty-six hundred and sixty-one people were found to be interested in biological processes as a result of the enrichment study. In molecular function, 353 points were earned, and 303 points were earned in cellular components. The target genes of differentially expressed miRNAs were mapped to the classical signal transduction pathway in KEGG to classify biological pathways in AMI compared to non-AMI.