**IDENTIFICATION OF POTENTIAL BIOMARKERS IN PANCREATIC ADENOCARCINOME OF MICRO-ARRAY GENE EXPRESSION DATA**

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(Received xxth January 20xx; accepted xxth April 20xx)

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**ABSTRACT.** We uncover molecular biomarkers using GSE16515 data set publicly reachable at NIH/NCBI Gene Expression Omnibus database. Using Biobase, GEOquery, gplots packages in R software 3.6 that is based on gene expression analysis, we detect 278 differentially expressed genes (DEGs) of up regulation, whereas we find 77 down-regulated gene. The gene ontology of pathway enrichments and KEGG enrichment analyses of DEGs were studied. 120 KEGG pathways related with pancreatic adenocarcinoma (PAAD) were detected, in which the PI3K/AKT signaling pathway was noted to be significant. The following 21 hub genes were detected through NetworkAnalyst on the basis of protein-protein interaction (PPI) network by the STRING tool: CDK1, CCNB1, CDC20, PPARG, MET, ISG15, LEF1, SFN, DMD, FN1, RUNX2, UBC, TOP2A, ECT2, WNT2, EFNA5, PAK3, PKM, ITGB4, NEK2, and ALB. In the TCGA database, the quantification of expression of PPARG and SFN were examined and showed similarity with the previous results that both of the genes were significantly upregulated in pancreatic adenocarcinoma tumor cells in comparison to normal cells. Other hub genes discussed in this study, may be used as potential targets for PAAD and related diseases diagnosis and treatment. Moreover, the constructed study of protein-protein interactions indicated that ‘amoebiasis’, ‘protein digestion and absorption’, ‘focal adhesion’, and ‘ECM-receptor interaction’ had a close association with PAAD. Furthermore, PI3K/AKT signaling pathway in PAAD was observed to be significant. Other hub genes discussed in the study, might be utilized as promising targets for PAAD and related diseases diagnosis and drug therapies.

Keywords: *PPARG, SFN, pancreatic adenocarcinoma, gene ontology pathway enrichment, PI3K/AKT signaling pathway*