IDENTIFICATION OF NS5B RESISTANCE-ASSOCIATED MUTATIONS IN HEPATITIS C VIRUS CIRCULATING IN TREATMENT NAÏVE CAMEROONIAN PATIENTS

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ABSTRACT

Background and Aims: NS5B polymerase inhibitors form the basis of current treatment for hepatitis C virus (HCV) infection. Direct-acting antivirals (DAAs) offer highly effective treatment. However, the presence of mutations associated with resistance, particularly at the level of non-structural polymerase protein 5B (NS5B), may reduce their efficacy. The aim of this study was to identify possible natural AAD mutations in the HCV NS5B gene associated with AAD resistance in treatment-naive Cameroonian patients with chronic hepatitis C.

Methods: Whole blood samples were collected. Plasma was then isolated and stored at -80°C for molecular analysis. Fragments of these genes were amplified with the specified primers and nucleotide sequences were obtained using the Sanger sequencing system and the resistance profile was analysed using Geno2pheno [hcv] 0.92.

Results: Analysis of the NS5B sequences revealed three genotypes, namely 1, 2 and 4, with numerous amino acid mutations. The significant S282T mutation, which confers high resistance to SOF, was found in one patient, while the NS5B C316N polymorphism associated with resistance was found in 16 sequences. The Q309R mutation associated with ribavirin resistance was detected in 19 genotype 1 sequences and the L320F polymerase inhibitor mutation was found in one genotype 4f sequence. The following mutations were associated with DAA resistance: E237G, M289L, A333V, D310N, V321A and V321I were found in different genotypes in our study.

Conclusion: Our study showed several different mutations in the NS5B gene in HCV patients who had not previously received DAA therapy. These mutations may increase the risk of future treatment failure.