

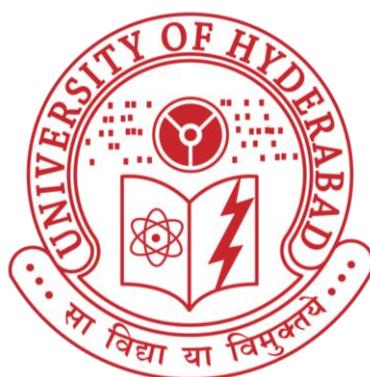
Anti-inflammatory Effects of 15-Lipoxygenase Metabolites of α -Linolenic acid: Studies on Signalling Pathways Involved

Thesis submitted for the degree of

DOCTOR OF PHILOSOPHY

By

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**Enrolment No. 08LAPH12
June, 2016**



University of Hyderabad

(A Central University established in 1974 by act of parliament)

Hyderabad-500 046, INDIA

CERTIFICATE

This is to certify that **Mr. Naresh Kumar** has carried out the research work embodied in the present thesis under my supervision and guidance for a full period prescribed under the Ph.D. ordinance of this University. We recommend his thesis entitled “**Anti-inflammatory Effects of 15-Lipoxygenase Metabolites of α -Linolenic acid: Studies on Signalling Pathways Involved**” for submission for the degree of Doctor of Philosophy of this University.

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DECLARATION

I hereby declare that the work embodied in this thesis entitled “**Anti-inflammatory Effects of 15-Lipoxygenase Metabolites of α -Linolenic acid: Studies on Signalling Pathways Involved**” has been carried out by me under the supervision of **Prof. P. Reddanna** and this work has not been submitted for any degree or diploma of any other university earlier.

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Table of Contents

Chapter 1: General Introduction	1
1.1 Inflammation	1
1.1.1 Introduction	1
1.1.2 Types of Inflammation	4
1.1.3 Inflammation meets cancer (7 th hallmark of cancer)	9
1.1.4 Inflammation: Anti-Tumor activity !!!	10
1.2 Inflammasome	11
1.2.1 Introduction	11
1.2.2 Inflammasome complex formation	12
1.2.3 NLRP3 Inflammasome	14
1.3 Polyunsaturated Fatty Acids	16
1.3.1 Introduction	16
1.3.2 Role of ω -6 and ω -3 PUFAs in inflammation	17
1.4 Eicosanoids	21
1.4.1 Introduction	21
1.4.2 Types of Eicosanoids	21
1.4.3 Cyclooxygenases (COX)	22
1.5 Lipoxygenases	23
1.5.1 Introduction	23
1.5.2 Distribution and Classification of LOXs	26
1.5.3 Role of Lipoxygenases in Plants and animals	27
Scope of Study	30
Chapter 2: Evaluation of the role of omega-6 and omega-3 PUFAs in inflammation in vitro by employing mouse macrophage cell line, RAW 264.7 as a model system	33
2.1 Introduction	34
2.2 Materials and methods	36
2.2.1 Chemicals and Reagents	36
2.2.2 Cell culture and Treatments	36
2.2.3 Cytotoxicity Assay	37
2.2.4 Nitrite Estimation	37

2.2.5	Estimation of IL-1 β _____	37
2.2.6	Measurement of Reactive Oxygen Species (ROS) _____	38
2.2.7	Analysis of Apoptosis by FACS _____	38
2.3	Statistical Analyses _____	38
2.4	Results _____	39
2.4.1	ω -6 and ω -3 PUFAs show less cytotoxic effect on RAW 264.7 cells. _____	39
2.4.2	Effects of ω -6 and ω -3 PUFAs on Nitrite level in culture medium in LPS induced RAW 264.7 Cells. _____	40
2.4.3	ω -6 and ω -3 PUFAs reduce Reactive Oxygen Species (ROS) generation in LPS induced RAW 264.7 cells. _____	41
2.4.4	ω -6 and ω -3 PUFAs show a decrease in IL-1 β level in culture medium in LPS induced RAW 264.7 Cells. _____	43
2.4.5	ω -3 PUFAs show increased apoptosis than ω -6 PUFAs in LPS induced RAW 264.7 Cells. _____	44
2.5	Discussion _____	46
<i>Chapter 3: Generation of 15-Lipoxygenase (15-LOX) metabolites of omega-6 and omega-3 PUFAs and their characterization</i> _____		49
3.1	Introduction _____	50
3.2	Materials and Methods _____	51
3.2.1	Chemicals and Reagents _____	51
3.2.2	Enzyme source _____	51
3.2.3	Homogenization and (NH ₄) ₂ SO ₄ precipitation of linseed seedling _____	52
3.2.1	Enzyme Assay _____	52
3.2.2	pH optimization _____	52
3.2.3	Temperature optimization _____	53
3.2.4	Clarification of sample _____	53
3.2.5	Desalting _____	53
3.2.6	Anion Exchange Chromatography _____	54
3.2.7	Biosynthesis of Linseed Lipoxygenase metabolites _____	54
3.2.8	Purification and analysis of metabolites on SP-HPLC _____	54
3.2.9	Characterization on LC-MS/MS _____	55
3.3	Statistical Analyses _____	55
3.4	Results _____	56
3.4.1	Linseed seedlings show abundant LOX activity during early days of germination _____	56

3.4.2	Linseed enzyme shows pH optima in alkaline pH range	58
3.4.3	Linseed enzyme uses ω -6 and ω -3 PUFAs as substrate	60
3.4.4	Purification of metabolites generated by linseed enzyme on preparative straight phase HPLC (SP-HPLC)	61
3.4.5	Analysis of metabolites generated by linseed enzyme and comparison with soybean LOX metabolites	65
3.4.6	Characterization of Linseed metabolites on LC-MS/MS	69
3.5	Discussion	72
Chapter 4: Study the effects of 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] on inflammation and elucidate the signaling pathways involved: in vitro and in vivo studies		75
4.1	Introduction	76
4.2	Materials and Methods	77
4.2.1	Chemicals and Reagents	77
4.2.2	Animals	78
4.2.3	Cell culture and Treatments	78
4.2.4	Isolation of Primary Peritoneal Macrophages	79
4.2.5	Cytotoxicity Assay	79
4.2.6	Nitrite Estimation	80
4.2.7	Estimation of IL-1 β , IL-10, PGD ₂ and PGE ₂	80
4.2.8	Measurement of Reactive Oxygen Species (ROS)	80
4.2.9	Anti-inflammatory Effects of ALA Metabolites <i>in vitro</i> employing RAW 264.7 cells and Mouse Peritoneal macrophages: Immunoblot Analysis	81
4.2.10	Anti-inflammatory Effects of ALA metabolites: Reverse Transcription Polymerase Chain Reaction (RT-PCR)	82
4.2.11	Analysis of the inflammasome, autophagy and NF- κ B translocation by confocal microscopy	83
4.2.12	Analysis of Apoptosis by FACS	84
4.2.13	Induction of Inflammation <i>in vivo</i> : Septic Shock with LPS	84
4.2.14	Induction of Inflammation <i>in vivo</i> : Cecal Ligation and Puncture (CLP) model	85
4.3	Statistical Analyses	86
4.4	Results	86
4.4.1	Hydroperoxy metabolites exhibit more cytotoxic effects on RAW 264.7 cells as compared to hydroxy metabolites of ALA	86

4.4.2	ALA metabolites reduce nitric oxide levels and ROS generation in RAW 264.7 cells and peritoneal macrophages	88
4.4.3	ALA metabolites inhibit the expression of iNOS and TNF- α in LPS stimulated RAW 264.7 cells	90
4.4.4	13-(S)-HPOTrE and 13-(S)-HOTrE inactivate inflammasome in PPAR- γ dependent manner in RAW 264.7 cells and peritoneal macrophages	93
4.4.5	ALA metabolites induce apoptosis in LPS treated RAW 264.7 cells	99
4.4.6	ALA metabolites extend BALB/c mice survival and show anti-inflammatory properties by regulating cytokines and inflammasome	102
4.5	Discussion	104
Chapter 5: Summary and conclusions		110
5.1	Linseed seedlings with abundant lipoxygenase activity	112
5.2	The linseed seedling enzyme is characterized as 15-LOX	112
5.3	The omgea-3 PUFAs (ALA, and DHA) efficiently show anti-inflammatory effects in comparison to omgea-6 PUFAs (AA, and LA)	114
5.4	ALA metabolites show anti-inflammatory effects in RAW 264.7 CELLS and mouse primary peritoneal macrophages	115
5.5	ALA metabolites extend survival of BALB/c mice and mediate anti-inflammatory effects by inactivating NLRP3 inflammasome: <i>in vivo</i> studies in sepsis model and CLP mice model	118
REFERENCES		121
Index		134
List of Publications and Manuscripts		135

List of Figures and Tables

Figure 1-1:	Inflammation: Five cardinal signs.	1
Figure 1-2 :	Acute inflammation, Resolution of Inflammation and development of chronic inflammation	7
Figure 1-3:	Inflammation: 7th Hallmark of Cancer	9
Figure 1-4:	Different types of inflammasomes	11
Figure 1-5:	Assembly and activation of NALP3 inflammasome	13
Figure 1-6:	Regulation of inflammasome	14
Figure 1-7:	Regulation of inflammasome by Cell stress and ion flux	15
Figure 1-8:	The conversion of ω-3 PUFAs and ω-6 PUFAs into longer chain unsaturated derivatives	17
Figure 1-9 :	Role of ω-6 and ω-3 PUFAs in Inflammation	19
Figure 1-10:	Summary of the anti-inflammatory actions of marine n-3 polyunsaturated fatty acids	20
Figure 1-11:	Mechanism of Lipoxygenase reaction	23
Figure 1-12:	3D structure of Glycine max (Soybean) lipoxygenases	24
Figure 1-13:	Substrate binding site in lipoxygenases	25
Figure 1-14:	The dioxygenation of ALA by lipoxygenases in Plants	28
Figure 2-1:	Effects of ω-6 PUFAs (AA, and LA) and ω-3 PUFAs (ALA, and DHA) on viability of mouse macrophage cell line, RAW 264.7 cells	39
Figure 2-2:	Effects of ω-6 PUFAs (AA, and LA) and ω-3 PUFAs (ALA, and DHA) on NO generation in RAW 264.7 cells	41
Figure 2-3:	Effects of ω-6 PUFAs (AA, and LA) and ω-3 PUFAs (ALA, and DHA) on ROS generation in RAW 264.7 cells	42
Figure 2-4:	Effects of ω-6 PUFAs (AA, and LA) and ω-3 PUFAs (ALA, and DHA) on IL-1β level in RAW 264.7 cells	44
Figure 2-5:	Flow cytometric analysis showing the effects of ω-6 PUFAs (AA, and LA) and ω-3 PUFAs (ALA, and DHA) on apoptosis in RAW 264.7 cells challenged with LPS	45
Figure 3-1:	Homogenization, Isolation and Purification of Linseed seedling enzyme	57
Figure 3-2:	pH optimization of Linseed seedling enzyme	59
Figure 3-3:	Temperature optimization of linseed seedling enzyme	60
Figure 3-4 :	Wavelength scan (210 - 300 nm) of HPLC peak collected from SP-HPLC	61

Figure 3-5 :	HPLC chromatograms of PUFAs metabolites generated using Linseed lipoxygenase	62
Figure 3-6:	HPLC analysis of hydroperoxy metabolites of ALA catalyzed by Linseed lipoxygenase	63
Figure 3-7:	HPLC analysis of hydroxy metabolites of ALA catalyzed by Linseed lipoxygenase	64
Figure 3-8:	Comparison of linseed hydroperoxy and hydroxy metabolites of ALA with soybean hydroperoxy (13-(S)-HPOTrE) and hydroxy (13-(S)-HOTrE) metabolites of ALA, respectively	66
Figure 3-9:	Comparison of linseed hydroperoxy and hydroxy metabolites of AA with soybean hydroperoxy (15-(S)-HPETE) and hydroxy (15-(S)-HETE) metabolites of AA	67
Figure 3-10:	Comparison of linseed hydroperoxy and hydroxy metabolites of LA with soybean hydroperoxy (13-(S)-HPODE) and hydroxy (13-(S)-HODE) metabolites of LA	68
Figure 3-11:	Comparison of linseed LOX metabolite of AA with soybean 15 LOX metabolites of AA (15-(S)-HETE)	69
Figure 3-12:	Comparison of linseed seedling LOX metabolite of AA with soybean 15 LOX metabolite of AA (15-(S)-HETE) on LC-MS/MS	70
Figure 3-13:	The fragmentation of hydroxy metabolite of linseed seedling LOX using AA as substrate, accounting for the peaks observed on LC-MS/MS	71
Table 1 :	List of Primers used for Semi-quantitative PCR	83
Figure 4-1:	Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on cells viability in RAW 264.7 cells	87
Figure 4-2:	Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on generation of NO and ROS in RAW 264.7 cells and mouse peritoneal macrophages	89
Figure 4-3:	Anti-inflammatory effect of 13-(S)-HPOTrE and 13-(S)-HOTrE is mediated by inhibition of iNOS and TNF-α	91
Figure 4-4:	ALA metabolites inhibit the expression of iNOS and TNF-α in LPS stimulated RAW 264.7 cells through NF-κB pathway	92
Figure 4-5:	ALA metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE, inhibit inflammasome complex in RAW 264.7 cells	94
Figure 4-6:	ALA metabolites inhibit inflammasome complex activation in mouse peritoneal macrophages	96
Figure 4-7:	ALA metabolites inhibit inflammasome complex activation in mouse peritoneal macrophages	97
Figure 4-8:	13-(S)-HPOTrE and 13-(S)-HOTrE show anti-inflammatory effects by upregulating expression of COX-2	98

List of Figures and Tables

Figure 4-9:	13-(S)-HPOTrE and 13-(S)-HOTrE induce apoptosis in LPS stimulated RAW 264.7 cells	100
Figure 4-10:	13-(S)-HPOTrE and 13-(S)-HOTrE inhibit Beclin-1 mediated autophagy in LPS stimulated RAW 264.7 cells	101
Figure 4-11:	Effects of ALA metabolites during sepsis in BALB/c mice	103
Figure 5-1:	Effects of ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE] on different cellular processes/mechanism during inflammation	119

1

List of Abbreviations

AA	:	Arachidonic acid
ALA	:	α -Linolenic Acid
BSA	:	Bovine serum albumin
CLP	:	Cecal Ligation and Puncture
COX	:	Cyclooxygenase
DAPI	:	4',6-diamidino-2-phenylindole
DCFH-DA	:	2',7'-Dichlorofluorescein Diacetate
DHA	:	Docosahexaenoic acid
DMEM	:	Dulbecco's Modified Eagle Medium
DMSO	:	Dimethyl sulfoxide
DNA	:	Deoxyribonucleic acid
EDTA	:	Ethylene diamine tetra acetic acid
EFA	:	Essential fatty acids
ELISA	:	Enzyme linked immunosorbent assay
EPA	:	Eicosapentaenoic acid
FACS	:	Fluorescence-activated cell Sorter
FBS	:	Fetal bovine serum
FFA	:	Free fatty acids
FITC	:	Fluorescein isothiocyanate
g	:	Gram
GC-MS	:	Gas chromatography-mass spectrometry
h	:	Hour(s)
HRP	:	Horseradish peroxidase
IL-1 β	:	Interleukin-1 β

List of Abbreviations

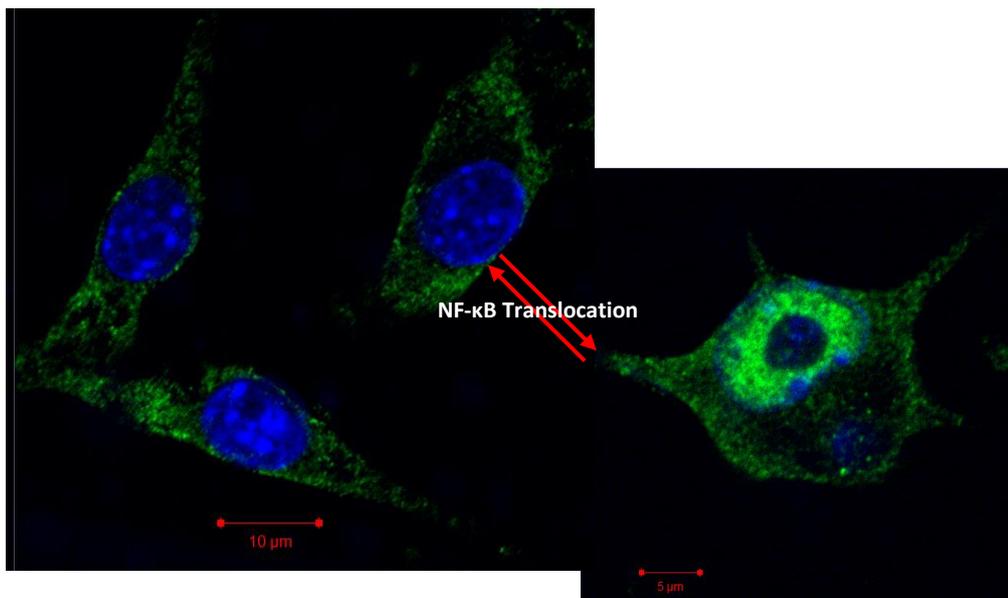
iNOS	:	Inducible nitric oxide synthase
kDa	:	Kilo Dalton
l	:	litre
LA	:	Linolenic acid
LOX	:	lipoxygenase
LPS	:	Lipopolysaccharide
LT	:	Leukotriene
LX	:	Lipoxin
mg	:	Milli gram
min	:	Minute(s)
mL	:	Milli liter
mM	:	Milli molar
mRNA	:	Messenger Ribonucleic acid
MTT	:	3-(4, 5-dimethylthiazol-2-yl)-2,5- Diphenyl tetrazolium bromide
NAC	:	N-acetylcystein
nm	:	Nano meter(s)
NO	:	Nitric oxide
NSAIDs	:	Non-steroidal anti-inflammatory drugs
PAGE	:	Polyacrylamide gel electrophoresis
PBS	:	Phosphate buffered saline
PCR	:	Polymerase chain reaction
PG	:	Prostaglandin
PI	:	Propidium iodide
PMSF	:	Phenyl methane sulphonyl fluoride
PUFAs	:	Polyunsaturated fatty acids

List of Abbreviations

ROS	:	Reactive oxygen species
RP-HPLC	:	Reverse phase- High pressure liquid chromatography
RT-PCR	:	Reverse transcription-polymerase chain Reaction
SDS	:	Sodium dodecyl sulfate
SP-HPLC	:	Straight phase-High pressure liquid chromatography
TNF- α	:	Tumor necrosis factor- α
Tris	:	Tris-(Hydroxymethyl) aminomethane
UV	:	Ultraviolet
μ M	:	Micro molar
$^{\circ}$ C	:	Degree centigrade/ Degree Celsius
13-(S)-HODE	:	13-(S)-hydroxyoctadecadienoic acid
13-(S)-HOTrE	:	13-(S)-hydroxyoctadecatrienoic acid
13-(S)-HPODE	:	13-(S)-hydroperoxyoctadecadienoic acid
13-(S)-HPOTrE	:	13-(S)-hydroperoxyoctadecatrienoic acid
15-(S)-HETE	:	15-(S)-hydroxyeicosatetraenoic acid
15-(S)-HPETE	:	15-(S)-hydroperoxyeicosatetraenoic acid

Chapter 1

GENERAL INTRODUCTION



1.1 INFLAMMATION

1.1.1 Introduction

Inflammation is the host's immune response towards any internal or external cue such as tissue damage, injury, infection, artificial agents, or immune disorders. In 1600 BC, Celsus explained four cardinal signs of inflammation as *ruber* (redness), *tumor* (swelling), *calor* (heat), and *dolor* (pain). Galen added the 5th sign of inflammation: *functio laesa* (loss of function) (Figure 1-1). Inflammatory response involves three events, vasodilation, increase in blood capillary permeability and the influx of phagocytes from blood capillaries to specific tissue. The initiation of the inflammatory response is mediated by a complex series of events through a variety of

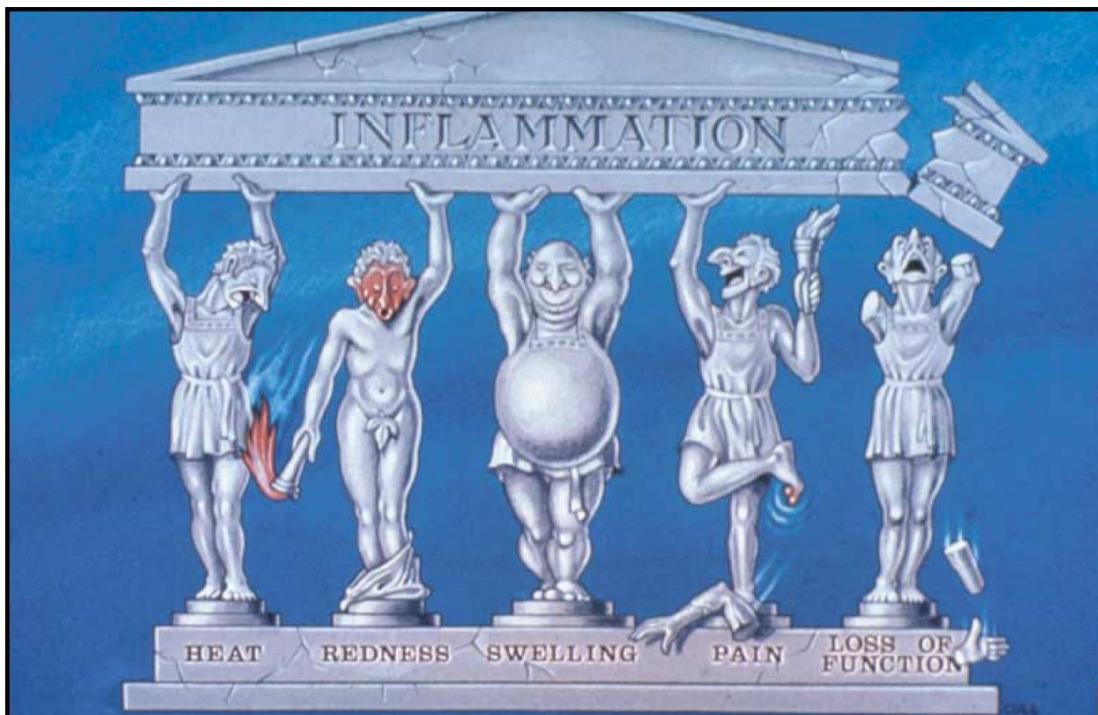


Figure 1-1: Inflammation: Five cardinal signs.

Source: Lawrence et al., Anti-inflammatory lipid mediators and insights into the resolution of inflammation. *Nat. Rev. Immunol.* 2, 787–795 (2002)

mediators. These mediators may be originated either from pathogenic microbes, from the molecules released by the damaged cells in case of tissue injury, or from some plasma enzymes or from the product of leukocytes (WBCs).

Vascular endothelial cell line serves as a guard for regulating the migration of molecules and leukocytes into the tissue. The movement of these molecules and leukocytes at the site of tissue injury through endothelium lining is called **extravasation**. This process is based on the interaction between **cell adhesion molecules (CAMs)** present on endothelium cells and migrating cells. CAMs are divided into four families based on the differences in the structure and the pattern of glycosylation: **selectin family, integrin family, mucin-like family and immunoglobulin superfamily**. As the initiation of inflammatory response originates, many cytokines and inflammatory mediators act on local blood capillaries and induce the expression of CAMs on the endothelial membrane. This state of vascular endothelium is called **inflamed** or **activated**. Generally, neutrophils are among the first cell type that binds to inflamed endothelium and extravasates into tissue. Neutrophils first recognize the inflamed endothelium and then attach strongly to adhesion molecules. Lymphocytes circulate continuously from the vascular system (Cardiovascular system and lymphatic system) to various lymphoid organs. The circulation process of lymphocytes increases the possibility of activated lymphocytes to encounter antigen, presented by antigen presenting cells and thus determine the removal of pathogens or microorganisms either by inhibiting their growth or by killing them.

Acute phase proteins are serum originated chemical mediators of the inflammatory response whose concentration can either increase or decrease in the

serum during inflammation thus called as **positive acute phase proteins** and **negative acute phase proteins** [1,2]. C- reactive protein, Serum amyloid, mannose binding lectin, complement factors, ferritin, and coagulation factors are positive acute phase proteins while albumin, retinol binding protein, and transferrin are negative acute phase proteins [3]. The majority of bacterial and fungal cell walls are composed of C-polysaccharide, providing strength to their cell wall and thus offering protection. However, the C-reactive protein uses these polysaccharides for pathogen identification. C-reactive protein binds to C-polysaccharide [4] leading to complement system activation which results in complement-mediated phagocytosis or lysis of pathogens [5], and thus avoiding any damage or infection by the microbes. Another factor, blood-clotting factor in blood circulatory system arrests the pathogen or toxic agent, locally in blood clots and limit the infection from spreading [6].

Histamine is an important chemical mediator of inflammatory response released by the various cell during inflammation. It is a biological molecule that plays various vital roles in the body. Apart from functioning as a neurotransmitter and maintaining a role in the physiology of digestive track, it has a critical role associated with local immune responses [7]. It causes vasodilation and increases the permeability of capillaries after binding to its receptor and thus recruits leukocytes and macrophages at the site of infection. Next, a significant group of inflammatory mediators is small peptide-kinin which is generally present in an inactive form in the blood. This peptide gets activated after tissue damage. Like histamine, it also causes vasodilation and increases the permeability of blood capillaries. Bradykinin- a type of kinin also activates pain receptors present in the skin. Such inflammatory mediators recruit neutrophils and macrophages at inflammatory site and assist in pathogen killing or its removal.

1.1.2 Types of Inflammation

Inflammation can be classified into two different groups, acute inflammation and chronic inflammation, based on time of persistence and tissue damage.

Acute Inflammation (Either Localized or Systemic inflammation):

The acute inflammation may be either localized or systemic in nature. Tissue injuries of any kind can induce rapid and acute immune response. The immediate immune response is initiated by chemical mediators [8]. These mediators appear at the site of tissue injuries within few seconds and start action in the microenvironment. As a consequence, edema (fluid accumulation) development takes place along with hallmarks of inflammation as described above [9]. Extravasation of leukocytes further increases swelling and blood flow in that area which further generates heat, and at the same time fluid from bloodstream exudates, activates kinin, and fibrinogen-blood clotting system. The plasma enzyme mediators- fibrinopeptide and bradykinin directly initiate vascular modification that takes place during the early local response. The complement system, however, plays an indirect role in local vascular changes through its complement anaphylatoxins-C3a, C4a, and C5a [10–12]. These molecules also induce mast cell degranulation to release histamine- a potent inflammatory mediator that induces smooth muscle contraction and vasodilation.

The tissue neutrophils actively participate at the site of inflammation within a minute after tissue damage or any infection encountered, however, the blood neutrophils extravasate from blood vessels to the local site of inflammation after few

hours of the onset of initial inflammatory response. After recruitment at the local site of inflammation, neutrophils devour invading particles, pathogens and/or other foreign particles and release chemical mediators that further enhance the inflammatory response. Generally, chemotactic chemokine- **Macrophage Inflammatory Proteins** (MIP-1) are released by neutrophils, which attract macrophages at the site of inflammation [7]. After 5-6 hours of initiation of the inflammatory response, macrophages arrive at the site of inflammation. Like neutrophil, these activated macrophages also phagocytose the pathogen and secret 3 different types of cytokines- IL-1 β , IL-6, and tumor necrosis factor- α (TNF- α) which further enhance the systemic and localized inflammatory responses. These cytokines work in paracrine fashion and increase expression of adhesion molecules on endothelial cells and increase permeability. As a result, extravasation of lymphocytes, neutrophils and monocytes take place, which are thus recruited, to the inflammation site. TNF- α and IL-1 β act in an autocrine manner, induce macrophages and endothelial cells to produce chemokine that in turn increases neutrophil influx in tissue. On the other hand, TNF- α and INF- γ activate macrophage and neutrophils to enhance the phagocytic properties and release of the lytic enzymes in tissue at inflammation site [9].

Mechanism of acute inflammation is beautifully planned which regulates its amplitude and time period to control tissue damage and starts tissue repair process. The presence of leukocytes, neutrophils, macrophages, monocytes and other phagocytic cells enhance pathogen clearance and increase tissue repair. Unlike TNF- α and INF- γ , TGF- β plays an anti-inflammatory role and inhibits leukocytes recruitment by inhibiting extravasation through endothelial layer [13] thus limiting the pro-inflammatory process. TGF- β also assists in tissue repairing by increasing the deposition

of extracellular matrix at the damaged tissue thus helping in wound healing. Hence, the inflammatory response terminates with the removal of pathogen followed by resolution of inflammation and tissue repair [9].

Systemic inflammatory response (Also called **Acute-Phase Response**) is a consequence of local inflammatory response and results from its failure to control the release of cytokines and acute phase proteins. In another way, it can be defined as the effects of local inflammation on different organs. The characteristics systemic inflammation includes the production of acute phase proteins in liver, initiation of fever, increase in leukocytes production and synthesis of hormones. The Cytokines-IL-1, TNF- α , and IL-6 act on the hypothalamus and induce fever which decreases microbial growth and its pathogenic effects. TNF- α , on the other hand, activates macrophages and endothelial cells to secrete colony stimulating factors such as GM-CSF, G-CSF, and M-CSF. These secreted CSFs activate hematopoiesis that leads to leukocytes production, which eliminates the infection. The serum components- C-reactive protein also assists the removal of pathogens and/or other foreign particles from the site of infection. It deposits opsonin C3b on pathogens and boosts its killing by phagocytic cells [10–12]. In worse circumstances, systemic inflammatory response leads to deleterious outcomes such as **systemic Inflammatory Response Syndrome (SIRS)** and **Multi Organ Dysfunction Syndrome (MODS)**.

Chronic Inflammation:

Chronic inflammation occurs when acute inflammatory response fails to eliminate pathogen and infection persists. Activation and assembly of macrophages for a prolonged period of time is the hallmark of chronic inflammation. These activated macrophages activate proliferation of fibroblasts and production of collagen. As a result, excess fibrous connective tissue is formed that leads to **fibrosis** and the aggregates of leukocytes and lymphocytes lead to **granulomas**.

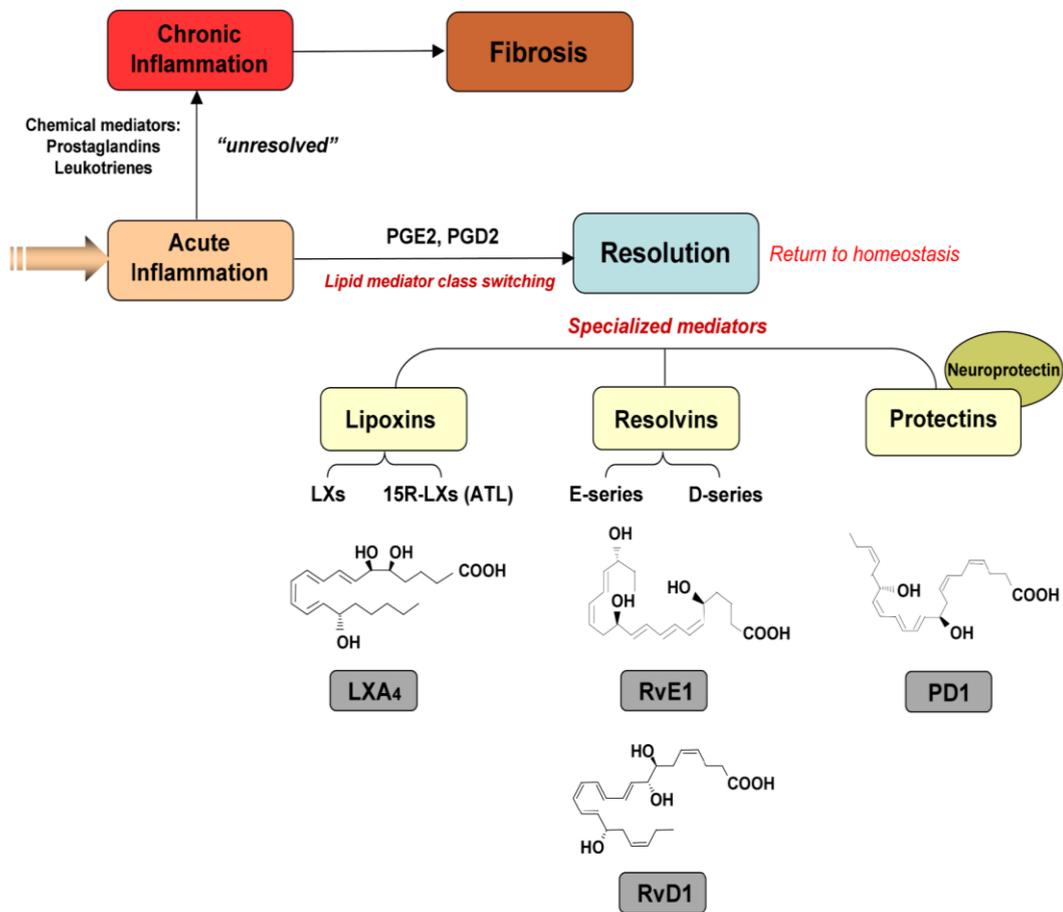


Figure 1-2 : *Acute inflammation, Resolution of Inflammation and development of chronic inflammation*

Source: Serhan et al., Resolving inflammation: dual anti-inflammatory and pro-resolution lipid mediators. *Nat. Rev. Immunol.* **8**, 349–361 (2008).

Players of Chronic inflammation: INF- γ and TNF- α

INF- γ and TNF- α are two cytokines which play a vital role in chronic inflammation development. The activated macrophages secrete TNF- α while T_C cells, NK cells and T_{H1} cells secrete INF- γ . The virus-infected cells, on the other hand, secrete interferons that protect the neighboring cells from the viral infections. [9]. However, the nature of interferons production depends on the type of a cell infected. The infected leukocytes produce INF- α , the fibroblast secrete INF- β , while NK cells and T cells produce INF- γ . Among the interferons, INF- γ has a unique characteristic- the pleiotropic effects that make it different from others. One of the remarkable effects of INF- γ is its capacity to activate macrophages. Activated macrophages produce more cytokines and increase the expression of MHC II molecules on membranes. As a result, these activated macrophages efficiently function as APC (Antigen presenting cells) and exhibit increased cytokine production and increased pathogens killing activity (phagocytic property) in comparison to non-activated macrophages. Other than phagocytic property, these activated macrophages also produce many hydrolytic enzymes, ROS and RNS (Reactive Nitrogen species) that kill microorganisms. However, these hydrolytic enzymes are also responsible for tissue damage, even leading to autoimmune disorders [14], in case the activation of macrophages persists for longer time period.

1.1.3 Inflammation meets cancer (7th hallmark of cancer)

The relation of inflammation with cancer was established long back in the 19th century. Based on multiple pieces of evidence from epidemiological and molecular studies; the general concept is that cancer and inflammation are interlinked. There are many points of control in chronic inflammation that increase the possibility of cancer development [14–16].

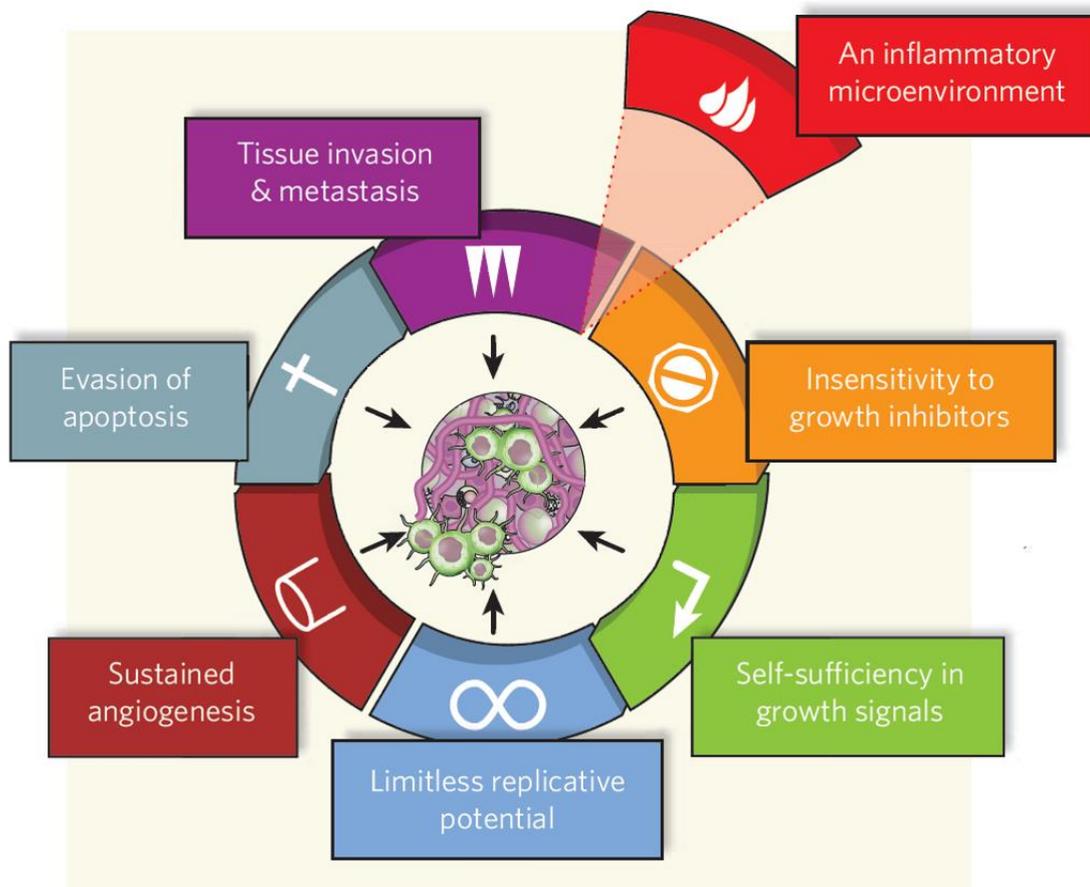


Figure 1-3: Inflammation: 7th Hallmark of Cancer

Source: Mantovani A. Cancer: Inflaming metastasis. *Nature* 457, 36–37 (2009)

Connecting Links between Inflammation and Cancer:

Inflammation and cancer share some common intermediates. Basically, two pathways correlate the functional relation of inflammation with cancer. These are extrinsic and intrinsic pathways [17,18]. In intrinsic pathways, genetic mutation or modification that originate neoplasia development also initiate the program related to inflammatory response and build microenvironment of inflammation [19]. Different oncogenes such as ras, and tyrosine kinase coordinate with pro-inflammatory switches such as an angiogenic switch to guide the development of inflammatory microenvironment. In extrinsic pathways, inflammatory response promotes cancer progression. The significant mediators of extrinsic and intrinsic pathways include transcription factors such as NF- κ B and STAT3, cytokines such as IL-1 β , IL-6, TNF- α and IL-23, and chemokines. NF- κ B is a key molecule of inflammation and adaptive immunity thus important for both inflammation and cancer progression [20,21].

1.1.4 Inflammation: Anti-Tumor activity !!!

In some tumor environments, the presence of inflammatory cells exhibit more prognosis and reveal the facts that inflammatory cells such as macrophages kill cancer cells [15,21,22]. Recently, studies indicated that NF- κ B is associated with balancing between the pro-tumor and anti-tumor activity of macrophages [23]. The exact mechanism, which triggers anti-cancer property of immune response, is not clear. In future, it will be interesting to find out the external stimuli to convert tumor-promoting environment (M2 macrophages and TH2) into the tumor-killing environment (M1 macrophages and TH1 cells).

1.2 INFLAMMASOME

1.2.1 Introduction

Germline encodes sensor to monitor signal of infection or tissue damage in extracellular and intracellular compartments. Inflammasome - multimeric protein complex is a key molecule associated with cytosolic surveillance. It is also called cytoplasmic equivalent to TLRs. This complex can be classified into two major families- **Nod-Like receptor family** (NLR family) and **PYHIN family** (Pyrin and HIN 2000). The human genome encodes 23 NLRs while mouse genome encodes 34 NLRs [24]. NLRs are composed of three domains: **a) Effector domain** (N-terminal domain) consists of either PYD, CARD (caspase recruitment domain) or BIR (Baculovirus inhibitor of apoptosis

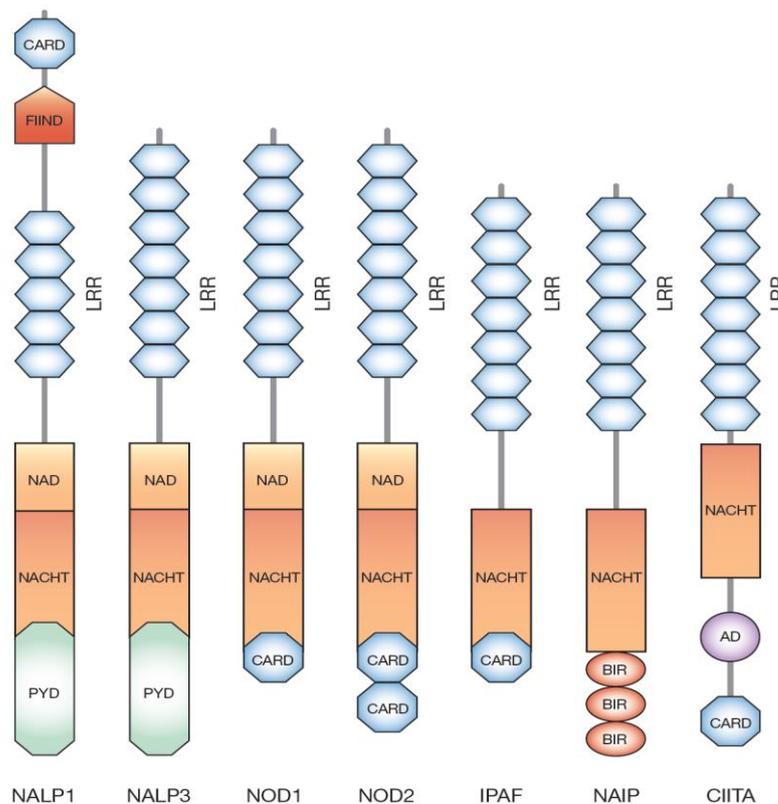


Figure 1-4: Different types of inflammasomes

Source: Church et al., Primer: inflammasomes and interleukin 1β in inflammatory disorders. *Nat. Clin. Pract. Rheumatol.* **4**, 34–42 (2008)

protein repeat), **b). Nucleotide binding domain** (NBD; NAD, NOD; or NATCH), **C). LLR domain** (Leucine-rich repeats-C terminal domain) [24].

NLRPs are the largest family having PYD proteins. 14 NLRP genes are present in the human genome. Among these; NLRP1, NLRP3, IPAF (NLRC4), NLRP6 and NLRP12 form inflammasome complexes. NLRPs consists of PYD domain, NACHT domain and variable LRRs (22-28 Leucine residue repeats) (Figure1-4) [25]. Activated Inflammasome complex processes pro-caspase-1 (Inactive form) into caspase-1 (Active form). Then Caspase-1 initiates processing of Pro-IL-1 β and Pro-IL 18 into their mature forms IL-1 β and IL 18, respectively [26]. These pro-inflammatory cytokines initiate the complex cascade of cytokines that have been implicated in inflammation, pain and even auto-immune disorders [27] .

1.2.2 Inflammasome complex formation

The initiation of oligomerization of NLRs takes place through intermediate NACHT domain [**NAIP** (neuronal apoptosis inhibitory protein), **CIITA** (class II MHC transcription activator), **HET-E** (incompatibility locus protein) and **TP1** (telomerase-associated protein)] while CARD domain of NLRs interacts with pro-caspase-1 that leads to its recruitment in the complex. Those NLRs in which CARD domain is lacking but containing PYDs domain, ASC adaptor (PYD domain + CARD domain) protein is required for interactions [28]. The PYD domain of ASC adaptor protein interacts with PYD domain of NLRs while CARD domain of ASC adaptor protein recruits pro-caspase-1 into inflammasome complex [28]. The activation of Inflammasome takes place by its oligomerization into big disc shape structure while ASC adaptor protein functions as a platform for protein-protein interactions.

Multimerization of proteins in Inflammasome complex initiates autoproteolytic cleavage of recruited pro-caspase-1. Pro-caspase-1 is fragmented into a large p35 fragment (CARD+caspase1) and a small p10 fragment. p35 fragment subsequently fragmented into p20 subunit and CARD [24]. An active caspase-1 enzyme consists of two p10s and two p20s subunits (Figure1-5).

Caspase-1 is cysteine protease specific to aspartate and cleaves IL-1 β and IL-18 at specific recognition site next to aspartic acid residues [29]. Inflammasome containing ASC adaptor induces autoproteolysis of pro-caspase-1 that promotes maturation of pro-inflammatory cytokines while ASC-independent caspase-1 multimeric complex initiates **pyroptosis**- a caspase-1 dependent programmed cell death [24] [28].

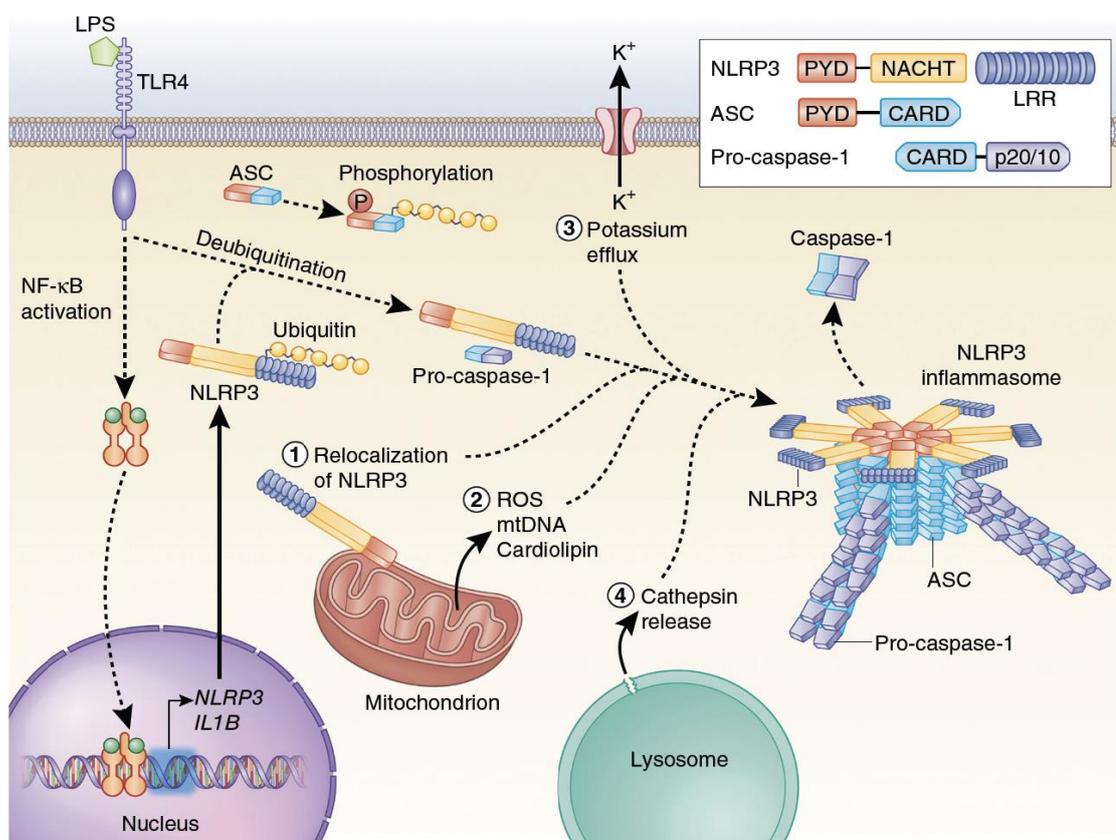


Figure 1-5: Assembly and activation of NALP3 inflammasome

Source: Guo et al., Inflammasomes: mechanism of action, role in disease, and therapeutics. *Nat. Med.* **21**, 677–87 (2015)

1.2.3 NLRP3 Inflammasome

The NLRP3 inflammasome (**N**OD, **L**RR, and **pyrin-containing domain-3**) is the best-studied member of NLRs family and activated by various types of stimuli such as pathogenic, environmental, endogenous or viral [24]. The pathogenic stimuli originated from the pathogens such as influenza A virus [30], *N. gonorrhoeae* [31], *L. monocytogenes* [32], *C. albicans* [33] *S. aureus* [34], and *K. pneumoniae* [35] trigger NLRP3 inflammasome. In addition, the endogenous signals that release during tissue damage such as hyaluronan, extracellular ATP, uric acid crystals also activate NLRP3 inflammasome complex [36] (Figure 1-6, 1-7).

Despite the identification of several NLRP3 activators and immunostimulatory properties of several molecules, the exact mechanism of NLRP3 activation is not much clear. However, the activation of NLRP3 is proposed by three different phenomena such

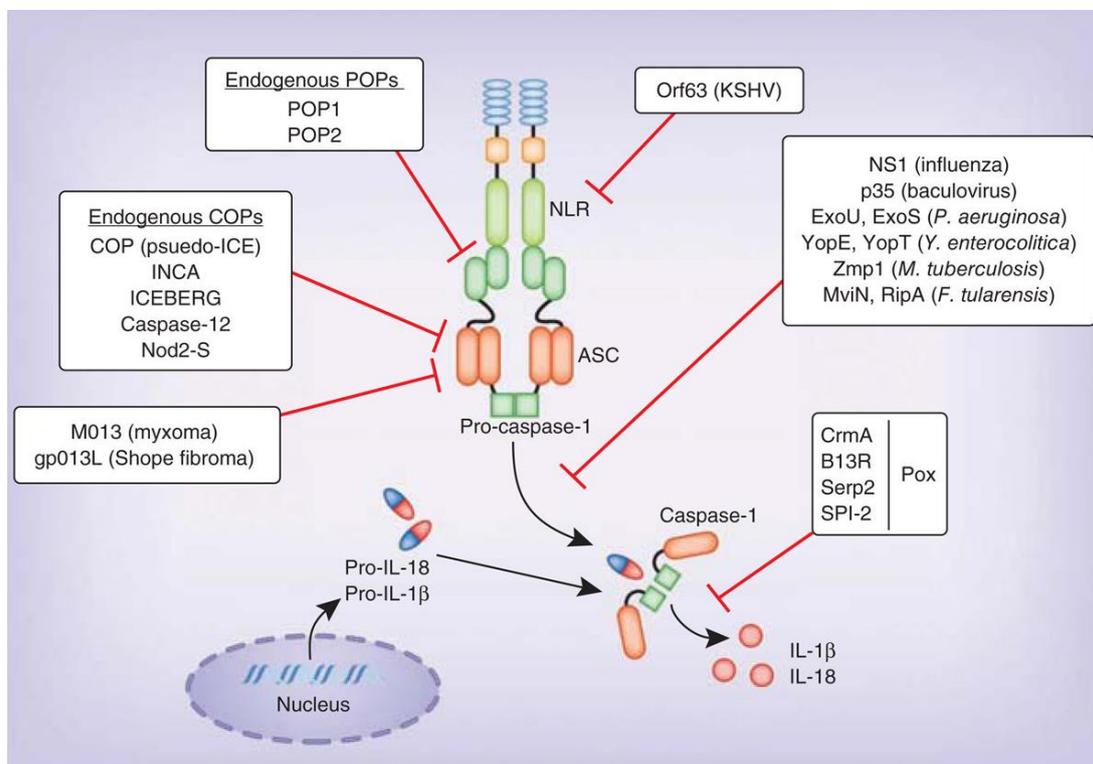


Figure 1-6: Regulation of inflammasome

Source: Rathinam *et al.*, Regulation of inflammasome signaling. *Nat. Immunol.* **13**, 332–333 (2012)

as ROS generation from mitochondria, potassium efflux, and phagolysosomal destabilization. The importance of NLRP3 can be determined by the fact that mutation [37] in *nalp3* gene gives rise to auto-inflammatory disorder and other several deformities [38–41].

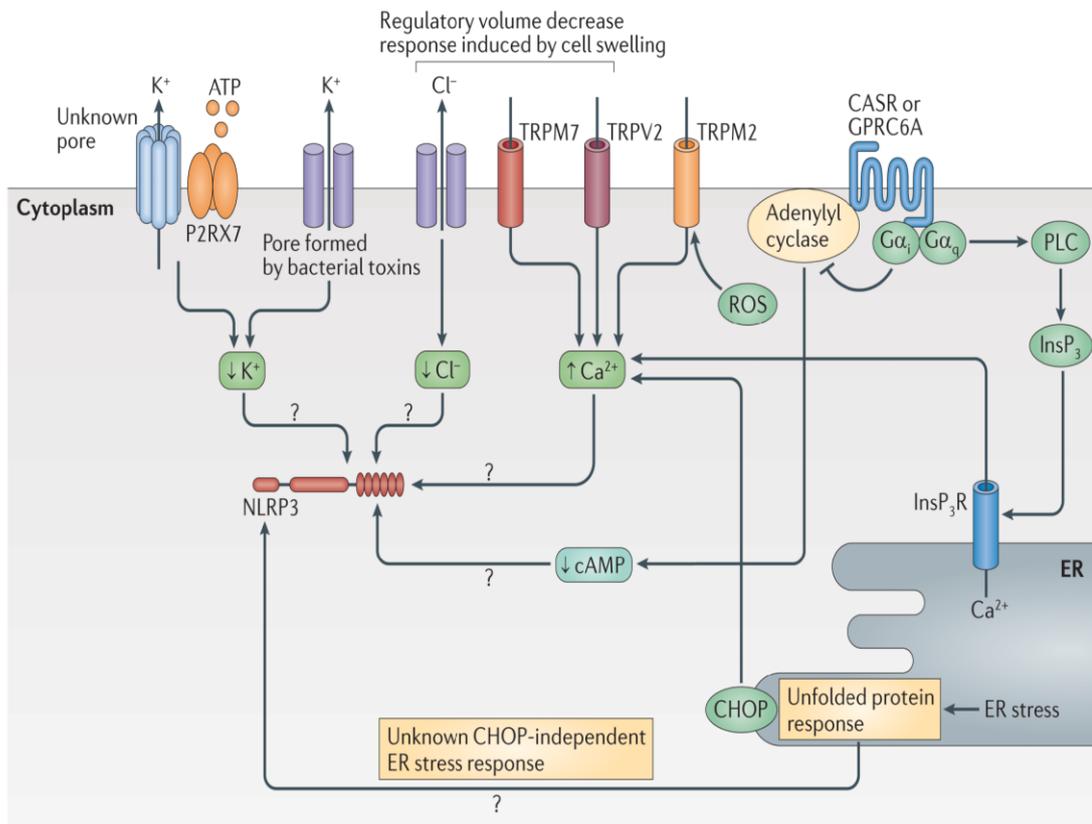


Figure 1-7: Regulation of inflammasome by Cell stress and ion flux

Source: Latz et al., Activation and regulation of the inflammasomes. *Nat. Rev. Immunol.* **13**, 397–411 (2013)

1.3 POLYUNSATURATED FATTY ACIDS

1.3.1 Introduction

Polyunsaturated fatty acids (PUFAs) are made up of long-chain carbon in which a methylene group separates multiple double bonds having cis-configuration. Based on the position of the double bond in carbon backbone, two major families of PUFAs, omega-6 (ω -6) and omega-3 (ω -3), have been characterized. Oleic acid (18:1 Δ 9) is a precursor for most of the plants PUFAs [42]. In the plants, Δ 12 desaturase introduces a double bond in Oleic acid at 12th position to form Linoleic acid (LA, 18:2 Δ 9, 12, ω -6). Further desaturation of LA on 15th position catalyzed by Δ 15 desaturase forms α -Linolenic acid (ALA, 18:3 Δ 9, 12, 15, ω -3). In animals, LA and ALA are required for the growth, reproduction, and other metabolic processes, however; animals lack the synthesis of these fatty acids. Therefore, LA and ALA are essential fatty acids and are made available to animals only through dietary sources. These essential fatty acids give rise to two series of PUFAs, omega- ω -6 series and ω -3 series. LA catalyzed by Δ 6 desaturase, elongase, and Δ 5 desaturase give rise to Arachidonic acid (AA, 20:4 Δ 5, 8, 11, 14). On the other hand, when these enzymes catalyze ALA then give rise to Eicosapentaenoic acid (EPA, 20:5 Δ 5, 8, 11, 14, 17). Further, elongase and Δ 4 desaturase catalyze EPA and generate Docosahexaenoic acid (DHA, 22:6 Δ 4, 7, 10, 13, 16, 19) (Figure 1-8) [43]. As with other complications, age, diabetes and food habit affect the enzymatic activities of these enzymes and thus alter the proportion of PUFAs in the body.

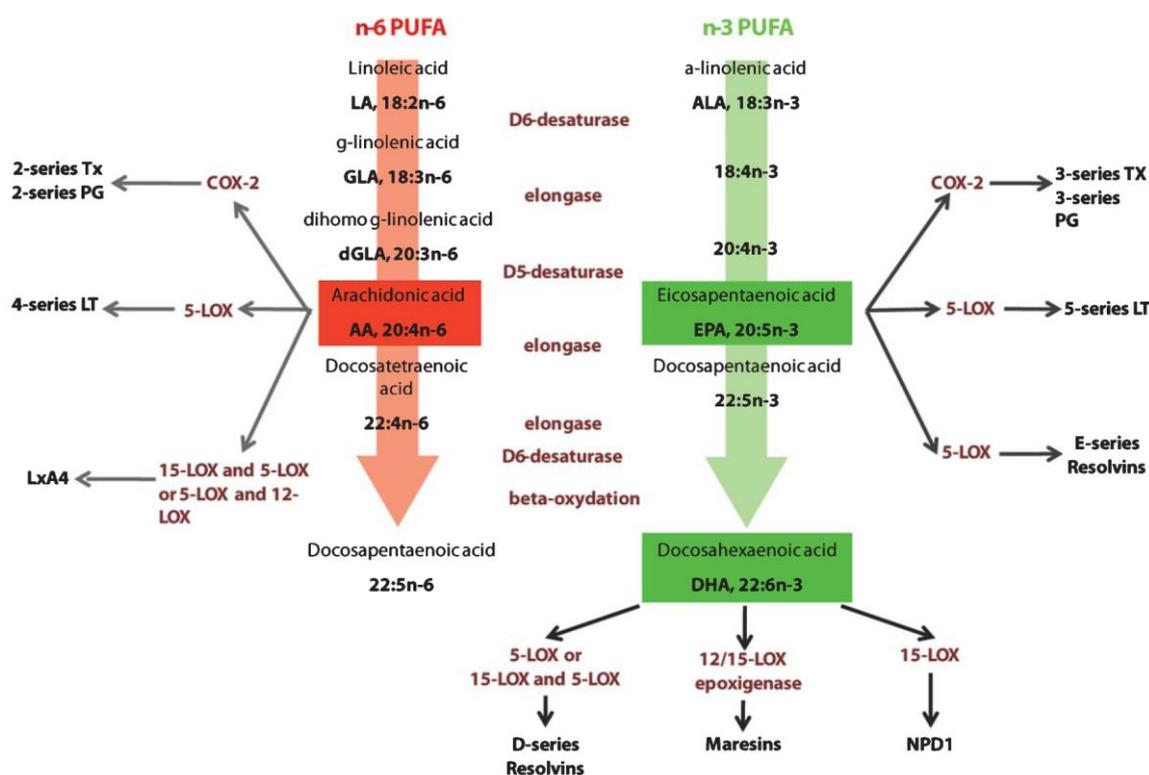


Figure 1-8: The conversion of ω -3 PUFAs and ω -6 PUFAs into longer chain unsaturated derivatives

Source: Layé *et al.*, N-3 polyunsaturated fatty acid and neuroinflammation in aging and Alzheimer's disease. *Nutr. Aging* 3, 33–47 (2015)

1.3.2 Role of ω -6 and ω -3 PUFAs in inflammation

Inflammation, in general, is the host's response of its immune system and is associated with the prognosis of various autoimmune disorders, arthritis, and cancer. However, the manifestation of inflammation is mediated through various chemical mediators including lipid molecules. Lipid mediators are among the biomolecules that are generated by LOXs and COXs pathways, whose nature depends on the types of PUFAs utilized as the substrate. The eicosanoids generated from AA include prostaglandins (PGs), leukotrienes (LTs), and Thromboxane (Tx). PLA2 releases free fatty acids (AA) from membrane phospholipids, which is acted upon by COX-2 and generates series-2 PGs and thromboxanes such as PGE2 and TXA2 while 5-LOX uses AA

as a substrate for generation of 4-series leukotrienes LTA₄, LTB₄, LTC₄, LTD₄ and LTE₄ and hydroperoxyeicosatetraenoic acids (HPETEs) and hydroxyeicosatetraenoic acids (HETEs). When ω -3 PUFAs such as EPA and DHA are available, then LOXs and COXs use these fatty acids and generate series-3 TXs and PGs; and series-5 LTs.

Now it is well established that there is a correlation between the increased ratio of ω -6 to ω -3 PUFAs and emergence of various metabolic disorders as well as life-threatening complications such as autoimmune disorders and cancer [44]. Several other findings also supported such type of relation in which the decrease in ω -6 PUFAs intake and/or increase ω -3 PUFAs intake (decrease ω -6 to ω -3 PUFAs ratio) reduces the severity of these diseases [45]. Based on several studies, the information suggests that during the ancient times the ratio of ω -6 to ω -3 PUFAs in the diet was 1/1 [44]. However, during the course of evolution the proportion of ω -3 PUFAs decreased drastically, a typical western diet contains 20% of ω -6 PUFA (AA) [46,47] while the proportion of ω -3 PUFA (ALA) is less than 1% [44,48,49] having average ratio of 15/1 to 16.7/1 (ω -6 to ω -3 PUFAs ratio) [44]. Observations based on several reports show that excessive high ratio of ω -6 to ω -3 PUFAs as present in western food habit, stimulate prognosis of numerous disorders and diseases such as cancer, cardiovascular diseases, autoimmune disorders, and inflammation [44]. However, a decreased ratio of 4/1 significantly reduced 70% mortality in cardiovascular disease while a 2.5/1 ratio was linked with a decrease in colorectal cancer [44]. Moreover, the ratio of 5/1 revealed beneficial effects on Asthma patients [44]. In converse to this, the ratio of 10/1 showed adverse consequences [44]. In another experiment, *C. elegans* fat 1, a gene which

converts ω -6 into ω -3 PUFAs has lowered the ratio of ω -6 to ω -3 PUFAs in treated mice and has shown a protective effect against pathological angiogenesis in the retina [50].

These studies demonstrate the role of ω -6 and ω -3 PUFAs and the importance of their ratio in the manifestation of various inflammatory disorders. In general, the ω -6 PUFAs are pro-inflammatory in nature while ω -3 PUFAs are anti-inflammatory (Figure 1-9).

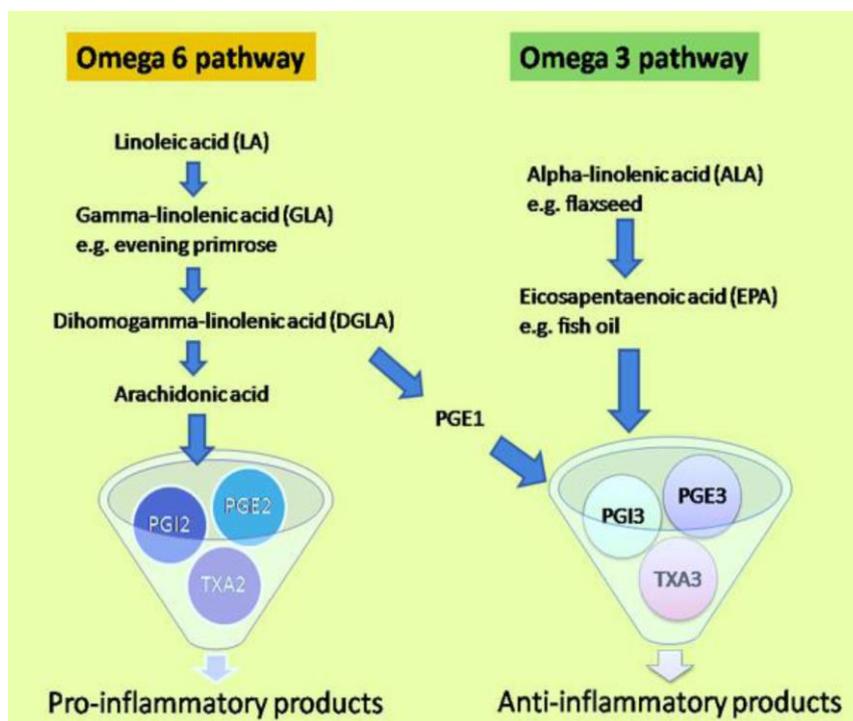


Figure 1-9 : Role of ω -6 and ω -3 PUFAs in Inflammation

The increase in the proportion of ω -3 PUFAs in cell membrane leads to a decrease of pro-inflammatory mediator generated by ω -6 fatty acids in several ways. The first one is a generation of differential metabolites of COX-2 and 5-LOX that depends on the type of substrate available. In ω -6 PUFAs rich diet, AA is dominant substrate among PUFAs available for eicosanoids synthesis that gives rise to the most effective pro-inflammatory mediators. On the other hand, intake of ω -3 PUFAs replaces

AA in the plasma membrane and thus decreases the availability of AA for eicosanoid biosynthesis. The lipid mediators generated by ω -3 PUFAs are less potent for inducing inflammation than the lipid mediators generated by AA [51]. One of the best examples is LTB₄- ω -6 PUFA based metabolite and LTB₅- ω -3 PUFA based metabolite, both generated by 5-LOX. Both metabolites are chemoattractant to neutrophils at the inflammatory site; however, LTB₅ attracts neutrophils with 10 times less efficiency than LTB₄. Next is antagonistic nature of ω -3 PUFAs based lipid mediators. In this scenario, apart from the generation of differential metabolites, the metabolites of ω -3 PUFAs bind to same receptors and thus act as antagonists for AA based lipid mediators. Moreover, COX-2 and 5-LOX generate E-series resolvins by using EPA as a substrate, which act as anti-inflammatory molecules. Therefore, the ratio of ω -3 fatty acids to ω -6 in the body is very important and sufficiently high ratio in the diet decreases the production of several pro-inflammatory mediators and supports resolution phase of inflammation thereby helping the body to maintain homeostasis (Figure 1-10).

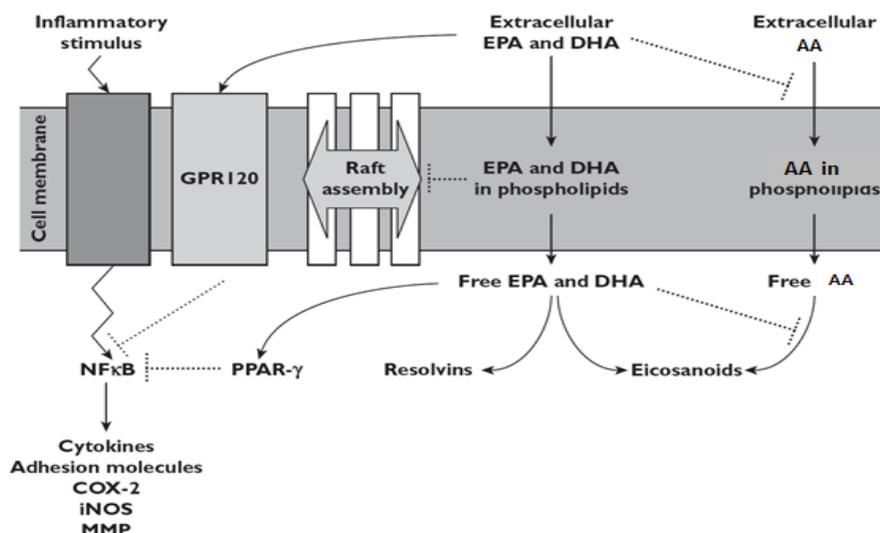


Figure 1-10: Summary of the anti-inflammatory actions of marine n-3 polyunsaturated fatty acids.

Source: Calder et al., Omega-3 polyunsaturated fatty acids and inflammatory processes: Nutrition or pharmacology? Br. J. Clin. Pharmacol. 75, n/a-n/a (2012)

1.4 EICOSANOIDS

1.4.1 Introduction

Eicosanoids term is generally used for 20 carbon fatty acids and their metabolites, which are very short-lived but active lipid mediators. These metabolites act mostly in a paracrine manner. In the early 1930s, Kurzrok and Lieb reported that human uterus either strongly contracted or relaxed in the presence of human seminal fluid. Von Euler and Goldblatt independently found out that lipid fraction of ram seminal vesicular gland contained this activity. This active fatty acid fraction was named as “**prostaglandin**” which later opened a sea of signaling molecules associated with countless significant signaling pathways. PGE₁ and PGF_{1 α} are first two prostaglandins isolated in the form of the crystal structure. The nomenclature is based on the backbone of 20 C acid in which C₈ and C₁₂ form a 5 C member ring also called **prostanoid acid**. E-series and F-series prostaglandins have keto and hydroxyl group, respectively, at C₉ position, while 1, 2 and 3 represent a number of double bonds present and α represent stereochemistry of hydroxyl group.

1.4.2 Types of Eicosanoids

Although prostaglandins were discovered first but now it is known that essential fatty acids are precursors for generation of eicosanoids. Eicosanoids include prostaglandins, prostacyclins, thromboxanes, leukotrienes and other oxygenated metabolites produced mainly through three enzymes: Cyclooxygenases (COX), Lipoxygenases (LOX) and Cyt 450 (epoxygenase). ω -6 (dihomo- γ - linolenic acid and AA)

and ω -3 PUFAs (EPA and DHA) are the precursors for eicosanoids biosynthesis. The non-enzymatic free radical peroxidation of PUFAs leads to the generation of prostaglandin-like molecules called **isoprostanes**. In plants, jasmonates generated from ALA are analogous to eicosanoids generated from AA.

Biosynthesis of eicosanoids starts as soon as the free fatty acids (FFA) are available in the cytoplasm. PLA2 releases FFA from cell membrane phospholipids in response to various physiological factors such as hormones, cytokines or tissue injuries. Cyclooxygenase pathways produce **prostanoids** (prostacyclins, thromboxanes, and prostaglandins) while lipoxygenase pathways produce leukotrienes, lipoxins, and hydroperoxyeicoastetraenoic acids (HPETEs) [52].

1.4.3 Cyclooxygenases (COX)

Cyclooxygenases (EC 1.14.99.1) are enzymes that oxygenate free PUFAs available in cytoplasm into prostanoids. They are also called as prostaglandin endoperoxide H synthases. COX includes two different forms-cyclooxygenase-1 (COX-1) which are generally constitutive and cyclooxygenase-2 (COX-2), an inducible form of COX. Both, COX-1 and COX-2 are very similar in structure and share 60% homology but are coded by two different genes.

1.5 LIPOXYGENASES

1.5.1 Introduction

Lipoxygenases (EC 1. 13. 11. 12); are members of a class of dioxygenases (non-heme iron-containing) which catalyze the addition of molecular oxygen to fatty acids containing at least one cis, cis-1, 4-pentadiene system and give rise to unsaturated fatty acid hydroperoxides. The mechanism of dioxygenation of fatty acids catalyzed by LOXs involves three main steps (Figure 1-11). First, abstraction of a hydrogen atom from the double allylic methylene carbon atom (the first and rate-limiting step). Second, conjugation of double bonds followed by rearrangement of the radical electron, and third, addition of molecular oxygen (this occurs at a diffusion-controlled rate under ambient O₂ concentrations) [53].

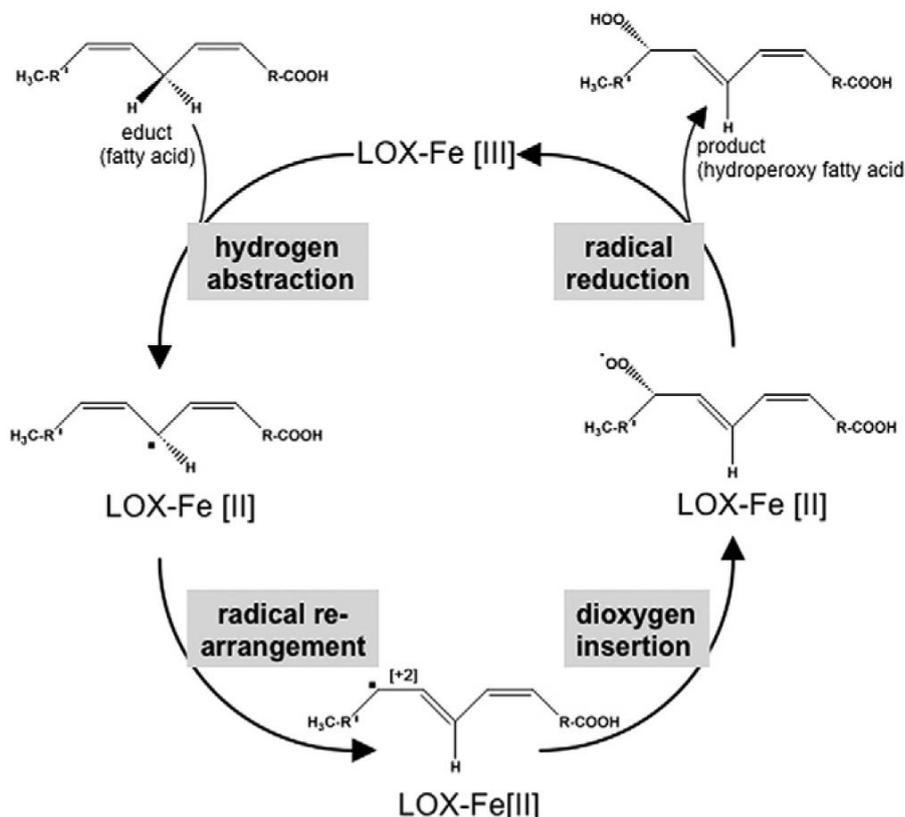


Figure 1-11: Mechanism of Lipoxygenase reaction

Source: Ivanov *et al.*, Molecular enzymology of lipoxygenases. *Arch. Biochem. Biophys.* **503**, 161–174 (2010)

Structure

The three-dimensional structure of soybean LOX-1 has been determined. It is a single polypeptide chain enzyme having two domains (Figure 1-12). The N-terminal domain contains 146 amino acid residues having β -barrel and called domain I while C-terminal domain contains 693 amino acid residues having a helix and called domain II [54]. The active site is present in the center of domain II and contains iron which is connected with 4 conserved Histidines and one Isoleucine [54]. Molecular oxygen and substrates reached to active site through two different cavities: cavity I and cavity II. Molecular oxygen reaches at the active site through cavity I while substrate such as AA

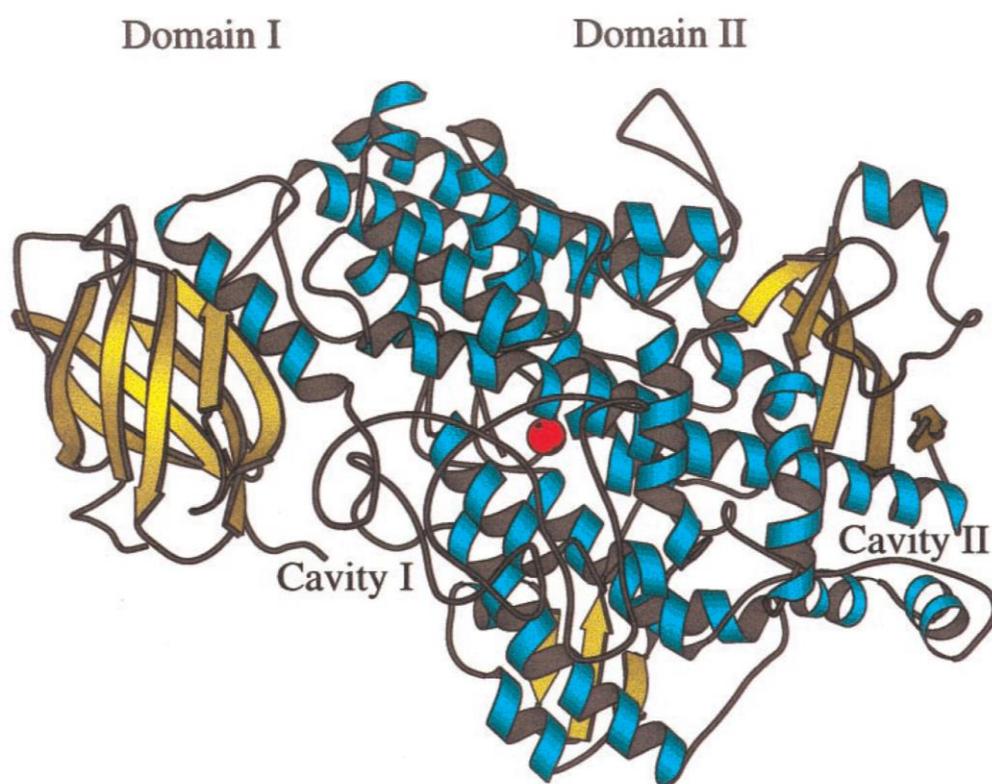


Figure 1-12: 3D structure of *Glycine max* (Soybean) lipoxygenases

Source: Ivanov *et al.*, Molecular enzymology of lipoxygenases. *Arch. Biochem. Biophys.* **503**, 161–174 (2010)

and other larger fatty acids reach through cavity II (Figure 1-13) [53]. Mammalian LOXs are lesser smaller in molecular mass (75-80 kDa) in comparison to plant LOXs (94-104 kDa) because it lacks domain I (N-terminal domain) as present in LOX-1 and other related plants LOXs [54]. The crystal structure of several mammal and plant LOXs available now, along with X-ray data of human 12-LOX. Most of the LOXs composed of single polypeptide chain like soybean LOX-1. However, LOXs in lower organisms may present in the form of fusion proteins where LOX domain attached to a different catalytic domain [53,55].

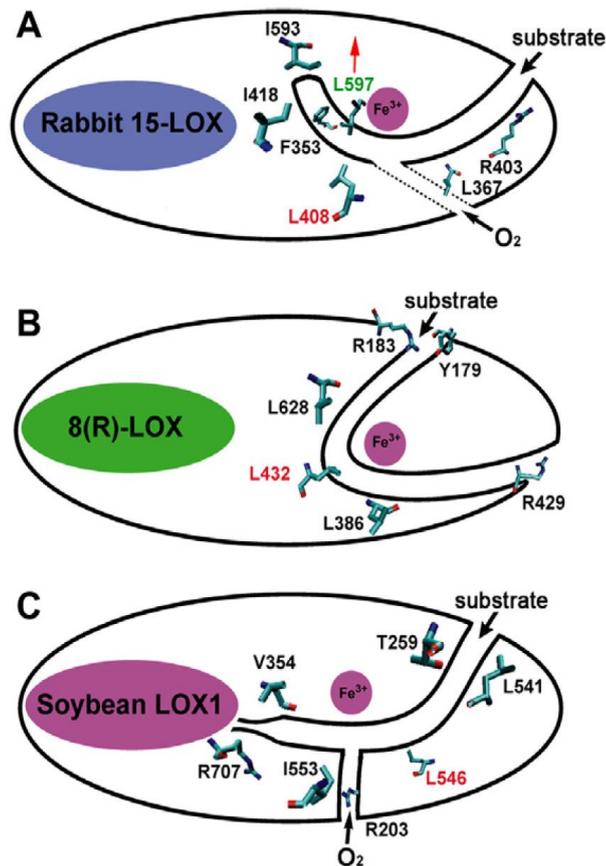


Figure 1-13: Substrate binding site in lipoxygenases

Source: Ivanov, I. *et al.* Molecular enzymology of lipoxygenases. *Arch. Biochem. Biophys.* **503**, 161–174 (2010)

1.5.2 Distribution and Classification of LOXs

LOXs are broadly distributed in mammals [56,57], aquatic organisms [58] and plant [59,60]. Recently, various prokaryotes also reported to have different LOXs isoforms [61–63]. LOXs sequences are found in eukaryotes and prokaryotes while not reported in archaea. In conventional nomenclature, animal LOXs are classified into five different types. These are 5-LOX, 8-LOX, 11-LOX, 12-LOX and 15-LOX [53]. Although in 1947, Theorell *et al*, [64] crystallized the lipoxygenase the progress was limited until 1974 when Axelrod and coworkers first separated and purified different isoforms of lipoxygenase from soybean (*Glycin max*) and further confirmed in 1988 that soybean cotyledons contain three isozymes (LOX-1, 2 and 3) [65,66]. All these are water soluble having 5.68, 6.25 and 6.15 isoelectric values, respectively. All LOXs contain one atom of non-heme iron/protein molecule. LOX-1, 2 and 3 are composed of 838, 865 and 859 amino acids having a molecular weight of 94, 97 and 96 kDa, respectively [67,68]. It also shows different pH optima, LOX-1 has optimum activity at pH 9.0 while LOX-2 and LOX-3 have around pH 6.5 and pH 7.0, respectively [69].

LOXs regiospecificity changed by surrounding pH and oxygen concentration. Soybean LOX-1 (15-LOX) catalyzes linoleate into 9-(S)-HPODE (25%) and 13-(S)-HPODE (75%) at pH 6.0 while at pH 9.0 it oxidizes linoleate exclusively into 13-(S)-HPODE [70]. 9-(S)-HPODE is formed from linoleic acid (non-dissociated carboxylic acid form) because substrate in this form can enter the active site of LOX in any orientation, however, carboxylate ion (linoleate) can be recognized only from $-\text{CH}_3$ end [70]. In normal condition, soybean LOX-1 oxidizes linoleate into 95% 13-(S)-HPODE. However, it loses its regiospecificity in low oxygen concentration and oxidizes linoleate into an equal

amount of 9- and 13-(S)-HPODE [71]. LOX-2 and LOX-3 oxidize linoleate into an equal amount of 9-(S)-HPODE and 13-(S)-HPODE product [69].

1.5.3 Role of Lipoxygenases in Plants and animals

LOXs are broadly expressed in animal and plant systems and initiate the production of signaling molecules. LOX pathways in plants and animals differ because of availability of substrate. In plants, linoleate and α -linolenate are the most abundant substrates while lacking arachidonic acid and eicosapentaenoic acid. However, in animals, the main fatty acids available as substrates are arachidonic acid and eicosapentaenoic acid [72]. Generally, LOXs prefer free PUFAs as substrates. However, some LOXs also act on esterified fatty acids *in vivo* suggesting a direct role of membrane lipids in the synthesis of oxylipins [73–75]. In the plant, the LOXs hydroperoxy metabolites of LA and ALA can be further metabolized by at least six different enzymes into different compounds (Figure 1-14).

Plant LOXs are generally present in seeds [69], have various functions such as lipid mobilization [73] and storage of proteins in vegetative plants [76]. It also plays vital

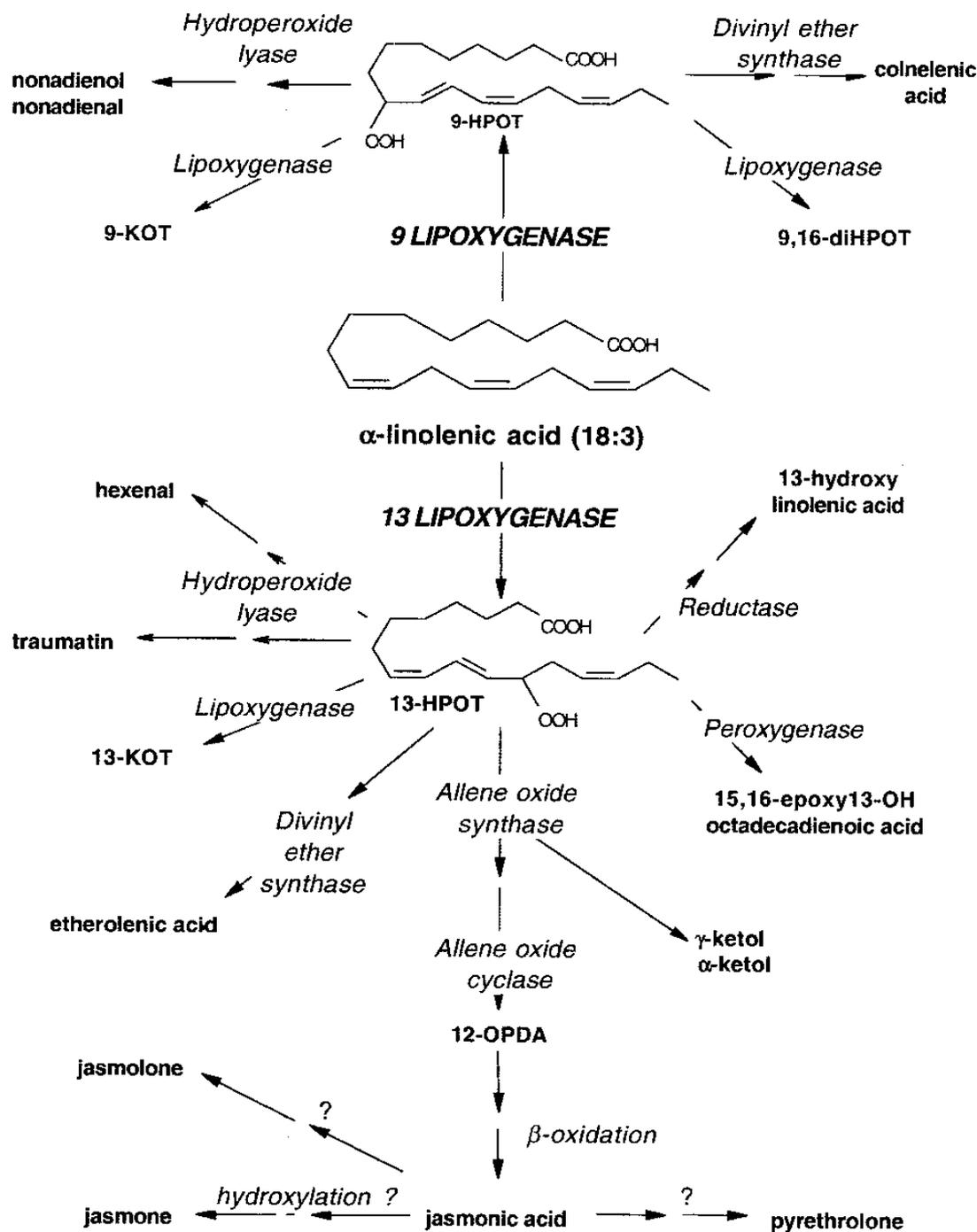


Figure 1-14: The dioxygenation of ALA by lipoxygenases in Plants

Source: Porta, H. Plant Lipoxygenases. Physiological and Molecular Features. *Plant Physiol.* **130**, 15–21 (2002)

roles during several developmental processes [69]. The expression of LOXs genes are associated with various biotic and abiotic factors such as pathogen attack [77], abscisic acid [77], jasmonates [78], deficiency of water [79], wound [79], drought, temperature [76].

In vegetative plants such as potato, LOXs are associated with tuber growth and development, most likely by oxylipin synthesis[80]. In legume plants, the presence of LOX mRNA and proteins is associated with the development of nodule[79].The presence of LOX activity and its regulation by ethylene during fruit ripening also advocates LOX defense role. The C₆ aldehydes of LOX metabolites also give aroma and flavor to tomato plants [81]. Plant tissues also synthesize **vegetative storage protein (VSP)**- a LOX family protein. There are three VSPs- VSPa (VSP27), VSPb (VSP29) and VSP94 in soybean, which stores amino acids and provides nitrogen and other nutrients if needed [82,83]. Lipoxins provide a defense to the plants from the wound as well as from herbivores [84]. Several studies reported induced expression of LOXs during wounding and herbivore attack in several plants including potatoes [78,85]. **Jasmonic acid (JA)** and **phytodienic acid** levels increase during wounding and herbivores attack where they function as signaling molecules [78,86]. They stimulate the synthesis of molecules such as C₆ volatile alcohols and aldehydes that protect against herbivores attack. These volatile molecules attract natural predators of attacking herbivores [87].

SCOPE OF STUDY

Inflammation is a crucial part of the immune response of a host to an infection or injury in order to sustain cellular homeostasis. Abnormal or uncontrolled inflammation is associated with various disorders mediated by hyperactivation of inflammasome complexes and up-regulation of pro-inflammatory enzymes like iNOS, LOXs, and COXs [88–92]. The inflammatory response generated by eicosanoids is known to be mediated by pro-inflammatory cytokines such as IL-1 β and tumor necrosis factor- α (TNF- α) [93].

A balanced diet is always known to be associated with proper maintenance of health. Imbalanced diet or nutritional deficiency, on the other hand, is associated with prognosis of various disorders and diseases [94]. Several studies also show that many of inflammatory disorders in the modern era are not caused by pathogens or injuries but due to altered lifestyles such as lack of physical activities, high calories food, and expose to toxic compounds in daily life [95]. Obesity, atherosclerosis, neurodegenerative diseases, type 2 diabetes, and asthma are the outcome of these conditions, wherein inflammation is a major component [95]. The impact of fatty acids on inflammation have been well established [96,97]. In several comparative studies, PUFAs have been shown to have several beneficial and protective properties [98] over saturated fatty acids when treated with pathogenic bacteria [98]. It is well established that the two types of PUFAs, ω -6, and ω -3 regulate homeostasis in body but have opposing effects [96,99]. The ω -6 PUFAs mediate the generation of eicosanoids family of lipid mediators such as prostaglandins, prostacyclin, and thromboxane maintain homeostasis. However, their uncontrolled production shifts the homeostasis towards pathogenesis. Dietary

intake of ω -3 PUFAs, on the other hand, increase the ratio of ALA, EPA, and DHA in the body [100,101], which leads to the generation of less potent pro-inflammatory mediators on one side and on the other side they compete with ω -6 mediated pro-inflammatory mediators for the same receptors [96,100]. Several of these studies demonstrated that beneficial effects of ω -3 PUFAs are mediated in part by their oxygenated metabolites mainly via the LOXs and COXs pathways. However, the downstream signaling pathways mediating these anti-inflammatory effects of ω -3 PUFAs have not been elucidated.

The present study, therefore, is aimed at understanding the signalling pathways involved in the mediation of anti-inflammatory effects of 13-(S)-hydroperoxy octadecatrienoic acid [13-(S)-HPOTrE] and 13-(S)-hydroxyoctadecatrienoic acid [13-(S)-HOTrE], the 15-LOX metabolites of alpha-linolenic acid (ALA), a ω -3 PUFA. As the macrophages actively participate during inflammation and secrete inflammatory mediators, it is a preferable cell type for inflammatory studies. However, established and immortalized cell lines are tools for various researchers working in the area of cell biology, immunology, and biochemistry. Hence RAW 264.7 cells, an immortalized cell line derived from male BALB/c mice, were employed in the present study. Moreover, RAW 264.7 cells are the most preferred for inflammatory studies because their fast growing nature with doubling time of 2-3 days, easy to handle, easy to propagate, expression of complement system factor-C3, high transfection efficiency ratio, and sensitivity to siRNA [102]. Hence, in the present study, the anti-inflammatory effects of 15-LOX metabolites of ALA (13-(S)-HPOTrE and 13-(S)-HOTrE) were elucidated on mouse macrophage cell line, RAW 264.7 cells. As RAW 264.7 cells are immortalized cell line, the primary peritoneal macrophages were also employed in this study. For further

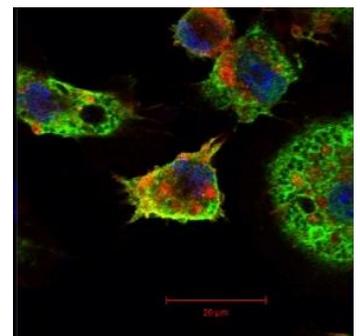
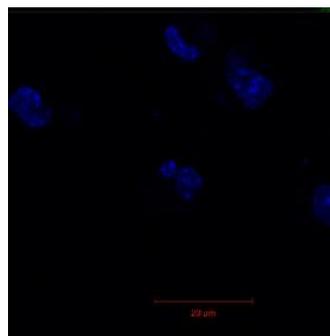
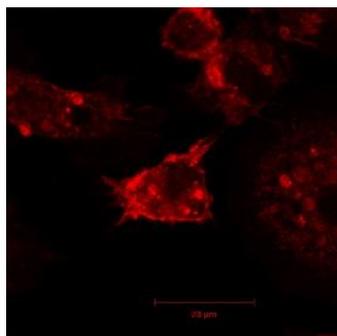
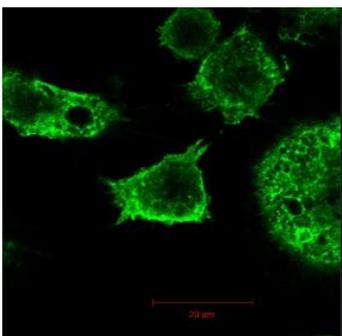
validation of these *in vitro* findings, studies were also carried *in vivo* on BALB/c male mice.

The specific objectives of the present study are:

1. Evaluate the role of ω -6 PUFAs and ω -3 PUFAs in inflammation *in vitro* by employing mouse macrophage cell line, RAW 264.7 as a model system.
2. Generation of 15-Lipoxygenase (15-LOX) metabolites of ω -6 and ω -3 PUFAs and their characterization.
3. Study the effects of 15- LOX metabolites of ALA (13-(S)-HPOTrE and 13-(S)-HOTrE) on inflammation *in vitro* and *in vivo* and elucidate the signalling pathways involved.

Chapter 2

EVALUATION OF THE ROLE OF OMEGA-6 AND OMEGA-3 PUFAS IN INFLAMMATION *IN VITRO* BY EMPLOYING MOUSE MACROPHAGE CELL LINE, RAW 264.7 AS A MODEL SYSTEM



2.1 INTRODUCTION

Inflammation is the host's immune response towards any cue like tissue damage, injury, infection, artificial agents, or immune disorders and it is associated with the prognosis of various autoimmune disorders, arthritis, and cancer. The state of inflammation depends on the severity of infection and pathogenesis. Neutrophils and tissue macrophages are among the initial mediators that migrate at the site of infection during initial inflammatory responses and generate a state of inflammation called acute inflammation. These inflammatory mediators are accompanied by infiltration of leukocytes, monocytes, and other phagocytic cells, which actively participate in the removal of pathogens and strengthen wound healing process. When acute inflammatory response fails to eliminate pathogen and infection still persists, then macrophages and other immune cells get activated and release cytokines such as $\text{INF-}\gamma$ and $\text{TNF-}\alpha$, that initiate the development of chronic inflammation. These activated macrophages produce many hydrolytic enzymes, ROS and NOS that kill microorganisms and help in removing pathogens.

It is well established that the two types of PUFAs, ω -6, and ω -3 regulate homeostasis in body but have opposing effects [96,99]. The ω -6 PUFAs mediate the generation of eicosanoids family of lipid mediators such as prostaglandins, prostacyclins, and thromboxanes, and shift the homeostasis towards pathogenesis. On the other hand, intake of ω -3 PUFAs increases the ratio of ALA, EPA, and DHA in the body [100,101] as a result less potent pro-inflammatory mediators are generated [96,100]. It is reported that beneficial effects of ω -3 PUFAs are mediated via the LOXs and COXs pathways

mainly by their oxygenated metabolites. However, the downstream signalling pathways mediating these anti-inflammatory effects of ω -3 PUFAs have not been elucidated.

In the present study, the role of ω -6 and ω -3 PUFAs in inflammation was studied on mouse macrophages cell line, RAW 264.7 cells. Cytotoxicity of ω -6 and ω -3 PUFAs was determined by MTT (3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyl tetrazolium bromide) assay. A low dose of endotoxin (LPS) was used to stimulate RAW 264.7 cells for generation of inflammatory state inside cells, and then pro-inflammatory markers and cytokines were analyzed.

2.2 MATERIALS AND METHODS

2.2.1 Chemicals and Reagents

Culture medium DMEM, penicillin, streptomycin, PBS, Trypsin-EDTA and fetal bovine serum (FBS) were purchased from Gibco. MTT, DCFH-DA (2'-7'-Dichlorodihydrofluorescein diacetate), LPS (lipopolysaccharide from *E. coli*, 0127:B8), and Griess reagent were purchased from Sigma-Aldrich, USA. Enzyme immunoassay kit for IL-1 β was purchased from R&D system, Inc. (MN, USA). AA, LA, ALA, and DHA were procured from Nu-Chek-Prep (MN, USA).

2.2.2 Cell culture and Treatments

The mouse macrophage cell line, RAW 264.7 cell was obtained from NCCS (Pune, India). It was grown and maintained in DMEM supplemented with 10% heat-inactivated FBS, 100 IU/ml penicillin, and 100 μ g/ml streptomycin in a humidified atmosphere with 5% CO₂ at 37°C. Subculturing of cells was done twice a week. Fresh culture medium was used before each treatment. For MTT assay, cells were pre-incubated with different concentrations (1, 10, 100 and 200 μ M) of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) for different time points (24 h, and 36 h). For apoptosis study and IL-1 β measurement, RAW 264.7 cells were pre-incubated with 100 μ M of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) for 3 h then primed with LPS (100 ng/ml) for 24 h. For IL-1 β measurements, RAW 264.7 cells were incubated with 1mM ATP for 30 min prior to end time point. While, for ROS measurement, RAW 264.7 cells were pre-incubated with 100 μ M of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) for 3 h then primed with LPS (100 ng/ml) 16 h.

2.2.3 Cytotoxicity Assay

Cytotoxicity of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) was assayed by MTT assay. To perform this assay, RAW 264.7 cells were seeded in 96 well plates at a density of 5×10^4 cells/well then treated with ω -6 PUFAs (AA, and LA), ω -3 PUFAs (ALA and DHA) at various concentrations (1, 10, 100 and 200 μ M) for different time points (24 h, and 36 h). Cell viability was measured colorimetrically by MTT assay as described by Mossman [103].

2.2.4 Nitrite Estimation

RAW 264.7 cells were seeded in 6 well plates for 12 h then pre-incubated with 100 μ M of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) for 3 h then stimulated with or without LPS (100 ng/ml) for the next 24 h. At the end of the time point, stable nitrite level in the culture supernatant was measured by Griess Reagent. For this, 50 μ l of cell culture medium was mixed with 50 μ l of Griess reagent and incubated at room temperature for 10 min in the dark. Then absorbance was measured at 540 nm using multi-mode ELISA reader (BioTek, SynergyMx). Nitrite level in samples was determined by using the standard curve of sodium nitrite. Culture medium was taken as blank for all experiments.

2.2.5 Estimation of IL-1 β

RAW 264.7 cells were seeded in 6 well plates for 12 h then pre-incubated with 100 μ M of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA and DHA) for 3 h then stimulated with or without LPS (100 ng/ml) for the next 24 h. Then cells were incubated with 1 mM ATP for 30 min prior to end time point. At the end of the time point, the culture supernatant was collected. Levels of IL-1 β (R&D system, Inc. MN, USA) in culture medium were measured by ELISA kit according to manufacturer's protocol. Their levels

in culture medium were determined by using standard curves of IL-1 β standard provided along with the kit.

2.2.6 Measurement of Reactive Oxygen Species (ROS)

RAW 264.7 cells were seeded in 6 well plates at a density of 2×10^5 cells/well then pre-incubated with 100 μ M of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) for 3 h. Then these cells were stimulated with or without LPS (1 μ g/ml) for next 16 h. After this, cells from each well were harvested and washed twice with PBS and further incubated with 10 mM of DCFH-DA for 30 min in dark at 37°C and then further washed twice with PBS. 10,000 cells per sample were taken for analysis. The quantification was performed on a Flow Cytometer and data analysis was done by Cell Quest software (FACS Calibur, Becton Dickinson, CA, USA) with excitation of DCF at λ 488 nm and emission at λ 525 nm.

2.2.7 Analysis of Apoptosis by FACS

RAW 264.7 cells were seeded in 6 well cultures plate. When cells were 60 % confluent, pre-incubated with 100 μ M of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA and DHA) and/or doxorubicin (10 μ M) for 3 h. Then stimulated with or without LPS (100 ng/ml) for 24 h. Staining of cells was done by Propidium iodide. Samples were run on Flow Cytometer (BD, LSR Fortessa, CA, USA) and data analyses were done on BD FACSDiva™ software.

2.3 STATISTICAL ANALYSES

All the experiments were performed in triplicates and the values represented as mean \pm SD. Data were correlated, analyzed and p-values were obtained using student's t-test. The p-value < 0.05 was considered as statistically significant.

2.4 RESULTS

2.4.1 ω -6 and ω -3 PUFAs show less cytotoxic effect on RAW 264.7 cells.

The cytotoxic effects of ω -6 and ω -3 PUFAs were evaluated by MTT assay on RAW 264.7 cells. There was no significant cytotoxicity of either ω -6 or ω -3 PUFAs at 24 h. Therefore, the percentage of cell death was calculated for 200 μ M PUFAs at 36 h. As shown in the

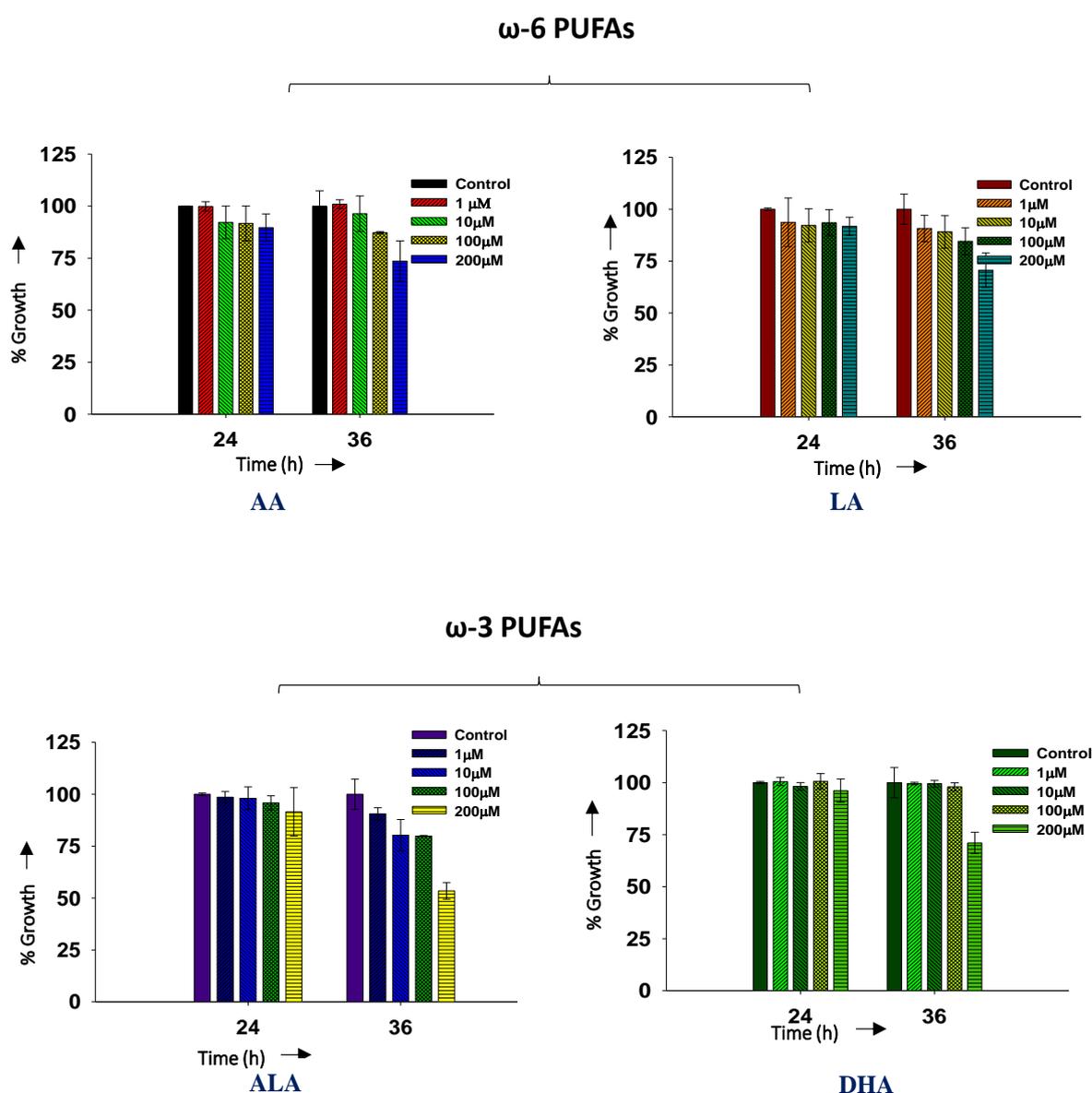


Figure 2-1: Effects of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) on viability of mouse macrophage cell line, RAW 264.7 cells. In MTT assay, cells were pre-incubated with different concentrations (1, 10, 100 and 200 μ M) of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) for different time points (24 h and 36 h). The percent cell growth following treatment was calculated, in comparison with untreated control cells.

figure 2-1, RAW 264.7 cells treated with ALA and DHA (ω -3 PUFAs) showed 46.6% and 29% cell death, respectively. However, AA and LA (ω -6 PUFAs) showed only 26.4% and 29.4% cell death, respectively; at 36 h. Treatment of these PUFAs decreased the growth of the cells in a dose and time-dependent manners. The cell death was less than 50% in RAW 264.7 cells treated with ω -6 and ω -3 PUFAs, therefore, IC50 values of any of PUFAs could not be calculated. Based on these results, further experiments were carried out at 100 μ M concentrations of ω -6 and ω -3 PUFAs.

2.4.2 Effects of ω -6 and ω -3 PUFAs on Nitrite level in culture medium in LPS induced RAW 264.7 Cells.

Next, it was aimed to evaluate the effects of ω -6 and ω -3 PUFAs on LPS induced inflammation by examining effects on pro-inflammatory chemical mediator: NO- a second messenger. For this, RAW 264.7 cells were first treated with or without PUFAs and challenged with LPS (100 ng/ml) as described in the methods. There was a significant elevation in NO production in RAW 264.7 cells when stimulated with LPS and this elevated level was reduced by 13% and 12.45% in the presence of ALA and DHA, respectively (Figure 2-2). However, there was no significant changes in NO level in AA and LA treated and LPS stimulated macrophages. The significant reduction in NO production by ALA and DHA suggests their strong anti-inflammatory effects on LPS stimulated macrophages.

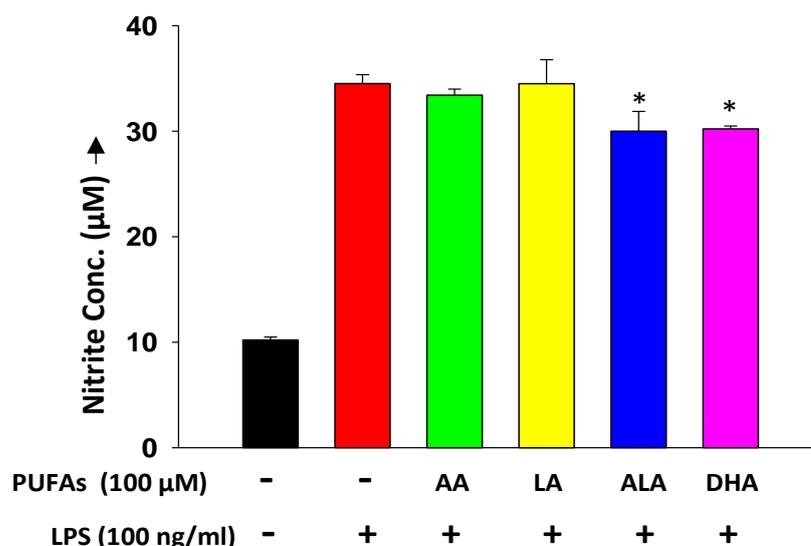


Figure 2-2: Effects of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) on NO generation in RAW 264.7 cells. Nitrite level measured in culture medium of RAW 264.7 cells pre-incubated with ω -6 PUFAs (100 μ M) and ω -3 PUFAs (100 μ M) for 3 h and further stimulated with or without LPS (100 ng/ml) for the next 24 h. ω -3 PUFAs reduced NO level more efficiently compared to ω -6 PUFAs. The values represent mean \pm SD of three independent experiments. * indicates significance ($p < 0.05$) compared to LPS alone treated cells.

2.4.3 ω -6 and ω -3 PUFAs reduce Reactive Oxygen Species (ROS) generation in LPS induced RAW 264.7 cells.

Next, it was aimed to evaluate the effects of ω -6 and ω -3 PUFAs on LPS induced inflammation by examining effects on pro-inflammatory chemical mediator: ROS- an oxidative stress marker. For this, RAW 264.7 cells were first treated with or without PUFAs and challenged with LPS (100 ng/ml) as described in the methods. There was a significant elevation in ROS production in RAW 264.7 cells, when stimulated with LPS and this elevated level was reduced by 73.1% and 88.2% in the presence of ALA and DHA, respectively (Figure 2-3). However, AA and LA (ω -6 PUFAs) showed 61.5% and

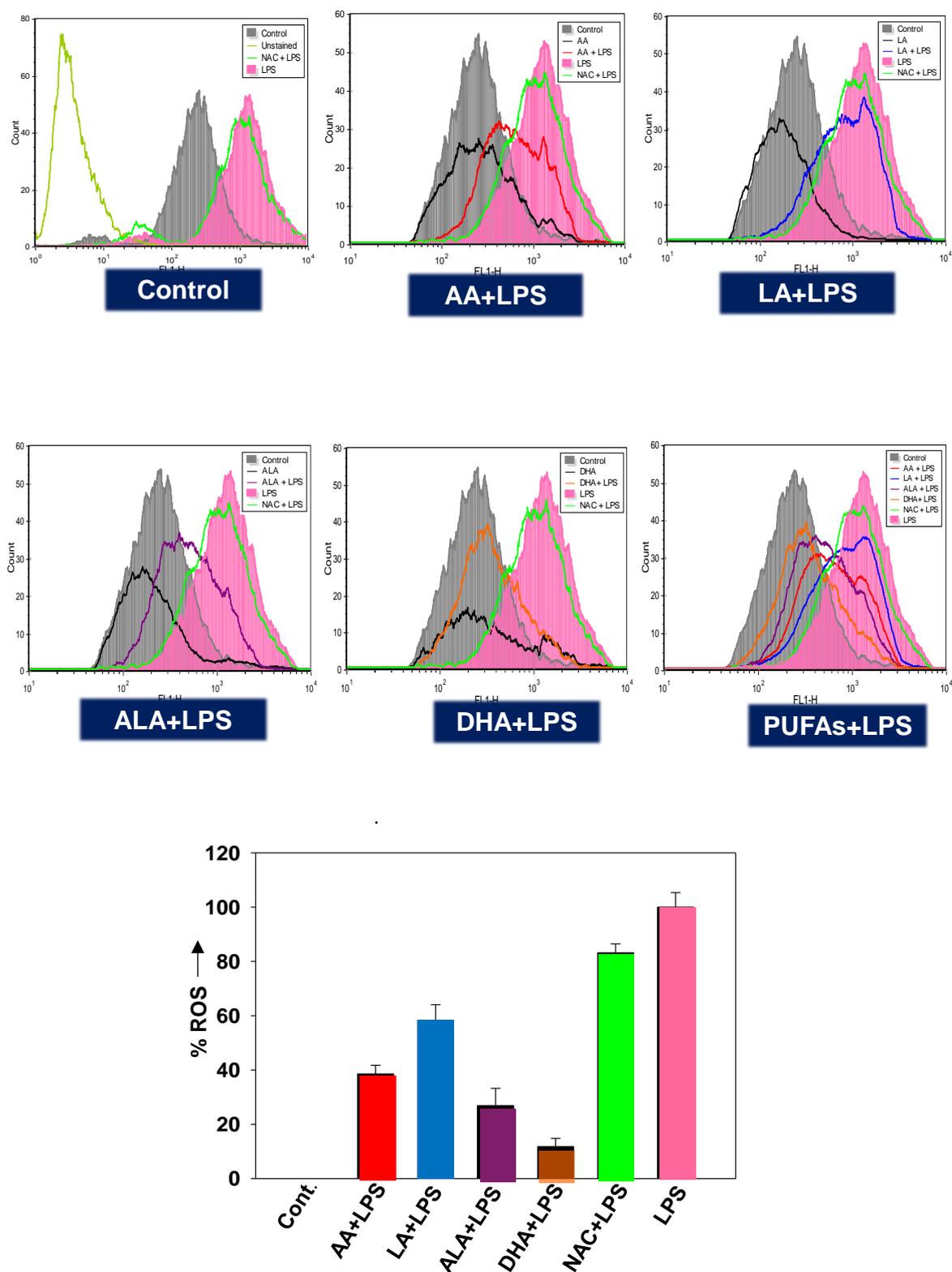


Figure 2-3: Effects of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) on ROS generation in RAW 264.7 cells. Intracellular ROS level measured in cells following pre-incubation with ω -6 PUFAs (100 μ M) and ω -3 PUFAs (100 μ M) for 3 h then stimulated with LPS for 16 h. ω -3 PUFAs reduced ROS level more efficiently compared to ω -6 PUFAs. N-Acetyl Cysteine (NAC, 5mM), a ROS inhibitor was used as positive control.

41.6% reduction in ROS generated by LPS stimulation. NAC- an anti-oxidant compound also decreased 16.8% ROS generated by LPS. The result showed that ω -3 PUFAs reduced LPS induced ROS generated in RAW 264.7 cells more efficiently than ω -6 PUFAs and even NAC- an anti-oxidant molecule.

2.4.4 ω -6 and ω -3 PUFAs show a decrease in IL-1 β level in culture medium in LPS induced RAW 264.7 Cells.

The identification of IL-1 β is registered in the 1980s [104] but its existence noticed in the form of Pus much before the advent of the microscope [27,105]. Its significance can be analyzed by the fact that before the 1980s, it was studied with different names such as haematopoietin 1, leukocytes endogenous mediators, catabolin, endogenous pyrogens depending on diverse functions noticed [105]. Now, it is well established that most potent molecule of innate immune system-IL-1 β , is also pro-inflammatory in nature. The above studies indicated the anti-inflammatory nature of ω -3 PUFAs. Therefore, it was aimed to evaluate the effects of ω -6 and ω -3 PUFAs on the level of pro-inflammatory cytokine-IL-1 β . The level of IL-1 β in the culture medium of RAW 264.7 cells were measured by ELISA kit. There was an increase in IL-1 β level in RAW 264.7 cells challenged with LPS. However, macrophages pre-treated with ω -6 and ω -3 PUFAs and challenged with LPS showed decreased IL-1 β level. The ω -3 PUFAs, ALA and DHA significantly decreased IL-1 β level by 52.7% and 54% respectively, while ω -6 PUFAs, AA, and LA decreased IL-1 β by 50% and 41.7%, respectively in LPS induced RAW 264.7 cells (Figure 2-4).

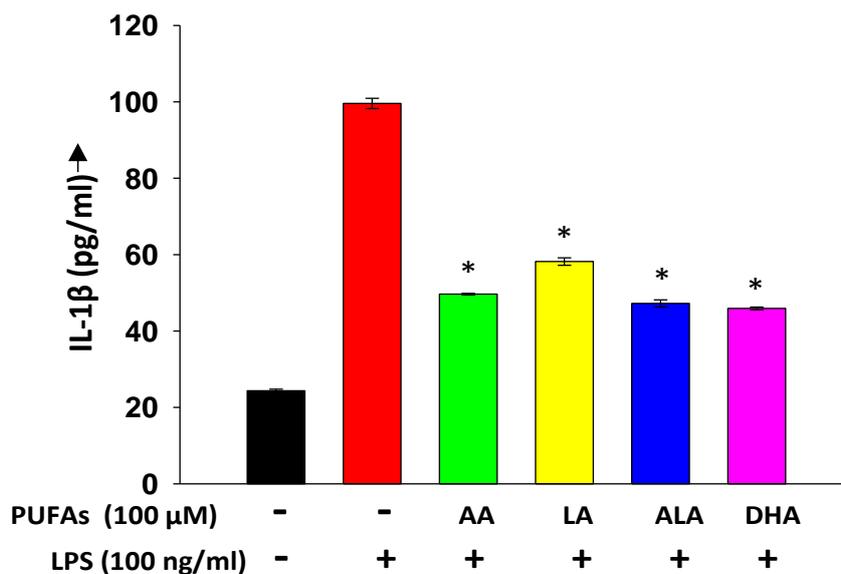


Figure 2-4: Effects of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) on IL-1 β level in RAW 264.7 cells. Cells were pre-incubated with 100 μ M of ω -6 PUFAs and ω -3 PUFAs for 3 h then stimulated with or without LPS (100 ng/ml) for the next 24 h. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated cells.

2.4.5 ω -3 PUFAs show increased apoptosis than ω -6 PUFAs in LPS induced RAW 264.7 Cells.

Apoptosis enhances anti-inflammatory effects and it plays a vital role in the resolution of inflammation [106]. Moreover, LPS and activated inflammasomes also induce autophagy in mesothelial cells [107]. Since ω -3 PUFAs showed anti-inflammatory effects, we examined whether they affected induction of apoptosis in LPS stimulated RAW 264.7 cells. FACS analysis of RAW 264.7 cells stimulated with LPS showed increased apoptosis. However, macrophages pre-treated with PUFAs and challenged with LPS showed a further increase in apoptosis. Macrophages pre-treated with ALA and DHA and challenged with LPS showed 47% and 57.6% increase in apoptosis while AA and LA showed 32.2% and 35.2% increase in apoptosis, respectively (Figure 2-5).

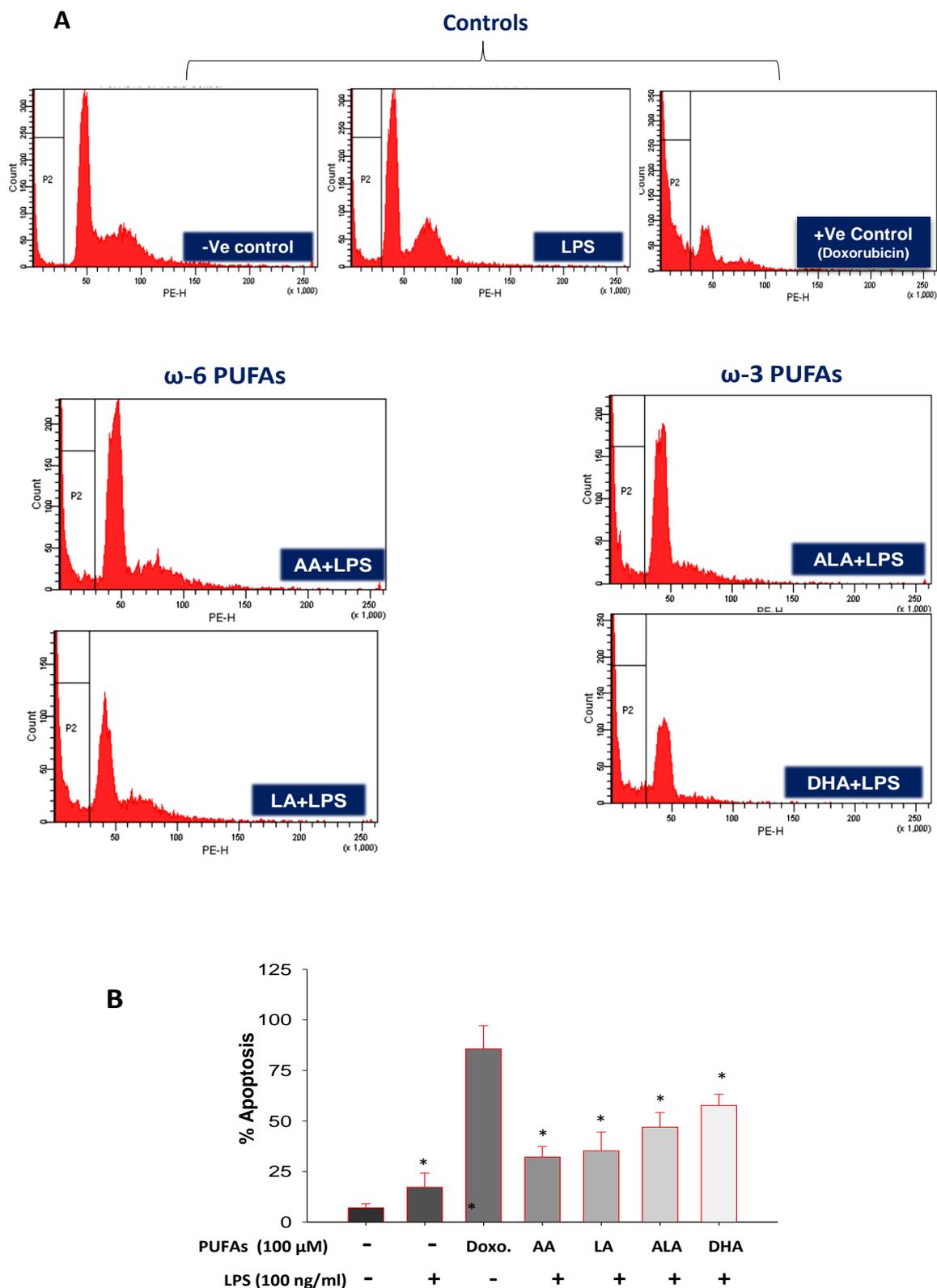


Figure 2-5: Flow cytometric analysis showing the effects of ω -6 PUFAs (AA, and LA) and ω -3 PUFAs (ALA, and DHA) on apoptosis in RAW 264.7 cells challenged with LPS. **A)** Apoptosis was assayed by Propidium iodide at 24 h, by flow cytometric analysis. The dead cells were gated and analysis was performed only on live cells. **B)** Bar graph representation of above studied apoptosis. *Indicates significance ($p < 0.05$) compared to LPS treated cells.

2.5 DISCUSSION

According to Merriam-Webster's Learner's Dictionary, "food" is defined as "Material consisting essentially of protein, carbohydrate, and fat used in the body of an organism to sustain growth, repair, and vital processes and to furnish energy" [108]. In addition to this, types of food (diet) is also associated with health, prognosis of various disorders and diseases [94]. Several studies also show that all the inflammatory diseases are not caused by foreign pathogens or injuries but seems to be linked with situations such as less or lack of physical activities, high calories food, and expose to toxic compounds in daily life [95]. Obesity, atherosclerosis, neurodegenerative diseases, type 2 diabetes, and asthma are the outcome of these conditions [95]. These states are also called **para-inflammation** or **chronic low-grade inflammation**. If these conditions persist for a longer time then contribute to further disease progression.

The dietary intake of PUFAs decides the ratio of ω -6 and ω -3 PUFAs in the body. Increased ratio of ω -6 to ω -3 PUFAs is hypothesized to elevate pro-inflammatory eicosanoid production and thus the onset of inflammatory diseases. A sufficiently high intake of ω -3 PUFAs, on the other hand, has shown to offer protection from inflammatory diseases by decreasing the production of pro-inflammatory eicosanoids, cytokines, ROS and RNS [100,101].

In the present study, mouse macrophage cell line, RAW 264.7 was used as *in vitro* model system to elucidate ω -6 and ω -3 PUFAs role in inflammation. The findings of the present study supports above thought wherein, FACS analysis of RAW 264.7 cells stimulated with LPS showed increased intracellular ROS level, while the macrophages

pre-treated with ω -6 and ω -3 PUFAs and stimulated with LPS showed a significant decrease in generation of ROS. ω -3 PUFAs, however, decreased the intracellular ROS level more efficiently as compared to ω -6 PUFAs. In MTT cytotoxicity assay, ω -6 PUFAs (AA, and LA) showed very less cytotoxic effects as compared to ω -3 PUFAs (ALA, and DHA) in RAW 264.7 cells. On the other hand, both, ω -6 and ω -3 PUFAs decreased IL-1 β level significantly.

NO is a signalling molecule and generally considered as a pro-inflammatory marker [46]. It also regulates growth and inhibition of cell type which are associated with inflammatory responses such as macrophages, immune cells and mast cells [109]. In the present study, NO level in culture medium was measured by Griess reagent. The results showed that LPS increase the level of NO generation in RAW 264.7 cells while macrophages pre-treated with ω -3 PUFAs showed decreased NO level. Nevertheless, among both ω -6 and ω -3 PUFAs, ω -3 PUFAs appear to be relatively more effective.

The apoptosis actively participates in the removal of neutrophils and other inflammatory mediators thus enhance strength during resolution phase. RAW 264.7 cells challenged with LPS showed increased apoptosis, which was further increased in macrophages pre-treated with ω -6 and ω -3 PUFAs and challenged with LPS. However, apoptosis induced by ω -3 PUFAs was more prominent than ω -6 PUFAs. Hence, the involvement of ω -3 PUFAs (ALA, and DHA) to increase apoptosis in comparison to ω -6 confirms its importance during the resolution of inflammation.

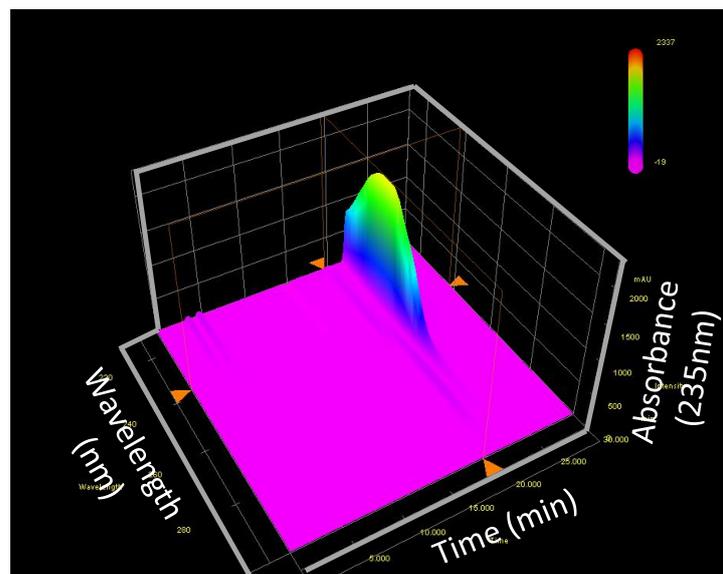
ALA is the precursor for EPA and DHA and the anti-inflammatory properties of ω -3 PUFAs might be mediated through various pathways. The maturation of inflammation mediated through various chemical mediators in which, lipid mediators

play a vital role. Lipid mediators are generated by LOXs and COXs pathways, whose nature depends on the types of PUFAs available. The ω -6 PUFAs generate eicosanoids family, which on excess production shift the homeostasis towards pathogenesis. On the other hand, ω -3 PUFAs gives raise to less potent pro-inflammatory mediators [96]. Also, the presence of EPA and DHA decreases the availability of AA for LOXs and COXs as substrate. As a result, on one side, there is an increase in the EPA and DHA-mediated eicosanoids generation while on the other side, there is a decrease in AA based eicosanoids and lipid mediators. Furthermore, DHA and EPA based eicosanoids and lipid mediators are less potent than AA based analogs [51].

It is also reported that ω -3 PUFAs show anti-inflammatory effects through several mechanisms [51,100], among these, NF- κ B and MAP kinase pathways are two major signalling cascades involved. In NF- κ B signalling pathway, it prevents the phosphorylation and degradation of I κ -B α protein by proteasome complex while in MAP kinase pathways it is mediated through JNK, ERK, p38 and AP-1 [110]. In addition, this effect also mediated by showing anti-oxidant properties by inhibiting the intracellular accumulation of peroxides [111]. Therefore, the reduction in production of NO and ROS by ω -3 PUFAs in LPS primed macrophage might be mediated through any of the above mechanisms, either directly or through their metabolites. In order to understand these mechanisms, further studies were undertaken to evaluate the anti-inflammatory effects of the metabolites of ω -3 PUFAs (Chapter 4). As this involves the pure metabolites of these PUFAs, their generation and characterization was taken up first by employing 15-lipoxygenase (Chapter 3).

Chapter 3

GENERATION OF 15-LIPOXYGENASE (15-LOX) METABOLITES OF OMEGA-6 AND OMEGA-3 PUFAS AND THEIR CHARACTERIZATION



3.1 INTRODUCTION

Lipoxygenases are found in various plants such as peas, green beans, peanuts, mung beans, soybean, mustard, cucumber and in cereals such as rice, oat, rye, corn barley, and wheat [69,112–115]. LOXs are also reported in vegetables such as potato tubers and brinjal [116,117]. However, soybean LOXs are well known and extensively studied for several decades. In soybeans, all the three lipoxygenase isozymes (lipoxygenase-1, 2 and 3) are water-soluble and globular proteins and consist of a single polypeptide of approximate 96 kDa molecular weight [69].

Linseed (*Linum usitatissimum*), also known as flaxseed, is a food and fiber yielding annual plant. The linseed seeds have been used for a long time as a source of food as well as for oil called linseed oil. Linseed is rich in fatty acids and consists 35-40% fatty acids out of which 8-10% saturated fatty acids, 15-20% monounsaturated and more than 70% ALA [118]. LOX activity has also been reported in linseed seeds [119]. In 1970, Zemmerman showed LOXs activity in linseed [120] that was further confirmed by Grosch [121] in 1976 and found that linseed seed LOXs perform catalysis similar to soybean LOX-1. On the other hand, In 1982, Vernoo demonstrated that unlike soybean, linseed seed lack LOX-2 activity [122].

All the plant LOXs studied above have a common feature, i.e., as the seedling develops there is an increase in LOXs activity in initial 50 to 72 h and further followed by a significant decrease. In rice, there was a 20 fold increase in LOXs activity in day three seedling [114]. So far, all the LOX activities in linseed were demonstrated in defatted seeds. In the present study, instead of linseed seed, we demonstrated LOXs activity in linseed seedling and found as a novel source of LOX enzyme and day two seedling

showed maximum enzyme activity. The enzyme was extracted and purified by column chromatography, enzyme activity was measured on oxygraph using Clark's Oxygen electrode and molecular mass determination was done by SDS-PAGE. Further, metabolites of AA, ALA, and LA were generated from two different enzyme sources- Linseed seedling enzymes as well as from soybean LOX (commercially available) and purified on HPLC. Co-chromatography was done to compare metabolites generated from these two different enzyme sources. Then these metabolites were also characterized on LC-MS/MS.

3.2 MATERIALS AND METHODS

3.2.1 Chemicals and Reagents

Column Chromatography matrices and Q Sepharose™ fast flow were purchased from Amersham Pharmacia Biotech, Uppsala, Sweden and G-50 Sephadex was obtained from Sigma chemical company, St. Louis, USA. All the solvents used for HPLC were of HPLC grade and procured from Merck Specialities Pvt. Ltd, Mumbai, India. AA, LA, and ALA were purchased from Nu-Chek Prep, Inc. MN, USA. Soybean Lipoxygenase (cat# L7395) was procured from Sigma, Saint Louis, Missouri, USA

3.2.2 Enzyme source

Dried ripe seeds of Linseed (*Linum usitatissimum*) were surface sterilized using 0.1% sodium hypochlorite for 15 min and subsequently washed in running tap water for 5-6 times. Then linseed seeds were soaked in tap water for overnight and allowed for germination at room temperature. Then seeds were washed rigorously in tap water to remove mucilage, kept for germination at room temperature in a humid environment for 4 days, and further stored in -80 °C for further studies.

3.2.3 Homogenization and $(\text{NH}_4)_2\text{SO}_4$ precipitation of linseed seedling

Germinated linseed seedlings (Day1-4) were homogenized in homogenization buffer (125 mM Tris-Cl buffer, pH 8.0 containing 1mM EDTA, 2 mM Ascorbic acid, and 2 mM Sodium metabisulphite) at 4°C. Then the homogenate was filtered by double-layered cheesecloth and centrifuged at 17000 rpm for 15 min and supernatant was collected. Then $(\text{NH}_4)_2\text{SO}_4$ was added under continuous stirring to the supernatant fraction to give a final concentration of 30% saturation and stirred for one hour at 4°C. The precipitated protein was removed by centrifugation at 17,000 rpm for 15 min at 4°C. The resulting supernatant was brought to 30-40% saturation by further addition of solid $(\text{NH}_4)_2\text{SO}_4$, stirred for one hour at 4°C, and then centrifuged at 17,000 rpm for 15 min at 4°C. Different fractions were obtained by ammonium sulphate fractionation. The homogenization and fractionation process were carried at 0-4°C.

3.2.1 Enzyme Assay

The LOX activity was measured by determining the O_2 consumption with Strathkelvin 782 oxygen system version 3.0, Model 782, Oxygen monitor equipped with Clark's oxygen probe and connected to the computer for data acquisition. The enzyme assay mixture consists of 2 ml enzyme assay buffer, 10 μl substrate (AA-133 μM ; ALA, and LA-266 μM), 25 μl linseed homogenate and double distilled water in a total volume of 3 ml reaction mixture. The reaction was carried out in an airtight chamber, molecular O_2 consumption was recorded and enzyme unit was calculated.

One Enzyme Unit= $\mu\text{mole of O}_2$ consumed/mg protein x min

3.2.2 pH optimization

The LOX activity in linseed seedling was measured by oxygraph at different pHs (pH 6.0 – pH 13.0). For this, Potassium phosphate, Tris-Cl, Sodium bicarbonate and

Potassium chloride buffer systems were used to obtain a wide range of enzyme assay buffers. The homogenates of different day's seedlings (Day1-4) of linseed were used to check enzyme activity at various pH ranges (pH 6.0 – pH 13.0).

3.2.3 Temperature optimization

The LOX activity in linseed seedling was measured by oxygraph compatible to measure enzyme activity at different temperatures. The various temperatures were achieved by attaching oxygraph with water bath fitted with temperature regulator. The enzyme activity in seedling homogenate was assayed at various temperature ranges (5.0-50°C).

3.2.4 Clarification of sample

The pellets obtained from Ammonium sulphate fractionations were redissolved in homogenization buffer containing 0.5 M CaCl₂ and 0.2% Dextran sulphate and kept for mild stirring at 4°C for 20 min and then centrifuged at 18,000 rpm for 40 min at 4°C. The supernatant was collected and further filtered through Whatman filter paper followed by Millipore filter of pore size 0.8 and 0.4 µm.

3.2.5 Desalting

Desalting of the sample was done by gel filtration chromatography. Sephadex G-50 matrix was packed into a glass column (30 x 350 mm) and equilibrated with 2 CV (Column Volume) equilibration buffer (50 mM Tris-Cl pH 8.50 containing 1 mM EDTA, 2 mM Ascorbic acid, and 2 mM Sodium metabisulphite). Then the sample was loaded onto the Sephadex G-50 column at 2-3 ml/min flow rate and different fractions were collected. Active fractions were pooled together and further purified by anion exchange chromatography.

3.2.6 Anion Exchange Chromatography

Q-Sepharose fast flow matrix was packed in column (20 x 100 mm) and equilibrated with 4 CV equilibration buffer (50 mM Tris-Cl pH 8.5 containing 100 mM KCl, 1 mM EDTA, 2 mM Ascorbic acid, and 2 mM Sodium metabisulphite). Then the sample was loaded onto the column at 0.8-1 ml/min flow rate. The column was washed with equilibration buffer to remove unbound proteins while bound proteins were eluted with 0.7 M linear KCl gradient at 1.5 ml/min flow rate.

3.2.7 Biosynthesis of Linseed Lipoyxygenase metabolites

Linseed enzyme was employed for synthesis of hydroperoxy and hydroxy metabolites of AA, LA, and ALA as per the method described earlier [123,124]. In brief, linseed enzyme was incubated with AA (133 μ M), LA (266 μ M), or ALA (266 μ M), in 100 mM Tris-Cl buffer, pH 8.0 for 3 min and the reaction was terminated by acidifying the reaction mixture to pH 3.0 with 6N HCl. The products formed were extracted with equal volumes of hexane: diethyl ether (1:1) twice and the organic solvent was evaporated under inert conditions. The dried products were then dissolved in HPLC mobile phase consisting of hexane: propane-2-ol: acetic acid (1000:15:1) for purification of these metabolites on HPLC. For biosynthesis of corresponding hydroxides, these dried hydroperoxy products were dissolved in methanol and reduced with sodium borohydride (NaBH_4) for 2 min. Then the reduced products were extracted in hexane diethyl system and separated on HPLC as mentioned above.

3.2.8 Purification and analysis of metabolites on SP-HPLC

The metabolites generated using different PUFAs as substrate were purified on preparatory straight phase HPLC (SP-HPLC) (Shimadzu LC 20AP) equipped with the autosampler- (SIL-10AF), detector (SPD-M20A) and connected to a computer with Shimadzu LC solution. The metabolites were separated on SP-HPLC using enable Silica

column (250 x 20mm) and HPLC mobile phase solvent system consisting of hexane: propane-2-ol: acetic acid (1000:15:1) at a flow rate of 6 ml/min and the eluents were monitored at 235 nm. The peaks showing characteristic absorption maximum at 235 nm, as analysed on UV/VIS Perkin Elmer lambda 35 spectrophotometer, were taken for further characterisation. The solvent was evaporated and metabolites were stored in 100% ethanol in an inert environment at -20°C. Analysis of metabolites was performed on analytical HPLC (Shimadzu LC 20AD, equipped with autosampler SIL-20AC HT and diode array detector (SPD-M20A) on Enable silica column (250 x 4.6mm) at 1 ml/min flow rate and solvent system mentioned above.

3.2.9 Characterization on LC-MS/MS

For characterization, equal concentration of linseed metabolites and Soybean 15-(S)-HETE (as the standard) were dissolved in MS grade solvent system separately. The Reverse phase solvent system (methanol: water, 80: 20) was used for purification and characterization of metabolites. These metabolites were injected in LC-MS/MS (LC: Agilent Technologies, 1200 series, Hystar Version 3.2, MS/MS: Bruker Daltonics, micrOTOFQ, micrOTOF control version 2.2) fitted with C-18 column. The fragmentation pattern of linseed metabolites and soybean metabolites were compared for identification

3.3 STATISTICAL ANALYSES

All the experiments were performed in triplicates and the values represented as mean \pm SD. Data were correlated, analyzed and p-values were obtained using student's t-test. The p-value <0.05 was considered as statistically significant.

3.4 RESULTS

3.4.1 Linseed seedlings show abundant LOX activity during early days of germination.

Several plants have shown LOX activity, which varies from type of tissue and their states. LOXs activity reported mostly in plant seeds while high enzymatic activity reported during germination. LOXs activities were also reported in defatted linseed seed [119,125], however, in this study, we report LOX activity in linseed seedlings. The germinated seedlings were homogenized in Tris-Cl buffer at pH 8.0 as described in methodology and fractionated by ammonium sulphate precipitation. The ammonium sulphate fraction of 30-50% showed more enzymatic activity than other fractions. Therefore, this fraction was used for further purification of the enzyme. The homogenates of different day's seedlings (Day1-Day4) of linseed were used to check its enzyme activity on oxygraph and abundant LOX-like activity was detected in linseed seedlings. Oxygraphic assay of linseed seedlings homogenate, using AA, LA, and ALA as the substrates, showed rapid incorporation of molecular O₂ (Figure 3-1). It was further confirmed by the characteristic spectrum of conjugated diene present in LOXs product, which was observed by the spectrophotometer-based assay.

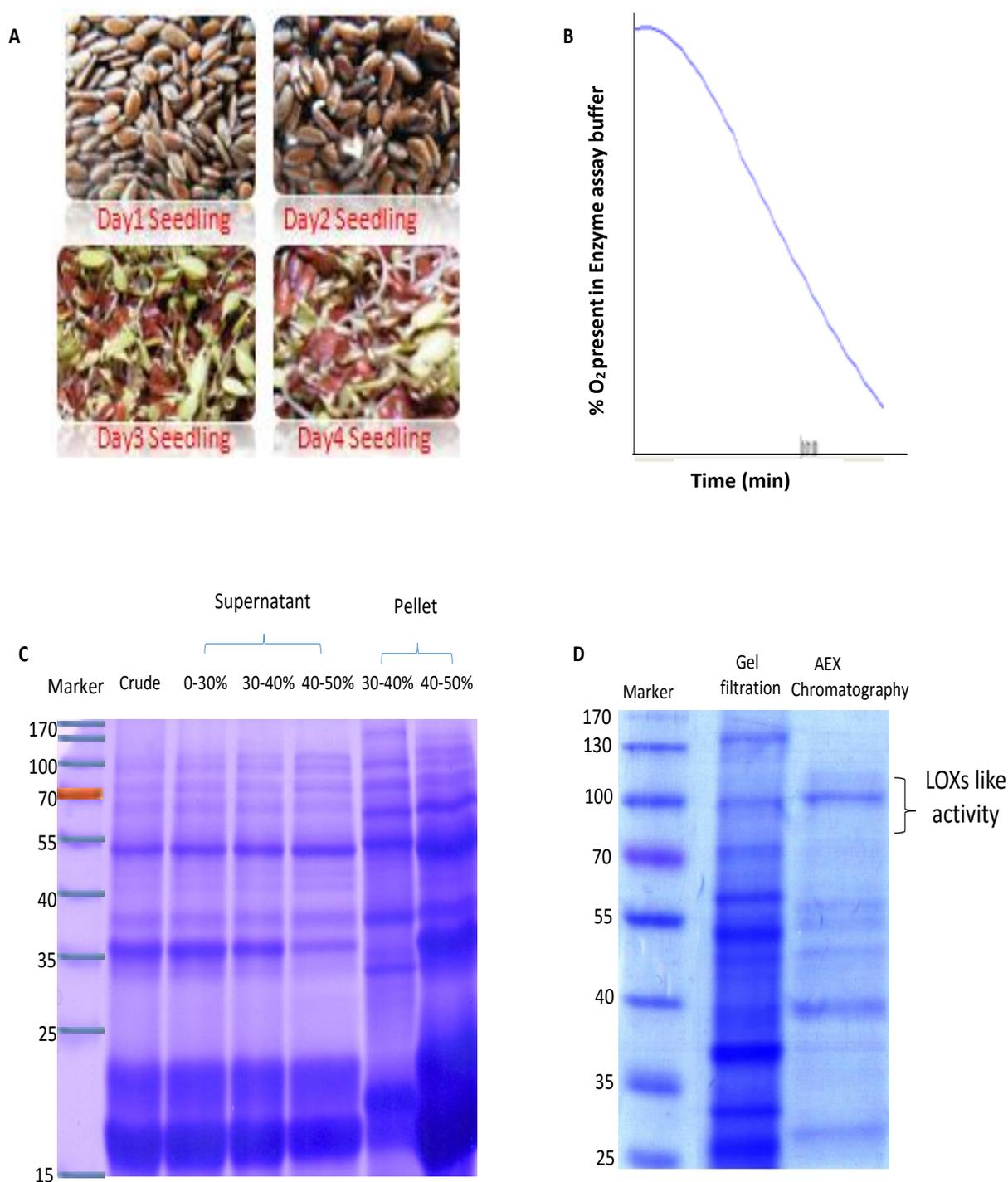


Figure 3-1: Homogenization, Isolation and Purification of Linseed seedling enzyme. **A)** Different days seedling of Linseed seeds showing the growth of radicle and plumule. **B)** A typical image of Oxygraph showing the enzymatic activities of linseed seedlings. **C)** SDS-PAGE showing proteins of different fractions obtained by ammonium sulphate fractionation of linseed seedling homogenate. **D).** SDS-PAGE showing partial purification of active enzyme fraction by chromatography.

3.4.2 Linseed enzyme shows pH optima in alkaline pH range

Enzyme assay was carried out as per the methods described in the methodology on an oxygraph (Strathkelvin 782 oxygen system version 3.0, Model 782). Enzyme activity was assayed in homogenates of different day's linseed seedlings (day1-4) against changing pH in a range of pH 6.0 to pH 13.0 at 25°C. The homogenate of day-1 linseed seedling showed two major pH optima, first at pH 10.0 and the second at pH 11.7. In addition, two minor peaks with pH optima of 9.5 and 6.8 were also recorded (Figure 3-2).

The enzyme activity in Day 2 homogenate of linseed seedlings was also analyzed at different pHs (pH 6.0 – 13.0). The optimum enzyme activity was observed at two different pHs. It showed two major pH optima, first at pH 9.7 and the second at pH 11.05. In addition, two minor peaks with pH optima of 8.2 and 12.4 were also recorded. The homogenate of day-3 linseed seedling showed one major pH optima at 11.03. In addition, four minor peaks with pH optima of 7.2, 9.0, 9.7 and 12.03 were also recorded. The enzyme activity in Day 4 homogenate of linseed seedlings was also analyzed at different pHs (pH 6.0 – 13.0). The maximum enzyme activity was observed at pH 9.6 and pH 11.10. Minor peaks of activity were also observed at pH 7.2 and pH 12.5.

When the specific activity of linseed enzyme at different pH was compared with those from different days of germination, enzymes of Day 2 linseed seedlings showed highest LOX specific activity. Four days analysis of LOX activity and pH optimization showed that linseed homogenate had two pH optima, first at pH 9.6 (\pm 0.07) and second at pH 11.2 (\pm 0.3). Further, linseed enzyme based enzymatic reactions were -

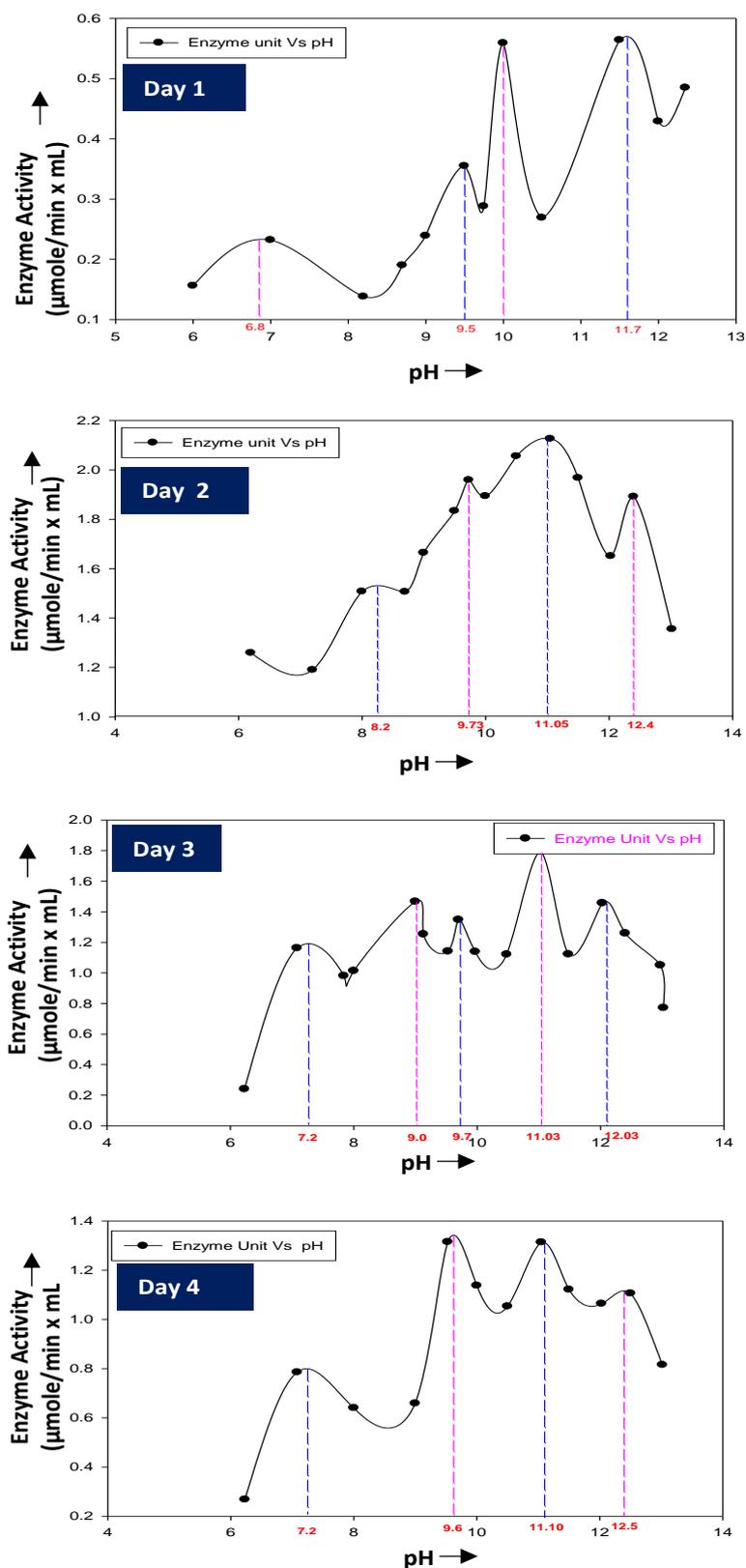


Figure 3-2: pH optimization of Linseed seedling enzyme. Different days linseed seedlings were homogenized in Tris-Cl buffer (125 mM, pH 8.0). Enzyme activity was assayed on oxygraph (Strathkelvin 782 oxygen system version 3.0, Model 782), at various pHs (pH 6.0-pH13.0) at 25°C.

performed at pH 9.6 only. Temperature optimization was performed on Oxygraph, which showed the optimum enzymatic activity of linseed seedling enzyme at 40°C (Figure 3-3).

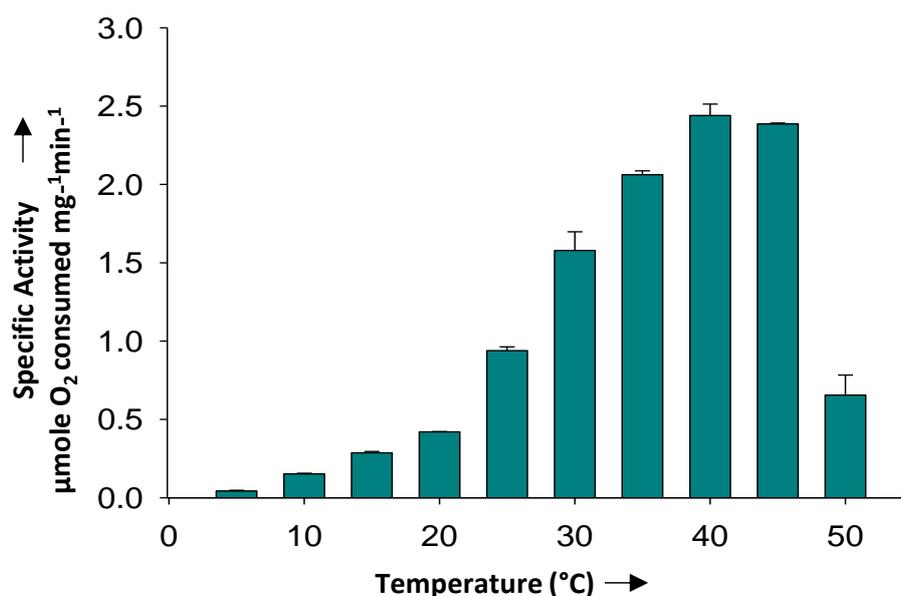


Figure 3-3: *Temperature optimization of linseed seedling enzyme.* Enzymatic activity was assayed on oxygraph (Strathkelvin 782 oxygen system version 3.0, Model 782) and the specific activity was calculated by determining protein contents, at various temperatures (5°C to 50 °C) at pH 9.6.

3.4.3 Linseed enzyme uses ω-6 and ω-3 PUFAs as substrate.

The linseed enzyme was incubated with ω-6 PUFAs (AA, and LA) and ω-3 PUFAs (ALA). The reaction mixtures were extracted with organic solvent (described in materials and methods) and purified on HPLC. The HPLC chromatogram showed the formation of products with both the ω-6 and ω-3 PUFAs having absorption maxima at 235 nm but different retention time (Rt) (Figure 3-5). The peaks were collected and wavelength scan was performed, which showed the characteristic spectrum of conjugated diene present in LOXs product (Figure 3-4).

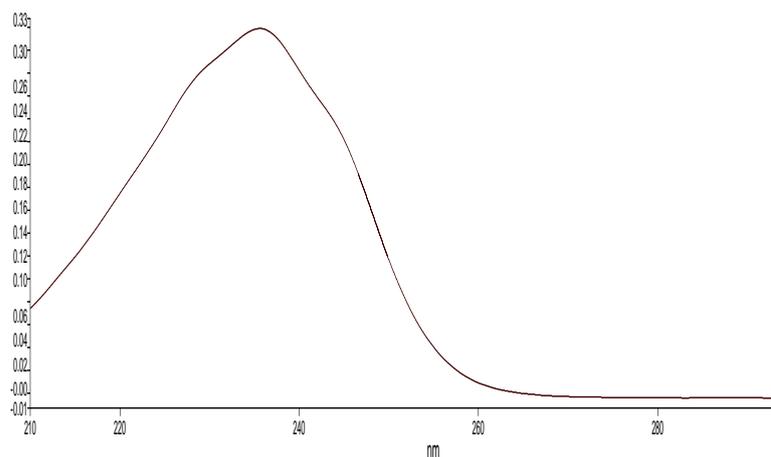


Figure 3-4 : Wavelength scan (210nm- 300nm) of HPLC peak collected from SP-HPLC. It is showing characteristic conjugated diene spectrum at 235 nm measured on UV/VIS spectrophotometer (Perkin Elmer lambda 35)

3.4.4 Purification of metabolites generated by linseed enzyme on preparative straight phase HPLC (SP-HPLC).

The metabolites of linseed enzyme were synthesized by employing partially purified homogenate of Day 2 seedling with AA, LA, and ALA as the substrates at pH 9.6 as described in methodology. The AA, ALA and LA metabolites catalyzed by linseed seedling enzyme were extracted into an organic solvent. The products were purified on SP-HPLC by preparative column. The retention times of hydroperoxy and hydroxy metabolites (products formed with reduction by NaBH_4) of AA were 21.3 and 15.0 min respectively, (Figure 3-5A). Similarly, the retention times of hydroperoxy and hydroxy products of ALA were 22.0 and 19.7 min (Figure 3-5B) respectively. The absorption spectra of the metabolites when recorded on UV-VIS spectrophotometer, showed-

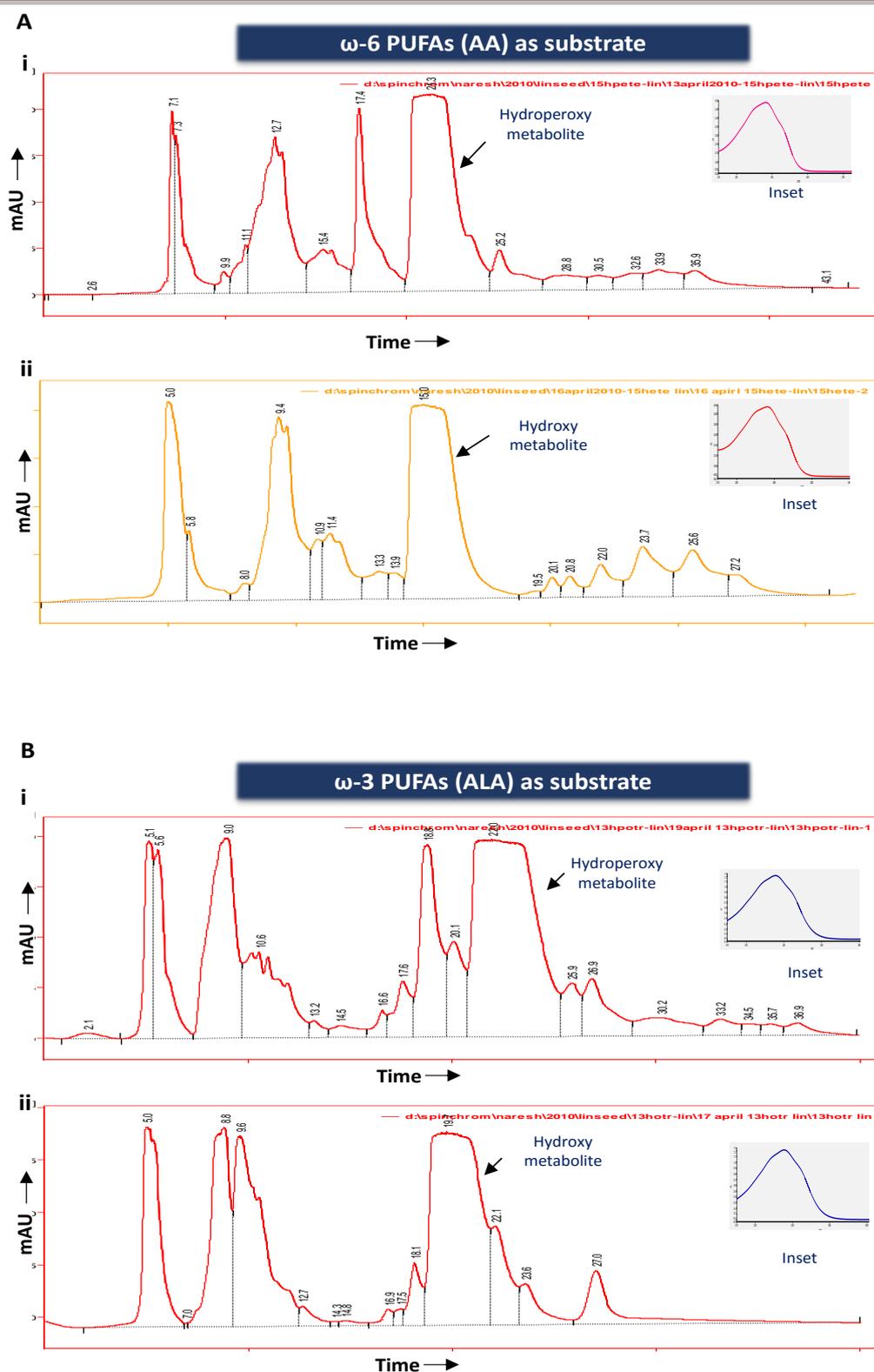


Figure 3-5 : HPLC chromatograms of PUFAs metabolites generated using Linseed lipoxygenase. The products were synthesized using linseed seedlings enzyme; ω -6 PUFA (AA) and ω -3 PUFA (ALA) were used as substrates. The products were purified on SP-HPLC system using hexane: propane-2-ol: acetic acid (1000:15:1) solvent system at 6 ml/min flow rate. **A).** i) Hydroperoxy and ii) hydroxy metabolites of ω -6 PUFA (AA) generated by employing Linseed seedlings lipoxygenase and purified on SP-HPLC. **B).** i) Hydroperoxy and ii) hydroxy metabolites of ω -3 PUFA (ALA) generated by employing Linseed seedlings lipoxygenase and purified on SP-HPLC. **(Inset)** The absorption spectra of the compounds when recorded on UV-VIS spectrophotometer, show characteristic conjugated diene spectra with maximum absorbance peaks at 235 nm.

Analysis of Linseed hydroperoxy metabolites of ALA on Analytical SP-HPLC

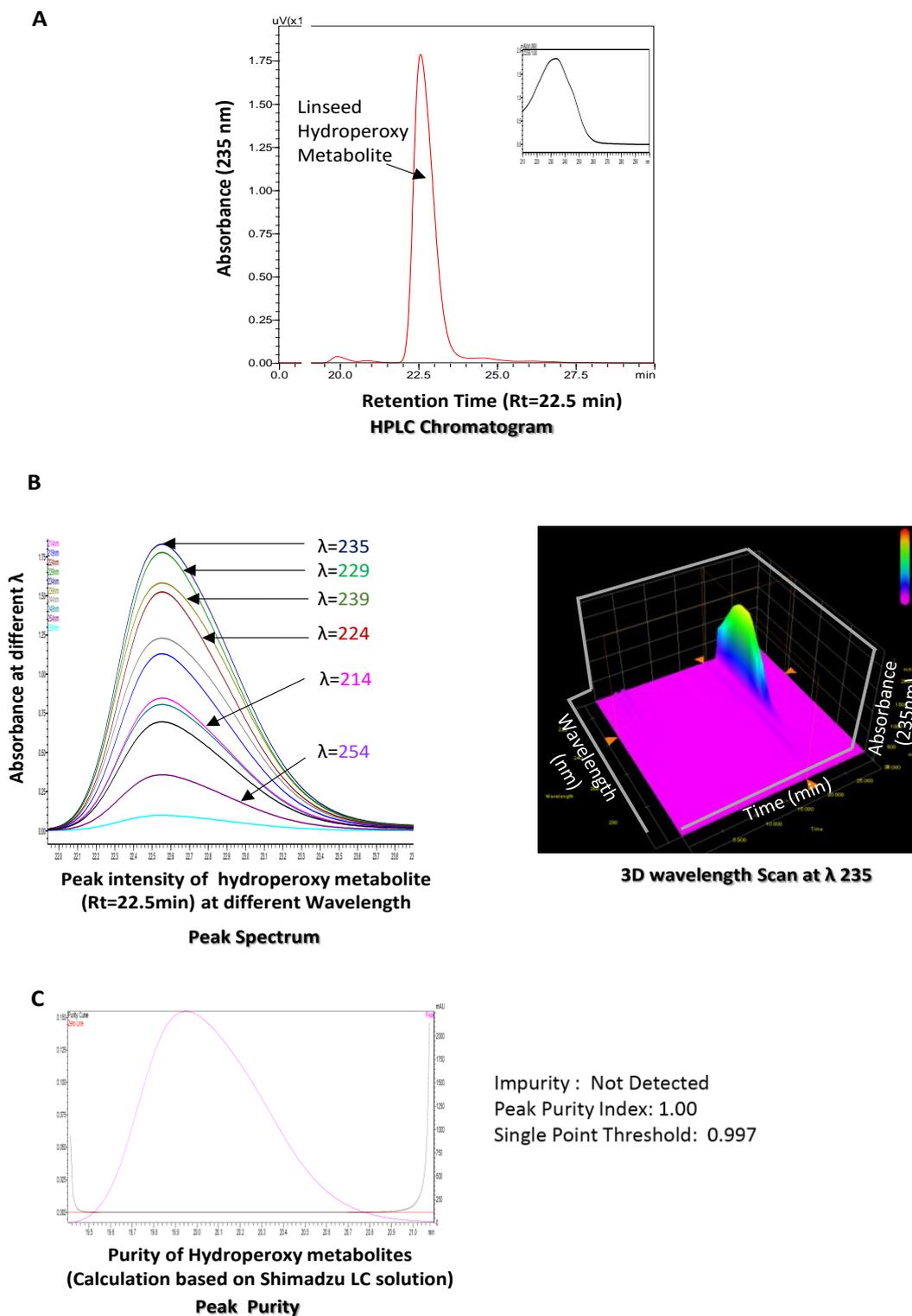


Figure 3-6: HPLC analysis of hydroperoxy metabolites of ALA catalyzed by Linseed lipoxygenase. **A)** HPLC chromatogram of hydroperoxy metabolite showing single and prominent peak (Rt=22.5 min). **B)** Image showing optimum absorbance of the peak (Rt=22.5 min) obtained above at 235 nm. The image showing real time absorbance of the selected peak at different wavelength obtained from HPLC PDA detector (Shimadzu, Japan). **C)** The image showing peak purity curve of the HPLC peak calculated by LC solution software associated with HPLC. It shows that the metabolite present in selected HPLC peak is free from impurity and having purity index 1.00.

Analysis of Linseed hydroxy metabolites of ALA On Analytical SP-HPLC

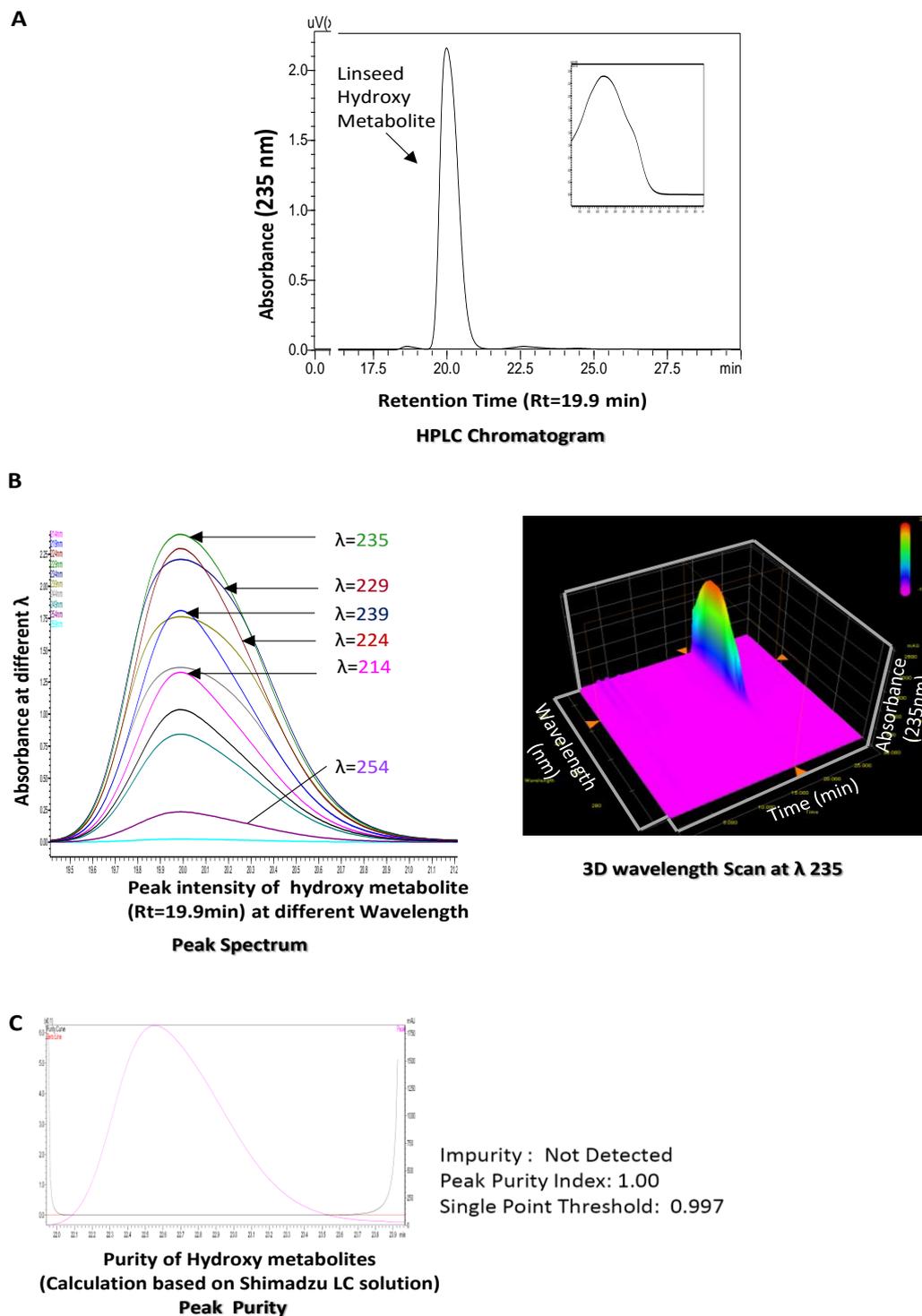


Figure 3-7: HPLC analysis of hydroxy metabolites of ALA catalyzed by Linseed lipoxygenase. **A)** HPLC chromatogram of hydroxy metabolites showing single and prominent peak (Rt=19.9 min). **B)** Image showing optimum absorbance of peak (Rt=19.9 min) obtained above at 235 nm. The image shows real time absorbance of the selected peak at different wavelength obtained from HPLC PDA detector (Shimadzu, Japan). **C)** The image showing peak purity curve of the HPLC peak calculated by LC solution software associated with HPLC. It shows that the metabolite present in selected HPLC peak is free from impurity and having purity index 1.00.

characteristic conjugated diene feature with peaks at 235 nm (Inset). The metabolites thus separated on SP-HPLC, were initially identified based on retention time in SP-HPLC solvent system. The purity of the metabolites was determined by peak purity curve, which showed 1.0 peak purity index and 0.997 single point threshold (Figure 3-6, 3-7).

3.4.5 Analysis of metabolites generated by linseed enzyme and comparison with soybean LOX metabolites.

The analysis of LOX activity of the enzyme from linseed seedling was initiated upon the reaction with PUFAs (AA, LA, and ALA) as substrate and purifying the hydroperoxy and hydroxy metabolites on SP-HPLC by preparative column. The wavelength scanning spectrum of the hydroperoxy product was observed on a spectrophotometer. The product showing absorption maximum at 235 nm was collected and then compared with soybean 15-LOX hydroperoxy and hydroxy metabolites of corresponding PUFAs by comparing retention times (Rt). The hydroperoxy and hydroxy metabolites of soybean LOX were considered as the standards. The prominent peak showed typical conjugated diene spectrum. The retention time of linseed hydroperoxy and hydroxy metabolites of ALA were 22.5 min and 19.5 min, respectively, while the retention time of hydroperoxy and hydroxy metabolites AA were 14.9 min and 8.8 min, respectively. The hydroperoxy and hydroxy metabolites of LA showed retention times of 22.8 min and 20.1 min, respectively. The HPLC chromatogram of linseed hydroperoxy and hydroxy metabolites of ALA when subjected to overlay with HPLC chromatogram of standard 13-(S)-HPOTrE and 13-(S)-HOTrE of soybean LOX, the two metabolites have shown same retention times corresponding to standard (Figure 3-8). The HPLC chromatogram of linseed hydroxy and

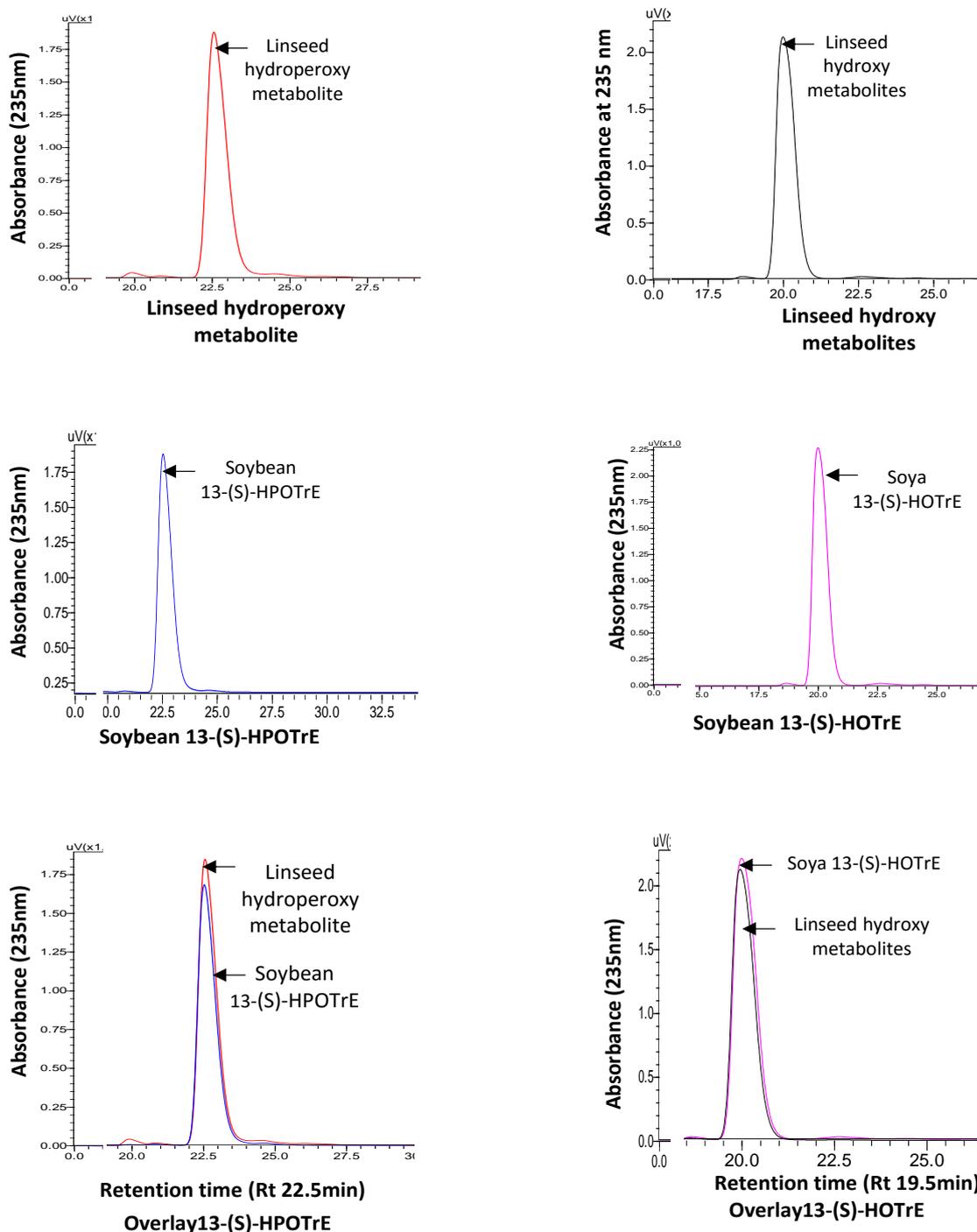


Figure 3-8: Comparison of linseed hydroperoxy and hydroxy metabolites of ALA with soybean hydroperoxy (13-(S)-HPOTrE) and hydroxy (13-(S)-HOTrE) metabolites of ALA, respectively. Overlay of HPLC chromatogram of linseed hydroperoxy (Red) and hydroxy (Black) metabolites of ALA over soybean (13-(S)-HPOTrE) (Blue) and (13-(S)-HOTrE) (pink) metabolites of ALA shows similarity of linseed hydroperoxy metabolite with 13-(S)-HPOTrE and hydroxy metabolite with 13-(S)-HOTrE. Analysis was performed on analytical SP-HPLC using hexane: propan-2-ol: acetic acid (1000:15:1) solvent system.

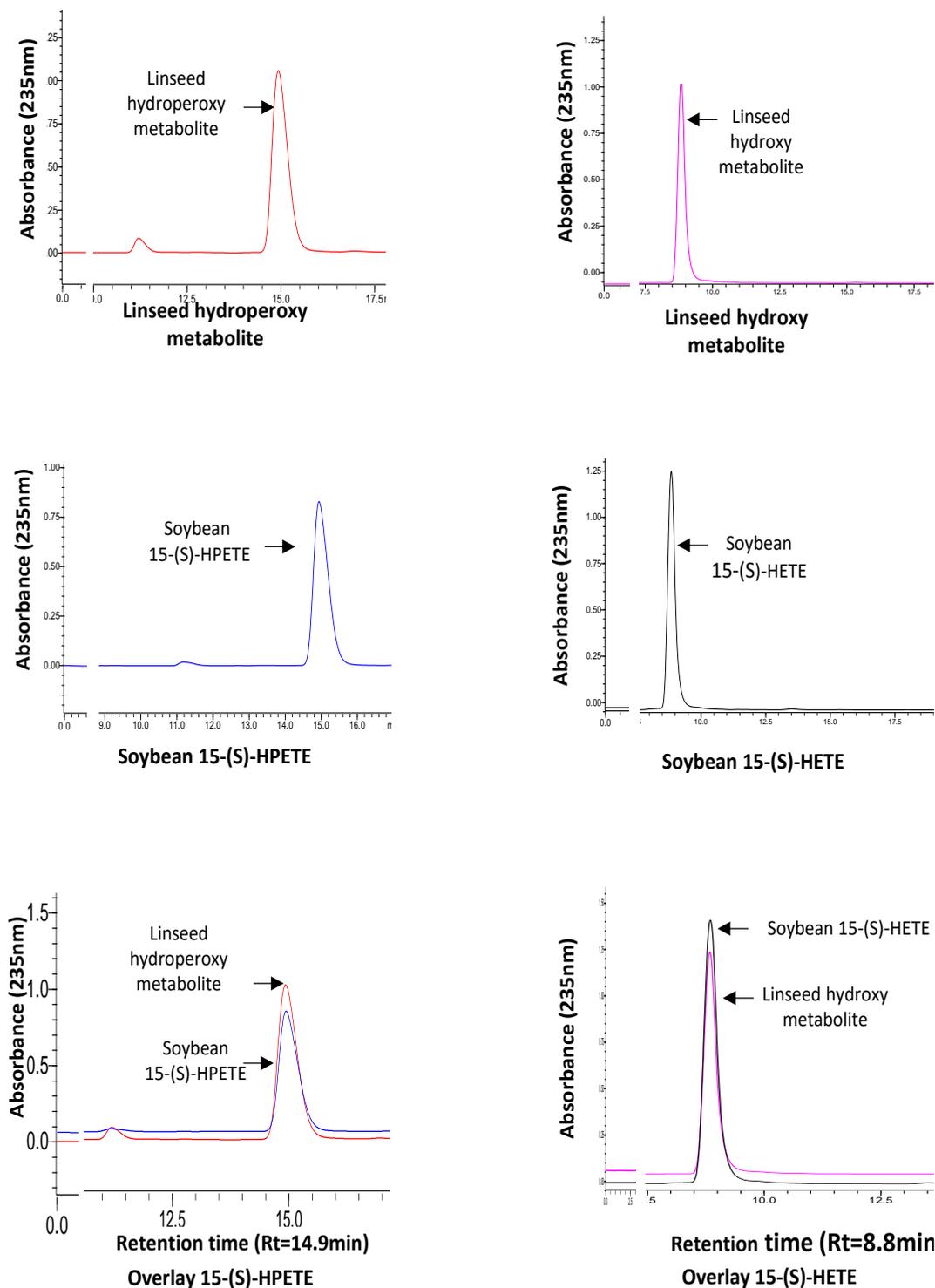


Figure 3-9: Comparison of linseed hydroperoxy and hydroxy metabolites of AA with soybean hydroperoxy (15-(S)-HPETE) and hydroxy (15-(S)-HETE) metabolites of AA. Overlay of HPLC chromatogram of linseed hydroperoxy (Red) and hydroxy (pink) metabolites of AA over soybean (15-(S)-HPETE) (Blue) and (15-(S)-HETE) (black) metabolites of AA shows similarity of linseed hydroperoxy metabolite with 15-(S)-HPETE and hydroxy metabolite with 15-(S)-HETE. Analysis was performed on analytical SP-HPLC using hexane: propan-2-ol: acetic acid (1000:15:1) solvent system.

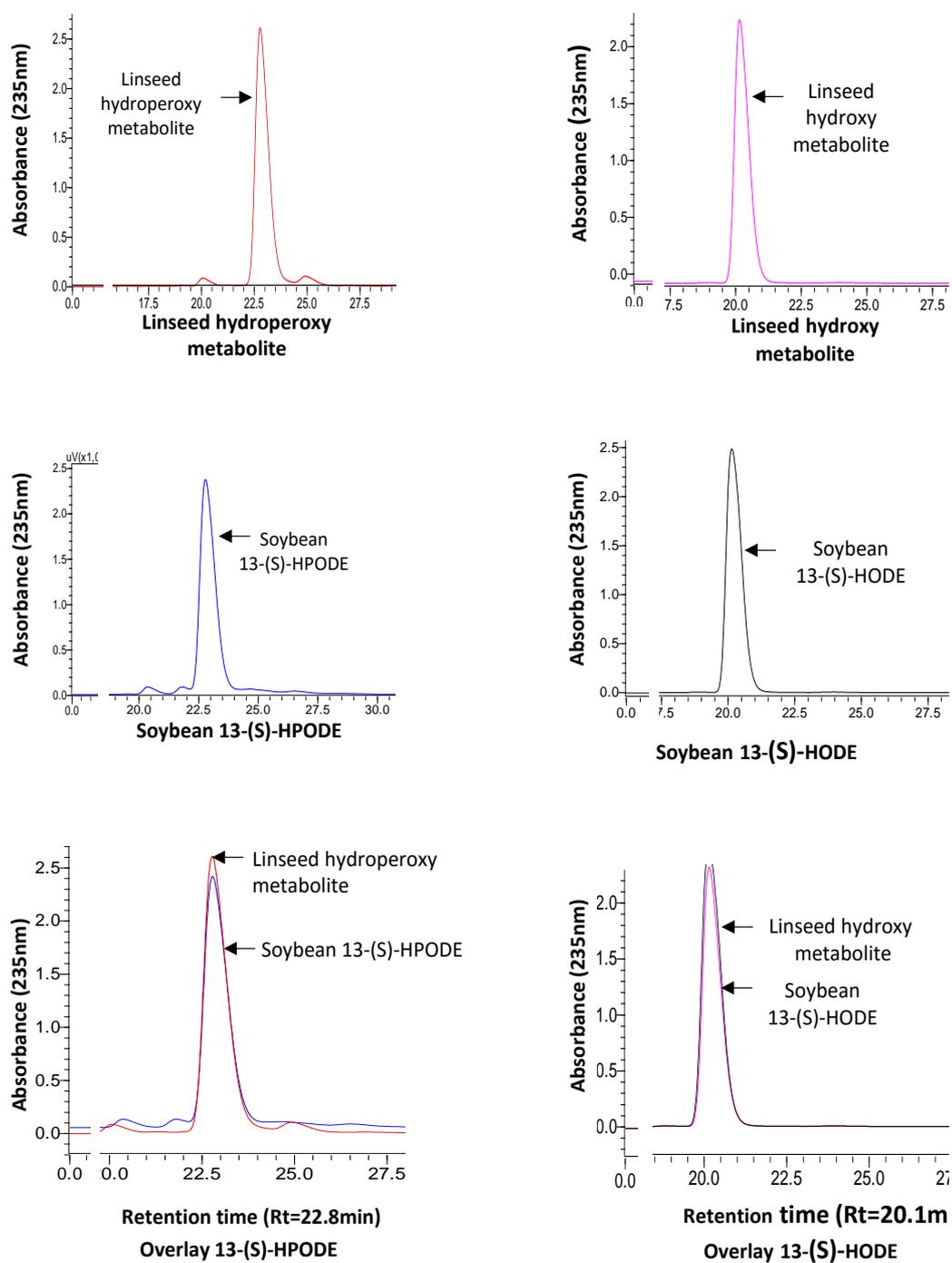


Figure 3-10 Comparison of linseed hydroperoxy and hydroxy metabolites of LA with soybean hydroperoxy (13-(S)-HPODE) and hydroxy (13-(S)-HODE) metabolites of LA. Overlay of HPLC chromatogram of linseed hydroperoxy (Red) and hydroxy (pink) metabolites of LA over soybean (13-(S)-HPODE) (Blue) and (13-(S)-HODE) (black) metabolites of LA shows similarity of linseed hydroperoxy metabolite with 13-(S)-HPODE and hydroxy metabolite with 13-(S)-HODE. Analysis was performed on analytical SP-HPLC using hexane: propan-2-ol: acetic acid (1000:15:1) solvent system.

and hydroperoxy metabolites of AA when subjected to overlay with HPLC chromatogram of standard 15-(S)-HPETE and 15-(S)-HETE of soybean LOX, the two metabolites have shown same retention times corresponding to standard (Figure 3-9). The similar pattern was observed when the HPLC chromatogram of linseed hydroperoxy and hydroxy metabolites of LA subjected to overlay with HPLC chromatogram of standard 13-(S)-HPODE and 13-(S)-HODE of soybean LOX, these two metabolites have also shown same retention times corresponding to standard (Figure 3-10).

3.4.6 Characterization of Linseed metabolites on LC-MS/MS.

Linseed hydroxy metabolite of AA, purified on SP-HPLC, was further characterized by LC-MS/MS. The metabolites were initially separated on the reverse phase solvent system (Methanol: water 80:20) using analytical silica column (C-18) at a flow rate of 1 ml/min on LC-MS/MS. Similarly, soybean 15-(S)-HETE (standard) was also subjected to LC-MS/MS. Linseed metabolite of AA and Soybean 15-(S)-HETE showed the same retention time (4.0 min) in LC-MS/MS (Figure 3-11). The major fragmentation detected in both linseed metabolite and soybean 15-(S)-HETE were identical with peaks at 321, 301, 251, 219 and 205 (Figure 3-12 and Figure 3-13).

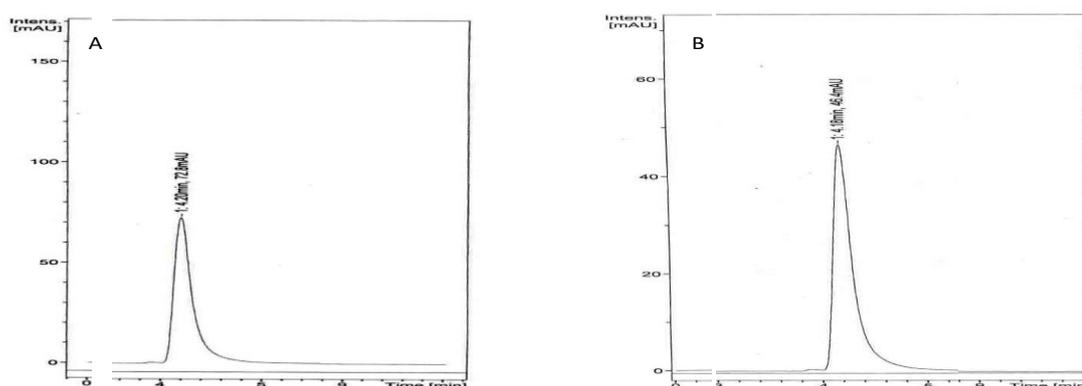


Figure 3-11: Comparison of linseed LOX metabolite of AA with soybean 15 LOX metabolites of AA (15-(S)-HETE) on LC-MS/MS using mobile phase solvent, Methanol: Water (80: 20). (A) RP-HPLC chromatogram showing linseed hydroxy metabolite of AA on LC-MS/MS, retention time 4.0 min. (B) RP-HPLC chromatogram showing soybean 15-(S)-HETE on LC-MS/MS, retention time 4.0 min.

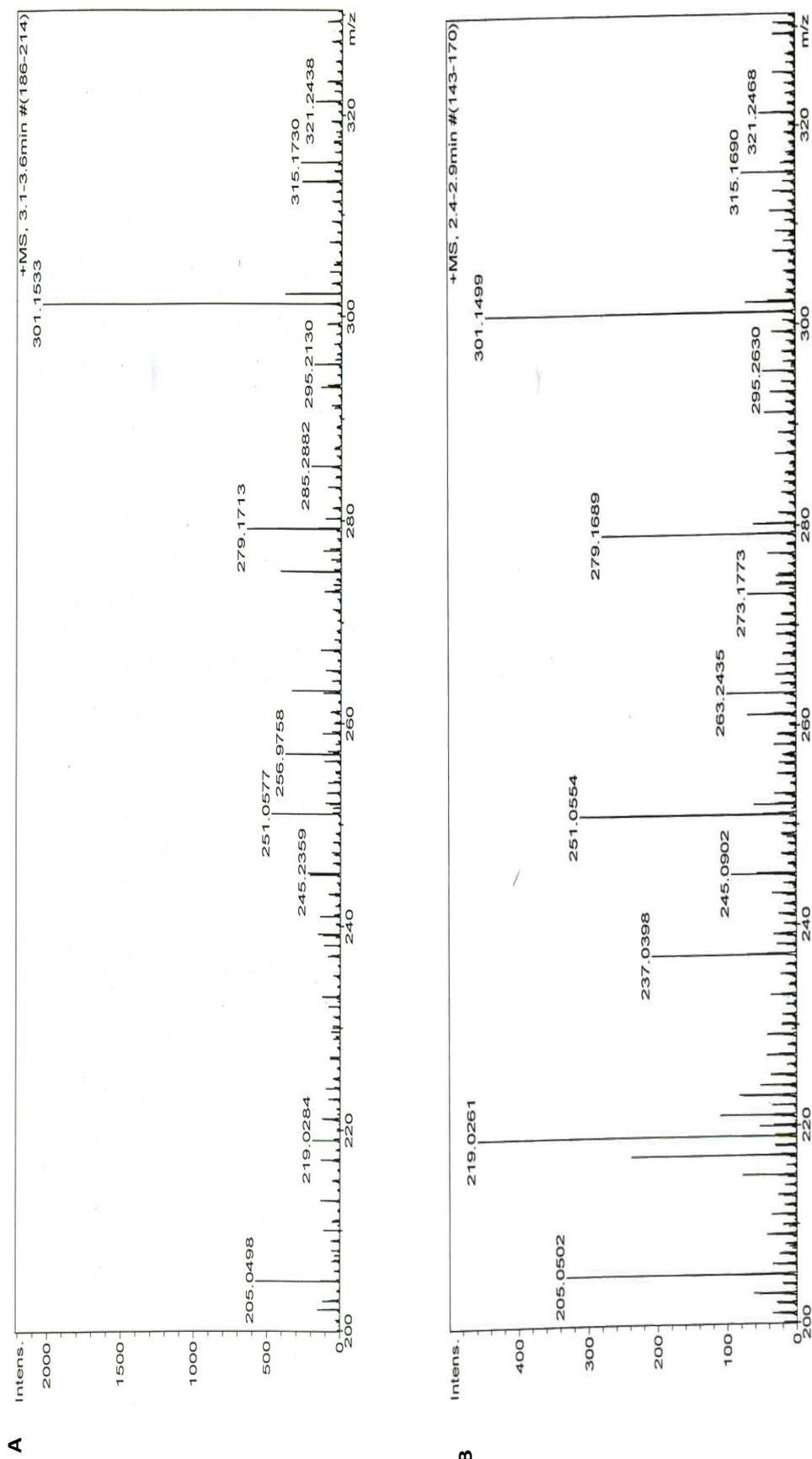


Figure 3-12: Comparison of linseed seedling LOX metabolite of AA with soybean 15 LOX metabolite of AA (15-(S)-HETE) on LC-MS/MS in positive mode at capillary volt 3800V and collision cell RF 120V_{pp}. A) Fragmentation pattern of Linseed hydroxy metabolite of AA in LC-MS/MS in positive mode. B) Fragmentation pattern of soybean 15-LOX metabolite 15-(S)-HETE in LC-MS/MS in positive mode.

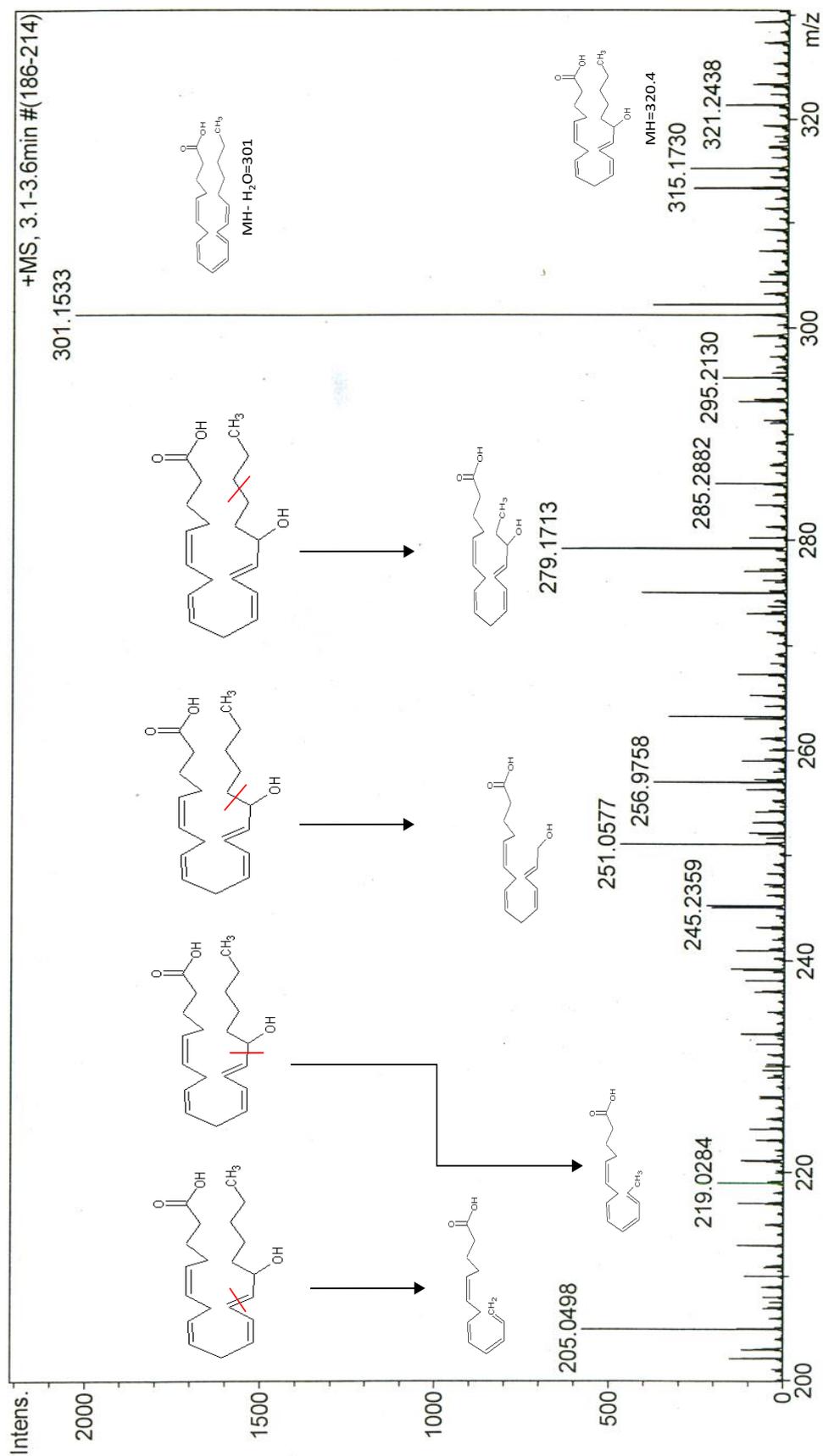


Figure 3-13: The fragmentation of hydroxy metabolite of linseed seedling LOX using AA as substrate, accounting for the peaks observed on LC-MS/MS. It is showing the characteristic fragmentation pattern of 15-(S)-HETE – a 15 LOX metabolite of soybean.

3.5 DISCUSSION

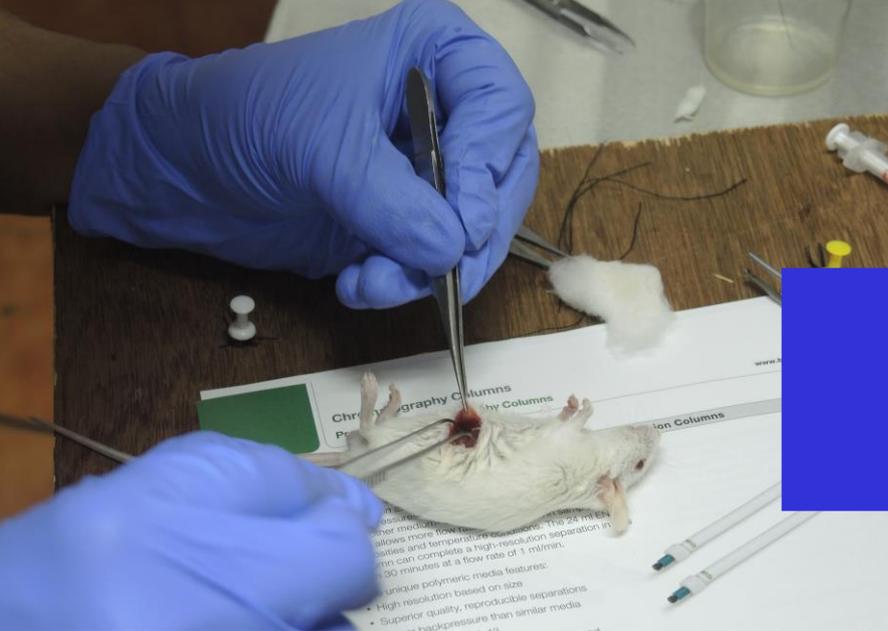
In plants, LOXs play vital role, which starts from seed germination to fruit ripening and plant senescence [126]. Several studies reported that there are many fold increase in LOXs expression during early hours of seed germination [114] and as the seedling develops, the LOXs activity decreases significantly. In the present study, linseed seedling showed abundant LOX activity. Enzymatic activity of seedling was assayed by oxygraph that measures molecular O₂ in the reaction chamber. It showed that linseed seedling contains enzymatic activity, which varies as the seedling develops. It was noticed that the specific activity of the enzyme of day 2 seedling was significantly higher in comparison to the enzyme of the day1-4 seedling. The increase in enzymatic activity in early linseed seedling and a significant decrease in day 3 and day 4 seedling supports the previous findings which reported in other plants during seed germination [114]. The linseed seedling enzyme used ω -6 (AA, LA) and ω -3 PUFAs (ALA) as substrates and showed rapid oxygen consumption, when measured on oxygraph, suggesting the possibility of LOX activity in the linseed seedlings. The enzyme activity of linseed seedling assayed at various pHs ranging from pH 6.0 to 13.0, showed several majors and minor peaks. The presence of such peaks reveals the possibility of different isoforms of LOXs showing different pH optima at different days. The possibility of 15-LOXs in linseed seedling was further strengthened by comparing metabolites of linseed seedling with metabolites of soybean 15-LOX on HPLC. In SP-HPLC, the stationary phase is hydrophilic (polar) in nature while mobile phase contains hydrophobic solvent (nonpolar solvent e.g. heptane, hexane) mixed with more polar solvent (e.g. ethyl acetate, isopropanol, chloroform). Silica and other organic groups such as amino and cyano are generally

used as stationary phase. The Linseed seedling enzyme also catalyzed AA, LA (ω -6 PUFAs) and ALA (ω -3 PUFA) and generated corresponding hydroperoxy metabolites while hydroxy metabolites were generated by further reduction of hydroperoxy metabolites. When purified on SP-HPLC, the soybean hydroperoxy metabolites of ALA, AA and LA (13-(S)-HPOTrE, 15-(S)-HPETE, and 13-(S)-HPODE) showed more retention times and eluted late as compared to corresponding hydroxy metabolites (13-(S)-HOTrE, 15-(S)-HETE, 13-(S)-HODE). The peak purity index showed the purity of PUFAs metabolites synthesized by linseed seedling enzyme.

The hydroperoxy and hydroxy metabolites of linseed seedling enzyme synthesized using ALA, AA, and LA, were compared with corresponding standard hydroperoxy and hydroxy metabolites of soybean LOX using same substrates on SP-HPLC. When the hydroperoxy metabolites of linseed seedlings using ALA as the substrate, compared with hydroperoxy metabolites (13-(S)-HPOTrE) of soybean LOX using ALA as the substrate, showed same retention time (22.5 min). Similarly when the hydroxy metabolites of linseed seedling using ALA as the substrate, compared with hydroxy metabolites (13-(S)-HOTrE) of soybean LOX using ALA as the substrate, also showed same retention time (19.5 min). Similarly, the hydroperoxy and hydroxy metabolites of seedling using ω -6 PUFAs (AA, and LA) as the substrates, showed same retention time of corresponding hydroperoxy and hydroxy metabolites of standard soybean 15-LOX. Thus, the HPLC chromatogram of the hydroperoxy and hydroxy metabolites of linseed seedlings overlay showed same retention times when compared to corresponding hydroperoxy and hydroxy metabolites of soya LOX.

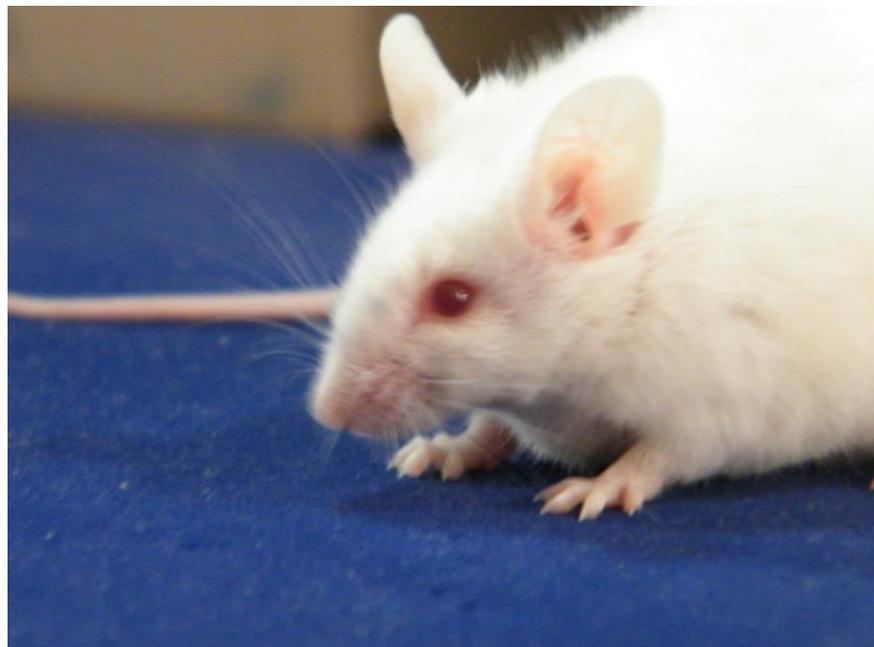
The overlay HPLC chromatogram of hydroperoxy and hydroxy metabolites of linseed seedling with standard soybean hydroperoxy and hydroxy metabolites indicate that linseed seedling enzyme might be 15-LOX, which might catalyze PUFAs and generated the same hydroperoxy and hydroxy metabolites as catalyzed by soybean 15-LOX.

The initial assays based on oxygraph indicated the possibility of LOXs in linseed seedling. Furthermore, the comparison of the retention times of hydroperoxy and hydroxy metabolites of linseed seedling enzyme with the hydroperoxy and hydroxy metabolites of soybean 15-LOX (standard) strengthen such a possibility. The presence of 15-LOX in linseed seedling was confirmed by analyzing the fragmentation patterns of the metabolite of linseed seedling with the corresponding metabolite of soybean 15-LOX on LC-MS/MS.



Chapter 4

**STUDY THE EFFECTS OF 15-LOX
METABOLITES OF ALA [13-(S)-HPOTRE
AND 13-(S)-HOTRE] ON INFLAMMATION
AND ELUCIDATE THE SIGNALLING PATHWAYS
INVOLVED: *IN VITRO* AND *IN VIVO* STUDIES**



4.1 INTRODUCTION

Inflammation is an essential part of host's response to infection or injury in order to maintain cellular homeostasis. Aberrant inflammation is associated with various disorders mediated by hyperactivation of inflammasome complexes and up-regulation of pro-inflammatory enzymes like iNOS, LOXs and COXs [88–92]. The inflammatory responses generated by eicosanoids, is known to be mediated by pro-inflammatory cytokines such as IL-1 β and TNF- α [93].

Increased ratio of ω -6 to ω -3 PUFAs is hypothesized to elevate pro-inflammatory eicosanoid production and thus the onset of inflammatory diseases. A sufficiently high intake of ω -3 PUFAs, on the other hand, is shown to offer protection from inflammatory diseases by decreasing the production of pro-inflammatory eicosanoids, cytokines, ROS and RNS [100,101]. In addition, it is reported that increasing ω -3 PUFAs tissue levels by dietary or genetic means decreases the pathological retinal angiogenesis by suppressing TNF- α [50]. These beneficial effects of ω -3 PUFAs appear to be mediated by the oxygenated metabolites formed via the LOXs and COXs pathways [97,127–130].

COX-2, an inducible enzyme that converts ω -6 PUFAs such as AA to pro-inflammatory prostaglandins, has been widely recognized as the major pathway responsible for inflammation as it triggers the production of other pro-inflammatory chemokines and cytokines [130]. However, this concept is challenged by recent findings on COX-2 derived oxidative metabolites of ω -3 PUFAs possessing anti-inflammatory and anti-oxidant properties [131,132]. These studies suggest that the ultimate pro/anti-inflammatory effects of COX-2 depend on the substrate on which these enzymes act, ω -6 or ω -3 PUFAs [133,134] and their down-stream metabolites-PGE₂ and/or PGD₂. While

PGE₂ is associated to shifting of M1 macrophages (pro-inflammatory) into M2 macrophages (anti-inflammatory) [135,136], PGD₂ exhibits anti-inflammatory effects by its conversion to PGJ₂ and subsequently 15-deoxy- $\Delta^{12,14}$ PGJ₂ (15d-PGJ₂) a well-known ligand with high affinity for peroxisome proliferator-activated receptor- γ (PPAR- γ) [137–139]. LOXs, on the other hand, are majorly classified into 5-, 12- and 15-LOXs, depending on the position at which AA is oxygenated. These LOX isoforms have been implicated in a variety of inflammatory and hyperproliferative and neurodegenerative diseases [140]. While 5-LOX is pro-inflammatory in nature [141], the 15-LOX exhibits anti-inflammatory properties [142,143]. Earlier we have shown the anti-inflammatory and anti-cancer properties of 15-LOX metabolites of AA and elucidated the mechanisms involved [144] [145] [17]. In the present study, we report the anti-inflammatory effects of 15-LOX metabolites of ALA, the precursor for EPA and DHA, on LPS stimulated mouse macrophage cell line, RAW 264.7 and primary peritoneal macrophages isolated from BALB/c mice and demonstrated that these effects are mediated by inactivating NLRP3 inflammasome complex through the PPAR- γ pathway. Further, we report on the extended survival of BALB/c mice in endotoxin-mediated septic shock and polymicrobial sepsis in CLP mouse model.

4.2 MATERIALS AND METHODS

4.2.1 Chemicals and Reagents

Culture medium DMEM, penicillin, streptomycin, PBS, Trypsin-EDTA and fetal bovine serum (FBS) were purchased from Gibco. MTT, 2'-7'-Dichlorodihydrofluorescein diacetate (DCFH-DA), LPS (lipopolysaccharide from *E. coli*, 0127:B8), Griess reagent, Dexamethasone (Dex) and GW9662 (2-chloro-5 nitrobenzanilide) were purchased from Sigma-Aldrich, USA. Anti-Beclin-1, anti-Caspase-1, anti-NF- κ B and anti-TNF- α antibodies

were purchased from Abcam (MA, USA). Anti-LC-3 antibody was purchased from Cell Signalling while anti-COX-2 antibody was obtained from Santa Cruz Biotechnology Inc. (Texas, USA). Anti-iNOS antibody was purchased from Thermo Fisher Scientific (MA, USA). Enzyme immunoassay kit for IL-1 β , IL-10 and PGE₂ were purchased from R&D system, Inc. (MN, USA) whereas PGD₂ assay kit was purchased from Cayman Chemical Company (Ann Arbor, MI, USA). AA, LA, ALA, and DHA were procured from Nu-Chek-Prep (MN, USA). The 15-LOX metabolites of ALA, 13-(S)-HPOTrE and 13-(S)-HOTrE, were generated essentially employing the methods described earlier for generation of 5-LOX metabolites [116,123,124].

4.2.2 Animals

BALB/c, male mice, 4-week old weighing 20-25 g were purchased from Centre for Cellular and Molecular Biology, Hyderabad, India. Mice were housed at constant room temperature (23 \pm 1 $^{\circ}$ C) and allowed to water and food *ad libitum* in 12 h dark/light cycle. The mice were kept at least 1 week in animal house before performing any experiment. The mice used in this study were handled carefully and according to the *Guide for the care and use of Laboratory animals* published by NIH (National Institute of Health). The experimental protocol was approved by Institutional Animal Ethics Committee (IAEC), University of Hyderabad, India.

4.2.3 Cell culture and Treatments

The mouse macrophage cell line, RAW 264.7 was obtained from NCCS (Pune, India). The cells were grown and maintained in DMEM supplemented with 10% heat-inactivated FBS, 100 IU/ml penicillin and 100 μ g/ml streptomycin in a humidified atmosphere with 5% CO₂ at 37 $^{\circ}$ C. Sub-culturing of cells was done twice a week. Fresh culture medium was used before each treatment. Cells were pre-incubated with

different concentrations (1, 50 and 100 μM) of ALA metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE or with Dexamethasone (10 μM) for 3 h then challenged with LPS (100 ng/ml) for different time points as mentioned in experiments. The anti-inflammatory drug, dexamethasone was used as positive control. For inhibitor study, cells were pre-incubated with 10 μM GW9662 for specific time periods as mentioned in experiments. For analysis of the inflammasomes and IL-1 β measurements, RAW 264.7 cells and peritoneal macrophages were incubated with 1mM ATP for 30 min prior to end time points.

4.2.4 Isolation of Primary Peritoneal Macrophages

Primary peritoneal macrophages were isolated from thioglycolate-elicited BALB/c male mice as described by Xia Zhang et al [146]. Briefly, in BALB/c male mice, 3% thioglycolate broth (1 ml) was injected through i.p. After 3 days, mice were euthanized by cervical dislocation. 5 ml ice-cold DMEM was injected into the peritoneal cavity. The abdomen was finger tapped 4-5 times and peritoneal lavage was aspirated and collected in a cold sterile centrifuge tube. Further, centrifugation was done at 1500 rpm for 5 min, pellets were resuspended in DMEM and cell counting was done by haemocytometer. The appropriate number of cells were grown and maintained in DMEM, macrophages enrichment was done by washing and removing unattached cells from culture plate, further grown as described above for RAW 264.7 cells, and treated with 13-(S)-HPOTrE and 13-(S)-HOTrE as mentioned in experiments for RAW 264.7 cells.

4.2.5 Cytotoxicity Assay

Cytotoxicity of ALA metabolites was assayed by MTT assay. To perform this assay, RAW 264.7 cells were seeded in 96 well plates at a density of 5×10^4 cells/well then treated with ω -6 PUFAs (AA, and LA), ω -3 PUFAs (ALA and DHA) and 15-LOX

metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] at various concentrations (1, 50, 100 and 200 μ M) for different time points. Cell viability was measured colorimetrically by MTT assay as described by Mossman [103].

4.2.6 Nitrite Estimation

RAW 264.7 cells were seeded in 6 well plates for 12 h then pre-incubated with different concentrations (1, 50 and 100 μ M) of ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE], or dexamethasone for 3 h then stimulated with or without LPS (100 ng/ml) for the next 24 h. At the end of the time point, stable nitrite level in the culture supernatant was measured by Griess Reagent. For this, 50 μ l of cell culture medium was mixed with 50 μ l of Griess reagent and incubated at room temperature for 10 min in the dark. Then absorbance was measured at 540 nm using multi-mode plate reader (BioTek, SynergyMx). Nitrite level in samples was determined by using the standard curve of sodium nitrite. Culture medium was taken as blank for all experiments.

4.2.7 Estimation of IL-1 β , IL-10, PGD₂ and PGE₂

Levels of IL-1 β , IL-10, PGE₂ and PGD₂ in culture medium were measured by ELISA kit according to manufacturer's protocol. Their levels in culture medium were determined by using standard curves of respective cytokine or prostaglandin standards provided along with the kit.

4.2.8 Measurement of Reactive Oxygen Species (ROS)

RAW 264.7 cells were seeded in 6 well plates at a density of 2×10^5 cells/well then pre-incubated with different concentrations (1, 50 and 100 μ M) of ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE] and/or N-Acetyl Cysteine (NAC, 5 mM), for 3 h. Then cells were further stimulated with or without LPS (1 μ g/ml) for next 16 h. After that cells from each well were harvested and washed twice with PBS and further

incubated with 10 mM DCFH-DA for 30 min in dark at 37°C and then two times washed with PBS. About 10,000 cells per sample were taken for analysis. The measurement was performed on a Flow Cytometer and data analysis was done by Cell Quest software (FACS Calibur, Becton Dickinson, CA, USA) with excitation of DCF at λ 488 nm and emission at λ 525 nm. Primary macrophages isolated from peritoneal cavity were seeded in 12 well plates and grown as mentioned earlier. Then pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE at 100 nM for 3 h. Then stimulated with LPS and ROS was measured as described above.

4.2.9 Anti-inflammatory Effects of ALA Metabolites in vitro employing RAW 264.7 cells and Mouse Peritoneal macrophages: Immunoblot Analysis

RAW 264.7 cells seeded in 100 mm plates at a density of 5×10^5 cells/well and after 12 h pre-incubated with different concentrations (1, 50 and 100 μ M) of either ALA metabolites or dexamethasone (10 μ M) for 3 h. For Immunoblot analysis of primary cells, mouse peritoneal macrophages were isolated and seeded in 60 mm plates. Then pre-treated with lower doses (100 nM and 400 nM) of ALA metabolites for 3 h. Cells were then stimulated with or without LPS (100 ng/ml) for next 24 h. Cells were harvested at the end of time point, pelleted down and stored at -80°C for further use. Cell pellets were lysed in RIPA buffer containing 1x protease inhibitor at 4°C. Protein estimation was done by Bradford method using BSA as standard. An equal amount of protein was loaded and separated on 8-15% SDS-PAGE and transferred to nitrocellulose membrane. Then membranes were blocked with 5% (w/v) fat-free dry milk in TBST for 1 h at room temperature followed by washing three times with TBST. Membranes were incubated with primary antibodies (0.5-1.0 μ g/ml) for 12 h at 4°C on a shaker incubator with gentle shaking followed by thrice washing with TBST. The membranes were then

incubated with respective secondary antibodies conjugated with HRP. Signals were then detected with western lightning plus ECL kit (PerkinElmer) and captured on Kodak Imaging System (KODAK Image station 4000 mm Pro).

4.2.10 Anti-inflammatory Effects of ALA metabolites: Reverse Transcription Polymerase Chain Reaction (RT-PCR)

RAW 264.7 cells were seeded in 6 well culture plate. At 60% confluency, cells were pre-incubated with different concentrations of either ALA metabolites (1, 50 and 100 μ M) or dexamethasone (10 μ M) for 3 h and then stimulated with LPS (100 ng/ml) for 24 h. Total cellular RNA was extracted from each well using TRIzol[®] Reagent according to the manufacturer's instructions (Invitrogen Bio Services, India, Pvt. Ltd). RNA quantification was performed by nanodrop (NanoDrop 2000TM, Thermo Scientific, DE, USA). cDNA of each sample was prepared by using 2 μ g of RNA, 1 μ l MLV reverse transcriptase, 1 mM dNTP and 1 μ l oligo dT according to manufacturer's standardized protocol (Promega Corporation, WI, USA). PCR analyses were performed on aliquots of the cDNA prepared to detect iNOS, TNF- α , NLRP3, Caspase-1, IL-1 β , IL-18, and GAPDH. The reactions were carried out in a volume of 20 μ l containing (final concentration) 1 U Taq DNA polymerase, 0.2 mM dNTP, 100 pM of forward primers and reverse primers (Table 1), and 10 μ l reaction buffer. After amplification, PCR products were electrophoresed on 1% agarose gels and visualized by ethidium bromide staining on UV irradiation (BIO-RAD, Universal hood II).

Table 1: List of Primers used for RT-PCR	
mRNA	Sequences of Primers
NLRP3	Forward Primer 5' CTT CCA GAC TGG TGA ACT GCTG 3', Reverse Primer 5' TCT CCA AGG GCA TTG CTT CG 3',
Caspase-1	Forward Primer 5' GAG CTT CAA TCA GCT CCA TCA G 3' Reverse Primer 5' AAT GTC CCG GGA AGA GGT AGA 3',
IL-1 β	Forward Primer 5' AGC TTC CTT GTG CAA GTG TC 3', Reverse Primer 5' AAG GGA GCT CCT TAA CAT GCC 3',
IL-18	Forward Primer 5' TTC CTC TTG GCC CAG GAA CAA TG 3' Reverse Primer 5' CAA GGC GCA TGT GTG CTA ATC 3'
GAPDH	Forward Primer 5' AGG TCA TCC CAG AGC TGA ACG 3' Reverse Primer 5' CAC CCT GTT GCT GTA GCC GTA T 3'.
iNOS	Forward primer: 5' CCG CAT GAG CTT GGT GTT TG 3' Reverse primer: 5' AGT GCT TCA GTC AGG AGG TTG 3'
TNF- α	Forward Primer 5' TGT AGC CCA CGT CGT AGC AAA 3' Reverse Primer 5' AGA GGC AAC CTG ACC ACT CT 3',

Table 1 : List of Primers used for Semi-quantitative PCR

4.2.11 Analysis of the inflammasome, autophagy and NF- κ B translocation by confocal microscopy

RAW 264.7 cells were seeded in 6 well culture plates on sterile culture grade coverslips. When cells were 60% confluent, pre-incubated with ALA metabolites (100 μ M) and/or with GW9662, PPAR- γ inhibitor, for 3 h, then stimulated with LPS (100 ng/ml) for 24 h. For the study of inflammasome and autophagy, stimulation of cells with LPS was done for 24 h and for NF- κ B translocation; it was done for 16 h. However, for study NF- κ B translocation on peritoneal macrophages, cells were treated with ALA

metabolites at lower concentration (100 nM) for 16 h. Fixation of cells was done by ice-cold 4% paraformaldehyde for 10 min at 4°C followed by washing in PBS with 0.2% Tween 20. Permeabilization in cells was done by ice-cold acetone: methanol (1:3) for 15 min at room temperature followed by washing in PBS with 0.2% Tween 20. To avoid nonspecific binding, blocking was done by incubating cells in 5% FBS in PBST for 1 h at room temperature followed by twice washing in PBS with 0.2% Tween 20. Cells were then incubated with targeted primary antibody (1:100 dilution) in 3% BSA in PBST for 12 h at 4°C followed by washing thrice in PBS with 0.2% tween 20. Cells were then incubated with the fluorescent conjugated respective secondary antibody (1:300 dilutions) in 3% BSA in PBST for 1 h at room temperature in the dark. Finally, washings were done and coverslips mounted on slides by anti-fade reagent with DAPI (ProLong Gold Antifade reagent, Invitrogen, USA). Image analysis was done on a confocal microscope (Zeiss LSM700, USA).

4.2.12 Analysis of Apoptosis by FACS

RAW 264.7 cells were seeded in 6 well cultures plate. When cells were 60 % confluent, pre-incubated with different concentrations of either ALA metabolites (1, 50 and 100 μ M) and/or doxorubicin (10 μ M) for 3 h, then stimulated with LPS (100 ng/ml) for 24 h. Staining of cells was done by FITC Annexin V Apoptosis Detection Kit (BD Biosciences, CA, USA), according to manufacturer's standardized protocol. Samples were run on Flow Cytometer (BD, LSR Fortessa, CA, USA) and data analyses were done on BD FACS Diva™ software.

4.2.13 Induction of Inflammation in vivo: Septic Shock with LPS

BALB/c male mice (20 to 25 g) were divided into 4 different groups (10 mice in each group), control, LPS, LPS+13-(S)-HPOTrE, and LPS+13-(S)-HOTrE. LPS was dissolved

in saline (0.9% NaCl) and injected (30 mg/kg body weight) intraperitoneally (i.p.) in all mice except control. In control mice, 0.9% saline was injected. ALA metabolites were dissolved in saline having Tween 80 (0.9% NaCl + 0.5% Tween 80). Two i.p. doses of 13-(S)-HPOTrE and 13-(S)-HOTrE (0.1 mg/kg body weight, 2.5 µg/mice) metabolites were injected, first at 1 h prior to LPS and second, soon after LPS administration. 250 µl saline with Tween 80 (vehicle control) was injected in control and LPS treated groups. All mice were kept in normal conditions with an extra vigilance. Mice were monitored initially at 2 h intervals for 12 h then for 4 days.

4.2.14 Induction of Inflammation *in vivo*: Cecal Ligation and Puncture (CLP) model

Cecal Ligation and Puncture was performed in BALB/c male mice (20 to 25 g). Mice were divided into 4 groups (5 mice/group), Sham, CLP, CLP+13-(S)-HPOTrE and CLP+13-(S)-HOTrE. The mice were anesthetized with 60 µg/g ketamine and 10 µg/g xylazine. After cleaning and disinfecting the lower abdomen by iodine solution to prevent infection, a 1.5 to 2 cm incision was made through linea alba. Then, the cecum was spotted and ligated with disinfected 3-0 silk suture and perforated twice using a 22-gauge needle. Wound strength was ensured by squeezing out a small amount of stool. Then the cecum was replaced into the abdomen, and the incision was closed properly. In Sham, mice undergone surgery but ligation and puncture were not performed. Tramadol hydrochloride (20 µg/g body wt.) was injected i.p. with 1 ml warm saline in all mice. In ALA metabolites treated mice, two i.p. doses of 13-(S)-HPOTrE and 13-(S)-HOTrE (0.1 mg/kg body weight, 2.5 µg/mice) metabolites were given, first at 1 h prior to CLP and second, soon after CLP surgery. Finally, all mice were kept at normal conditions

with an extra vigilance. The mice were sacrificed after 24 h of CLP surgery then blood, peritoneal fluid, and liver were collected.

4.3 STATISTICAL ANALYSES

All the experiments were performed in triplicates and the values represented as mean \pm SD. Data were correlated, analyzed and p-values were obtained using student's t-test. The p-value <0.05 was considered as statistically significant.

4.4 RESULTS

4.4.1 Hydroperoxy metabolites exhibit more cytotoxic effects on RAW 264.7 cells as compared to hydroxy metabolites of ALA.

The cytotoxic effects of 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] on RAW 264.7 cells were evaluated by MTT assay. Among these metabolites, 13-(S)-HPOTrE showed a more cytotoxic effect compared to the hydroxy metabolite, 13-(S)-HOTrE, when incubated at different concentrations for 24 h (Figure 4-1). Treatment with both metabolites decreased the proliferation of the cells in a dose and time-dependent manner. However, 13-(S)-HPOTrE and 13-(S)-HOTrE showed more cytotoxic effects when compared to ω -3 (ALA, and DHA) and ω -6 (AA, and LA) PUFAs (Figure 2-1). A 50% decrease in RAW 264.7 cell proliferation was observed at a concentration (IC₅₀ value) of 114 μ M 13-(S)-HPOTrE, which was much lower than 13-(S)-HOTrE ($>200\mu$ M) at 24 h. Based on these results, further experiments on RAW 264.7 cells were carried out up to 100 μ M concentration of ALA metabolites for analysis of their anti-inflammatory effects.

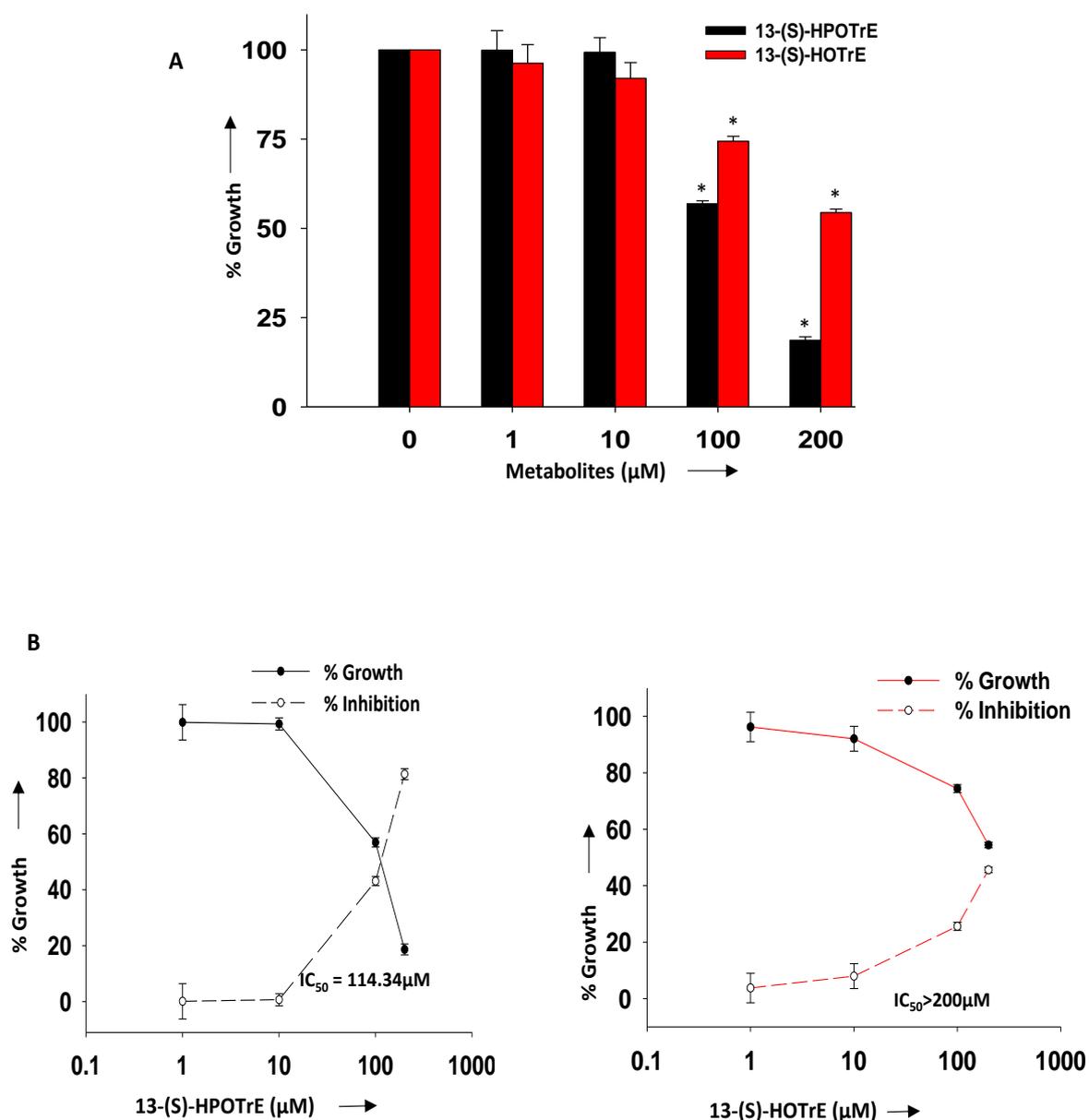


Figure 4-1: Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on cells viability in RAW 264.7 cells. **A)** Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on the viability of RAW 264.7 cells were measured by MTT assay. Cells were treated with different concentrations (1, 10, 100 and 200 μM) of ALA metabolites for 24 h. The percent cell growth following treatment was calculated, in comparison with untreated control cells. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) when compared with untreated control cells. **B)** IC_{50} values of 13-(S)-HPOTrE and 13-(S)-HOTrE calculated at 24 h. The values represent mean \pm SD of three independent experiments.

4.4.2 ALA metabolites reduce nitric oxide levels and ROS generation in RAW 264.7 cells and peritoneal macrophages.

Next, it was aimed to evaluate the effects of ALA metabolites on LPS induced inflammation by examining effects on pro-inflammatory parameters: NO- a second messenger and ROS- an oxidative stress marker. For this, RAW 264.7 cells were first treated with or without metabolites and challenged with LPS as described in the methods. There was significant elevation in NO production and ROS generation in cells when stimulated with LPS and this elevated NO level was reduced by 52.7% and 29% in the presence of 13-(S)-HPOTrE and 13-(S)-HOTrE at 100 μ M, respectively (Figure 4-2A). Similarly, LPS stimulated RAW 264.7 cells, pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE, resulted in the reduction of ROS generation, in a dose-dependent manner and at 100 μ M concentration, decreased ROS generation by 96.4% and 92.7% respectively (Figure 4.2B). Not only ALA metabolites, the substrate fatty acid ALA also showed the similar pattern of decreased NO and ROS production in LPS stimulated RAW 264.7 cells, though lower (89.5 % and 8.6%) compared to its metabolites (Figure 2-2, 2-3). Similar effects were observed on ROS level when the mouse peritoneal macrophages were pre-treated with ALA metabolites at lower doses (100 nM) and then challenged with LPS (Figure 4.2C). The significant reduction in the production of the pro-inflammatory markers by the ALA metabolites suggests their strong anti-inflammatory effects on LPS stimulated macrophages.

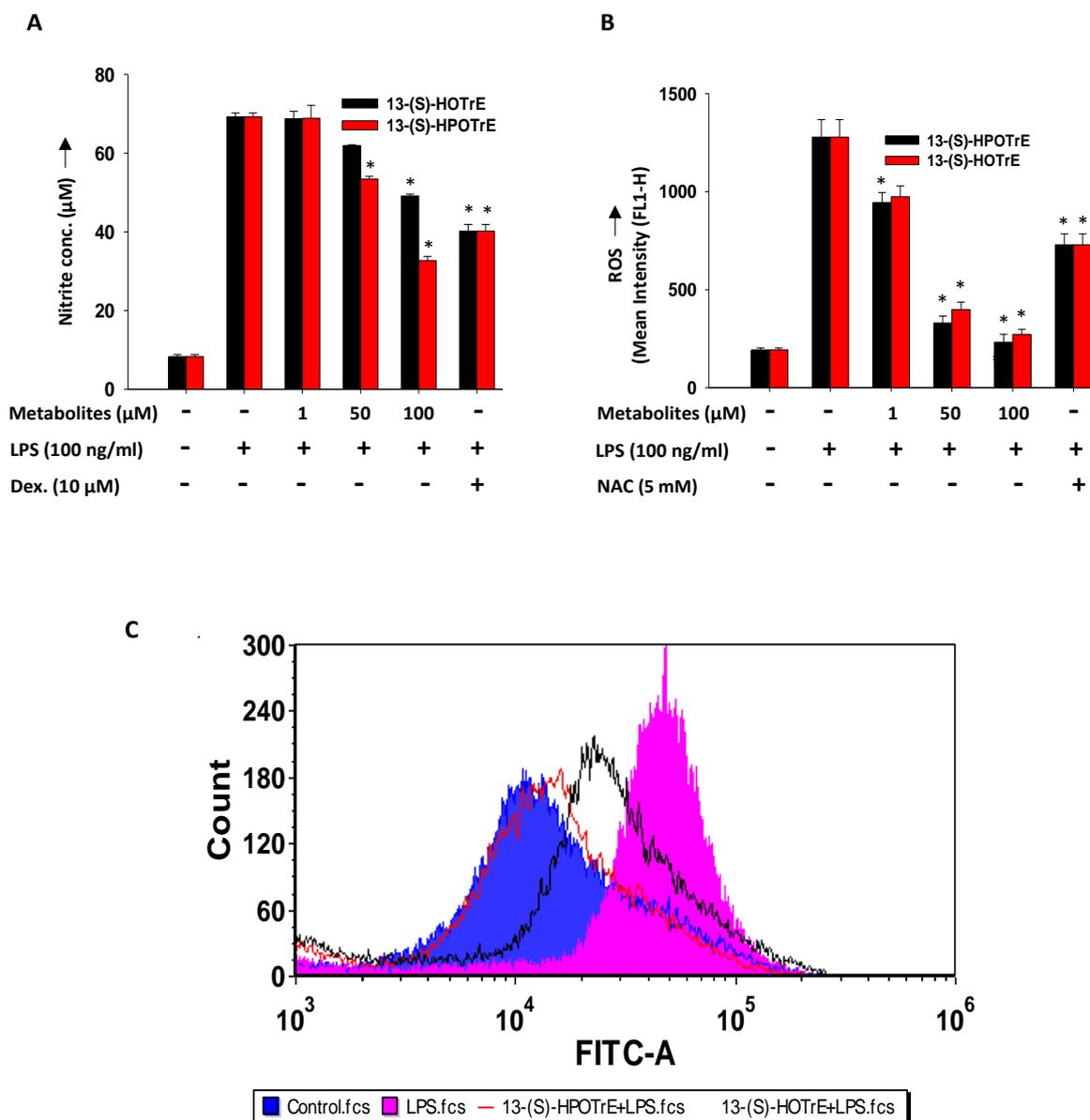


Figure 4-2: Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on generation of NO and ROS in RAW 264.7 cells and mouse peritoneal macrophages. **A**) Nitrite levels in the culture medium of RAW 264.7 cells pre-incubated with different concentrations (1, 50 and 100 μM) of ALA metabolites or dexamethasone (10 μM) for 3 h. Then stimulated with or without LPS (100 ng/ml) for the next 24 h. 13-(S)-HPOTrE showed more effective dose-dependent reduction in NO level as compared to 13-(S)-HOTrE. Dexamethasone, a steroidal anti-inflammatory drug that suppresses NO production, is used as positive control. *Indicates significance ($p < 0.05$) compared to LPS treated cells. **B**) Intracellular ROS level in RAW 264.7 cells following pretreatment with 100 μM of ALA metabolites for 3 h then stimulated with LPS for 16 h. 13-(S)-HPOTrE reduced ROS level more efficiently compared to 13-(S)-HOTrE. N-Acetyl Cysteine (NAC, 5 mM), a ROS inhibitor is used as positive control. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated cells. **C**) Intracellular ROS level in peritoneal macrophages following pre-incubation with 100 nM ALA metabolites for 3 h then challenged with LPS for 16 h. Similar to above result, 13-(S)-HPOTrE reduced ROS level more efficiently compared to 13-(S)-HOTrE. This is representative FACS chromatogram of the three independent experiments.

4.4.3 ALA metabolites inhibit the expression of iNOS and TNF- α in LPS stimulated RAW 264.7 cells.

iNOS is an enzyme associated with regulation of NO and ROS generation in monocytes, macrophages, and other cells [147]. The expression of iNOS and TNF- α , in RAW 264.7 cells stimulated with LPS in the presence and/or absence of ALA metabolites was studied. 13-(S)-HPOTrE and 13-(S)-HOTrE showed no effect on the expressions of either iNOS or TNF- α as compared to untreated RAW 264.7 cells, while LPS induced their expression. However, their expression in RAW 264.7 cells, pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE and then challenged with LPS, was reduced in a dose-dependent manner (Figure 4-3A). The transcript levels of iNOS and TNF- α were also analyzed by semi-quantitative PCR. In LPS treated RAW 264.7 cells, the transcript levels of iNOS and TNF- α were increased but were reduced by pre-treatment with 13-(S)-HPOTrE and 13-(S)-HOTrE in a dose-dependent manner (Figure 4-3B).

NF- κ B is known to regulate the expression of various pro-inflammatory genes, including iNOS and TNF- α [148,149] and ALA metabolites may affect its translocation to the nucleus to regulate gene expression. Therefore, the activation of NF- κ B was monitored for its translocation to the nucleus by confocal microscopy. While LPS stimulation of RAW 264.7 cells showed a marked translocation of NF- κ B, 13-(S)-HPOTrE and 13-(S)-HOTrE pre-treatments resulted in a decrease in NF- κ B translocation (Figure 4-4A). Very similar effects were observed on NF- κ B translocation when the mouse peritoneal macrophages were treated with 13-(S)-HPOTrE and 13-(S)-HOTrE at a lower dose (100 nM) and then challenged with LPS (Figure 4-4B).

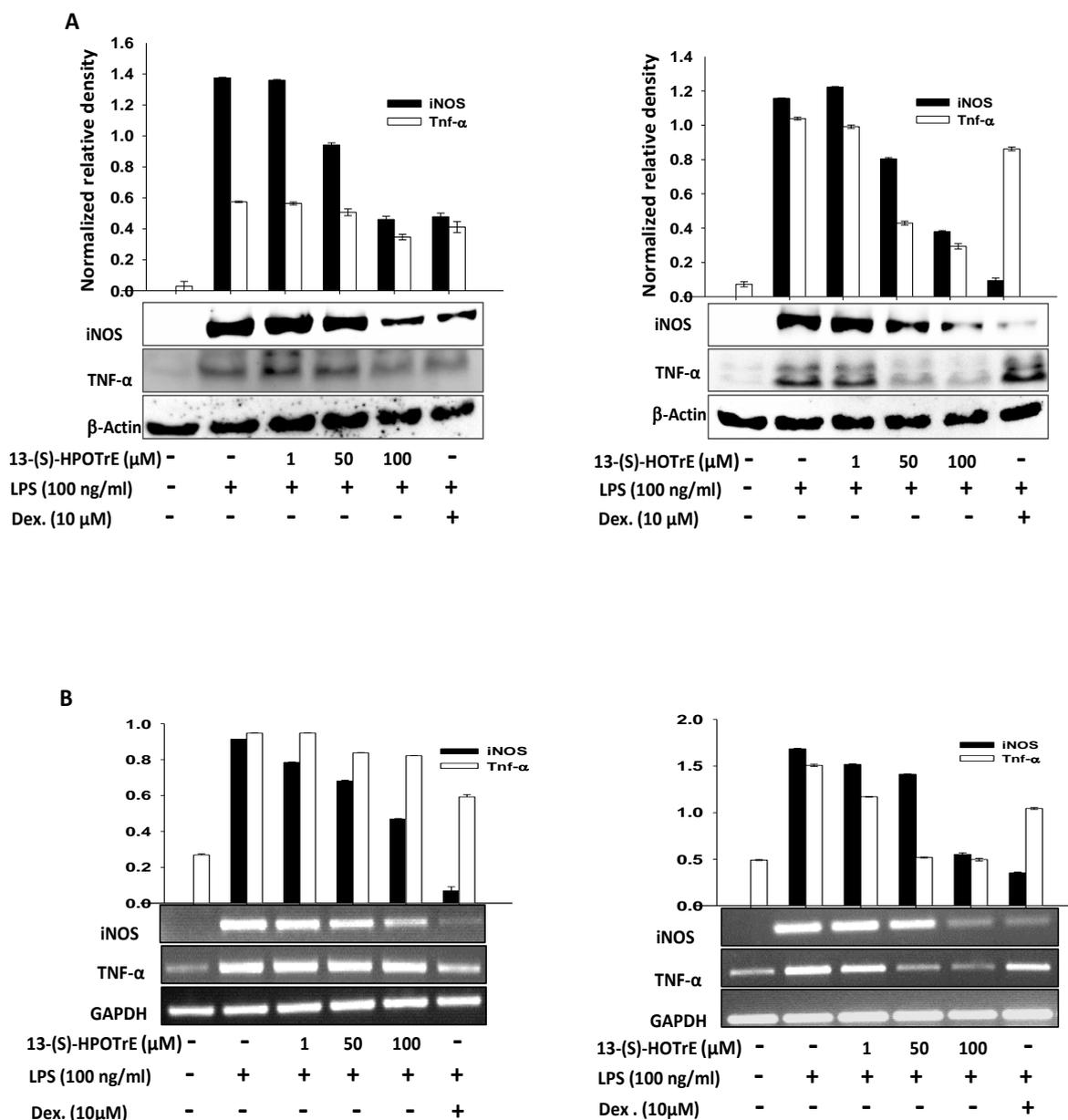


Figure 4-3: Anti-inflammatory effect of 13-(S)-HPOTrE and 13-(S)-HOTrE is mediated by inhibition of *iNOS* and *TNF-α*. **A)** Immunoblot analysis showing the expression of *iNOS* and *TNF-α* following treatment with 13-(S)-HPOTrE and 13-(S)-HOTrE (1, 50 and 100 μM) concentrations for 3 h and then stimulated with LPS for 24 h. β-Actin is used as an internal control. Dexamethasone (10 μM) is used as positive control. These are representative blots of the three independent experiments. **B)** RT-PCR analysis of transcripts of *iNOS* and *TNF-α* in RAW 264.7 cells pre-treated with ALA metabolites for 3 h then stimulated with LPS (100ng/ml) for 24 h. GAPDH is used as an internal control. Dexamethasone is used as positive control. These are representative gel images of the three independent experiments. The relative band intensities were measured by quantitative scanning densitometry (Image J).

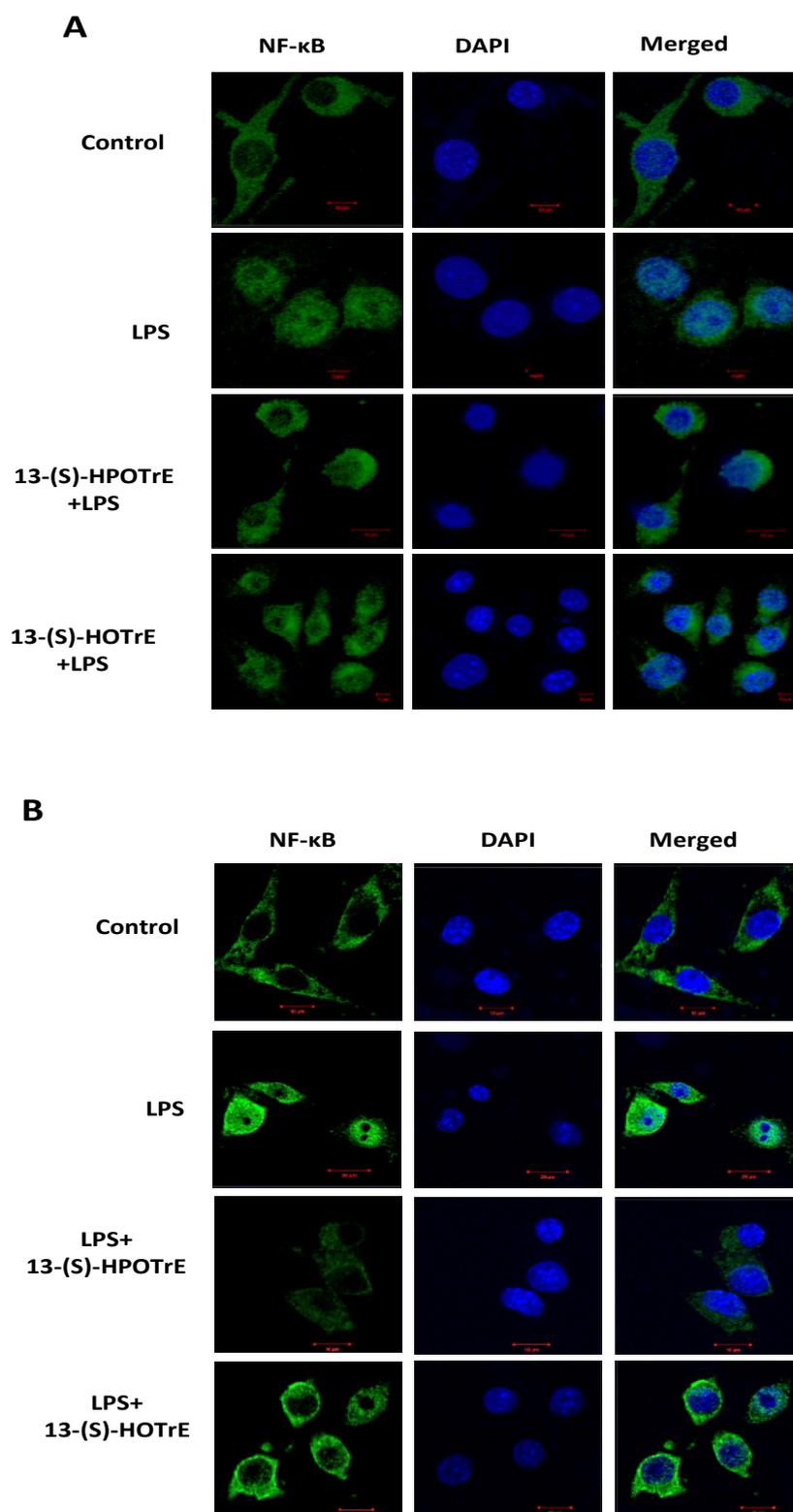


Figure 4-4: ALA metabolites inhibit the expression of *iNOS* and *TNF- α* in LPS stimulated RAW 264.7 cells through NF- κ B pathway. **A)** Immunofluorescence microscopy of RAW 264.7 cells pre-treated with or without ALA metabolites (100 μ M) for 3 h and then with LPS for 16 h. Immunostained for NF- κ B (Green) and DAPI (Blue). Bar Scale: 10 μ m. The image show representative of three independent experiments. **B)** Immunofluorescence microscopy of peritoneal macrophages pre-treated with or without ALA metabolites (100 nM) for 3 h and then challenged with LPS for 16 h. Immunostained for NF- κ B (Green) and DAPI (Blue), Bar Scale: 10 μ m. The image show representative of three independent experiments.

4.4.4 13-(S)-HPOTrE and 13-(S)-HOTrE inactivate inflammasome in PPAR- γ dependent manner in RAW 264.7 cells and peritoneal macrophages.

It is well known that NLRP3 inflammasome, an intracellular sensor that detects pathogens and sterile inflammation, gets activated in part through NF- κ B in response to LPS treatment [150–152]. For analyzing, the effects of 15-LOX metabolites of ALA on NLRP3 inflammasome activation in LPS stimulated RAW 264.7 cells, the level of gene transcripts associated with inflammasome complex were quantified by semi-quantitative PCR. An increased transcript level of NLRP3, caspase-1, IL-1 β and IL-18 in LPS activated RAW 264.7 cells showed an efficient dose-dependent reduction on treatment with both 13-(S)-HPOTrE and 13-(S)-HOTrE (Figure 4-5A). Since activated inflammasomes initiate the processing and secretion of IL-1 β [153,154], we measured the level of IL-1 β , in the culture medium of RAW 264.7 cells by ELISA. These studies showed a 4.4 fold increase in the level of IL-1 β in response to LPS treatment in RAW 264.7 cells and this elevated level of IL-1 β was significantly reduced by the treatment of 13-(S)-HPOTrE and 13-(S)-HOTrE, in a dose-dependent manner (Figure 4-5B). At 100 μ M concentration, 13-(S)-HPOTrE and 13-(S)-HOTrE reduced IL-1 β levels by 86.4% and 23% respectively.

LOX metabolites are natural ligands of PPAR- γ [155–158]. Interestingly, PPAR- γ and their coactivators were shown to promote macrophage's anti-inflammatory properties to increase insulin sensitivity [159]. In the present scenario, we studied the involvement of PPAR- γ on the NLRP3 inflammasome activation in LPS treated RAW 264.7 cells and peritoneal macrophages. Immunofluorescence microscopy studies showed activation of NLRP3 inflammasome complex along with upregulation of

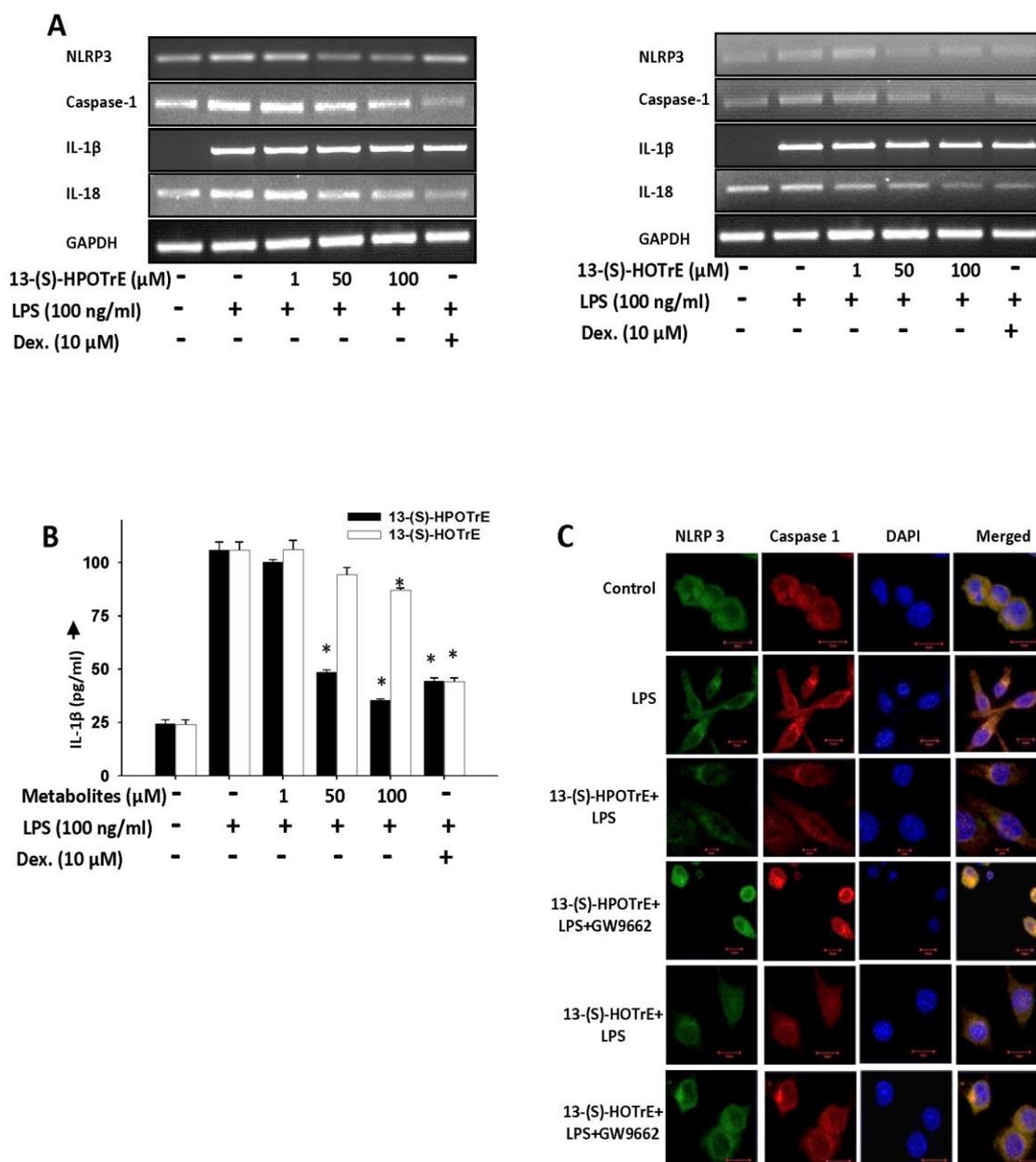


Figure 4-5: ALA metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE, inhibit inflammasome complex in RAW 264.7 cells. **A**) In semi-quantitative PCR analysis, 13-(S)-HPOTrE, and 13-(S)-HOTrE showed decrease in transcript level of NLRP3, caspase-1, IL-1β and IL-18 at various concentrations (1, 50 and 100 μM) pre-incubated for 3 h then stimulated with LPS for 24 h. GAPDH is used as an internal control. **B**) Estimation of IL-1β levels in the culture medium of cells as per the treatment described in (A). Dexamethasone (10 μM) is used as positive control. The values represent mean ± SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS alone treated cells. **C**) Immunofluorescence microscopy of RAW 264.7 cells pre-treated with ALA metabolites (100 μM) for 3 h then stimulated with LPS for 24 h. Immunostained for NLRP3 (Green), caspase-1 (Red) and DAPI (Blue). Bars Scale: 10 μm. Data show representative of three independent experiments.

caspace-1 upon LPS treatment in RAW 264.7 cells (Figure 4-5C). However, pre-treatment of RAW 264.7 cells with 13-(S)-HPOTrE or 13-(S)-HOTrE and then challenged with LPS resulted in inactivation of NLRP3 inflammasome and thus downregulation of caspace-1. Interestingly, these effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on inflammasome and caspace-1 were reversed when co-incubated with GW9662, a PPAR- γ antagonist.

To validate the findings observed in RAW 264.7 cells, further, studies were taken up on peritoneal macrophages at much lower doses (100 nM and 400 nM) of 13-(S)-HPOTrE and 13-(S)-HOTrE. Immunoblot analysis showed an increase in the expression of NLRP3 in LPS challenged peritoneal macrophages while cells pre-treated with ALA metabolites and challenged with LPS showed a reduction in the expression of NLRP3 (Figure 4-6A). Next, the IL-1 β cytokine was probed in the culture medium by immunoblot analysis and quantified by ELISA. As shown in figure 4-6A & 4-6B, peritoneal macrophages pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE and then challenged with LPS reduced the level of IL-1 β by 59.5% and 54.5% respectively, when compared to LPS alone challenged macrophages. These metabolites also increased the levels of anti-inflammatory cytokine-IL-10 in culture medium (Figure 4-6C). Similarly, the involvement of PPAR- γ in the regulation of inflammasome by ALA metabolites was validated on peritoneal macrophages at lower concentrations. Immunofluorescent microscopy showed decreased expression of NLRP3 inflammasome and caspace-1 in macrophages pre-treated with ALA metabolites and challenged with LPS. However, the effects of ALA metabolites were reversed when co-incubated with GW9662, PPAR- γ antagonist (Figure 4-7). The foregoing results suggest that inactivation of the inflammasome by 13-(S)-HPOTrE and 13-(S)-HOTrE in LPS challenged RAW 264.7 cells

and peritoneal macrophages is mediated through PPAR- γ dependent pathway. Immunoblot analysis of the LPS stimulated RAW 264.7 cells revealed an increase in the COX-2 expression (Figure 4-8A). The LPS induced expression of COX-2 was further enhanced by both 13-(S)-HPOTrE and 13-(S)-HOTrE in a dose-dependent manner.

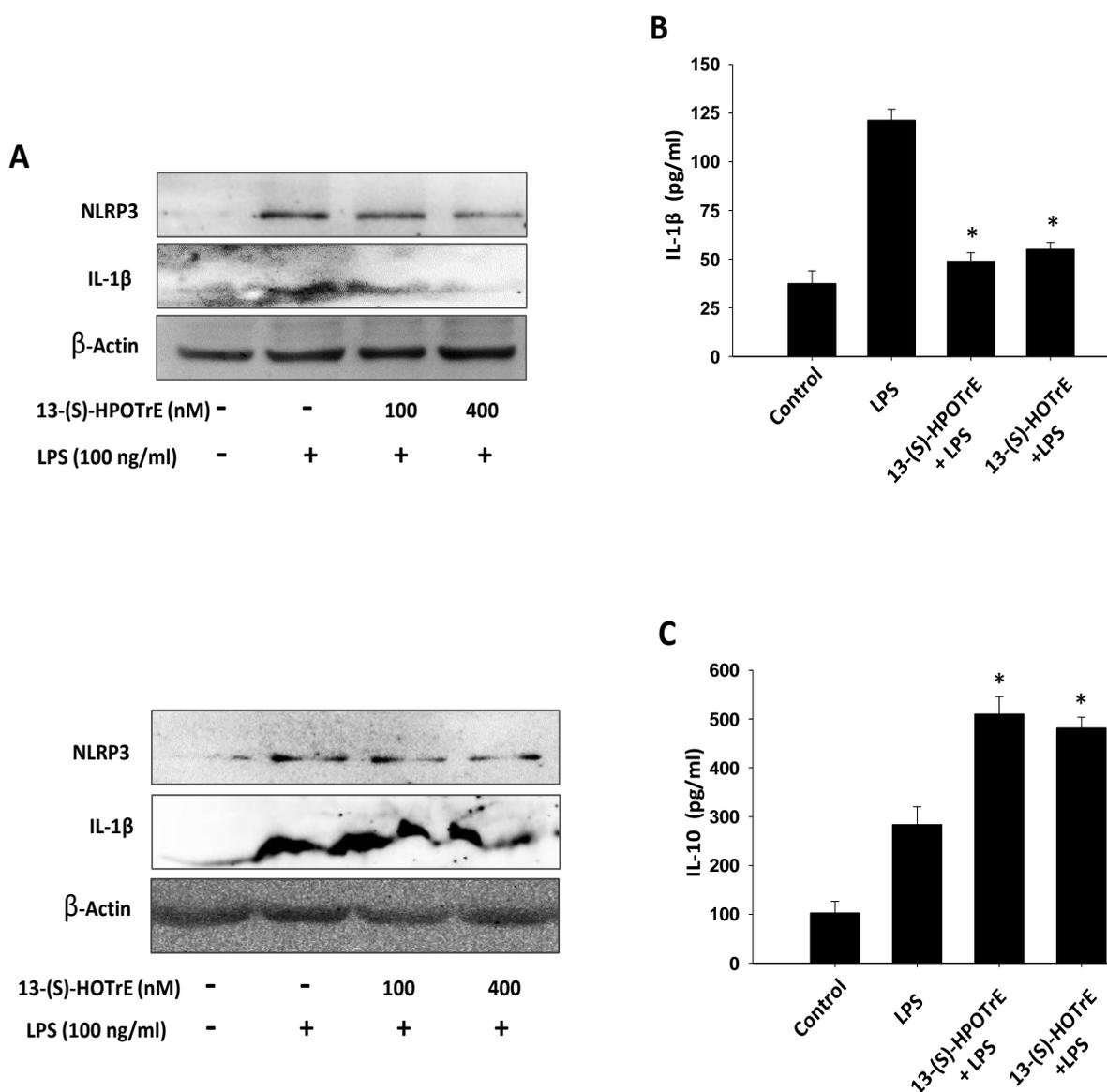


Figure 4-6: ALA metabolites inhibit inflammasome complex activation in mouse peritoneal macrophages. **A)** Immunoblot analysis of NLRP3 and IL-1 β (in culture medium) expression in peritoneal macrophages, pre-incubated with ALA metabolites (100 nM and 400 nM) for 3 h then challenged with LPS (100 ng/ml) for next 24 h. β -Actin is used as an internal control. **B)** Estimation of IL-1 β levels in the culture medium by ELISA as per the treatment described above. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated peritoneal macrophages. **C)** Estimation of IL-10 levels in the culture medium by ELISA as per the treatment described above (at 100 nM). The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated peritoneal macrophages.

Coinciding with the changes observed in COX-2, the downstream metabolites of COX-2, PGE₂ and PGD₂, also showed similar trend of enhanced production with LPS treatment (Figure 4-8B). These studies reveal that COX-2, a key enzyme involved in mediating inflammation, may also be playing a role in the resolution of inflammation through the generation of PGD₂ which is a PPAR- γ ligand [133].

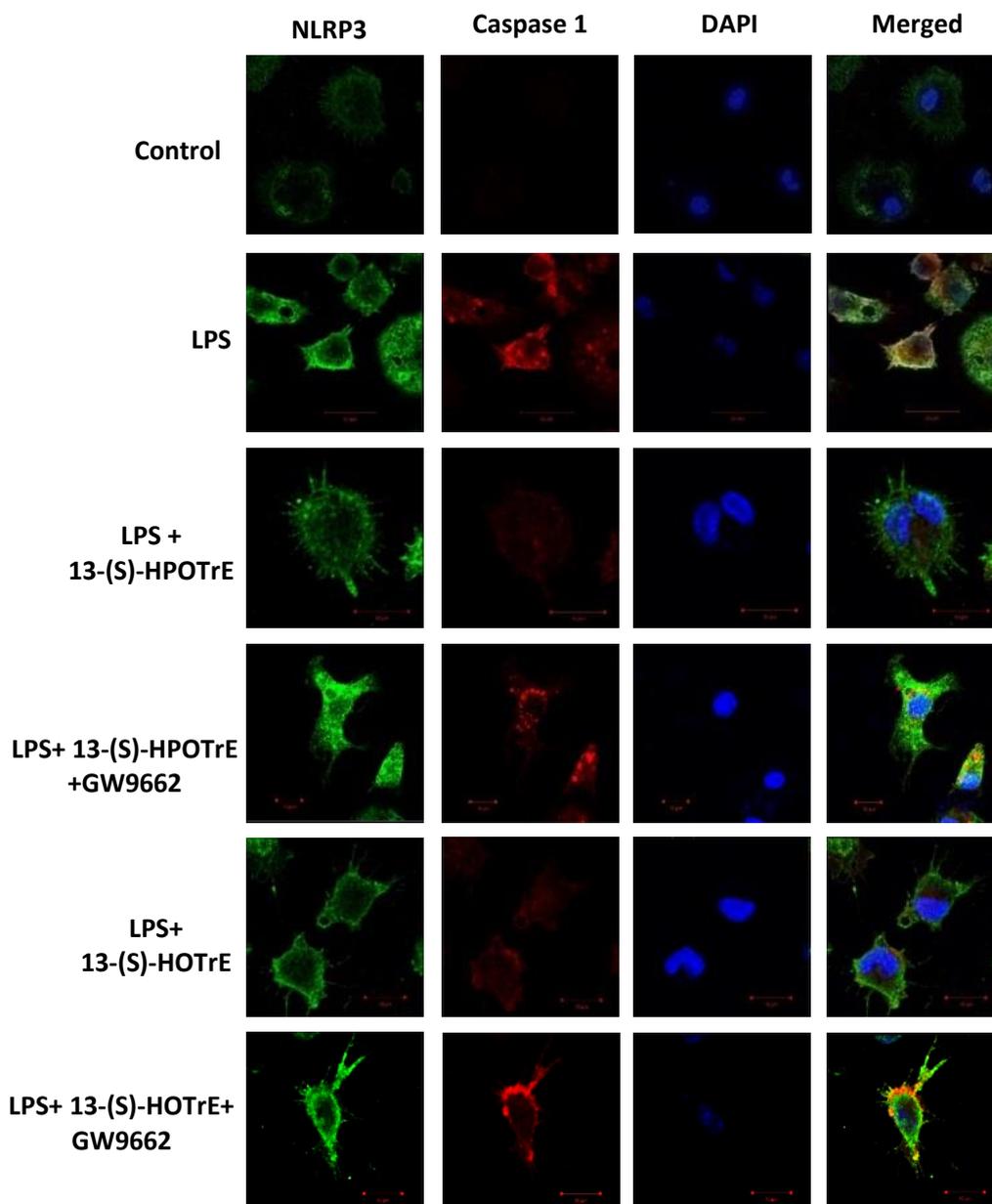


Figure 4-7: *ALA metabolites inhibit inflammasome complex activation in mouse peritoneal macrophages.* Immunofluorescence microscopy of peritoneal macrophages treated with ALA metabolites (100 nM) for 3 h then stimulated with LPS for 24 h. Immunostained for NLRP3 (Green), caspase-1 (Red) and DAPI (Blue). Bars Scale: 10 μ m. Images show representative of three independent experiments.

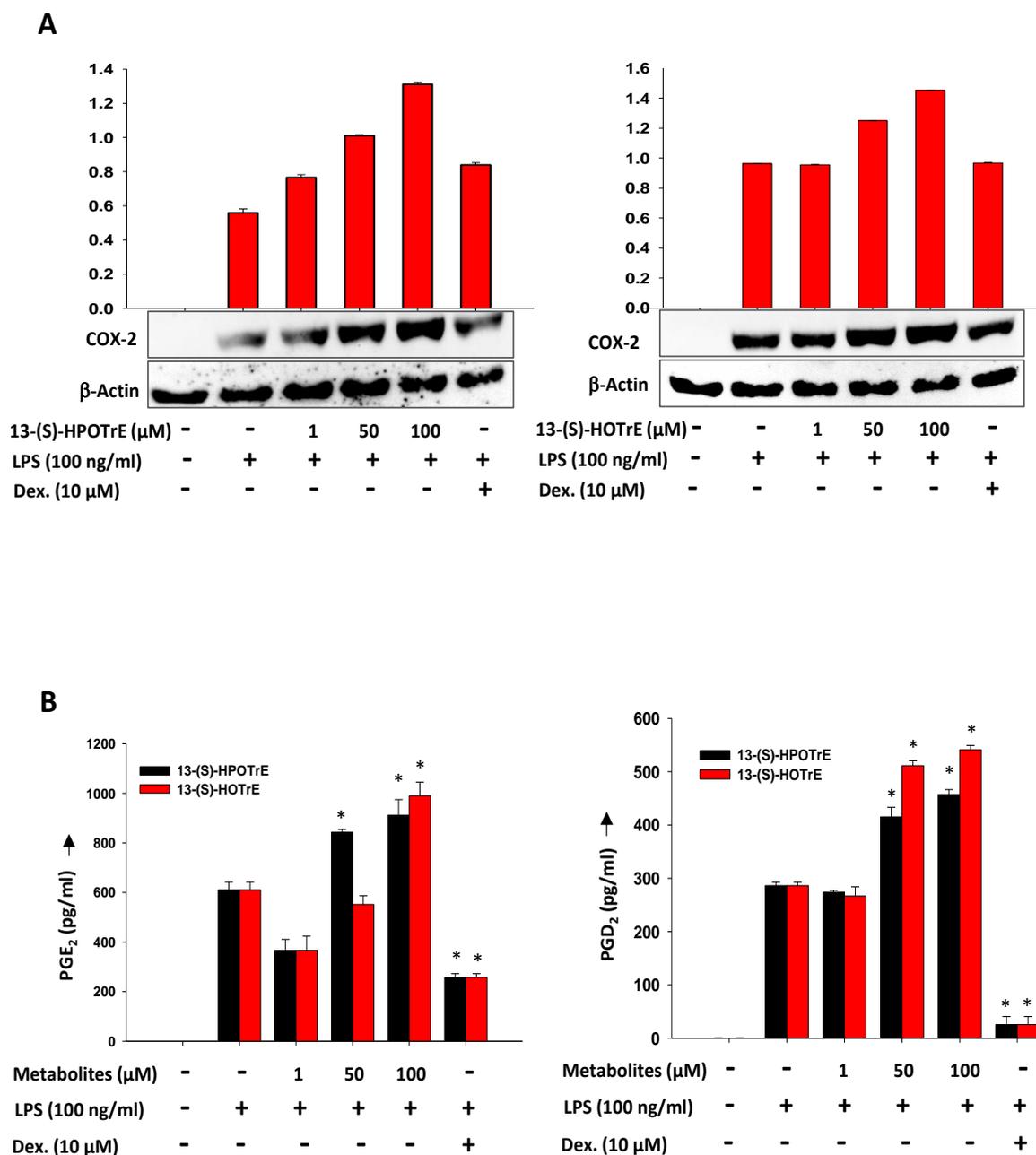


Figure 4-8: *13-(S)-HPOTrE and 13-(S)-HOTrE show anti-inflammatory effects by upregulating expression of COX-2.* **A)** Immunoblot analysis of COX-2 expression in RAW 264.7 cells pre-incubated with ALA metabolites at different concentrations (1, 50 and 100 μM) for 3 h then further stimulated by LPS (100 ng/ml) for next 24 h. β-Actin is used as an internal control and Dexamethasone is used as positive control. Western blot shows representative of three independent experiments. **B)** Estimation of PGE₂ and PGD₂ level in the culture medium of RAW 264.7 cells when pre-incubated with ALA metabolites for 3 h and then stimulated with LPS for 24 h. Dexamethasone is used as positive control. The values represent mean ± SD of three independent experiments. *Indicates significance (p < 0.05) compared to LPS treated cells.

4.4.5 ALA metabolites induce apoptosis in LPS treated RAW 264.7 cells.

It is known that apoptosis plays a vital role in the resolution of inflammation and Beclin-1 dependent inhibition of autophagy by apoptosis enhances its anti-inflammatory effects [106]. Apoptosis blocks Beclin-1 dependent autophagy by blocking autophagosome synthesis [160]. Moreover, LPS and activated inflammasomes also induce autophagy in mesothelial cells [107]. Since ALA metabolites showed anti-inflammatory effects, we examined whether they affect induction of apoptosis and autophagy in LPS stimulated RAW 264.7 cells. 13-(S)-HPOTrE treatment increased apoptosis in LPS challenged RAW 264.7 cells in a dose-dependent manner (Figure 4-9) although, 13-(S)-HPOTrE and 13-(S)-HOTrE showed no effect on apoptosis in unchallenged cells. A significant increase in autophagy with the enhanced conversion of soluble LC3-I into lipid bound LC3-II and increased puncta formation were observed in LPS challenged RAW 264.7 cells. However, these effects were greatly reduced or undetectable in RAW 264.7 cells pre-treated with ALA metabolites and challenged with LPS (Figure 4-10A, B). Moreover, immunoblot analysis also showed induced expression of beclin-1, an autophagic marker, which was greatly reduced when RAW 264.7 cells was treated with ALA metabolites in a dose-dependent manner (Figure 4-10C).

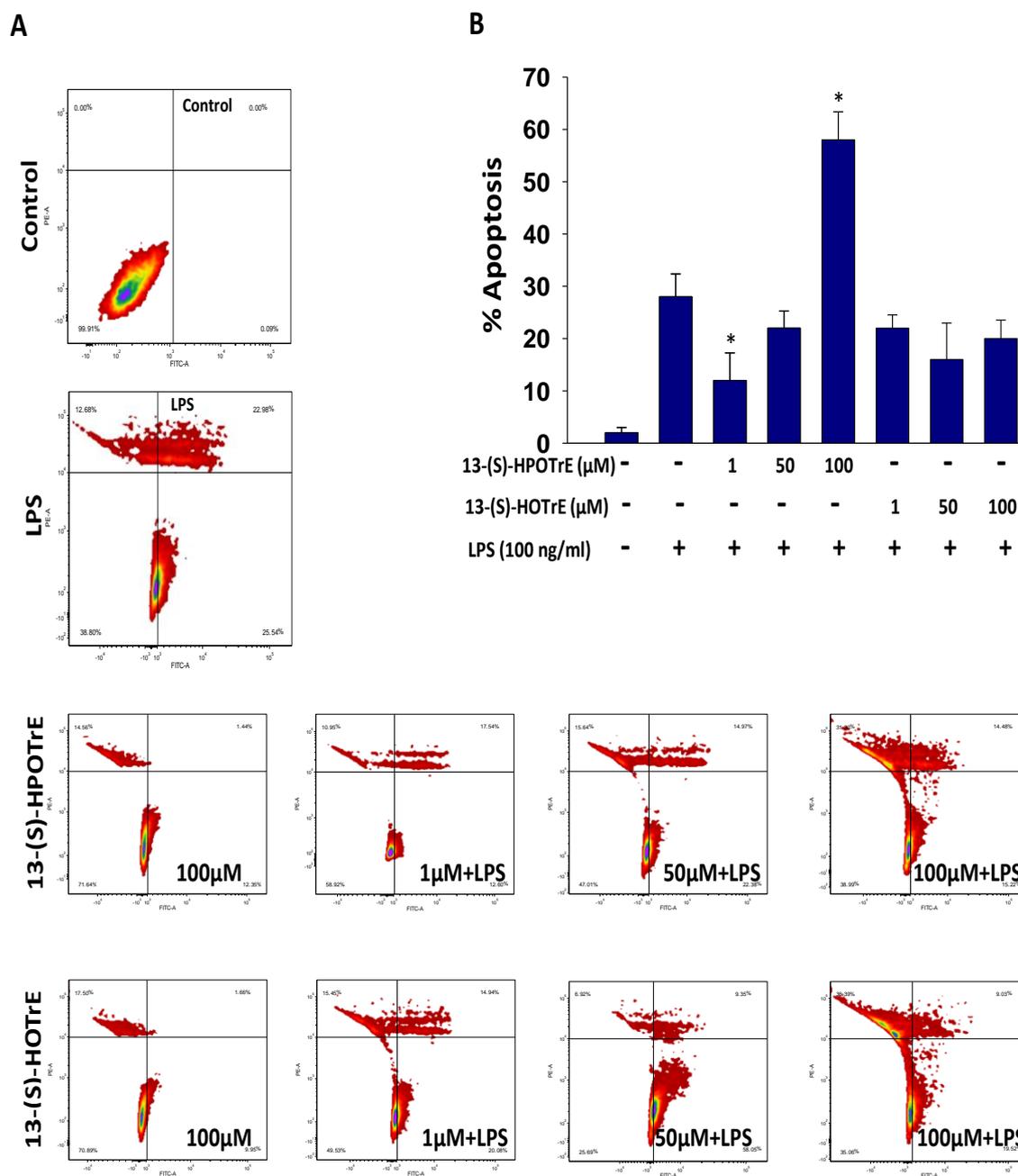
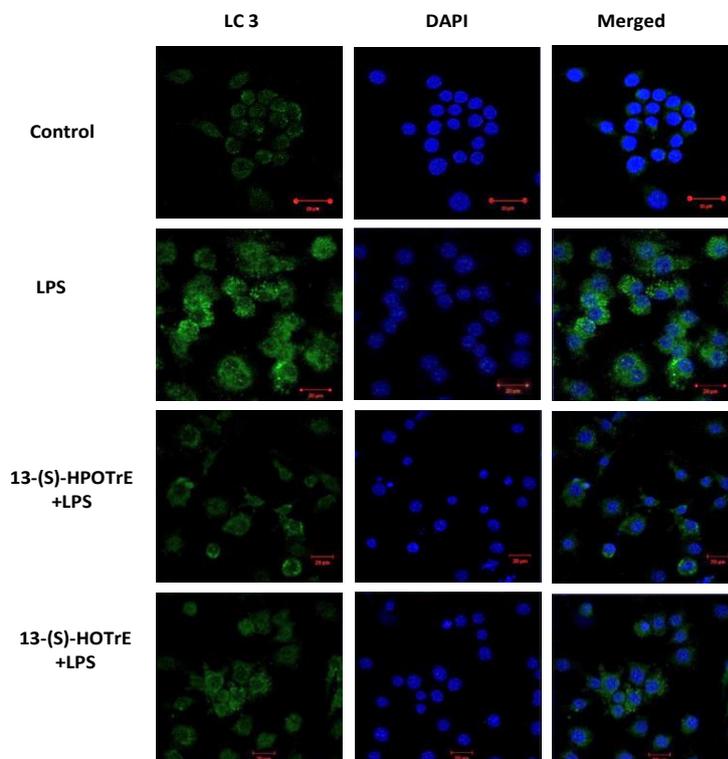
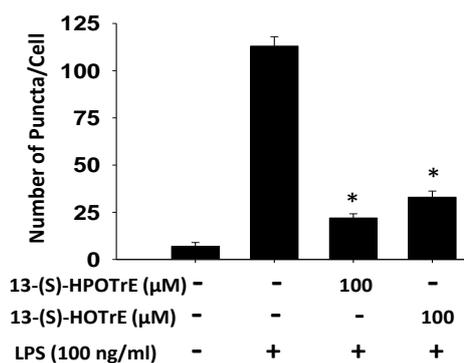


Figure 4-9: *13-(S)-HPOTrE and 13-(S)-HOTrE induce apoptosis in LPS stimulated RAW 264.7 cells.* **A)** Flow cytometric analysis showing the effects of ALA metabolites on apoptosis in RAW 264.7 cells challenged with LPS. Apoptosis is assayed by Propidium Iodide and FITC conjugated Annexin V at 24 h, by flow cytometric Analysis. The apoptosis level was calculated as % of AnnexinV⁺ PI⁻ cells in density plot distribution. The dead cells were gated and analysis was performed only on live cells. *Indicates significance ($p < 0.05$) compared to LPS treated cells. **B)** Bar graph is representation of above data.

A



B



C

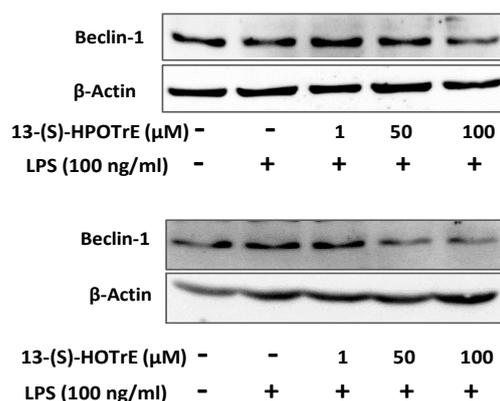


Figure 4-10: *13-(S)-HPOTrE and 13-(S)-HOTrE inhibit Beclin-1 mediated autophagy in LPS stimulated RAW 264.7 cells.* **A)** Confocal microscopy of RAW 264.7 cells treated with or without ALA metabolites (100 μM) for 3 h then challenged with LPS for 24 h. Immunostained for LC 3 (Green) and DAPI (Blue). Bars Scale: 10 μm. Images show representative of three experiments. **B)** Bar graph shows puncta/cell calculated by ImageJ LC3 macro.*Indicates significance ($p < 0.05$) compared to LPS treated cells. **C)** Beclin-1 Immunoblotting of RAW 264.7 cells pre-incubated with ALA metabolites for 3 h and then challenged with LPS for 24 h. Western blots show representative of three independent experiments.

4.4.6 ALA metabolites extend BALB/c mice survival and show anti-inflammatory properties by regulating cytokines and inflammasome.

Septic shock is a complication of inflammation in which infections or toxins induce an inflammatory response in the entire body. Endotoxin-mediated septic shock is often integrated with high mortality [161]. On the other hand, saturated fatty acid had shown major impact on the survival of mice in bacterial infection [98] and these ALA metabolites showed anti-inflammatory effects in *in vitro* model system. We then wanted to validate the effects of ALA metabolites *in vivo* on the survival of mice in septic shock induced by LPS in toxemia model. These studies showed features of septic shock in all the mice received LPS such as increase in heartbeat rate, decrease in body weight, apathy, dullness and diarrhea, which began to die within 12 h. Contrary to this, the mice pre-treated with ALA metabolites and then challenged with LPS were quite active. However, loss of weight was observed in all except control mice. The results from this experiment showed that survival rate in ALA metabolites pre-treated mice were 40% and 10% extended than LPS alone challenged mice (Figure 4-11A).

Since ALA metabolites showed a decrease in mortality rate in mice with endotoxin-mediated septic shock, studies were further extended to mice with sepsis induced by polymicrobial infection in a CLP mouse model. Results showed up-regulation of iNOS and NLRP3 expression in CLP mice and their down-regulation in mice pre-treated with ALA metabolites (Figure 4-11B). The levels of IL-1 β and IL-10 were increased in liver tissue and serum of CLP mice. However, the level of pro-inflammatory cytokine-IL-1 β was decreased while the level of anti-inflammatory cytokine-IL-10 was further increased in mice treated with ALA metabolites (Figure 4-11C).

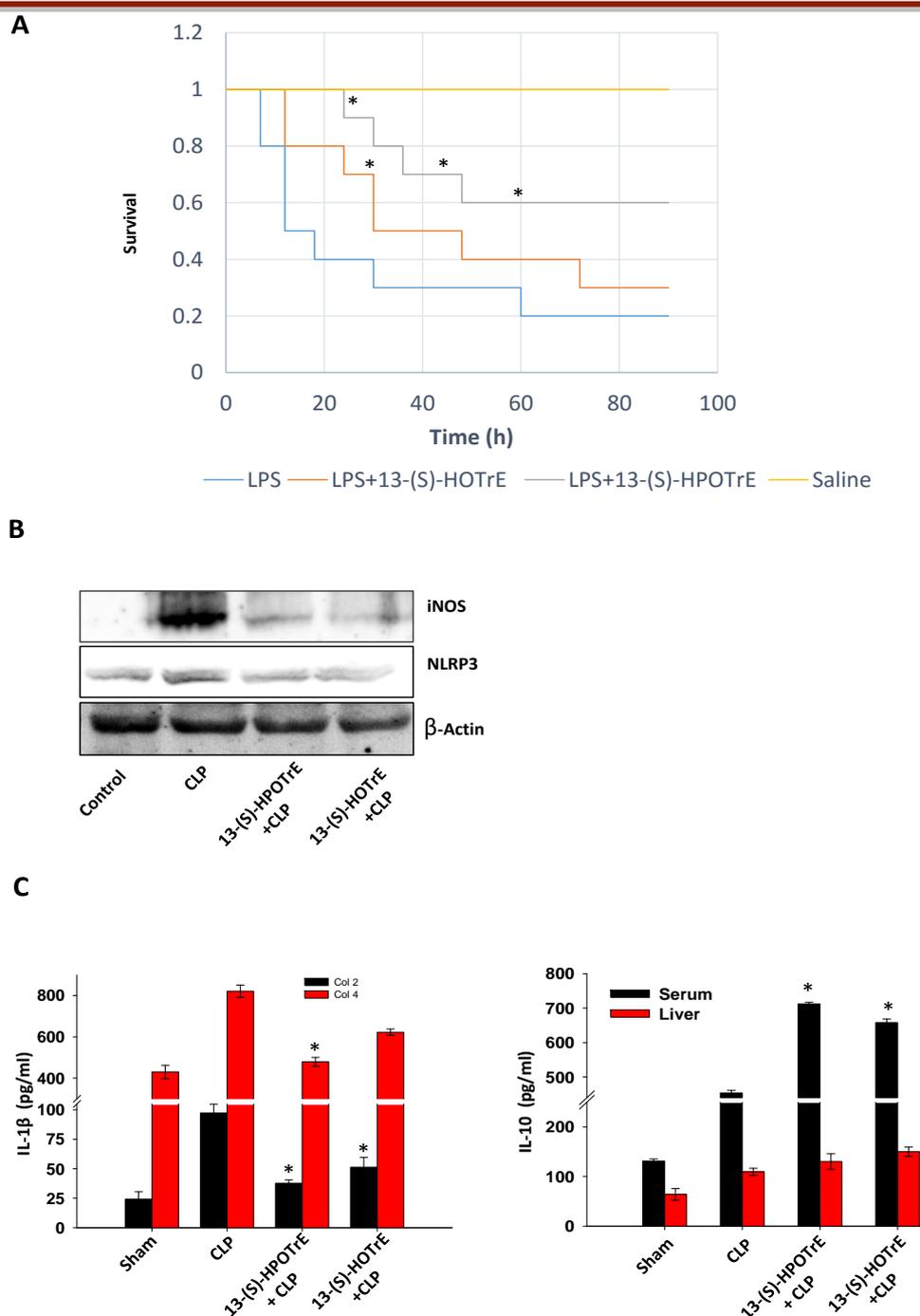


Figure 4-11: Effects of ALA metabolites during sepsis in BALB/c mice. **A)** ALA metabolites showed an increase in survival of BALB/c mice ($n=10$ mice/group) in endotoxin-induced Septic Shock in toxemia model. LPS (30 mg/kg) was injected i.p. and mice were monitored for 4 days then mortality was calculated. ALA metabolites showed decreased mortality rate in metabolites treated and LPS challenged mice as compared to LPS challenged mice. The survival curve is plotted on Kaplan-Meier method. *Indicates significance ($p<0.05$) compared to LPS treated mice. **B)** Sepsis was induced by polymicrobial infection in CLP mouse model ($n=5$ mice/group). Immunoblot analysis of iNOS and NLRP3 expression in CLP mice model, pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE (0.1 mg/kg, 2.5 μ g/mice) as described in methodology. Mice were sacrificed after 24 h of CLP and tissues were collected. β -Actin is used as an internal control. **C)** Estimation of IL-1 β and IL-10 cytokines levels in serum and liver tissue. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p<0.05$) compared to CLP mice.

4.5 DISCUSSION

The ratio of ω -6 PUFAs: ω -3 PUFAs in cell membranes reflect the physiological status of the tissues and regulate the inflammatory response to a variety of external or internal stimuli and thus maintenance of cellular homeostasis [100,101]. ω -3 PUFAs are known to exhibit anti-inflammatory effects and reduce the oxidative stress in the cells [51,100]. The findings of the present study also support this concept wherein ALA, ω -3 PUFA, and its metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE, significantly reduced the production of NO and ROS, as well as inflammatory cytokines, in LPS stimulated RAW 264.7 cells and in mouse peritoneal macrophages. Further studies on *in vivo* sepsis model and CLP mice model demonstrated the protective role of 13-(S)-HPOTrE and 13-(S)-HOTrE as evidenced by a decrease in the mortality rate and by the reduction of pro-inflammatory markers, in ALA metabolites treated BALB/c mice.

From previous studies, it has been established that ω -3 PUFAs exert their anti-inflammatory effects through several mechanisms, one of which being NF- κ B signalling [51,100]. ω -3 PUFAs prevent the phosphorylation and degradation of I κ -B α protein by proteasome complex, thus inhibiting NF- κ B signalling pathways [110]. The present study shows that 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] inhibit the translocation of NF- κ B to the nucleus, along with the reduction of NO and ROS in LPS stimulated RAW 264.7 cells and peritoneal mouse macrophages. ALA metabolites also inhibited the activation of NLRP3 inflammasome as well as downstream signalling molecules such as caspase-1 and IL-1 β at both transcriptional as well as translational levels. Interestingly, these effects of ALA metabolites on NLRP3 inflammasome were

blocked by the PPAR- γ antagonist-GW9662. These studies comprehensively suggest that inactivation of LPS induced NLRP3 inflammasome by 13-(S)-HPOTrE or 13-(S)-HOTrE in RAW 264.7 cells and peritoneal macrophages is dependent on PPAR- γ . Indeed a number of studies have shown that several PUFAs metabolites are ligands of PPAR- γ [137], further supporting such a possibility.

Recent studies have established that the inducible isoform of COX, COX-2, has dual roles, pro-and anti-inflammatory, depending on the downstream metabolites generated [129,162]. In the early stages, it is shown that COX-2 induction is mainly associated with the generation of pro-inflammatory prostaglandins, whereas at later stages the downstream metabolite is PGD₂, a ligand for PPAR- γ [133], which has been observed to possess anti-inflammatory roles [163]. In the present study, an increase in the expression of COX-2 and its downstream metabolites (PGE₂ and PGD₂) was observed in RAW 264.7 cells pre-treated with ALA metabolites and then stimulated with LPS. Here, COX-2 may be playing an anti-inflammatory role by shifting PGE₂ dominated prostaglandins in LPS stimulated macrophages to PGD₂ dominated prostaglandins upon treatment with ALA metabolites. It has been reported that PGD₂ derivative PGJ₂ and their metabolites ¹² Δ PGJ₂ and 15d-PGJ₂, often derived from induced COX-2, exhibit their anti-inflammatory effects in various *in vivo* systems [131,138,164]. In the present study the induced expression of COX-2 and increased the formation of PGD₂ upon treatment with ALA metabolites in LPS stimulated macrophages may be mediating the anti-inflammatory effects through its downstream metabolite, 15d-PGJ₂ a natural ligand for PPAR- γ [165]. This hypothesis is supported by the observation that PPAR- γ is maintaining the anti-inflammatory state, by inhibiting inflammasome and IL-1 β , via induced COX-2 generated downstream metabolites, and when PPAR- γ is inhibited, it is

failing to inactivate the inflammasome. The reverse effects of ALA metabolites on inflammasome and caspase-1, when co-incubated with the PPAR- γ antagonist GW9662 supports such a possibility.

Macrophage differentiation, their subtypes and function depend on its surrounding environment. After differentiation, macrophages polarized into two subtypes, M1 and M2 with characteristic phenotypes and exhibit different behaviors [166]. While, the activation of M1 macrophage is associated with increased expression of iNOS [167] and increased level of pro-inflammatory cytokines such as TNF- α , IL-1 β and IL-6 [19], the activation of M2 macrophages is associated with increased level of anti-inflammatory cytokines-IL-10 and scavenger receptor A [19]. LPS stimulated pro-inflammatory state is associated with M1 subtype macrophage, on the other hand, PPAR- γ activation and increased PGE₂ [135,136] is associated with shifting of M1 macrophages into M2 macrophages subtypes [168,169]. In the present study, ALA metabolites activated PPAR- γ , and increased PGE₂ level that might be responsible for shifting of M1 to M2 macrophages subtypes and thereby mediating anti-inflammatory effects. Furthermore, an increased cytokine IL-10 as well as decreased expression of iNOS and TNF- α which are associated with M2 subtype macrophages, further strengthen such a possibility.

Apoptosis is the major mechanism for safe clearance of PMNLs at inflammatory sites and thus limit pro-inflammatory signals and promote resolution of inflammation rather than persistence of tissue damage [170]. In the present study, 13-(S)-HPOTrE showed a dose-dependent increase in apoptosis in LPS activated RAW 264.7 cells and it is previously reported that activation of PPAR- γ induces apoptosis in differentiated

naive macrophages [171]. Therefore, it is possible that the apoptotic effects of 13-(S)-HPOTrE might be mediated through PPAR- γ dependent pathway. There is a correlation between apoptosis and regulation of autophagy. It is reported that apoptosis inhibits beclin-1 mediated autophagy [160]. It supports the present findings on immunofluorescence microscopy with LC3, in which pre-treatment of ALA metabolites remarkably diminished autophagy in LPS challenged RAW 264.7 cells. Furthermore, in immunoblot analysis, a decrease in beclin-1 expression was observed in ALA metabolites pre-treated and challenged with LPS. From these studies, it can be concluded that these ALA metabolites inhibit beclin-1 mediated autophagy through induction of apoptosis.

Sepsis is a critical state of the body because of systemic immune response induced by pathogens, microbes or endotoxins, also called systemic inflammatory response syndrome [172]. In endotoxin-induced septic shock model, mice pre-treated with ALA metabolites showed a significant decrease in mortality rate. Moreover, in another *in vivo* study, in CLP mouse model, mice treated with these ALA metabolites showed decrease in expression of NLRP3. It also showed reduction in IL-1 β levels while elevation in IL-10 cytokine level as well. Thus, the *in vitro* anti-inflammatory effects of 13-(S)-HPOTrE and 13-(S)-HOTrE observed in RAW 264.7 cells and peritoneal macrophages also have been demonstrated *in vivo* as evidenced by the extension in the survival of mice in endotoxin-induced septic shock in toxemia model and inactivated inflammasome in polymicrobial-induced sepsis in CLP model.

In the present study, the hydroperoxy [13(S)-HPOTrE] and hydroxy [13(S)-HOTrE] metabolites of ALA showed anti-inflammatory effects, though the hydroperoxy

metabolite being more potent. As the hydroperoxy metabolite [13(S)-HPOTrE] is getting converted to the corresponding hydroxy [13(S)-HOTrE] metabolite with increasing period of time because of the reducing environment created by serum in culture medium, the effects of 13(S)-HPOTrE observed in the present study may be mediated by both the hydroperoxy and hydroxy metabolites of ALA.

The anti-inflammatory properties of ALA (ω -3 PUFA) observed in the present study thus are quite contrasting to those of AA (ω -6 PUFA) metabolites, wherein the hydroperoxy (15-(S)-HPETE) and hydroxy (15-(S)-HETE) metabolites of AA showed contrasting effects on angiogenesis, which is critically associated with inflammation [145,173,174]. While 15(S)-HPETE showed anti-angiogenic effects [145], the 15(S)-HETE induced angiogenesis [174] in adipose tissue. Also, such differential effects of the hydroperoxy and hydroxy metabolites of 15-LOX on angiogenesis were observed in human umbilical vein endothelial cells (HUVECs) [173]. Similar differential effects of hydroperoxy and hydroxy metabolites of 15-LOX with AA as the substrate were reported on chronic myeloid leukemia cell line [144]. Interestingly, in the present study, the hydroperoxy and hydroxy metabolites of ALA showed anti-inflammatory effects, however, the hydroperoxy metabolite being more potent than the hydroxy metabolite. These findings, thus strongly advocate the beneficial effects of ω -3 PUFAs in counteracting various inflammatory disorders, which are mainly mediated by the metabolites of ω -6 PUFAs.

In summary, ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE] exhibit anti-inflammatory effects in LPS challenged RAW 264.7 cells and mouse peritoneal macrophages by down-regulating LPS induced pro-inflammatory markers and by

inactivating the NLRP3 inflammasome complex. Additionally, the anti-inflammatory effects of ALA metabolites were mediated by the induction of apoptosis and inhibition of autophagy in the LPS challenged macrophages. These anti-inflammatory effects of ALA metabolites appear to be mediated by the inactivation of NLRP3 inflammasome complex and decrease in pro-inflammatory cytokines/enzymes along with simultaneous increase in anti-inflammatory cytokines. The present study also demonstrates the protective effects of ALA metabolites *in vivo* as evidenced by the extended survival of BALB/c mice in LPS induced septic shock.

Chapter 5

SUMMARY AND CONCLUSIONS

Inflammation is an essential part of host's response to infection or injury in order to maintain cellular homeostasis. Aberrant inflammation is associated with various disorders mediated by hyperactivation of inflammasome complexes and up-regulation of pro-inflammatory enzymes like iNOS [88,89] LOXs, and COXs [90–92]. The inflammatory response generated by eicosanoids is known to be mediated by pro-inflammatory cytokines such as IL-1 β and TNF- α [93]. The types of PUFAs present and their ratio in cell membranes reflect the physiological status of the tissues and regulate the inflammatory response to a variety of external or internal stimuli and thus maintain cellular homeostasis [100,101].

The dietary intake of PUFAs such as AA, LA and ALA directly affects the ratio of ω -6 and ω -3 PUFAs in the cell membranes. The higher amount of ω -6 PUFAs is hypothesized to increase the pro-inflammatory eicosanoids production and thus the onset of various types of inflammatory disorders. A sufficiently high intake of ω -3 PUFAs, on the other hand, is shown to offer protection from inflammatory diseases by decreasing the production of pro-inflammatory eicosanoids, cytokines, ROS and RNS [51,100]. This concept is also supported by the findings of the present study wherein ω -3 PUFA, ALA and its metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE], significantly reduce the production of pro-inflammatory mediators such as NO and ROS, as well as inflammatory cytokines, in LPS stimulated RAW 264.7 cells and in mouse peritoneal macrophages *in vitro*. Further, *in vivo* sepsis model and CLP mice model studies also demonstrates the protective effects of ALA metabolites as evidenced by a decrease in the mortality rate and by the maintenance of anti-inflammatory properties, in treated mice. For these studies, the 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-

HOTrE] were generated by employing novel 15-LOX source, linseed seedlings (*Linum usitatissimum*).

Linseed seedlings with abundant lipoxygenase activity

In the plants, LOXs play vital role during seed germination, growth, fruit ripening, and plant senescence [126]. Several studies reported that there are many folds increase in expression of LOXs during seed germination [114]. The present study also showed that the enzymatic activity of linseed seedlings increased during early days and further decreased as the seedlings mature. The specific activity of Day 2 linseed seedlings enzyme was significantly higher in comparison to the enzyme from other days seedlings. The linseed seedlings enzyme used both ω -6 and ω -3 PUFAs as substrates. Further, pH was optimized by measuring the enzyme activity of linseed seedlings at various pHs (pH 6.0 to 13.0), which showed many majors and minor peaks. The presence of such diverse pH optima reveals the possibility of different isoforms of LOXs. The possibility of 15-LOXs in linseed seedlings was further strengthened by comparing metabolites of linseed seedlings with metabolites of soybean 15-LOX on HPLC.

The linseed seedling enzyme is characterized as 15-LOX.

The Linseed seedling enzyme oxygenated PUFAs (AA, LA, and ALA) and generated corresponding hydroperoxy metabolites while hydroxy metabolites were generated by further reduction of hydroperoxy metabolites. When purified on SP-HPLC, the linseed seedlings hydroperoxy and hydroxy metabolites and soybean 15-LOX hydroperoxy [13-(S)-HPOTrE, 15-(S)-HPETE, and 13-(S)-HPODE] and hydroxy metabolites [13-(S)-HOTrE, 15-(S)-HETE, 13-(S)-HODE] showed very similar retention times

respectively and were co-eluted when linseed LOX metabolites were co-injected with those of soybean 15-LOX metabolites, suggesting that linseed enzyme is 15-LOX.

The new generation PDA detector associated with HPLC can efficiently detect any type of impurity if present in major peak such as impurity having either same elution time, or any minor peak eluting in the same area with major peak. The peak purity index obtained from this detector confirmed the purity of PUFAs metabolites synthesized by linseed seedling enzyme and separated on HPLC showed purity index of 1.00, a characteristic feature of a pure compound. These hydroperoxy and hydroxy metabolites of linseed seedlings enzyme synthesized using ALA, AA, and LA, were compared with corresponding standard hydroperoxy and hydroxy metabolites of soybean 15-LOX on SP-HPLC. When the hydroperoxy metabolites of linseed seedlings using ALA, AA, and LA as the substrate, compared with corresponding hydroperoxy metabolites [13-(S)-HPOTrE, 15-(S)-HPETE, and 13-(S)-HPODE] of soybean 15-LOX, showed same retention times. Similarly, the hydroxy metabolites of linseed seedlings using ALA, AA, and LA as the substrate, compared with corresponding hydroxy metabolites [13-(S)-HOTrE, 15-(S)-HETE, and 13-(S)-HODE] of soybean 15-LOX, also showed same retention times. The overlay HPLC chromatogram of hydroperoxy and hydroxy metabolites of linseed seedlings with standard soybean 15-LOX hydroperoxy and hydroxy metabolites indicated that linseed seedling enzyme might be 15-LOX.

The initial assays based on oxygraph indicated the possibility of LOXs in linseed seedling. Furthermore, the comparison of the retention time of hydroperoxy and hydroxy metabolites of linseed LOX with the hydroperoxy and hydroxy metabolites of soybean 15-LOX (standard) strengthens such a possibility. Finally, the presence of 15-

LOX in linseed seedlings was confirmed by analyzing the fragmentation patterns of a metabolite of linseed seedling with the corresponding metabolite of soybean 15-LOX on LC-MS/MS.

The omega-3 PUFAs (ALA, and DHA) efficiently show anti-inflammatory effects in comparison to omega-6 PUFAs (AA, and LA).

In the present study, mouse macrophage cell line, RAW 264.7 was used as *in vitro* model system to elucidate the ω -6 and ω -3 PUFAs role in inflammation. The findings of the present study support the previous reports regarding ω -6 and ω -3 PUFAs ratio in the body and their significances. While RAW 264.7 cells stimulated with LPS increased intracellular ROS levels, the macrophages pre-treated with ω -6 and ω -3 PUFAs and then stimulated with LPS showed a significant decrease in ROS generation. ω -3 PUFAs were more efficient in decreasing the intracellular ROS level as compared to ω -6 PUFAs.

NO is considered as a pro-inflammatory marker which regulates growth and inhibition of various cell types such as macrophages, immune cells and mast cells [46,109]. When their level in culture medium was measured, the result showed that macrophages pre-treated with ω -3 and ω -6 PUFAs decreased NO level in comparison to LPS alone treated macrophages. Again, ω -3 PUFAs were more effective in decreasing NO level compared to ω -6 PUFAs. The apoptosis provides strength to resolution phase of inflammation by removing the actively participating pro-inflammatory cells from the site of inflammation. RAW 264.7 cells challenged with LPS showed increased apoptosis, which was further increased in macrophages pre-treated with ω -6 and ω -3 PUFAs and challenged with LPS. However, apoptosis induced by ω -3 PUFAs was more prominent

than ω -6 PUFAs. These studies clearly demonstrate that ω -3 PUFAs (ALA, DHA) are more effective in either decreasing ROS generation or in inducing apoptosis when compared to ω -6 PUFAs and thus in the resolution of inflammation.

ALA metabolites show anti-inflammatory effects in RAW 264.7 CELLS and mouse primary peritoneal macrophages.

The studies presented in the earlier chapter suggest the possibility that the anti-inflammatory effects of ω -3 PUFAs might be mediated through their oxygenated metabolites generated through LOXs and COXs pathways. Based on this assumption, the *in vitro* studies on RAW 264.7 cells and mouse primary peritoneal macrophages were performed, which established the anti-inflammatory role of 15-LOX metabolites of ALA [13-(S)-HPOTrE, and 13-(S)-HOTrE]. The findings of the present study show the anti-inflammatory effects of these metabolites mediated by reducing the production of NO and ROS, as well as inflammatory cytokines, in LPS stimulated RAW 264.7 cells and in mouse peritoneal macrophages isolated from BALB/c mice. Further, the studies indicate that the anti-inflammatory effects of ALA metabolites are mediated by inactivation of NLRP3 inflammasome complex through the PPAR- γ dependent pathway.

Based on immunofluorescent confocal microscopy studies and FACS analysis, it is clear that the ALA metabolites inhibit the translocation of NF- κ B to the nucleus, along with the reduction of NO (in culture medium) and ROS in LPS stimulated RAW 264.7 cells and peritoneal mouse macrophages. ALA metabolites also inhibit the activation of NLRP3 inflammasome as well as downstream signalling molecules such as caspase-1 and IL-1 β at both transcriptional as well as translational levels. Interestingly, these effects of ALA metabolites on NLRP3 inflammasome were blocked by GW9662- a PPAR- γ antagonist. These studies systematically suggest that the inactivation of LPS induced

NLRP3 inflammasome by ALA metabolites in RAW 264.7 cells and peritoneal macrophages is mediated through PPAR- γ dependent pathway. Indeed, several studies have shown that PUFAs metabolites are ligands of PPAR- γ [137], further supporting such a possibility.

COX-2 functions as both pro-and anti-inflammatory marker, depending on the period and types of downstream metabolites generated [129,162]. In the early stages, it generates pro-inflammatory prostaglandins, whereas at later stages the downstream metabolite is PGD₂, a ligand for PPAR- γ [133], which has been observed to possess anti-inflammatory effects [163]. In this study, an increase in the expression of COX-2 and its downstream metabolites (PGE₂, and PGD₂) was observed in RAW 264.7 cells pre-treated with ALA metabolites and then stimulated with LPS. Here, COX-2 may be playing an anti-inflammatory role by its down-stream metabolite- PGD₂. It has been reported that PGD₂ derivative PGJ₂ and their metabolites ¹² Δ PGJ₂ and 15d-PGJ₂, often derived from induced COX-2, exhibit their anti-inflammatory effects in various *in vivo* systems [131,138,164]. In the present study the induced expression of COX-2 and increased the formation of PGD₂ upon treatment with ALA metabolites in LPS stimulated macrophages may be mediating the anti-inflammatory effects through its downstream metabolite, 15d-PGJ₂ a natural ligand for PPAR- γ [165]. This hypothesis is supported by the observation that PPAR- γ is maintaining the anti-inflammatory state, by inhibiting inflammasome and IL-1 β , via induced COX-2 metabolites. This is further supported by the fact that PPAR- γ antagonist GW9662 could successfully block the ALA metabolites mediated inactivation of the inflammasome.

The surrounding environment affects the differentiation, subtypes and function of macrophages. Macrophages polarized into two subtypes, M1 and M2 after differentiation along with characteristic phenotypes that exhibit different behaviors [166]. While, the activation of M1 macrophages is associated with increased expression of iNOS [167] and increased level of pro-inflammatory cytokines such as TNF- α , IL-1 β and IL-6 [19], the activation of M2 macrophages is associated with increased level of anti-inflammatory cytokines-IL-10 and scavenger receptor A [19]. LPS stimulated pro-inflammatory state is associated with M1 subtype macrophages, on the other hand, PPAR- γ activation and increased PGE₂ [135,136] shift the M1 macrophages into M2 macrophages [168,169]. In the present study, ALA metabolites activated PPAR- γ , and increased PGE₂ level that might be responsible for shifting of M1 to M2 macrophages subtypes and thereby mediating anti-inflammatory effects. Furthermore, an increased cytokine IL-10 as well as decreased expression of iNOS and TNF- α further strengthens such a possibility.

Apoptosis is the key machinery for clearance of pro-inflammatory cells from the inflammatory sites and support resolution phase of inflammation [170] and the activation of PPAR- γ induces apoptosis in differentiated naive macrophages [171]. In the present study 13-(S)-HPOTrE showed an increase in apoptosis in LPS stimulated RAW 264.7 cells. Therefore, it is possible that the apoptotic effects of 13-(S)-HPOTrE might be mediated through PPAR- γ dependent pathway. Further, there is a correlation between apoptosis and regulation of autophagy. It is reported that apoptosis inhibits beclin-1 mediated autophagy [160]. Again, it supports the present findings on immunofluorescence microscopy with LC3 in LPS challenged RAW 264.7 cells, in which pre-treatment of ALA metabolites remarkably diminished autophagy. Furthermore, in

immunoblot analysis, decrease in beclin-1 protein expression was observed in ALA metabolites pre-treated cells when challenged with LPS. From these studies, it can be concluded that ALA metabolites inhibit beclin-1 mediated autophagy through induction of apoptosis.

ALA metabolites extend survival of BALB/c mice and mediate anti-inflammatory effects by inactivating NLRP3 inflammasome: in vivo studies in sepsis model and CLP mice model.

The anti-inflammatory effects of ALA metabolites were further demonstrated *in vivo* in both the animal models, sepsis model induced by LPS and CLP mice model. These studies confirm the protective effects of 13-(S)-HPOTrE and 13-(S)-HOTrE as evidenced by a decrease in the mortality rate and by the maintenance of anti-inflammatory properties, in ALA metabolites treated BALB/c mice.

In LPS induced septic shock model, there was a significant decrease in the mortality rate in the mice pre-treated with ALA metabolites. Moreover, in another *in vivo* study, polymicrobial induced CLP mouse model, there was decrease in NLRP3 inflammasome expression in the mice treated with these ALA metabolites. It also showed reduction in pro-inflammatory cytokine- IL-1 β levels along with elevation in anti-inflammatory cytokine- IL-10 levels. Thus, the *in vitro* anti-inflammatory effects of ALA metabolites observed in RAW 264.7 cells and peritoneal macrophages were further demonstrated *in vivo* as evidenced by the extension in the survival of mice in LPS-induced septic shock in toxemia model and inactivation of inflammasome in polymicrobial-induced sepsis in CLP model.

In conclusion the present study demonstrates that the ω -3 PUFAs (ALA, and DHA) exhibit significant anti-inflammatory effects *in vitro* in RAW 264.7 cells, much

higher than ω -6 PUFAs (AA, and LA), by reducing pro-inflammatory markers such as ROS, IL-1 β , and NO. Further, the studies demonstrate that the LOX metabolites of ω -3 PUFAs

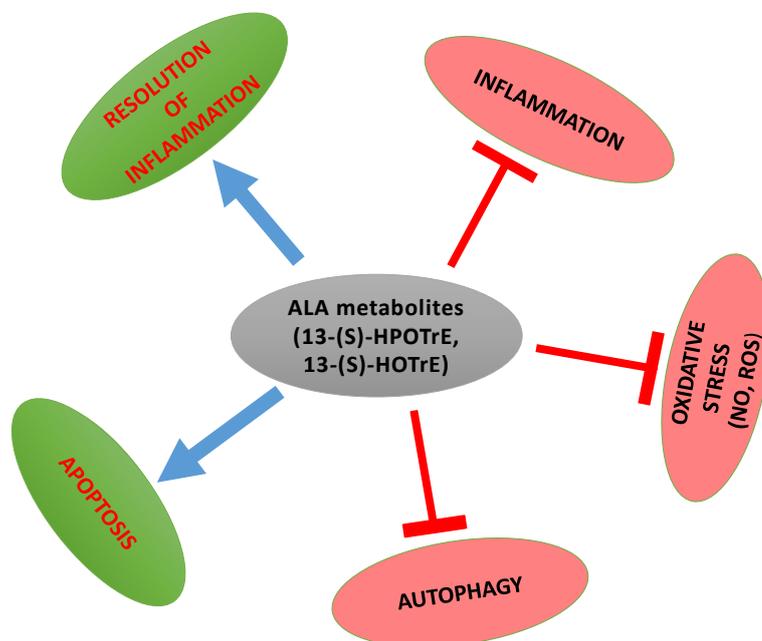


Figure 5-1: Effects of ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE] on different cellular processes/mechanism during inflammation. Blue arrow- Positive effects, Red arrow- Negative effects

Information based on: Kumar, N. *et al.* 15-Lipoxygenase metabolites of α -linolenic acid, [13-(S)-HPOTrE and 13-(S)-HOTrE], mediate anti-inflammatory effects by inactivating NLRP3 inflammasome. *Sci. Rep.* 6, 31649 (2016).

are much more potent than the ω -6 PUFAs in exhibiting the anti-inflammatory effects, both *in vitro* and *in vivo*. The hydroperoxy and hydroxy metabolites of ALA, [13-(S)-HPOTrE and 13-(S)-HOTrE], exhibit their anti-inflammatory effects by down-regulating LPS induced pro-inflammatory markers and by inactivating the NLRP3 inflammasome complex in LPS challenged RAW 264.7 cells as well as in mouse peritoneal macrophages. Further, the ALA metabolites were shown to mediate the anti-inflammatory effects by the induction of apoptosis, inhibition of autophagy, inactivation of NLRP3 inflammasome complex and decrease in pro-inflammatory cytokines or enzymes along with simultaneous increase in anti-inflammatory cytokines. This study also

demonstrates for the first time the protective role of ALA metabolites *in vivo* in LPS-induced septic shock in toxemia model and inactivation of inflammasome in polymicrobial induced sepsis in CLP model, through induction of various anti-inflammatory pathways.

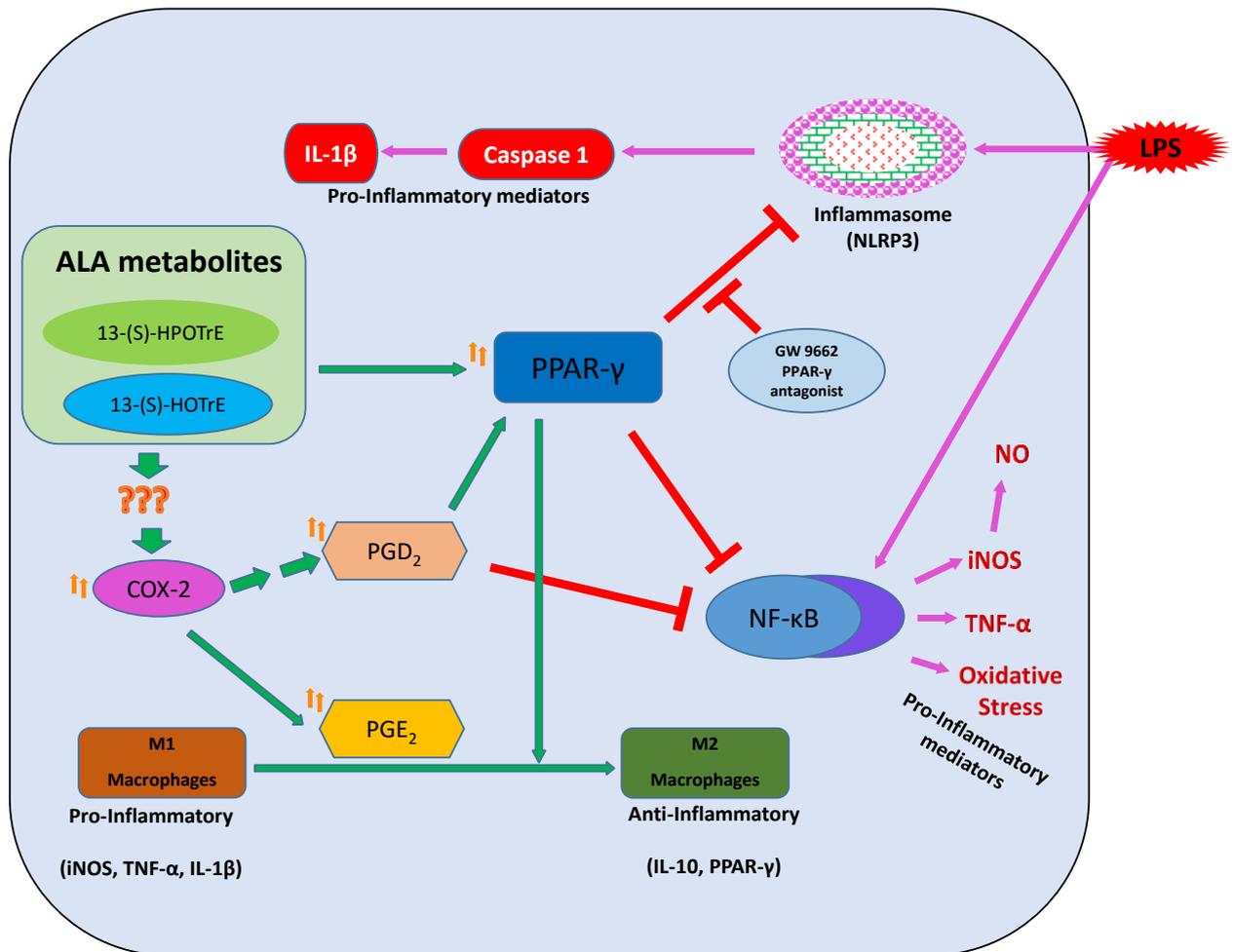


Figure : ALA metabolites mediate anti-inflammatory effects through PPAR-γ dependent pathways

Information based on: Kumar, N. *et al.* 15-Lipoxygenase metabolites of α -linolenic acid, [13-(S)-HPOTrE and 13-(S)-HOTrE], mediate anti-inflammatory effects by inactivating NLRP3 inflammasome. *Sci. Rep.* 6, 31649 (2016).



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INDEX

- chronic low-grade inflammation, 46
- Cyclooxygenases (COX), 22
- Eicosanoids, 21
- essential fatty acids, 16
- Essential fatty acids, 21
- free fatty acids, 22
- Inflammation, 1
- isoprostanes, 22
- Isoprostanes, 22
- Jasmonic acid, 29
- Lipid mediators, 17, 47
- Lipoxin, 29
- Lipoxygenases, 23
- NLRP3 Inflammasome, 14
- Nod-Like receptor family, 11
- para-inflammation, 46
- phytodienic acid, 29
- Polyunsaturated Fatty Acids, 16
- positive acute phase proteins and
 - negative acute phase proteins, 3
- prostaglandin, 21
- prostaglandin endoperoxide H synthases,
 - 22
- prostanoic acid, 21
- PYHIN family, 11
- pyroptosis, 14
- Types of Eicosanoids, 21
- vegetative storage protein (VSP), 29

LIST OF PUBLICATIONS AND MANUSCRIPTS

1. **Kumar, N.**, Gupta, G., Kotha, A., Fatima, N., Karnati, R., Gorla, G.V., Voorigiri, P., & Reddanna, P. 15-Lipoxygenase metabolites of α -linolenic acid, [13-(S)-HPOTrE and 13-(S)-HOTrE], mediate anti-inflammatory effects by inactivating NLRP3 inflammasome. ***Nature Sci. Rep.*** 6, 31649 (2016).
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SCIENTIFIC REPORTS

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15-Lipoxygenase metabolites of α -linolenic acid, [13-(S)-HPOTrE and 13-(S)-HOTrE], mediate anti-inflammatory effects by inactivating NLRP3 inflammasome

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The ratio of ω -6 to ω -3 polyunsaturated fatty acids (PUFAs) appears to be critical in the regulation of various pathophysiological processes and to maintain cellular homeostasis. While a high proportion of dietary intake of ω -6 PUFAs is associated with various inflammatory disorders, higher intake of ω -3 PUFAs is known to offer protection. It is now well established that beneficial effects of ω -3 PUFAs are mediated in part by their oxygenated metabolites mainly via the lipoxygenase (LOX) and cyclooxygenase (COX) pathways. However, the down-stream signaling pathways that are involved in these anti-inflammatory effects of ω -3 PUFAs have not been elucidated. The present study evaluates the effects of 15-LOX metabolites of α -linolenic acid (ALA, ω -3 PUFA) on lipopolysaccharide (LPS) induced inflammation in RAW 264.7 cells and peritoneal macrophages. Further, the effect of these metabolites on the survival of BALB/c mice in LPS mediated septic shock and also polymicrobial sepsis in Cecal Ligation and Puncture (CLP) mouse model was studied. These studies reveal the anti-inflammatory effects of 13-(S)-hydroperoxyoctadecatrienoic acid [13-(S)-HPOTrE] and 13-(S)-hydroxyoctadecatrienoic acid [13-(S)-HOTrE] by inactivating NLRP3 inflammasome complex through the PPAR- γ pathway. Additionally, both metabolites also deactivated autophagy and induced apoptosis. In mediating all these effects 13-(S)-HPOTrE was more potent than 13-(S)-HOTrE.

Inflammation is an essential part of host's response to infection or injury in order to maintain cellular homeostasis. Aberrant inflammation is associated with various disorders mediated by hyperactivation of inflammasome complexes and up-regulation of pro-inflammatory enzymes like inducible nitric oxide synthase (iNOS)^{1,2}, LOX³ and COX^{4,5}. The inflammatory response generated by eicosanoids, the oxygenated metabolites of PUFAs such as arachidonic acid (AA) is known to be mediated by pro-inflammatory cytokines such as IL-1 β and tumor necrosis factor- α (TNF- α)⁶.

Increased ratio of ω -6 to ω -3 PUFAs is hypothesized to elevate pro-inflammatory eicosanoid production and thus the onset of inflammatory diseases. A sufficiently high intake of ω -3 PUFAs, on the other hand, was shown to offer protection from inflammatory diseases by decreasing the production of pro-inflammatory eicosanoids, cytokines, ROS and RNS^{7,8}. In addition, it is reported that increasing ω -3 PUFAs tissue levels by dietary or genetic means decrease the pathological retinal angiogenesis by suppressing TNF- α ⁹. These beneficial effects of ω -3 PUFAs appear to be mediated by the oxygenated metabolites formed via the LOX and COX pathways¹⁰⁻¹⁴.

COX-2, an inducible enzyme that converts ω -6 PUFAs such as AA to pro-inflammatory prostaglandins, has been widely recognized as the major pathway responsible for inflammation as it triggers the production of other pro-inflammatory chemokines and cytokines¹⁴. However, this concept is challenged by recent findings on COX-2 derived oxidative metabolites of ω -3 PUFAs possessing anti-inflammatory and anti-oxidant properties^{15,16}. These studies suggest that the ultimate pro/anti-inflammatory effects of COX depend on the substrate

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on which these enzymes act, ω -6 or ω -3 PUFAs^{17,18} and their down-stream metabolites-PGE₂ and/or PGD₂. While PGE₂ is generally pro-inflammatory in nature¹³, PGD₂ exhibits anti-inflammatory effects by its conversion to PGJ₂ and subsequently 15-deoxy- Δ ^{12,14} PGJ₂ (15d-PGJ₂) a well-known ligand with high affinity for peroxisome proliferator-activated receptor- γ (PPAR- γ)^{19–21}. LOXs, on the other hand, are majorly classified into 5-, 12- and 15-LOXs, depending on the position at which AA is oxygenated. These LOX isoforms have been implicated in a variety of inflammatory and hyperproliferative and neurodegenerative diseases²². While 5-LOX is pro-inflammatory in nature²³, the 15-LOX exhibits anti-inflammatory properties^{24,25}. Earlier we have shown the anti-inflammatory and anti-cancer properties of 15-LOX metabolites of AA and elucidated the mechanisms involved^{26–28}. In the present study, we report the anti-inflammatory effects of 15-LOX metabolites of ALA, the precursor for eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), on LPS stimulated mouse macrophage cell line, RAW 264.7 and primary peritoneal macrophages isolated from BALB/c mice and demonstrated that these effects are mediated by inactivating NLRP3 inflammasome complex through the PPAR- γ pathway. Further, we report on the extended survival of BALB/c mice in endotoxin-mediated septic shock and polymicrobial sepsis in CLP mouse model.

Results

Hydroperoxy metabolites exhibit more cytotoxic effects on RAW 264.7 cells as compared to hydroxy metabolites of ALA. The cytotoxic effects of 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] on RAW 264.7 cells were evaluated by MTT (3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyl tetrazolium bromide) assay. Among this, hydroperoxy metabolite, 13-(S)-HPOTrE showed more cytotoxic effect compared to the hydroxy metabolite, 13-(S)-HOTrE, when incubated at different concentrations for 24 h (Fig. 1A). Treatment with both metabolites decreased the proliferation of the cells in a dose and time-dependent manner. However, 13-(S)-HPOTrE and 13-(S)-HOTrE showed more cytotoxic effects when compared to ω -3 (ALA & DHA) and ω -6 (AA & Linoleic acid-LA) PUFAs (Supplementary Figure S1). A 50% decrease in RAW 264.7 cell proliferation was observed at a concentration (IC₅₀ value) of 114 μ M 13-(S)-HPOTrE, which was much lower than 13-(S)-HOTrE (>200 μ M) at 24 h. Based on these results, further experiments on RAW 264.7 cells were carried out up to 100 μ M concentration of ALA metabolites for analysis of their anti-inflammatory effects.

ALA metabolites reduce nitric oxide levels and ROS generation in RAW 264.7 cells and peritoneal macrophages. Next, it was aimed to evaluate the effects of ALA metabolites on LPS induced inflammation by examining effects on pro-inflammatory parameters: NO- a second messenger and ROS- an oxidative stress marker. For this, RAW 264.7 cells were first treated with and/or without metabolites and challenged with LPS as described in the methods. There was significant elevation in NO production and ROS generation in cells when stimulated with LPS and this elevated NO level was reduced by 52.7% and 29% in the presence of 13-(S)-HPOTrE and 13-(S)-HOTrE at 100 μ M, respectively (Fig. 1B). Similarly, LPS stimulated RAW 264.7 cells, pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE, resulted in the reduction of ROS generation, in a dose-dependent manner and at 100 μ M concentration, decreased ROS generation by 96.4% and 92.7% respectively (Fig. 1C). Not only ALA metabolites, the substrate fatty acid ALA also showed the similar pattern of decreased ROS and NO production in LPS stimulated RAW 264.7 cells, though lower (18.6% and 89.5%) compared to its metabolites (Supplementary Figure S2). Similar effects were observed on ROS level when the mouse peritoneal macrophages were pre-treated with ALA metabolites at lower doses (100 nM) and then challenged with LPS (Fig. 1D). The significant reduction in the production of the pro-inflammatory markers by the ALA metabolites suggest their strong anti-inflammatory effects on LPS stimulated macrophages.

ALA metabolites inhibit the expression of iNOS and TNF- α in LPS stimulated RAW 264.7 cells. iNOS is an enzyme associated with regulation of NO and ROS generation in monocytes, macrophages, and other cells²⁹. The expression of iNOS and TNF- α , in RAW 264.7 cells stimulated with LPS in the presence and/or absence of ALA metabolites was studied. 13-(S)-HPOTrE or 13-(S)-HOTrE showed no effect on the expressions of either iNOS or TNF- α as compared to untreated RAW 264.7 cells (Supplementary Figure S3), while LPS induced their expression. However, their expression in RAW 264.7 cells, pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE and then challenged with LPS, was reduced in a dose-dependent manner (Fig. 2A). The transcript levels of iNOS and TNF- α were also analyzed by semi-quantitative PCR. In LPS treated RAW 264.7 cells, the transcript levels of iNOS and TNF- α were increased but were reduced by pre-treatment with 13-(S)-HPOTrE and 13-(S)-HOTrE in a dose-dependent manner (Supplementary Figure S4). NF- κ B is known to regulate the expression of various pro-inflammatory genes, including iNOS and TNF- α ^{30,31} and ALA metabolites may affect its translocation to the nucleus to regulate gene expression. Therefore the activation of NF- κ B was monitored for its translocation to the nucleus by confocal microscopy. While LPS stimulation of RAW 264.7 cells showed a marked translocation of NF- κ B, 13-(S)-HPOTrE and 13-(S)-HOTrE pre-treatments resulted in a decrease in NF- κ B translocation (Fig. 2B). Very similar effects were observed on NF- κ B translocation when the mouse peritoneal macrophages were treated with 13-(S)-HPOTrE and 13-(S)-HOTrE at a lower dose (100 nM) and then challenged with LPS (Fig. 2C).

13-(S)-HPOTrE and 13-(S)-HOTrE inactivate inflammasome in PPAR- γ dependent manner in RAW 264.7 cells and peritoneal macrophages. It is well known that NLRP3 inflammasome, an intracellular sensor that detects pathogens and sterile inflammation, gets activated in part through NF- κ B in response to LPS treatment^{32–34}. For analyzing the effects of 15-LOX metabolites of ALA on NLRP3 inflammasome activation in LPS stimulated RAW 264.7 cells, the level of gene transcripts associated with inflammasome complex were quantified by semi-quantitative PCR. An increased transcript level of NLRP3, caspase-1, IL-1 β and IL-18 in LPS activated RAW 264.7 cells showed an efficient dose-dependent reduction on treatment with both 13-(S)-HPOTrE

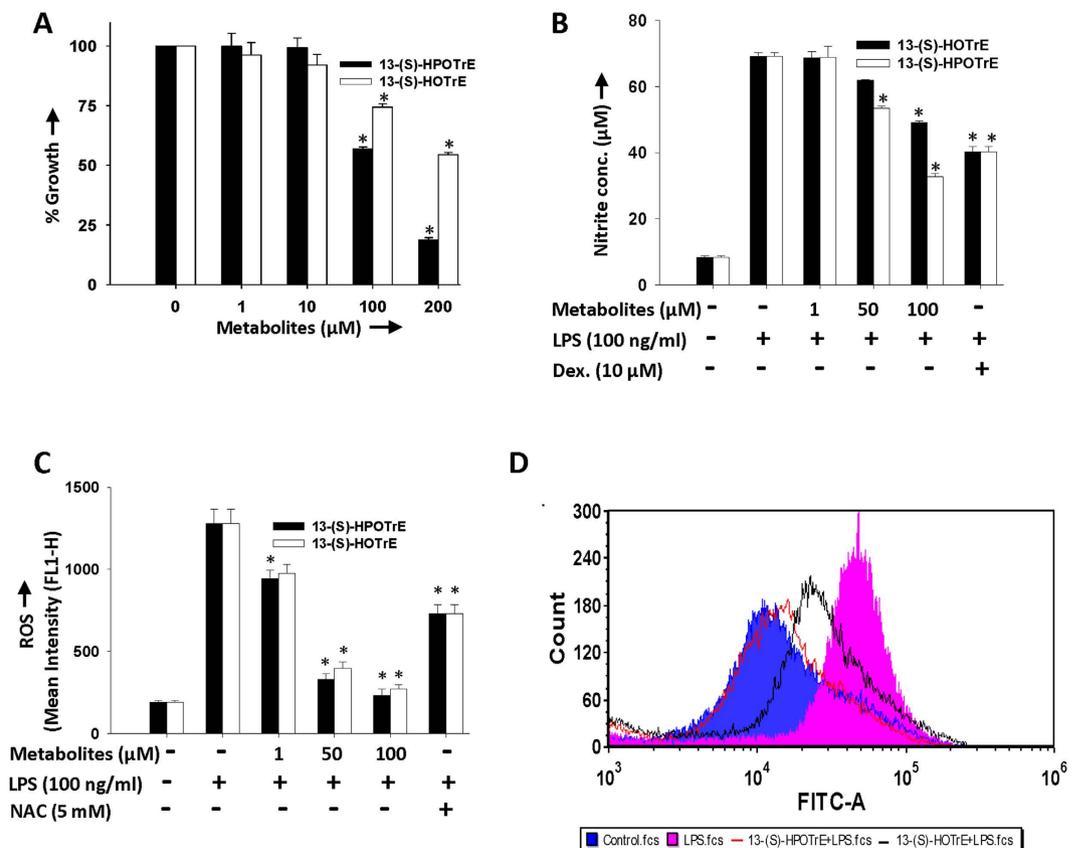


Figure 1. Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on cells viability, generation of NO and ROS in RAW 264.7 cells and mouse peritoneal macrophages. **(A)** Effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on the viability of RAW 264.7 cells were measured by MTT assay. Cells were treated with different concentrations (1, 10, 100 and 200 μM) of ALA metabolites for 24 h. The percent cell growth following treatment was calculated, in comparison with untreated control cells. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) when compared with untreated control cells. **(B)** Nitrite levels in the culture medium of RAW 264.7 cells pre-incubated with different concentrations (1, 50 and 100 μM) of ALA metabolites or dexamethasone (10 μM) for 3 h and further stimulated with or without LPS (100 ng/ml) for the next 24 h. 13-(S)-HPOTrE showed more effective dose-dependent reduction in NO level as compared to 13-(S)-HOTrE. Dexamethasone, a steroidal anti-inflammatory drug that suppresses NO production, is used as positive control. *Indicates significance ($p < 0.05$) compared to LPS treated cells. **(C)** Intracellular ROS level in RAW 264.7 cells following pretreatment with 100 μM of ALA metabolites for 3 h then stimulated with LPS for 16 h. 13-(S)-HPOTrE reduced ROS level more efficiently compared to 13-(S)-HOTrE. N-Acetyl Cysteine (NAC, 5 mM), a ROS inhibitor was used as positive control. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated cells. **(D)** Intracellular ROS level in peritoneal macrophages following pre-incubation with 100 nM ALA metabolites for 3 h then challenged with LPS for 16 h. Similar to above result, 13-(S)-HPOTrE reduced ROS level more efficiently compared to 13-(S)-HOTrE. This is representative FACS chromatogram of the three independent experiments.

and 13-(S)-HOTrE (Fig. 3A). Since activated inflammasomes initiate the processing and secretion of IL-1 β ^{35,36}, we measured the level of IL-1 β , in the culture medium of RAW 264.7 cells by ELISA. These studies showed a 4.4 fold increase in the level of IL-1 β in response to LPS treatment in RAW 264.7 cells and this elevated level of IL-1 β was significantly reduced by the treatment of 13-(S)-HPOTrE and 13-(S)-HOTrE, in a dose-dependent manner (Fig. 3B). At 100 μM concentration, 13-(S)-HPOTrE and 13-(S)-HOTrE reduced IL-1 β levels by 86.4% and 23% respectively.

LOX metabolites are natural ligands of PPAR- γ ³⁷⁻⁴⁰. Interestingly, PPAR- γ and their coactivators were shown to promote macrophage's anti-inflammatory properties to increase insulin sensitivity⁴¹. In the present scenario, we studied the involvement of PPAR- γ on the NLRP3 inflammasome activation in LPS treated RAW 264.7 cells and peritoneal macrophages. Immunofluorescence microscopy studies showed activation of NLRP3 inflammasome complex along with upregulation of caspase-1 upon LPS treatment in RAW 264.7 cells (Fig. 3C). However, pre-treatment of RAW 264.7 cells with 13-(S)-HPOTrE or 13-(S)-HOTrE and then challenged with LPS resulted in inactivation of NLRP3 inflammasome and thus downregulation of caspase-1. Interestingly, these effects of 13-(S)-HPOTrE and 13-(S)-HOTrE on inflammasome and caspase-1 were reversed when co-incubated with GW9662, a PPAR- γ antagonist.

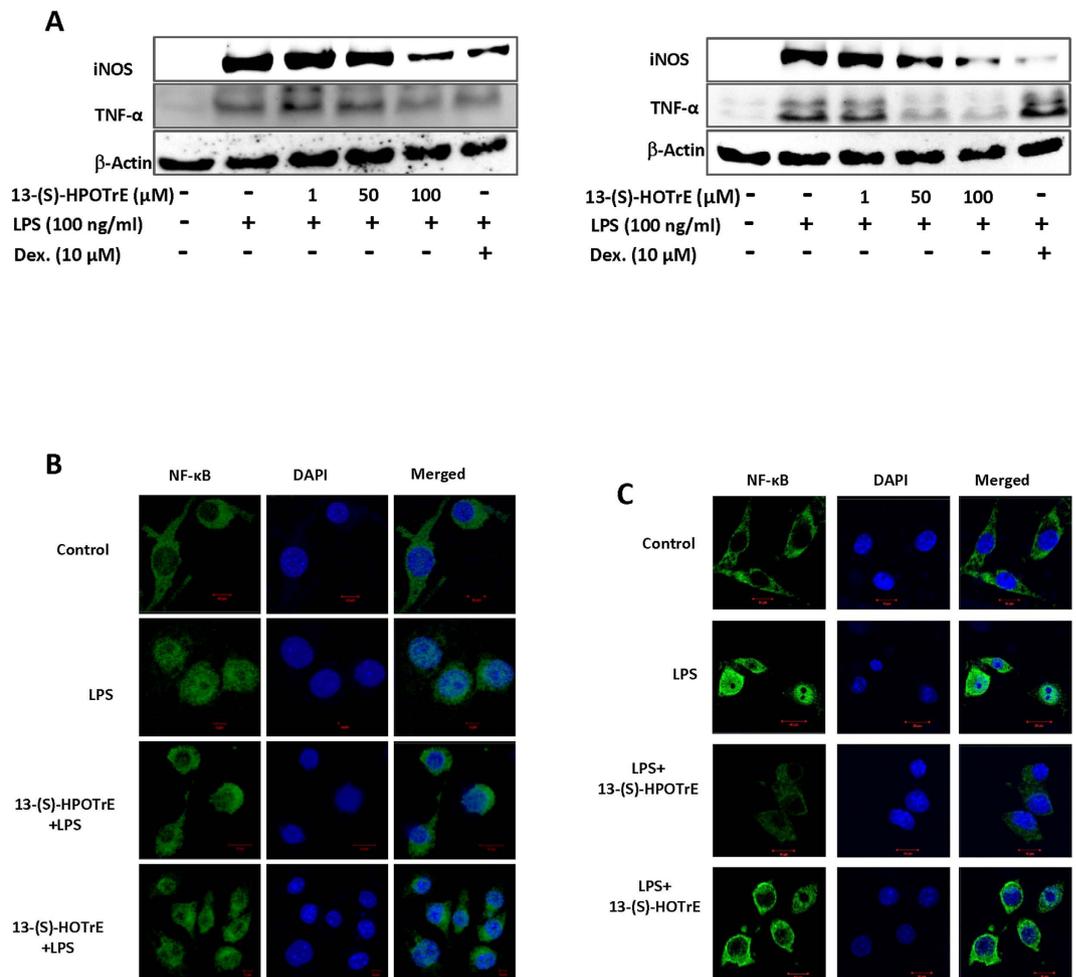


Figure 2. Anti-inflammatory effect of 13-(S)-HPOTrE and 13-(S)-HOTrE is mediated by inhibition of iNOS and TNF- α . (A) Immunoblot analysis showing the expression of iNOS and TNF- α following treatment with 13-(S)-HPOTrE and 13-(S)-HOTrE (1, 50 and 100 μM) concentrations for 3 h and then stimulated with LPS for 24 h. β -Actin was used as an internal control. Dexamethasone (10 μM) was used as positive control. These are representative blots of the three independent experiments. (B) Immunofluorescence microscopy of RAW 264.7 cells pre-treated with or without ALA metabolites (100 μM) for 3 h and then with LPS for 16 h. Immunostained for NF- κB (Green) and DAPI (Blue). Bar Scale: 10 μm . The image showed representative of three independent experiments. (C) Immunofluorescence microscopy of peritoneal macrophages pre-treated with or without ALA metabolites (100 nM) for 3 h and then challenged with LPS for 16 h. Immunostained for NF- κB (Green) and DAPI (Blue), Bar Scale: 10 μm . The image showed representative of three independent experiments.

To validate the findings observed in RAW 264.7 cells, further, studies were taken up on peritoneal macrophages at much lower doses (100 nM and 400 nM) of 13-(S)-HPOTrE and 13-(S)-HOTrE. Immunoblot analysis showed an increase in the expression of NLRP3 in LPS challenged peritoneal macrophages while cells pre-treated with ALA metabolites and challenged with LPS showed a reduction in the expression of NLRP3 (Fig. 4A). Next, the IL-1 β cytokine was probed in the culture medium by immunoblot analysis and quantified by ELISA. As shown in Fig. 4A,B, peritoneal macrophages pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE and then challenged with LPS reduced the level of IL-1 β by 59.5% and 54.5% respectively, when compared to LPS alone challenged macrophages. Similarly, the involvement of PPAR- γ in the regulation of inflammasome by ALA metabolites was validated on peritoneal macrophages at lower concentrations. Immunofluorescent microscopy showed decreased the expression of NLRP3 inflammasome and caspase-1 in macrophages pre-treated with ALA metabolites and challenged with LPS. However, the effects of ALA metabolites were reversed when co-incubated with GW9662, PPAR- γ antagonist (Fig. 4C). These metabolites also increased the levels of anti-inflammatory cytokine-IL-10 in culture medium (Fig. 4D).

The foregoing results suggest that inactivation of the inflammasome by 13-(S)-HPOTrE and 13-(S)-HOTrE in LPS challenged RAW 264.7 cells and peritoneal macrophages is mediated through PPAR- γ dependent pathway. Immunoblot analysis of the LPS stimulated RAW 264.7 cells revealed an increase in the COX-2 expression (Fig. 5A). The LPS induced expression of COX-2 was further enhanced by both 13-(S)-HPOTrE and 13-(S)-HOTrE in a dose-dependent manner. Coinciding with the changes observed in COX-2, the downstream

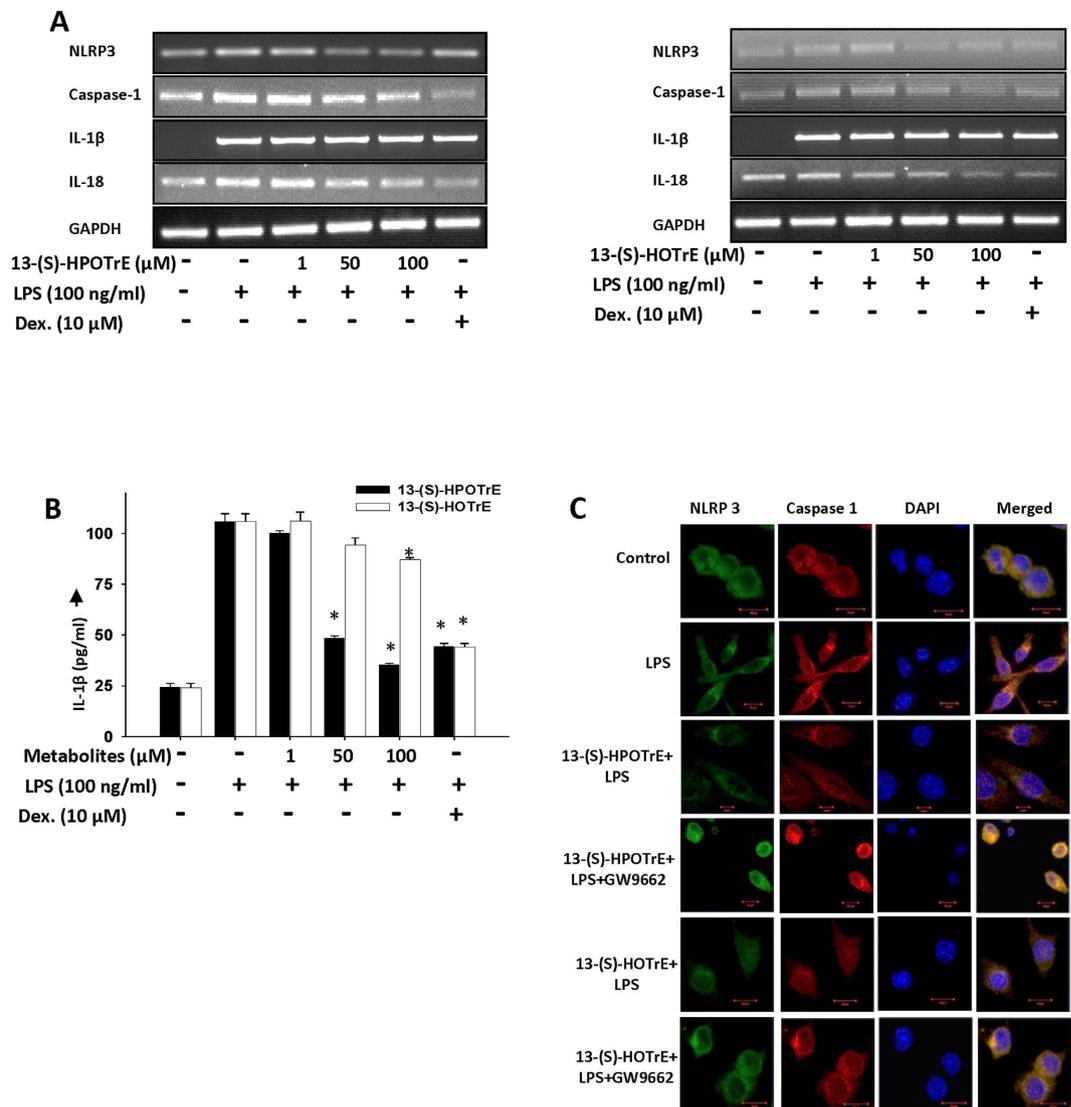


Figure 3. ALA metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE, inhibit inflammasome complex in RAW 264.7 cells. (A) In semi-quantitative PCR analysis, 13-(S)-HPOTrE, and 13-(S)-HOTrE showed decrease in transcript level of NLRP3, caspase-1, IL-1 β and IL-18 at various concentrations (1, 50 and 100 μ M) pre-incubated for 3 h then stimulated with LPS for 24 h. GAPDH was used as an internal control. (B) Estimation of IL-1 β levels in the culture medium of cells as per the treatment described in (A). Dexamethasone (10 μ M) was used as positive control. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS alone treated cells. (C) Immunofluorescence microscopy of RAW 264.7 cells pre-treated with ALA metabolites (100 μ M) for 3 h then stimulated with LPS for 24 h. Immunostained for NLRP3 (Green), caspase-1 (Red) and DAPI (Blue). Bars Scale: 10 μ m. Data show representative of three independent experiments.

metabolites of COX-2, PGE₂ and PGD₂ also showed similar trend of enhanced production with LPS treatment (Fig. 5B). These studies reveal that COX-2, a key enzyme involved in mediating inflammation, may also be playing a role in the resolution of inflammation through the generation of PGD₂ which is a PPAR- γ ligand¹⁷.

ALA metabolites induce apoptosis in LPS treated RAW 264.7 cells. It is known that apoptosis plays a vital role in the resolution of inflammation and Beclin-1 dependent inhibition of autophagy by apoptosis enhances its anti-inflammatory effects⁴². Apoptosis blocks Beclin-1 dependent autophagy by blocking autophagosome synthesis⁴³. Moreover, LPS and activated inflammasomes also induce autophagy in mesothelial cells⁴⁴. Since ALA metabolites showed anti-inflammatory effects, we examined whether they affect induction of apoptosis and autophagy in LPS stimulated RAW 264.7 cells. 13-(S)-HPOTrE treatment increased apoptosis in LPS challenged RAW 264.7 cells in a dose-dependent manner (Fig. 6A) although, 13-(S)-HPOTrE and 13-(S)-HOTrE showed no effect on apoptosis in unchallenged cells (Supplementary Figure S5). A significant increase in autophagy with the enhanced conversion of soluble LC3-I into lipid bound LC3-II and increased puncta formation was observed in LPS challenged RAW 264.7 cells. However, these effects were greatly reduced or undetectable in RAW 264.7

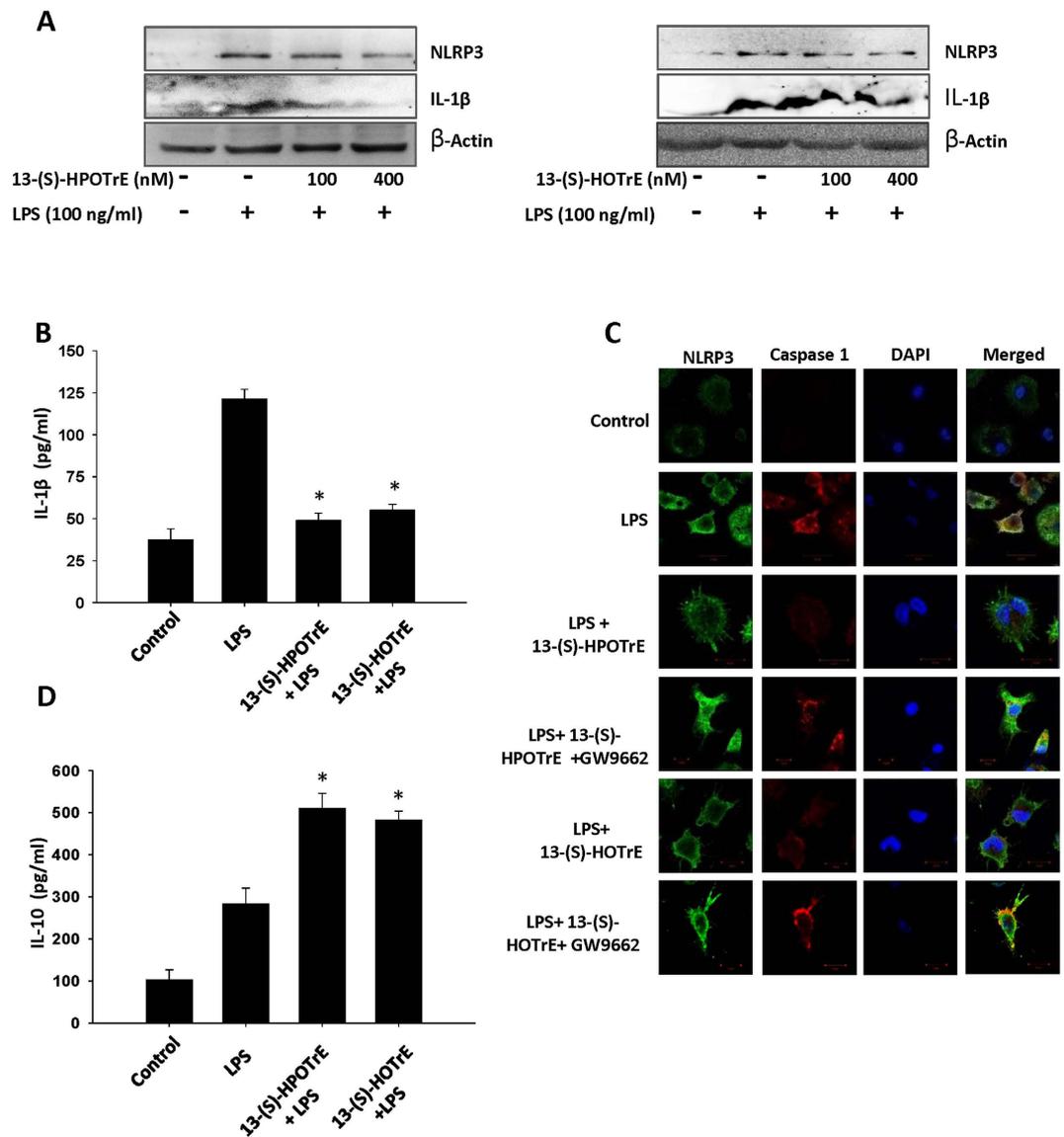


Figure 4. ALA metabolites inhibit inflammasome complex activation in mouse peritoneal macrophages. (A) Immunoblot analysis of NLRP3 and IL-1 β (in culture medium) expression in peritoneal macrophages, pre-incubated with ALA metabolites (100 nM and 400 nM) for 3 h then challenged with LPS (100 ng/ml) for next 24 h. β -Actin was used as an internal control. (B) Estimation of IL-1 β levels in the culture medium by ELISA as per the treatment described above. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated peritoneal macrophages. (C) Immunofluorescence microscopy of peritoneal macrophages treated with ALA metabolites (100 nM) for 3 h then stimulated with LPS for 24 h. Immunostained for NLRP3 (Green), caspase-1 (Red) and DAPI (Blue). Bars Scale: 10 μ m. Images show representative of three independent experiments. (D) Estimation of IL-10 levels in the culture medium by ELISA as per the treatment described above (at 100 nM). The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to LPS treated peritoneal macrophages.

cells pre-treated with ALA metabolites and challenged with LPS (Fig. 6B). Moreover, immunoblot analysis also showed induced expression of beclin-1, an autophagic marker, which was greatly reduced when RAW 264.7 cells were treated with ALA metabolites in a dose-dependent manner (Fig. 6C).

ALA metabolites extend BALB/c mice survival and show anti-inflammatory properties by regulating cytokines and inflammasome. Septic shock is a complication of inflammation in which an infection or toxin induces inflammatory response in the entire body. Endotoxin-mediated septic shock is often integrated with high mortality⁴⁵. On the other hand, saturated fatty acid had shown major impact on the survival of mice in bacterial infection⁴⁶ and these ALA metabolites showed anti-inflammatory effects in *in vitro* model system. We then wanted to validate the effects of ALA metabolites *in vivo* on the survival of mice in a septic shock induced by LPS in toxemia model. These studies showed features of septic shock in all the mice received LPS such as an increase in heartbeat rate, decrease in body weight, apathy, dullness and diarrhea, which began to die

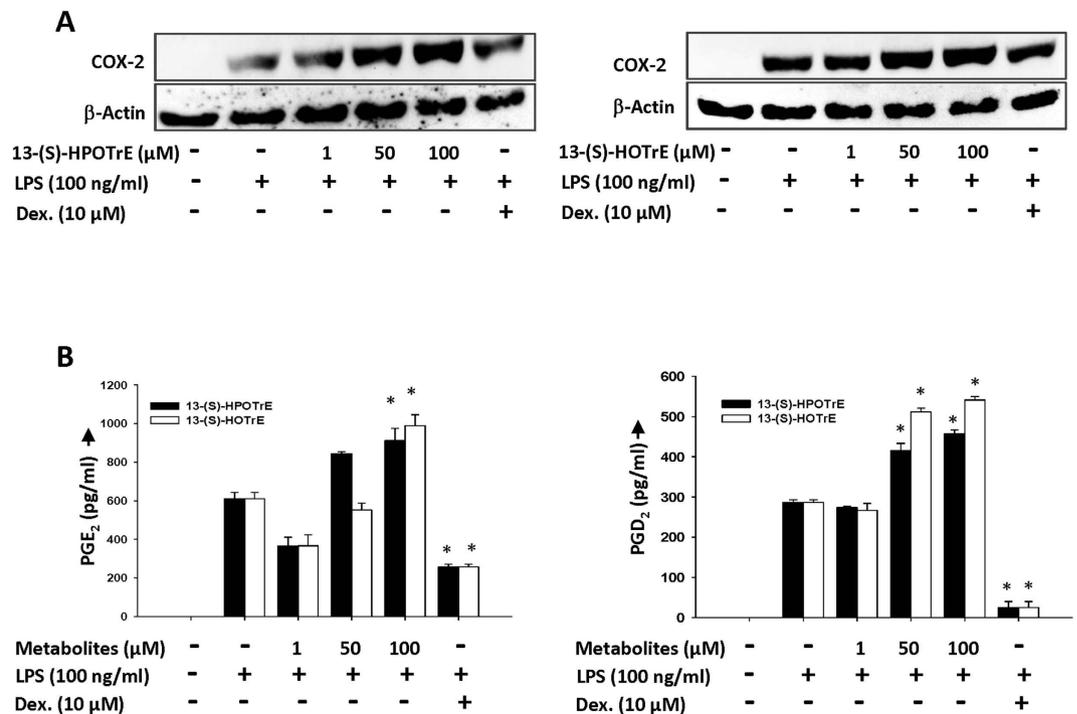


Figure 5. 13-(S)-HPOTrE and 13-(S)-HOTrE show anti-inflammatory effects by upregulating expression of COX-2. (A) Immunoblot analysis of COX-2 expression in RAW 264.7 cells pre-incubated with ALA metabolites at different concentrations (1, 50 and 100 μM) for 3 h then further stimulated by LPS (100 ng/ml) for next 24 h. β-Actin was used as an internal control and Dexamethasone was used as positive control. Western blot shows representative of three independent experiments. (B) Estimation of PGE₂ and PGD₂ level in the culture medium of RAW 264.7 cells when pre-incubated with ALA metabolites for 3 h and then stimulated with LPS for 24 h. Dexamethasone was used as positive control. The values represent mean ± SD of three independent experiments. *Indicates significance (p < 0.05) compared to LPS treated cells.

within 12 h. Contrary to this, the mice pre-treated with ALA metabolites and then challenged with LPS were quite active. However, loss of weight was observed in all except control mice. The result from this experiment showed that survival rate in ALA metabolites pre-treated mice were 40% and 10% extended than LPS alone challenged mice (Fig. 7A).

Since ALA metabolites showed a decrease in mortality rate in mice with endotoxin-mediated septic shock, the study was further extended to mice with sepsis induced by polymicrobial infection in a CLP mouse model. Results showed upregulation of iNOS and NLRP3 expression in CLP mice and their down-regulation in mice pre-treated with ALA metabolites (Fig. 7B). The levels of IL-1β and IL-10 were increased in liver tissue and serum of CLP mice. However, the level of pro-inflammatory cytokine-IL-1β was decreased while the level of anti-inflammatory cytokine-IL-10 was further increased in mice treated with ALA metabolites (Fig. 7C).

Discussion

The ratio of ω-6 PUFAs: ω-3 PUFAs in cell membranes reflects the physiological status of the tissues and regulates the inflammatory response to a variety of external or internal stimuli and thus maintains cellular homeostasis^{7,8}. ω-3 PUFAs are known to exhibit anti-inflammatory effects and reduce the oxidative stress in the cells^{7,47}. The findings of the present study also support this concept wherein ALA, ω-3 PUFA, and its metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE, significantly reduced the production of NO and ROS, as well as inflammatory cytokines, in LPS stimulated RAW 264.7 cells and in mouse peritoneal macrophages. Further studies on *in vivo* sepsis model and CLP mice model demonstrated the protective role of 13-(S)-HPOTrE and 13-(S)-HOTrE as evidenced by a decrease in the mortality rate and by the maintenance of anti-inflammatory properties, in ALA metabolites treated BALB/c mice.

From previous studies, it has been established that ω-3 PUFAs exert their anti-inflammatory effects through several mechanisms, one of which being NF-κB signaling^{7,47}. ω-3 PUFAs prevent the phosphorylation and degradation of IκB-β protein by proteasome complex, thus inhibiting NF-κB signaling pathways⁴⁸. The present study shows that 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] inhibit the translocation of NF-κB to the nucleus, along with the reduction of NO and ROS in LPS stimulated RAW 264.7 cells and peritoneal mouse macrophages. ALA metabolites also inhibited the activation of NLRP3 inflammasome as well as downstream signaling molecules such as caspase-1 and IL-1β at both transcriptional as well as translational levels. Interestingly, these effects of ALA metabolites on NLRP3 inflammasome were blocked by the PPAR-γ antagonist-GW9662. These studies comprehensively suggest that inactivation of LPS induced NLRP3 inflammasome by 13-(S)-HPOTrE or 13-(S)-HOTrE in RAW 264.7 cells and peritoneal macrophages is dependent on

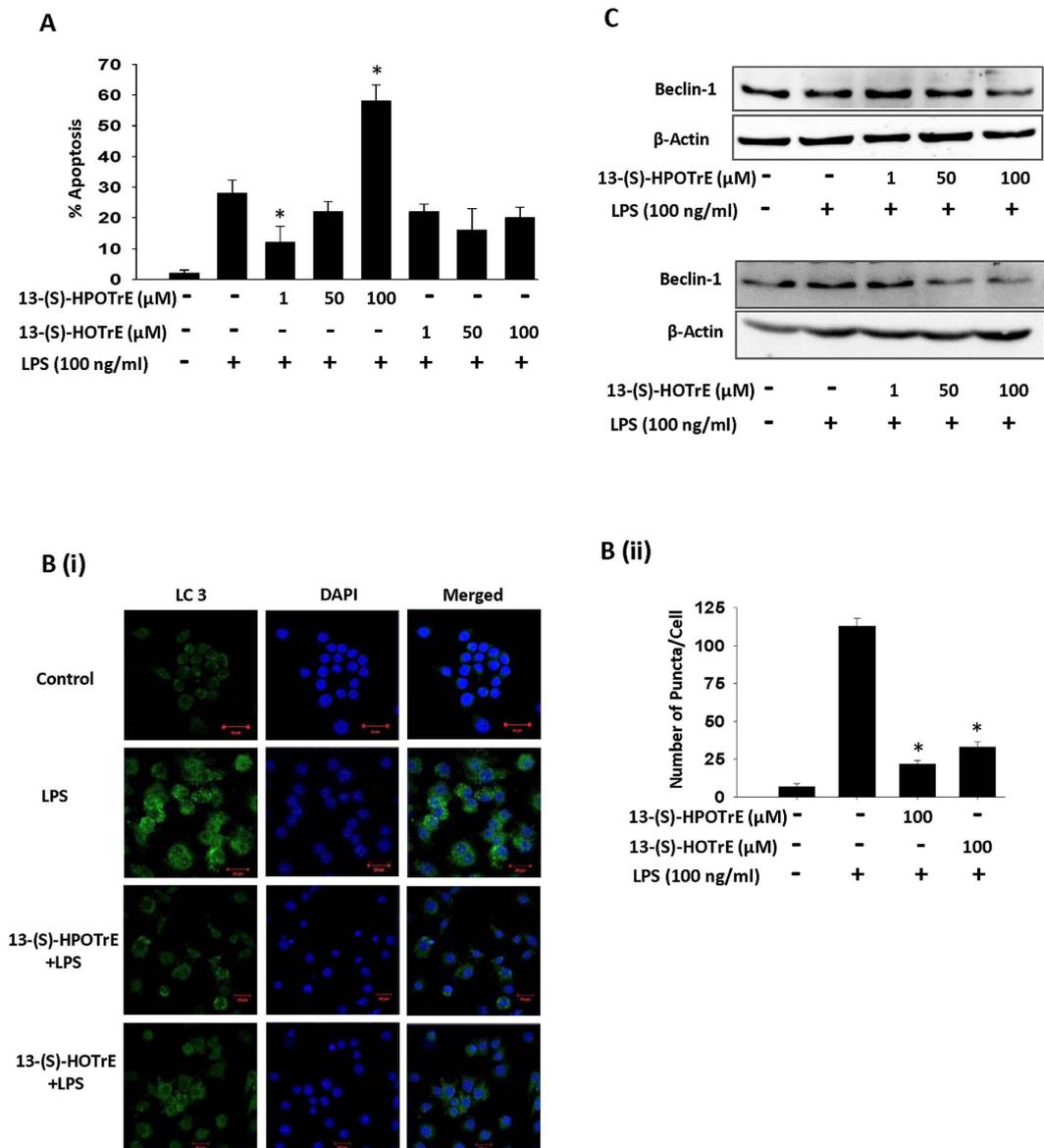


Figure 6. 13-(S)-HPOTrE and 13-(S)-HOTrE inhibit Beclin-1 mediated autophagy in LPS stimulated RAW 264.7 cells. (A) Flow cytometric analysis showing the effects of ALA metabolites on apoptosis in RAW 264.7 cells challenged with LPS. Apoptosis was assayed by Propidium Iodide and FITC conjugated Annexin V at 24 h, by flow cytometric Analysis. The apoptosis level was calculated as % of AnnexinV⁺ PI⁻ cells in density plot distribution. The dead cells were gated and analysis was performed only on live cells. *Indicates significance ($p < 0.05$) compared to LPS treated cells. (B) (i) Confocal microscopy of RAW 264.7 cells treated with or without ALA metabolites (100 μM) for 3 h then challenged with LPS for 24 h. Immunostained for LC 3 (Green) and DAPI (Blue). Bars Scale: 10 μm. Images show representative of three experiments. (ii) Bar graph shows puncta/cell calculated by ImageJ LC3 macro. *Indicates significance ($p < 0.05$) compared to LPS treated cells. (C) Beclin-1 Immunoblotting of RAW 264.7 cells pre-incubated with ALA metabolites for 3 h and then challenged with LPS for 24 h. Western blots show representative of three independent experiments.

PPAR- γ . Indeed a number of studies have shown that several PUFA metabolites are ligands of PPAR- γ ¹⁹, further supporting such a possibility.

Recent studies have established that the inducible isoform of COX, COX-2, has dual roles, pro- and anti-inflammatory, depending on the downstream metabolites generated^{13,49}. In the early stages, it is shown that COX-2 induction is mainly associated with the generation of pro-inflammatory prostaglandins, whereas at later stages the downstream metabolite is PGD₂, a ligand for PPAR- γ ¹⁷, which has been observed to possess anti-inflammatory roles⁵⁰. In the present study, an increase in the expression of COX-2 and its downstream metabolites (PGE₂ and PGD₂) was observed in RAW 264.7 cells pre-treated with ALA metabolites and then stimulated with LPS. Here, COX-2 may be playing an anti-inflammatory role by shifting PGE₂ dominated prostaglandins in LPS stimulated macrophages to PGD₂ dominated prostaglandins upon treatment with ALA metabolites. It has been reported that PGD₂ derivative PGJ₂ and their metabolites ¹²Δ PGJ₂ and 15d-PGJ₂, often derived from

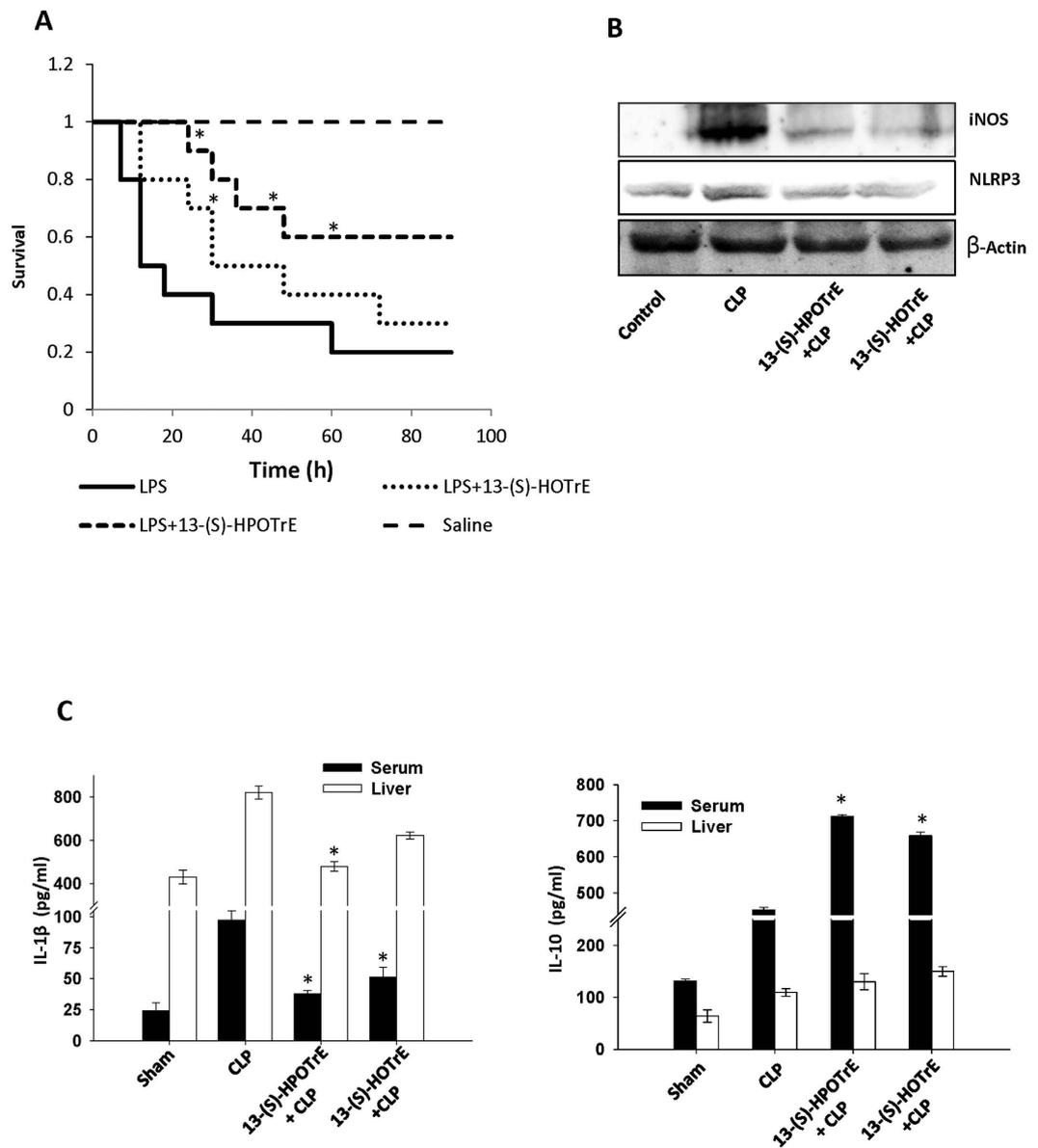


Figure 7. Effects of ALA metabolites during sepsis in BALB/c mice. (A) ALA metabolites showed an increase in survival of BALB/c mice ($n = 10$ mice/group) in endotoxin-induced Septic Shock in toxemia model. LPS (30 mg/kg) was injected i.p. and mice were monitored for 4 days then mortality was calculated. ALA metabolites showed decreased mortality rate in metabolites treated and LPS challenged mice as compared to LPS challenged mice. The survival curve is plotted on Kaplan-Meier method. *Indicates significance ($p < 0.05$) compared to LPS treated mice. (B) Sepsis was induced by polymicrobial infection in CLP mouse model ($n = 5$ mice/group). Immunoblot analysis of iNOS and NLRP3 expression in CLP mice, pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE (0.1 mg/kg, 2.5 μ g/mice) as described in methodology. Mice were sacrificed after 24 h of CLP and tissues were collected. β -Actin was used as an internal control. (C) Estimation of IL-1 β and IL-10 cytokines levels in serum and liver tissue. The values represent mean \pm SD of three independent experiments. *Indicates significance ($p < 0.05$) compared to CLP mice.

induced COX-2, exhibit their anti-inflammatory effects in various *in vivo* systems^{20,15,51}. In the present study, the induced expression of COX-2 and increased formation of PGD₂ upon treatment with ALA metabolites in LPS stimulated macrophages may be mediating the anti-inflammatory effects through its downstream metabolite, 15d-PGJ₂ a natural ligand for PPAR- γ ⁵². This hypothesis is supported by the observation that PPAR- γ is maintaining the anti-inflammatory state, by inhibiting inflammasome and IL-1 β , via induced COX-2 generated downstream metabolites, and when PPAR- γ is inhibited, it is failing to inactivate the inflammasome. The reversed effects of ALA metabolites on inflammasome and caspase-1, when co-incubated with the PPAR- γ antagonist GW9662 support such a possibility.

Macrophage differentiation, their subtypes and function depend on its surrounding environment. After differentiation, macrophages polarized into two subtypes, M1 and M2 with characteristic phenotypes and exhibit

different behaviours⁵³. While, the activation of M1 macrophage is associated with increased expression of iNOS⁵⁴ and increased level of pro-inflammatory cytokines such as TNF- α , IL-1 β and IL-6⁵⁵, the activation of M2 macrophages is associated with increased level of anti-inflammatory cytokines-IL-10 and scavenger receptor A⁵⁵. LPS stimulated pro-inflammatory state is associated with M1 subtype macrophage, on the other hand, PPAR- γ activation and increased PGE₂^{56,57} is associated with shifting of M1 macrophages into M2 macrophages subtypes^{58,59}. In the present study, ALA metabolites activated PPAR- γ , and also increased PGE₂ level that might be responsible for shifting of M1 to M2 macrophages subtypes and thereby mediating anti-inflammatory effects. Furthermore, an increased cytokine IL-10 as well as decreased expression of iNOS and TNF- α which are associated to M2 subtype macrophages further strengthen such possibility.

Apoptosis is the major mechanism for safe clearance of PMNLs at inflammatory sites and thus limit pro-inflammatory signals and promote resolution of inflammation rather than persistence of tissue damage⁶⁰. In the present study, 13-(S)-HPOTrE showed a dose-dependent increase in apoptosis in LPS activated RAW 264.7 cells and it is previously reported that activation of PPAR- γ induces apoptosis in differentiated naive macrophages⁶¹. Therefore, it is possible that the apoptotic effects of 13-(S)-HPOTrE might be mediated through PPAR- γ dependent pathway. There is a correlation between apoptosis and regulation of autophagy. It is reported that apoptosis inhibits beclin-1 mediated autophagy⁴³. It supports the present findings on immunofluorescence microscopy with LC3, in which pre-treatment of ALA metabolites remarkably diminished autophagy in LPS challenged RAW 264.7 cells. Furthermore, in immunoblot analysis, a decrease in beclin-1 expression was observed in ALA metabolites pre-treated and challenged with LPS. From these studies, it can be concluded that these ALA metabolites inhibit beclin-1 mediated autophagy through induction of apoptosis.

Sepsis is a critical state of the body because of systemic immune response induced by pathogens, microbes or endotoxins, also called systemic inflammatory response syndrome⁶². In endotoxin-induced septic shock model, mice pre-treated with ALA metabolites showed a significant decrease in mortality rate. Moreover, in another *in vivo* study, in CLP mouse model, mice treated with these ALA metabolites showed a decrease in expression of NLRP3. It also showed a reduction in IL-1 β levels while elevation in IL-10 cytokine level as well. Thus the *in vitro* anti-inflammatory effects of 13-(S)-HPOTrE and 13-(S)-HOTrE observed in RAW 264.7 cells and peritoneal macrophages also have been demonstrated *in vivo* as evidenced by the extension in the survival of mice in endotoxin-induced septic shock in toxemia model and inactivated inflammasome in polymicrobial induced sepsis in CLP model.

In the present study, the hydroperoxy [13(S)-HPOTrE] and hydroxy [13(S)-HOTrE] metabolites of ALA showed anti-inflammatory effects, though the hydroperoxy metabolite being more potent. As the hydroperoxy metabolite [13(S)-HPOTrE] is getting converted to the corresponding hydroxy [13(S)-HOTrE] metabolite with increasing period of time because of the reducing environment created by serum in culture medium, the effects of 13(S)-HPOTrE observed in the present study may be mediated by both the hydroperoxy and hydroxy metabolites of ALA.

The anti-inflammatory properties of ALA (ω -3 PUFA) observed in the present study thus are quite contrasting to those of AA (ω -6 PUFA) metabolites, wherein the hydroperoxy (15-(S)-HPETE) and hydroxy (15-(S)-HETE) metabolites of AA showed contrasting effects on angiogenesis, which is critically associated with inflammation^{27,63,64}. While 15(S)-HPETE showed anti-angiogenic effects²⁷, the 15(S)-HETE induced angiogenesis⁶⁴ in adipose tissue. Also, such differential effects of the hydroperoxy and hydroxy metabolites of 15-LOX on angiogenesis were observed in human umbilical vein endothelial cells (HUVECs)⁶³. Similar differential effects of hydroperoxy and hydroxy metabolites of 15-LOX with AA as the substrate were reported on chronic myeloid leukemia cell line²⁶. Interestingly, in the present study, the hydroperoxy and hydroxy metabolites of ALA showed anti-inflammatory effects, however, the hydroperoxy metabolite being more potent than the hydroxy metabolite. These findings, thus strongly advocate the beneficial effects of ω -3 PUFAs in counteracting various inflammatory disorders, which are mainly mediated by the metabolites of ω -6 PUFAs.

In summary, ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE] exhibit anti-inflammatory effects in LPS challenged RAW 264.7 cells and mouse peritoneal macrophages by down-regulating LPS induced pro-inflammatory markers and by inactivating the NLRP3 inflammasome complex. Additionally, the anti-inflammatory effects of ALA metabolites were mediated by the induction of apoptosis and inhibition of autophagy in the LPS challenged macrophages. These anti-inflammatory effects of ALA metabolites appear to be mediated by the inactivation of NLRP3 inflammasome complex and decrease in pro-inflammatory cytokines/enzymes along with a simultaneous increase in anti-inflammatory cytokines. The present study also demonstrates the protective effects of ALA metabolites *in vivo* as evidenced by the extended survival of BALB/c mice in LPS induced septic shock.

Materials and Methods

Chemicals and Reagents. Culture medium DMEM, penicillin, streptomycin, PBS, Trypsin-EDTA and fetal bovine serum (FBS) were purchased from Gibco. MTT, 2',7'-Dichlorodihydrofluorescein diacetate (DCFH-DA), LPS (lipopolysaccharide from *E. coli*, 0127:B8), Griess reagent, Dexamethasone (Dex) and GW9662 were purchased from Sigma-Aldrich, USA. Anti-Beclin-1, anti-Caspase-1, anti-NF- κ B and anti-TNF- α antibodies were purchased from Abcam (MA, USA). Anti-LC-3 antibody was purchased from Cell Signaling while Anti-COX-2 antibody was obtained from Santa Cruz Biotechnology Inc. (Texas, USA). Anti-iNOS antibody was purchased from Thermo Fisher Scientific (MA, USA). Enzyme immunoassay kit for IL-1 β , IL-10 and PGE₂ were purchased from R&D system, Inc. (MN, USA) whereas PGD₂ assay kit was purchased from Cayman Chemical Company (Ann Arbor, MI, USA). AA, LA, ALA and DHA were procured from Nu-Chek-Prep (MN, USA). The 15-LOX metabolites of ALA, 13-(S)-HPOTrE and 13-(S)-HOTrE, were generated (Supplementary Figure S6) essentially employing the methods described earlier for generation of 5-LOX metabolites⁶⁵⁻⁶⁷.

Cell culture and Treatments. The mouse macrophage cell line, RAW 264.7 was obtained from NCCS (Pune, India) grown and maintained in DMEM supplemented with 10% heat-inactivated fetal bovine serum (FBS), 100 IU/ml penicillin and 100 µg/ml streptomycin in a humidified atmosphere with 5% CO₂ at 37 °C. Subculturing of cells was done twice a week. Fresh culture medium was used before each treatment. Cells were pre-incubated with different concentrations (1, 50 and 100 µM) of ALA metabolites, 13-(S)-HPOTrE and 13-(S)-HOTrE or with Dexamethasone (10 µM) for 3 h then challenged with LPS (100 ng/ml) for different time points as mentioned in experiments. The anti-inflammatory drug, dexamethasone was used as positive control. For inhibitor study, cells were pre-incubated with 10 µM GW9662 (2-chloro-5-nitrobenzanilide), for specific time period as mentioned in experiments. For analysis of the inflammasomes and IL-1 β measurements, RAW 264.7 cells and peritoneal macrophages were incubated with 1 mM ATP for 30 min prior to end time points.

Animal. BALB/c, male mice, 4-week old weighing 20–25 g were purchased from Centre for Cellular and Molecular Biology, Hyderabad, India. Mice were housed at constant room temperature (23 ± 1 °C) and allowed to water and food *ad libitum* in 12 h dark/light cycle. The mice were kept at least 1 week in animal house before performing any experiment. The mice used in this study were handled carefully and according to the *Guide for the care and use of Laboratory animals* published by NIH (National Institute of Health). The experimental protocol was approved by Institutional Animal Ethics Committee (IAEC), University of Hyderabad, India.

LPS Induced Septic Shock. BALB/c male mice (20 to 25 g) were divided into 4 different groups (10 mice in each group), control, LPS, LPS+13-(S)-HPOTrE and LPS+13-(S)-HOTrE. LPS was dissolved in saline (0.9% NaCl) and injected (30 mg/kg body weight) intraperitoneal (i.p.) in all mice except control. In control mice, 0.9% saline was injected. ALA metabolites were dissolved in saline having Tween 80 (0.9% NaCl + 0.5% Tween 80). Two i.p. doses of 13-(S)-HPOTrE and 13-(S)-HOTrE (0.1 mg/kg body weight, 2.5 µg/mice) metabolites were injected, first at 1 h prior to LPS and second, soon after LPS administration. 250 µl saline with Tween 80 (vehicle control) was injected in control and LPS treated groups. All mice were kept in normal conditions with an extra vigilance. Mice were monitored initially at 2 h intervals for 12 h then for 4 days.

Cecal Ligation and Puncture (CLP) model. Cecal Ligation and Puncture was performed in BALB/c male mice (20 to 25 g). Mice were divided into 4 groups (5 mice/group), Sham, CLP, CLP+13-(S)-HPOTrE and CLP+13-(S)-HOTrE. The mice were anesthetized with 60 µg/g ketamine and 10 µg/g xylazine. After cleaning and disinfecting the lower abdomen by iodine solution to prevent infection, a 1.5 to 2 cm incision was made through linea alba. Then, the cecum was spotted and ligated with disinfected 3–0 silk suture and perforated twice using a 22-gauge needle. Wound strength was ensured by squeezing out a small amount of stool. Then the cecum was replaced into the abdomen, and the incision was closed properly. In Sham, mice undergone surgery but ligation and puncture were not performed. Tramadol hydrochloride (20 µg/g body wt.) was injected i.p. with 1 ml warm saline in all mice. In ALA metabolites treated mice, two i.p. doses of 13-(S)-HPOTrE and 13-(S)-HOTrE (0.1 mg/kg body weight, 2.5 µg/mice) metabolites were given, first at 1 h prior to CLP and second, soon after CLP surgery. Finally, all mice were kept at normal conditions with an extra vigilance. The mice were sacrificed after 24 h of CLP surgery then blood, peritoneal fluid and liver were collected.

Isolation of Primary Peritoneal Macrophages. Primary peritoneal macrophages were isolated from thioglycolate-elicited BALB/c male mice as described by Xia Zhang *et al.*⁶⁸. Briefly, in BALB/c male mice, 3% thioglycolate broth (1 ml) was injected through i.p. After 3 days, mice were euthanized by cervical dislocation. 5 ml ice-cold DMEM was injected into the peritoneal cavity. The abdomen was finger tapped 4–5 times and peritoneal lavage was aspirated and collected in a cold sterile centrifuge tube. Further, centrifugation was done at 1500 rpm for 5 min, pellets were resuspended in DMEM and cell counting was done by haemocytometer. Appropriate number of cells were grown and maintained in DMEM, macrophages enrichment was done by washing and removing unattached cells from culture plate, further grown as described above for RAW 264.7 cells, and treated with 13-(S)-HPOTrE and 13-(S)-HOTrE as mentioned in experiments for RAW 264.7 cells.

Cytotoxicity Assay. Cytotoxicity of PUFAs and their metabolites were assayed by MTT assay. To perform this assay, RAW 264.7 cells were seeded in 96 well plates at a density of 5×10^4 cells/well then treated with ω -6 PUFAs (AA and LA), ω -3 PUFAs (ALA and DHA) and 15-LOX metabolites of ALA [13-(S)-HPOTrE and 13-(S)-HOTrE] at various concentrations (1, 50, 100 and 200 µM) for different time points. Cell viability was measured colorimetrically by MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide) assay as described by Mossman⁶⁹.

Nitrite Estimation. RAW 264.7 cells were seeded in 6 well plates for 12 h then pre-incubated with different concentrations (1, 50 and 100 µM) of ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE], or dexamethasone for 3 h then stimulated with or without LPS (100 ng/ml) for the next 24 h. At the end of the time point, stable nitrite level in the culture supernatant was measured by Griess Reagent. For this, 50 µl of cell culture medium was mixed with 50 µl of Griess reagent and incubated at room temperature for 10 min in the dark. Then absorbance was measured at 540 nm using multi-mode plate reader (BioTek, SynergyMx). Nitrite level in samples was determined by using the standard curve of sodium nitrite. Culture medium was taken as blank for all experiments.

Estimation of IL-1 β , IL-10, PGE₂ and PGD₂. Levels of IL-1 β , IL-10, PGE₂ and PGD₂ in culture medium were measured by ELISA kit according to manufacturer's protocol. Their levels in culture medium were determined by using standard curves of respective cytokine or prostaglandin standards provided along with the kit.

Measurement of Reactive Oxygen Species (ROS). RAW 264.7 cells were seeded in 6 well plates at a density of 2×10^5 cells/well then pre-incubated with different concentrations (1, 50 and $100 \mu\text{M}$) of ALA metabolites [13-(S)-HPOTrE and 13-(S)-HOTrE] and/or N-Acetyl Cysteine (NAC, 5 mM), for 3 h. Then cells were further stimulated with or without LPS ($1 \mu\text{g}/\text{ml}$) for next 16 h. After that cells from each well were harvested and washed twice with PBS and further incubated with 10 mM DCFH-DA for 30 min in dark at 37°C and then two times washed with PBS. About 10,000 cells per sample were taken for analysis. The measurement was performed on a Flow Cytometer and data analysis was done by Cell Quest software (FACS Calibur, Becton Dickinson, CA, USA) with excitation of DCF at $\lambda 488 \text{ nm}$ and emission at $\lambda 525 \text{ nm}$. Primary macrophages isolated from peritoneal cavity were seeded in 12 well plate and grown as mentioned earlier. Then pre-treated with 13-(S)-HPOTrE and 13-(S)-HOTrE at 100 nM for 3 h. Then stimulated with LPS and ROS was measured as described above.

Immunoblot Analysis. RAW 264.7 cells seeded in 100 mm plates at a density of 5×10^5 cells/well and then after 12 h pre-incubated with different concentrations (1, 50 and $100 \mu\text{M}$) of either ALA metabolites or dexamethasone ($10 \mu\text{M}$) for 3 h. For Immunoblot analysis of primary cells, mouse peritoneal macrophages were isolated and seeded in 60 mm plates. Then pre-treated with lower doses (100 nM and 400 nM) of ALA metabolites for 3 h. Cells were then stimulated with or without LPS ($100 \text{ ng}/\text{ml}$) for next 24 h. Cells were harvested at the end of time point, pelleted down and stored at -80°C for further use. Cell pellets were lysed in RIPA buffer containing 1x protease inhibitor at 4°C . Protein estimation was done by Bradford method using BSA as standard. An equal amount of protein was loaded and separated on 8–15% SDS-PAGE and transferred to nitrocellulose membrane. Then membranes were blocked with 5% (w/v) fat-free dry milk in TBST for 1 h at room temperature followed by washing three times with TBST. Membranes were incubated with primary antibodies ($0.5\text{--}1.0 \mu\text{g}/\text{ml}$) for 12 h at 4°C on a shaker incubator with gentle shaking followed by thrice washing with TBST. The membranes were then incubated with respective secondary antibodies conjugated with HRP. Signals were then detected with western lightning plus ECL kit (PerkinElmer) and captured on Kodak Imaging System (KODAK Image station 4000 mm Pro).

Reverse Transcription Polymerase Chain Reaction (RT-PCR). RAW 264.7 cells were seeded in 6 well culture plate. At 60% confluency, cells were pre-incubated with different concentrations of either ALA metabolites (1, 50 and $100 \mu\text{M}$) or dexamethasone ($10 \mu\text{M}$) for 3 h and then stimulated with LPS ($100 \text{ ng}/\text{ml}$) for 24 h. Total cellular RNA was extracted from each well using TRIzol[®] Reagent according to the manufacturer's instructions (Invitrogen Bio Services, India, Pvt. Ltd). RNA quantification was performed by nanodrop (NanoDrop 2000TM, Thermo Scientific, DE, USA). cDNA of each sample was prepared by using $2 \mu\text{g}$ of RNA, $1 \mu\text{l}$ MLV reverse transcriptase, 1 mM dNTP and $1 \mu\text{l}$ oligo dT according to manufacturer's standardized protocol (Promega Corporation, WI, USA). PCR analyses were performed on aliquots of the cDNA prepared to detect iNOS, TNF- α , NLRP3, Caspase-1, IL-1 β , IL-18 and GAPDH. The reactions were carried out in a volume of $20 \mu\text{l}$ containing (final concentration) 1 U Taq DNA polymerase, 0.2 mM dNTP, 100 pM of forward primers and reverse primers (Supplementary Table S1), and $10 \mu\text{l}$ reaction buffer. After amplification, PCR products were electrophoresed on 1% agarose gels and visualized by ethidium bromide staining on UV irradiation (BIO-RAD, Universal hood II).

Analysis of the inflammasome, autophagy and NF- κB translocation by confocal microscopy. RAW 264.7 cells were seeded in 6 well culture plates on sterile culture grade coverslips. When cells were 60% confluent, cells were pre-incubated with ALA metabolites ($100 \mu\text{M}$) and/or with GW9662, PPAR- γ inhibitor, for 3 h, then stimulated with LPS ($100 \text{ ng}/\text{ml}$) for 24 h. For the study of inflammasome and autophagy, stimulation of cells with LPS was done for 24 h and for NF- κB translocation, it was done for 16 h. However, for study NF- κB translocation on peritoneal macrophages, cells were treated with ALA metabolites at lower concentration (100 nM) for 16 h. Fixation of cells was done by ice-cold 4% paraformaldehyde for 10 min at 4°C followed by washing in PBS with 0.2% Tween 20. Permeabilization in cells was done by ice-cold acetone: methanol (1:3) for 15 min at room temperature followed by washing in PBS with 0.2% Tween 20. To avoid nonspecific binding, blocking was done by incubating cells in 5% FBS in PBST for 1 h at room temperature followed by twice washing in PBS with 0.2% Tween 20. Cells were then incubated with targeted primary antibody (1:100 dilution) in 3% BSA in PBST for 12 h at 4°C followed by washing thrice in PBS with 0.2% tween 20. Cells were then incubated with the fluorescent conjugated respective secondary antibody (1:300 dilutions) in 3% BSA in PBST for 1 h at room temperature in the dark. Finally, washings were done and coverslips mounted on slides by anti-fade reagent with DAPI (ProLong Gold Antifade reagent, Invitrogen, USA). Image analysis was done on a confocal microscope (Zeiss LSM700, USA).

Analysis of Apoptosis by FACS. RAW 264.7 cells were seeded in 6 well cultures plate. When cells were 60% confluent, cells were pre-incubated with different concentrations of either ALA metabolites (1, 50 and $100 \mu\text{M}$) and/or doxorubicin ($10 \mu\text{M}$) for 3 h, then stimulated with LPS ($100 \text{ ng}/\text{ml}$) for 24 h. Staining of cells was done by FITC Annexin V Apoptosis Detection Kit (BD Biosciences, CA, USA), according to manufacturer's standardized protocol. Samples were run on Flow Cytometer (BD, LSR Fortessa, CA, USA) and data analyses were done on BD FACS Diva[™] software.

Statistical Analyses. All the experiments were performed in triplicates and the values represented as mean \pm SD. Data were correlated, analyzed and p-values were obtained using student's t-test. The p-value < 0.05 was considered as statistically significant.

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Author Contributions

N.K. and P.R. designed research, N.K. performed the experiments, N.K. and R.K. analyzed the data, N.K. and N.F. drafted manuscript. N.K., P.R., G.G., K.A., G.V.R. and P.V.G. reviewed the manuscript. All the authors approved the manuscript.

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Isolation and characterization of gallic acid and methyl gallate from the seed coats of *Givotia rottleriformis* Griff. and their anti-proliferative effect on human epidermoid carcinoma A431 cells

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ABSTRACT

Gallic acid (GA) and its derivative methyl gallate (MG) are well studied plant phenolics. They have exhibited anticancer effects in several cancer cell lines. However, the presence of GA/MG in the seed coats of *Givotia rottleriformis* and their inhibitory effect on human epidermoid carcinoma (A431) skin cancer cells were not reported. In this study we have isolated and chemically characterized the bioactive compounds GA and MG from the bioassay guided methanolic (MeOH) seed coat extracts of *G. rottleriformis*. The fractions obtained from open silica column chromatography were subjected to in vitro enzymatic assays. Among seven fractions we found that only fractions 5 and 6 showed significant inhibition activity toward COX-1 with an IC₅₀ value of 28 µg/mL and 9.3 µg/mL and COX-2 with an IC₅₀ value of 35 µg/mL and 7.0 µg/mL respectively. However, we could not find 5-LOX enzyme inhibition activity. MG (10 mg/g DW) and GA (6 mg/g DW) were the major compounds of seed coats. Cell viability was analyzed by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) assay, which showed that GA/MG significantly reduced the growth of A431 cells with an IC₅₀ value of 25 µg/mL and 53 µg/mL and 11 µg/mL and 43 µg/mL at 24 h and 48 h, respectively. However the cytotoxic effect of GA/MG on HaCaT normal skin keratinocyte cell line was found to be less. Western blot analysis has shown that GA/MG treatment down regulated Bcl-2 and up regulated cleaved caspase-3 with respect to increasing doses. Our results conclude that GA and MG have potential anticancer effects and can be used as therapeutic agents for skin cancers.

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1. Introduction

Skin diseases are becoming more common worldwide, because of increasing environmental pollutants, such as chemical hazards and radiations. Diverse factors influence skin cancers, e.g. solar radiation, UV irradiation. More than one million new skin cancer cases were reported annually in USA [1]. Increasing incidence of skin cancers was reported in AIDS (Acquired immune deficiency syndrome)

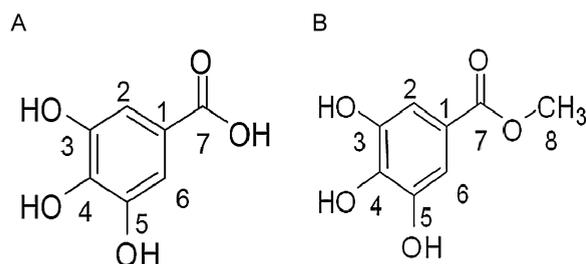


Fig. 1. Chemical structure of (A) gallic acid and (B) methyl gallate.

patients [2]. The cancer chemoprevention by natural agents such as phytochemicals, minerals and vitamins were shown to have effective results on various malignancies [3,4]. The curcumin isolated from plants inhibits UV-irradiation-induced oxidative stress and enhanced apoptosis in A431 cells [1,5]. The isolated resveratrol from plants was reported to have potential anti-cancer effect that enhanced apoptosis in A431 cells [6].

In this study we used the seed coats of *Givotia rottleriformis*, a tree species that belongs to Euphorbiaceae family. This plant grows in limited areas and particularly in the forests of Andhra Pradesh, Karnataka, Tamil Nadu and West Bengal in India. In our previous study we have observed that the seeds of this plant were rich in phenolics [7] and were reported to have anti-rheumatic, anti-psoriatic and anti-dandruff medicinal properties [8].

The gallic acid is isolated from plants [9,10] and the antioxidant and anticancer effect of GA were well reported in most of the cancer cells [9,11–17]. Many of GA derived chemical derivatives were also shown to have good anticancer properties [18]. Methyl gallate, a methyl ester of GA, was also isolated from several plants [19,20]. The biosynthesis of GA and MG takes place via dihydroshikimate, a derivative of phenylpropanoid biosynthesis [21]. The anticancer and anti oxidant effects of MG was reported in different cancer cells [22–27]. In addition MG was also shown to have anti-bacterial and anti-viral properties [28–30].

Cyclooxygenases (COX-1 and COX-2) and lipoxygenases (5-LOX, 12-LOX, 15-LOXa and 15-LOXb) are the key enzymes of arachidonic acid (AA) metabolism [31]. Previous reports suggested that inducible form of COX-1 and COX-2 leads to the biosynthesis of prostaglandins and thus causes inflammation and cancer [32–34]. Inhibition of 5-LOX blocks production of 5-LOX metabolites and triggers apoptosis in prostate cancer cells [35]. Therefore, identification of natural dual COX-2/5-LOX inhibitors is an interesting area of research to control cancer progression [36].

The over expression of Bcl-2 protein causes reduction of apoptosis in cancer cells [37–40]. In contrast, the up-regulation of cleaved caspase-3 activated by other caspases [41,42], enhances apoptosis and thus reduces cancer cell survival [43–45].

In the present study, we have isolated GA and MG from the seed coats of *G. rottleriformis* using chromatographic techniques and chemically characterized them using IR, NMR and LC–MS analysis (Fig. 1). The inhibitory effect of

GA or MG on COX-1, COX-2 and 5-LOX was determined. We further studied the cytotoxic effect of purified GA and MG on human epidermoid carcinoma (A431) skin cancer cell line and normal human skin keratinocyte cell line HaCaT using MTT assay. The apoptotic effect of GA/MG was studied by western blotting analysis of Bcl-2 and cleaved caspase-3 in a dose dependent manner.

2. Materials and methods

2.1. General procedure

IR spectra was determined in the KBr pellet using a JASCO FT-IR model 5300 spectrophotometer with polystyrene as reference. NMR spectra were recorded at 400 MHz for ^1H NMR and 100 MHz for ^{13}C NMR on Bruker-Avance-400 spectrometer with chloroform-d as solvent and tetramethylsilane (TMS) as reference ($\delta=0$ ppm) in DMSO- d_6 at 25 °C. The chemical shift was expressed in δ , downfield from the signal of internal TMS. Mass spectra were recorded using LC–MS-2010 (Shimadzu).

2.2. Plant materials

Mature and dry seeds of *G. rottleriformis* were collected during summer from Regional Forest Research Centre (RFRC), Rajahmundry, Andhra Pradesh, India.

2.3. Cell lines and reagents

A431 skin cancer cell line and normal HaCaT skin cell line were obtained from National Centre for Cell Science (NCCS), Pune, India. Dulbecco's modified Eagle's medium (DMEM), fetal bovine serum (FBS), phosphate buffered saline (PBS), penicillin and streptomycin were purchased from GIBCO, Ltd. (BRL Life Technologies, Inc., Grand Island, NY). MTT [3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide] and dimethyl sulfoxide (DMSO) were obtained from Sigma; poly-L-lysine, glutaraldehyde, proteinase inhibitor K, propidium iodide (PI), phenyl methyl sulfonyl fluoride (PMSF), luepeptin, aprotinin, pepstatin A, trypsin, Tween 20, Triton X-100, TMPD (*N,N,N,N'*-tetramethyl-*p*-phenylenediamine) were purchased from Sigma Chemical Company (St. Louis, USA). The primary antibodies for Bcl-2 and cleaved caspase-3 were obtained from Upstate Biotechnology (Charlottesville, VA, USA). The GA and MG were purified from the seed coats of *G. rottleriformis*. All other chemicals and reagents used in the study were obtained either from Merck or Sigma.

2.4. Extraction and reverse phase HPLC analysis of crude extract

The seed coats were macerated into fine powder and were extracted in methanol (MeOH). The crude extract was filtered using Whatman No.1 filter paper and was concentrated using Rotavapor (R3, Buchi). The extract was further analyzed with RP-HPLC (Shimadzu) using C18 reverse phase column (Shim-pack column with dimensions 250 mm \times 4.6 mm, particle size 5 μM), with flow rate of

6 mL/min and detection at 280 nm. The mobile phase used was a complex gradient of solvent-A (water:acetic acid, 1000:1), and solvent-B (MeOH:acetic acid, 1000:1).

2.5. Open silica column and RP-HPLC

The crude extract (10 g) was chromatographed using (Acme's) silica gel (100–200 mesh). Hexane and ethyl acetate was used as a mobile phase. Each fraction was passed through a thin layer chromatography (TLC) using silica gel plates (Merck 60F²⁵⁴) and visualized by irradiation with UV light and/or by iodine vapors. COX-1, COX-2 and 5-LOX assays were performed for all the fractions (see below). Only fractions that showed significant bioactivity were resolved using RP-HPLC (method mentioned above), isolated and concentrated by lyophilizer. The purified compounds were stored at room temperature and were used for bioassays and further analysis.

2.6. Isolation of COX-1 enzyme

We isolated COX-1 enzyme from Ram seminal vesicles using Hemler and Lands [46] method with slight modifications. In brief, Ram seminal vesicles were minced and homogenized in Tris-HCl (pH 8.0) buffer for 1 min; the homogenate was filtered through cheese cloth and centrifuged at $13,000 \times g$ at 4 °C for 30 min. Finally 0.01% sodium azide was added to the supernatant. It was stored as small aliquots at –80 °C and was used as COX-1 enzyme source.

2.7. Isolation of COX-2 enzyme

The enzyme COX-2 was isolated according to the method of Reddy et al. [47] with slight modifications. In brief, human recombinant COX-2 enzyme was expressed in Sf-9 cells. Cells were pelleted down by centrifugation at 2000 rpm and the cells were further resuspended in 50 mM Tris-HCl buffer (pH 7.2) and sonicated for 3 min followed by centrifugation at $90,000 \times g$ at 4 °C for 1 h 20 min using ultracentrifuge (Hitachi, Himac CP-100 α). The obtained pellet was re-suspended in 2.5 mM Tris-HCl buffer (pH 7.2), 0.8% Tween 20, 1 mM phenol, and 0.5% glycerol. It was stored as small aliquots at –80 °C and used as COX-2 enzyme source.

2.8. COX-1 and COX-2 enzyme activity

We used the method of Copeland et al. [48] with slight modifications to measure the enzymatic activities of both COX-1 and COX-2, based on the chromogenic assay and oxidation of TMPD during the reduction of prostaglandin G₂ (PGG₂) to prostaglandin H₂ (PGH₂). In brief, the assay mixture contained Tris-HCl buffer (100 mM, pH 8.0), hematin (15 μ M), EDTA (3 μ M), enzyme (COX-1 or COX-2) and test compound. The assay mixture was pre-incubated at 25 °C for 15 min and the reaction was initiated by addition of AA and TMPD to a final volume of 1 mL. The activity was measured by estimating the rate of TMPD oxidation with an increase in absorbance at 603 nm during 1 min. A low rate of non-enzymatic TMPD oxidation observed in the absence of

COX-1 or COX-2 enzymes was used as control reaction and was subtracted from the test experimental values while calculating the percent inhibition.

2.9. 5-LOX assay

The 5-LOX enzyme was extracted from potato tubers and assayed according to Reddanna et al. [49]. The enzyme activity was measured using polarographic method with a Clark's oxygen electrode on Strathkelvin instruments, model 782, RC-300. The typical reaction mixture contained 50–100 μ L of enzyme and 10 μ L of substrate (133 μ M of AA), 100 mM phosphate buffer (pH 6.3) in a total volume of 3 mL. The rate of decrease in the oxygen concentration was taken as a measure of enzyme activity. The stock solutions of the test compounds were freshly prepared before use and were dissolved in DMSO. Various concentrations of the test compound were prepared and the 5-LOX was initiated by the addition of the substrate. The assay was performed at 25 °C and the maximum slope generated was taken for calculating the activity. The percent inhibition was calculated by the comparison of 5-LOX activity in the presence or absence of the inhibitor and IC₅₀ value was calculated from the concentration–inhibition response curve.

2.10. Cell culture

A431 cells and HaCaT cells were grown as a monolayer in petriplates and supplemented with DMEM that contains 10% heat inactivated FBS, 100 IU/mL penicillin, 100 μ g/mL streptomycin, 2 mM L-glutamine and maintained at 37 °C in a humidified atmosphere with 5% CO₂. The cells were sub-cultured twice in a week and the exponentially growing cells were used for the analysis.

2.11. MTT assay

A431 cells and HaCaT cells (5×10^3 cells per well) were seeded in 96 well plates and were treated with or without GA/MG at various concentrations (0.1, 10, 25, 50 and 100 μ g/mL) in a final volume of 100 μ L and incubated for 24 h and 48 h. Later 20 μ L of MTT (5 mg/mL in PBS) was added to each well and incubated for an additional 3 h at 37 °C. The culture medium was removed and 50 μ L of DMSO was added to each well to dissolve the purple-blue formazan crystals and optical density was measured at 570 nm using ELISA multi mode plate reader (SYNERGYMX, Biotek).

2.12. Preparation of whole cell extract and Western blot analysis

The cells were treated with or without GA or MG at various concentrations (25, 50 and 100 μ g/mL) for 24 h. Then the cells were washed with PBS and harvested by trypsinization and finally cell pellets were resuspended in RIPA buffer containing 1 \times protease inhibitor cocktail followed by incubation for 30 min at 4 °C with frequent vortex. The lysate was centrifuged at 10,000 rpm for 30 min and the supernatant was collected as whole-cell extract

[50]. The protein concentration was estimated by Bradford method Bradford [51]. The total protein was resolved on 12% SDS-PAGE and transferred onto nitrocellulose (NC) membrane. The NC membrane was then incubated in 5% (w/v) non-fat dry milk powder at room temperature for 1 h to block non-specific sites. The NC membrane was incubated with the primary antibody of interest for 12 h at 4 °C under shaking (cleaved caspase-3, and Bcl-2) and washed thrice with TBST. The NC membrane was again incubated with the respective secondary antibody conjugated with HRP for 1 h at room temperature, and again washed thrice with TBST. The blot was developed by adding HRP substrate (PerkinElmer; Western lightning Plus-ECL).

2.13. Statistical analyses

The data was presented graphically as the mean \pm standard deviation (SD). Statistical analysis was done using Sigma Plot 12.0 software and the graphs were plotted using Graph pad prism 6.0 software.

3. Results

3.1. RP-HPLC analysis and column chromatography of seed coat extract

The crude seed coat extract subjected to RP-HPLC and the resolved chromatogram showed 10 major peaks at different retention times (RTs). Peak-1 eluted at 9.0 min, peak-2 at 25.9 min, peak-3 at 28.6 min, peak-4 at 33.1 min, peak-5 at 40.8 min, peak-6 at 42.1 min, peak-7 at 44.7 min, peak-8 at 47.7 min, peak-9 at 50.0 min and peak-10 at 57.0 min (Fig. 2). The crude seed coat extract (10 g) was fractionated into one to seven fractions, fraction 1 (0.6 g), fraction 2 (5.0 g), fraction 3 (1 g), fraction 4 (0.8 g), fraction 5 (1.0 g), fraction 6 (1.2 g), fraction 7 (0.4 g) according to the polarity using open silica chromatography and the purity of each fraction was monitored with TLC.

3.2. COX-1, COX-2 and 5-LOX enzymatic assays

COX-1, COX-2 and 5-LOX activity were estimated for fractions 1–7. However, only fractions 5 and 6 inhibited COX-1 with an IC₅₀ value of 7 μ g/mL and 5.1 μ g/mL and COX-2 with an IC₅₀ value of 9 μ g/mL and 6.44 μ g/mL respectively (Fig. 3A–D). None of the fractions showed 5-LOX inhibition activity.

3.3. Isolation and chemical characterization of active compound from fraction 5

The bioassay guided fraction 5 that showed only a single peak at RT of 41.5 min, when resolved by RP-HPLC was collected (Fig. 4A). The isolated compound was subjected to IR, ¹H, ¹³C NMR and LC–MS analysis and identified as MG (Supplementary Fig. S1–S4). IR (KBr) cm⁻¹: 3506 (O–H), 1697 (●C=O), 1618 (C=C), 1541, 1471, 1439, 1313, 1251, 1195, 1037, 767, 746 (Supplementary Fig. S1). ¹H NMR (400 MHz, CDCl₃) δ ppm: 7.26 (S, 2H, A), 4.01 (S, 2H, B) (Supplementary Fig. S2). ¹³C NMR (200 MHz, CDCl₃) δ ppm: 165.67 (C7,

●C=O) 144.10 (C3, C5), 136.99 (C4), 118.82 (C1) 107.86 (C2, C5) 50.36 (C8) (Supplementary Fig. S3). The molecular mass of isolated MG was determined as 184 using LC–MS analysis (Supplementary Fig. S4).

3.4. Isolation and chemical characterization of active compound from fraction 6

RP-HPLC chromatogram of fraction 6 that showed a mixture of 3 compounds eluted at different RTs, C1 (600 mg) at RT 27.49 min, C2 (250 mg) at RT 40.8 min and C3 (350 mg) at RT 51.4 min were isolated separately (Fig. 4B). MTT assay results showed that significant inhibition of A431 cell proliferation was seen when treated with C1, whereas treatment with C2 or C3 did not show any inhibitory effect on cell proliferation. The active C1 was subjected to IR, ¹H, ¹³C NMR and LC–MS analysis and its chemical structure was identified as GA. IR (KBr) cm⁻¹ 33.71 (–COOH), 3057 (C–H), 1705 (=C=O), 1620 (C=C), 1452, 1338, 1248, 1026, 702 (Supplementary Fig. S5). ¹H NMR δ ppm: 12.52 (S, H acid OH), 7.22 (S, 2H) (Supplementary Fig. S6). ¹³C NMR δ ppm: 167.01 (C7=C=O), 143.98 (C3, C5), 136.61 (C4), 119.87 (C1) 108.14 (C2, C6); (Supplementary Fig. S7). The mass of the purified GA was determined as 169 by LC–MS (Supplementary Fig. S8).

3.5. MTT assay

Dose and time dependent effect of GA and MG on A431 and HaCaT cell proliferation was investigated. A431 cells that were treated with various concentrations of GA/MG (1, 10, 25, 50 and 100 μ g/mL) showed significantly reduced cell proliferation due to enhanced cell death (Fig. 5A and B). GA treatment enhanced A431 cell death in a dose dependent manner with calculated IC₅₀ value of 25 μ g/mL at 24 h. The cell death was increased further when the GA treatment time increased to 48 h with an IC₅₀ value of 11 μ g/mL (Fig. 5Ai–iv). Similarly MG treatment also reduced A431 cell proliferation in a dose dependent manner. MG treatment showed reduced A431 cell proliferation with an IC₅₀ value of 53 μ g/mL at 24 h. However when the MG treatment time increased to 48 h the rate of cell death also increased further with an IC₅₀ value of 43 μ g/mL (Fig. 5Bi–iv). HaCaT cells that were treated with same GA concentrations (1, 10, 25, and 100 μ g/mL) showed low level of reduction in cell proliferation with the calculated IC₅₀ values of 84.2 μ g/mL at 24 h and 64.4 μ g/mL at 48 h, respectively (Fig. 6Ai–iv). MG treatment also showed reduced effect on HaCaT cell proliferation with an IC₅₀ value of 79.4 μ g/mL at 48 h (Fig. 6Bi–iv).

3.6. Western blot analysis

Treatment of A431 cells with GA and MG down regulated Bcl-2 and thus enhanced apoptosis in dose (25, 50 and 100 μ g/mL) dependent manner (Fig. 7Ai and Bi). The cleaved caspase-3 was also induced in a dose dependent manner with increasing doses of GA and MG treatment (Figs. 7Aii and 6Bii). β -Actin was used as a loading control (Fig. 7Aiii and Biii).

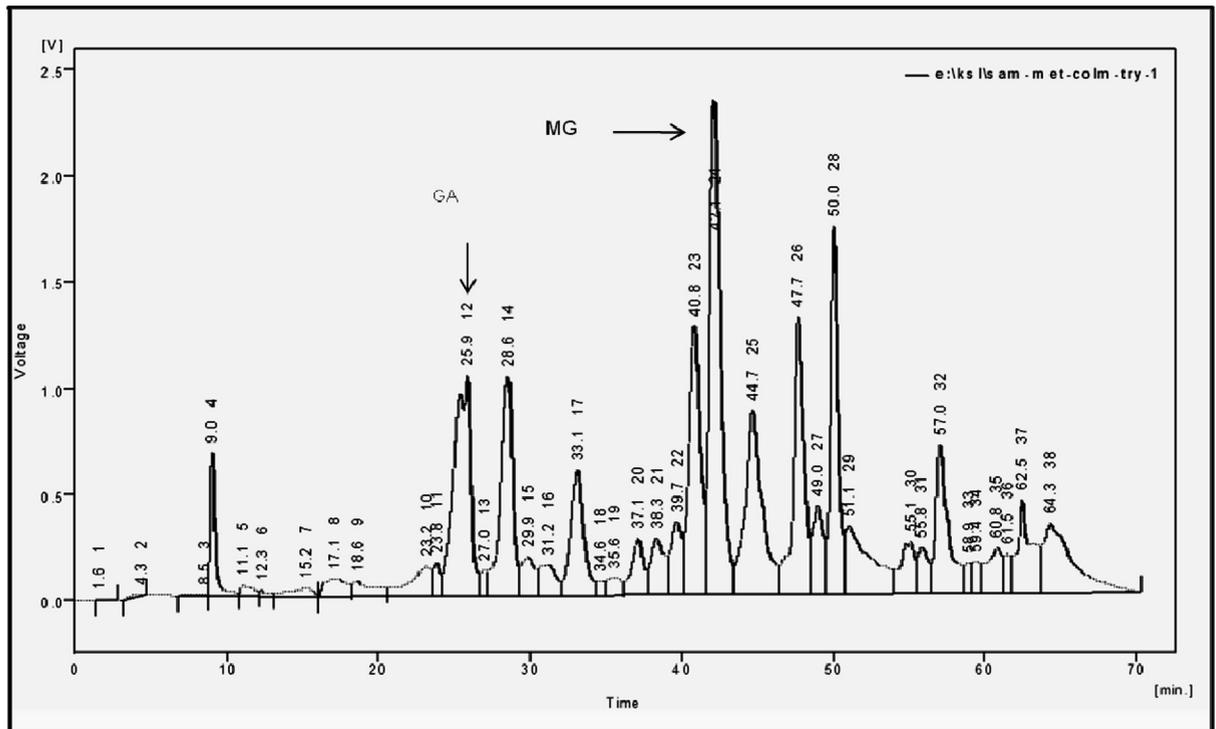


Fig. 2. High-performance liquid chromatography (HPLC) analysis of crude extract of *G. rotleriformis* seed coats using a reverse phase C_{18} column. High-performance liquid chromatography (HPLC) chromatogram showing crude compounds resolved at their respective retention times (RTs).

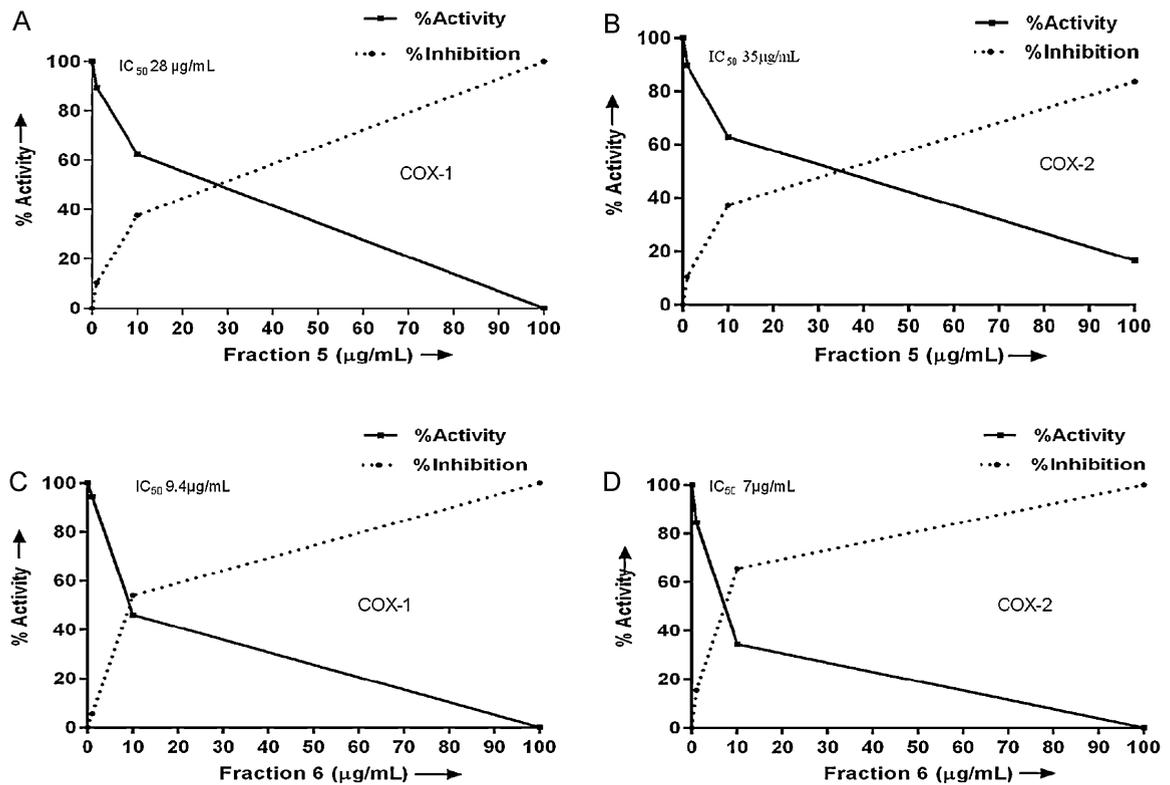


Fig. 3. COX-1 and COX-2 inhibition activity of fractions 5 and 6. (A) COX-1 inhibition of fraction 5, (B) COX-2 inhibition of fraction 5, (C) COX-1 inhibition of fraction 6 and (D) COX-2 inhibition of fraction 6.

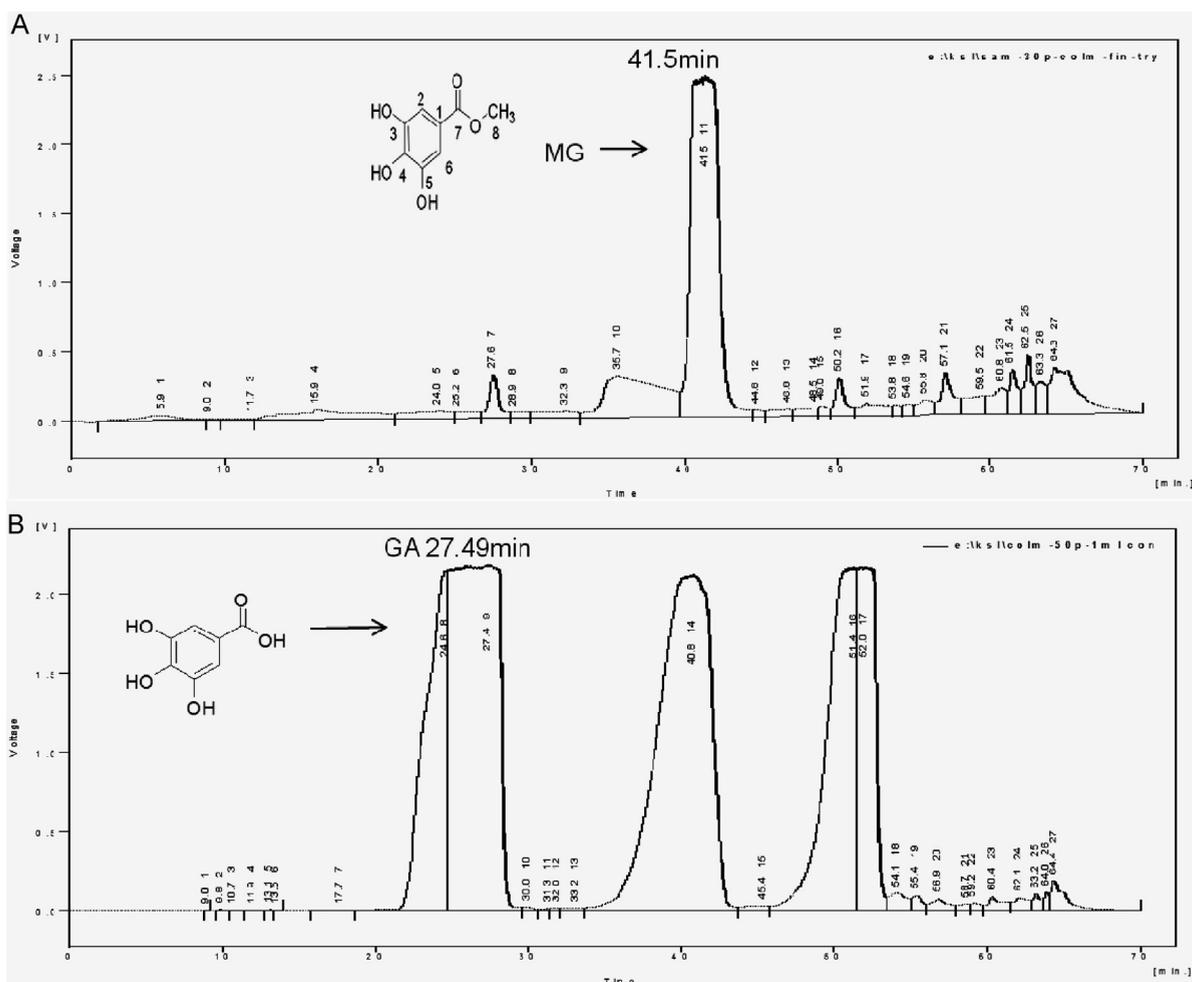


Fig. 4. Purification of methyl gallate (MG) from fraction 5 and gallic acid (GA) from fraction 6 by high-performance liquid chromatography (HPLC) using a reverse phase C₁₈ column. (A) MG from fraction 5. (B). GA from fraction 6.

4. Discussion

Plants synthesize a wide range of metabolites for their survival, growth, development and protection from a broad spectrum of bacterial, fungal and viral pathogens. Some of the plant metabolites work as anti-oxidant and anticancer drugs because of their toxic effect toward cancer cells [6,26,52]. In this study we isolated GA and MG as major metabolites from the seed coats of *G. rotteriformis*. The total seed coat extract was fractionated and subjected to COX-1/COX-2/5-LOX assays and cytotoxic efficiency was conducted on A431 cells and HaCaT cells. The HPLC chromatogram data of MeOH seed coat extract revealed a group of peaks that were fractionated from one to seven by open silica column chromatography. Among all the fractions, only 5 and 6 fractions significantly inhibited COX-1 and COX-2 enzyme activity (Fig. 3a–d). However, these fractions did not show any significant inhibition on 5-LOX enzyme activity. Earlier studies have demonstrated that COXs and LOXs are the key enzymes that play an important role in inflammation and carcinogenesis [10,11,52]. Only 5 and 6 chromatographed fractions that inhibited

the A431 cell proliferation was further subjected to active compound isolation by RP-HPLC. The active compounds of fractions 5 and 6 were purified by RP-HPLC (Fig. 4A and B) and were identified as GA and MG using IR, NMR and LC–MS analysis. GA and MG are natural constituents isolated from different plants [19,25,29]. Phenylpropanoid metabolism produce enormous array of secondary metabolites. The biosynthesis of GA and its derivative MG takes place via phenylpropanoid metabolism [21]. Our results suggest that MG (10 mg/g DW) and GA (6 mg/g DW) are the major compounds of the seed coats of this plant. We have also isolated several phenylpropanoid metabolites both known and unknown and studied their role in inducing plant immunity (Samuel et al., unpublished data). It was well demonstrated that some plant compounds such as curcumin, resveratrol and α -santalol suppressed cell proliferation and enhanced apoptosis in A431 cells [1,5,6].

Treatment of A431 cells with GA/MG suppressed cell survival by enhanced apoptosis in a dose and time dependent manner (Fig. 5Ai–iv and Bi–iv). The cytotoxic effect of GA and MG was investigated in various cancer cells [11,26,53–55]. The GA isolated from *Terminalia bellerica*

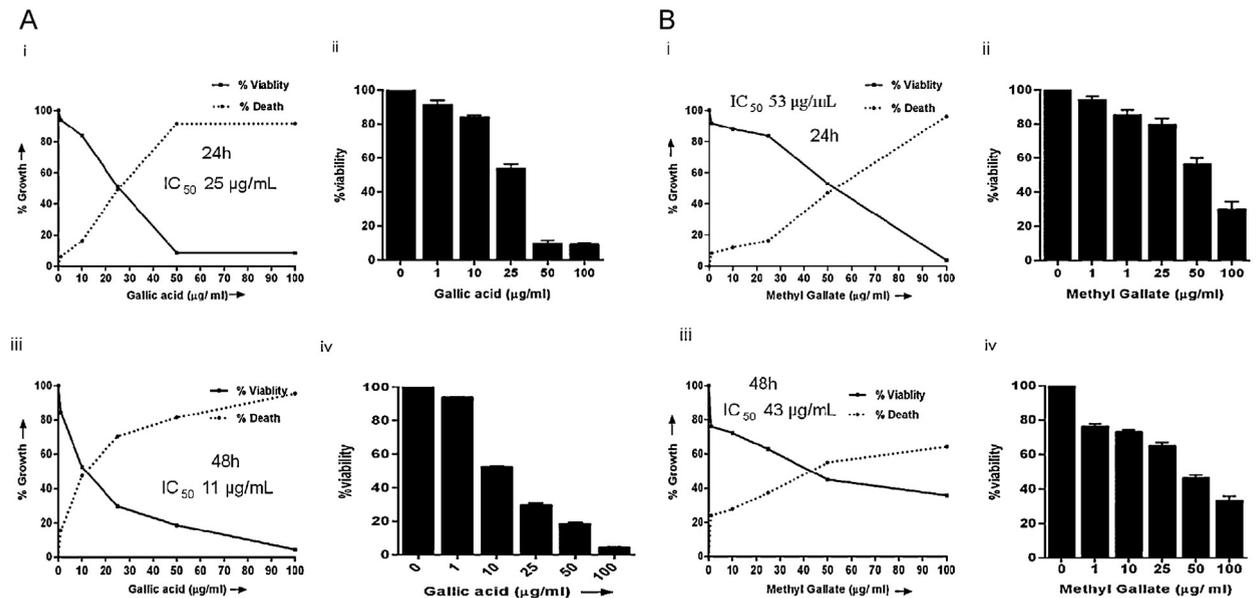


Fig. 5. Gallic acid (GA) and methyl gallate (MG) reduced the cell viability of A431 cells. Cells were seeded at a density of 1×10^6 cells/mL in 96 well polystyrene culture plates and maintained at 37 °C with 5% (v/v) CO₂ for 1 day. After 24 h the cells were incubated with GA/MG at the indicated concentrations for 24 h and 48 h and then processed for MTT assay. (Ai–iv) Percentage of cell death and viability of A431 cells treated with GA in a dose dependent manner at 24 h and 48 h. (Bi–iv) Percentage of cell death and viability of A431 cells after treatment with MG at 24 h and 48 h. The data presented as the mean \pm SD of three independent experiments. The bars represent statistical significance over control ($P < 0.05$).

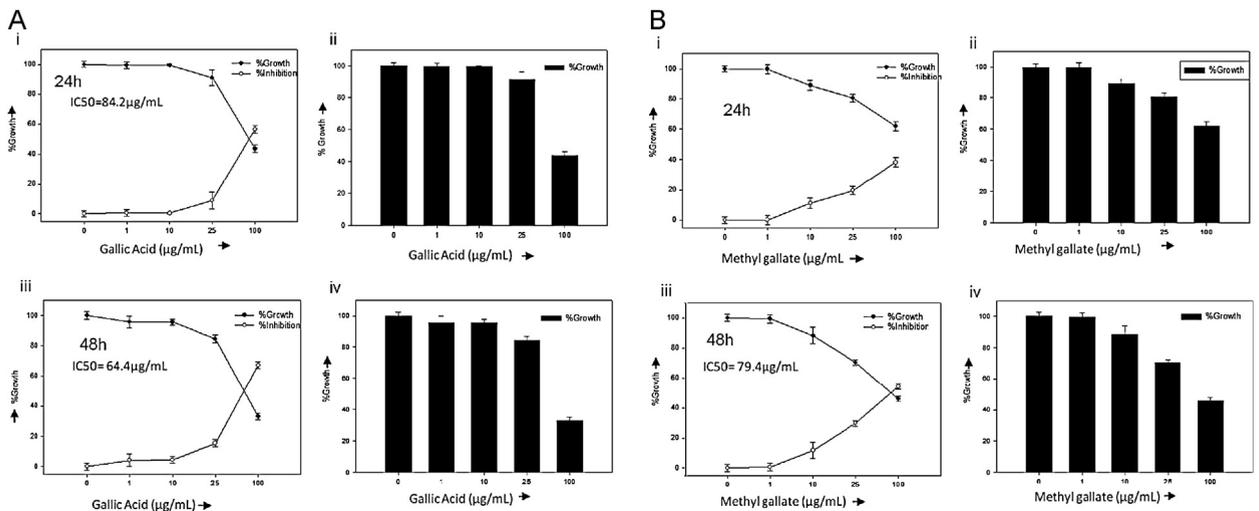


Fig. 6. Gallic acid (GA) and methyl gallate (MG) reduced the cell viability of HaCaT normal skin keratinocyte cell line. Cells were seeded at a density of 1×10^6 cells/mL in 96 well polystyrene culture plates at 37 °C with 5% (v/v) CO₂ for 1 day. After 24 h the cells were incubated with GA/MG at the indicated concentrations for 24 h and 48 h and then processed for MTT assay. (Ai–iv) Percentage of cell death and viability in HaCaT cells when treated with GA in a dose dependent manner at 24 h and 48 h. (Bi–iv) Percentage of cell death and viability in HaCaT cells when treated with MG in a dose dependent manner at 24 h and 48 h. The data presented as the mean \pm SD of three independent experiments. Bars represent statistical significance over control ($P < 0.05$).

potentially inhibited COX-1 and COX-2 enzymes in a concentration dependent manner [10]. Similarly, MG also showed dual COX-2/5-LOX inhibitory activity; however, 5-LOX inhibition was based on the leukotriene C₄ [36]. Similar results were observed with our data with GA inhibiting both COX-1 and COX-2 enzymes in a dose dependent manner [10]. The inhibition of COX-2 enzyme by MG was similar as that mentioned by Kim et al. [36]. The COX-1 activity of fraction 5 and the purified MG were the same (IC₅₀ value

of 28 μg/mL). Here we report for the first time the COX-1 inhibition activity of MG. We have not observed any effect of GA on 5-LOX activity and our results were consistent with the findings from previous reports [10]. Whereas the 5-LOX activity of MG could not be observed even at increasing concentrations though it was earlier reported that MG exhibits 5-LOX inhibition activity [36].

The anti-oxidant and anti-proliferative effects of GA/MG were well studied [11,19,20,22,26,28,30,53]. In our results,

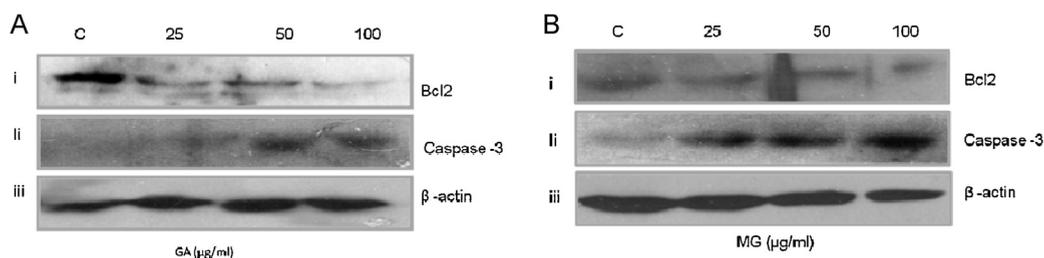


Fig. 7. Western blotting analysis showing Bcl-2 and cleaved caspase-3 protein up regulation in A431 cells that were treated with purified gallic acid (GA)/methyl gallate (MG). (Ai) A431 cells treated with GA down regulated Bcl-2 expression with respect to increasing doses. (Aii) Up regulation of the expression of cleaved caspase-3 in GA treated A431 cells. (Bi) Down regulation of the expression of Bcl-2 levels with increasing doses of MG treated A431 cells. (Bii) Up regulation of the expression of cleaved caspase-3 with increasing doses of MG treated A431 cells.

the treatment of A431 cells with purified GA suppressed the growth of A431 cells in a dose dependent manner with an IC_{50} value of 25 $\mu\text{g}/\text{mL}$ and 11 $\mu\text{g}/\text{mL}$ at 24 h and 48 h, respectively (Fig. 5Ai–iv). On the other hand, GA has shown much less cytotoxic effect on HaCaT normal skin keratinocyte cell line and showed IC_{50} value of 84.2 $\mu\text{g}/\text{mL}$ and 62.4 $\mu\text{g}/\text{mL}$ at 24 h and 48 h, respectively (Fig. 6Ai–iv). The anti-proliferative and apoptotic properties of phytochemicals were demonstrated in A431 cells [1,5,6]. However this is the first observation that reported the effect of GA on A431 cells. Similarly MG reduced the cell proliferation with an IC_{50} value of 53 $\mu\text{g}/\text{mL}$ and 48 $\mu\text{g}/\text{mL}$ at 24 h and 48 h respectively (Fig. 5Bi–iv). In the same way, normal skin HaCaT cells that were treated with MG showed less cytotoxicity with an IC_{50} value of 79.4 $\mu\text{g}/\text{mL}$ than A431 cancer cells (Fig. 6Bi–iv). It was suggested by previous reports that MG inhibits cancer cells [25,53]. Our data showed that the treatment of A431 cells with GA and MG down regulated Bcl-2 (Fig. 7Ai and Bi). Bcl-2 promotes cell proliferation and reduced apoptosis in cancer cells [56–59]. Treatment of A431 cells with GA or MG also upregulated the protein levels of cleaved caspase-3 in a dose dependent manner (Fig. 7Aii and Bii). Caspase-3 was reported as an apoptotic marker protein, the expression of which enhances apoptosis, cleaves key cellular proteins and promotes cell death in cancer cells [56,60–62]. Apart from cancer, because of antioxidant property of GA, GA and its ester derivatives were widely used as additives in food industry [63]. In summary, this study demonstrates that the seeds coats of *G. rottleriiformis* are a rich source of GA/MG and may play significant role in treatment of various cancers. These results demonstrate and encourage the need of further studies to establish the role of GA or MG as potential anti-inflammatory drugs to avoid the risk of various skin and other cancer problems.

Conflict of interest

The author has received grants from University Grants commission, Council of Scientific and Industrial Research, and Department of Science and Technology, during the conduct of the study.

Transparency document

The [Transparency document](#) associated with this article can be found in the online version.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at [doi:10.1016/j.toxrep.2015.03.001](https://doi.org/10.1016/j.toxrep.2015.03.001).

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Evaluation of *Cissus quadrangularis* extracts as an inhibitor of COX, 5-LOX, and proinflammatory mediators

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ABSTRACT

Ethnopharmacological relevance: *Cissus quadrangularis* is an ancient medicinal plant. It is an active ingredient of one Ayurvedic formula called "Laksha Gogglu". Its stem is used in food preparation in India. Traditionally it is used to treat various diseases like asthma, indigestion, ear diseases, irregular menstruation, skin diseases, piles, fractured bones, etc.

Aim of the study: This study aimed to evaluate the ability of the plant extracts to inhibit cyclooxygenase (COX-1), cyclooxygenase (COX-2), and 5-lipoxygenase (5-LOX) enzyme activity. Western blot analysis was also carried out in the quest to determine the effect of active acetone fraction of *Cissus quadrangularis* (AFCQ) on proinflammatory mediators as acetone extract is found to be the most effective in this study.

Materials and methods: The differential extract of the stem were tested for enzyme inhibition of COX and 5-LOX using spectroscopic and polarigraphic method. Effective acetone extract was partially purified by silica column, one of the active fraction showed dual inhibition against COX and 5-LOX. Western blotting shows downregulation of proinflammatory mediators as well as upregulation of phase-II enzymes.

Results: AFCQ extract showed COX and 5-LOX inhibition with IC₅₀ values of 7 µg/ml, 0.4 µg/ml, and 20 µg/ml for COX-1, COX-2 and 5-LOX respectively. It also showed anti-inflammatory activity on RAW 264.7 cell line with IC₅₀ value 65 µg/ml. In addition to this it is showing inhibition of proinflammatory mediators like iNOS and TNFα, along with translocation of Nrf-2 and upregulation of HO-1.

Conclusion: AFCQ is a COX and 5-LOX inhibitor isolated from the stems of *Cissus quadrangularis*. It is also effectively downregulate the iNOS, TNFα, and upregulation of HO-1.

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1. Introduction

Cissus quadrangularis is an ancient medicinal plant that has been used in many traditional medicines. Traditionally it is used to treat diverse diseases like rheumatic diseases, allergies, skin diseases, piles, fracture, and bone diseases (Udupa et al., 1965; Deka et al., 1994). It is an active ingredient of Ayurvedic formula called "Laksha Gogglu" which is used for alleviating pain, reducing inflammation and promoting the healing of wounds or simple fracture (Kulkarni, 2001). Stem of *Cissus quadrangularis* is very important part of the plant and used as raw drug in Indian folk medicine (Panda, 1990). Leaves of *Cissus quadrangularis* is used to treat anorexia whereas dried powder of stem with honey is taken orally to reduce pain and inflammation. The stem and leaf of the *Cissus quadrangularis* are used in food preparation in India. Numerous

studies demonstrated that methanolic and petroleum ether extract of the whole plant are used in treating osteoporosis and fracture (Deka et al., 1994; Shirwaikar et al., 2003; Sharpa et al., 2007). It possesses antioxidant (Jainu and Shyamaladevi, 2005), anti-inflammatory, antibacterial (Kashikar and George, 2006; Thakur et al., 2009), antiviral (Balasubramaniana et al., 2010), and antiulcerogenic (Jainu and Shyamaladevi, 2004, 2006; Jainu et al., 2010) properties. It has also solved the problems of weight loss and various metabolic syndromes (Oben et al., 2006, 2007). Phytochemical studies of *Cissus quadrangularis* have shown the presence of several phytochemical constituents, such as ascorbic acid, flavonoids, and triterpenoids (Potu et al., 2010).

Inflammatory and pathogenic condition activates the enzymes cyclooxygenase (COX) and 5-lipoxygenase (5-LOX). COX and 5-LOX are the key enzymes in the synthesis of prostanoid and eicosonoids from poly unsaturated fatty acids (PUFAs), which are involved in various inflammatory and allergic disorders (Martel-Pelletier et al., 2003; Daniel et al., 2004). Nuclear factor E2 p45-related factor 2 (Nrf-2) is a member of leucine zipper transcription family

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responsible for upregulation of genes of phase-II enzymes in response to oxidative stress and LPS treatment (Annukka et al., 2008). Heme oxygenase-1 (HO-1) is the phase-II enzyme catalyzes the degradation reaction of heme to convert biliverdin further to bilirubin. Deficiency of HO-1 isozyme reveals severe damage of iron metabolism, which leads to liver, and kidney oxidative damage and inflammation. Consequently HO-1 expression increases cell resistance to oxidative injury (Daniel et al., 2004). Inducible nitric oxide synthase (iNOS) and tumour necrosis factor alpha (TNF α) are the proinflammatory mediators. The concentration of iNOS is elevated in injury and inflammation, while TNF α is mainly formed through monocytes and activated macrophages. It is pleiotropic proinflammatory cytokine with many actions like fever, macrophage activation, etc., that are central to the pathogenesis.

In the present study, we have examined the in vitro anti-inflammatory activity of different extracts of *Cissus quadrangularis* on COX, 5-LOX and proinflammatory mediators. Inhibition of COX-1 and COX-2 were evaluated by using chromogenic assay and inhibition of 5-LOX was evaluated by using polarographic method. Whole plant of *Cissus quadrangularis* was extracted with different organic solvents and the acetone extract gave the potential inhibition of COX and 5-LOX. Consequently number of partially purified fraction of acetone extract we have screened to examine the inhibition of COX and 5-LOX. Single active acetone fraction of *Cissus quadrangularis* have shown potent inhibition hence called AFCQ. AFCQ was further used to evaluate the eventual mechanism essentially its anti-inflammatory effect in LPS induced inflammation. We found that AFCQ have potentially inhibited COX-2, iNOS, and TNF α expression in LPS treated murine macrophages RAW 264.7 cells. Upregulation of HO-1 expression connected with activation and expression of Nrf-2 might be related in the anti-inflammatory activity of AFCQ.

2. Materials and methods

2.1. Plant material

Plant material was collected from Vidarbha region of Maharashtra in March 2008. The plants were authenticated at the Department of Botany, Rashtrasant Tukdoji Maharaj Nagpur University, Nagpur and voucher specimens were deposited in the herbarium. Botanical name is *Cissus quadrangularis* and voucher specimen number is 9433.

2.2. Preparation of extracts of *Cissus quadrangularis*

The stem of *Cissus quadrangularis* was shade dried for five to six months, powdered, and extracted successively using Soxhlet apparatus with hexane, chloroform, acetone, ethyl acetate, methanol, ethanol, and water in the increasing polarity index. 250 g of dried plant powder was taken for the extraction. All extracts were concentrated to dryness using rotary evaporator. We obtained hexane extract 7.27 g, chloroform extract 5.10 g, acetone extract 2.17 g, ethyl acetate 1.7 g, methanol extract 3.53 g, ethanol extract 1.2 g, and water extract 1 g. The concentrated dry extracts were again dissolved in dimethyl sulphoxide (DMSO), mixed and vortexed for few min and then centrifuged 2000 \times g for 10 min. Supernatant was subsequently used to check the inhibition of COX-1, COX-2, and 5-LOX.

2.3. Partial purification of acetone extract by column chromatography

Acetone extract partially purified by column chromatography. Active acetone extract passed through open silica column. We obtained around thirteen different fractions, this fractions were

dried using rotary vacuum evaporator. Dried fractions again used to verify the inhibition of COX-1, COX-2, and 5-LOX. Out of thirteen fraction ninth fraction shows potent inhibition of COX and 5-LOX, hence called active fraction of *Cissus quadrangularis* (AFCQ) and used in further studies.

2.4. Reagents and chemicals

Phosphate buffered saline (PBS), RPMI 1640; fetal bovine serum (FBS), penicillin and streptomycin were purchased from Gibco BRL. TMPD (N,N,N-tetramethyl-*p*-phenylenediamine), Hematin, Trypsin, MTT (3-(4,5-dimethylthiazol-2-yl)-diphenyl tetrazolium bromide), β -actin antibody and lipopolysaccharide or LPS (*Escherichia coli* serotype), nitro blue tetrazolium (NBT) and 5-bromo-4-chloro-3-indolyl phosphate (BCIP) were purchased from Sigma–Aldrich chemical company (St. Louis, USA). Antibodies for COX-2, HO-1, TNF α , Nrf-2, iNOS and alkaline phosphatase conjugated anti-mouse, anti-goat and anti-rabbit antibodies were purchased from Santa Cruz Biotechnology (Santa Cruz, CA, USA). All other chemicals and solvents for chromatography were of HPLC grade. All other chemicals and solvents were of analytical grade purchased from authorized standard companies.

2.5. Extraction and isolation of cyclooxygenase-1 enzyme. (from Ram seminal vesicles)

Ram seminal vesicles were collected from local slaughter house and stored at -80°C . Before starting the experiment, the ram seminal vesicles were taken out from -80°C and kept at 4°C overnight in refrigerator. All the process of Extraction and isolation were carried out below 7°C .

2.5.1. Preparation of microsomes as a source of cyclooxygenase-1

Preparation of microsome was carried out, according to the method of Hemler et al. (1976), with some modifications. Ram seminal vesicles were ground in a grinder. The ground material was homogenized with a waring blender in buffer containing 0.05 M Tris–HCl (pH 8), 5 mM EDTA disodium salt, 5 mM diethyl dithiocarbamate and 0.01% sodium azide. The homogenate was centrifuged at 13,000 \times g for 15 min, 4°C . The supernatant was filtered through cheesecloth. The filtered supernatant was again centrifuged at 42,000 rpm for 1 h 10 min, 4°C by using ultracentrifuge (Himac, CP-100 α HITACHI) to obtain microsomal pellet. This microsomal pellet was rehomogenized with a motor-driven Potter-Elvehjem homogenizer, connected to a teflon pestle in a buffer containing 0.05 M Tris–HCl (pH 8), 0.1 mM EDTA disodium salt, 0.1 mM diethyl dithiocarbamate and 0.01% sodium azide. This microsome fraction was stored as small aliquots at -80°C , and used for further studies as enzyme source.

2.6. Extraction and isolation of cyclooxygenase-2 enzyme (from Sf9 insect cell line)

2.6.1. Preparation of microsomes as a source of cyclooxygenase-2

Preparation of microsome was carried out according to the method of Reddy et al. (2000), with some modifications. Human recombinant COX-2 expressed in *Spodoptera frugiperda*. *Spodoptera frugiperda* (Sf9) cells were maintained at 28°C in Grace's insect culture medium. Insect Cells at 60% confluency were infected with recombinant baculovirus containing human COX-2. After 72 h of infection, the cells were collected by centrifugation at 2000 \times g for 5 min at 4°C . The pellet was suspended in minimum volume of Tris–HCl buffer (50 mM, pH 7.2) containing 5 mM EDTA, 300 mM sucrose, 5 mM diethyl thiocarbamate, 1 $\mu\text{g/ml}$ pepstatin, 1 mM phenol and sonicated for 3 min. The cell lysate was centrifuged at 100,000 \times g for 1 h 10 min at 4°C by using ultracentrifuge (Himac,

CP-100 α HITACHI), and the microsomal pellet obtained was suspended in Tris–HCl buffer (2.5 mM, pH 7.2) containing 0.5% glycerol, 0.8% Tween 20 and 1 mM phenol. This solubilized microsomal fraction was stored as small aliquots at -80°C and used as enzyme source for further studies.

2.6.2. Cyclooxygenase (COX-1 and COX-2) assay

Enzymatic activities of COX-1 and COX-2 were measured according to the method of [Copeland et al. \(1994\)](#), with slight modifications using a chromogenic assay based on the oxidation of N,N,N-tetramethyl-*p*-phenylene diamine (TMPD), during the reduction of PGG₂ to PGH₂ ([Egan et al., 1976](#); [Pagels et al., 1983](#)). The assay mixture contained Tris–HCl buffer (0.5 M), hematin (5 mM), EDTA (0.5 M), enzyme (COX-1 or COX-2) and the test compound. The mixture was pre-incubated at 25°C for 5 min and then the reaction was initiated by the addition of substrate AA and TMPD, in total volume of 1 ml reaction mixture. The enzyme activity was determined by estimating the rate of TMPD oxidation for the first 60 s of the reaction by following the increase in absorbance at 603 nm. A low rate of non-enzymatic oxidation, observed in the absence of COX-1 and COX-2, was subtracted from the experimental value while calculating the percent inhibition.

2.7. Purification and assay of 5-lipoxygenase (5-LOX)

Purification of 5-LOX from potato tubers was carried out and assayed according to the method of [Reddanna et al. \(1990\)](#). Enzyme activity was measured using polarographic method with a Clark's oxygen electrode on Strathkelvin Instruments (model 782, RC-300). Typical reaction mixture contained 50–100 μl of enzyme and 10 μl of substrate (Arachidonic acid, 40 mM) and final volume made to 3 ml with 100 mM potassium phosphate buffer of pH 6.3. Since LOX is an oxygen-consuming enzyme, the rate of decrease in oxygen was taken as a measure of enzyme activity. Reaction was allowed to proceed at 25°C and the maximum slope generated was taken for calculating enzyme activity. The enzyme activity was expressed as moles of oxygen consumed min/mg protein.

2.8. Cell culture and treatment

RAW 264.7 cell line was maintained in monolayer in tissue culture petri dishes in RPMI-1640 medium supplemented with 10% heat inactivated fetal bovine serum (FBS), 100 IU/ml penicillin, 100 $\mu\text{g/ml}$ streptomycin and 2 mM L-glutamine. The cultured cells were passaged twice a week. Cell cultures were maintained in a humidified atmosphere with 5% CO₂ at 37°C . Before the treatment with test compound, cells were washed with PBS and fresh complete medium was added. The cells were incubated in the presence and absence of different concentration (50 $\mu\text{g/ml}$, 1 $\mu\text{g/ml}$, 10 ng/ml) of AFCQ, and stimulated with lipopolysaccharide (1 $\mu\text{g/ml}$) for 24 h. At the end of the treatment cells were washed with PBS and harvested to prepared cytoplasmic and nuclear extract for protein expression.

2.8.1. Cell proliferation assay of RAW 264.7 cell line

Cell proliferation was assessed by MTT (3-(4,5-dimethylthiazol-2-yl)-diphenyl tetrazolium bromide) assay as described by [Mosmann \(1983\)](#). The RAW 264.7 cell line used in this study were maintained in tissue culture petri dishes in complete RPMI-1640 medium. The cell line was maintained in a humidified atmosphere with 5% CO₂ at 37°C . The cultured cells were passaged twice a week, seeding at a density of 5×10^4 cells per well in 96-well plates before the day of experiment. Before the treatment with test compound cells were washed with PBS and fresh complete RPMI-1640 medium was added, in the presence or absence of different concentration (100 $\mu\text{g/ml}$, 10 $\mu\text{g/ml}$, 1 $\mu\text{g/ml}$, 0.1 ng/ml) of AFCQ and

were incubated for different time points (3, 6, 12, 24, and 48 h) in a final volume of 100 μl . At the end of the treatment, 20 μl of MTT (5 mg/ml) was added to each well and incubated for 4 h at 37°C . The purple blue formazan precipitate was dissolved in 100 μl of DMSO and the optical density was measured at 570 nm on Synergy Mx, Bio-tek Instruments, Inc. micro titer plate reader. Each concentration was tested in three different experiments run in four replicates.

2.9. Preparation of cell extract and Western blot analysis

Cell pellets were lysed in lysis buffer (150 mM NaCl, 10 mM Tris–HCl, 1% Tween 20, 1 mM EDTA, 1 mM PMSF). Lysates were sonicated for 5 sec and centrifuged at $10,000 \times g$ for 5 min. Protein concentrations were estimated by Bradford method, using BSA as a standard. Cell extracts were boiled in Laemmli sample buffer, resolved by SDS-PAGE on 12% polyacrylamide gels, and electroblotted onto nitrocellulose membrane. Membrane was stained with 0.5% ponceau in 1% acetic acid to confirm transfer of protein on membrane. Non-specific binding sites were blocked by incubating the membrane in 5% dried milk (fat free) in TBST solution, overnight at 4°C . Blots were incubated with primary antibodies of COX-2 (1:1000 dilution), iNOS (1:500 dilution), TNF α (1:500 dilution), Nrf-2 (1:1000 dilution), HO-1 (1:1000 dilution) and β -actin (1:1000 dilution) dissolved in 5% bovine serum albumin solution prepared in TBST for overnight at 4°C . Subsequently, blots were probed with a secondary antibodies of anti-goat, anti-mouse and anti-rabbit conjugated with alkaline phosphatase and incubated for 1 h at room temperature. After washing, protein expression was detected using Western blot detection reagent, nitro blue tetrazolium (NBT) and 5-bromo-4-chloro-3-indolyl phosphate (BCIP). NBT serve as oxidant and BCIP is the alkaline phosphatase substrate which gives dark blue dye.

2.9.1. Nuclear protein extraction

RAW 264.7 macrophages (3×10^6 cells/plate) were plated in 100-mm plates. Then, cells were treated with 1 $\mu\text{g/ml}$ of LPS in the presence or absence of different concentration (50 $\mu\text{g/ml}$, 1 $\mu\text{g/ml}$, 10 ng/ml) of AFCQ for 24 h. Treated cells were scraped in cold PBS on ice, and centrifuged at 1000 rpm for 2 min at 4°C . Each cell pellet was resuspended in 100 μl of cold lysis buffer (20 mM Tris–HCl, pH 7.5, 10 mM Magnesium acetate, 1% nonidet P-40, 1 mM PMSF). Cell suspensions were incubated on ice for 10 min and mixed by vortex stirring every 5 min. After incubation, Cell suspensions were centrifuged at 13,000 rpm for 15 min at 4°C . Supernatant (Cytoplasmic extract) removed and nuclear pellet was resuspended in 100 μl of nuclear protein extraction buffer (420 mM NaCl, 10 mM HEPES, 10 mM MgCl₂, 1 mM EDTA, 0.1 mM DTT and 25% glycerol) incubated for 30 min on ice with intermittent vortexing of 10 sec each every 5 min. Followed, cell suspensions were centrifuged at 13,000 rpm for 30 min at 4°C and supernatant were collected in new microcentrifuge tube as nuclear protein extracts. Protein concentrations were estimated by Bradford method, using BSA as a standard. Level and translocation of Nrf-2, HO-1 and β -actin in nuclear protein extract were determined by Western blotting analysis as described above.

2.10. Statistical analysis of data

All the data analysis was completed using the Sigma Plot 10 software. Numerical data, obtained from all the experiments, were presented as mean \pm S.D. of three independent experiments, *P*-values were determined using the unpaired Student's *t*-test. *P*-value of less than 0.05 was considered as significant.

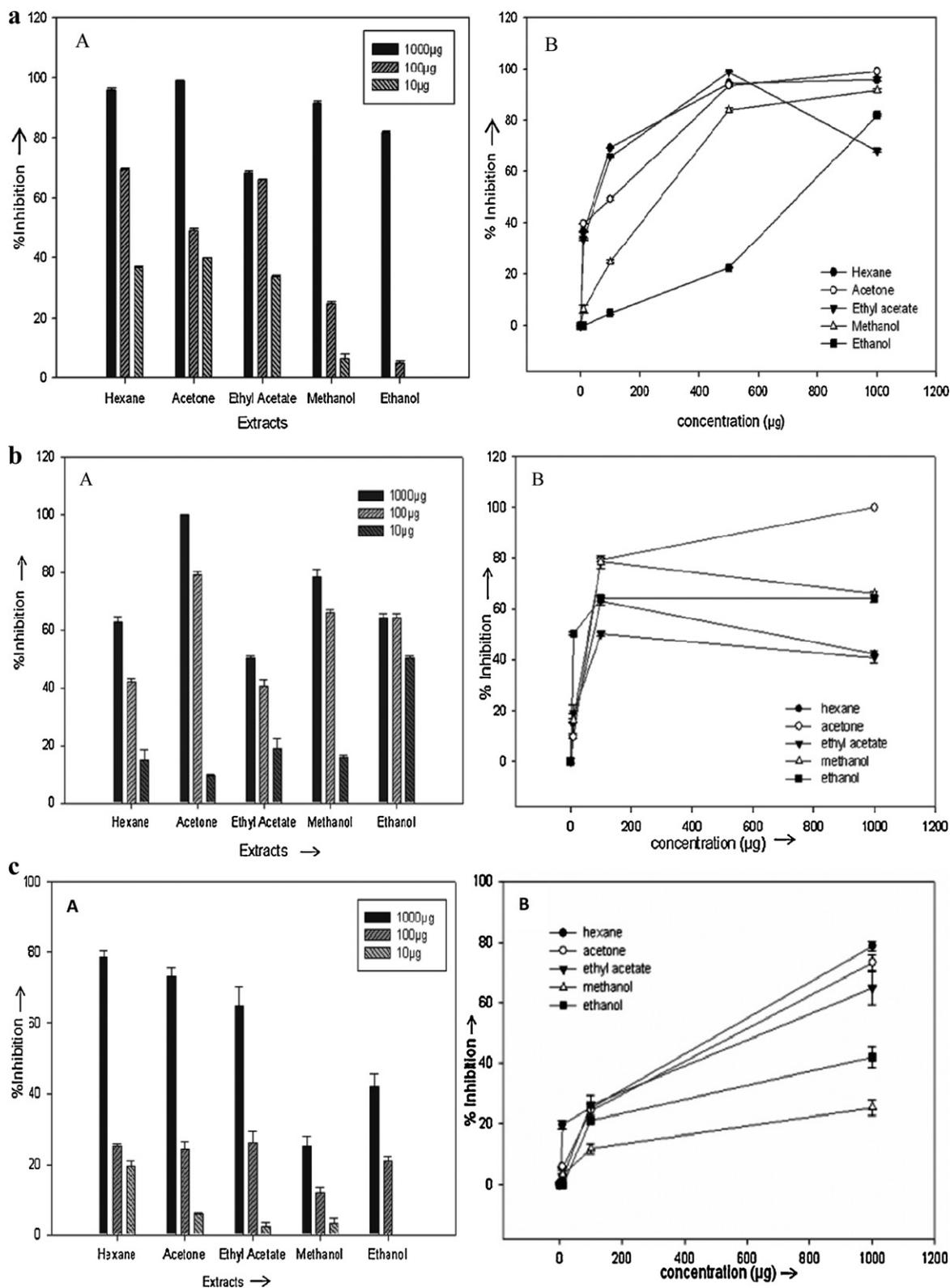


Fig. 1. (a) Effect of *Cissus quadrangularis* extracts on the enzyme activity of cyclooxygenase-1. The inhibition properties of extracts were checked through spectroscopic method. The enzyme was incubated with different concentration (as shown in graph) of extracts for 5 min at 25 °C and the enzyme activity was observed by the oxidation of TMPD in presence of AA. Dose dependent inhibition of enzyme activity of COX-1 by hexane, acetone, ethyl acetate, methanol, and ethanol extracts were observed. Data are mean ± S.D. of three independent experiments. (b) Effect of *Cissus quadrangularis* extracts on the enzyme activity of cyclooxygenase-2. The inhibition properties of extracts were checked through spectroscopic method. The enzyme was incubated with different concentration (as shown in graph) of extracts for 5 min at 25 °C and the enzyme activity was examined by the oxidation of TMPD in presence of AA. Dose dependent inhibition of enzyme activity of COX-2 by hexane, acetone, ethyl acetate, methanol, and ethanol extracts were observed. Data are mean ± S.D. of three independent experiments. (c) Effect of *Cissus quadrangularis* extracts on the enzyme activity of 5-lipoxygenase. The inhibition properties of extracts were checked through polarographic method with a Clark's oxygen electrode. The enzyme was incubated with different concentration (as shown in graph) of extracts for 5 min at 25 °C and the enzyme activity was examined by the rate of decrease in oxygen in presence of AA. Dose dependent inhibition of enzyme activity of 5-LOX by hexane, acetone, ethyl acetate, methanol, and ethanol extracts were observed. Data are mean ± S.D. of three independent experiments.

Table 1

IC₅₀ values (µg/ml) of all extracts of *Cissus quadrangularis*, hexane, acetone ethyl acetate, methanol, and ethanol showed inhibition on activity of cyclooxygenase-1, cyclooxygenase-2, and 5-lipoxygenase enzymes were isolated from ram seminal vesicles, Sf9 cell line and potato tubers. The enzyme activity inhibition was estimated by decrease in the oxygen concentration in presence of extracts.

Plant extract (crude)	IC ₅₀ values (µg/ml)				
	Hexane	Acetone	Ethyl acetate	Methanol	Ethanol
COX-1	47.976	106.46	55.98	271.54	71.35
COX-2	441	25.9	100	59.29	65.81
5-LOX	367.86	550	654.9	-	-

3. Results

3.1. Effect of different extracts on cyclooxygenase enzyme activity.

Preliminary studies with the plant extracts of *Cissus quadrangularis* exhibited inhibitory activity against both cyclooxygenase (COX-1 and COX-2) enzymes. The IC₅₀ values of all extracts are obtained on the inhibitory effect on COX-1 and COX-2 enzymes were given in Table 1. Hexane, acetone, ethyl acetate, methanol, and ethanol extracts of *Cissus quadrangularis* showed satisfactorily inhibition of enzyme COX-1 and COX-2 in dose dependent manner (1000 µg/ml, 100 µg/ml, 10 µg/ml) in (Fig. 1a and b), while chloroform and water extracts showed negligible inhibition against COX-1 and COX-2. Whereas the acetone extract showed potent inhibition of COX-1 and COX-2 with IC₅₀ values of 106.46 µg/ml and 25.9 µg/ml, respectively, with 4-fold preference towards COX-2.

3.2. Inhibition of lipoxygenase enzyme activity

Inhibition of 5-LOX enzyme activity by the plant extracts was recorded as percentage inhibition, in terms of reducing enzyme activity. The enzyme activity inhibition was estimated by decrease in the oxygen concentration in presence of extracts. IC₅₀ values of all extracts are given in Table 1. Bar graph (Fig. 1c) showing the comparison between hexane, acetone, ethyl acetate, methanol and ethanol extracts. From Fig. 1c we portrayed that the Acetone extract showed potent inhibition of 5-LOX enzyme with an IC₅₀ value 550 µg/ml.

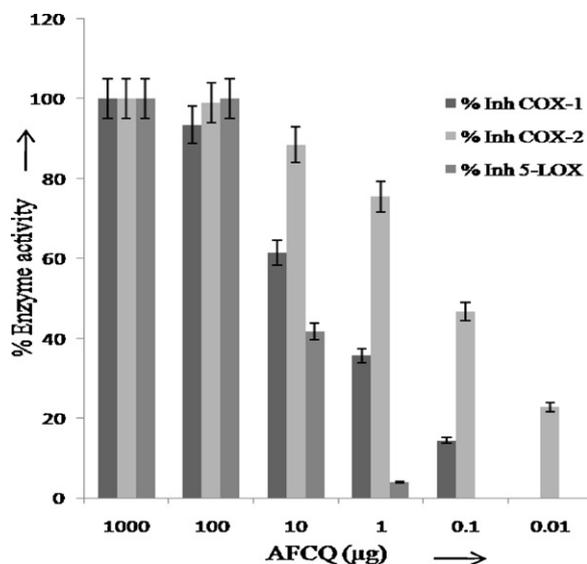


Fig. 2. Enzymatic inhibition activity of AFCQ on COX-1, COX-2 and 5-LOX. AFCQ more specifically inhibited COX-2 than COX-1 with 18-fold preference. The IC₅₀ values for COX-1, COX-2 and 5-LOX were 7 µg/ml, 0.4 µg/ml, and 20 µg/ml, respectively. Data are mean ± SD of three independent experiments.

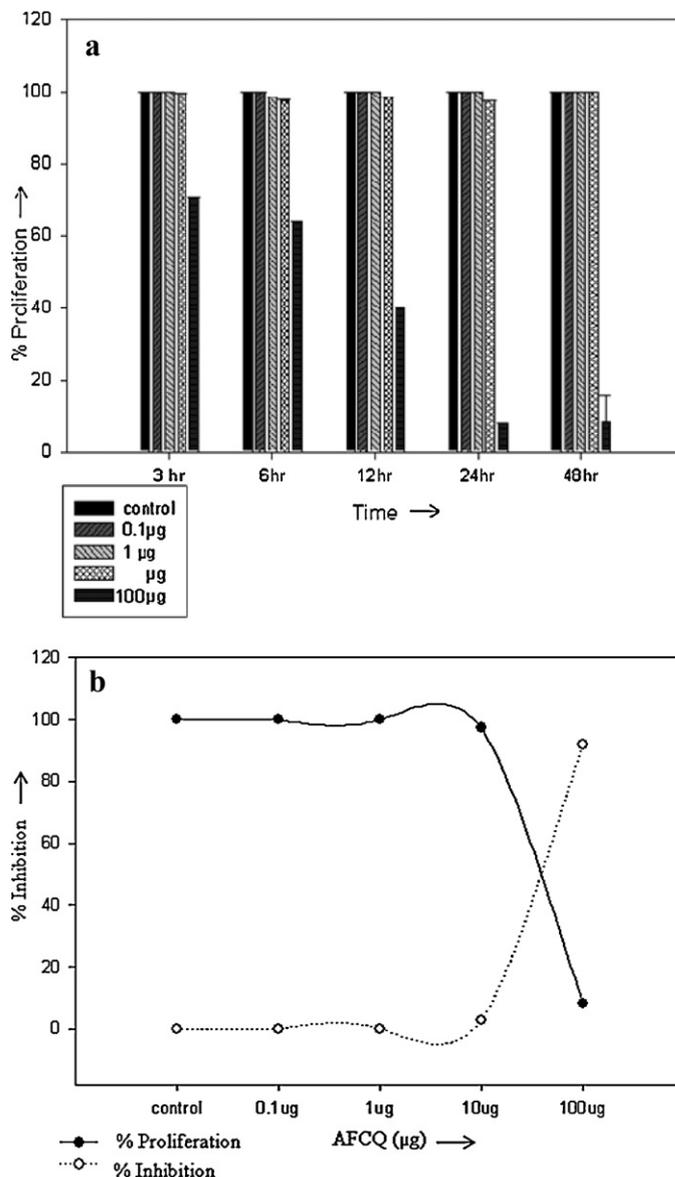


Fig. 3. (a) Effect of AFCQ on the proliferation of RAW 264.7 cell line. The cells were incubated with different concentrations (as shown in graph) of AFCQ for different time points (3, 6, 12, 24, and 48 h) and the cell viability was examined by MTT assay. Dose dependent inhibition was observed. Data are mean ± SD of three independent experiments. (b) IC₅₀ value of AFCQ on RAW 264.7 cell line at 24 h was obtained 65 µg/ml. The cells were incubated with different concentrations (100 µg/ml, 10 µg/ml, 1 µg/ml, and 0.1 ng/ml) of AFCQ for 24 h and the cell viability was checked by MTT assay. Data are mean ± SD of three independent experiments.

3.2.1. Column chromatography, phytochemical study and inhibitory effect of AFCQ on COX and 5-LOX activity

The acetone extract of *Cissus quadrangularis* was fractionated through open silica column chromatography. We obtained around 13 fractions, all fractions were dried and concentrated by using rotary vacuum evaporator and checked for inhibitory action on COX and 5-LOX. Twelfth fraction showed inhibition on COX-1 and COX-2 activity only. Ninth fraction showed dose dependent inhibition of COX-1, COX-2, and 5-LOX (Fig. 2) with IC₅₀ values of 7 µg/ml, 0.4 µg/ml, and 20 µg/ml. The phytochemical studies of the AFCQ have showed the presence of tannin compounds. Partially purified AFCQ was used in all the experiments.

3.3. *In vitro* anti-inflammatory studies

RAW 264.7 cell lines was used in the present study for the evaluation of anti-inflammatory effect of AFCQ. RAW 264.7 cell line was incubated with different concentration of AFCQ (100 µg/ml, 10 µg/ml, 1 µg/ml, and 0.1 µg/ml) for different time points 3, 6, 12, 24, and 48 h. Cell viability was evaluated by MTT assay (Fig. 3a). AFCQ showed wide anti-inflammatory properties in dose dependent manner. The IC₅₀ values of AFCQ for RAW 264.7 cell line was 65 µg/ml (Fig. 3b).

3.4. Effects of AFCQ on expression of iNOS, COX-2, TNFα

The potential anti-inflammatory effect of AFCQ were investigated by using murine macrophage cells, RAW 264.7, which can produce iNOS, COX-2, and TNFα upon stimulation with LPS. Cells were preincubated with AFCQ (50 µg/ml, 1 µg/ml, and 10 ng/ml,) for 3 h, and stimulated with or without LPS (1 µg/ml) for 24 h. iNOS, COX-2, and TNFα provide as key mediators of inflammation and thus the agents that suppress their expression have remedial importance for inflammatory diseases. iNOS, COX-2, and TNFα protein levels were markedly up-regulated in response to LPS treatment (Fig. 4), and AFCQ inhibited the expression of these proteins in a dose dependent manner. This study demonstrated the anti-inflammatory activity of AFCQ through down regulation of iNOS, COX-2, and TNFα.

3.5. Effects of AFCQ on expression of HO-1 and Nrf-2

Murine macrophage RAW 264.7 cells were preincubated with AFCQ (50 µg/ml, 1 µg/ml and 10 ng/ml) for 3 h, and stimulated with or without LPS (1 µg/ml) for 24 h. This study showing the translocation of Nrf-2 from cytoplasm to nucleus it leads to upregulation of anti-inflammatory protein HO-1 in dose dependent manner. Nrf-2 is in the cytosol under normal situation. But when it is activated, it get separated from keap-1 protein and phosphorylated, after that translocated to the nucleus, and binds to a promoter region called ARE, which is concerned in the regulation of downstream gene expression. Therefore we studied the effect of AFCQ on intracellular localization of Nrf-2 in RAW 264.7 cells. Western blot analysis of cytoplasmic extract exposed that Nrf-2 was translocated into the nucleus by AFCQ treatment at lower dose too in (Fig. 5). Whereas Western blot analysis of nuclear extract

Cytoplasmic Extract

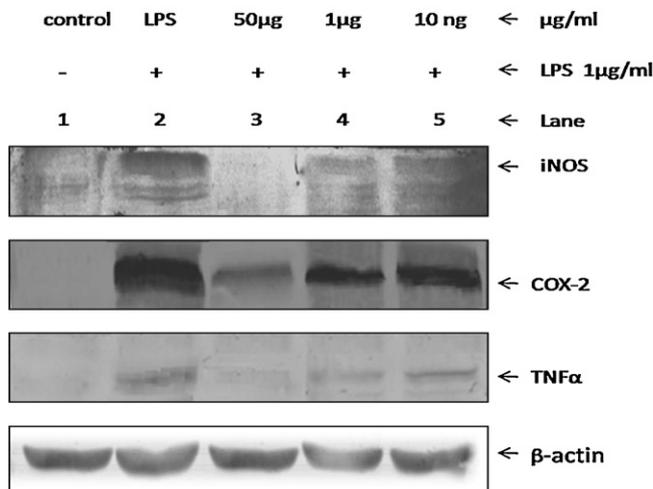


Fig. 4. AFCQ shows anti-inflammatory activity against LPS stimulated RAW 264.7 cells. Cells were preincubated with AFCQ (50 µg/ml, 1 µg/ml and 10 ng/ml,) for 3 h, and stimulated with or without LPS (1 µg/ml) for additional 24 h. iNOS, COX-2 and TNFα protein expression levels were monitored by Western blot analysis, β-actin was used as loading control.

showed that AFCQ increased nuclear levels of Nrf-2 protein, indicating translocation from the cytoplasm into the nucleus (Fig. 5). Nrf-2 is a transcription factor regulating expression of phase-II antioxidant enzymes including HO-1 which are involved in the regulation of acute inflammatory responses. Western blot analysis of cytoplasmic and nuclear extract of AFCQ treated LPS stimulated RAW 264.7 cells showed increased level of HO-1 in cytoplasmic extract (Fig. 5) along with its level was decreased in nuclear extract (Fig. 5). HO-1 is a antioxidant enzymes induced in inflammatory or oxidative condition. AFCQ exerts anti-inflammatory activity through activating the translocation of Nrf-2 molecule from cytoplasm to nucleus and hence increasing the transcription of phase-II antioxidant enzyme HO-1 (Fig. 5). Here we found that lower concentration of AFCQ also activated the Nrf-2 for translocation (Fig. 5) and hence expression of antioxidant protein HO-1 was upregulated in cytoplasmic extract at lower dose.

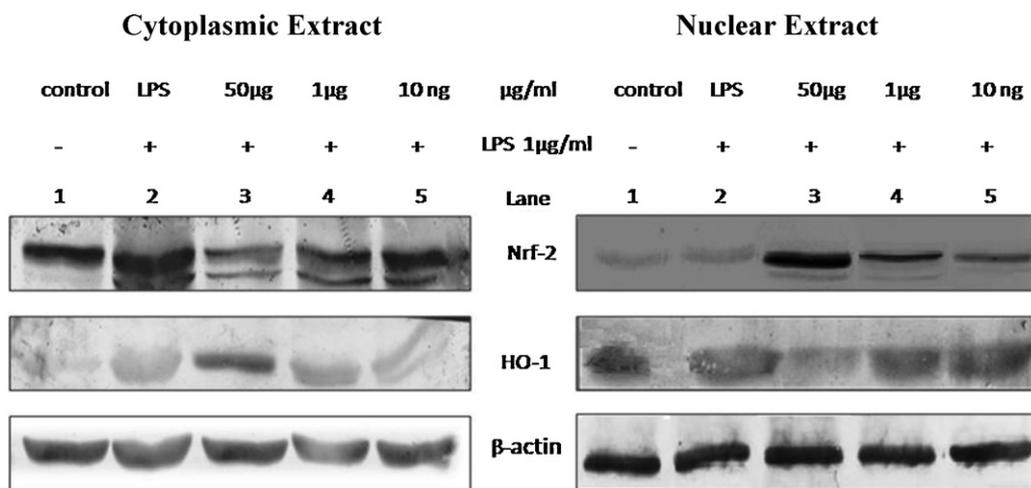


Fig. 5. RAW 264.7 cells were preincubated with AFCQ (50 µg/ml, 1 µg/ml, and 10 ng/ml) for 3 h, and stimulated with or without LPS (1 µg/ml) for 24 h and the levels of Nrf2 and HO-1 protein in cytoplasmic and nuclear fractions were analyzed by Western blot analysis. β-actin was used as loading markers for cytoplasmic and nuclear fractions, respectively.

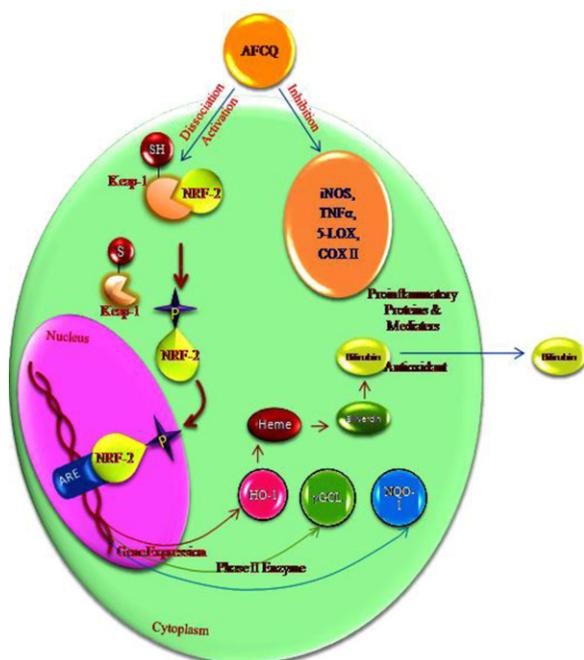


Fig. 6. Figure shows the effect of AFCQ on the Nrf-2 molecule which in turn increases the gene expression of antioxidant enzymes HO-1. It leads to the formation of bilirubin. AFCQ is also shows inhibition on the proinflammatory cytokines and mediators like TNF α , iNOS, 5-LOX, and COX-2.

4. Discussion

Almost all diseases are characterized by the inflammation and pain in response to different conditions like injuries, infection, etc. Inflammation and pain indicate the presence of COX and 5-LOX. The enzyme COX has two isoforms, COX-1 and COX-2. COX-1 is the constitutive enzyme, COX-2 is an inducible enzyme and its level is always found elevated in abnormal conditions like inflammation, arthritis and in carcinogenesis. Non steroidal anti-inflammatory drugs (NSAIDs) inhibit COX-2, but have many side effects, like cardiac failure, gastric ulcer, stroke, etc. (Pairet et al., 1996). A number of drugs, used in the treatment of chronic diseases, have been developed over the past few decades but these drugs have a lot of side effects. A very good example is of Aspirin which results in gastric ulceration, Vioxx (Rofecoxib) which results in heart attack, stroke, and serious cardiovascular events. That might be the reason behind its ban. Plant extracts are striking sources of new drugs. Traditional medicinal plant *Cissus quadrangularis*, commonly known as bone setter, is frequently used as a common food item in India. It is an edible plant found throughout the tropical parts of the world like India, Africa, Thailand, and Philippines (Parisuthiman et al., 2009). It is a multipurpose plant, used traditionally for different healing treatments. Our present study deals with COX and 5-LOX inhibition by using differential extracts of *Cissus quadrangularis*. Based on polarity, extraction was performed and six different extracts were prepared, viz. hexane, chloroform, acetone, ethyl acetate, methanol, and ethanol. Out of all these six extracts, acetone extract showed potent inhibition of COX-1, COX-2, and 5-LOX. Results show that acetone extract exhibit an effective inhibitor of both COX and 5-LOX. AFCQ is the active fraction of acetone extract isolated by column chromatography has shown inhibition on COX-1, COX-2, and 5-LOX enzyme activity with IC₅₀ values of 7 μ g/ml, 0.4 μ g/ml, and 20 μ g/ml. The phytochemical study of the AFCQ has shown the presence of tannin compounds. Partially purified AFCQ on cell proliferation of RAW 264.7 cell line shows IC₅₀ value 65 μ g/ml at 24 h. iNOS, COX-2, 5-LOX, and TNF α are key mediators of inflammation. The transcription factor Nrf-2 regulates the basal

and inducible expression of numerous detoxifying and antioxidant genes. Western blotting studies have shown the downregulation of iNOS, COX-2, and TNF α by AFCQ treatment. In addition AFCQ have activated the translocation of Nrf-2 molecule which leads to increase in the synthesis of the antioxidant proteins HO-1, NQO-1, and γ GCL, here we have verified the upregulation of HO-1. Isolation and characterization of active principle from AFCQ is in progress in our laboratory. Further studies with these extracts on arthritis, cancer and in other chronic diseases are also going on.

5. Conclusion

According to experimental results, AFCQ obtained from *Cissus quadrangularis*, was found to have better anti-inflammatory activity. AFCQ might be helping in the dissociation the Nrf-2-Keap-1 complex which in turn leads to activation of Nrf-2 protein by phosphorylation and translocation from cytoplasm into nucleus. Phosphorylated Nrf-2 binds with ARE which in turn activates the gene expression of phase-II enzymes. The antioxidant proteins like HO-1 get expressed through the Nrf-2 Pathway. It leads to synthesis of antioxidant like bilirubin. AFCQ also inhibit proinflammatory cytokines and mediators like TNF α , iNOS, 5-LOX, and COX-2 (Fig. 6). This might be due to the effect of the tannin compounds present in the AFCQ. Further studies are necessary to isolate active compounds and to elucidate their exact mechanism of action.

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6

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