

Université de Montréal

**Regulation of microsomal prostaglandin E₂ synthase-1
and 5-lipoxygenase-activating protein/5-lipoxygenase by
4-hydroxynonenal in human osteoarthritic chondrocytes**

By

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Postdoctoral Studies in partial fulfillment of the requirements
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4-hydroxynonenal in human osteoarthritic chondrocytes**

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RÉSUMÉ

L'arthrose (OA) est une maladie dégénérative et multifactorielle caractérisée par une destruction de cartilage, une formation d'ostéophytes et une inflammation au niveau de la membrane synoviale. Le 4-hydroxynonéal (HNE), un produit final de la peroxydation lipidique, a été identifié récemment comme un facteur catabolique et un médiateur inflammatoire dans le cartilage arthrosique humain. Notre projet vise à étudier l'effet du HNE sur la régulation de la prostaglandine E₂ synthase-1 microsomale (mPGES-1) et de la protéine activante 5-lipoxygénase (FLAP)/5-lipoxygénase (5-LOX) dans les chondrocytes arthrosiques humains. Lorsque les cellules sont traitées une seule fois avec 10 µM HNE, les résultats de Western blot et de PCR en temps réel montrent que l'expression de la cyclooxygénase-2 (COX-2) et de la mPGES-1 augmente de manière significative et atteint respectivement le maximum après 8 et 16 heures d'incubation puis diminue graduellement. Cependant, lorsque les cellules sont traitées plusieurs fois avec 10 µM HNE à 2 heures d'intervalle, l'expression de la COX-2 et de la mPGES-1 augmente en fonction du temps sans subir une baisse après 24 heures d'incubation. Le HNE induit l'activité du promoteur de la mPGES-1 via l'activation du facteur de transcription Egr-1. L'investigation de la 2^{ème} voie du métabolisme de l'acide arachidonique, à savoir 5-LOX/FLAP, montre que le HNE induit l'expression de FLAP après 24 heures de stimulation et celle de 5-LOX seulement après 48 heures. Ceci semble survenir à l'étape de transcription au cours de laquelle HNE induit l'expression de l'ARNm et l'activité du

promoteur du gène 5-LOX. Nous avons démontré aussi que le niveau de leukotriène B₄ (LTB₄) augmente et suit le même profil que celui de la 5-LOX. L'étude des mécanismes moléculaires susceptibles d'être impliqués dans la régulation de la 5-LOX/FLAP par le HNE montre que ce dernier stimule leur expression via l'action de prostaglandine E₂ (PGE₂) et du facteur de croissance transformant-beta 1 (TGF-β1).

En conclusion, notre étude démontre que le HNE induit à court-terme d'incubation la voie de COX-2/mPGES-1 puis par la suite stimule celle de FLAP/5-LOX à long-terme d'incubation dans les chondrocytes arthrosiques humains. Ces résultats suggèrent que la mPGES-1 et 5-LOX/FLAP sont des potentielles cibles thérapeutiques intéressantes pour contrôler la production de PGE₂ et LTB₄ dans OA.

Mots clés:

Arthrose, Inflammation, Chondrocytes, Peroxydation lipidique, 4-hydroxynonéal, Cyclooxygénase-2, Prostaglandine E₂ synthase-1 microsomale, Prostaglandine E₂, 5-lipoxygénase, Protéine activante 5-lipoxygénase, Leukotriène B₄.

SUMMARY

4-hydroxynonenal (HNE), a lipid peroxidation end-product, is produced abundantly in osteoarthritic (OA) articular tissues. Recently, we reported that HNE-induced cyclooxygenase-2 (COX-2) decreased gradually in human OA chondrocytes after 8 h of incubation. This study aimed to investigate whether COX-2 down-regulation is attributed to HNE depletion and is responsible for the switch from COX-2 to 5-lipoxygenase-activating protein (FLAP)/5-lipoxygenase (5-LOX). Treatment of chondrocytes with 10 μ M HNE induced prostaglandin E₂ (PGE₂) release as well as COX-2 and microsomal prostaglandin E₂ synthase-1 (mPGES-1) expression at the protein and mRNA levels, with a plateau reached at 8-16 h of incubation, followed by a subsequent decline. However, 8 repeated treatments with 10 μ M HNE prevented the reduction of COX-2 and mPGES-1 expression. We demonstrated that HNE induced mPGES-1 promoter activity mainly through transcription factor Egr-1 activation. On the other hand, when COX-2 expression decreased, leukotriene B₄ (LTB₄) level rose after a long period of stimulation (48 and 72 h). At the mRNA level, HNE induced FLAP and 5-LOX expression after 24 and 48 h of stimulation, respectively. The addition of a nonspecific COX-2 inhibitor (naproxen) to cultured chondrocytes revealed that FLAP and 5-LOX regulation by HNE required PGE₂ production. Furthermore, our data showed that 10 μ M HNE significantly induced transforming growth factor-beta 1 (TGF- β 1) production. The addition of anti-TGF- β antibody to culture medium reduced HNE-induced 5-LOX/FLAP expression by 40%, indicating the

involvement of a TGF- β 1-dependent mechanism. Our data demonstrate that the shunt to the FLAP/5-LOX pathway in HNE-induced human OA chondrocytes is attributed to COX-2 inhibition, probably due to HNE depletion. PGE₂ and TGF- β 1 are suggested to be involved in this regulation. Further experiments are in progress to determine other molecular mechanisms underlying this switch in OA chondrocytes.

Key words:

Osteoarthritis, Inflammation, Chondrocytes, Lipid peroxidation, 4-hydroxynonenal, Cyclooxygenase-2, Microsomal prostaglandin E₂ synthase-1, Prostaglandin E₂, 5-lipoxygenase, 5-lipoxygenase-activating protein, Leukotriene B₄.

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LIST OF ABBREVIATIONS

5-LOX: 5-lipoxygenase

AA: Arachidonic acid

ADAMTS: A disintegrin and metalloprotease with thrombospondin motifs

Col: Collagen

Col II: Type II collagen

Col V: Type V collagen

COX: Cyclooxygenase

COX-2: Cyclooxygenase-2

cPGES: Cytosolic prostaglandin E₂ synthase

cPLA₂: Cytosolic phospholipase A₂

CYS: Cysteine

cys-LTs: Cysteinyl-leukotrienes

DHN: Dihydroxy-2-nonene alcohol

ECM: Extracellular matrix

Egr-1: Early growth response protein-1

EIA: Enzyme immunoassay

FLAP: 5-lipoxygenase-activating protein

GM-CSF: Granulocyte/macrophage colony-stimulating factor

GSH: Glutathione

GST: Glutathione-S-transferase

HIS: Histidine

HNA: 4-hydroxy-2-nonenic acid
HNE: 4-hydroxynonenal
IL-1 β : Interleukin-1 beta
iNOS: Inducible nitric oxide synthase
JNK: c-Jun N-terminal kinases
LOX: Lipoxygenase
LPO: Lipid peroxidation
LPS: Lipopolysaccharides
LTB₄: Leukotriene B₄
LTs: Leukotrienes
LYS: Lysine
MAPK: Mitogen-activated protein kinases
MDA: Malondialdehyde
MMPs: Matrix metalloproteinases
mPGES-1: Microsomal prostaglandin E₂ synthase-1
NF- κ B: Nuclear factor-kappa B
NO: Nitric oxide
O₂⁻: Superoxide anion
OA: Osteoarthritis
PG: Proteoglycan
PGE₂: Prostaglandin E₂
PGES: Prostaglandin E₂ synthase
PGH₂: Prostaglandin H₂

PPAR γ : Peroxisome proliferator-activated receptor gamma

RA: Rheumatoid arthritis

ROS: Reactive oxygen species

TGF- β 1: Transforming growth factor-beta 1

TIMP: Tissue inhibitor of metalloproteinases

TNF- α : Tumor necrosis factor alpha

VDR: Vitamin D receptors

VDRE: Vitamin D receptor element

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CHAPTER I: INTRODUCTION

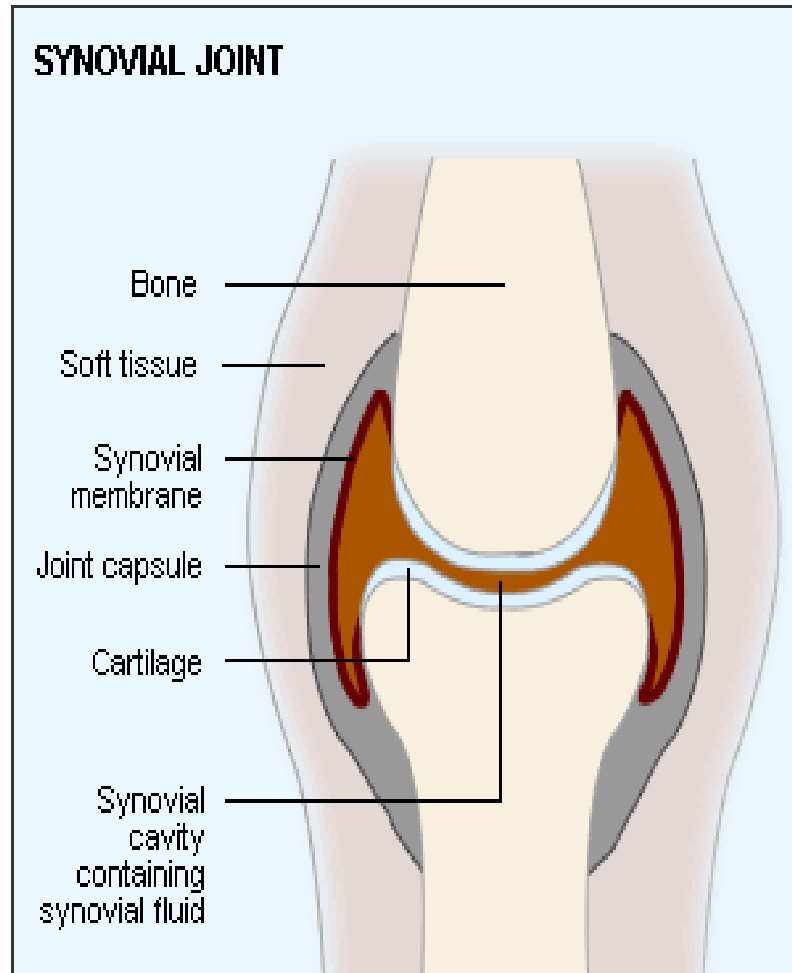
1. SYNOVIAL JOINTS AND ARTICULAR CARTILAGE

Synovial joints are structures consisting of bone, hyaline cartilage, synovial membrane and joint capsule filled with synovial fluid (**Fig. 1**). Synovial fluid serves as a protective barrier by preventing contact between surfaces and provides nutrients to the hyaline cartilage (Schmidt et al., 2007). The latter covers the surface of bone and provides low-friction gliding surface with strong compressive strength and resistance; therefore it facilitates the movement of bones without difficulties and pain. Destruction of cartilage brings extreme pain during the movement, which we often see in osteoarthritis (OA) patients. In this section, we will discuss the structure, composition and biochemical characteristics of cartilage.

1.1 Structure

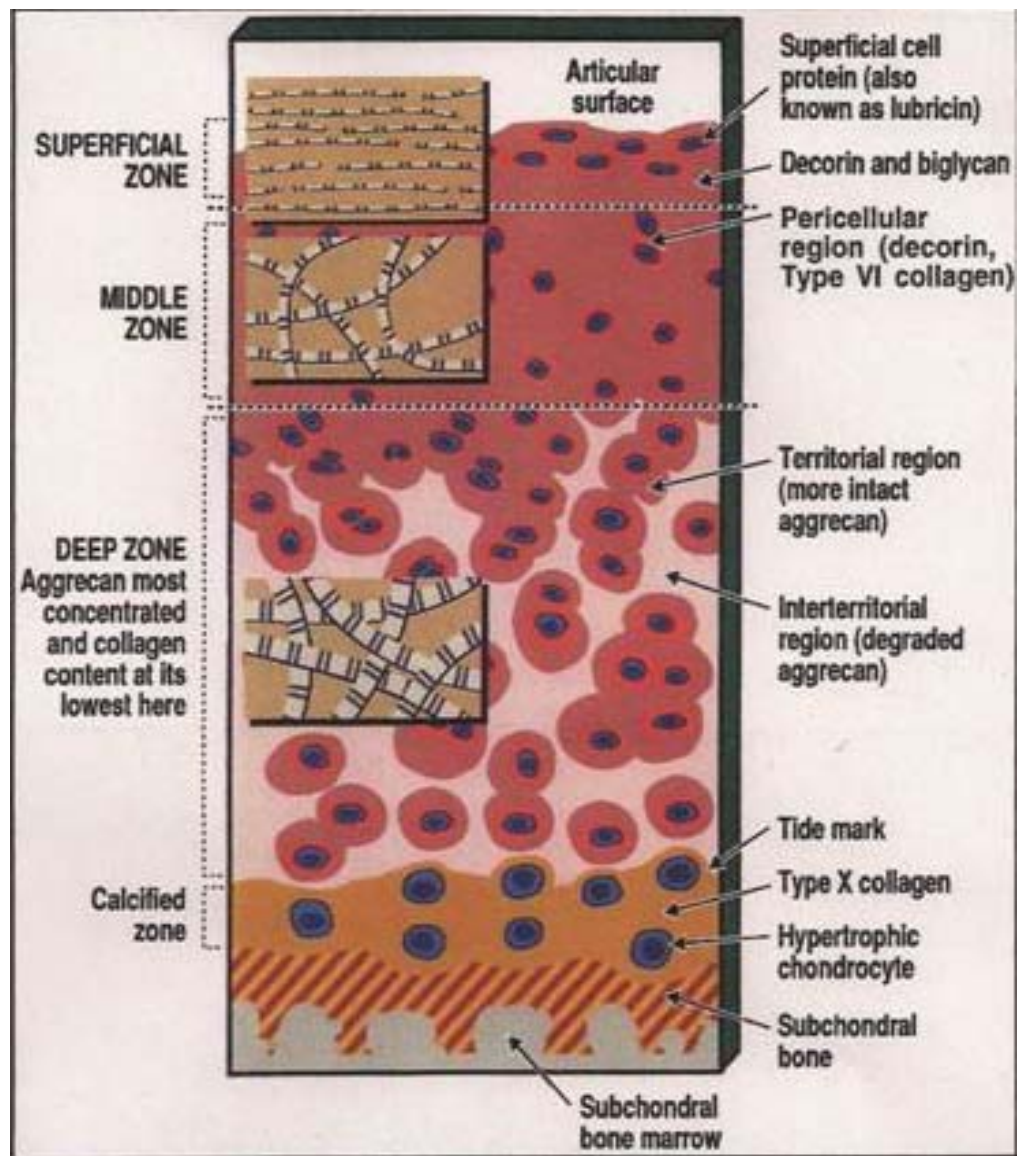
Morphologically, the hyaline cartilage is a connective tissue, which divides into four layers from the exterior to interior: superficial zone, transitional (middle zone), deep zone and calcified zone. The thickness of different layers depends on the inside component and the intensity of force applied (Poole et al., 2001).

The superficial zone is the thinnest layer consisting of flattened cells aligned parallel to the surface. It is covered by the protein lubricin and synovial fluid. This parallel arrangement gives the greatest tensile strength to cartilage (**Fig. 2**). The transitional zone of extracellular matrix (ECM) is formed by spheroid shaped cells with lower cell density and high concentration of



myDr, CMPMedica Australia, 2000-2009

Figure 1: Structure of synovial joint



(Poole et al., 2001)

Figure 2: Structure of articular cartilage in adults

macromolecules, such as proteoglycans and collagens (Bhosale and Richardson, 2008).

Chondrocytes present in the deep zone have spheroid shape with perpendicular arrangement. Highest level of proteoglycan is observed in this zone. The calcified zone, the most profound zone of hyaline cartilage, contains low quantity of cells. However, the chondrocytes in this zone are special because they show hypertrophic phenotype and have capacity of synthesizing type V collagen (Col V) (**Fig. 2**). This feature provides an important structural integrity to the less elastic subchondral bone (Aigner and McKenna, 2002).

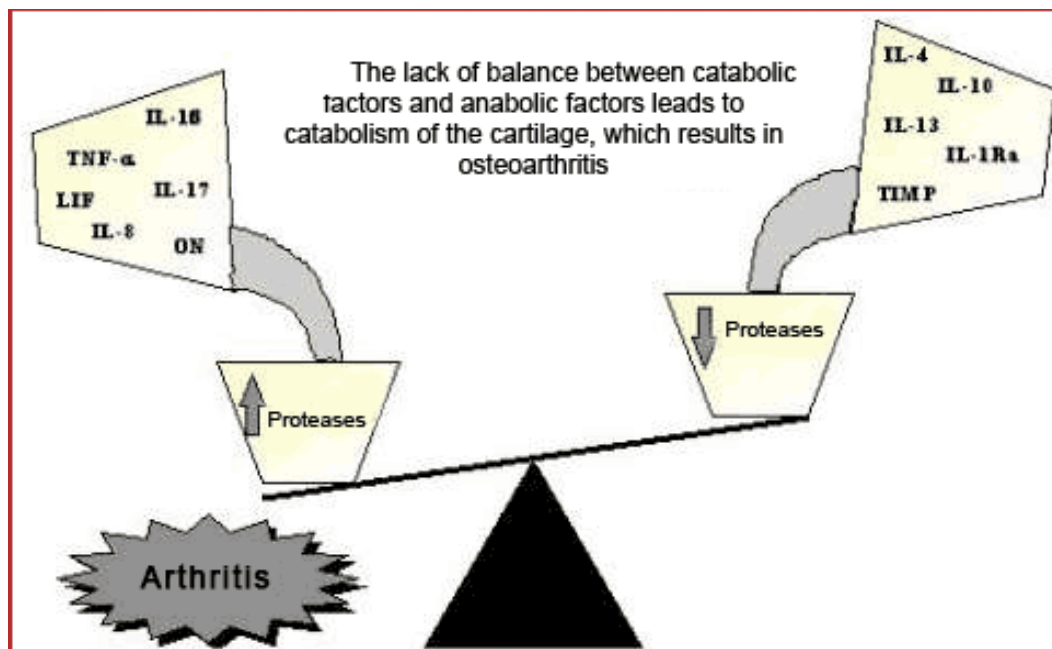
1.2 Composition

The hyaline cartilage is an avascular and alymphatic ECM composed of only chondrocytes. This ECM consists of 70% of water and 30% of collagen (Col), proteoglycan (PG) and elastic fibers. There exists many types of collagen including type II collagen (Col II), Col VI, Col IX, Col X and Col XI; among them Col II is the most abundantly present in ECM. These components help to maintain the tension and the movement of articulations as well as to provide essential nutrients for chondrocytes (Gardner, 1983;Bhosale and Richardson, 2008).

1.3 Metabolic and biochemical characteristics

The characteristics of cartilage are determined by the structure and functions of molecules presenting in the ECM. Chondrocytes existing in the cartilage are very active and able to secrete various molecules such as cytokines, growth factors and enzymes. Interleukin-1 beta (IL-1 β) and tumor necrosis factor alpha (TNF- α) produced abundantly by chondrocytes can generate different cellular responses through various signal pathways. For example, IL-1 β stimulates inducible nitric oxide synthase (iNOS) expression through p38 Mitogen-activated protein kinases (MAPK) pathway (Badger et al., 1998). It can also stimulate nuclear factor-kappa B (NF- κ B) that translocates to the nucleus to activate various genes. Furthermore, cyclooxygenase-2 (COX-2) and prostaglandin E₂ (PGE₂) synthesis were determined to be upregulated by IL-1 β and TNF- α in explants of human OA knee menisci (LeGrand et al., 2001).

As ECM is an avascular and alymphatic tissue, the transport of nutrients to chondrocytes is through diffusion. In normal cartilage, degradation (catabolism) and repair (anabolism) are in equilibrium, which is controlled by the synthesis of ECM components such as collagen, matrix metalloproteinases (MMPs) and tissue inhibitor of metalloproteinases (TIMP). In OA, catabolism is more active than anabolism. The overproduction of MMPs extensively degrades cartilage components, which cannot be repaired by anabolism mediator TIMP and results in OA (**Fig. 3**).



(csbioactive website, osteoarthritis)

Figure 3: imbalance between anabolic factors (anti-inflammatory) and catabolic factors (inflammatory), leading to the destruction of cartilage.

2. OSTEOARTHRITIS (OA)

2.1 Definition and classification

OA is the most common form of arthritis and one of the most pervasive diseases in the Western society. According to the Arthritis Society, approximately 3 million Canadians suffer from OA. OA is a disease that affects a subset of the joints of the body, particularly the hips, knees and distal interphalangeal joints of the hands (Oliveria et al., 1995;Dieppe et al., 2002). Examination of an OA joint by arthroscopy or open surgery confirms a dramatic loss of articular cartilage (Gardner, 1983;Radin et al., 1991;Kerin et al., 2002). Histological examination of the cartilage confirms the gross anatomy and reveals a striking loss of ECM components (Poole, 1999;Felson et al., 2000). Depending on the region being examined, cartilage may be devoid of chondrocytes, presumably as a result of cell death, or contains clusters of chondrocytes that have undergone division, possibly in response to ECM depletion (Sandell and Aigner, 2001). Some chondrocytes appear to be synthesizing ECM at an elevated rate, as if attempting repair, while the synthetic rates of other chondrocytes are depressed (Haq et al., 2003). It is generally thought that an elevated ECM synthesis is a feature of early OA, while reduced synthetic rates occur later in the disease. Loss of articular cartilage is a progressive condition that develops in response to a variety of stimuli: mechanical or environmental, and is orchestrated by growth factors and cytokines acting through several signaling cascades (Radin et al., 1991;Pelletier et al., 1993;Arend and Dayer, 1995;Westacott and Sharif, 1996;Kerin et al., 2002). The cartilage

degradation is characterized by the loss of ECM components and qualitative changes of collagen. The precise mechanisms responsible for the initiation of cartilage degradation remain to be clarified.

OA is classified into two groups: primary (idiopathic) and secondary. Primary OA is the most common form and has no known cause, although it is often related to aging and heredity. Secondary OA is related to antecedent factors including trauma, congenital or developmental diseases, metabolic diseases, endocrine diseases and other bone diseases.

2.2 Epidemiology of OA

2.2.1 Prevalence and incidence of OA

OA is an extremely common joint disorder in the whole population. Its high prevalence and the frequency of OA-related physical disability make OA, especially in the elderly, one of the leading causes of disability. OA of the hip and knee represent two of the most significant causes of adult pain and physical disability. OA has a higher prevalence, and more often exhibits a generalized distribution in women than in men. Before the age of 50, men have a higher prevalence than women, but after the age of 50, women have a higher prevalence. This sex difference in prevalence further increases with age (Felson and Zhang, 1998; Nevitt et al., 2001). Overall, OA occurs frequently in knees, hands, hips,

back, neck, wrists and ankles. Many people have joint symptoms without X-ray change and vice versa.

2.2.2 Risk factors for OA

Risk factors for OA include systemic and local biomechanical factors

Systemic factors:

Age, sex and ethnicity: the most potent systemic vulnerabilities are an increasing age and the female gender. Disease incidence and prevalence increase dramatically with age. The Framingham study found that 27% of those aged 63 to 70 had radiographic evidence of knee OA, increasing to 44% in the over 80 age group (Felson et al., 1995). Racial factor is another systemic factor with Asian people having very low rates of hip OA (Haq et al., 2003).

Genetics: OA is a group of clinically heterogeneous disorders. Many genes have been linked to OA. There is most concordance with chromosomes 2q, 4 and 16. Families have been found with rare autosomal dominant patterns of inheritance of OA. The defective genes are often coding for structural proteins of the ECM of the joint and collagen (Haq et al., 2003; Gabay et al., 2008).

Hormonal status: some women after age 50 develop “menopausal arthritis” at the time of menopause. These gender- and age-related prevalence patterns are consistent with a role for post-menopausal hormone deficiency in increasing the risk of OA. Estrogen loss has been strongly implicated as a risk factor.

Epidemiologic studies provide evidence that estrogen replacement therapy is associated with a reduction in the risk of knee and hip OA (Nevitt et al., 2001).

Nutritional factors: people with lower vitamin C and vitamin D levels in blood have a threefold risk of progression of knee OA (Hunter et al., 2002). Vitamin C protects against damage by reactive oxygen species (ROS) and serves as a cofactor for enzymes contributing to Col II synthesis. Low dietary vitamin D intake increases the risk of knee OA progression (Bergink et al., 2009).

Local biomechanical factors

Obesity: many recent studies allow us to better understand the relationships between OA and obesity (Gabay et al., 2008). Although it is evident that mechanical components contribute to joint destruction in overweight people, OA is considered not only a disease of articular cartilage but also a systemic disorder in which circulating factors linked to altered lipid and glucose metabolism may explain the diversity of pathophysiological changes found in generalised OA. However, the potential contribution of adipose-derived cytokines in OA would not preclude the involvement of other mechanisms, including activation of mechanoreceptors and vascular dysfunction in the subchondral bone.

Major joint injury: with a major joint injury, a person can sustain permanent damage of many of the structures within a joint. This damage alters its biomechanics, increases stress across particular areas of the joint and often

dramatically increases the risk of OA. The Framingham study found men with a history of knee injuries had a relative risk of 3.5 for subsequent knee OA; for women the relative risk was 2.2 (Felson, 1990).

Occupational and athletic activities: OA is common in those performing heavy physical works, especially if this involves knees bending, squatting, or kneeling. Dockers and miners have been found to have a higher prevalence of knee OA than those in sedentary jobs (Partridge and Duthie, 1968). Epidemiologic study has demonstrated that participation in certain competitive sports increases the risk for OA (Buckwalter and Lane, 1997b). Sports activities that appear to increase the risk for OA include those that demand high-intensity, acute, direct joint impact as a result of contact with other participants, playing surfaces, or equipment (Buckwalter and Lane, 1997a). Repetitive joint impact and torsional loading also appear to be associated with joint degeneration.

3. PATHOPHYSIOLOGY OF OA

OA is one of the most frequent health problems for older people. It is a multifactorial degenerative joint disease characterized by the destruction of articular cartilage and synovial inflammation. The principal factors can be sex, gene, strenuous exercise, excess weight and injury (Hunter et al., 2002; Ouedraogo et al., 2008). The pathophysiology of OA is not completely understood, but its progression is being evaluated. The development of OA is usually separated into

three stages. Stage I is the imbalance between anabolic and catabolic metabolism, in which excessively synthesized proteases damage the cartilage matrix (**Fig. 3**). During stage II, the erosion of cartilage surface and inflammation of synovial membrane are observed, and the breakdown products are released into the synovial fluid. In stage III, these products are ingested by the synovial cells through phagocytosis, which is accompanied by the production of protease and proinflammatory cytokines (Martel-Pelletier, 2004). OA does not only cause the deterioration of cartilage but also the synovial membrane where an inflammatory reaction is often present. In this section, we will discuss the factors mediating in the development of OA, such as MMPs, aggrecanase protease, cytokines and ROS.

3.1 Matrix metalloproteinases (MMPs) and aggrecanases

MMPs are considered to be the main proteases responsible for proteolytic degradation of collagen and aggrecan in cartilage ECM (Martel-Pelletier et al., 2001). The expression of several MMPs was elevated in synovial tissues of OA patients. Degradation of Col II in the matrix is an irreversible step in OA and it was thought to be catalyzed by the MMP-1. Newer evidences showed that MMP-13 also has this effect and is the most reactive MMP in the degradation of OA cartilage. It targets Col II five times more rapidly than MMP-1 (Reboul et al., 1996). More members of MMPs (MMP-3, MMP-8, MMP-14) were identified. MMP-3 and MMP-14 degrade proteoglycan and are involved in the activation of other pro-MMPs. All of these MMPs are able to degrade different types of

collagen with different extents and mechanisms (Moilanen et al., 2003). Several aggrecanases have been identified: A disintegrin and metalloprotease with thrombospondin motifs (ADAMTS)-1, ADAMTS-4 and ADAMTS-5. They are members of the ADAMTS family of aggrecanases. They degrade aggrecans during cartilage destruction (Nagase and Kashiwagi, 2003).

3.2 Roles of cytokines in OA

Proinflammatory cytokines produced during synovial membrane inflammation upregulate MMPs gene expression and promote further progression of cartilage lesions in OA. They are synthesized by activated synoviocytes and by articular cartilage itself (Fernandes et al., 2002). Enhanced amounts of these mediators are found in OA synovial tissues compared to normal tissues. Among the cytokines, IL-1 β and TNF- α are considered to be the principal mediators of joint destruction. It is evident that, in animal model experiments, inhibiting IL-1 β synthesis and activity prevent cartilage damage, whereas blocking TNF- α reduces inflammation. This suggests that TNF- α drives inflammatory process and that IL-1 β is more responsible for cartilage destruction (Martel-Pelletier, 2004). The main action of IL-1 β is to suppress proteoglycan and collagen synthesis in parallel with the release of destructive protease in chondrocytes. Other cytokines involved in the development of OA include IL-8, IL-17 and IL-6. It has been showed that IL-6 deficient mice have a reduced joint inflammation (Van de Loo et al., 1997). These cytokines increase the number of inflammatory cells by upregulating other

proinflammatory cytokines, enhance the production of MMPs and stimulate the production of oxidative and inflammatory products synthesized by 5-lipoxygenase (5-LOX) (Guerne et al., 1989; Schroder, 1989). Use of specific anti-cytokine was found to reduce cartilage destruction in animal model; therefore, it was thought to be a treatment in the development of OA.

Several anti-inflammatory cytokines (IL-4, IL-10 and IL-13) were also found at an increased level in synovial tissues. They have a protective role from the degradation of cartilage. They decrease the production of IL-1 β , TNF- α and MMPs, upregulate TIMP-1 and inhibit PGE₂ release (Hart et al., 1989; Jovanovic et al., 1998). Since IL-4 exerts its effect at the translational level and IL-10 at the transcriptional level, synergic protection was observed when these two cytokines are given as a combination therapy (Joosten et al., 1997). In this context, modulation of cytokines that control the gene expression of MMPs becomes the target for drug development in the treatment of OA.

3.3 Reactive oxygen species (ROS)

ROS are produced by chondrocytes and synoviocytes in response to mechanical stress and inflammatory mediators. Recently, ROS were found to be involved in the degradation of cartilage (Henrotin et al., 2003). The main ROS produced in OA are nitric oxide (NO) and superoxide anion (O₂⁻). NO is synthesized mainly by iNOS enzyme. The production of NO is stimulated by IL-

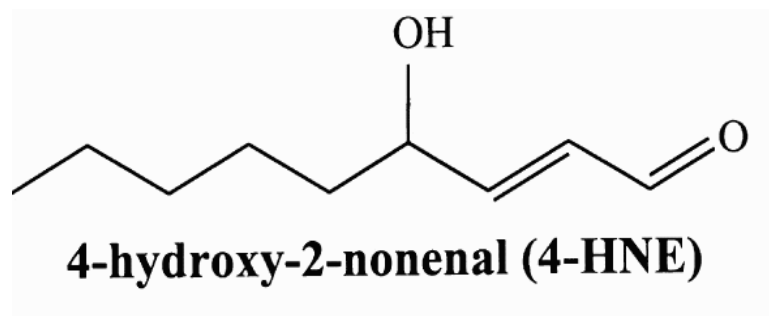
1 β , TNF- α and lipopolysaccharides (LPS) and is inhibited by anti-inflammatory cytokines such as IL-4 and IL-10 (Stadler et al., 1991). In OA, an insufficient antioxidant capacity is not able to detoxify ROS; therefore oxidative stress will take place. Increased ROS induces chondrocyte apoptosis and cartilage matrix breakdown by upregulating the expression of MMPs (MMP-3 and MMP-13). It also modulates the production of pro-inflammatory mediators. However, some evidence had demonstrated that ROS are produced at a low level in chondrocytes and may contribute to the maintenance of cartilage homeostasis. It was observed that a decrease in levels of ROS reduces the ability of articular chondrocytes to regulate pH (Milner et al., 2007;Gibson et al., 2009).

4. 4-HYDROXYNONENAL (HNE)

4.1 Synthesis and characteristics of HNE

Oxidative stress initiates many signaling cascades of cellular functions including inflammation, cell proliferation and chemoattraction. Under oxidative stress, lipid peroxidation (LPO) of membrane polyunsaturated fatty acids proceeds through a free radical chain reaction to yield lipid peroxides. They are subsequently decomposed and generate several end products such as aldehydes.

HNE was identified to be the most produced and cytotoxic aldehyde during lipid peroxidation. Due to its long half-life and α - β double bond, HNE can react easily with nucleic acids, proteins and phospholipids (**Fig. 4**). It also functions as a



(Pappa et al., 2003)

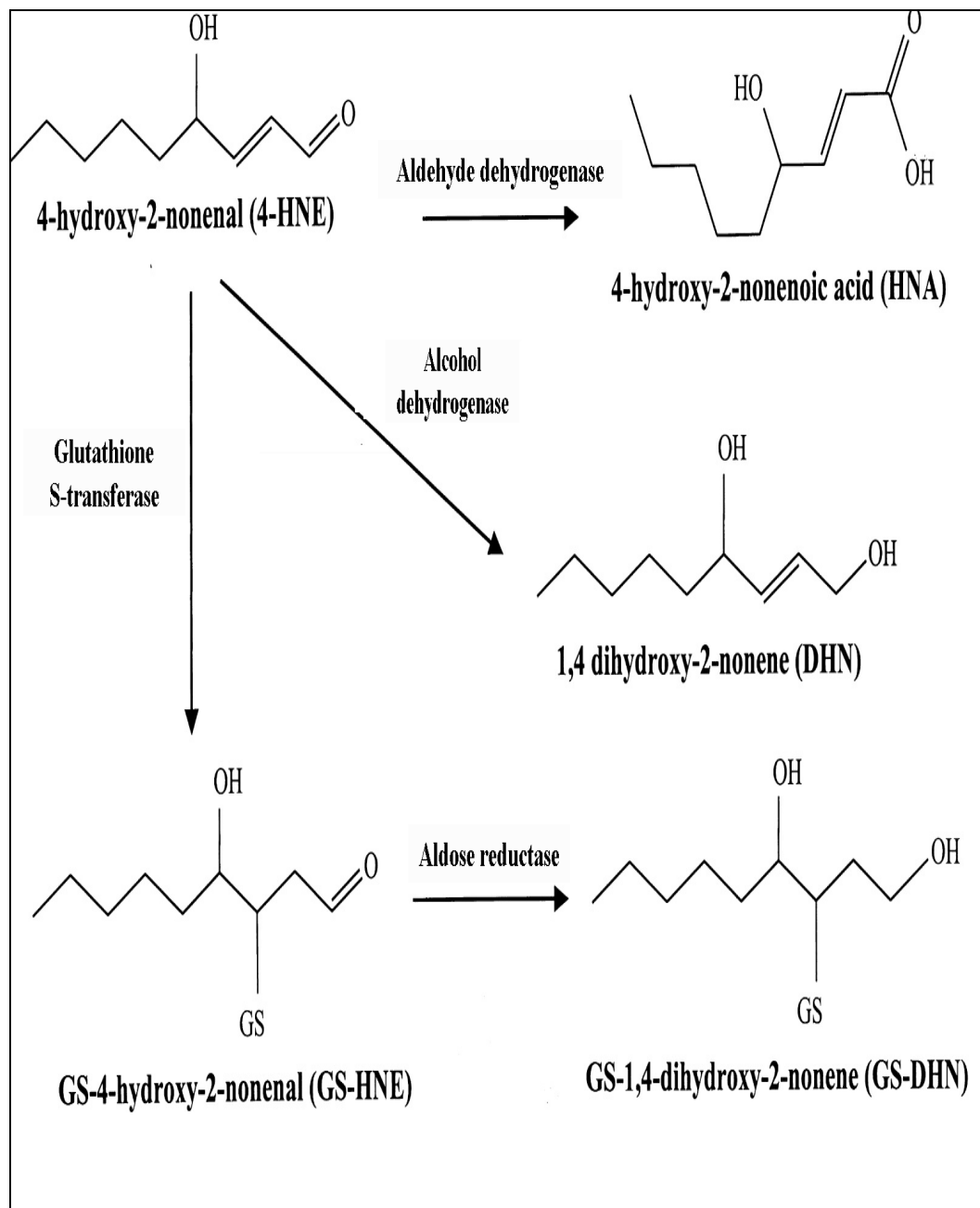
Figure 4: Structure of HNE with an α - β double bond and a hydroxyl group

bioactive molecule that affects numerous cell functions, including chemotactic activity, signaling transduction and gene expression (Esterbauer et al., 1991; Catala, 2009). Increased level of HNE was found in plasma, various organs and cells under oxidative stress conditions and in many rheumatological diseases, such as liver damage and chronic lymphedema (Comporti, 1985; Poli et al., 1987; Siems et al., 2002). Therefore, HNE Michael adduct can serve as a biomarker for the presence of oxidative stress and tissue damage (Zarkovic, 2003). A previous study also demonstrated higher HNE concentration in synovial fluids and in chondrocytes of OA patients compared to normal subjects (Morquette et al., 2006). The topic of HNE recently became controversial because HNE was found to be a normal constituent of membrane in mammals, at low concentration, without toxicity.

4.2 Metabolism of HNE

A low level of HNE is normally present in mammalian cells. Obviously, organisms have several enzymatic pathways to detoxify HNE in order to protect proteins and lipids from damage by aldehydic products. The best characterized HNE-metabolizing enzymes include the glutathione-S-transferase (GST), aldose reductase, aldehyde dehydrogenase and alcohol dehydrogenase (**Fig. 5**) (Pappa et al., 2003). HNE can be modified to non-toxic products through the following reactions: 1) Michael addition of glutathione (GSH) to HNE to produce GS-HNE, 2) the oxidation of HNE to 4-hydroxy-2-nonenic acid (HNA), 3) the reduction to

unreactive 1,4-dihydroxy-2-nonenal (DHN), 4) the interaction with carnosine, a dipeptide (beta-alanyl-L-histidine) present in high concentration in skeletal muscle (Aldini et al., 2002). Carnosine has numerous antioxidant properties and is able to scavenge ROS and unsaturated aldehydes formed during oxidative stress (Quinn et al., 1992; Babizhayev et al., 1994). Even with the rapid HNE metabolism, HNE-caused protein modification can occur. In different mammalian cells including hepatocytes, tumor cells and synovial fibroblasts, HNE metabolism is limited and a high level of protein-HNE adducts was observed after the addition of HNE (Siems and Grune, 2003). These HNE-modified proteins are believed to be involved in many impaired cells-related diseases. In this context, the degradation of intracellular HNE becomes one important part of the antioxidative defense systems.



(Modified from Pappa et al., 2003)

Figure 5: Metabolism of HNE

4.3 HNE binding proteins

HNE has a hydroxyl group and an α - β double bond, which make it highly reactive with specific amino acids of some proteins by the reaction of Michael addition to their particular functional groups. They were identified to be sulfhydryl group of cysteine, imidazole group of histidine and ϵ -amino group of lysine (Uchida and Stadtman, 1992a;Uchida and Stadtman, 1992b;Szweda et al., 1993). HNE can interact with many different cell proteins because it is quite stable and can pass through subcellular compartments. Several HNE-binding proteins were found, including glutamate transporter, proteasome and glyceraldehyde-3-phosphate dehydrogenase (Blanc et al., 1998;Okada et al., 1999;Tsuchiya et al., 2005). Due to its property of damaging DNA and proteins in cellular compartments, HNE was thought to be responsible for various pathophysiological effects associated with oxidative stress.

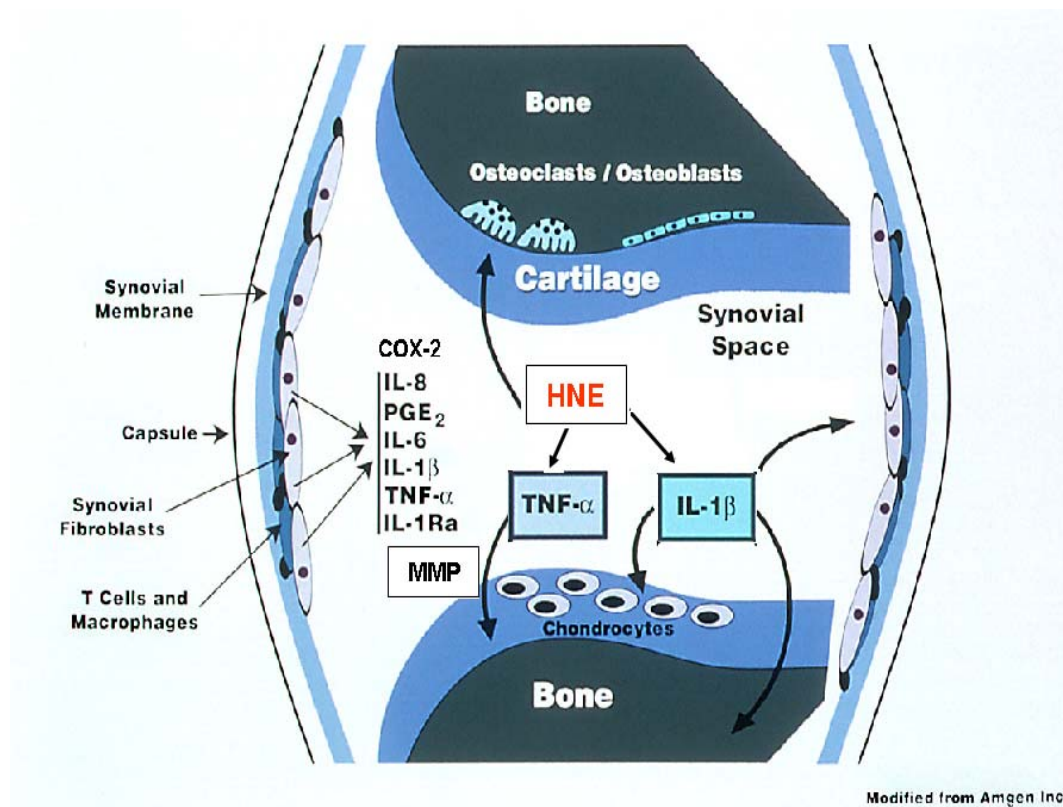
4.4 HNE and signaling pathways

Many studies suggested that HNE at low concentrations could be considered as a modulator of pathophysiological events by activating various signaling mechanisms, such as mitogen-activated protein kinases (MAPK), c-Jun N-terminal kinases (JNK) and caspase pathways. Apoptosis is one example of intracellular responses under oxidative stress in which caspases cascade is activated by HNE (Liu et al., 2000;Vaillancourt et al., 2008). Interestingly, increasing evidence showed that HNE stimulates the production of MMPs,

including MMP-2, MMP-9, and MMP-13 through ERK and p38 MAPK pathway in various cell types (Seo et al., 2010; Lee et al., 2010). HNE also induces COX-2 expression through p38 MAPK (**Fig. 6**) (Kumagai et al., 2004). The roles of MMPs and inflammatory mediators in cartilage destruction have been extensively studied and defined. These findings suggest that HNE may be involved in the pathophysiology of OA in association with inflammatory responses.

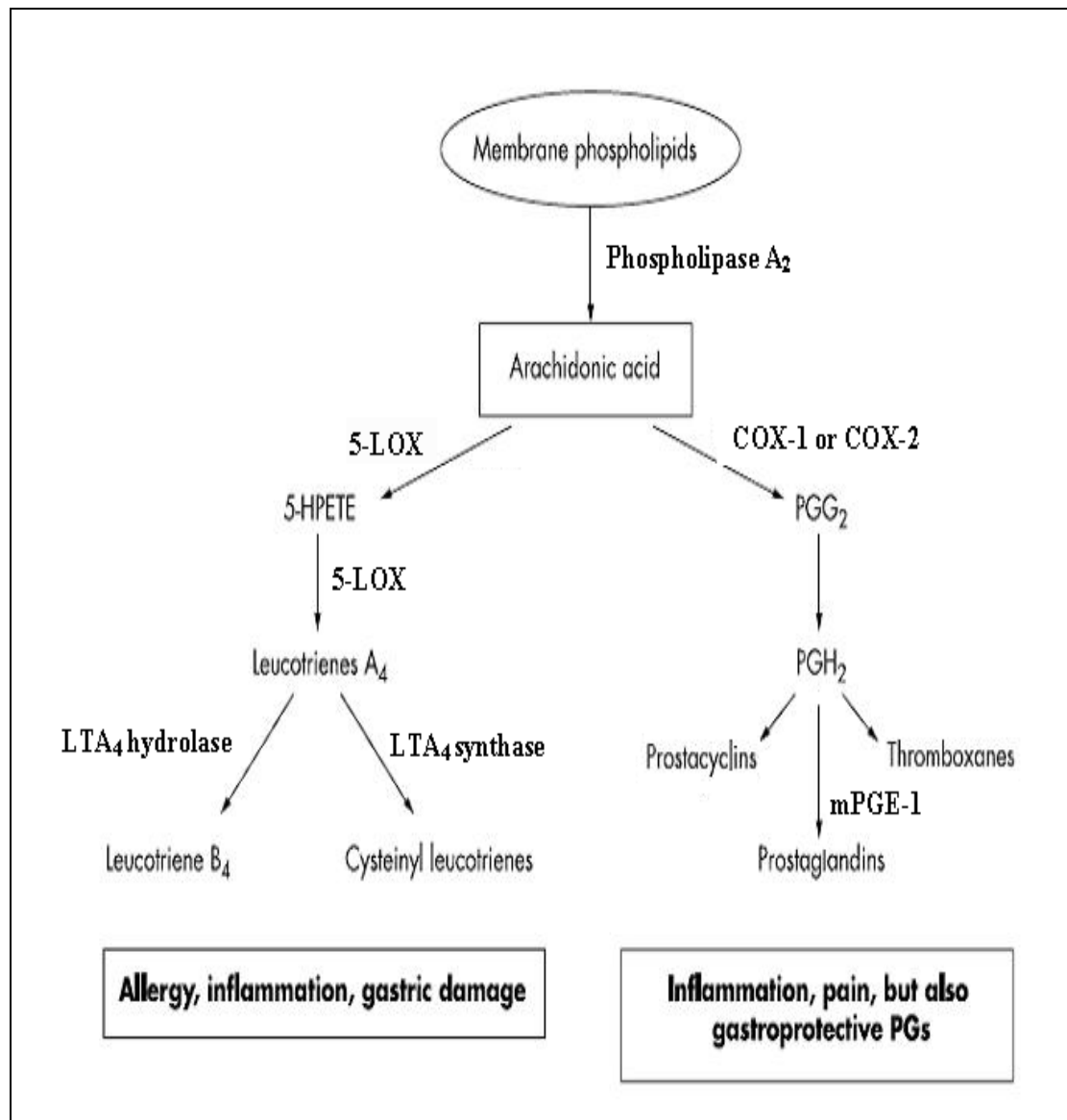
5. ARACHIDONIC ACID METABOLISM

During its metabolism, arachidonic acid (AA) is released from hydrolysis of cell membrane phospholipids by cytosolic phospholipase A₂ enzyme (cPLA₂). AA is then oxygenated to form PGG₂ by COXs, which subsequently reduce PGG₂ to the unstable intermediate called prostaglandin H₂ (PGH₂). PGH₂ quickly transform to prostacyclins, thromboxanes and prostaglandins by prostaglandin E₂ synthase (PGES) (Smith et al., 2000; Park et al., 2006). Another AA metabolism pathway is catalyzed by 5-lipoxygenase-activating protein (FLAP)/5-lipoxygenase (5-LOX), which are the pivotal enzymes to yield leukotrienes (LTs) (**Fig. 7**). The amount of eicosanoid production is dependent on the release of AA by cPLA₂ (Park et al., 2006). The production and the regulation of these enzymes are discussed in detail in the following sections.



(Modified from Amgen Inc.)

Figure 6: Role of HNE in the development of OA.



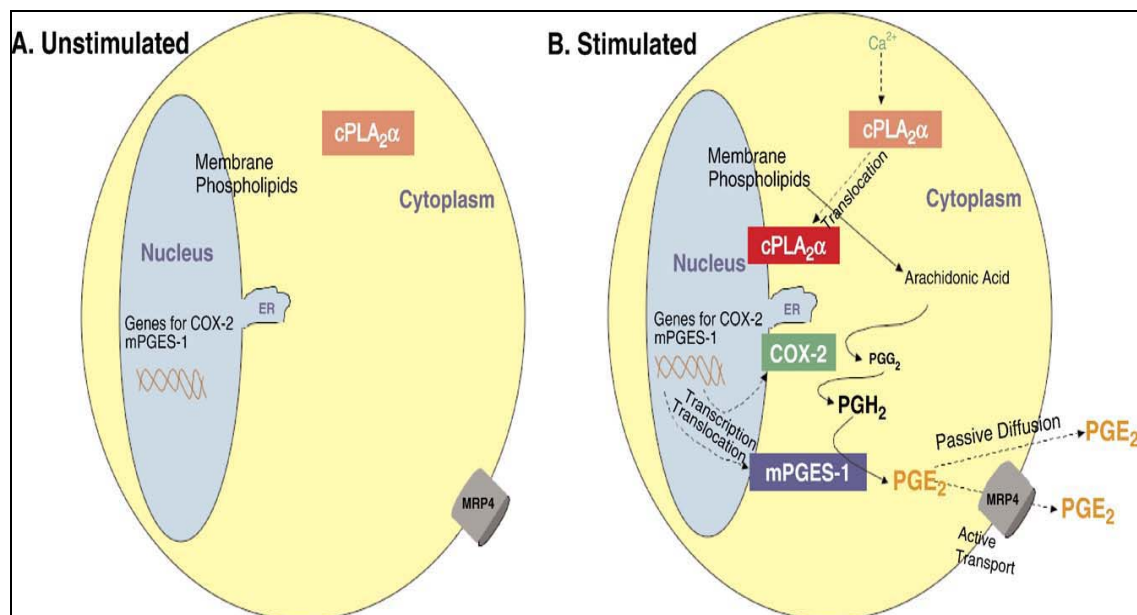
(Modified from Martel-Pelletier et al., 2003)

Figure 7: Arachidonic acid metabolism

5.1 Cyclooxygenase (COX)

Two COX isoforms have been identified: COX-1 and COX-2. They are encoded by different genes and expressed in different manners. COX-1 is a membrane-bound heme-containing glycoprotein expressed ubiquitously under normal conditions, whereas COX-2 is inducible and expressed by various stimuli (Martel-Pelletier et al., 2003; Uchida, 2008). Stimulation induces influx of calcium into the cell, leading to the translocation of cPLA₂ from the cytosol to the nuclear membrane where it enzymatically hydrolyzes membrane phospholipids to liberate AA (**Fig. 8**) (Park et al., 2006). Different stimuli that can induce COX-2 expression include pro-inflammatory IL-1 β , TNF- α and growth factors, which promote prostaglandins synthesis and lead to further inflammation and carcinogenesis (FitzGerald, 2003). HNE was found to stimulate the expression of COX-2 and PGE₂ production in chondrocytes, suggesting it may induce OA development through inflammatory processes (Vaillancourt et al., 2007).

In human rheumatoid arthritis (RA) synovial membranes, immunostaining with anti-COX-2 antisera revealed the presence of COX-2 in infiltrating mononuclear cells, endothelial cells of blood vessels, and subsynovial fibroblast-like cells. IL-1 β and phorbol myristate acetate enhance *de novo* mRNA and protein synthesis of COX-2 in RA synovial membrane and cultured synovial fibroblasts.



(Park et al., 2006)

Figure 8: COX-2 expression in the absence or presence of stimulations

COX-2 is also expressed in cartilage specimens from OA patients (Amin et al., 1997; Siegle et al., 1998). Osteoarthritic cartilage spontaneously releases PGE₂ in levels at least 50-fold higher than the normal cartilage and 18-fold higher than normal cartilage stimulated with cytokines and endotoxin. The production of PGE₂ was sensitive to the translation inhibitor Cycloheximide, indicating the inducible aspect of this mediator. These observations indicate that COX-2 expression is upregulated in arthritic synovial membranes and cartilage, and suggest that selective inhibition of COX-2 may result in the amelioration of arthritic diseases.

5.2 Prostaglandin E₂ synthase (PGES)

The terminal enzyme found in the COX pathway is called PGES, which collaborates with COX in the synthesis of prostaglandins from PGH₂. Three isoforms of PGES have been determined: cytosolic PGES (cPGES), microsomal PGES-1 (mPGES-1) and mPGES-2. cPGES is preferentially coupled with COX-1 to immediately produce PGE₂, whereas mPGES-1 is inducible as COX-2, both work together to promote late synthesis of PGE₂ (Fahmi, 2004). mPGES-2 is not well studied at present and its function is still unclear.

At transcriptional level, mPGES-1 expression is regulated by transcriptional factors such as early growth response protein-1 (Egr-1) and nuclear factor-kappa B (NF-κB) (Cheng et al., 2004; Ackerman et al., 2008). The regulation of mPGES-1 by Egr-1 was found through two Egr-1 binding motifs

(tandem GC boxes) that are located in the proximal region of the mPGES-1 promoter (Naraba et al., 2002;Subbaramaiah et al., 2004). On the other hand, mPGES-1 expression can be inhibited by a nuclear receptor called peroxisome proliferator-activated receptor gamma (PPAR γ), which acts as a protector with anti-inflammatory and chondroprotective properties (Afif et al., 2007).

Recently, the characteristics, regulations and roles of mPGES-1 in inflammation have been studied in various cells, including vein endothelial cells, chondrocytes, synoviocytes. mPGES-1 has been identified to be a membrane bound microsomal enzyme, which is induced by glutathione and upregulated by proinflammatory stimuli, such as IL-1 β , TNF- α and LPS at both mRNA and protein level (Stichtenoth et al., 2001;Uracz et al., 2002;Kojima et al., 2004).

5.3 Prostaglandin E₂ (PGE₂)

PGE₂ is an end product of AA through COX pathway. Its role as an inflammatory mediator is well known and its regulation mechanism is extensively studied. The group of Yucel-Lindberg investigated the effects of AA, PLA₂ and PGE₂ on the expression of mPGES-1 in fibroblasts. Interestingly, they found that cPLA₂ inhibitors downregulated mPGES-1 expression, which is upregulated by the addition of AA and PGE₂. These findings showed that the expression of mPGES-1 is regulated by PGE₂ through positive feedback regulation, amount of AA and functional cPLA₂ enzyme (Yucel-Lindberg et al., 2006). The effect of

PGE₂ on the enhancement of mPGES expression was also found in synovial fibroblasts from patients with RA (Kojima et al., 2003). Another study showed that PGE₂ has a regulatory function on the biosynthesis of leukotriene B₄ (LTB₄) and 5-LOX/FLAP expression. It decreases the production of LTB₄ by inhibiting FLAP via IL-10 dependent mechanism in dendritic cells, but without any effect on 5-LOX (Harizi et al., 2003). Recently, PGE₂ produced by synovial COX-2 was shown to be involved not only in inflammation, but also in the modulation of the degradation of cartilage proteoglycan mediated by IL-1 β (Hardy et al., 2002).

5.4 5-lipoxygenase (5-LOX)

5-LOX is a pivotal enzyme that catalyzes the first two steps in the biosynthesis of LTs, including LTB₄ and cysteinyl-leukotrienes (cys-LTs). 5-LOX first catalyzes the conversion of AA to unstable epoxide intermediate LTA₄, which is subsequently transformed to either LTB₄ by LTA₄ hydrolase or cys-LTs by LTA₄ synthase (**Fig 7**). These LTs are pro-inflammatory lipids mediators that are involved in asthma, inflammation, allergy and phagocyte chemotaxis (Wardlaw et al., 1989; Bigby, 1999).

5.5 Regulation of 5-LOX expression

5-LOX contains a large catalytic domain consisting of a non-heme iron atom and an ATP binding site, which are crucial for the catalytic potential of 5-LOX (Aparoy et al., 2008). Calcium and ATP are two important factors that

influence 5-LOX activation. In an environment without these two factors, the enzyme activity of 5-LOX is limited, but can be recovered by the addition of Ca^{2+} (Rouzer and Samuelsson, 1987). Interestingly, the increase in 5-LOX activity by ATP only happens in the presence of Ca^{2+} (Noguchi et al., 1996). Ca^{2+} plays an important role in the movement of 5-LOX to the nuclear membrane, allowing its binding with FLAP.

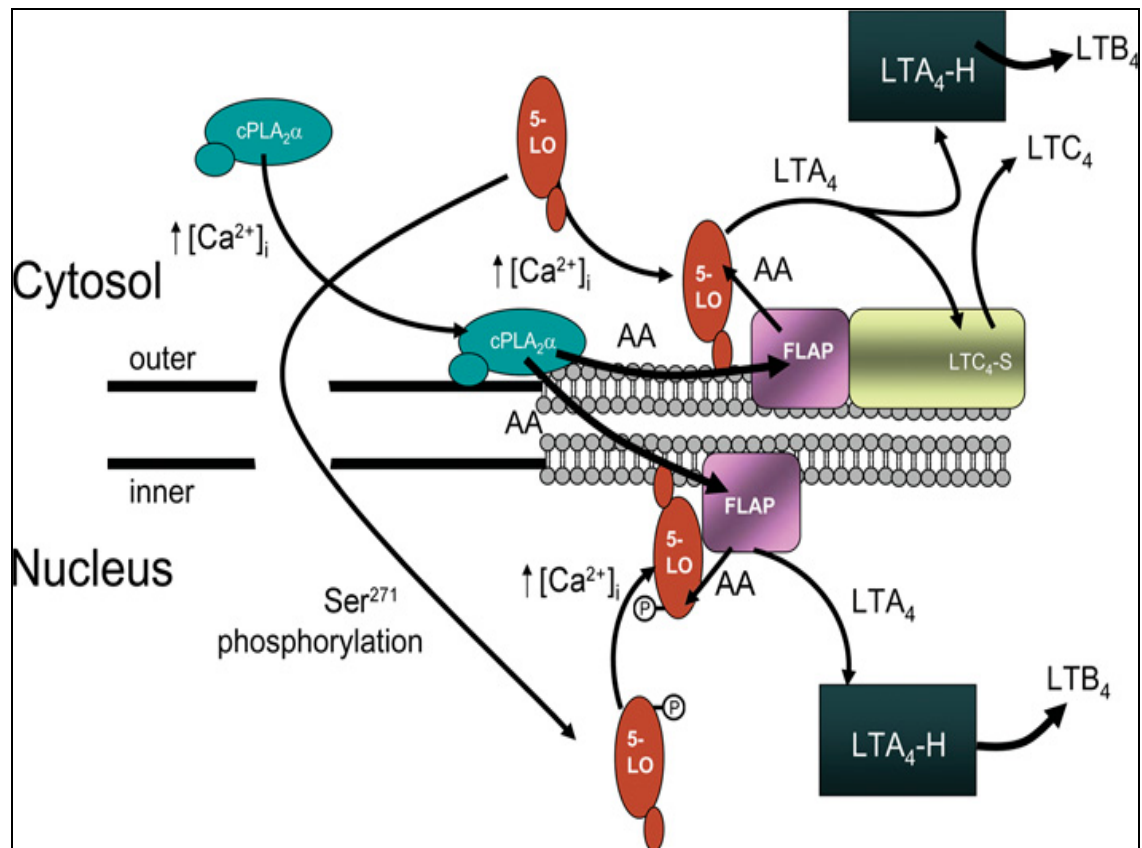
5-LOX is highly expressed in leukocytes, cancer cells and especially in differentiated cells. The expressions of 5-LOX mRNA and protein are induced by transforming growth factor-beta 1 (TGF- β 1) and dihydroxyvitamin D₃, DMSO and granulocyte/macrophage colony-stimulating factor (GM-CSF) in human monocytic Mono Mac 6, leukemia HL-60 cells and granulocytes (Krump and Borgeat, 1994; Brungs et al., 1994). These findings suggested that TGF- β 1, dihydroxyvitamin D₃ and GM-CSF act as differentiation inducers and promote 5-LOX synthesis in various cells (Krump and Borgeat, 1994; Harle et al., 1999). 5-LOX transcription activity increases when 5-LOX promoter construct is cotransfected with Egr-1 expression vector (Cheng et al., 2004). The transcription factor Egr-1 binds to GC sequences and interacts with transcriptional coactivators. This indicates that inducible 5-LOX gene transcription is mediated by Egr-1 and maybe by other transcriptional factors in GC rich promoter region (Silverman et al., 1998). 5-LOX expression can also be stimulated by dihydroxyvitamin D₃, which is synthesized in synovial fluid of patients with inflammatory arthritis. In OA cartilage, Tetlow and Woolley indicated that 5-LOX promoter contains a

vitamin D receptor element (VDRE), which induces 5-LOX expression by interaction with vitamin D receptors (VDR) (Tetlow and Woolley, 2001).

5.6 5-lipoxygenase-activating protein (FLAP)

FLAP is a nuclear membrane bound protein that collaborates with 5-LOX. When cells are stimulated, cPLA₂ and 5-LOX migrate to the nuclear membrane. FLAP helps the binding of 5-LOX with AA and the efficient utilization of AA released from phospholipids, leading to the biosynthesis of LTs (**Fig. 9**) (Murphy and Gijon, 2007). It has been shown that transformation of AA by 5-LOX is efficiently blocked in cells missing FLAP. Even FLAP is required for the LTs biosynthesis from endogenous AA, but metabolism of exogenous AA does not need FLAP.

This observation suggests that FLAP is not mandatory but can facilitate and enhance 5-LOX activity (Coffey et al., 1994). Furthermore, the expression of 5-LOX and FLAP as well as LTB₄ synthesis are enhanced in various inflammatory conditions, such as OA, systemic sclerosis and asthma (Chu et al., 2000;Kowal-Bielecka et al., 2001;Lascelles et al., 2009).



(Murphy RC, 2007)

Figure 9: Intracellular organization of the critical enzymes involved in leukotriene biosynthesis

6. OBJECTIVES AND HYPOTHESIS

Recently, we reported that the induction of COX-2 decreased dramatically after 8 hours of incubation with HNE, an end product of lipid peroxidation. HNE was thought to be involved in the pathophysiology of OA due to its ability to induce the expression of MMP-13 and COX-2, leading to destruction of cartilage and synovial inflammation. This study aimed to investigate the regulation of mPGES-1, FLAP and 5-LOX expression by HNE as well as the biosynthesis of PGE₂ and LTB₄ in human OA chondrocytes with different periods of incubation. We hypothesize that COX-2 and mPGES-1 down-regulation is attributed to HNE depletion and is responsible for the switch from COX-2 to FLAP/5-LOX pathway, resulting in the decrease of PGE₂ production and an increase of LTB₄. It has been shown that there is a switch of COX pathway to FLAP/5-LOX in the presence of low PGE₂. This study is also to investigate the involvement of transforming growth factor-beta 1 (TGF-β1) in this switch. In addition, increased LTB₄ level in synovial tissues was observed in OA patients who usually take COX-2 inhibitors. Therefore, our hypothesis is that HNE may be involved in the switch from COX-2 to FLAP/LOX pathway in human OA chondrocytes.

CHAPTER II:
MATERIALS AND METHODS

Specimen selection and chondrocyte culture

Human OA articular cartilage was obtained from OA patients aged 67 ± 9 years (mean \pm SD) who underwent total knee arthroplasty. Informed consent had been obtained from patients with OA for the use of their tissues for research purposes. All patients were evaluated by rheumatologists who followed American College of Rheumatology criteria (Altman et al., 1986). The experimental protocol and use of human tissues were approved by the Research Ethics Board of Hôpital du Sacré-Cœur de Montréal. OA cartilage (femoral condyles and tibial plateaus) was obtained under aseptic conditions and carefully dissected from the underlying bone in each specimen (Benderdour et al., 2002). OA chondrocytes were extracted by sequential enzymatic digestion with 1 mg/ml of pronase (Sigma, Oakville, Ontario, Canada) for 1 h at 37°C, then with 2 mg/ml of type IV collagenase (Sigma) for 6 h in Dulbecco's modified Eagle's medium (DMEM; Gibco BRL, Burlington, Ontario, Canada) supplemented with 10% heat-inactivated fetal bovine serum (FBS; Invitrogen Life Technology, Inc., Grand Island, NY, USA), 100 units/ml of penicillin and 100 μ g/ml of streptomycin (Invitrogen Life Technology, Inc.). The cells were seeded at high density in culture flasks at 37°C in a humidified atmosphere of 5% CO₂/95% air until they were confluent and ready for the experiments. First-passage cells were employed to ensure their phenotype and seeded at 10^5 cells/cm² in culture tissue plates. The DMEM containing 2% FBS and antibiotics was replaced 24 h before the experiments were performed in this medium with the factors under study for different incubation time periods.

Chondrocytes were treated with single addition of 10 μ M HNE for increasing times (0 to 72 h) or with repeated treatments by adding 10 μ M HNE to the cultures at t=2, 4, 6, 8, 10, 12, 16, 24 h. For drug exposure, cells were pre-treated with 50 μ M naproxen or 100 μ g/ml anti-transforming growth factor-beta 1 (TGF- β 1) antibody for 1 h, followed by a second incubation for 24 or 72 h in the presence or absence of 10 μ M HNE.

Protein detection by Western blotting

Twenty micrograms of total proteins from chondrocyte lysates treated with HNE under the indicated conditions were loaded for discontinuous 4-12% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Protein transfer and immunodetection as well as semi-quantitative measurements were performed as described previously (Morquette et al., 2006). The primary antibodies were rabbit anti-COX-2, anti-mPGES-1 (Cayman Chemical-Cedarlane, Hornby, Ontario, Canada), anti- β -actin and anti-Egr-1 (Santa Cruz Biotechnology, Santa Cruz, CA, USA). After serial washes, primary antibodies were detected by goat anti-rabbit immunoglobulin G conjugated to horseradish peroxidase (Jackson ImmunoResearch Laboratories, Inc., West Grove, PA, USA). Immunoreactive proteins were detected with SuperSignal blotting substrate (Pierce Biotechnology, Inc., Rockford, IL, USA) and exposed to clear-blue x-ray film (Pierce).

RNA extraction and reverse transcription-polymerase chain reaction (RT-PCR)

Total RNA was isolated with TRIzol reagent according to the manufacturer's instructions. RNA was quantitated with RiboGreen RNA quantitation kit (Molecular Probes, Eugene, OR, USA), dissolved in diethylpyrocarbonate-treated H₂O, and stored at -80°C until used. One microgram of total RNA was reverse-transcribed with Moloney murine leukemia virus reverse transcriptase (Fermentas, Burlington, Ontario, Canada), as detailed in the manufacturer's guidelines. One-fiftieth of the reverse transcriptase reaction product was analyzed by traditional PCR or real-time quantitative PCR. The following sense and antisense specific primers (purchased from Bio-Corp, Inc., Montreal, Quebec, Canada), were tested: human mPGES-1, 5'-GAA GAA GGC CTT TGC CAA C-3' (sense) and 5'-GGA AGA CCA GGA AGT GCA TC-3' (antisense); human 5-LOX, 5'-CTG TTC CTG GGC ATG TAC CC-3' (sense) and 5'-GAC ATC TAT CAG TGG TCG TG-3' (antisense); human FLAP, 5'-AAT GGG AGG AGC TTC CAG AG-3' (sense) and 5'-ACC AAC CCC ATA TTC AGC AG-3' (antisense); human GAPDH, 5'-CAG AAC ATC ATC CCT GCC TCT-3' (sense) and 5'-GCT TGA CAA AGT GGT CGT TGA G-3' (antisense).

Quantitative PCR analysis was performed in a total volume of 50 µl containing template DNA, 200 nM sense and antisense primers, 25 µl of SYBR Green Master Mix (Qiagen, Mississauga, Ontario, Canada), and 0.5 units of uracil-

N-glycosylase (UNG; Epicentre Technologies, Madison, WI, USA). After incubation at 50°C for 2 min (UNG reaction) and at 95°C for 10 min (UNG inactivation and activation of AmpliTaq Gold enzyme), the mixtures were subjected to 40 amplification cycles (15 s at 95°C for denaturation and 1 min for annealing and extension at 60°C). Incorporation of SYBR Green dye into the PCR products was monitored in real time with a Mx3000 real-time PCR systems (Stratagene, La Jolla, CA, USA), to determine the threshold cycle (C_t) at which exponential amplification of PCR products begins. After PCR, dissociation curves were generated with 1 peak, indicating amplification specificity. A C_t value was obtained from each amplification curve with the software provided by the manufacturer (Stratagene).

Relative mRNA expression in chondrocytes was quantified according to the $\Delta\Delta C_t$ method, as detailed in the manufacturer's guidelines (Stratagene). A ΔC_t value was first calculated by subtracting the C_t value for the housekeeping gene GAPDH from the C_t value for each sample. A $\Delta\Delta C_t$ value was then calculated by subtracting the ΔC_t value for the controls (unstimulated cells) from the ΔC_t value for each treatment. Fold changes compared with the controls were then determined by $2^{-\Delta\Delta C_t}$. Each PCR generated only the expected specific amplicon, as shown by melting temperature profiles of the final product and gel electrophoresis of the test PCRs. Each PCR was performed in triplicate on 2 separate occasions for each independent experiment.

PGE₂, LTB₄ and transforming growth factor-beta 1 (TGF-β1 enzyme immunoassay

After incubation, the culture medium from cultured OA chondrocytes was collected and PGE₂ and LTB₄ levels were measured with specific commercial kits for PGE₂ (Cayman Chemical), LTB₄ and TGF-β1 (R&D Systems, Minneapolis, MN, USA), according to the manufacturer's instructions. Detection sensitivity was 9, 13.7, 4.6 pg/ml, respectively. All assays were in triplicate.

Plasmids and transient transfection

The human mPGES-1 promoter construct (-538/-28) was a gift from Dr. Terry J. Smith (University of California, Los Angeles, CA, USA) (Han et al., 2002). The pEgr-1Mutx3-TK-Luc reporter construct was generously provided by Dr. Yuqing E. Chen (Morehouse School of Medicine, Atlanta, GA, USA) (Fu et al., 2002). The 5-LOX promoter construct was kindly donated by Dr. Dieter Steinhilber (University of Frankfurt, Frankfurt, Germany). Subconfluent human OA chondrocytes were transiently transfected in 12-well cluster plates with lipofectamine 2000TM reagents (Invitrogen Life Technology, Inc.), according to the manufacturer's protocol. Briefly, transfections were conducted for 6 h with DNA lipofectamine complexes containing 10 μl of lipofectamine reagent, 2 μg DNA plasmid and 0.5 μg of pCMV-β-gal (as a transfection efficiency control). After washing, the cells were stimulated with 10 μM HNE for different incubation periods, depending on the experiments. Luciferase activity was determined in

cellular extracts with commercially-available kits (Luciferase assay system, Promega Corporation, Madison, WI, USA). The data were normalized to β -gal level, which was quantified by a specific ELISA (Roche Applied Science, Laval, Quebec, Canada).

Statistical analysis

For the time course experiments, all quantitative results were expressed as means \pm SEM. The data were compared by ANOVA. *p* values less than 0.05 were considered to be statistically significant and contrast tests were against the control (time = 0 h). Two-way ANOVA was used to analyze the results from the experiments with treatments of two factors, such as HNE and naproxen or HNE and TGF- β 1. Their interaction and main effects are reported in the figures.

CHAPTER III: RESULTS

Single or repeated treatments with HNE regulate differently PGE₂ release and COX-2 protein expression

As described in our previous report, COX-2 expression decreased gradually after 8 h of chondrocyte incubation with 10 μ M HNE. To examine whether this reduction is attributable to HNE depletion, cells were stimulated with either one or repeated 10 μ M HNE treatments for different incubation periods (0 to 24 h, n = 3 independent experiments). Chondrocyte stimulation with 10 μ M HNE (1 treatment) showed that COX-2 protein expression and PGE₂ release increased within 4 h and plateaued at 8 h of incubation, before declining at 16 and 24 h (Fig. 1A & 1C). PGE₂ and COX-2 reached maximum levels of 157.5 ± 33 ng/ 10^5 cells and 340% of control values, respectively. However, in experiments where the cells were stimulated repeatedly, COX-2 expression and PGE₂ release were enhanced after 4 h and 8 h of incubation respectively, with maximum values obtained at 24 h (Fig. 1B & 1D). Maximum PGE₂ and COX-2 values were 210 ± 29 ng/ 10^5 cells and 400% of control values, respectively. HNE was cytotoxic at >20 μ M and significantly decreased cell viability (data not included).

Induction of mPGES-1 protein and mRNA expression by single or repeated treatment with HNE

To gain insights into the role of HNE in the modulation of mPGES-1, the inducible form of PGES involved in the terminal step of PGE₂ synthesis, we

Figure 10

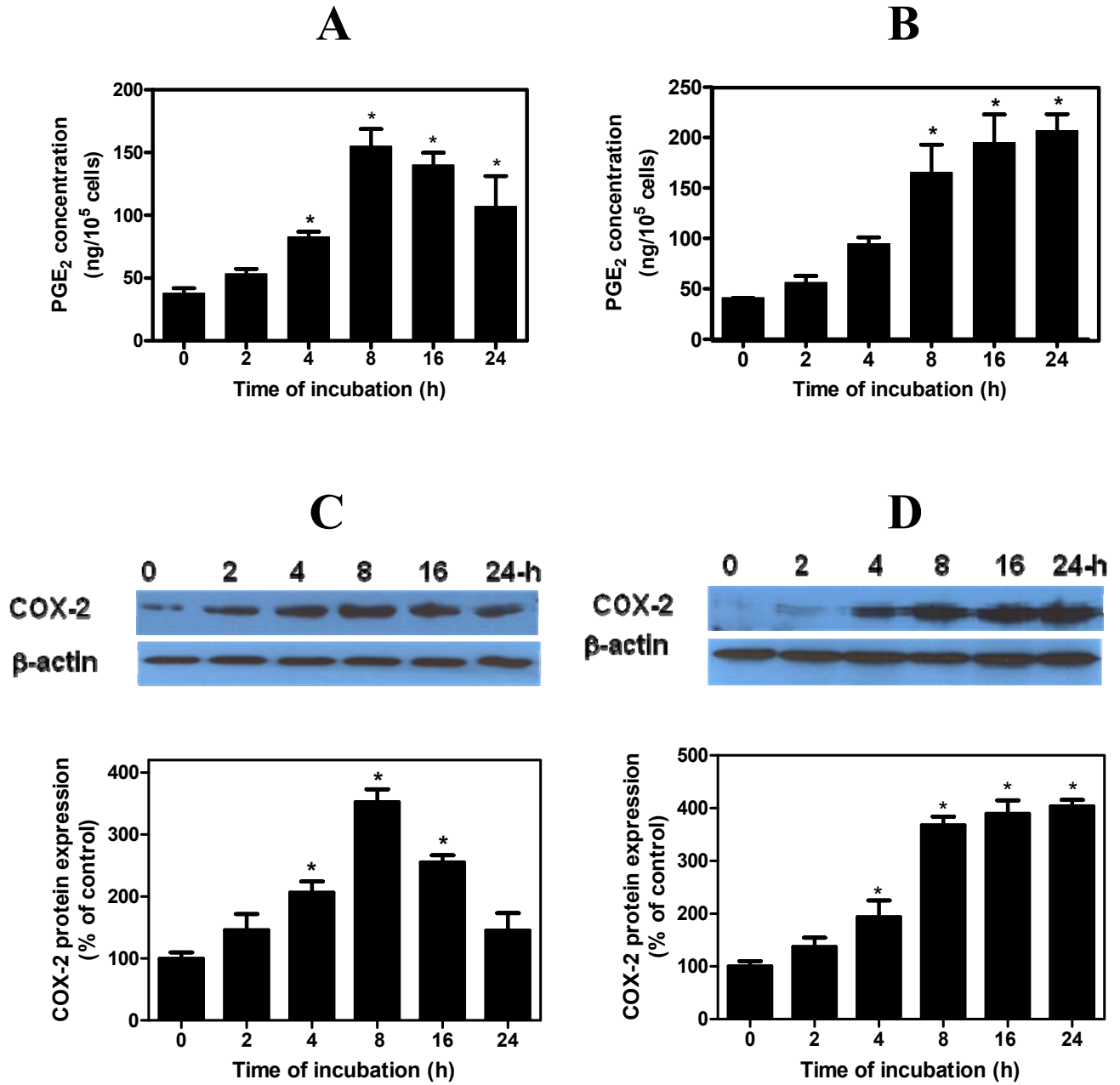


Figure 10. HNE-induced PGE₂ production and COX-2 expression in human OA chondrocytes

Cells were stimulated once (A & C) or repeatedly (B & D) with 10 μ M HNE every 2 h for different incubation periods, as indicated above. PGE₂ concentration (A & B) was measured by enzyme immunoassay (EIA) commercial kit. COX-2 protein expression (C & D) was analyzed by Western blotting. The data are means \pm SEM of $n = 3$ and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA: * $p < 0.05$.

evaluated its effect on the expression of this enzyme in human OA chondrocytes treated once or several times for different incubation periods ($n = 3$ independent experiments). As depicted in Figures 2A and 2C, one treatment with $10 \mu\text{M}$ HNE significantly increased mPGES-1 protein and mRNA levels, which plateaued at 16 h but then declined at 24 h. mPGES-1 protein and mRNA reached maximum levels of 230 and 214% of control values, respectively. However, repeated treatments with $10 \mu\text{M}$ HNE enhanced mPGES-1 protein and mRNA levels, with maximum value attained at 24 h (Fig. 2B and 2C). The maximum levels of mPGES-1 protein and mRNA were 430 and 300% of the controls, respectively.

HNE-induced mPGES-1 and 3xEgr-1 binding site promoter activities

In our previous report, we have reported that HNE induced COX-2 transcription through ATF-2/CREB-1 transactivation (Vaillancourt et al., 2007). In the present study, we further examined whether HNE induced mPGES-1 at transcriptional level through Egr-1 transactivation. Firstly, to determine whether changes in mPGES-1 mRNA levels can be ascribed to alteration in promoter activity, chondrocytes were transiently transfected with human mPGES-1 promoter-luciferase reporter genes ($n = 3$ independent experiments). Treatment of transfected cells with $10 \mu\text{M}$ HNE for increasing periods of incubation led to a time-dependent increment of mPGES-1 promoter activity (Fig. 3A). Maximum promoter activity was 331% at 16 h compared to the controls. These data are

Figure 11

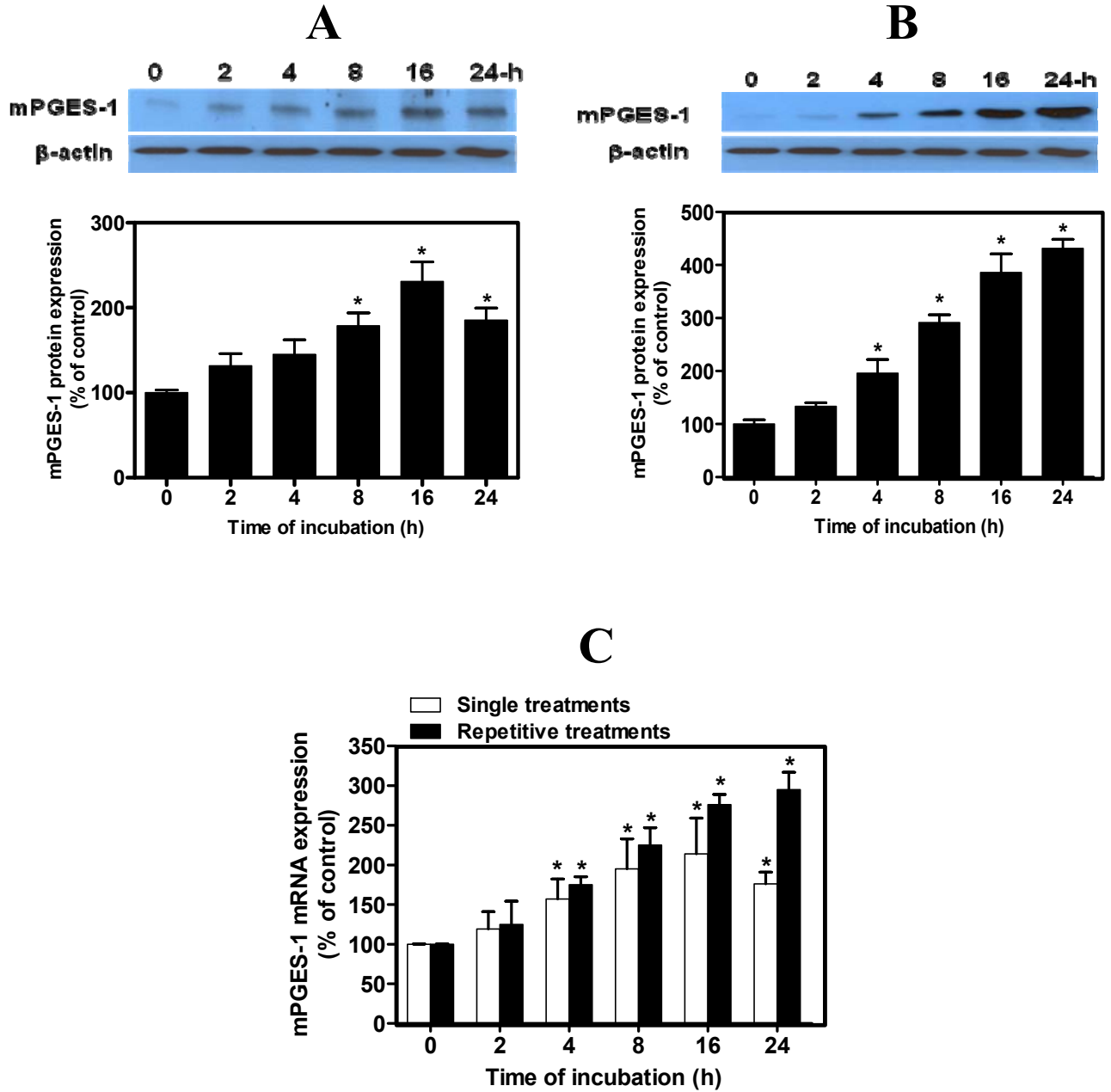


Figure 11. HNE-induced mPGES-1 protein and mRNA expression in human OA chondrocytes

Cells were stimulated with 10 μ M HNE once (A & C) or repeatedly (B & C) with 10 μ M HNE every 2 h for different incubation periods, as indicated above. mPGES-1 protein (A & B) and mRNA (C) were measured respectively by Western blotting and real-time RT-PCR. The data are means \pm SEM of $n = 3$ and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA: * $p < 0.05$.

Figure 12

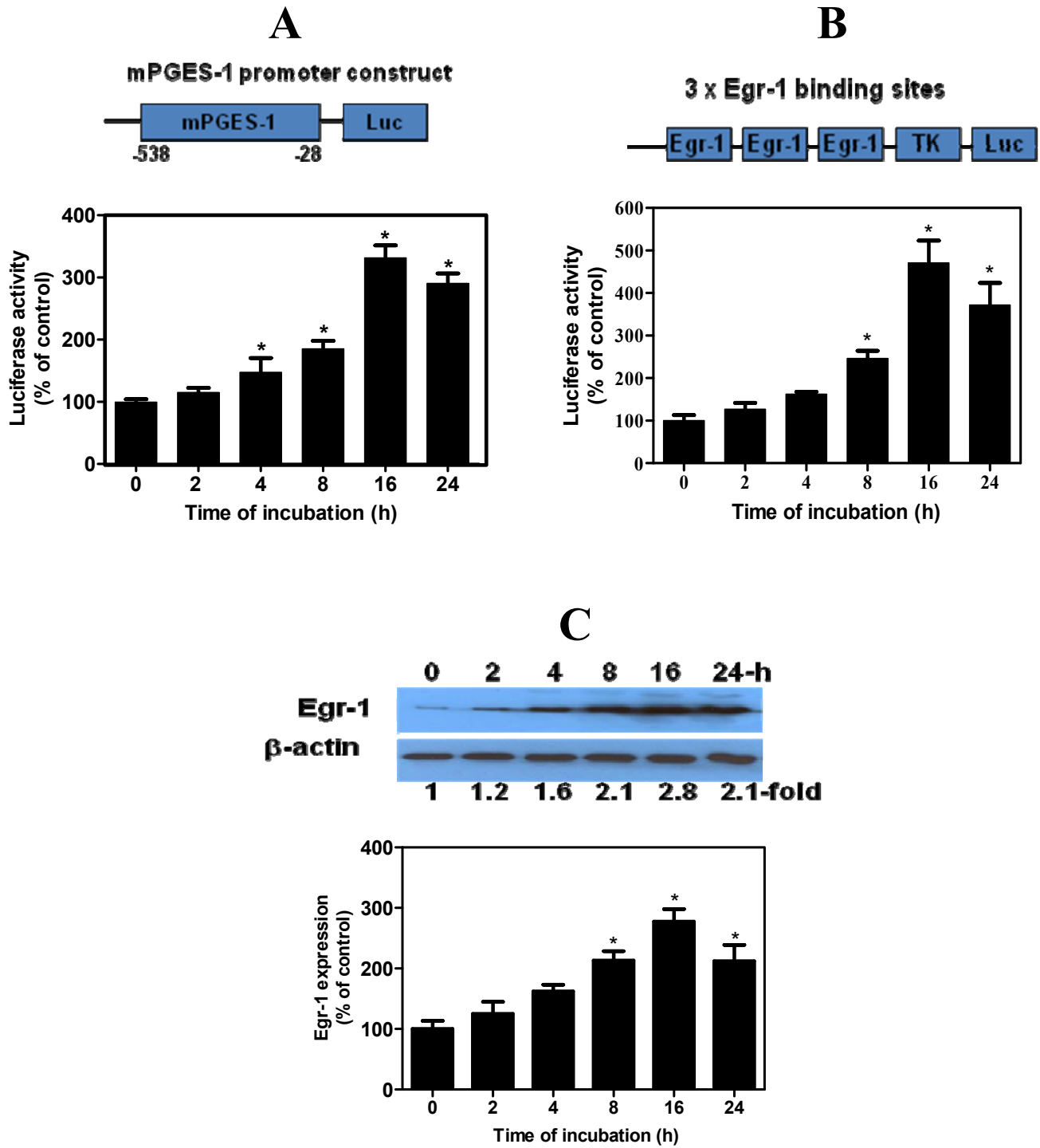


Figure 12. HNE-activated mPGES-1 promoter

Chondrocytes were transfected with mPGES-1-Luc (A) or p3xEgr-1-Luc (B) containing 3 Egr-1 binding sites. The next day, they were incubated with 10 μ M HNE for increasing incubation time periods. Luciferase activity was measured in cell extracts and normalized to β -galactosidase activity. (C) OA chondrocytes were treated with 10 μ M HNE at increasing time of incubation and then Egr-1 protein expression was evaluated in cellular extract by Western blot. The data are means \pm SEM of $n = 3$ and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA: * $p < 0.05$.

consistent with the regulation of mPGES-1 expression by HNE at the transcription level. The transcription factor Egr-1 has been shown to play a crucial role in mPGES-1 transcription. Therefore, we analyzed the effect of HNE on the transcriptional activation of a synthetic luciferase reporter construct containing 3 tandem repeats of the putative Egr-1 binding sequence pEgr-1×3-TK-Luc. As seen in Figure 3B, HNE increased luciferase activity of the above construct, and this activation was time-dependent. Maximum promoter activity reached 450% at 16 h compared to the controls (Fig. 3B). Western blot analysis revealed that single treatment with 10 μ M HNE induced Egr-1 protein expression by 280% compared to untreated cells after 16 h of incubation (Fig. 3C). Collectively, these data suggest that Egr-1 may be one of the transcription factors involved in HNE-induced mPGES-1 promoter activity.

HNE-induced LTB₄ release through 5-LOX and FLAP up-regulation

LTB₄ is an end product of an inflammatory signaling pathway. It has been found to regulate the synthesis of other catabolic factors involved in the pathophysiology of OA (Martel-Pelletier et al., 2004). Human OA chondrocytes (n = 5 independent experiments) were stimulated with 10 μ M HNE for different incubation periods. HNE-induced changes in LTB₄ level was measured with EIA commercial kits. LTB₄ release (Fig. 4A) was induced only after 48 h incubation period, with a further increase after 72 h of treatment (66.6 ± 3.7 pg/10⁵ cells).

Figure 13

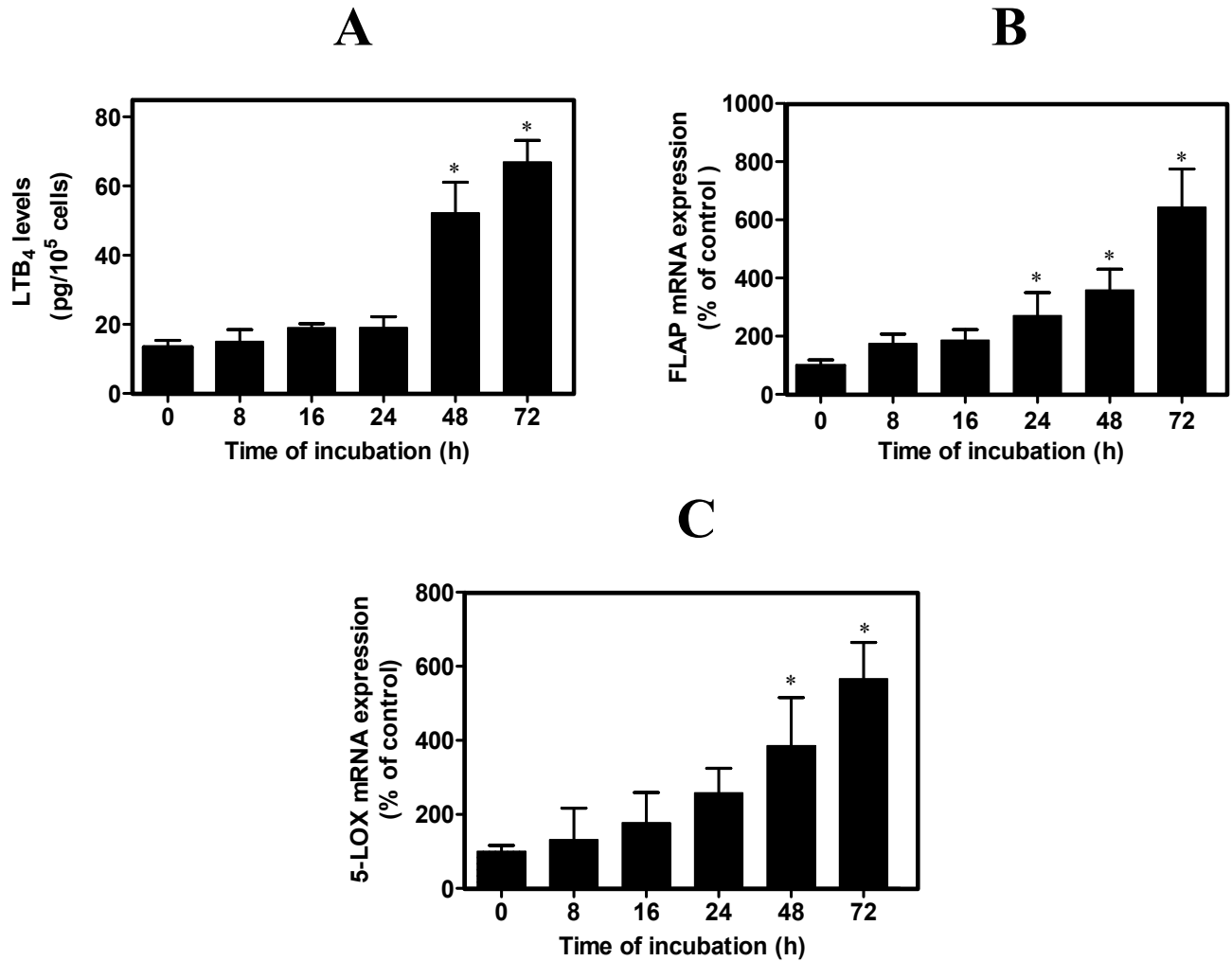


Figure 13. HNE-induced LTB₄ biosynthesis and 5-LOX and FLAP mRNA expression in human OA chondrocytes

Cells were treated with 10 μ M of HNE for different incubation time periods, as indicated above. LTB₄ production (A) was evaluated by EIA commercial kit. FLAP (B) and 5-LOX (C) mRNA expression was measured by real-time RT-PCR. The data are means \pm SEM of $n = 5$ and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA: * $p < 0.05$.

5-LOX and FLAP are essential proteins responsible for LTB₄ synthesis. To determine whether augmented LTB₄ production induced by HNE is related to 5-LOX and FLAP synthesis, we further examined the effect of HNE on their mRNA expression. As shown in Figures 4B and 4C, our data disclosed that both FLAP and 5-LOX mRNA expression rose significantly but differentially after incubation in human OA chondrocytes. FLAP mRNA expression occurred earlier, after 24 h of incubation, compared to 5-LOX (48 h). Maximum FLAP and 5-LOX levels were 644% and 566% of control values, respectively.

HNE-induced 5-LOX promoter activity

To more accurately identify whether HNE-induced 5-LOX at the transcription level, the 5-LOX promoter construct with luciferase gene reporter was transiently transfected into human OA chondrocytes, followed by stimulation with 10 μ M HNE (n = 3 independent experiments). Compared to unstimulated cells, HNE induced 5-LOX gene promoter activity in transfected chondrocytes. 5-LOX promoter activity increased significantly by 310% and 580% after 48 and 72 h of incubation, respectively (Fig. 5). These data indicated that HNE regulates 5-LOX mRNA expression at transcriptional level.

Figure 14

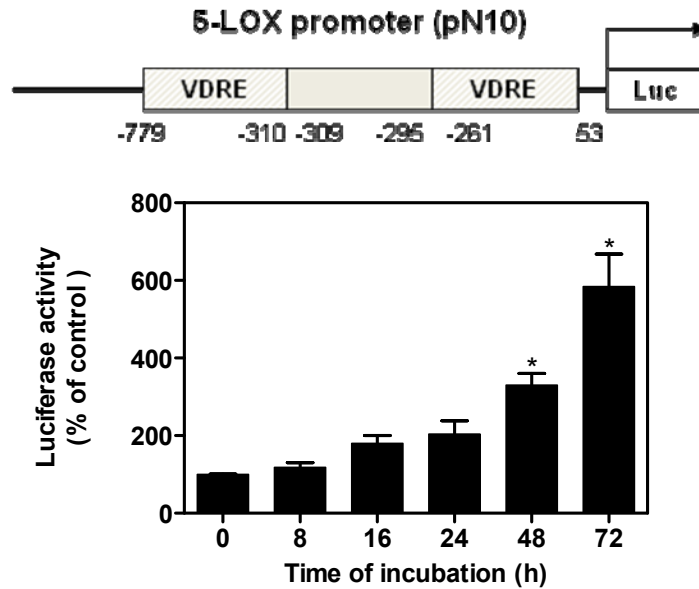


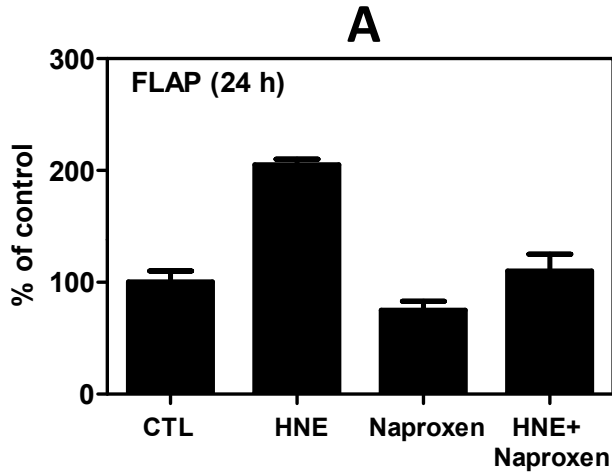
Figure 14. HNE-activated 5-LOX promoter in human OA chondrocytes

Cells were transfected with human 5-LOX promoter. The next day, they were incubated with 10 μ M HNE for increasing incubation time periods. Luciferase activity was measured in cell extracts and normalized to β -galactosidase activity. The data are means \pm SEM of $n = 3$ and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA: * $p < 0.05$.

Effect of COX inhibition on FLAP and 5-LOX expression

Further experiments were aimed at elucidating the role of PGE₂ in HNE-induced 5-LOX and FLAP expression in OA chondrocytes. Firstly, cells were treated with 50 μM naproxen (a non-selective COX inhibitor) for 1 h followed by another treatment of 10 μM HNE for 24 or 72 h (n = 3 independent experiments). Our real-time RT-PCR results demonstrated that HNE induced FLAP expression after 24 h of treatment (210% of control) and the level was even higher after 72 h (315% of control) (Fig. 6A and 6B). In contrast, FLAP expression was diminished by naproxen after 24 and 72 h (75% of control). HNE-induced FLAP expression was also abolished by naproxen, which prevents PGE₂ production. HNE did not induce 5-LOX expression after 24 h of incubation. It stimulated 5-LOX expression only after 72 h by 600% above control values (Fig. 6D). However, incubation of cells with naproxen caused a consistent increase of 5-LOX mRNA level by 330% and 570% of control values after 24 and 72 h of incubation, respectively (Fig. 6C & 6D). We observed that PGE₂ has different effects on the expression of FLAP and 5-LOX. It has been indicated that the inhibition of PGE₂ up-regulates 5-LOX while down-regulating FLAP gene expression (Martel-Pelletier et al., 2004). We showed that the production of PGE₂ during 24 h of HNE incubation prevents 5-LOX expression. However, between 24 and 72 h, the level of PGE₂ (35 ± 15 (control) vs. 55 ± 21 (72 h), not significant) was low due to the decrease in COX-2 expression, which allows 5-LOX to be expressed (Fig. 4C). All these data suggest that PGE₂ has opposite effects on 5-LOX and FLAP regulation by HNE.

Figure 15

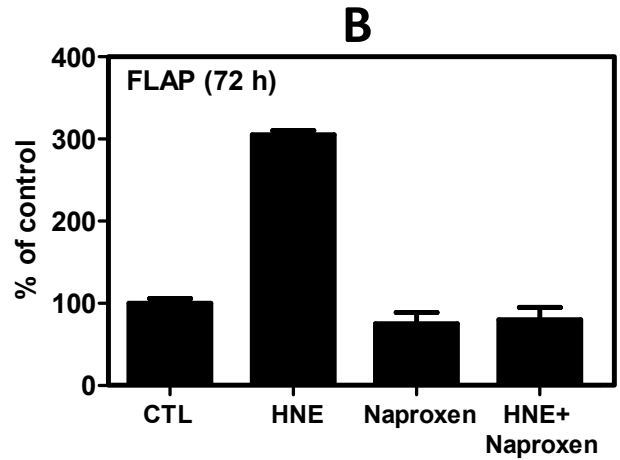


Two-way ANOVA

HNE: $F(1,8) = 47.1, p < 0.05$

Naproxen: $F(1,8) = 34.9, p < 0.05$

HNE + Naproxen: $F(1,8) = 11.7, p < 0.05$

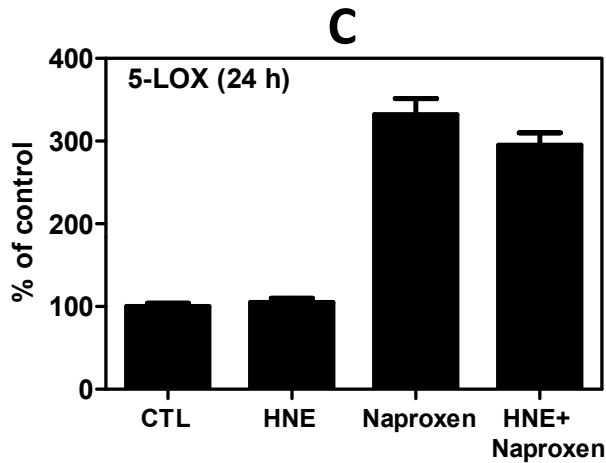


Two-way ANOVA

HNE: $F(1,8) = 92.1, p < 0.05$

Naproxen: $F(1,8) = 130.6, p < 0.05$

HNE + Naproxen: $F(1,8) = 83.6, p < 0.05$

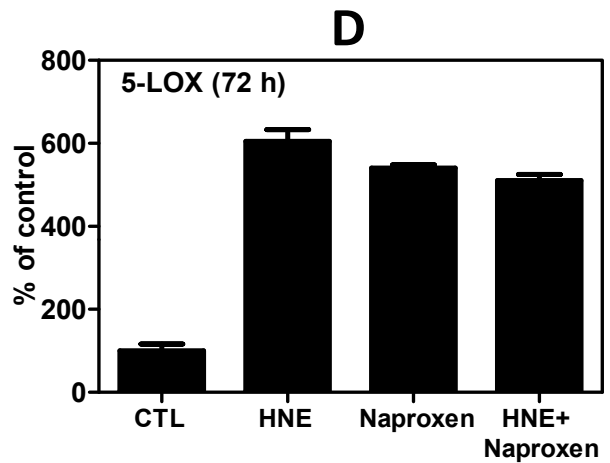


Two-way ANOVA

HNE: $F(1,8) = \text{NS}$

Naproxen: $F(1,8) = 272.3, p < 0.05$

HNE + Naproxen: $F(1,8) = \text{NS}$



Two-way ANOVA

HNE: $F(1,8) = 167.1, p < 0.05$

Naproxen: $F(1,8) = 88.2, p < 0.05$

HNE + Naproxen: $F(1,8) = 212.0, p < 0.05$

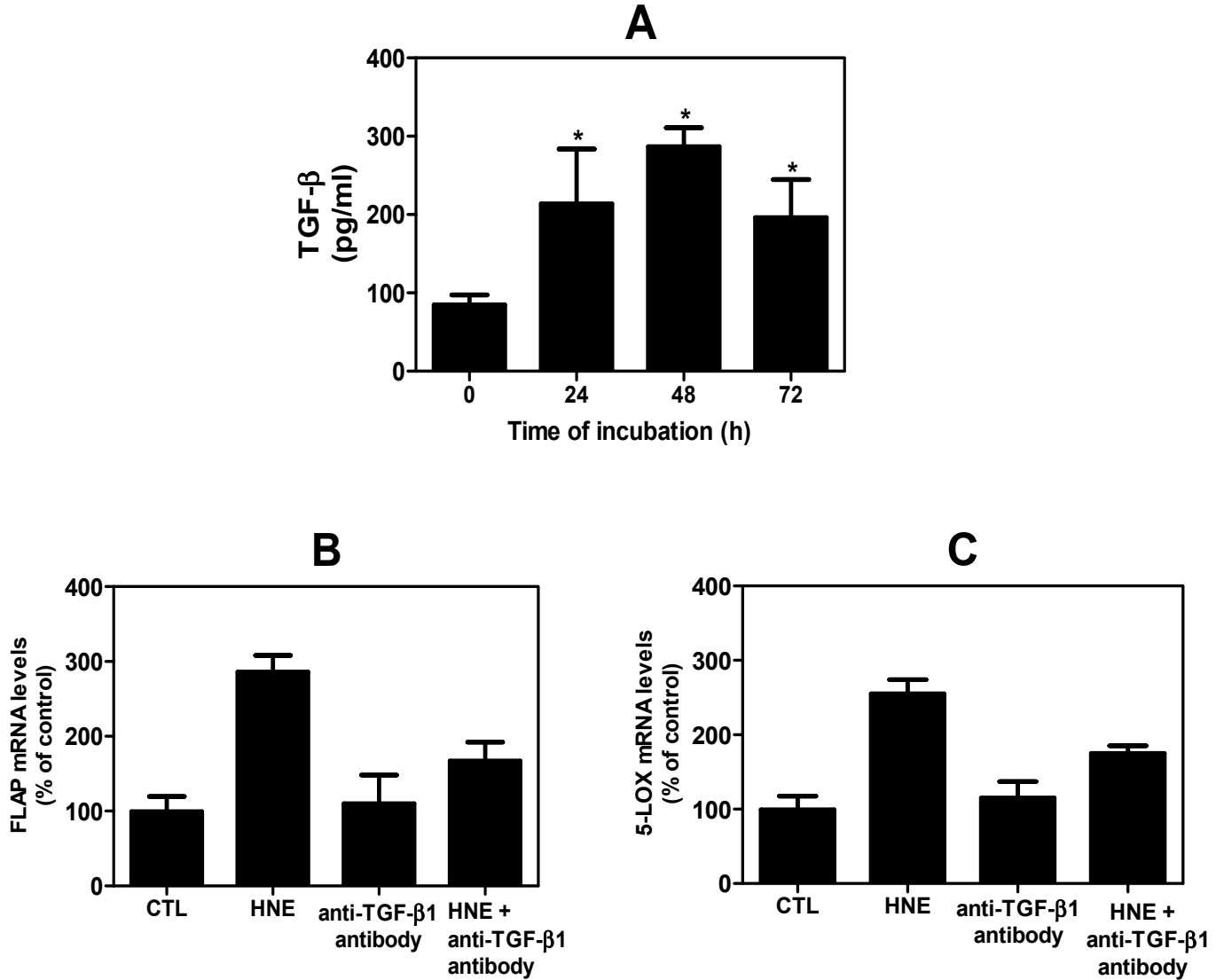
Figure 15. HNE-induced FLAP/5-LOX expression is PGE₂-dependent in human OA chondrocytes

Cells were treated with 50 μ M naproxen, 10 μ M HNE or both for 24 or 72 h. FLAP (A & B) and 5-LOX (C & D) mRNA expression was evaluated by real-time RT-PCR. The data are means \pm SEM of n = 3 and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA.

HNE induction of 5-LOX/FLAP mRNA is TGF- β 1-dependent

In other experiments, we determined whether TGF- β 1 production could be involved in HNE-induced 5-LOX/FLAP expression. Chondrocytes were treated or not with 10 μ M HNE for 72 h in the presence or absence of 100 μ g/ml of TGF- β 1 antibody. As illustrated in Figure 7, 10 μ M HNE elevated TGF- β 1 levels in chondrocyte culture media (n = 3 independent experiments) to 210, 288 and 201 pg/ml at 24, 48, 72 h of incubation respectively. Interestingly, the addition of anti-TGF- β 1 antibody (TGF- β 1 neutralization) to cultured cells attenuated HNE-induced 5-LOX and FLAP by 50-65%, from 255% to 175% for 5-LOX mRNA and from 286% to 167% for FLAP mRNA expression. It has been showed that TGF- β 1 induced a marked enhancement in FLAP and 5-LOX mRNA levels (Martel-Pelletier et al., 2004). Our data suggest that 5-LOX and FLAP regulation by HNE is partially mediated via TGF- β 1 production.

Figure 16



Two-way ANOVA

HNE: $F(1,8) = 11.9, p < 0.05$

Anti-TGF-β1 Ab: $F(1,8) = 60.3, p < 0.05$

HNE + Anti-TGF-β1 Ab: $F(1,8) = 17.1, p < 0.05$

Two-way ANOVA

HNE: $F(1,8) = 9.8, p < 0.05$

Anti-TGF-β1 Ab: $F(1,8) = 109.8, p < 0.05$

HNE + Anti-TGF-β1 Ab: $F(1,8) = 21.6, p < 0.05$

Figure 16. HNE-induced FLAP/5-LOX expression is TGF- β 1-dependent in human OA chondrocytes

TGF- β 1 level (A) was measured with ELISA commercial kits and expressed as pg/ml. (B & C) Cells were treated with 10 μ M HNE for 72 h in the presence or absence of anti-TGF- β 1 antibody, 5-LOX and FLAP mRNA levels were then assessed by real-time RT-PCR. The data are means \pm SEM of n = 3 and contrast test is against the control (time = 0 h). The significance was calculated by ANOVA: * $p < 0.05$.

CHAPTER IV: DISCUSSION

HNE: A pathophysiological modulator

Numerous studies have shown that oxidative stress was involved in the pathophysiology of OA, caused by the excessive production of ROS and an insufficient availability of antioxidants to detoxify ROS (Chen et al., 2008; Davies et al., 2008; Roman-Blas et al., 2009). ROS induces LPO of membrane polyunsaturated fatty acids, leading to the production of aldehydes from AA. Similar to free radicals, aldehydes are electrophiles that bind to the nucleophilic groups of proteins, (amino)phospholipids and nucleic acids, but their relatively longer half-life made them candidates for the propagation of damage to neighbouring cells. Among the aldehydes, HNE is considered to be the most reactive species because of its α,β -double bond, which make HNE more susceptible to nucleophilic attack (Uchida, 2003). Whether aldehydes are “second toxic messengers”, as first hypothesized by Esterbauer (Esterbauer et al., 1991), or merely represent changed markers of extensive tissue damage (Halliwell and Chirico, 1993), has long been a subject of controversies. This situation recently changed, when HNE was found to be a normal constituent of mammalian tissue membranes (Poli et al., 2008). One specific property of HNE is its ability to bind to proteins. The α,β -double bond of HNE reacts readily with specific amino acid and coenzyme residues of proteins via Michael-type addition: the sulfhydryl group of cysteine (CYS) or lipoic acid, the ϵ -amino group of lysine (LYS), or the imidazol function of histidine (HIS).

HNE occupies a prominent place in the hierarchy of LPO end-products and growing evidence supports it as a (patho)physiological modulator of signal transduction, transcriptional regulation, and post-translational modification of proteins (Uchida, 2003;Poli et al., 2008). It is found to be involved in many diseases where oxidative stress is increased, including atherosclerosis, neurodegenerative disorders and cancers (Cerbone et al., 2007;Mattson, 2009). The relevance of HNE to joint biology and pathology is now becoming clearer. In our previous study, we have reported for the first time that the level of HNE was significantly increased in synovial fluids of patients with OA compared to normal subjects and in OA chondrocytes and osteoblasts treated with ROS donors (Morquette et al., 2006;Shi et al., 2006). These data are consistent with the results reported by Grigolo and colleagues, (Grigolo et al., 2003) who found higher levels of both malondialdehyde (MDA) and HNE in human OA synoviocytes compared to normal cells. Furthermore, we demonstrated that HNE induced transcriptional and post-translational modification of Col II and MMP-13, suggesting that HNE could play a role in cartilage degradation in OA (Morquette et al., 2006). In another study, we have identified two distinct mechanisms of action of HNE in OA chondrocytes, which include upregulation of COX-2 via ATF/CREB activation and inhibition of iNOS via NF- κ B inactivation (Vaillancourt et al., 2007). In this previous study, we showed that COX-2 expression at protein and mRNA levels was detectable within 2 h of incubation with 10 μ M of HNE and plateaued at 8 h of incubation before declining afterwards. Moreover, we revealed

that HNE-induced COX-2 production expression required the activation of p38 MAPK signaling pathway. Furthermore, overexpression of WT p38 MAPK in OA chondrocytes enhanced HNE-induced COX-2 protein expression and promoter activity. Interestingly, this induction is specific for HNE since other aldehydes, such as acrolein and 2-nonenal, possessing an analogous functionality to HNE were all inactive in terms of COX-2 expression in these cells (Kumagai et al., 2000).

Regulation of COX-2 and mPGES-1 by HNE

In the present study, we have extended our investigation to evaluate the potential role of HNE in inflammatory response in OA. With the ultimate goal of clarifying this role, we documented firstly the ability of HNE to modulate COX-2 and mPGES-1 as well as the production of PGE₂, using two types of stimulation: single and repeated treatments. We have observed that 10 μ M HNE (with one treatment) induced PGE₂ release as well as COX-2 and mPGES-1 expression at protein and mRNA levels and plateaued at 8 h of incubation before declining afterwards at 16 and 24 h respectively in OA chondrocytes. These data are in concordance with our previously reported COX-2 data and are supported by other studies indicating that HNE-induced COX-2 expression and PGE₂ release declined rapidly in various cell lines, such as rat liver RL34 epithelial cells and RAW264.7 macrophages (Kumagai et al., 2000; Kumagai et al., 2002; Kumagai et al., 2004; Vaillancourt et al., 2007). Interestingly, our results indicated that the

reductions of COX-2 and mPGES-1 expression at 16 h and 24 h were completely abolished by repetitive stimulation of cells with 10 μ M HNE (8 treatments at regular interval of 2 h), supporting the hypothesis that the decrease of COX-2 and mPGES-1 expression is linked to HNE metabolism in chondrocytes. Mammalian cells have developed multiple enzymatic pathways for the detoxification of HNE. The best characterized of these enzymes include the aldehyde dehydrogenase and alcohol dehydrogenase (Esterbauer et al., 1991; Ullrich et al., 1997). The estimated half-life of HNE in cells was approximately 1 h (Pizzimenti et al., 2002).

Since the regulation of mPGES-1 by HNE had not yet been reported, we extended our investigation to determine whether changes in mRNA levels can be ascribed to changes in promoter activity. To do so, human OA chondrocytes were transiently transfected with the human mPGES-1 promoter-luciferase reporter gene. Treatment of transfected cells with 10 μ M HNE at increasing periods of incubation led to a time-dependent increase of the mPGES-1 promoter activity. These data are consistent with the regulation of mPGES-1 expression by HNE at the transcriptional level. The mPGES-1 promoter construct contains several proximal regulation sites, such as Egr-1 and NF- κ B (Cheng et al., 2004; Ackerman et al., 2008). Emerging evidence suggests that the transcriptional induction of mPGES-1 by cytokines and growth factors is controlled primarily by Egr-1 through two Egr-1 binding motifs identified in the proximal promoter region of the mPGES-1 region (Cheng et al., 2004). Thus, we hypothesized that induction of

Egr-1 activity by HNE could be the mechanism by which HNE exerts its inducer effect on mPGES-1 transcription. To gain insight into the mechanism of HNE-mediated mPGES-1 expression through Egr-1 activation, OA chondrocytes were transiently transfected with the synthetic luciferase reporter construct containing three tandem repeats of Egr-1 motif. Data showed that HNE induced the transcriptional activity of the above construct, suggesting the implication of this transcription factor in HNE-induced transcriptional activity of mPGES-1 promoter. In our Western blot analysis, we observed that 10 μ M HNE increased Egr-1 protein expression in a time-dependent manner. Recently, ROS were reported to enhance Egr-1 expression, which in turn contributes to the elevated level of mPGES-1 in inflamed cells (Hasan and Schafer, 2008). Cheng et al. 2004 examined the role of PPAR γ in the regulation of mPGES-1 in OA cartilage; the authors showed that PPAR γ activation suppresses mPGES-1 expression via negative interference with Egr-1. Altogether, this is the first evidence supporting that mPGES-1 up-regulation by HNE required Egr-1 transcriptional activity and expression in OA chondrocytes.

Regulation of FLAP and 5-LOX by HNE

FLAP and 5-LOX are two primary enzymes involved in LTB₄ biosynthesis. Moreover, recent investigations of how FLAP activates 5-LOX propose that 5-LOX does not actually bind FLAP, but rather that FLAP binds arachidonic acid and presents it to 5-LOX in such a manner that 5-LOX becomes fully

enzymatically active (Peters-Golden, 1998). The expressions of 5-LOX and FLAP have been variably documented in different cells and tissues. Usually, significant levels are found in bone marrow-derived cells, such as neutrophils, dendritic cells and some lymphocytes but 5-LOX and FLAP levels are not detectable in undifferentiated cells (Peters-Golden and Brock, 2003). 5-LOX and FLAP are highly enhanced by TGF- β 1 and dihydroxyvitamin D₃, followed by increased production of LTB₄ (Brungs et al., 1995; Martel-Pelletier et al., 2004). We deciphered the role of HNE in 5-LOX and FLAP expression in order to determine the mechanism underlying the modulation of LTB₄ biosynthesis in human OA chondrocytes.

Our data suggested a potential 5-LOX and FLAP up-regulation by HNE, occurring at least in part, at the transcriptional level, as determined by real-time quantitative RT-PCR and transient transfection experiments. HNE-induced both FLAP and 5-LOX mRNA expression in a time-dependent but different fashion. The expression of FLAP is activated earlier than that of 5-LOX, which occurs only after 48 hours of HNE stimulation. In the same pattern as 5-LOX expression, HNE enhanced LTB₄ release after 48 and 72 h of incubation. However, our attempts to detect 5-LOX and FLAP protein by Western blot in total cellular protein extracts were unsuccessful probably because of their low level as indicated by Martel-Pelletier et al., 2004. Thereafter, to determine whether the regulation of 5-LOX mRNA by HNE occurred at transcriptional level, we carried out transient transfection studies. Human OA chondrocytes were transfected with a human 5-

LOX promoter (-779 to +53) region/luciferase reporter gene construct and stimulated with 10 μ M HNE at different times of incubation. Data showed that HNE increased the luciferase activity of the 5-LOX promoter only after 48 hours of incubation. The 5-LOX promoter sequence contains consensus binding sites for several transcriptional factors, including Sp1, Egr-1, VDR, NF- κ B and AP family members. The FLAP promoter sequence contains a TATA box and glucocorticoid receptor binding sites (Peters-Golden and Brock, 2003). The investigation of the activation of the transcriptional factors associated with these promoters can help us to gain insight into how HNE regulates 5-LOX and FLAP expression at transcriptional level.

These results were consistent with a previous report of Martel-Pelletier et al., 2004 showing that 5-LOX expression is activated in late fashion, leading to the late increase in LTB₄ production (Martel-Pelletier et al., 2004). The authors showed that FLAP mRNA level was significantly enhanced after short period (20 h) of treatment with TGF- β 1 and 1,25-dihydroxyvitamin D₃, whereas 5-LOX mRNA level increased only after 72 h (Martel-Pelletier et al., 2004). These authors suggested that the reason for the late increase in 5-LOX mRNA may be that TGF- β 1 induces only an accumulation of 5-LOX mRNA and not a true up-regulation of the gene expression per se. The increase in LTB₄ production upon HNE stimulation occurred late (48 h) after the beginning of the stimulation. This coincided with the time at which the 5-LOX mRNA level was increased and the

FLAP gene expression remained high. These data confirm that LTB₄ production depends on the regulation of both 5-LOX and FLAP. Other studies demonstrated, however, that the increase in LTB₄ production was related mainly to up-regulation of the FLAP gene (Peters-Golden and Brock, 2003) or to a combination with an increase in the activity and/or expression of 5-LOX (Steinhilber et al., 1993; Brungs et al., 1995).

Role of PGE₂ and TGF-β1 in 5-LOX and FLAP expression

PGE₂ does not only participate in inflammation by itself, but may also regulate the effects of other inflammatory mediators, resulting in greater inflammatory and immune responses. Several studies reported that eicosanoid products of AA metabolism are important modulators of COX and 5-LOX pathways in various types of cells. For example, 5-LOX activity can be inhibited by some metabolites of the LOX pathway. PGE₂ can inhibit the synthesis of LTB₄ in rat neutrophils and chondrocytes (Ham et al., 1983). Another study showed that the expression of mPGES-1 is regulated by PGE₂ that may act as an enhancer of mPGES-1 in IL-1β stimulated rheumatoid synovial fibroblasts (Kojima et al., 2003). All these findings help us to better understand how PGE₂ and LTB₄ induced by HNE modulate various cell responses and AA metabolism in OA chondrocytes. Several studies showed that both FLAP and 5-LOX expressions were regulated by PGE₂ (Harizi et al., 2003; Martel-Pelletier et al., 2004). Our results put this observation in evidence. PGE₂ regulates FLAP and 5-LOX expression in different manners. The non-specific inhibitor of COXs naproxen abolishes HNE-induced

FLAP expression in OA chondrocytes after 24 and 72 h of incubation. In contrast, naproxen stimulates 5-LOX expression compared to unstimulated cells. We observed that 5-LOX is expressed only after 72 h of HNE incubation when the level of PGE₂ was low. This suggests that PGE₂ stimulates FLAP expression but inhibits 5-LOX expression. Important advances have been made concerning the role of PGE₂ in metabolism of articular tissues. It was found to be involved not only in inflammation responses but may regulate the effects of other inflammatory mediators. Therefore, more pharmaceutical companies put their interest in mPGES-1, the protein synthesizing PGE₂, to treat arthritis due to its inducible form and functional link with COX-2 (Fahmi, 2004). In contrast, PGE₂ inhibits 5-LOX after long stimulation time where 5-LOX just starts to be expressed. Our results are different than what the group of Harizi had obtained. They observed that PGE₂ reduces LTB₄ release by inhibiting FLAP via IL-10 dependent mechanism in dendritic cells, but without any effect on 5-LOX (Harizi et al., 2003). This suggests that PGE₂ regulates the expression of FLAP and 5-LOX differently depending on the types of cells.

The actual therapies to treat OA are limited to reducing the pain in affected joints by using either non-selective NSAID or the selective COX-2 drugs. Production of both PGE₂ and LTB₄ requires the existence of arachidonic acid, but their synthesis is through different pathways, COX and 5-LOX pathway respectively, therefore one of the pathways is favorably to be used depending on the condition. Long-term inhibition of COX causes the switch from COX to 5-

LOX pathway. This is observed in OA patients treated with COX-2 inhibitors (Maxis et al., 2006). In our study, we also demonstrated that lower PGE₂ production favors 5-LOX pathway in HNE-treated OA chondrocytes, leading to the synthesis of LTB₄. However, LTs have greater potential in inflammation process and may be more harmful than PGE₂ in various tissues due to their chemotactic property (Griffiths et al., 1995). For this reason, drugs that can inhibit both COX and LOX attract pharmaceutical attention in the treatment of inflammatory diseases. Tepoxalin and licofelone (ML3000) are drugs identified to have this function (Knight et al., 1996;Paredes et al., 2002). Today, licofelone is in phase III clinical development. It does not only lower the production of PGE₂ and LTB₄ but also can modify abnormal bone remodeling in OA; thus it was thought to be useful to treat OA (Paredes et al., 2002).

In addition to the involvement of PGE₂ in HNE-induced 5-LOX/FLAP, we found additional data supporting the role of TGF-β1 in this process. Our findings showed that HNE induced TGF-β1 and that TGF-β1 neutralization by using anti-TGF-β1 antibody attenuates HNE-induced 5-LOX and FLAP after 72 h of incubation. These results suggest that the regulation of 5-LOX/FLAP by HNE is mediated partially via TGF-β1 production. Leonarduzzi et al. 1997 were the first to demonstrate that HNE induced TGF-β1 production. Furthermore, there are a number of reports supporting the role of TGF-β1 in 5-LOX and FLAP expression through activation of smad 3/4 (Brungs et al., 1995;Martel-Pelletier et al.,

2004;Seuter et al., 2006). All these findings suggest that HNE stimulates the production of TGF- β 1, which probably induces the expression of 5-LOX and FLAP through smad 3/4 involvement.

CHAPTER V: CONCLUSION

High levels of ROS and HNE are present in OA synovial tissues. Our study has several important implications and suggests that HNE production in OA articular tissues contributes to inflammatory responses in OA. We investigated the effect of HNE on the production of inflammatory mediators PGE₂ and LTB₄ and on the expression of COX-2, mPGES-1 and FLAP/5-LOX, the primary enzymes responsible for their biosynthesis. HNE induces differently the production of PGE₂ and LTB₄. Depletion of PGE₂ promotes LTB₄ formation, leading to the switch of AA metabolism from COX to FLAP/5-LOX pathway. The expression of FLAP and mainly 5-LOX increase after HNE stimulation when that of COX-2 and mPGES-1 decrease. In addition, the expression of FLAP happens earlier than that 5-LOX, which induces late biosynthesis of LTB₄. Furthermore, PGE₂ and TGF-β1 have regulatory effect on the expression of FLAP and 5-LOX at mRNA level.

A lot of perspectives are given by this study. Activations of certain transcriptional factors involved in the regulation of mPGES-1 and 5-LOX by HNE remain to be investigated, such as smad 2/3 and VDR for mPGES-1 and 5-LOX promoter studies. This will help us to better understand the role of smad 2/3 and VDR in mPGES-1 and 5-LOX expression. Also, it will be interesting to study the mechanism underlying the switch of pathways in AA metabolism.

Pathogenesis of OA is mainly characterized by inflammatory and catabolic process in parallel with high presence of several mediators, including ROS, HNE,

NO and PGE₂. We gave evidence that HNE stimulates the production of pro-inflammatory mediators PGE₂ and LTB₄ in human OA chondrocytes. Importantly, these factors do not only provoke inflammatory response but may also be involved in cartilage destruction. High concentration of PGE₂ can inhibit collagen synthesis in differentiated osteoblasts and LTB₄ has been identified to be a potent factor that induces TNF- α , IL-1 β and MMPs. In a pharmaceutical point of view, inhibition of both the prostaglandins and LTs biosynthesis pathway is better than single interference due to the additive anti-inflammatory effectiveness and lower gastrointestinal toxicity. Therefore, a drug that has this effect may become an innovative treatment of OA and other inflammatory diseases. This study helps us to better understand the regulation of inflammatory factors and primary enzymes involved in OA by HNE.

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