LetPub 结果：

【简要总结】

Yes, the gut microbiome has been extensively studied in hepatocellular carcinoma (HCC) across multiple etiologies including nonalcoholic fatty liver disease (NAFLD), cirrhosis, and viral hepatitis. Investigations consistently demonstrate distinct microbial signatures in HCC patients compared to those with cirrhosis alone or healthy controls. For instance, patients with NAFLD-related cirrhosis and HCC display elevated fecal calprotectin, heightened systemic inflammation, and microbiota shifts featuring increased Bacteroides and Ruminococcaceae alongside reduced Bifidobacterium and Akkermansia, patterns that correlate with monocyte activation and pro-inflammatory cytokines [1]. Parallel work profiling 419 fecal samples across Chinese regions identified 30 microbial markers achieving strong diagnostic performance (AUC 80.64%) for early HCC, marked by depletion of butyrate producers and enrichment of lipopolysaccharide-producing taxa [2]. Similar dysbiotic trajectories, including expanded Erysipelotrichaceae and altered Bacteroides/Prevotella ratios, appear in other cirrhosis cohorts and associate with NOD-like receptor pathway activation [3]. These alterations escala compensated cirrhosis through decompensated stages to HCC-asso modulated further by host factors such as excess weight and diet [4

具体研究结果直接对应原始文献[2]，30个微生物标志物及AUC 80.64%均可由原文核实，证据来源清晰

Beyond diagnostic associations, microbiome features influence treatment outcomes and intratumoral microenvironments in HCC. Responders to anti-PD-1 immunotherapy exhibit greater taxonomic richness, stable beta-diversity trajectories, and enrichment of Akkermansia muciniphila and Ruminococcaceae species linked to carbohydrate metabolism pathways [5]. Integrated microbiome-transcriptome analyses in HBV-related HCC further connect Bacteroides, Lachnospiracea incertae sedis, and Clostridium XIVa to tumor immune microenvironment genes, potentially mediated by serum bile acids, enabling outcome prediction models with AUC values reaching 81% [6]. Viable intratumoral bacteria have also been cultured from HCC tissues, revealing cytosolic localization in hepatocytes and erythrocytes and yielding machine-learning signatures for tumor classification [7]. Collectively, these studies establish the gut-liver axis as a mechanistic contributor to hepatocarcinogenesis and highlight microbial biomarkers for early detection, prognosis, and therapeutic stratification in HCC.

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文章要点：Demonstrates distinct gut microbiota and inflammatory profiles in NAFLD-HCC versus cirrhosis without HCC.

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作者：Zhigang Ren; Ang Li; Jianwen Jiang; Lin Zhou; Zujiang Yu; Haifeng Lu; Haiyang Xie; Xiaolong Chen; Li Shao; Ruiqing Zhang; Shaoyan Xu; Hua Zhang; Guangying Cui; Xinhua Chen; Ranran Sun; Hao Wen; Jan Lerut; Quancheng Kan; Lanjuan Li; Shusen Zheng
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作者：Federico Piñero; Martín Vázquez; Patricia Baré; Cristian Rohr; Manuel Mendiz ábal; Mariela Sciara; Cristina Alonso; Fabi án Fay; Marcelo Silva
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作者：Jian-Hang Huang; Jie Wang; Xiaoqiang; Jun Li; Xing Liu; Jia Fan; Jiabin Cai; Feng Li
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文章要点：Provides first evidence of viable intratumoral bacteria usable for HCC prediction.

针对具体HCC研究场景直接推荐原始研究，而非仅停留在综述