CANCER BIOMARKERS

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ABSTRACT

Cancer biomarkers are biological molecules that indicate the presence, progression, and therapeutic response of cancer, playing a crucial role in improving diagnosis and personalized medicine. We investigate biomarkers for early diagnosis and prognosis of gastric cancer. For this purpose, the ten microarray based gene expression datasets were retrieved from the GEO database and analyzed by GEO2R to identify differentially expressed genes. Datasets were arranged in subsets of different dataset combinations to identify common DEGs. The gene ontology and functional pathway enrichment analysis of common DEGs was performed by the DAVID tool. A pan cancer analysis was conducted using the UALCAN database. Survival analysis of common DEGs was done by Kaplan Meier plotter. A total of 71 common DEGs were identified in different combinations of datasets. Among them, only five DEGs namely, ATP4B, ATP4A, CCKBR, KCNJ15 and KCNJ16 were detected to be common in all the datasets. The GO and pathway analysis showed that the identified DEGs are involved in gastric acid secretion and collecting duct acid secretion pathways. Further expression validation of these five genes using three additional datasets confirmed their differential expression in gastric cancer samples. The pan cancer analysis also revealed aberrant expression of DEGs in various cancers. The survival analysis showed the association of these 5 DEGs with poor survival of gastric cancer patients. In recent years, targeted mass spectrometry (MS) has emerged as a valuable quantitative tool for tumor markers. Despite frequent identification of potentially novel cancer biomarkers in discovery proteomics studies and longstanding clinical use of targeted MS for small molecule quantification, few targeted MS based proteomic assays have been developed for routine analysis of tumor markers in clinical settings.

REFERENCES

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