Level: 200 Bioinformatics.

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

Abstract:

Stsegment elevation myocardial infarction (STEMI), nonstsegment 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 (CKMB) 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. 8MicroRNAs (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 1822 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. 9 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 qRTPCR findings of differentially expressed miRNAs were consistent with the results of highthroughput sequencing.The qRTPCR 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.

Related Work:

The findings of major studies on the relationship between miRNA and AMI were summarised. According to studies, the serum miR1 level in AMI patients increased dramatically relative to non-AMI controls and returned to normal after 2 weeks of drug treatment.The serum level of miR1 in mice with coronary artery ligature increased rapidly after the onset of AMI in a model of myocardial infarction in mice with coronary artery ligature.The serum miR133 level in AMI patients increased by 4.4 times compared to the normal control group and returned to normal after 7 days. The researchers also discovered that serum miR133 was linked to cTnT, but that miR133 peaked before cTnT.The levels of serum miR133a and miR133b were also linked to a rise in troponin levels, and the level of miR133a was also linked to the risk of death in AMI patients.MiR208 was not expressed in normal myocardium, according to a review of miRNA in cardiac myocytes from AMI patients. MiR208 was discovered to have a higher cardiac specificitythan miR1, miR133, or miR499. Furthermore, miR208 was highly expressed in the AMI rat model at 1 hour after coronary artery ligation, peaked at 3 hours, and gradually decreased at 612 hours., disappeared after 24 hours.MiR499, like miR208, was not found in healthy human serum but was found to be elevated in the serum of AMI patients. It was not found in congestive heart failure or normal heart.The researchers discovered that the serum miR4995p in NSTEMI patients was 80 times higher than the stable control group after analysing 92 patients with NSTEMI. As a result, miR499 can be used as a biomarker to diagnose AMI.

Finally, the informativeness for AMI diagnosis was investigated using the ROC curves of four upregulated miRNAs and four downregulated miRNAs. Four upregulated miRNAs had AUCs of 0.936, 0.919, 0.936, and 0.965, while two downregulated miRNAs had AUCs of 0.688 and 0.716.The high specificity and sensitivity of the denoted threshold score of circulating miR935p,miR1265p, miR199a5p, and miR499a5p for detection of AMI from non-AMI control group wereachieved by using the denoted threshold score of circulating miR935p, miR1265p, miR199a5p, and miR499a5p.As a result, the data showed that circulating miRNAs had a significant role in AMI diagnosis, corroborating previous findings that circulating miRNAs could be used to diagnose AMI as novel biomarkers.The remaining 92 upregulated miRNAs and 81 downregulated miRNAs will be subjected to ROC analysis in order to identify further candidate miRNAs with diagnostic value.

METHOD:

All of the participants in this study went to Meizhou People's Hospital's Department of Cardiovascular Diseases for cardiovascular meditation or examination. Cardiovascular risk factors, chest discomfort complaints, ischemia abnormalities in the ECG, or increased myocardial enzymes were all used as inclusion criteria.Impaired left ventricular ejection fraction of less than 45 percent, congestive cardiac failure, chronic renal or hepatic disease, AMI, and malignant illness are all exclusion criteria. Laboratory testing, electrocardiography (ECG), and coronary angiography were performed on all participants in this study.Coronary angiography, dynamic ECG evolution, and dynamic changes in serum markers were used to detect acute myocardial infarction. STEMI was diagnosed in individuals who had ST-segment elevation, while NSTEMI was diagnosed in individuals who did not have ST-segment elevation.This study had twenty-two participants, with 12 males and 10 females (a ratio of 1.2:1). Twenty-two participants were chosen for the study, and they were divided into two groups: non-AMI and AMI, both of whom went to Meizhou People's Hospital (Huangtang Hospital),From February 2016 to April 2017, 38 people aged 38 to 73 years old were treated at Meizhou Hospital affiliated with Sun Yat-sen University in Guangdong, China. The study was carried out in accordance with the Declaration of Helsinki and was approved by the Meizhou People's Hospital Ethics Committee (Huangtang Hospital).

RESULTS:

In the study, 16 AMI patients and 6 non-AMI controls were enlisted. Table 1 shows the clinical features of the 22 participants in this investigation. Systolic blood pressure, total cholesterol, and LDL-C were all greater in AMI patients than in non-AMI controls (P =.003,.021, and.016, respectively).Between the AMI patients and the non-AMI controls, there were no statistical differences in age, smoking, drinking, diastolic blood pressure, hypertension, diabetes, hyperlipidemia, triglycerides, or HDL-C.