Results: 101 SOPPs were performed. Subsequent care was affected in 86 (85%) cases. Surgery was planned for 29 (29%) patients. A cause other than IPMN for MD dilatation was found in 28 (28%) cases. In 35 (35%) cases a side branch IPMN diagnosis without malignant or high-grade dysplasia was suspected. Post-SOPP pancreatitis occurred 20 (20%) times. A decrease in odds of post-SOPP pancreatitis was seen as the MD diameter increases (OR 0.714 for 1.0mm increase in MD diameter, CI 95% 0.514 - 0.993, p=0.045). A lower probability for post-SOPP pancreatitis was seen if the MD diameter is $\geq$ 7.0mm (OR 0.334, CI 95% 0.120 - 0.928, p=0.035). We found no correlation between complications and the use of prophylactic NSAIDs and pancreatic stents or PS timing.
Conclusions: SOPP aids clinical decision-making in suspected MD-IPMNs. The risk for pancreatitis decreases as the diameter of the MD increases.

EP02C-091
PREVENTING OF POSTOPERATIVE COMPLICATIONS IN PATIENTS AFTER PANCREATICODUODENECTOMY

L. Pererva[1], V. Kopchak[1], K. Kopchak[2], I. Khomiak[1], O. Duvalko[1], V. Shkarban[1], V. Trachuk[1], P. Azadov[1] and S. Lynnyk[1]
[1]Shalimov National Institute of Surgery and Transplantology, Pancreatic and Bile Ducts Surgery, Kyev, Ukraine, and [2]National Cancer Institute, Department of Abdominal Surgery, Kyev, Ukraine

Introduction: To develop a prevention system that allows to reduce frequency of postoperative pancreatic fistula and severe postoperative complications after pancreaticoduodenectomy.
Methods: In our department results of 217 pancreaticoduodenectomy were analyzed in the period from January 2017 to December 2020. In the main group we proposed pancreatic fistula prevention system and assessment of sarcopenia that were applied in 127 patients (from November 2018 to December 2020). In patients with high risk of pancreatic fistula we performed pancreato-jejunostomy with external drainage of the main pancreatic duct (stent) during the reconstructive stage after pancreaticoduodenectomy. The comparison group was comprised of 90 patients. They were operated in the period from January 2017 to October 2018 without assessment of the pancreatic fistula risk and presence of sarcopenia. Decision on the type of pancreatic anastomosis was based on surgeon's preference.
Results: The level of postoperative complications was significantly higher in the comparison group 28 (30.4%) and 23 (18.1%) in the main group (c^2= 4.95, p = 0.03). The level of postoperative pancreatic fistula grade B or C was in 17 (18.5%) in the comparison group, which is significantly higher than in the main group, where the fistula gr. B occurred in 11 (8.7%) patient (c^2= 4.9, p = 0.03).
Conclusions: The developed prevention system allowed to reduce significantly the incidence of postoperative pancreatic fistula from 18.5% to 8.7% and the number of postoperative complications from 30.4% to 18.1%.

EP02C-092
COMPREHENSIVE BIOINFORMATICAL ANALYSIS IDENTIFIES HETEROGENEITY OF GENOMICS AND TUMOR MICROENVIRONMENT BETWEEN PANCREATIC ADENOSQUAMOUS CARCINOMA AND PANCREATIC DUCTAL ADENOCARCINOMA

C. Cao[1,2], L. Yin[1,2], Y. Lu[1,2], J. Chen[1,2], H. Yuan[1,2], W. Gao[1,2], J. Wu[1,2], Y. Miao[1,2], Z. Lu[1,2] and K. Jiang[1,2]
[1]The First Affiliated Hospital of Nanjing Medical University, Pancreas Center, Nanjing, China, and [2]Pancreas Institute of Nanjing Medical University, Nanjing, China

Introduction: Pancreatic adenosquamous carcinoma (PASC) is a rare subtype of pancreatic malignancies which presents different biological and clinical features with classic pancreatic ductal adenocarcinoma. However, no comprehensive comparative analysis of genomics and tumor microenvironment (TME) between PASCs and PDACs has been reported. This study is to determine genomic and TME difference between PASCs and PDACs via bioinformatical approach.
Method: RNA-seq, mutation and clinical data of ICGC (International Cancer Genome Consortium) cohort were downloaded and collected from CBioPortal website. R package maftools and GenVisR were applied to analyze mutated genes and Deseq2 was used to screen differentially expressed genes (DEGs). Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG) and protein-protein interaction (PPI)analysis were also performed. Online tools ESTIMATE, MCPcounter and CIBERSORT were used to determine the stromal and immune scores of transcriptome datasets.
Results: SMAD4 mutation rate was significantly lower in PASCs (0/12, 0%) than PDACs (19/70, 27.1%) while CC2D2A mutation was prevalent in PASCs (2/7, 16.67%) with none in PDACs (0/70, 0%). 869 significant DEGs(log2 Fold Change>2, false discovery rate (FDR)< 0.05) were identified, including 583 down-regulated genes and 286 up-regulated genes in PASCs. DEGs were enriched in pathway of maturity onset of diabetes of the young, GO terms of epidermis development, cornification and skin development. TME analysis showed that the proportions of resting and activated NK cells, and neutrophils were significantly higher in PDACs than PASCs.
Conclusions: There are genomic and TME differences between PASCs and PDACs which can possibly contribute to the clinical differences.

EP02C-093
INCIDENCE, RISK FACTORS AND OUTCOMES OF JEJUNAL VARIX OF THE AFFERENT LOOP AFTER PANCREATODUODENECTOMY

M. D'Silva[1], Y. -S. Yoon[1], J. S. Lee[1], J. Y. Cho[1], H. W. Lee[1], B. Lee[1], M. Kim[1] and H. -S. Han[1]
[1]Seoul National University Bundang Hospital, General Surgery, Seongnam, Korea, Republic of