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GENE EXPRESSION PROFILING AND PROGNOSTIC IMPLICATIONS IN PANCREATIC DUCTAL ADENOCARCINOMA: IDENTIFICATION OF KEY MOLECULAR MARKERS FOR TARGETED THERAPIES

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Background : Pancreatic ductal adenocarcinoma (PDAC) is one of the deadliest types of cancer, with a high mortality rate and limited therapeutic options. Identifying molecular markers and relevant biological pathways is crucial for improving prognosis and developing targeted therapies. This study aimed to analyze differentially expressed genes (DEGs) and evaluate their functional and clinical significance in PDAC

Methods : Gene expression profiles from pancreatic tumor and non-tumor tissues were obtained from the GEO database. Differential expression analysis was performed using limma to identify DEGs ($p<0.01$). Functional enrichment was conducted using DAVID and Enrich to analyze Gene Ontology terms and KEGG pathways. Protein-protein interaction networks were constructed using Cytoscape to identify hub genes. Additionally, mutation analysis of candidate genes was conducted using dbSNP, Prosite, SIFT, and PolyPhen to assess the functional impact of genetic variations.

Results : Among the identified genes, LAMC2, LAMB3, KCNN4, TSPAN1, and MLPH were significantly upregulated and associated with poor prognosis. Functional enrichment analysis revealed the involvement of these genes in extracellular matrix remodeling, cell adhesion, and cancer-related signaling pathways. PPI network analysis identified these genes as central hubs in oncogenic networks. Mutation analysis revealed several pathogenic variants in these genes, potentially affecting tumor progression and therapy resistance.

Conclusions : This study identified key molecular markers, including LAMC2, LAMB3, KCNN4, TSPAN1, and MLPH, which are associated with PDAC progression and poor prognosis. The integration of pathway enrichment analysis, PPI networks, and mutation analysis provides insights into their potential as diagnostic biomarkers and therapeutic targets.

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