Results The results show precise expression levels for each of the 60 markers in the assay in each individual cell in the sample, maintaining spatial information about each cell. Dozens of immune cell subtypes were identified and quantified based on protein expression profiles. Spatial analysis of the samples reveals quantifiable heterogeneity of immune cell infiltration within the tumor samples, demonstrating the utility of the ChipCytometry platform for in-depth immune profiling in clinical samples.

Conclusions The ChipCytometry platform enables simultaneous detection of multiple protein markers on a single tissue section for deep immune cell profiling in the tumor microenvironment. Combined with the single-cell spatial information, such data sets provide an opportunity for the discovery of new complex multiplexed biomarker signatures to inform therapeutic development.

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immunohistochemistry. Paraffin sections were stained with hematoxylin and eosin (H&E) or Ki67 according to standard methods. For immunohistochemistry, cryosections were stained overnight at 4°C with fluorescent antibodies.

Results H&E images confirmed that transgenic Apc1322T mice lacking IL-25 had smaller tumours and showed less dysplasia than Apc1322T mice with normal IL-25 expression. Ki67 staining showed that tumours express higher Ki67 levels than adjacent normal intestinal tissue. The tumour-associated tertiary lymphoid structures (TATLS) of Apc1322T mice lacking IL-25 appeared larger, indicating a more robust anti-tumour immune response.

Likewise, Apc1322T mice lacking ILC2s had smaller, less dysplastic tumours. TATLS in these mice were bigger than mice with ILC2s but smaller than Apc1322T mice lacking IL-25, indicating that IL-25 may act via additional protumourigenic cell types.

Immunohistochemistry confirmed the presence of ILC2s, as well as MDSCs the tumours of Apc1322T mice, suggesting that these cells create an immunosuppressive niche.

Conclusions This pilot study confirms that genetic ablation of either IL-25 or ILC2s promotes anti-tumour immune reactions and decreases tumour size, correlating with reduced intestinal tumour proliferative capacity and dysplasia. Mice lacking IL-25 or ILC2s had larger TATLS, which are known to be associated with improved prognosis in patients. This study, along with previous data, highlights the potential therapeutic benefit of targeting the IL-25-ILC2 axis for colorectal cancer. Further studies are required to bring this from bench to bedside.

REFERENCE


PO2.07 INNATE IMMUNITY ATLAS OF HEPATOCELLULAR CARCINOMA UNRAVELS THE DIFFERENTIATION HIERARCHY OF MYELOID NK CELLS AND MDSCS

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Background Hepatocellular carcinoma (HCC) environmental risk factors include viral infection, alcohol abuse and the metabolic syndrome. While there is evidence that boosting the activity of tumour-specific T cells might benefit patients with HCC, the underlying liver soil (cirrhosis, NASH) renders this cancer’s tumour microenvironment somewhat unique. Despite a significant therapeutic advance in the treatment of advanced HCC, ~75% of patients do not respond to immunotherapies for unclear reasons. Such a heterogeneous response highlights the need to further explore etiology- and organ-specific immunity towards improved patient stratification and the development of new combination therapies.

Materials and Methods With the objective to characterize the innate immunity landscapes of HCC, we employed droplet-based 3′ scRNA-seq of CD45+ panTCRβ CD19+ cells, freshly isolated from tumors or adjacent non-tumoral livers of 10 HCC patients. In parallel, we used spatial transcriptomics (10x Genomics, Visium platform) to localize identified cell populations with respect to tumor and tissue features. Functional validation was carried in ex vivo co-culture experiment-susing patient-derived cells and in vivo using mouse models.

Results We present the most comprehensive atlas to date of hepatic innate immunity cells (~100,000 single cell transcripts). Besides describing the remarkable diversity of innate immunity cell states, our study identified and functionally characterized previously unexplored subsets of cytotoxic cells with myeloid features (myeNK) and novel myeloid-derived suppressor cell (MDSC) differentiation states. We computed signaling entropy at the single-cell level to characterize the differentiation hierarchy of these poorly annotated cells and show that myeNK cells are highly differentiated and exhibit potent lytic activity against cancer cells. Our analysis also distinguished three main MDSC lineages, a granulocytic (G-MDSC), a monocytic (M-MDSC) and an ‘immature’ subset with TAM-like features. This latter lineage presents the highest entropy and is the most immunosuppressive. Finally, we identified a discriminatory expression of the inflammatory receptor TREM1 on MDSCs, particularly in NASH setting, and unraveled this receptor as a potential therapeutic target in HCC.

Conclusions Our data support the stratification of patients according to etiology to define optimal therapeutic regimens and identify TREM1 high MDSC as deleterious effectors of HCC.