

**Republic of Iraq  
Ministry of Higher Education  
and Scientific Research  
University of Diyala  
College of Medicine**



# **Prevalence of SEN Virus and Pegivirus (GBV-C) among Patients on Maintenance Hemodialysis in Al-Kindy Dialysis Center in Baghdad**

**A Thesis**

Submitted to Council College of Medicine - University of  
Diyala as Partial Fulfillment of the Requirements for the  
master's degree of Sciences in Medical Microbiology

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بِسْمِ اللّٰهِ الرَّحْمٰنِ الرَّحِیْمِ

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We, certify that this thesis entitled (**Prevalence of SEN Virus and Pegivirus (GBV-C) among Patients on Maintenance Hemodialysis in Al-Kindy Dialysis Center in Baghdad**) has been conducted under my supervision at the College of Medicine, University of Diyala, as partial fulfilment of the requirements for the Master Degree of Science in Medical Microbiology.



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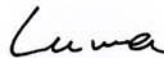


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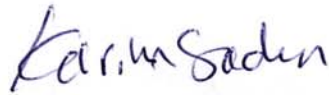
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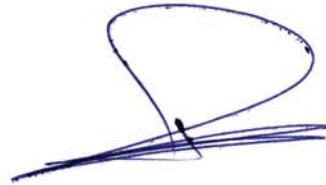
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## *Dedication*

*I dedicate the current study ...*

*To my dear and lovely mother for her  
encouragement and support. To my father  
who taught me the first letter.*

*To my lovely wife and lovely children*

*Yosef, Dawood, and Ibrahim*

# ***Acknowledgment***

*First, In the Name of Allah, the Most Gracious, The Most Merciful, the first who deserve all thanks and appreciation for granting me with well, strength and help to accomplish the current study.*

*I would like to express my sincere gratitude to my supervisors **Professor Dr. Ismail Ibrahim Latif**, and their continuous guidance, support, patience, motivation, enthusiasm helped me to complete my study.*

*I would like to express my sincere gratitude to my supervisor **Assistant Professor Dr. Arwa M. Abdullah** Her guidance helped me all the time for her continuous support of my master study and for her patience, motivation, enthusiasm.*

*I wish to express my sincere thanks to DR. Nawar satea' the chief of (Dialysis center in Al-Kindy training hospital). Great thanks go to the staff of Dialysis center and Lab staff of AL-Kindy hospital for their help and support.*

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*Hayder*

# Abstract

Abstract text consisting of multiple lines of placeholder text.







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## List of Abbreviations

Abbreviation	Meaning
<b>AASLD</b>	American Association for the study of liver diseases
<b>ALP</b>	Alkaline phosphate
<b>ALT</b>	Alanine aminotransferase
<b>AST</b>	Aspartate amino transferase
<b>β</b>	Beta
<b>cDNA</b>	Complementary DNA
<b>CKD</b>	Chronic kidney diseases
<b>DNA</b>	Deoxyribonucleic acid
<b>dNTPs</b>	Deoxynucleotide triphosphates
<b>E1</b>	Envelope protein- 1
<b>E2</b>	Envelope protein- 2
<b>EDTA</b>	Ethylenediaminetetraacetic acid
<b>EIA</b>	Enzyme Immunoassay
<b>ELISA</b>	Enzyme linked immunosorbent assay
<b>ESRD</b>	End stage renal diseases
<b>FDA</b>	Food and drugs administration
<b>GTs</b>	Genotypes
<b>HAV</b>	Hepatitis A virus
<b>HBV</b>	Hepatitis B virus
<b>HCV</b>	Hepatitis C virus
<b>HCWs</b>	Health care workers
<b>HD</b>	Hemodialysis
<b>HIV</b>	Human immune deficiency virus
<b>ICTV</b>	International committee on taxonomy of viruses
<b>IFN I</b>	Interferon type one
<b>IgG</b>	Immunoglobulin G

<b>IL</b>	Interleukin
<b>ISGs</b>	Interferon stimulating genes
<b>IV</b>	Intravenous
<b>KT</b>	Kidney transplantation
<b>NANB</b>	Non-A non B hepatitis
<b>NAT</b>	Nucleic Acid Testing
<b>NK</b>	Natural killer cell
<b>NNIs</b>	Non-nucleotide inhibitors
<b>NS</b>	Nonstructural
<b>NS2</b>	Nonstructural region 2
<b>NS3</b>	Nonstructural region 3
<b>NS4</b>	Nonstructural region 4
<b>NS5</b>	Nonstructural region 5
<b>ORF</b>	Open reading frame
<b>PBMC</b>	Peripheral blood mononuclear cell
<b>PCR</b>	Polymerase chain reaction
<b>PH</b>	Power of hydrogen
<b>RdRp</b>	RNA dependent RNA polymerase
<b>RNA</b>	Ribonucleic acid
<b>RRT</b>	Renal replacement therapy
<b>RT-PCR</b>	Real-time Polymerase chain reaction
<b>SPSS</b>	Statistically package for social science
<b>TRAIL</b>	Tumor necrosis factor related apoptosis inducing ligand
<b>Treg</b>	T- regulatory cell
<b>USA</b>	United States of America
<b>WHO</b>	World health organization

# **Chapter One**

## **Introduction**

## 1. 1 Introduction

It is well known that patients underlying dialysis treatment, and in particular hemodialysis (HD), are more susceptible risk for viral infections. This is due to their underlying low cellular immunity, which increases their susceptibility to infection. In addition, the process of hemodialysis need blood, that causes to exposure to infectious materials through the extracorporeal circulation for a prolonged period. Moreover, HD patients may require a blood transfusion, frequent hospitalizations, and surgery, which increase opportunities for nosocomial infection exposure (Bernieh, 2015). Approximately 1% of transfusion-associated hepatitis and 2% of community-acquired hepatitis cases do not have a defined etiology, suggesting the existence of an additional causative agent (Al-Quaili, 2010). Patients on long-term hemodialysis are especially susceptible to parenterally transmitted agents and therefore represent an important population for analysis of the clinical and epidemiological implications of newly identified agents (Forns et al., 1999). Perhaps one of the most common viral infections are caused by hepatotropic or other hepatitis-associated viruses, including hepatitis B virus (HBV), hepatitis C virus (HCV), and hepatitis G virus (GBV-C) (Darendeli et al., 2005), and SEN Virus (Abd El-Hady et al., 2006).

In 1995-1996, GBV-C was described as putative agents that accounted for the unexplained non-A to non-E hepatitis. The virus's genome is consisting of single-stranded RNA with positive polarity., and belongs to the flaviviruses family. It only has one open reading frame, which encodes the viral polyprotein. There is contrary information as to whether or not GBV-C replicates in the liver. The clinical significance of GBV-C infection in humans it is still to be establish and few data in patients on HD are available (Darendeli *et al.*, 2005; Bernieh, 2015). A high rate of GBV-C infection has been extensively reported in several countries in the last stage of renal failure and in chronic HD patients, ranging from 6 to 44 percent. Analysis of the 5-untranslated region (5'UTR) suggests

that GBV-C variations may be split into five genotypes. Genotype 1 is common in the western and central African countries □ genotype 2 is widespread in Europe, North and East Africa, Pa□istan and □apan □ genotype 3 occurs across Asia □ genotype 4 occurs in South East Asia □ genotype 5 in South African countries is prevalent (□□darendeli et al., 2□□5).

SEN virus (SENV), was discovered in 1999, the name for the SENV was derived from the initials of the first identified patient (Abbasi et al., 2□16 □ Abd El-Hady et al., 2□□6). SENV is a small, single-stranded, non-enveloped circular □NA virus (Abd El-Hady et al., 2□□6) and belongs to the Ciconiidae family (Abbasi et al., 2□16) It is probably accounting for many cases of non-A-E hepatitis. This virus is parenterally transmitted, and therefore, appropriate screening of blood and blood products could control its spread. In addition, this virus appears capable of co-infecting patients who have other types of viral disease raising the possibility that it may aggravate their clinical course and □or their response to treatment. Phylogenetic analysis of SENV isolates had demonstrated the existence of eight highly divergent genotypes (A-H). Genotypes SENV-□ and SENV-H are more prevalent in patients with transfusion-associated non A-E hepatitis (Al-□u□aili, 2□1□). The high prevalence of SENV observed among patients with HIV, HBV, HCV infections indicate a shared route of transmission (Abbasi et al., 2□16). The association of SENV infection with hepatocyte damage or serum levels of aminotransferase remains uncertain. The role of SENV infection in patients on maintenance hemodialysis is also far from clear (□ai et al., 2□□5) □ therefore, the present study try to determine the prevalence of SENV (SENV-□ and SENV-H strains) and GBV-C among hemodialysis patients and some of their clinical significance in Al-□indy center for dialysis □ Baghdad.

**1.2 Aims of the study:**

The aims of this study as is formulated to:

1. Determine the prevalence of SEN-V infection in hemodialysis patients by nested PCR.
2. Determine the prevalence of GBV-C infection in hemodialysis patients by reverse nested PCR.
3. Evaluate any possible association between SEN-V and GBV-C with HCV and their clinical importance in hemodialysis patients by biochemical test (ALT and AST).
4. The association of SENV and GBV-C with demographic, clinical characteristics and some risk factors.