Name(s)	Project Number
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Project Title

Identification of Novel Biomarkers for the Early Diagnosis of Acute Myocardial Infarction

Abstract

Objectives

Heart disease is one of the leading causes of death worldwide. As the death rates due to heart disease continue to grow throughout the years, it is necessary to find a non-invasive method for early diagnosis because time is crucial in acute myocardial infarctions (AMIs). The purpose of this project is to find certain genes that are differentially expressed in AMI patients relative to the healthy population to be used as potential biomarkers for AMIs.

Methods

Gene expression data from AMI patients relative to the healthy population were obtained through the NCBI Gene Expression Omnibus. The data of the common genes found in the peripheral blood of patients with first-time acute myocardial infarction under two studies were analyzed through two methods. The heat cluster maps gave a visual depiction of the contrast of gene expression among the populations. The statistical analysis was conducted on a spreadsheet software by calculating the ratios and p-values between the gene expression groups. Then, the common genes identified in both studies were further analyzed to find the common biological pathways through the Panther Gene Ontology Consortium.

Results

From the comparison of the two studies, sixty-four commonly expressed genes between AMI patients were discovered. In addition, the classification of the genes into their respective pathway ontologies through Panther indicated that there is the greatest variance among the categories in the molecular function ontology as well as the cellular component with variances between the largest and smallest amount of genes of 13 and 14, respectively. For reassurance, the statistical analysis of the expression rates of the genes of interest resulted in a p-value of less than 0.01, meaning that there is 99.99 percent confidence in the data.

Conclusions

The 99.99 percent statistical confidence is a reassurance that the data came from the same sources. Among the sixty-four genes, one or more may be potential biomarkers for they were expressed by AMI patients in both studies and aren't highly expressed by the healthy population. The pathway analysis suggests that it is likely for the potential biomarker to have binding and catalytic activity and be located on cells due to the great amount of genes in those categories. This experiment served to begin the process of searching for a potential biomarker that will allow the early diagnosis of AMIs. It narrows over fifty-thousand potential expressed genes to sixty-four and gives indications as to where the desired biomarker may be located and what function it plays in the human body.

Summary Statement

A meta-analysis approach was utilized to compare the expression rates of over 50,000 genes in acute myocardial infarction patients relative to the healthy population to be used as potential biomarkers for early diagnosis.

Help Received