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Basic Study

Role of RNA secondary structure in emergence of compartment specific hepatitis B virus immune escape variants

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Abstract

AIM: To investigate the role of subgenotype specific RNA secondary structure in the compartment specific selection of HBV immune escape mutations.

METHODS: This study was based on the analysis of the specific observation of HBV subgenotype A1 in the serum/ plasma, while subgenotype A2 with G145R mutation in the peripheral blood leukocytes (PBLs). Genetic variability found among the two subgenotypes was used for prediction and comparison of the full length pregenomic RNA (pgRNA) secondary structure and base pairings. RNA secondary structures were predicted for 37°C using the Vienna RNA fold server, using default parameters. Visualization and detailed analysis was done using RNA shapes program.

RESULTS: In this analysis, using similar algorithm and conditions, entirely different pgRNA secondary structures for subgenotype A1 and subgenotype A2 were predicted, suggesting different base pairing patterns within the two subgenotypes of genotype A, specifically, in

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