factors for NAFLD were significant predictors of liver pathology. The phenomenon of methotrexate-related hepatotoxicity is likely to have been historically over-estimated. Our results suggest that this cohort had NAFLD as the underlying cause of liver fibrosis. The STrATIFY study continues to recruit participants.

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P1 | **LONG TERM ABDOMINAL DRAIN FOR PALLIATION IN ADVANCE LIVER CIRRHOSIS: A SURVEY OF RISKS & BARRIERS**

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**Introduction** Ascites is a leading cause of hospital admission in patients with cirrhosis, with up to a third developing refractory ascites (RA.) RA has a median transplant free survival of 6 months,[1] yet palliation remains sub-optimal and practice varies widely. Long term ascitic drains (LTAD) are standard of care in malignant ascites but there is a paucity of data to support use in advanced cirrhosis. Our aim was to establish current views and practices of gastroenterologists and hepatologists towards LTAD as a palliative intervention in advanced cirrhosis.

**Methods** An electronic survey of 10 questions was designed by a focus group of four hepatologists with a special interest in palliative management of advanced cirrhosis. The survey included seven questions with fixed quantitative options and three exploratory questions with free text space. The survey was logged on survey monkey and distributed electronically via the BASL website and also to relevant departments in Brighton and North East London, with reminder emails in four and eight weeks.

**Results** The survey was completed by 210 respondents over 16 weeks with 99% completion rates for all questions with quantitative endpoints. Respondents included Hepatologists (36.8%,) specialist nurses (24.4%,) gastroenterologists (16.3%) and trainees (15.3%.) Ninety-six percent of respondents looked after patients with RA and 70% had experience of LTAD. All respondents had access to large volume paracentesis, 86.1% to TIPSS, 67% to LTAD and 6% to the Alpha pump. The commonest deterrent to use of LTAD was infection risk (90%), followed by community management of LTAD in these complex patients (56.5%). Patient/carer dissatisfaction (as reported by clinicians) did not seem to be a major cause of concern.

Fifty-six percent of those with experience reported clinical consequences (bleeding, infection, renal impairment) 41.4% reported technical issues and 35.8% inadequate community support. Additional themes emerged, including: lack of clear guidance on use of LTAD in advanced cirrhosis, the role of human albumin solution, monitoring of renal function and funding.

**Conclusions** This national survey of clinicians managing RA in the setting of advanced cirrhosis shows that the majority would be willing to consider LTAD, the main deterrent being infection risk. Additional concerns identified were: lack of training, funding concerns and absence of clear guidelines on community management of LTAD. Our survey highlights the need for a robustly designed randomised controlled trial to assess palliative interventions for the management of RA in advanced cirrhosis.

## REFERENCE

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P2 | **PDLIM5 IN HEPATIC STELLATE CELLS IS UPSTREAM OF PRO-FIBROTIC YAP1 MECHANO-TRANSDUCTION**

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**Introduction** Liver fibrosis is excessive remodelling of the extracellular matrix (ECM) leading to tissue scarring and eventually impaired liver function. Hepatic stellate cells (HSCs) are the key cellular drivers of liver fibrosis responsible for the formation of stiffened fibrotic ECM in response to liver injury. Activation of HSCs is driven and maintained by increased matrix stiffness. Yes Associated Protein1 (YAP1) appears to be a critical mechano-regulator of HSC activation and fibrotic gene expression. Functional disruption of YAP1 reduces liver fibrosis; we therefore sought to identify how external cues from the ECM are transduced by the HSC cytoskeleton, and regulate YAP1 activity. We identify Enigma family protein PDLIM5 as a potential driver of YAP1 mechano-activation.

**Methods** Human liver tissue was from the Manchester Biobank (ethical approval NW1260/22). Primary human or mouse HSCs were isolated using standard liver perfusion, digestion and density gradient centrifugation. Total RNA extracted from quiescent and activated mouse (mHSCs) was used for RNA-seq following the HISeq Illumina protocol and identification of differentially expression genes (DEG) by DESeq2. PDLIM5 gene and protein expression was characterized in immortalized human HSCs (LX-2 cells) and primary HSCs by qPCR, western blot (WB) and immunocytochemistry (ICC). siRNA was used to disrupt PDLIM5 expression in LX-2 cells. qPCR, WB and ICC were used to assay LX-2 phenotype.

**Results** The transcriptome analysis of activated mHSCs revealed 6053 DEGs. Gene ontology analyses showed that the activated HSC transcriptome is characterized biologically by expression of genes related to ECM organization and secretion, and genes implicated in the regulation of the actin cytoskeleton. The transcriptome of activated HSCs had significantly increased expression of Enigma protein coding genes including PDLIM5. Enigma proteins are cytoskeleton associated proteins