Potential Impact of Gut Lactobacillus Acidophilus and Bifidobacterium Bifidum on Hepatic Histopathological Changes in Non-Cirrhotic Hepatitis C Virus Patients with Different Viral Load

Abstract:

Background: Composition of gut microbiota has recently been suggested as a key factor persuading the pathogenesis of numerous human diseases including hepatic cirrhosis. Objective: To evaluate the potential impact of Lactobacillus acidophilus and Bifidobacterium bifidum microbiota on the progression of hepatic histopathological changes among patients with non-cirrhotic chronic hepatitis C (HCV) infection with different viral load. Additionally, to assess fecal composition of Lactobacillus acidophilus ATCC-4356 and Bifidobacterium bifidum ATCC-11863 microbiota genotypes. Material and methods: This study was carried out on 40 non-cirrhotic chronically infected HCV patients, and 10 healthy-controls. Liver biopsy and HCV genomic viral load were assessed for all patients after full clinical examination. Lactobacillus acidophilus ATCC-4356 and Bifidobacterium bifidum ATCC-11863 microbiota were assessed in all fecal samples using PCR assay, after counting total lactic acid bacteria. Results: There was a significantly higher difference between the count of both total lactic acid and Lactobacillus acidophilus of healthy controls compared to patients (P-value < 0.001). Though the count of total lactic acid bacteria, and Lactobacillus acidophilus were higher in the cases with early stage of fibrosis (score ≤ 1) compared to those with score > 1, there were no statistically significant differences with both the serum level of hepatitis C viremia ($P = 0.850$ and 0.977 respectively) and the score of fibrosis ($P = 0.246$ and 0.260 respectively). Genotypic analysis for the composition of the studied microbiota revealed that diversity was higher in healthy controls compared to patients. Conclusions: The progression of hepatic fibrosis in HCV chronically infected patients seems to be plausible based on finding the altered Lactobacillus acidophilus and Bifidobacterium bifidum gut microbiota composition. Thus, modulation of these microbiota seems to be a promising target for prevention and control of HCV infection.

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