

## Association of Transmission Risk Factors Among HCV-infected Bangladeshi Patients With Different Genotypes

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**Abstract :** Globally, an estimated 58 million people have chronic hepatitis C virus infection, with about 1.5 million new infections occurring per year. The hepatitis C virus is a blood-borne virus, and most infections occur through exposure to blood from unsafe injection practices, unsafe health care, unscreened blood transfusion, injection drug use, and sexual practices that lead to exposure to blood. Hepatitis C virus (HCV) causes chronic infections that mainly affect the liver leading to liver diseases. This study aimed to determine whether there is any significant association between HCV transmission risk factors in relation to genotypes in HCV-infected Bangladeshi patients. After quantification of HCV viral load, 36 samples were randomly selected for HCV genotyping and risk factor measurement. A greater proportion of genotype 1 ( $p > 0.05$ ) patients (40%) underwent blood transfusion compared to patients (22.6%) with genotype 3 infections. More genotype 1 patient underwent surgery and invasive procedures (20%), and rather than those with genotype 3 patients (16.1%). The history of IDUs (25.8%) and sexual exposure (3.2%) are only prevalent in genotype 3 patients and absent in patients with genotype 1 ( $p > 0.05$ ). There was no significant statistical difference found in HCV transmission risk factors (blood transfusion, IDUs, Surgery & interventions, sexual transmission) between patients infected with genotypes 1 and 3. In HCV infection, genotype may have no relation to transmission risk factors among Bangladeshi patients.

**Keywords :** HCV genotype, alanine aminotransferase (ALT), HCV viral load, IDUs

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