Ain Shams University Faculty of Science Biochemistry Department



The Role of MicroRNA in Hepatitis C Infection

A Thesis

Submitted for the Degree of Master of Science as a partial fulfillment for requirements of the Master of Science Biochemistry Department

By

Fatma El-Zahraa Mohamed Mohamed Khorshed

B.Sc. (Biotechnology / Biomolecular Chemistry)
Cairo University
2010

Under supervision of

Prof. Dr. Amina M.Medhat

Professor of Biochemistry Faculty of Science Ain Shams University

Prof.Dr. Mahmoud H. Romeih

Professor and Head of Biochemistry & Molecular Biology & Medicinal Chemistry Departments Theodor Bilharz Research Institute

Dr. Samah M. Mohamed

Lecturer of Biochemistry
Biochemistry and Molecular Biology Department
Theodor Bilharz Research Institute

2016

I declare that this thesis has been composed by myself and that the work which is recorded here has been done by myself. It has not been submitted for a degree at this or any other university.

Fatma El-Zahraa Mohamed

Dedication

I dedicate this work to my father, mother, brother, husband, friends and those from whom I have learned, whenever and wherever they are.

Fatma El-Zahraa Mohamed

ACKNOWLEDGMENTS

I wish to express my thanks and gratitude to *Prof. Dr. Amina Mohamed Medhat*, Professor of Biochemistry,
Faculty of Science, Ain Shams University, for her kind supervision, instructive guidance, invaluable assistance, moral support and kind advices.

The words can never express my infinite gratitude to *Prof. Dr. Mahmoud Hassan Romeih*, Professor of Biochemistry and Head of Biochemistry and Molecular Biology and Medicinal Chemistry Departments, Theodor Bilharz Research Institute, for his creative guidance, tremendous effort, intelligent remarks motivated me a lot to finish up this work and tutorial support in revision all details of this thesis.

My deepest thanks and appreciation to *Dr. Samah Mamdouh Mohamed*, Lecturer of Biochemistry,

Biochemistry and Molecular Biology department, Theodor

Bilharz Research Institute, for her strong support, patience
and the interest she showed in my work during the study

period. I owe my deepest thanks for her great supervision

throughout this work.

I would like to thank *Prof. Dr. Mohamed Ali Saber*, Professor of Biochemistry, Biochemistry and Molecular Biology department, Theodor Bilharz Research Institute for his kind help, assistance and his effort in revising this thesis and *Prof. Dr. Mohamed Abbas Shemis*, Professor of Biochemistry and Head of Biochemistry and Molecular Biology department, Theodor Bilharz Research Institute for his support.

This work has been supported by Science and Technology Development Fund (STDF) project (ID: 1763) and Theodor Bilharz Research Institute project (ID: 17C).

Finally, I am grateful to all my colleagues at Biochemistry and Molecular Biology Department, Theodor Bilharz Research Institute for incorporation and sharing their scientific knowledge whenever possible.

CONTENTS

		Pag€
	Abstract	i
	List of Abbreviations	ii
	List of Figures	viii
	List of Tables	xi
	Introduction	xiii
	Aim of the Work	xvi
1.	Review of Literature	
1.1.	Hepatitis C virus	1
1.1.1.	HCV genome	1
1.1.2.	HCV genotypes	3
1.1.3.	HCV genotype 4	3
1.1.4.	HCV in Egypt	4
1.2.	HCV treatment	4
1.2.1.	Interferons	5
1.2.1.1.	Interferon and HCV	5
1.2.1.2.	Ribavirin	6
1.2.1.3.	Pegylated interferon	7
1.2.1.4.	Responding and non-responding to	7
	interferon therapy	
1.2.2.	Protease inhibitors and polymerase	9
	inhibitors	
1.3.	MicroRNAs	11
1.3.1.	MicroRNAs discovery	11
1.3.2.	MicroRNAs in the genome	12
1.3.3.	MicroRNAs biogenesis	13
1.3.3.1.	MicroRNAs processing in the nucleus	13
1.3.3.2.	MicroRNAs maturation in the cytoplasm	16
1.3.4.	Functional features of microRNAs	18
1.3.5.	MicroRNAs silencing performance	18
1.3.6.	MicroRNAs and HCV	19
1.3.6.1.	Direct interaction of cellular miRNAs to	19
	HCV genome	
1.3.6.2.	MicroRNAs and interferon	20
1.3.7.	MicroRNAs in blood	20
1.3.7.1.	MiR-21	21
1.3.7.2.	MiR-155	23

1.3.7.3.	MiR-196b	24
1.3.7.3.	MiR-1900	25
1.3.7.4.	Interferon stimulated genes	26
1.4.1.	MxA gene	26
1.4.1.	MxA induction by interferons	27
1.4.2.	MxA and MicroRNAs	29
1.4.5.	MXA and MICIORNAS	29
2.	Subjects and Methods	
2.1.	Subjects	
2.1.1.	Patients and healthy blood donors	30
2.1.2.	Equipments and supplies	32
2.2.	Methods	
2.2.1.	Samples collection and preparation	33
2.2.2.	Biochemical measurements	33
2.2.2.1.	Measurements of ALT activity	33
2.2.2.2.	Measurements of AST activity	35
2.2.3.	HCV-RNA quantification	37
2.2.3.1.	HCV-RNA extraction	37
2.2.3.2.	HCV viral load quantification	40
2.2.4.	MicroRNAs quantification	42
2.2.4.1.	MicroRNAs extraction	42
2.2.4.2.	MicroRNAs amplification	46
2.2.5.	MxA-mRNA quantification	49
2.2.5.1.	MxA-mRNA extraction	50
2.2.5.2.	MxA-mRNA amplification	50
2.2.6.	Relative quantification measurements	52
2.2.6.1.	Relative quantification for microRNAs	53
2.2.6.2.	Relative quantification for MxA-mRNA	54
2.2.7.	Statistical analysis	54
3.	Results	56
4.	Discussion	86
5.	Summary	97
6.	References	102
7.		
	Arabic Summary	
8.	Arabic Abstract	

ABSTRACT

Background: Hepatitis C virus (HCV) infection is the major cause for chronic hepatitis. Interferons (IFNs) are a large family of proteins involved in antiviral defense and used for HCV treatment. Large numbers of Egyptian patients are not responding to the combined pegylated interferon alpha /ribavirin therapy. MicroRNAs (miRNAs) are class of post transcription regulators that play important role in HCV life cycle and interfering with interferon signaling or production.

Aim: To find a predictive measure for the response to the combined pegylated interferon alpha /ribavirin therapy using miR-20a, miR-155, miR-21 and miR-196b with evaluating MxA-mRNA expression levels as a positive control for interferon action.

Methods: This study was conducted on 100 patients, 50 responders and 50 non-responders with HCV and 20 healthy controls. MiRNAs and MxA-mRNA were isolated from serum and blood sequentially and the expression levels were quantified using quantitative PCR (qPCR).

Results: All the studied miRNAs; miR-20a, miR-155, miR-21 and miR-196b were up regulated in non-responders compared to responders patients. These data were confirmed by the inhibition of MxA-mRNA levels in non-responders compared to responders patients. Receiver operator characteristic (ROC) analysis revealed that the cut-off value for responding to the combined pegylated interferon alpha /ribavirin therapy for miR-20a, miR-155, miR-21 and miR-196b is >1, >2.26, >1.57 and >2.49 respectively.

Conclusion: The circulating miRNAs; miR-20a, miR-155, miR-21 and miR-196b in serum are promising biomarkers for predicting the responding HCV-4 Egyptian patients to the combined pegylated interferon alpha /ribavirin therapy.

LIST OF ABBREVIATIONS

A Adenosine

ADARs Adenosine deaminases acting on RNA

Ago2 Argonaute-2

ALT Alanine aminotransferase

AST Aspartate aminotransferase

AUC Area under curve

bps Base pairs

C.elegens Caenorhabditis elegens

cal Calibrators

cDNA Complementary DNA

CHC Chronic hepatitis C

Ct Cycle threshold

D. melanogaster Drosophila melanogaster

DGCR8 DiGeorge critical region 8

dNTPs Deoxynucleotide triphosphate

dsDNA Double stranded DNA

dT Deoxy- thymine nucleotide

dTTP Deoxythymidine triphosphate

EDTA Ethylenediaminetetraacetic acid

FA Fanconi Anemia

FADD Fas associated protein with death domain

FRET Fluorescent resonance energy transfer

GAPDH Glyceraldehyde 3-phosphate dehydrogenase

GTPases Guanosine triphosphatase

HBV Hepatitis B virus

HCC Hepatocellular carcinoma

HCV Hepatitis C virus

HCV-4 HCV genotype 4

HIV Human immunodeficiency virus

HMOX1 Heme oxygenase 1

Huh7 Human hepatocarcinoma cell line

IC internal control

IFITM1 Interferon induced transmembrane protein 1

IFNs Interferons

IFN-α Interferon alpha

IFN-β Interferon beta

IFN-γ Interferon gamma

IFN-λ Interferon lambda

IGF2BP1 Insulin like growth factor 2 mRNA binding

protein 1

IL Interleukin

IRAK1 Interleukin-1 receptor-associated kinase 1

IRF-1 Interferon regulatory factor 1

IRF-2 Interferon regulatory factor 2

ISGF3 IFN-stimulated gene factor 3

ISGs Interferon stimulated genes

ISRE IFN-stimulated response element

MIR155HG MiR-155 host gene

miRNAs MicroRNAs

MxA Myxovirus resistance A

MyD88 Myeloid differentiation primary response

gene 88

NF-kB Nuclear factor kappa-light-chain-enhancer of

activated B cells

NK Natural killer

NS Non-structural

NS5A Nonstructural 5A protein coding region

nt Nucleotide

PACT protein activator of PKR

PBMCs Peripheral blood mononuclear cells

PCR Polymerase chain reaction

Peg- IFN-α Pegylated interferon alpha

PEG-IFN-RBV Pegylated interferon alpha plus ribavirin

Pre-miRNA Precursor miRNA

Pri-miRNA Primary miRNA transcripts

qPCR Quantitative polymerase chain reaction

RIP Receptor interacting protein

RISC RNA induced silencing complex

RLC RISC loading complex

RNase Ribonuclease

ROC Receiver operating characteristic

RT Reverse transcription

RT-PCR Reverse transcription PCR

RT-qPCR Quantitative reverse transcription PCR

Tth Thermostable polymerase enzyme

RVR Rapid virological response

siRNA Small interfering RNA

Smad7 Mothers against Decapentaplegic homolog 7

snoRNA Small nucleolar RNA

SOCS1 Suppressor of Cytokine Signaling 1

ssDNA Single stranded DNA

STDF Science and technology development fund in

Egypt

SVR Sustained virological response

TBRI Theodor Bilharz Research institute

TGF-β Transforming growth factor beta

TLRs Toll-like receptors

Tm Melting temperature

TMEM49 Transmembrane protein 49

TNFα Tumor necrosis factor alpha

TRBP Tar RNA binding protein

TU Transcription unit

UNG Uracil N-glycosylase

USP18 Ubiquitin Specific Peptidase 18

UTRs Untranslated regions

LIST OF FIGURES

Figure	Title	page
Figure (1)	Genomic organization of hepatitis C polyprotein	2
Figure (2)	MicroRNA genomic location and gene structure	13
Figure (3)	Characterization of the full-length pri-MIRN21	22
Figure (4)	Schematic representation of the MIR155HG	23
Figure (5)	Hsa-miR-196 on chromosome 7 within intronic region of hox gene cluster	24
Figure (6)	MxA gene expression depends on type I or type III IFN signaling	28
Figure (7)	Standard curve for HCV-RNA quantification	42