In our cohort we were able to show a better overall survival and recurrence-free survival for the larger margin width group (>0.5cm), but without achieving statistical significance. It should be emphasized, that resections with scarce margins or even R1 resections have a significant survival benefit over the irresectable group.

TP12-02
PROGNOSTIC SUBTYPES OF INTRAHEPATIC CHOLANGIOCARCINOMA BY INTEGRATIVE MOLECULAR - CLINICAL ANALYSIS AND SUBTYPE-SPECIFIC POTENTIAL TARGETED APPROACH

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Background: Although molecular characterization of intrahepatic cholangiocarcinoma(CCA) has been studied recently, integrative analysis between molecular and clinical characterization has not been established yet. We analyzed RNA sequencing data with annotated clinical data for clarifying genomic features of intrahepatic CCA, molecular specific clinical features and evaluating therapeutic potential based on molecular subtypes.
Methods: We performed next generation RNA sequencing of 30 surgically resected intrahepatic CCA from Korean patients. RNA expression, variants and fusions were analyzed with clinical, pathologic features. RNA sequences from 32 intrahepatic CCA resected from USA were used for validation.
Results: Patients were classified into 2 subclasses based on unsupervised clustering, which showed a significant difference 5-year survival. The validation cohort of USA data also revealed two subclasses with significant differences in survival. Two subclasses had different clinical and pathologic features for higher CEA and CA19-9 levels, underlying cholangitis and bile duct type pathology in the poor prognostic subclass and more frequent hepatitis and cholangiolar type of pathology in better prognostic subclass (Figure1). On pathway analysis, liver related signatures were enriched in better prognosis subclass. In poor prognosis subclass, inflammation related pathways were enriched and KRAS mutation was more frequent. Cholangiocarcinoma cell lines which have similar gene expression pattern with better prognosis subclass were sensitive to gemcitabine.
Conclusion: Two molecular subtypes of intrahepatic CCA with distinct clinical, biological and prognostic differences were identified. With clinical and pathological characteristics, molecular subtypes can be predicted and different signaling pathways of subtypes may lead to more rational targeted approaches to treatment.

TP12-03
16S RDNA MICROBIOME COMPOSITION PATTERN ANALYSIS AS A DIAGNOSTIC BIOMARKER FOR BILIARY TRACT CANCER

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Background: The aim of this study is to investigate the composition of microbiota in biliary tract cancer patients and healthy adults by metagenome analysis, and evaluate its potential values as biomarkers for biliary tract cancer.
Methods: Patients who were diagnosed with biliary tract cancer or benign inflammation were enrolled in this study. The control group consisted of healthy adults who presented with no history of significant medical issues. We isolated bacteria-derived extracellular vesicles in the plasma and investigated whether bacteria-derived EVs in plasma are useful for the metagenome analysis. The microbiome composition was investigated with 16S rDNA metagenome analysis. We evaluated each microbiome to ensure suitability for the biliary tract cancer prediction model.
Results: A total of 155 patients were included in this study; 24 patients with diagnosed biliary tract cancers, 43 diagnosed with cholecystitis or cholangitis, and 88 healthy adults. The microbiome composition pattern of the biliary tract cancer differed from the microbiome composition pattern seen in healthy adult group in beta diversity analysis. The percent composition of microbiota was found to be different from the phylum to genus level. We discovered that the composition of *Bifidobacteriaceae, and Pseudomonaceae families, Corynebacteriaceae Corynebacterium, Oxalobacteraceae Ralstonia*, and *Comamonadaceae Comamonas* species could be used to develop a biliary tract cancer prediction model.
Conclusion: Biliary tract cancer patients have altered microbiome composition, which represents a promising biomarker to differentiate malignant biliary tract disease from normal control group.

TP12-04
THE NEW CRITERIA FOR RADICAL SURGICAL OPERATION IN THE PATIENTS WITH HILAR CHOLANGIOCARCINOMA

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