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The gut microbiome's role in Egyptian liver disease patients across different etiologies

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Dysbiosis in the gut microbiome, particularly concerning the synchronous cross-talk between the gut and the liver, has been associated with various diseases. This study examines the gut microbiome's role in liver diseases among Egyptian patients, with a focus on the hepatitis C virus (HCV) and hepatocellular carcinoma (HCC), both of which are highly prevalent in Egypt. Utilizing shotgun metagenomic sequencing, we analyzed microbial gene catalogs and taxonomic profiles from 46 Egyptian patients categorized into five groups: healthy individuals, liver disease patients of different etiologies, post-HCV, treated HCV, and HCV-HCC patients. The results revealed that healthy and treated HCV patients exhibited distinct microbial profiles characterized by an abundance of beneficial bacteria, *Faecalibacterium* and *Bifidobacterium* ($p < 0.05$), associated with anti-inflammatory short-chain fatty acid production. Conversely, liver disease and HCC patients displayed increased pathogenic bacteria, *Enterobacteriaceae* ($p < 0.05$), and genes linked to inflammation and oncogenesis, including lipopolysaccharide biosynthesis. These findings suggest a novel dominance of *Faecalibacterium* in healthy Egyptians, likely attributable to fiber-rich diets, and cytochrome P450 genes as potential HCC biomarkers, possibly connected to aflatoxin exposure. Treated HCV patients showed significant microbiome recovery, reflecting effective antiviral therapy. These findings emphasize that Egypt-specific factors, such as persistent resistance genes post-HCV due to antibiotic use and the prominence of bile acid metabolism genes, are influenced by high HCV prevalence and environmental exposures like aflatoxins. These dynamics distinguish this study from global research, establishing a new agenda for regional microbiome studies as a detailed perspective of the broader picture.