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Analysis of variant *IFNL4* rs368234815 by simple PCR-RFLP technique is as effective as PCR sequencing in Egyptian patients chronically infected with HCV genotype 4

Background: Hepatitis C viral infection is an endemic health problem in Egypt with the highest prevalence rate worldwide. Several host and viral factors could affect the response to antiviral treatment among the most important host genetic factors, *IFNL4* rs368234815 variant that is classified as a deletion/insertion genetic variation (TT/ Δ G), that proved to have an important role in spontaneous and treatment induced clearance of HCV infection.

Aim: This study aimed to validate a simple, cheap and rapid polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method for analysis of *IFNL4* rs368234815 dinucleotide variant in comparison to the reference PCR sequencing technique

Subjects & Methods: *IFNL4* rs368234815 variant was genotyped using two methods; a simple PCR-RFLP method and PCR sequencing method as a reference method in 40 patients chronically infected with HCV genotype 4.

Results: Genotyping results of *IFNL4* rs368234815 variant with PCR-RFLP were concordant with PCR sequencing method in all studied patients with 100% analytical sensitivity and specificity.

Conclusion: We strongly suggest a validated, simple and rapid PCR-RFLP method for genotyping of common *IFNL4* rs368234815 that is more cost-effective than PCR sequencing.

Biography

Salwa Hamdi Gomaa has completed her PhD in 2009 from Alexandria University, Egypt. She has published more than 10 papers in reputed journals.

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