

Impact Analysis of the Hepatitis C Virus F Protein Deletion on Viral Replication and Pathogenic Infection

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Abstract: Objective: investigating the influence of the hepatitis C virus F protein deletion on viral replication and pathogenic infection and the results were analyzed. Methods: the experimental method selected biochemical methods, the first step, the preparation of the hepatitis C virus RNA transcript; the second step, according to the result of the correlation detection culture experiments, including: PCR technology, the detection of infectious replication, immunofluorescence, transfection, etc. Finally, the relevant results to collate, record and analyze. Results: the introduction of the mutant gene expression and the number of the original number of genes expression was no significant difference in the expression levels of the two groups and the core protein also no significant difference ($P < 0.05$); F protein expression in tumor tissue than other tissues, indicating HCC formation and F protein has some relevance; Core protein and the wild-type core protein contains a single mutation in the structure remained the same; F-deficient secondary structure of the core protein has more variations. Conclusion: HCV F translation and replication process of the missing protein of the virus had no effect on viral translation, reproduction and medical treatment to increase the resistance of the secondary structure of the core protein.

Introduction

Hepatitis C virus infection is the culprit leading to chronic liver disease and the resulting infection can be further developed into cirrhosis, fatty liver and liver cancer and other serious diseases [1]. There are about 170 million carriers of hepatitis C virus worldwide, and about 100,000 people have developed cancer patients. It is generally believed that the route of transmission of hepatitis C virus includes blood and blood products, the current drug for hepatitis C virus treatment only interferon and the drug's response rate is very low, side effects are more expensive, does not meet the requirements, and Hepatitis C virus vaccine is still in the research stage [3]. The hepatitis C virus genome consists of two parts, which are located in the middle of the open reading frame and at both ends of the non-coding region (conservative), the length can reach 9600bp. The noncoding region is indispensable for the viral RNA replication process and the translation process [4-5]. A single open reading frame translates as many as 3,000 amino acid residues, which are polyprotein precursors, which can be cleaved into six nonstructural proteins and 10 species under the dual action of viral proteases and host cells Structural proteins (E1, E2, C and P7). This year, some laboratories have found a viral protein called the reading frame shift protein, also known as core + 1 protein. In addition, there are also found that the endogenous codon can also produce F protein, the starting site is mainly located in the 85/87 codon was named core + 1 / S [6]. From the discovery of F protein to now has more than ten years of history, but the human biology of its red to know little about how to understand the hepatitis C virus F protein is how the virus infection, disease and replication process, the study observed the process of viral translation and replication in the absence of F protein, and further analyzes how the secondary structure of the core protein changes after its deletion.

Materials and Methods

Reagents and Instruments. The name of the reagent and the instrument and the details of the

manufacturer are shown in Table 1.

Table 1 Reagent and instrument name and manufacturer

Reagent or instrument name	Production company or individual
QuikChang LinghningSite-Directed Mutagenesis Kit	Stratagene Corporation (USA) products
Isopropyl thiogalactoside	Beijing tripod biotechnology limited liability company
5-bromo-4-chloro-3-indole- β -D galactoside	Beijing tripod biotechnology limited liability company
NZ amines	Beijing tripod biotechnology limited liability company
Yeast extract	Beijing tripod biotechnology limited liability company
14ml BD Falcon Polypropylene Tube	Shanghai Ya Yi Science Experimental Equipment Co., Ltd
HCV NS5A monoclonal antibody	Charles M .Riceprofessor
T7 in vitro transcription kit	Promrga company
M-MLV reverse transcriptase	Promrga company
Fetal bovine serum	America invitorgen company
DMEM	America invitorgen company
Opti-MEM	America invitorgen company
Alex488 goat anti-mouse fluorescent	America invitorgen company
FITC-goat anti-human IgG	America invitorgen company
Lipofectamine 2000	America invitorgen company
RNA extraction reagent	Shanghai Huashun Biological Engineering Company

Construction of Cell Lines and Plasmids. The introduction of the kit was carried out in the presence of PFL-J6JFH1 as template, and the number of introduced mutations was 5, and the purpose of introducing these mutations was to terminate the replication of all known F proteins, and this process did not Change the amino acid sequence of hepatitis C virus.

Preparation of Viral RNA Transcripts. In the first step, the linearization treatment: the plasmid is linearized by XbaI; the second step, in vitro transcription: the preparation of RNA in vitro transcripts by T7 transcription kit; the third step, purity and integrity detection: reagent A mixture of phenol, isoamyl alcohol and chloroform at a volume ratio of 25: 1: 24 was selected and the purity and integrity of the mixture were tested by electrophoresis with 1.5% agarose gel.

RNA Transcript Transfection and Cell Culture. Transfection of RNA transcripts: 1000 g of trypsin digested cells were washed and centrifuged, separated, washed, resuspended, diluted, mixed and clicked (270V, 100m Ω) and then transferred to a constant temperature incubator (5% CO₂, 37 ° C).

Cell culture: The culture medium, additives and conditions required for transfection are shown in Table 2.

Table 2 Transfection of the desired culture medium, additives and conditions

Cell name	Name of the culture medium, conditions, and additives								
	Culture medium	temperature	CO ₂	Fetal bovine serum	L-glutamine	NEAA	Streptomycin	penicillin	Incubator
Huh7.5.1	DMEM	37°C	5%	10%	2mmol/ml	0.1mmol/L	100g/ml	100U/ml	Saturation humidity

Quantification of PCR. The specific primers were introduced into the non-coding region of HCV5 'and transfected. After three days, the total RNA of the transfected cells or the supernatant RNA was extracted to quantitatively detect the hepatitis C virus RNA in the cells. The concentration of hepatitis C virus RNA was calculated.

Fluorescence Observation. The transfected cells were cultured and cultured on a cell culture plate (96-well cell culture plate) and then incubated in an incubator (37 ° C, 5% CO₂). After the culture was complete (about 48 hours) Discard the supernatant; add about 100 ul of methanol to each well and allow to stand for about 20 min in an environment at -20 ° C; wash with PBS for 5 minutes each time, then add Triton X-100 (1: 100), FITC-goat anti-human (1: 100) or Alex488 goat anti-mouse fluorescence (1: 100), followed by darkness feeding (1) Hour), and finally a fluorescence microscope to check and take pictures.

Virus Titer Detection. The cell supernatant was collected at different times and centrifuged at about 3000 g to remove the cell debris, and then stored at -80 ° C. Into the incubator to continue culture, and finally the virus titer detection.

Statistical Analysis. The data of the study were collated and collated. The comparison between the measurement data and the technical data was carried out by using the t test and the χ^2 test. The data were sorted out and the statistical analysis showed that EXEL and spss16.0 were different, respectively, and the difference was statistically significant [7].

Results

There was no significant difference between the expression of the mutated gene and the expression of the original gene. There was no significant difference in the expression level of the two groups (P <0.05).

Table 3 Comparison of the number of introduced mutant genes with the original gene expression

gene	J6 Core gene	J6CΔF (F protein gene deletion)
Core gene (5.0 × 10 ⁵) expression	3.6×10 ⁵	3.7×10 ⁵
P Value	<0.05	

F protein deficiency on the pathogenicity of the virus: F protein expression in the tumor tissue is higher than other tissues, indicating that the formation of liver cancer and F protein has certain relevance.

The secondary structure of RNA on the translation of the virus, the process of replication and pathogenicity: a single mutation containing the core protein and wild-type core protein in the structure of the basic consistent; F deletion of the core protein secondary structure has more Many changes.

Discussion and Conclusion

The F protein is produced by transcoding the core coding sequence of the hepatitis C virus. It is generally believed that the coding of the core protein and the sequence encoding the F protein overlap each other. The initiation site of the internal translation of the gene is thought to be codon 26 [8-11]. The coding position of the Core + 1 / S protein (the shortest F protein) is a gene of the

core protein coding region (85-87), which is considered to be the starting point for the internal translation of the F protein [12]. So far, there have been a variety of mapping proteins, but their biological function is still very clear [13-15].

In order to gain a better understanding of the biological functions of the F protein and to determine how it affects the replication, translation and pathogenesis of the hepatitis C virus, the study was conducted on wild-type J6JFH1 and self-constructed mutants (J6JFH1 / Δ F) Contrast and analysis. The results showed that the expression level of the protein of the mutant hepatitis C virus was much lower than that of the previous one. At the same time, the level of the RNA of the virus also decreased significantly (decreased by nearly 95%), and the virus particles in the supernatant the number is also significantly reduced [16].

The RNA of the mutant RNA was transfected into Huh7.5.1 cells, and the expression of intracellular virus protein was detected. The titer of the virus RNA and virus in the supernatant were detected. The results showed that the wild type and mutant there is no significant difference between them [17]. Since the introduction of mutations may lead to changes in the secondary structure of the hepatitis C virus core gene, the secondary structure of the core gene can influence the process of replication and translation of hepatitis C virus RNA; further the secondary structure of the core gene Analysis, the results show that the process of translation and replication of the virus by the core gene secondary structure changes; the specific process to be further studied [18].

In summary, the virus replication, translation, pathogenicity and F protein deletion or not, but the core gene changes in the secondary structure will cause the virus translation and replication process changes, there is a correlation between the two.

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