**DeepSeek 结果：**

Yes, the gut microbiome has been extensively studied in hepatocellular carcinoma (HCC). Research in this area has advanced significantly, with investigations spanning multiple aspects: the identification of specific microbial signatures, the underlying mechanisms of disease promotion, and the potential for novel diagnostic and therapeutic applications.
The current body of evidence highlights the gut microbiome's role across various etiologies and stages of HCC through a diverse range of study designs.
 Key Research Findings
The literature reveals several significant ways the gut microbiome is implicated in HCC:

Disease-Specific Microbial Signatures: Numerous studies have identified distinct microbiota compositions that differentiate HCC patients from healthy individuals and those with liver cirrhosis.

研究对象表述不够准确：该研究整合分析涉及gut与liver microbiome，此处以“ liver microbiota ”概括后又用于回答gut microbiome问题，需区分样本来源

A 2026 integrative analysis of 13 studies found that liver microbiota showed significant differences in diversity between HCC patients and non-cancer controls, and identified Blautia and Streptococcus as potential biomarkers common to both the gut and liver.

A 2025 study on Egyptian patients with HCV-related HCC observed gut dysbiosis with a marked enrichment of specific species, including Bifidobacterium, Fusobacterium, Providencia, and Pseudomonas aeruginosa.

具体研究发现未就地标注Citation，需根据后续Study Focus自行对应文献来源

A 2025 pilot study comparing patients at different stages found that the abundance of genera like Bulleidia, Pantoea, Clostridium_Q, Rothia, and Streptococcus was significantly increased in HCC, while beneficial taxa such as Akkermansia and Butyricimonas were depleted.

Mechanistic Links to Disease Progression: Research is uncovering how gut microbes promote liver cancer. A pivotal 2026 study published in Cancer Discovery demonstrated that certain gut pathobionts, like Bacteroides fragilis, can translocate from the gut to the liver, triggering oncogenic pathways that facilitate HCC development. This supports the concept of the "gut-liver axis" , where increased intestinal permeability and microbial products promote inflammation and carcinogenesis.

Diagnostic and Therapeutic Potential: The distinct microbial fingerprints are being explored as tools for early diagnosis and treatment.

Microbiome-based predictive models have shown high discriminative ability for HCC, with a gut model achieving an AUC of 0.8064 and a liver model achieving an AUC of 0.9645. This suggests microbial biomarkers could be valuable for non-invasive early screening.

Reviews highlight the potential of modulating the gut microbiota (e.g., with probiotics or fecal microbiota transplantation) to improve the efficacy of HCC immunotherapy.

Summary of Study References

| Study Focus | Key Finding | Reference |
| --- | --- | --- |
| Obesity-related dysbiosis | Fecal microbiota from obese mice promoted HCC tumor growth in a mouse model. | https://www.tandfonline.com/doi/full/10.1080/20565623.2025.2599729 |
| Mucosa-associated microbiota | Identified distinct microbial patterns in the gut mucosa of HCC patients, linked to inflammation and carcinogenesis. | https://pubmed.ncbi.nlm.nih.gov/41361834/#1<br>https://link.springer.com/article/10.1186/s13099-025-00767-4#1 |
| MASLD-associated HCC | Investigated the interaction between gut microbiome and host gene expression to identify diagnostic biomarkers for MASLD-HCC. | https://link.springer.com/article/10.1186/s13099-025-00782-5?fromPaywallRec=false#1 |
| HCV-related HCC | Found a correlation between specific gut microbes (e.g., Fusobacterium) and inflammatory biomarkers like MMP9 | https://library.nih.go.kr/ncmiklib/search/Retrieve?an=edsdoj.40ac4ec79aa47a5be7090d64f356e9e&dbid=edsdoj&highlight=AND&type=other#1<br>https://link.springer.com/article/10.1038/s41598-025-28663-6?fromPaywallRec=false#1 |

研究结论错配：原文与MMP9显著正相关的是Porphyromonas；Fusobacterium主要表现为HCC患者中富集

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| | in Egyptian patients. | |
| Gut pathobiont translocation | Demonstrated that gut Bacteroides fragilis can translocate to the liver to activate oncogenic pathways and promote HCC. | https://aacrjournals.org/cancerdiscovery/article-split/doi/10.1158/2159-8290.CD-25-1355/785669/#skipNav#1 |
| Multi-study integration | Integrated data from 13 studies to identify shared microbial biomarkers and build predictive models for HCC. | https://link.springer.com/article/10.1186/s13568-026-02082-w?fromPaywallRec=false#1 |
| Comprehensive review | Summarized the role of gut microbiota in HCC proliferation, diagnosis, and immunotherapy response. | https://ouci.dntb.gov.ua/en/works/lxLrab1G/#1<br>https://www.sciencedirect.com/science/article/abs/pii/S0882401025009982#1<br>https://www.kci.go.kr/kciportal/landing/article.kci?arti_id=ART003210448 |

Reference呈现形式不统一：主要以URL作为文献入口，未统一列出作者、题名、期刊、年份及DOI

In summary, the gut microbiome is now recognized as a key player in HCC. The field is moving from describing associations to understanding causal mechanisms and translating these findings into clinical applications, such as non-invasive biomarkers and novel therapeutic strategies.

If you're interested in a specific area, like a particular cause of HCC (e.g., viral hepatitis vs. fatty liver disease) or its role in immunotherapy, I can provide more focused information.

以上结果来自 **DeepSeek V4**