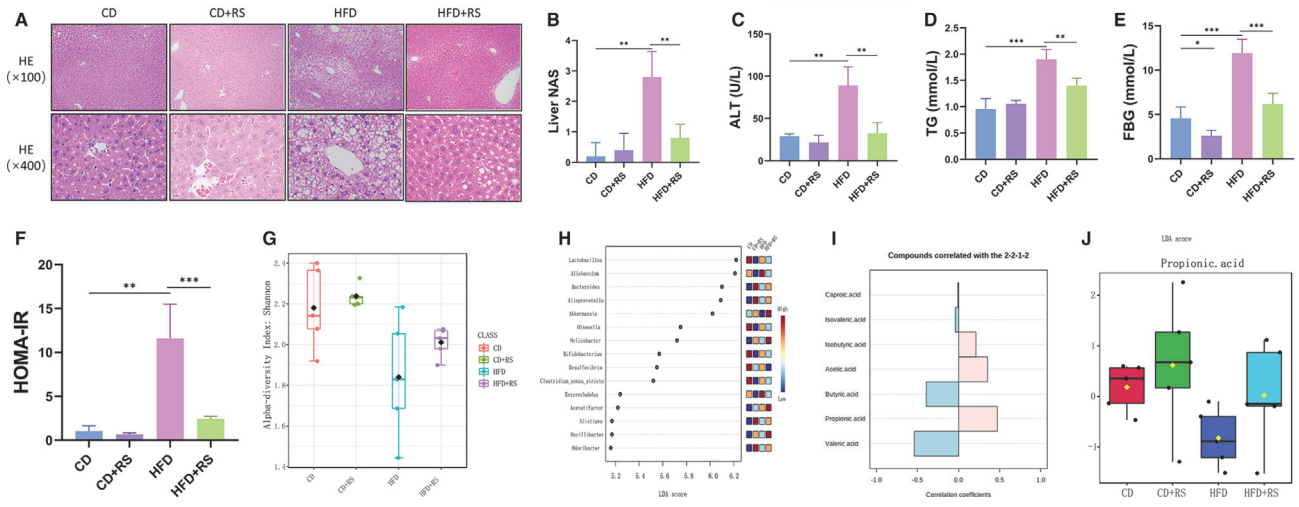

Abstract IDDF2021-ABS-0207 Figure 1

0207 Figure 1d Type 2 resistant starch improves liver steatosis induced by high-fat diet; Serum levels of TG in mice (**P<0.01, ***P<0.001) (IDDF2021-ABS-0207 Figure 1e Type 2 resistant starch improves liver steatosis induced by high-fat diet; Serum levels of FBG in mice (*P<0.05, ***P<0.001)) (IDDF2021-ABS-0207 Figure 1f Type 2 resistant starch improves liver steatosis induced by high-fat diet; Serum levels of HOMA-IR in mice (**P<0.01, ***P<0.001)). The α diversity of intestinal microflora was decreased in HFD group mice compared with CD group mice, but slightly increased after RS2 intervention (IDDF2021-ABS-0207 Figure 1g Type 2 resistant starch improves liver steatosis induced by high-fat diet; Alpha diversity). LEfSe analysis showed that the abundance of Akkermansia (LDA=6.02) was decreased in the HFD group mice compared with CD group mice and increased significantly after RS2 intervention, indicating that it was a biomarker of NAFLD mice (IDDF2021-ABS-0207 Figure 1h Type 2 resistant starch improves liver steatosis induced by high-fat diet; LEfSe analysis). The concentration of valeric acid in portal vein blood was negatively correlated with the abundance of Akkermansia (r=-0.54, P=0.014), and propionic acid was positively correlated with the abundance of Akkermansia (r=0.47, P=0.036) (IDDF2021-ABS-0207 Figure 1i Type 2 resistant starch improves liver steatosis induced by high-fat diet; Correlation analysis of SCFA and intervention) (IDDF2021-ABS-0207 Figure 1j Type 2 resistant starch improves liver steatosis induced by high-fat diet; Concentration of propanoic acid in portal vein blood. CD, control diet; HFD, high-fat diet; RS, type 2 resistant starch).

Conclusions RS2 intervention can improve liver steatosis, liver function, serum lipid and serum glucose levels and insulin resistance in NAFLD mice, The α diversity of intestinal microflora in RS2 treated mice was increased too. Akkermansia is a biomarker of NAFLD mice, which is significantly increased after RS2 treatment. The concentration of propionic acid in portal vein blood of mice increased after RS2 treatment and was positively correlated with the abundance of Akkermansia.

Diwen Shou and Chuangyu Cao contributed equally to this work.

Basic Gastronenterology

IDDF2021-ABS-0013 THE METHOD FOR OBTAINING A REPRODUCIBLE MODEL OF TUBERCULOUS PERITONITIS IN RABBITS

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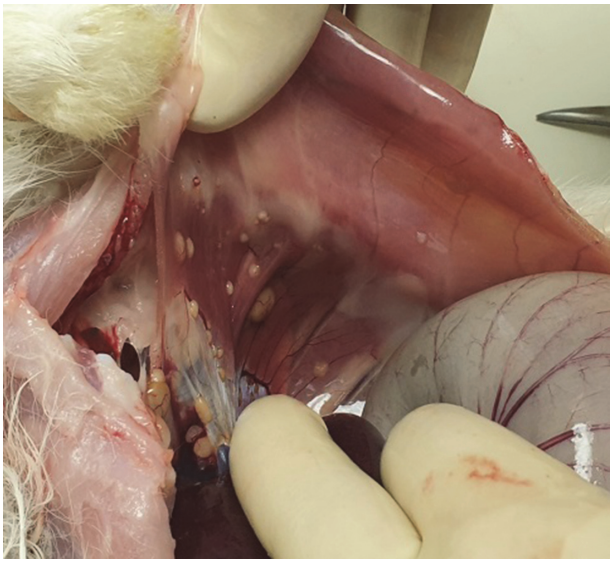
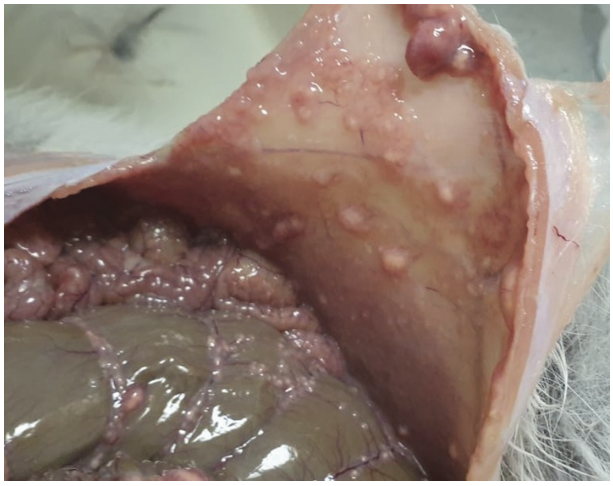
10.1136/gutjnl-2021-IDDF.21

Background The unsatisfactory results of the diagnosis and treatment of tuberculosis peritonitis as well as the high rate of disability and mortality in this disease require further study of the pathogenesis of its progression, the features of morphology, and the development of new treatment methods. To this end, we have created a reproducible model of chronic tuberculous peritonitis to study the pathophysiological mechanisms of its development.

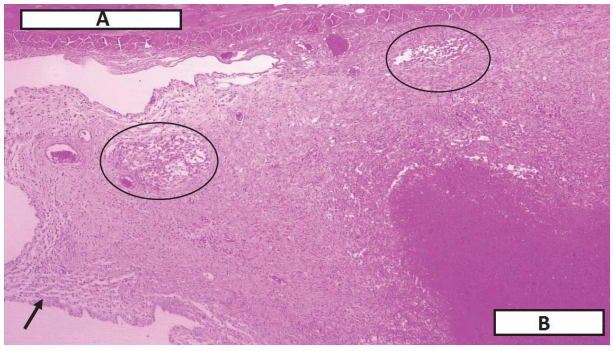
Methods Approved by the Local Ethics Committee, the study was performed using 10 male rabbits of the 'Soviet Chinchilla' breed. All the work with model animals was carried out in accordance with international standards for the humane treatment of laboratory animals. Rabbits underwent intraperitoneal administration of mycobacterium tuberculosis (MBT), modeling tuberculosis peritonitis according to our proposed method which included intravenous administration of TNF inhibitor and intraperitoneal inoculation of iron (III) hydroxide of the sucrose complex. As a result, local and general immunosuppression led to active development of MBT in the peritoneum layers causing specific inflammation. The animals were removed from the experiment on the 44th day after infection. Samples of the parietal and visceral peritoneum, intestines, lungs, lymph nodes, parenchymal organs were collected for morphological examination.



Abstract IDDF2021-ABS-0013 Figure 1



Abstract IDDF2021-ABS-0013 Figure 2



Abstract IDDF2021-ABS-0013 Figure 3

Results During the autopsy of rabbits, the presence of serous-fibrinous effusion, characteristic tubercular formations on the peritoneum, polymorphic adhesive process due to the organization of exudate in the abdominal cavity was noted. It was proved in the experiment that all animals developed tuberculous peritonitis with a lesion of the large omentum and serous integuments of internal organs (IDDF2021-ABS-0013 Figure 1. Autopsy the adhesive process and gray tubercles are disseminated on the parietal and visceral peritoneum)(IDDF2021-ABS-0013 Figure 2. Autopsy gray tubercles on the parietal peritoneum). A molecular genetic study of fragments of the omentum and peritoneum revealed the DNA of mycobacterium tuberculosis. Histological examination of the fragments of the peritoneum and the omentum showed an area of caseous necrosis and granuloma-like clusters of macrophages (IDDF2021-ABS-0013 Figure 3), single clusters of acid-resistant mycobacteria were detected when the preparations were stained according to Ziehl-Neelsen.

Conclusions The developed method of modeling tuberculosis peritonitis is close to the real human disease in clinical and morphological manifestations and allows us to study the dynamics and mechanisms of the development of a specific infectious process in the abdominal cavity.

IDDF2021-ABS-0028 MICROBIOLOGIC RISK FACTORS OF RECURRENT CHOLEDOCHOLITHIASIS POST ENDOSCOPIC SPHINCTEROTOMY

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10.1136/gutjnl-2021-IDDF.22

Background Bile microbiome has a profound influence on recurrence in choledocholithiasis patients post endoscopic sphincterotomy (EST), but the key pathogens and their function on the biliary tract remain unclear.

Methods In this study, the next-generation sequencing techniques were applied to investigate the biliary microbial characteristics of the recurrent patient's post EST and analyze the metabolic functions of the key pathogens, in the hope of finding out the risk factors of recurrence post EST.

Results Results revealed the distinct clustering of biliary microbiota in recurrent choledocholithiasis from those without recurrence, and a higher relative abundance of Fusobacterium and Neisseria with the absence of Lactobacillus were observed in the bile of the recurrent patients. Functional analysis showed the changes of the microbiome might lead to worse metabolism of carbohydrate and amino acids and more biosynthesis of glycan and other secondary metabolites in the biliary tract, indicating microbiologic influence on recurrence of choledocholithiasis. And survival analysis found out the presence of Lactobacillales in bile might be effective in the prediction of recurrence post EST.