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Introduction and Objectives: Hepatocellular carcinoma (HCC) is the third cause of cancer-related death worldwide. Assessment of genetic components has been used to better stratify those at risk. However, most studies have been performed in Asian or Caucasian populations. Tolloid-like protein 1 (*TLL1*) is one such SNP that has been shown to increase risk in hepatitis C virus (HCV)-associated HCC. We evaluated the risk association of TLL1 in a South American cohort.

Materials and Methods: This is a cross-sectional analysis performed in South Americans with HCC as well as cirrhotic controls through the ESCALON network. We analyzed 120 HCC blood samples and 293 cirrhotic controls from Argentina, Chile, Brazil, Colombia, Ecuador and Peru. The pathogenic variant of *TLL1* (rs1704200) was evaluated using TaqMan-genotyping assay. Multiple logistic regression was used to establish the association between *TLL1* and HCC.

Results: The median age of HCC patients was 68 years (IQR 62-72) and of cirrhotics 64 years IQR 68-70). The most common underlying liver disease in both groups was Non-alcoholic fatty liver disease (NAFLD) at 58% and 59%, respectively. The proportion of individuals who developed HCC with a *TLL1* pathogenic variant (AT/TT) was 18.2% in the South American cohort. The calculated Odds-Ratio (OR) for HCC among South Americans with the TLL1 variant was 0.69 (CI 0.37-1.29), suggesting a non-significant decrease odds for HCC. Interestingly, different results were found when examining HCV-associated HCC (11% of the cases and 6% of controls). The OR for HCV-associated HCC in Latin Americans was 2.07 (CI 0.93-4.58), suggesting a non-significant increased odd of being diagnosed with HCC in South Americans with the variant.

Conclusions: *TLL1* mutations do not seem to associate with HCC development in South American patients with liver disease. However, preliminary results show that the presence of *TLL1* SNP could confer an increased risk for HCC in South Americans with HCV infection.

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P-5 THREE-DIMENSIONAL SINGLE-CELL ATLAS OF LIVER TISSUE ARCHITECTURE

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Introduction and Objectives: The liver is an organ that performs a wide variety of functions that are highly dependent on its complex 3D structure. Geometrical models (digital representations of tissues) represent a versatile technique to characterize 3D tissues as well as to get quantitative insights into the link between their structure and function. Until now, these models have only focused on some tissue (sinusoids and bile canaliculi) and cellular components (hepatocytes), leaving out important cellular populations such as stellate cells and Kupffer cells. One of the major bottlenecks for a complete tissue reconstruction is the limitation on the number of markers that can be imaged by fluorescence microscopy (up to 4-5). This study aimed to generate a "3D single-cell atlas of liver tissue architecture", i.e., a full 3D geometrical model which includes all tissue and cellular components simultaneously.

Materials and Methods: We overcome the technical constraints by using deep tissue immunostaining, multiphoton microscopy, deep learning techniques, and 3D image processing. As a proof of concept, we used the 3D atlas to describe the morphological changes that occur in the mouse liver during post-natal early development and adulthood.

Results: We described how liver tissue architecture progressed from post-natal day one to adulthood by a novel set of morphometric cellular and tissue parameters. Our analysis revealed unknown details about the spatial organization of different liver cell types. Unexpected spatiotemporal patterns of non-parenchymal cells and hepatocytes with differing in size, number of nuclei, and DNA content were uncovered. We also provided information regarding the remodeling of the bile canaliculi and sinusoidal networks.

Conclusions: These findings revealed novel characteristics of liver heterogeneity and have important implications for both the structural organization of liver tissue and its functional features. 3D single-cell atlas will provide a powerful tool to understand liver tissue architecture under both physiological and pathological conditions.

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P-6 PATTERNS OF ANTIBIOTIC RESISTANCE IN PATIENTS WITH CIRRHOSIS AND SPONTANEOUS BACTERIAL INFECTIONS: ANALYSES OF THE MULTICENTER STUDY FROM ARGENTINA AND URUGUAY

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