

YMDD and FLLAQ Mutations in Chronic Hepatitis B Patients

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Abstract

Background and Objective: Lamivudine is the first orally available drug approved for treatment of chronic hepatitis B. Mutations at the YMDD and FLLAQ motifs in the domains of HBV polymerase gene contribute resistance to lamivudine. This study was aimed to determine the rate of YMDD and FLLAQ mutants in hepatitis B patients in Golestan Province, Iran.

Material and methods: In this cross sectional study, 120 patients with chronic HBV infection were recruited. Of them, 55 were treated and 65 untreated with Lamivudine. HBV DNA extractions from plasma and polymerase chain reaction (PCR) were performed. For detection of Lamivudine mutants direct sequencing and alignment of products were applied using reference sequence from Gene Bank database.

Results: the average age of patients was 36.31 ± 10.07 , which 35% of them were female and 65% were male. Mutations at the YMDD and FLLAQ motifs in the domains of HBV polymerase gene were detected in 12 of 55 patients (21.81%) treated with Lamivudine while no mutation was observed in untreated patients. The YMDD and FLLAQ mutants were detected in 9.16% (11/120) and 0.83% (1/120) of chronic HBV patients, respectively.

Conclusion: Usual HBV mutations, which play an important role in lamivudine resistance, detected in this study are similar to other studies.

Key words: Hepatitis B Viruse, YMDD Mutation, Lamivudine, Iran.

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