

GUT DYSBIOSIS IN PATIENTS WITH NON-ALCOHOLIC FATTY LIVER DISEASE

MD. SANAULLAH HAQUE¹

Background: Non-alcoholic fatty liver disease (NAFLD) is a multifactorial condition with a rapidly increasing global prevalence. Emerging evidence suggests that gut microbiome dysbiosis plays a crucial role in the progression from NAFLD to non-alcoholic steatohepatitis (NASH). However, there is a paucity of data regarding gut microbial alterations in biopsy-proven NAFLD patients in the Asian population, particularly in Bangladesh.

Methods: This observational study was conducted at the Department of Hepatology, Bangladesh Medical University, from November 2023 to August 2024. A total of 40 participants were enrolled, including 10 patients with NASH, 20 with non-NASH NAFLD (diagnosed by liver biopsy and NAFLD Activity Score), and 10 healthy controls. Fecal DNA was extracted and analyzed using next-generation sequencing (NGS) targeting the hypervariable region of 16S rRNA on the Illumina HiSeq platform. Microbial diversity was assessed using alpha diversity (Observed species, Chao1, Shannon index) and beta diversity (Bray–Curtis dissimilarity index). Statistical analyses were performed using SPSS version 26, applying Chi-square test, Student's t-test, and ANOVA as appropriate. **Results:** A significant difference in beta diversity was observed between healthy controls and NASH patients based on the Bray–Curtis dissimilarity index ($P = 0.042$). Alpha diversity indices demonstrated a decreasing trend from controls to non-NASH and further to NASH patients; however, these differences did not reach statistical significance between subgroups. Taxonomic analysis revealed a shift in gut microbial composition, with a reduction in beneficial bacterial populations and an increase in pro-inflammatory or potentially pathogenic taxa in NAFLD patients. This was reflected in an altered Firmicutes/Bacteroidetes (F/B) ratio. **Conclusion:** This study demonstrates a significant association between gut dysbiosis and NAFLD progression in the Bangladeshi population. The observed reduction in microbial diversity and increased abundance of pathogenic bacteria suggest a contributory role of the gut microbiome in the transition from NAFLD to NASH. These findings underscore the potential of microbiome-targeted therapies as a novel approach in the management of NAFLD.

Keywords: Non-alcoholic fatty liver disease, NAFLD, Gut microbiome dysbiosis, Non-alcoholic steatohepatitis, NASH.

Date of submission: 11.04.2026

Date of acceptance: 29.04.2026

DOI: <https://doi.org/10.3329/bjm.v37i20.89333>

Citation: Haque MS. Gut Dysbiosis in Patients with Non-alcoholic Fatty Liver Diseas. *Bangladesh J Medicine* 2026; Vol. 37, No. 2(1): pp. 214.

Affiliation:

1. Registrar, National Gastroliver Institute and Hospital, Dhaka, Bangladesh. E-mail: mdsanaullah.rmc@gmail.com