**Introduction/Objective:** Pancreatic ductal adenocarcinoma (PDAC) is a leading cause of cancer-related death in the United States. Determining the genetic alterations involved in the formation of PDAC and its precursor, pancreatic intraepithelial neoplasia (PanIN), may lead to earlier detection and new therapeutic options. We performed an analysis of the genetic alterations responsible for the progression of the normal pancreatic tissue to PanIN and ultimately from PanIN to PDAC.

**Methods/Case Report:** Initially, we used the continuous bioinformatic analysis in such a way that the RNA-seq datasets were extracted from the Biojupies database. We separately analyzed two datasets that included PDAC and PanIN, where their differentially expressed genes (DEGs) were obtained by comparison with controls. A Venn diagram was drawn to visualize the overlapping and non-overlapping DEGs in both groups. Using the Enrichr and ShinyGO databases, we examined the cell signaling pathways and ontologies of up/down-regulated genes. We mapped the protein network of important genes involved in cancer pathways by the STRING database. Finally, the shared and non-shared candidate proteins in the PDAC and PanIN pathways with the GEPIA database were confirmed in human samples.

**Results (if a Case Study enter NA):** We found six shared genes in PDAC and PanIN including RAC1, RAP1A, ITGA5, RHOA, FZD2, and FN1, which appear to take part in the transition of PanIN to PDAC. Our result showed that the aforementioned genes are critical in the cell cycle, angiogenesis, and cell death processes. In the next step, the DEGs analysis in both PDAC and PanIN revealed the role of candidate genes (COX5B, NME2, MGLL, and PAICS for PanIN and PRKCA, PLCG2, NOS3, and PTK2 for PDAC) in cellular aging, MAPK, and PI3K/Akt signaling pathways.

**Conclusion:** Our findings showed that the overexpression of RAC1, RAP1A, ITGA5, RHOA, FZD2, and FN1 may have an important role in PanIN shifting to PDAC.

**Clinico-pathological and Molecular Features of Pancreatic Acinar Cell Carcinoma: Association with BRCA2 Mutation**

*G. Goyal, J.V. Reusner, K.K. Haye, R. Tondon; Pathology, Hospital of University of Pennsylvania, Philadelphia, Pennsylvania, United States*

**Introduction/Objective:** Pancreatic acinar cell carcinoma (ACC) is a rare neoplasm of exocrine epithelial origin and accounts to <1% of primary neoplasms of pancreas.

**Methods/Case Report:** The cases diagnosed as ACC were retrieved from Pathology data base between January 2010 to July 2021. A retrospective review of clinical, pathological, molecular findings along with follow up was performed.

**Results (if a Case Study enter NA):** Eight patients with resection specimens were identified over a period of 11 years. Median age of diagnosis was 74.5 yrs with M: F ratio of 3:1 and size range of 1.8 to 10.9 cm. The tumor was located in body/tail (5) and head of pancreas (3). Immunohistochemical stains for BCL10 and trypsin were utilized in 4 cases. One patient had lymph node metastasis and two patients had liver metastasis at the time of presentation. One patient presented with lipase hypersecretion syndrome. Four cases (50%) had pT3 stage. Follow-up period was available in 7 patients and ranged from 1-3 yrs, of which 3 died within 2 yrs of surgery while 4 patients were disease free. Three patients (35%) were found to have germline (1) and somatic BRCA2 mutations (2). These patients received platinum-based chemotherapy and were free from recurrence upon follow-up of 3 yrs.

**Conclusion:** Pancreatic ACC is a rare entity. In our study, 35% (3/8) cases were associated with somatic/germline BRCA2 mutations. Our results suggest that patients with ACC should undergo genetic testing for BRCA 1/2 mutations. This would not only enable treatment of these patients with specific targeted therapies, but also aid in screening of their families.

**Pathology Informatics**

**Do we need Diagnostic Decision Support For Pathologists in Anatomic Pathology Laboratory Information System (APLIS)?**

*S.S. Sonawane; Pathology, SBMF, Logansport, Indiana, United States*

**Introduction/Objective:** On a typical day, pathologists spend time not just looking at the slides but have various information needs in order to facilitate the sign-out. This study was performed to find out various resources utilized by pathologists to facilitate the sign-out and if having the diagnostic decision support in APLIS will improve the sign-out experience? To answer these questions a survey was created.

**Methods/Case Report:** An anonymous Google survey of 10 questions inquiring about practice setting, training level, work experience, various resources utilized to facilitate daily sign-out, time spent to find the information, and ways the sign-out experience can be enhanced was created and distributed among the pathologists via a social media platform.