

Abstract

Novel genome-wide methylation profile of Pancreatic Ductal Adenocarcinoma patients in Indian population along with key modulated pathways and its associated disease defining genes

Submitted by Akash Bararia (Index No.: 24/22/Life Sc./27)

Pancreatic ductal adenocarcinoma (PDAC) is a lethal cancer with a poor prognosis globally. Epigenetic changes, particularly DNA methylation, have a significant role in PDAC. Our study focused on the epigenetic landscape of PDAC in Indian patients and identified methylation markers like *NPY* and *FAIM2*, associated with poor prognosis. The study used DNA methylome analysis and compared findings with global datasets. The research highlighted the importance of ethnic factors in epigenetic research and identified potential diagnostic and therapeutic targets for PDAC in India. In our previous study, researchers found differences in genetic and epigenetic features of PDAC patients from India compared to worldwide patterns. Enrichment analysis revealed the significance of "regulation of ion transport" genes, with specific genes like *KCNJ5* showing variations in methylation and expression between Indian and Western populations. Several small molecule/ drugs targeting *Kcnj5* identified through CMap database based on their high enrichment score are Amiloride and Vernakalant hydrochloride which are FDA approved. The study also identified novel gene interactions in PDAC that could impact treatment strategies.

Understanding DNA methylation and its effects on tumor characteristics is crucial for developing new treatments, particularly in advanced PDAC cases. Targeting epigenetic changes in signalling pathway-associated genes may offer new therapeutic options. Integrating machine learning and artificial intelligence in precision oncology can enhance prognostication and treatment selection in PanCa patients. Machine learning methods, combined with bioinformatics, can help identify new prognostic and predictive biomarkers for PDAC. Research into epigenetic processes and gene expression dysregulation in PDAC is ongoing to improve diagnosis and treatment outcomes. Measuring Methylation-regulated Differentially Expressed Genes (MeDEGs) may provide valuable insights for enhancing prognostic tools and targeted therapies for PDAC. MeDEGs obtained by us includes genes (*MOGAT2*, *MIA*, *CD68*, *CD36*, *TFF1*, *S100P*, and *MUC13*) that are novel to our observation in PanCa but are previously reported in other cancer types., studies like these shed light on the complex interplay between genetics, epigenetics, and environmental factors in PDAC. By identifying novel methylation markers, researchers aim to improve the diagnosis, prognosis, and treatment of this deadly cancer. Collaboration across institutions and countries is essential for advancing our understanding of PDAC and developing targeted therapies for improved patient outcomes.


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