

A Cytokine Profile in Response to Stimulation of Peripheral Blood Mononuclear Cells by HCV C33

Thesis

Submitted for partial fulfillment of master degree in
Clinical and Chemical Pathology

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2011

لمحة عن استجابة المؤثرات الطرفية الخلوية بعد تحفيز
الخلايا واحدة النواة باستخدام ببتايد سى 33 الخاص
بالالتهاب
الكبدى الفيروسى سى

رسالة

توطئة للحصول على درجة الماجستير
فى الباثولوجيا الاكلينيكية والكيمائية

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Summary

Hepatitis C virus (HCV) infection has become a global health problem with around 130–170 million infected people worldwide.

The majority of those infected enter a chronic disease state and further develop liver cirrhosis, hepatocellular carcinoma. Although combination therapy with pegylated interferon and ribavirin is available, only 55% of the infected patients show a favorable response.

This response greatly varies with the HCV genotype involved in the infection. Furthermore, the combination therapy is expensive and the associated side effects limit their usage.

HCV is a small, enveloped, positive sense single strand ribonucleic acid (RNA) virus of the family Flaviviridae consisting of the structural proteins (core, envelope 1 and 2) and the nonstructural proteins (NS2, NS3, NS4, NS5).

Most HCV proteins have a clearly defined role in the viral replication cycle and may also facilitate immune evasion by altering cell signaling pathways involved in host defense.

The NS3 is a multifunctional protein, with a serine protease which responsible for the polyprotein cleavage and RNA helicase/NTPase which is indispensable for RNA replication.

2011

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List of Abbreviations

5-PL	: Five-Parameter Logistic curve
aa	: Amino acids
Ag	: Antigen
ALT	: Alanine aminotransferase
APC	: Antigen presenting cells
ARF	: Alternative reading frame
bDNA	: branched DNA
CARs	: Coxsackie virus B adenovirus receptors
CD	: Cluster of differentiation
CDC	: Centers for disease control and prevention
CFSE	: Carboxyfluorescein diacetate succinimidyl ester
CLDN-1	: Claudin-1
CpG	: Unmethylated cytosine preceding guanosine motif
CTL	: Cytotoxic T lymphocyte
DC	: Dendritic cells
DC-SIGN	: Dendritic cell-specific intercellular adhesion molecule-3-grabbing non-integrin
EC1	: extracellular loop-1
EIA	: Enzyme immuno assay
EIF2A	: Eukaryotic translation initiation factor 2, alpha subunit
ELISA	: Enzyme-linked immunosorbent assay
ELISpot	: Enzyme linked immunospot
ER	: Endoplasmic reticulum
F	: Frameshift
FasL	: Fasligand
GAG	: Glycosaminoglycans
HBV	: Hepatitis B virus
HCC	: Hepatocellular carcinoma
HCV	: Hepatitis C virus
HCWs	: Health care workers
HDL	: High density lipoproteins
HIV	: Human Immune Deficiency Virus
HMW	: High-molecular-weight
HS	: Highly Significant

HVR	: Hypervariable regions
IDU	: Intravenous drug use
IFNγ	: Interferon -gamma
IL2	: Interlukin2
IRES	: Internal ribosome entry site
IRF	: Interferon regulatory factor
ISDR	: Interferon sensitivity determining region
ISDR	: Interferon sensitivity determining region
JAMs	: Junction-associated molecules
LD	: Lipid droplets
LDL	: Low density lipoprotein
LDLR	: Low density lipoprotein receptor
LEL	: Large extracellular loop
LPS	: Lipopolysaccharide
L-SIGN	: Liver/lymph node-specific intercellular adhesion molecule-3-grabbing integrin
M/M	: Monocytes/macrophages
MAF	: Macrophage activating factors
MDC	: Myeloid dendritic cells
MHC	: Major histocompatibility complex
Mo-DC	: Monocyte-derived dendritic cells
NCR	: Non-coding region
NK	: Natural killer cells
NKT	: Natural killer T cells
NS	: Nonstructural protein
NS	: Non-Significant
NTPase	: Nucleoside triphosphatase
NTR	: Nontranslated regions
NTR IRES	: Non translated region-internal ribosome entry site
ODN	: Oligodeoxynucleotide
ORF	: Open -reading frame
PAT	: Parenteral antischistosomal therapy
PBMCs	: Peripheral blood mononuclear cells
PCR	: Polymerase chain reaction
PDC	: Plasmacytoid dendritic cells
PE	: Phycoerythrin
PEG-IFN α	: Pegylated interferon- α

PI	: Proliferation index
PKR	: Protein kinase receptor
PM	: Plasma membrane
RdRp	: RNA-dependent RNA polymerase
RF	: Replicative form
RFU	: Relative fluorescence units
RI RNA	: Replicative intermediate Ribonucleic acid
RIBA	: Recombinant immuno blot assay
RIG-I	: Retinoic-acid-inducible gene
RT-PCR	: Real Time Polymerase chain reaction
Sig	: Significant
SL	: Stem loops
SPSS	: Statistical Package for Social Sciences
SR-BI	: Scavenger receptor class B type I
ssRNA	: Single stranded genomic HCV RNA
STAT	: Signal transducer and activator of transcription
SVR	: Sustained virological response
TCR	: T-cell receptor
Th	: T helper cell
TLR	: Toll-like receptors
TMA	: Transcription mediated amplification
TNF	: Tumour necrosis factor
TRAIL	: TNF-related apoptosis-inducing ligand
Treg	: Regulatory T cells
TRIF	: Toll/interleukin-1 receptor domain-containing adapter inducing interferon- β
UTR	: Untranslated region
VLDL	: Very-low-density lipoproteins.
VL	: Viral loads
WHO	: World health organization

Introduction

Hepatitis C virus (HCV) infection is a major world health problem; In most cases (60–85 %), HCV infection progresses to chronic liver disease, which can lead to liver cirrhosis and hepatocellular carcinoma (*Burlone and Budkowska, 2009*).

HCV is a small, enveloped virus. HCV has a single-stranded positive sense RNA genome, encoding a polyprotein of about 3000 amino acids, which is cleaved into structural (core, E1 and E2) and non-structural (p7, NS2, NS3, NS4A, NS4B, NS5A and NS5B) proteins by host and viral proteases (*Burlone and Budkowska, 2009*).

Hepatitis C viruses interfere with the complex cytokine network brought about by the immune system and liver cells in order to prevent an effective immune response, capable of viral control (*Larrubia et al., 2009*).

Successful viral clearance is associated with a vigorous antiviral T-cell response. Both CD4 and CD8 T cells contribute to virus control (*Chang et al., 2001*).

CD4+ cell responses are critical to both the generation and maintenance of antiviral immune responses; they secrete cytokines that augment antibody production by B cells and prime CD8+ cells (*Koziel, 2005*).

CD8+ T cells The effector function of CTLs consists of both the cytolysis of infected cells and the production of cytokines that lead to clearance of virus (e.g., TNF- α and IFN γ) (*Koziel, 2005*).

The imbalance between T helper cell Th1 (IL-2, IL-12, IFN γ) cytokines and Th2 (IL-10) cytokines affect the outcome of HCV infection. The defect in both IL-12 and IFN γ production may contribute to persistence of HCV infection (*Sarih et al., 2000*).

Interferon γ (IFN- γ), a cytokine that plays an important role in inducing and modulating an array of immune responses, including the activation and differentiation of T cells, B cells, NK cells, macrophages. The secretion of IFN- γ is in response to IL-2 and IL-12 (*Gattoni et al., 2006*).

Tumor necrosis factor (TNF)- α and IFN- γ and can purge viruses from infected cells noncytopathically. Also control viral infections indirectly, by modulating induction, amplification, recruitment, and effector functions of the immune response and by upregulating antigen processing (*Guidotti and Chisari, 2001*).

Strong and persistent cell-mediated immune responses have been reported in HCV- seronegative individuals with documented exposure to HCV in the absence of detectable viral RNA (*Post et al., 2004*).

HCV-specific CD4+T cell responses persist in acutely infected individuals who permanently cleared the virus, and disappear in patients whose viraemia subsequently recurred (*Chang et al., 2001*).

HCV-specific CD8+T cell responses that are associated with spontaneous viral clearance tend to be multi-specific and polyclonal (*Lauer et al., 2005*).

Aim of the Work

The aim of the work is to detect a panel of cytokines IL2, IFN- γ and TNF α of cell culture supernatant from unstimulated and stimulated peripheral mononuclear cells (PBMCs) by HCV specific C33 peptide.

Hepatitis C Virus

I. Structure of Hepatitis C Virus:

The hepatitis C virus (HCV), identified in 1988 through molecular biological techniques, is an enveloped virus that is classified as a separate genus in the Flaviviridae family. The HCV genome is a single-stranded, positive-sense RNA molecule approximately 9.5 kilobases (kb) in length. Within an infected person, HCV exists as a population of closely related heterogeneous variants, called quasispecies, that result from the rapid development of mutations in the viral genome (*Moyer et al., 1999*).

The putative infectious virus particle is composed of a nucleocapsid or ribonucleoprotein complex bearing the HCV genome; this inner structure is surrounded by a phospholipid bilayer, into which E1 and E2 envelope glycoproteins are anchored. However, infectious HCV particles become tightly associated with very-low-density lipoproteins (VLDL) during virus assembly and are (co-)secreted with VLDL (*Burlone and Budkowska, 2009*).

Various forms of HCV virions appear to exist in the blood of infected individuals: virions bound to very low density lipoproteins (VLDL), low-density lipoproteins (LDL), immunoglobulins, and free circulating virions. Moreover, it is speculated that the association with LDL and/or VLDL protects the virus against neutralization by HCV-specific antibodies (*Nahmias et al., 2006*).