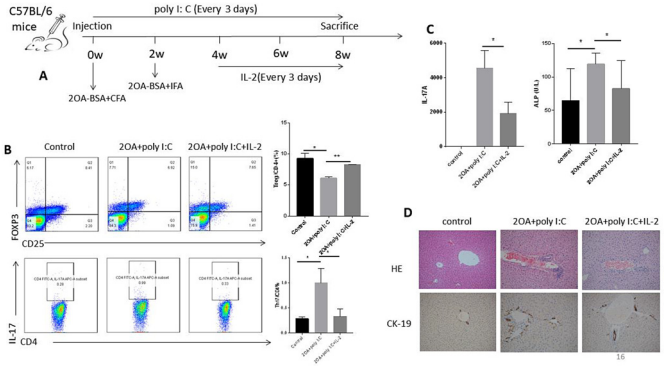

Conclusion: The PBC mouse model was successfully induced by the combination of 2OA-BSA and poly I:C and it can model human disease early status. Low-dose IL-2 inhibited PBC by augmenting Treg and decreasing Th17 numbers, which paly important role in the pathogenesis of the PBC. The improvement of biochemical indexes and liver histopathology, suggesting that low-dose IL-2 treatment may be considered as novel therapy for PBC in the future.

OS021

Cholangiocytes cleave surface CD100 from biliary infiltrating T cells and mediate pathogenic Th17 differentiation

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Background and aims: Chronic inflammation surrounding bile ducts contributes to the disease pathogenesis of most cholangiopathies, but the mechanism enabling pathogenic immune cells to adapt and survive in the biliary environment remains largely unknown. We have recently reported a variant of CD100 to be the causal mutation for a familial form of primary sclerosing cholangitis (PSC). Herein, we investigate how CD100 participates in the biliary local inflammation and its relevance to the differentiation of pathogenic immune cells.
Method: CD100 expression was assessed by spatial transcriptomics (10x Genomics) and *in situ* immunohistochemistry (IHC) in explanted livers of patients with PSC (n = 4–6) and other cholangiopathies (Ctrl, n = 4–5). Soluble CD100 (sCD100) was measured by ELISA in paired serum, plasma, and bile samples (n = 11–19). Biliary infiltrating immune cells were collected from endoscopic retrograde cholangiopancreatography brush samples (Ctrl, n = 6; PSC, n = 6) and surface expression of CD100 was evaluated by flow cytometry. To model pathogenic interactions between immune cells and cholangiocytes, splenic cells isolated from C57BL/6 wild-type (WT) and CD100 mutated mice were co-cultured with small or large cholangiocytes. Altered gene expression was assessed with RNA sequencing of purified cell subsets after co-culture.
Results: Spatial transcriptomics revealed *SEMA4D/CD100* RNA expression in all examined livers and demonstrated the localization in *KRT19*$^{+}$ bile duct regions (Ctrl, 7–40%; PSC, 11–94%). In contrast, CD100 protein expression measured by IHC was nearly undetectable in diseased periductal areas of the PSC livers. Moreover, surface expression of CD100 on biliary infiltrating immune cells was reduced and accompanied by increased sCD100 in plasma and bile from PSC patients, suggesting that CD100 is cleaved from the surface of immune cells in regions adjacent to the bile ducts. In co-culture experiments, we observed that activated immune cells adhered to cholangiocytes and correlated with the death of large but not small cholangiocytes. T cells were dominant (49.9–64.4%) in the adherent immune population and lost their surface CD100 expression. RNA sequencing data showed increased *Adamts4* in co-cultured cholangiocytes which appeared to cleave CD100. Genes involved in anti-apoptosis and T-helper 17 (Th17) differentiation were enriched in adherent T cells and further upregulated in T cells with mutated CD100.
Conclusion: Cholangiocytes induce cleavage of CD100 on biliary infiltrating T cells that facilitates persistent inflammation and local Th17 differentiation. These findings highlight a novel pathway in the liver with cholangiocyte-driven Th17 cell differentiation that is associated with CD100 cytoplasmic signaling. Targeting this pathogenic pathway serves as an attractive target for mitigating bile duct inflammation in PSC.

OS022

Novel approach combining whole liver single-cell RNA sequencing and spatial gene profiling using Nanostring GEOMX enables identification of specific cell sub-populations and pathways regulated by CCL24

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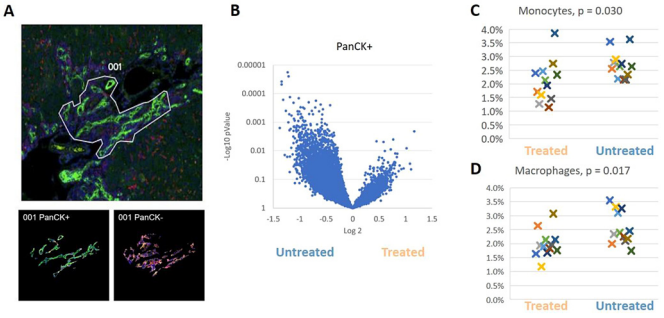
Background and aims: CCL24 (Eotaxin-2) is a chemokine that regulates profibrotic and proinflammatory activities through the CCR3 receptor. We previously demonstrated that CM-101, a CCL24 blocking antibody, improves liver inflammation, fibrosis and cholangitis in the Mdr2 knockout (Mdr2 -/-) mouse model. Characterization of CCL24 expression in relation to the different cell populations in Mdr2-/- mice and its inhibition effect on cholangiocytes and immune response was studied using two gene expression methods.
Method: Identification of cell population, including immune cells and CCL24 expressing cells in livers of Mdr2-/- mice was done by scRNA seq from whole liver. NanoString's technology was utilized for gene expression studies, focusing on the bile-duct injury sites. In this system segmenting of cholangiocytes (Pan-CK+) and immune cells (Pan-CK–) cells was done in liver sections from Mdr2-/-mice non-treated or treated with CM-101.
Results: Mdr2-/- mice treated with CM-101 resulted in reductions in: serum ALP, liver inflammation, liver peribiliary collagen deposition and cholangiocytes proliferation. Using whole liver scRNA seq we demonstrated that CCL24 is expressed in macrophage cells. This analysis identified a few specific disease relevant immune sub-populations, however it is missing crucial information that relates to cell localization. To overcome this, we used NanoString to characterize the alternations in peribiliary transcriptome following CM-101 treatment. Spatial profiling separated cholangiocytes (PanCK+) and non-cholangiocytes (PanCK–) peribiliary cells, distinguishing cholastatic, proinflammatory and profibrotic effects. Gene set enrichment analysis showed reduction in proliferation and senescence pathways in PanCK+ cells, whereas PanCK- cells showed reduction in ECM remodeling pathways and increased metabolic pathways. Cell deconvolution of the heterogeneous PanCK- population revealed alternation in the peribiliary immune cells, marked by reduction in macrophages and monocytes following treatment with CM-101.

Conclusion: Augmenting whole liver scRNA seq with spatial transcriptome analysis, is a novel approach to identify cell populations and pathways specific to the damaged peribiliary area. Using this approach we demonstrated that CCL24 regulates cholestatic, inflammatory and fibrotic liver damage, and its underling mechanisms. Understanding the underling mechanisms of CCL24 blockade and its ability to prevent liver injury in animal supports its role in PSC and its potential beneficial effect for PSC patients.



OS023

T regulatory cells promote bile duct regeneration through modulating ductular reaction in a model of cholestatic liver injury

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Background and aims: Reduced regulatory T cells (Tregs) and increased bile duct senescence are observed in primary sclerosing cholangitis (PSC) patients, with the degree of cholangiocyte senescence linking to disease severity and prognosis. Cholangiocytes can act as facultative liver progenitor cells through ductular reaction during extensive liver damage, whether this process is impaired during PSC remains to be investigated. The role of Tregs in modulating tissue resident progenitor cells have been shown in multiple organs, but this remains unclear in the context of liver regeneration. We aim to use transgenic murine models to investigate the cause of reduced Tregs in the liver and whether the lack of Tregs in the liver affect bile duct regeneration and senescence.
Method: Foxp3^{GFP}DTR transgenic mice were used to reduce Tregs number in a dose dependant manner. 50% of Tregs were depleted to avoid triggering systematic autoimmunity whilst cholestatic liver injury was induced by the feeding of 3, 5-diethoxycarbonyl-1, 4-dyhydrocollidine (DDC) diet and compared to the control group with intact Tregs population. We generated the Foxp3^{GFPCreERT}tdTom^{loxSTOPlox} mice to investigate Tregs stability. Tamoxifen was injected intraperitoneally to induce tdTom expression in Foxp3 Tregs and cell fate was investigated after DDC diet to determine Tregs stability. CD4 T-cells were isolated and co-cultured with intrahepatic cholangiocytes organoids to confirm the effect of CD4 T-cells on cholangiocytes.
Results: Mice with reduced Tregs have a lower tolerance to the feeding of DDC diet, with rapid weight loss and two times higher periportal fibrosis than the control group. Histological findings showed that the reduction in Tregs decrease the magnitude of Ck19^{+} ductular reaction by 30%. A two-fold increase in Ck19+p21+ senescing cholangiocytes was observed in the group with reduced Tregs after DDC induced liver injury. Transcriptional analysis of liver tissue revealed downregulation of *Yap1*, *Sox9* and *Ctgf*, suggesting the Yap pathway is affected following Tregs reduction. This is further confirmed with immunohistochemistry showing a two-fold reduction in the number of Yap and Sox9 expressing Ck19+ cholangiocytes. The Foxp3 fate mapping experiments showed that the labelled Tregs population reduces Foxp3 expression after DDC diet indicating that the stability of Tregs decreases during liver injury.
Conclusion: Our results demonstrated that the role of Tregs in promoting bile duct regeneration by modulating ductular reaction through the Hippo-Yap pathway. Furthermore, the observation that Foxp3 Tregs become unstable in an injured microenvironment in mice may explain the lack of Tregs seen in PSC patients. These show the potential of using Tregs to promote liver regeneration but also highlights the stability of Tregs should be taken into consideration when designing cell based Tregs therapy.

OS024

Deep learning for automatic diagnosis and morphologic characterisation of malignant biliary strictures using digital cholangioscopy: a pilot study

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Background and aims: Patients with indeterminate biliary strictures (BS) pose a significant diagnostic challenge. Digital cholangioscopy (DC) has enabled morphologic characterization as well as the performance of visually guided biopsies. However, the diagnostic yield of DC remains suboptimal, and the visual characterization of these lesions has significant interobserver variability. Recently, the development of artificial intelligence (AI) algorithms, particularly convolutional neural networks (CNNs) for interpretation of endoscopic images has generated intense interest. We aimed to develop a CNN-based system for simultaneous automatic detection of malignant BS in D-SOC images and identification of three morphologic features: nodules (NN), papillary projections (PP) and tumor vessels (TV).
Method: We developed and validated a CNN based on DC images (Spyglass DS II, Boston Scientific, USA). Each frame was labeled as normal/benign finding or as a malignant lesion if definite histologic evidence of biliary malignancy was available. Moreover, we evaluated the performance of the CNN for the detection of morphologic features associated with histology-proved biliary malignancy: NN, PP, and TV. The image dataset was split for constitution of training and validation datasets. The performance of the CNN was measured by calculating the accuracy, area under the curve (AUC), sensitivity, specificity, positive and negative predictive values (PPV and NPV, respectively).
Results: We included 23 595 images from 125 patients (20719 of malignant BS and 2876 of normal or benign findings). The model had a sensitivity of 98.9%, a specificity of 97.7% and an overall accuracy of 98.7%. The AUC was 1.00.
Additionally, the model comprised 2876 images of NN, 1675 images showing PP, and 4153 images of YV. The accuracy for the automatic detection of each of these features was, respectively, 96.9%, 96.1%, and 91.5%.
Conclusion: We developed a combined CNN for automatic detection of malignant BS as well as the automatic identification of morphologic features associated with increased probability of malignancy. The application of AI models to DC may increase its diagnostic yield for patients with indeterminate BS. Furthermore, accurate real-time automatic identification of features associated with increased probability of malignancy may help to guide biopsies, thus increasing their rentability.