

Is Single-Strand Conformation Polymorphism Analysis of the Full 5-Untranslated Region an Adequate Approach To Study Hepatitis C Virus Quasispecies Distribution?

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Abstract

Single-strand conformation polymorphism (SSCP) analysis is used by many laboratories to study the quasispecies distribution of the hepatitis C virus (HCV). Here we question the validity of this experimental approach, as conclusions are drawn from the analysis of the migration patterns of two ssDNA molecules and not from RNA. Using previously characterized mutants of the HCV 5 untranslated regions, we show that contrary to what has been predicted, SSCP migration patterns of DNA amplicons with differences in their nucleotide sequences generated from the full 5 UTR of HCV are not necessarily unique.