Abstract P085 Table 1 Table demonstrating a comparison of demographic, clinical and prognostic scores between patients assessed via VTA and FTFA. Results from t tests are displayed as mean (SD). Results from Mann Whitney U tests are displayed as median (IQR). Results from Fisher's exact tests are presented as number (%). Statistical significance was determined by a p value <0.05 and signified by *

Variable	N	VTA (n=19)	N	FTFA (n=30)	P value
Age	19	57.0 (49.0–60.0)	30	61.5 (56.8–64.3)	0.05
Sex (male)	19	13 (68.4%)	30	18 (60.0%)	0.76
Current/Ex-smoker	19	8 (42.1%)	29	14 (48.3%)	0.77
ARLD	19	9 (47.4%)	30	9 (30.0%)	0.24
NAFLD	19	2 (10.5%)	30	5 (16.7%)	0.69
Autoimmune liver diseases (PBC/PSC/AIH)	19	6 (31.6%)	30	13 (43.3%)	0.55
Redo transplantation	19	1 (5.3%)	30	0 (0.0%)	0.39
HCC	19	0 (0.0%)	30	2 (6.7%)	0.52
UKELD	19	54.5 (5.7)	30	54.1 (6.0)	0.81
MELD	19	12 (10.3–16.8)	30	10 (6.8–13.5)	0.10
CP score	19	8.6 (2.7)	30	7.8 (1.6)	0.24
Time from referral to completion of assessment	19	62 (48.0–125.0)	28	42 (21.0–54.5)	0.01*
Patient listed for transplant	19	18 (94.7%)	30	26 (86.7%)	0.64

Initially, face-to-face assessments occurred more frequently as the VTA pathway was established. This reversed with VTA being more common than face-to-face assessments in 2021. There was a trend for patients undergoing VTA to be younger than those undergoing face-to-face assessment. No significant differences were observed when comparing sex, smoking status, disease aetiologies, prognostic scores and listing status. The VTA pathway was associated with a significantly longer time from DIP to full discussion: – this likely reflects that patients were assessed who had been waiting from the pre-pandemic era via VTA and initial obstacles encountered as part of a new program. No difference was observed in time from listing to transplantation (table 1) – however, long-term outcomes are currently limited.

Conclusion VTA is feasible and will increase access to transplantation. Long-term post-transplant outcome data is required to fully assess the pathway.

P086

THE BILE ACID METABOLISM PATHWAY IS A SIGNIFICANT METABOLIC CHARACTERISTIC OF POSTOPERATIVE RECURRENCE OF HEPATOCELLULAR CARCINOMA UNDERGOING LIVER TRANSPLANTATION BEYOND MILAN CRITERIA

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Purpose Liver transplantation is one of the most important treatments for hepatocellular carcinoma (HCC), especially advanced HCC. But the prediction and prevention of postoperative recurrence of hepatocellular carcinoma undergoing liver transplantation beyond Milan criteria are still unknown. More and more evidence showed that metabolic biological progress plays a vital role in initial carcinogenesis and recurrence of HCC. Due to the high risk and lack of donor liver, it is urgent to reveal the mechanism of postoperative recurrence of HCC undergoing liver transplantation beyond Milan criteria. In our research, we used bioinformatics methods to find the metabolic characteristic of postoperative recurrence of hepatocellular carcinoma undergoing liver transplantation beyond Milan criteria.

Method We downloaded the data from Gene Expression Omnibus, TCGA, and normal liver tissues in the GTEx database, and we focused on the biological functions of metabolism-related genes. Firstly, we ran the Limma algorithm to find differential expression genes between recurrence and non-recurrence cancerous tissue of hepatocellular carcinoma undergoing liver transplantation beyond Milan criteria. Secondly, Gene Set Enrichment Analysis (GSEA) and Gene Set Variant Analysis (GSVA) were utilized to calculate the scores of the differential expression metabolism-related genes and gene sets. Finally, Kaplan-Meier analysis and Cox regression analysis were used to verify the clinical significance of the result. Bioinformatics methods are used to analyze the genomics, transcriptomics, and clinical data.

Results By analyzing the data from GEO, TCGA, and normal liver tissues of GTEx, metabolism-related gene sets were selected for further research. We ran the GSEA algorithm, and we found 'HALLMARK_BILE_ACID_METABOLISM' had the highest enrichment score. And we ran GSVA to confirm the importance of the 'HALLMARK_BILE_ACID_METABOLISM' gene set in HCC. Moreover, it's obvious the higher score of 'HALLMARK_BILE_ACID_METABOLISM' is relevant to the worse overall survival ($P < 0.01$) and median survival ($P < 0.01$).

Conclusion Our work revealed the importance of the bile acid metabolism pathway in postoperative recurrence of hepatocellular carcinoma undergoing liver transplantation beyond Milan criteria. It helps us to understand the mechanism of the bile acid metabolism pathway of hepatocellular carcinoma recurrence. It also helps us to predict the recurrence of HCC undergoing liver transplantation beyond Milan criteria. Targeting the bile acid metabolism pathway will be a hopeful strategy to predict and prevent the recurrence of hepatocellular carcinoma after liver transplantation.

P087

LIVER TRANSPLANT IN GLYCOGEN STORAGE DISEASE TYPE 1A; A CASE THAT DISPUTES CURRENT GUIDELINES

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Glycogen Storage Disease Type 1 (GSD1) is a rare autosomal recessive condition with an estimated incidence of around 1 in 100,000 births annually. GSD Type 1a describes