## An Exploration of the Pancreatic Cancer miRNome during the Progression of the Disease

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**Abstract :** Pancreatic Ductal Adenocarcinoma is a well-recognised cause of cancer death with a five-year survival rate of about 9%, and its incidence in India has been found to be increased manifold in recent years. Due to delayed detection, this highly metastatic disease has a poor prognosis. Several molecular alterations happen during the progression of the disease from precancerous conditions, and many such alterations could be investigated for their biomarker potential. MicroRNAs have been shown to be prognostic for PDAC patients in a variety of studies. We hereby used NGS technologies to evaluate the role of small RNA changes during pancreatic cancer development from chronic pancreatitis. Plasma samples were collected from pancreatic cancer patients (n=16), chronic pancreatitis patients (n=8), and also from normal individuals (n=16). Pancreatic tumour tissue (n=5) and adjacent normal tissue samples (n=5) were also collected. Sequencing of small RNAs was carried out after small RNAs were isolated from plasma samples and tissue samples. We find that certain microRNAs are highly deregulated in pancreatic cancer patients in comparison to normal samples. A combinatorial analysis of plasma and tissue microRNAs and subsequent exploration of their targets and altered molecular pathways could not only identify potential biomarkers for disease diagnosis but also help to understand the underlying mechanism.

Keywords: small RNA sequencing, pancreatic cancer, biomarkers, tissue sample

Conference Title: ICSRNAS 2023: International Conference on Small RNA Sequencing

**Conference Location :** Prague, Czechia **Conference Dates :** September 04-05, 2023