Prevalence of HCV Antibodies in haemodialysis patients in Cairo governate (Sector E)

Thesis

Submitted for partial fulfillment of master degree in internal medicine

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2013


بسم الله الرحمن الرحيم
وَأَنْزَلَ اللهُ عَلَيْكَ الْكِتَابَ
وَالْحِكْمَةَ وَعَلَّمَكَ مَا لَمْ تَكُنْ تَعْلَمُ
وَكَانَ فَضْلُ اللهِ عَلَيْكَ عَظِيمًا
صدق الله العظيم
سورة النساء
آية (113)

Acknowledgments

*First and foremost, I feel always indebted to **Allah**, the most Kind and the most Merciful*

*I would like to express my sincere thanks and my deepest appreciation to **Prof. Dr.EMAN IBRAHEIM SARHAN ,** Professor of internal medicine & nephrology, Faculty of Medicine –Ain-Shams University for her supervision, guidance, valuable advice, helpful directions throughout the whole work.*

*My deepest gratitude and respect to **Dr.SAHAR MAHMOUD SHAWKY,** Assistant prof. of internal medicine & nephrology, Faculty of Medicine –Ain-Shams University, for her keen interest, constant support and continuous encouragement during the conduction of this work.*

*My extreme thanks to **Dr.CHERRY REDA KAMEL,** Lecturer of internal medicine & nephrology , Faculty of Medicine – Ain-Shams University, for her sincere guidance and supervision .*

*I would like to dedicate this essay to my **family** to express to them my deep gratitude.*

RANIA ABDALLAH

List of Contents

INTRODUCTION.....**1**

AIM OF THE WORK.....**4**

REVIEW OF LITTERATURE.....

Chapter 1: Hepatitis C Virus Infection.....**5**

Chapter 2: HepatitisC Virus Infection in Hemodialysis Patients...**38**

Chapter 3: Infection Control Measures**.....72**

PATIENTS AND METHODS.....**84**

RESULTS.....**86**

DISCUSSION.....**100**

SUMMARY.....**109**

CONCLUSION **112**

RECOMMENDATIONS.....**113**

REFERENCES.....**115**

ARABIC SUMMARY.....**146**

List of Abbreviations

ALT	Alanine aminotransferase
AST	Aspartate aminotransferase
A-V fistula	Arterio-venous fistula
CDC	Centers for Disease Control and Prevention
CKD	Chronic kidney disease
CRF	Chronic renal failure
DNA	Deoxyribonucleic acid
DOPPS	Dialysis Outcomes and Practice Patterns Study
E1	Envelope protein1.
E2	Envelope protein2 .
EDHS	Egyptian demographic health survey
EIA	Enzyme Immuno Assay
ELISA	Enzyme Linked Immunosorbent Assay
EM	Electron microscopy
EOT	End-of-therapy
EPO	Erythropoietin
ESRD	End-stage renal disease
ETR	End of treatment response
EVR	Early virologic response
FSGS	Focal segmental glomerulosclerosis

GN	Glomerulonephritis
HAV	Hepatitis A Virus
HBsAg	Hepatitis B surface antigen
HBV	Hepatitis B virus
HCC	Hepatocellullar Carcinoma
HCcAg	Hepatitis C core antigen
HCV	Hepatitis C virus
HCV RNA	Hepatitis C virus ribonucleic acid.
HD	Heamodialysis
HIV	Human immunodeficiency virus
IFN	Interferon
IgA	ImmunoglobulinA
IgG	Immunoglobulin G
IL	Interleukin
IV	Intravenous
KDIGO	Kidney Disease: Improving Global Outcomes
LFTs	liver function tests
LM	light microscopy
MICS	Malnutrition–inflammation complex syndrome
MN	Membranous nephropathy
MMWR	Mortality and Morbidity Weekly Report.
MPGN	Membranoproliferative glomerulonephritis

NAT	Nucleic acid test(ing)
NHL	Non Hodgkin's lymphoma
NLI	National Liver Institute
PAT	Parenteral antischistosomal treatment.
PCR	Polymerase chain reaction
PEG	Polyethylene glycol
PEGIFN	Pegylated IFN
PS	Polysulfone membrane
PTDM	Post transplant diabetes mellitus
RF	Rheumatoid factor
RIBA	Recombinant immunoblot assay.
RNA	Ribonucleic acid.
RT.	Renal transplantation
RTR	Renal transplant recipient.
RT-PCR	Reverse transcriptase polymerase chain reaction
SS	Sjogren syndrome
SVR	Sustained virologic response
TFG	Transforming growth factor
TMA	Transcription-mediated amplification
TNF	Tumor necrosis factor
WHO	World Health Organization

List of Tables

Table	Title	Page
Table 1	Hepatitis C estimated prevalence and number of infected patients	9
Table 2	Interpretation of HCV Assays.	35
Table 3	Annual reports of Egyptian Registry from 1996 to 2008	44
Table 4	Prevalence of HCV infection in HD patients from various countries.	45
Table 5	HCV diagnostic tests for dialysis patients	55
Table 6	Pharmacokinetic parameters of two PEG-INF alfa formulations	63
Table 7	Trials with pegylated interferon alfa-2a in dialysis patients with chronic HCV infection	65
Table 8	Age, sex, HBV and HCV status of the studied group	91
Table 9	Causes of renal failure in the studied group	91
Table 10	Sero-convertion status with frequency of blood transfusion, surgery, family history of HCV and dialysis in other centers in the studied group	93
Table 11	Comparison between HCV sero-converters and free cases regarding age and duration of dialysis free from HCV.	94
Table 12	Categorical risk factors for seroconversion – Univariate analysis	95
Table 13	Risk factors for seroconversion – Multivariable analysis using logistic regression	96

List of Figures

Figure	Title	Page
Figure 1	Genetic structure of HCV.	**6**
Figure 2	Global Prevalence of Hepatitis C Virus	**10**
Figure 3	Hepatitis C virus in Egypt compared to other countries in the world**.**	**11**
Figure 4	Natural history of HCV infection.	**18**
Figure 5 A **Figure 5B** **Figure 5C**	Typical light microscopic findings of HCV-related MPGN. Electron microscopic demonstrations of sub endothelial electron-dense deposits. intracapillary accumulation of electron-dense material characteristic of precipitated cryoglobulins.	**27**
Figure	**): Individualization of treatment of HCV infection in dialysis patients.**	
Figure 7	Conceptual model of factors influencing adherence to hand hygiene practices **.**	**76**
Figure 8	Causes of renal failure in cairo governate sector(E)..	**92**
Figure 9	Prevalence of HCV and HBV infection at time of study.	**97**
Figure 10	Prevalence of HCV and HBV infection at start of dialysis.	**98**
Figure 11	HCV sero-convertion status**.**	**99**

INTRODUCTION

Hepatitis C is the most common cause of chronic viral liver disease in haemodialysis patients (**Hinrichsen et al.,2002**) Hemodialysis (HD) patients have an increased risk of exposure to hepatitis C virus (HCV). The relevance of HCV infection in HD patients is due to the documented increased risk of death due to chronic liver disease in these patients, particularly after kidney transplantation (**Nemati et al., 2009**).

The natural course of hepatitis C in haemodialysis patients is not well understood. It seems to differ from that in other HCV patients (**Simon et al., 1994).** Liver function tests are close to or near normal in many case (**Guh et al.,1995**) But the mortality of HCV infected haemodialysis patients seems to be enhanced compared with HCV negative haemodialysis patients in preliminary studies (**Stehman-Breen et al.,1998).** Thus patients with HCV on chronic haemodialysis are at increased risk of death, which suggests that the focus should be directed more to identification and prevention of hepatitis C infection in haemodialysis patients.

The prevalence of HCV infection among HD patients varies from country to country and from one center to another. The reported prevalence of HCV infection among dialysis patients in developed countries ranges from 3.6 to 20%; (**Jadoul et al.,**

2004). it is much higher in developing countries (**jaiswal et al., 2002**). The prevalence of anti-HCV among dialysis patients was 0.4% in the in the United Kingdom (2004), 8.4% in the United States (2000), 43.9% in Saudi Arabia (2001), 30% in India (2002), and 41% in Turkey (2001) (**Tokars et al., 2002**). In Egypt according to the Egyptian renal registry the prevalence is 52.1 % (**Afifi 2009)**.

Several risk factors are suggested to be related to HCV dissemination in HD centers. Repeated blood transfusions, shared dialysis machines, surgery, nosocomial route and multi-dose drug vials are the major suggested routes for spread of HCV infection in HD unit (**Nobakht Haghighi et al., 2001**). Partial immunosuppression found in HD patients, resulting in a poor antibody response, may play a role in sensitizing them to acquire the infection through uncommon ways.

The extensive use of recombinant erythropoietin to correct renal anemia in haemodialysis patients resulted in a significant reduction in blood transfusions. However, previous studies have shown that de novo infections in single haemodialysis units may still occur in the absence of other parenteral risk factors (**Fabrizi et al., 1998**).

In recent years, HCV viraemia (HCV-RNA) has been routinely detected by polymerase chain reaction (PCR) (**Gretch et al.,1995**). In 1993, Bukh and colleagues were the first to

describe the fact that HCV viraemia can occur without detection of HCV antibodies. This has been confirmed by several authors in small patient populations (**Seeling et al.,1994**). Most epidemiological studies in haemodialysis patients have been performed using serological testing of hepatitis C antibodies only(**Fabrizi et al., 1993**). Several prevalence studies of hepatitis C have been undertaken. There is a wide range in HCV antibody positivity and HCV viraemia within the studies, ranging from 1% up to 91%.

AIM OF THE WORK

This work aims to study the prevalence of HCV antibodies among haemodialysis patients in some dialysis hospitals in south cairo (sector E) .

Also this work aims to predict the factors that share in increasing the prevalence of this problem and to give the recommendations for preventing transmission of HCV infection.

Chapter1

Hepatitis C virus infection

Epidemiology of hepatitis C virus

The first demonstration that most cases of transfusion-associated hepatitis were caused by neither hepatitis A virus (HAV) nor hepatitis B virus (HBV) came in 1975.This new form of disease was called non-A non-B hepatitis ***(Purcell., 1994).***

In 1989 this virus was identified, cloned and named hepatitis C virus ***(Houghton.,1996***).

HCV is a major public health problem and a leading cause of chronic liver disease ***(William., 2006).*** The mortality related to HCV infection (death from liver failure or hepatocellular carcinoma) will continue to increase over the next two decades ***(Deuffic-Burban et al., 2007).***

It has been estimated that there are over 170 million with HCV infection worldwide , with an increasing incidence of new infections (3-4 million every year) **(WHO.**,**2007**). In the U.S., the prevalence of HCV infection between the years 1999 and 2002 was 1.6%, equating to about 4.1 million persons positive for antibody to hepatitis C, 80% of whom are estimated to be viremic ***(Armstrong et al., 2006).***

Genetic structure of HCV

The viral genome is a single stranded RNA of approximately 9,600 nucleotides which has been classified as a separate genus, designated hepacivirus, belonging to the Flaviviridae family. There is a single open reading frame -containing two non coding regions at the 5´ and 3´ ends- which encodes for a polyprotein precursor of about 3000 amino acids, which is processed by viral and cellular proteins to generate structural (core, E1, E2, p7) and non structural (NS2, NS3, NS4 A+ B, NS5 A+B) polypeptides ***(Mondell.i, 2003).***

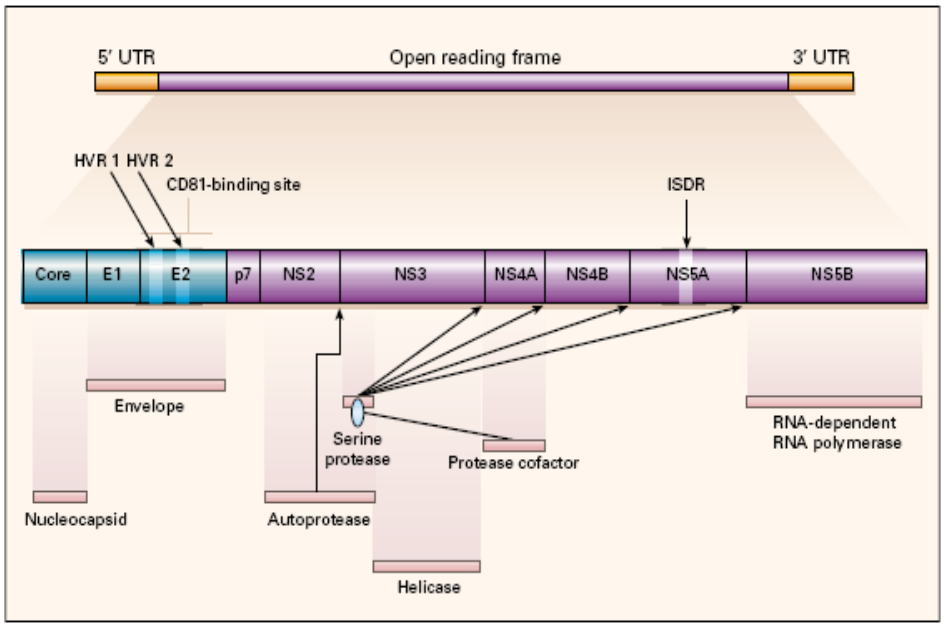

Figure (1): Genetic structure of HCV **(Lauer & Walker 2001).**