Characterization of Blood Immune Cells in patients with Decompensated Cirrhosis (SDC, UDC, and pre-ACLF): A pilot study

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Acknowledgements: We particularly acknowledge all the clinicians who participated in the study: Caraceni P., Bongiovanni D., Trebicka J., Gu W., Verbeeck A., Carlo A., Campion D. We also acknowledge all the DECISION team who participated directly or indirectly in the elaboration of this poster. We finally acknowledge all the patients for their participation.

INTRODUCTION

Liver cirrhosis has been traditionally classified into 2 major states: **compensated cirrhosis** and **decompensated cirrhosis**. The last is characterized by the occurrence of complications (ascites, variceal bleeding, and hepatic encephalopathy), which are associated with poor survival and quality of life (1).

Recently, more in detail, 4 pathophysiological/prognostic groups in patients with decompensated cirrhosis have been proposed (2):

Data Analysis

Seurat 4.0.1 was used to perform clustering analysis of single-cell data (4). Azimuth "refence-based mapping" pipeline was used in order to validate cell annotation (5).

NAVARRABIOME

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Cell Proportion across Samples

Healthy	SDC	UDC	pre-ACLF
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DECISION

- Stable decompensated cirrhosis (SDC)
- Unstable decompensated cirrhosis (UDC)
- Pre-acute-on-chronic liver failure (pre-ACLF)
- ACLF

However, the biological mechanisms involved in decompensation of cirrhosis and its progression need to be well-defined.

OBJECTIVE

Patients with cirrhosis present their immune system altered, indicated by an increase in circulating immune-deficient monocytes. The aim of this study is to estimate *changes in cell-type proportion* as well to perform *differential expression* analysis between different stages of decompensated cirrhosis at cell-type level.

SAMPLE OF STUDY & DATA ANALYSIS

Baseline Characteristics

	DECISION de novo recruitment					
	Healthy	SDC	UDC	Pre-ACLF	<i>p</i> value	
Patients	3	6	6	7	-	
Characteristics						
Age, median (range)	56 (56 - 60)	59.5 (54 - 81)	55.5 (43 - 57)	70 (49 - 79)	0.134	
Female Sex, yes, n (%)	1 (33)	2 (33)	0	2 (29)	0.479	
Diabetes mellitus, yes, n (%)	-	2 (33)	2 (33)	3 (43)	0.614	
CKD, yes, n (%)	-	0	0	2 (29)	0.194	
Cardiovascular disease, yes, n (%)	-	0	1 (17)	1 (14)	0.672	
BMI >30, yes, n (%)	-	2 (33)	0	0	0.118	
COPD, yes, n (%)	-	0	0	1 (14)	0.523	
HCC, yes, n (%)	-	0	0	1 (14)	0.523	
Alcohol Consumption, active, n (%)	-	1 (17)	2 (33)	1 (14)	0.643	
Etiology of cirrhosis, n (%)						
Alcohol	-	1 (17)	3 (50)	2 (29)	0.452	
Viral (HBV/HCV)	-	1 (17)	1 (17)	0	0.259	
NAFLD	-	2 (33)	1 (17)	2 (29)	0.828	
Alcohol and viral	-	0	0	2 (29)	0.147	
Alcohol and NAFLD	-	1 (17)	1 (17)	0	0.521	
other	-	1 (17)	0	1 (14)	0.591	



Differential Expression Analysis (SDC/UDC/pre-ACLF vs Healthy)



Data Generation

Preliminary analysis is based on a pilot study. It consists on single-cell RNAseq Gene Expression analysis (GEX) of peripheral Blood Mononuclear Cells (PBMCs) from 3 patients (1 SDC, 1 UDC and 1 pre-ACLF) and one healthy donor.



Data Processing

Cell Ranger Software 5.0.1. (3) was used to perform simple demultiplexing, barcode processing and single-cell 3' gene counting using standards default parameters and human build hg38.

NEXT STEPS

- 1) Complete studio with all samples
- 2) Multiomic solution to study Immunology: GEX + Surface proteins + TCR + BCR
- 3) Differ and study the stages of decompensation of cirrhosis at cell level
- 4) Integration of scRNAseq data with genome-wide association studies

REFERENCES

Sequencing Control

	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Reads Mapped Confidently to Genome/ Transcriptome
ealthy	8,327	17,015	1,531	141,682,646	84.50% - 72.50%
DC	6,597	21,445	1,930	141,474,048	86.40% - 73.60%
DC	5,237	25,257	1,759	132,272,104	83.40% - 71.70%
e-ACLF	8,218	13,252	1,398	108,902,141	82.80% - 71%

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This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 847949. This reflects only the view of the authors, and the *European Commission* is not responsible for any use that may be made of the information it contains.

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