Seroprevalence of Anti-Helicobacter pylori Antibodies in Hepatitis C Patients

M.Sc.Thesis

In

Medical Microbiology and Immunology.

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Cairo University
2011

بسم الله الرحمن الرحيم

صدق الله العظيم

سورة طه- آية (١١٤)

Acknowledgment

First of all, my thankfulness is to ***ALLAH***, who gave me the power to perform this work.

It is a pleasure to express my sincere gratitude and thankfulness to **Prof. Dr. Sohair Elattar Ahmed Anwar Elattar,** Professor of Microbiology and Immunology, Faculty of Medicine, Cairo University, who faithfully helped me in finishing this thesis. I will never forget her kind supervision and endless help through the whole study.

No word can express my everlasting obligation to **Dr. Nadia Mohamed Hassan Madany,** Lecturer of Microbiology and Immunology, Cairo University, for her sincere help and precious advice. I will never forget her beneficial instructions on the final touches of this thesis.

I owe too much to **Dr. Hanaa Hanna Morcos**, Consultant of Microbiology and Immunology, National Hepatology and Tropical Medicine Research Institute, for her endless guidance she gave me through this work. She spent many of her private time helping me and her constructive criticism will never be forgotten.

Finally, I will never forget to thank all my patients, to whom this study was carried out, without their cooperation this thesis was never going to appear.

Abstract

In this study, we were aiming to find a relation between *H.pylori* and progression of HCV related liver disease by comparing the sero-prevalence of *H.pylori* in HCV sero-negative and sero-positive (cirrhotic & non-cirrhotic) patients. *H.pylori* status was investigated using ELIZA technique in 30HCV positive cirrhotic patients, 30HCV positive non-cirrhotic patients and 20healthy controls.The study showed higher prevalence of both *H.pylori* IgG & IgA in cirrhotics (100%,80%) respectively, than non-cirrhotics (90%,46.7%) and controls (65%,20%). No relation was found between *H.pylori* infection and sex or age.

Key words: HCV, *H.pylori*,IgG,IgM.

CONTENT

LIST OF ABBREVIATIONS

ALT	Alanine aminotransferase
AST	Aspartate aminotransferase
C protein	Core protein
Cag A	Cytotoxin-Associated gene A
CDT	Cytolethal distending toxin
CIA	Chemiluminescence immunoassay
DNA	Deoxyribonucleic acid
E proteins	Envelope glycoproteins
EIA	Enzyme immunoassays
ELISA	Enzyme linked immune-sorbent assay
ER	Endoplasmic reticulum
ETR	End-of-treatment response
EVR	Early virological response
FDA	Food and Drug Administration
GBV-B	GB virus B
GBV-C	GB virus C
GERD	Gastro-esophageal reflux disease
GIT	Gastrointestinal tract
GSA	Gel shift assay
H.pylori	*Helicobacter pylori*
HDA	Heteroduplex analysis
HAV	Hepatitis A virus
HBV	Hepatitis B virus

HCC	Hepatocellular Carcinoma
HCV	Hepatitis C virus
HE	Hepatic encephalopathy
HIV	Human immune deficiency virus
HLA	Human leukocyte antigen
HRP	Horseradish peroxidase
HVR1	First hypervariable region
ICAM-1	Intercellular adhesion molecule 1
IFN	Interferon
Ig	Immunoglobulin
IL	Interleukin
IRES	Internal ribosome entry site
KD	Kilo dalton
LD	Lipid droplets
LDL	Low-density lipoprotein
LPS	Lipopolysaccharides
MALT	Mucosa-associated lymphoid tissue
MHC	Major histocompatibility complex
NCR	Non-coding regions
NIH	National Institute of Health
NK	Natural killer
NS	Non – structural
NTR	Non-translated regions
ORF	Open reading frame
PCR	Polymerase chain reaction

PEG	Polyethylene glycol
PEG-IFN	Pegylated Interferon
PPI	Proton pump inhibitor
RIBA	Recombinant immunoblot assay
RNA	Ribonucleic acid
RVR	Rapid virological response
SabA	Sialic acid-binding adhesin
SL	Stem loop
spp.	Species
SSCP	Single-strand conformational polymorphism
SVR	Sustained virological response
Tc	Cytotoxic T cells
Th	Helper T cell
TMA	Transcription-mediated amplification
TMB	Tetra-methyl benzidine
TNF- α	Tumour necrosis factor α
UTR	Untranslated regions
Vac A	Vacuolating Toxin A

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INTRODUCTION

Hepatitis C is a non-cytopathic hepatotrophic virus having a single stranded, positive sense linear 9.5 kb RNA genome. Hepatitis C virus (HCV) was first discovered in 1989 by ***Michael Houghton*** and colleagues at Chiron. It was rapidly recognized that the new virus was responsible for the majority of cases of non-A, non-B hepatitis. HCV infection is the leading cause of acute, chronic hepatitis, liver cirrhosis and hepatocellular carcinoma. There are more than 170 million chronic carriers worldwide who are at risk of developing liver cirrhosis and/or hepatocellular carcinoma ***(Kim, 2002; Watanabe et al., 2005)***.

Cirrhosis is a late stage of progressive hepatic fibrosis. It is considered to be irreversible in its advanced stages and the only option may be liver transplantation. Patients with cirrhosis are susceptible to various complications which increase the morbidity and mortality and reduce their life expectancy ***(Dore et al., 2004)***.

Knowing risk factors that lead to progression of hepatitis to cirrhosis is important to prevent its occurrence. HBV and HIV co-infection are of these factors, also acquiring the infection at a young or old age (>40 years), excess alcohol consumption, male gender and schistosomiasis ***(Al-Mahtab, 2010)***.

However, even in the absence of these factors, disease progression is still occurring in some patients, suggesting the role of other factors. Patients with liver cirrhosis are frequently subjected to a number of disorders of the gastric mucosa and peptic lesions in the gastro duodenal mucosa, and considering that *Helicobacter pylori* (*H.pylori*) infection is an important factor in the pathogenesis of peptic ulcer, it is reasonable to postulate *H.pylori* as a putative risk factor in HCV progression ***(Queiroz et al., 2006)***.

In addition, detection of *H. pylori* DNA in the liver tissue of patients with chronic hepatitis C and hepatocellular carcinoma (HCC) has been reported ***(Ponzetto et al., 2000)*** and *H. pylori* strain was isolated from the liver of a patient with cirrhosis ***(Queiroz et al., 2001)***.

H.pylori, a non-invasive Gram negative bacterial pathogen of the human stomach, infects about 50% of the population worldwide. The incidence rises steadily with age. Infection by *H.pylori* causes gastritis initially and, if allowed to persist, can induce a range of pathologies. It is the causative agent of most peptic ulcers, and other serious outcomes such as atrophic gastritis, intestinal metaplasia, and gastric cancer are correlated with long-term infections ***(Baldwin et al., 2007)***.

Detection and eradication of gastric *H.pylori* is easy and relatively inexpensive; hence the interest in exploring its involvement in diseases arising outside the stomach including liver diseases. Many studies have discussed the relation between *H.pylori* and liver diseases including HCV-related hepatic diseases and their results were controversial.

AIM OF THE WORK

This work was done to analyze serum antibody levels to *Helicobacter pylori* in patients with chronic hepatitis C virus divided into cirrhotic and non-cirrhotic and compare results with corresponding parameters for a healthy control group, to explore a possible association of *Helicobacter pylori* with HCV-related liver disease, and relate results to age and sex.