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Regulation
of macrophage lipoprotein lipase expression
by peroxisome proliferator-activated
receptor agonists

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This thesis entitled
"Regulation of macrophage lipoprotein lipase expression
by peroxisome proliferator-activated receptor agonists"

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RÉSUMÉ

L'athérosclérose est une complication importante du diabète de type 2. La lipoprotéine lipase (LPL), une enzyme produite par les macrophages dans la paroi artérielle favorise le développement de l'athérosclérose et est surexprimée dans le diabète humain. Les *peroxisome proliferator-activated receptors* (PPARs) sont des facteurs de transcription qui médient divers effets pléiotropiques incluant la régulation de gènes impliqués dans le métabolisme lipidique tels le gène de la LPL et ceux contrôlant l'inflammation. Dans la présente étude, nous avons déterminé l'effet des agonistes de PPAR alpha (α) et gamma (γ) sur l'expression de la LPL macrophagique. Nos résultats démontrent que l'incubation des cellules THP-1 et des macrophages dérivés de monocytes humains en présence de ligands de PPAR α et PPAR γ augmentent l'expression du gène de la LPL, sa masse immunoreactive, et son activité de manière dose- et temps-dépendants. Les ligands de PPAR semblent moduler l'expression du gène de la LPL en augmentant la liaison des PPARs à l'élément de réponse des PPARs (PPRE) situé dans le promoteur du gène de la LPL. Ces agonistes agissent également à un niveau posttranscriptionnel. En effet, ils régulent l'expression génique de la LPL en augmentant la demi-vie de son ARNm dans les cellules THP-1. La présente étude démontre pour la première fois un effet direct des agonistes de PPAR sur l'expression génique et la sécrétion de la LPL macrophagique. Une compréhension détaillée du rôle des PPARs dans la régulation de la biologie vasculaire et le développement de nouveaux ligands de PPAR dissociant les propriétés pro- et anti-athérogéniques de ces agents offrira de nouvelles stratégies dans le traitement de l'athérosclérose.

SUMMARY

Atherosclerosis is a major complication of type 2 diabetes. Lipoprotein lipase (LPL), an enzyme produced by macrophages in the arterial wall favors the development of atherosclerosis and is upregulated in human diabetes. Peroxisome proliferator-activated receptors (PPARs) are transcription factors which mediate pleiotropic effects including regulation of genes involved in lipid metabolism such as LPL and control of inflammation. In the present study, we determined the effect of PPAR alpha (α) and gamma (γ) agonists on macrophage LPL control. Our results show that incubation of THP-1 and human monocyte-derived macrophages in the presence of PPAR α or PPAR γ ligands enhance LPL gene expression, immunoreactive mass, and activity in a dose-, time-, and ligand affinity-dependent manner. PPAR ligands appear to modulate macrophage LPL gene expression through PPAR binding to a specific response element termed peroxisome proliferator responsive element (PPRE) in the promoter of the LPL gene. These compounds also act at the posttranscriptional level to regulate macrophage LPL mRNA expression as reflected by the slower rate of decay of LPL mRNA in THP-1 cells exposed to PPAR α and γ ligands. The present study provides the first evidence of a direct regulatory effect of PPAR agonists on human macrophage LPL gene expression and secretion. A detailed understanding of the role of PPARs in the regulation of vascular biology and the development of novel PPAR ligands that dissociate pro- and anti-atherogenic properties will offer new strategies in the treatment of atherosclerosis.

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LIST OF ABBREVIATIONS

AA	: arachidonic acid
ACS	: acyl-CoA synthetase
AGEs	: advanced glycation end products
AP-1, -2	: activated protein –1 and 2
ApoCII	: apolipoprotein CII
BRL49653	: rosiglitazone
cAMP	: cyclic adenosine monophosphate
CHD	: coronary heart disease
COX-2	: cyclo-oxygenase 2
<i>C. pneumoniae</i>	: <i>Chlamydia pneumoniae</i>
CPT-1	: carnitine palmitoyltransferase
CS	: cystathionine synthase
DBD	: DNA-binding domain
EPA	: eicosapentaenoic acid
FAT	: fatty acid translocase
FATP	: fatty acid transport protein
FFA	: free fatty acids
FGF-2	: fibroblast growth factor –2
FSE	: fat specific element
GH	: growth hormone
GRE	: glucocorticoid responsive element

HDL	: high-density lipoprotein
HETE	: hydroxyeicosatetraenoic acid
HF-3	: hepatic factor-3
HODE	: hydroxyoctadecenoic acid
<i>H. pylori</i>	: <i>Helicobacter pylori</i>
HSPG	: heparan sulfate proteoglycans
ICAM-1	: intercellular adhesion molecule-1
IFN- γ	: interferon- γ
IL-1	: interleukin-1
IL-6	: interleukin-6
IL-8	: interleukin-8
IL-12	: interleukin-12
iNOS	: inducible NO synthase
LA	: linoleic acid
LDL	: low-density lipoproteins
LFA-1	: lymphocyte function-related antigen-1
LIF	: leukemia inhibitory factor
LP	: lipoprotein
Lp(a)	: lipoprotein (a)
Lp(β)	: lipoprotein (β)
LPL	: lipoprotein lipase
LPS	: lipopolysaccharide
LTB ₄	: leukotriene B ₄

MAPK	: mitogen-activated protein kinase
MCP-1	: monocyte chemotactic protein-1
M-CSF	: macrophage-colony stimulating factor
MMP	: matrix metalloproteinases
MTHFR	: methylenetetrahydrofolate reductase
NF- κ B	: "nuclear factor-kappa B"
NO	: nitric oxide
NOS	: nitric oxide synthase
OA	: oleic acid
Oct-1	: octamer-1
O ₂ ^{-•}	: superoxide anion
oxLDL	: oxidized low-density lipoprotein
PA	: palmitic acid
PAI-1	: plasminogen activator inhibitor-1
PDGF	: platelet-derived growth factor
PGs	: prostaglandins
PKC	: protein kinase C
PLC	: phospholipase C
PPAR	: peroxisome proliferator-activated receptors
PPRE	: PPAR response element
RAS	: renin-angiotensin system
ROS	: reactive oxygen species
RXR	: retinoic acid receptors

SA : stearic acid

SMCs : smooth muscle cells

sPLA2 : secreted phospholipase A2

SP1 : stimulatory protein1

TGF- β : transforming growth factor β

TG : triglycerides

TNF- α : tumor necrosis factor α

TZDs : thiazolidinediones

TRE : thyroid responsive element

Type II sPLA2 : type II-secreted phospholipase

VCAM-1 : vascular cell adhesion molecule-1

VEGF : vascular endothelial growth factor

VLDL : very low-density lipoproteins

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DEDICATION

I dedicate my work to my loving and caring parents, who have always been there to encourage and support me. You both taught me the importance of friendship, respect, and love, for all aspects of life. I dedicate my work to my husband and lovely daughter, whose love and strength have sustained my energy to complete this work. In addition, I dedicate this work to my brother, as well as my best friends, who through their goodness of nature have given me, as the song goes, "the wind beneath my wings."

I. INTRODUCTION

I. Introduction

I.I. Atherosclerosis

I.I.1. General

Atherosclerosis is a chronic, multifactorial and progressive disease characterized by the accumulation of lipids and fibrous elements in the large and medium arteries. Epidemiological studies over the past 50 years have identified numerous risk factors for atherosclerosis. These can be grouped into factors with an important genetic component and those that are largely environmental. Among the primary events in atherosclerosis are the accumulation of low density lipoproteins (LDL) in the subendothelial space [Guyton et al. 1996, Van De Graff et al. 1992] and the adhesion of inflammatory cells, namely monocytes and T-lymphocytes, to the endothelium. The notion that atherosclerosis is an immune-mediated inflammatory disease is now widely accepted and provides the basis for the development of new strategies in the diagnosis and management of this disease.

I.I.2. Development and progression of the atherosclerotic lesion

I.I.2.1. Endothelial dysfunction in atherosclerosis

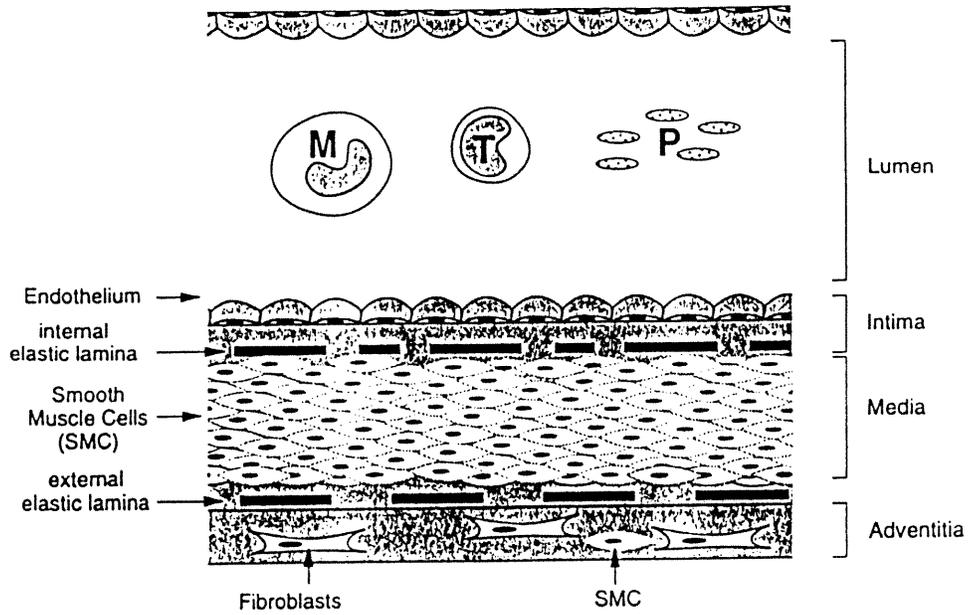
The vascular endothelium is considered to be a monolayer layer acting as a selectively permeable barrier between blood and tissues. It is a dynamic and heterogeneous organ. It has secretory, synthetic, metabolic, and immunological functions and can generate effector molecules, such as nitric oxide (NO),

prostacyclin, platelet-derived growth factor (PDGF), angiotensin II, and endothelin [Gotlieb et al. 1996] that regulate thrombosis, inflammation, vascular tone and vascular remodeling. The endothelium has important anti-coagulant and fibrinolytic functions. Endothelial dysfunction is closely linked to the occurrence of vascular diseases and precedes the development of atherosclerosis. It is characterized by major functional alterations, including decreased vasodilatory response, increased vascular permeability and enhanced pro-thrombotic and pro-coagulant activities. Increased endothelial permeability is considered as one of the earliest events in atherogenesis. Increased permeability of endothelium to macromolecules such as LDL and enhanced migration of inflammatory cells to the subintimal space through the effect of oxidized LDL (oxLDL) [Rajavashisth et al. 1990], monocyte chemoattractant protein 1 (MCP-1), interleukin-8 (IL-8), PDGF, macrophage-colony stimulating factor (M-CSF), and osteopontin [Giachelli et al. 1998] (**Figure 1, A and B**) result in the formation of early atherosclerotic lesions or fatty streaks.

I.I.2.2. Fatty-streak lesion

As mentioned above, early atherosclerotic lesions, or fatty streaks are characterized by the accumulation of LDL and the migration of monocytes and lymphocytes into the subendothelial space of the arterial wall. Fatty streaks initially consist of lipid-laden monocytes and macrophages (foam cells) mixed together with variable numbers of T lymphocytes [Ross 1999]. Rosenfeld et al. [1990] found that the formation of foam cells is mediated mainly by M-CSF, tumor

A



B

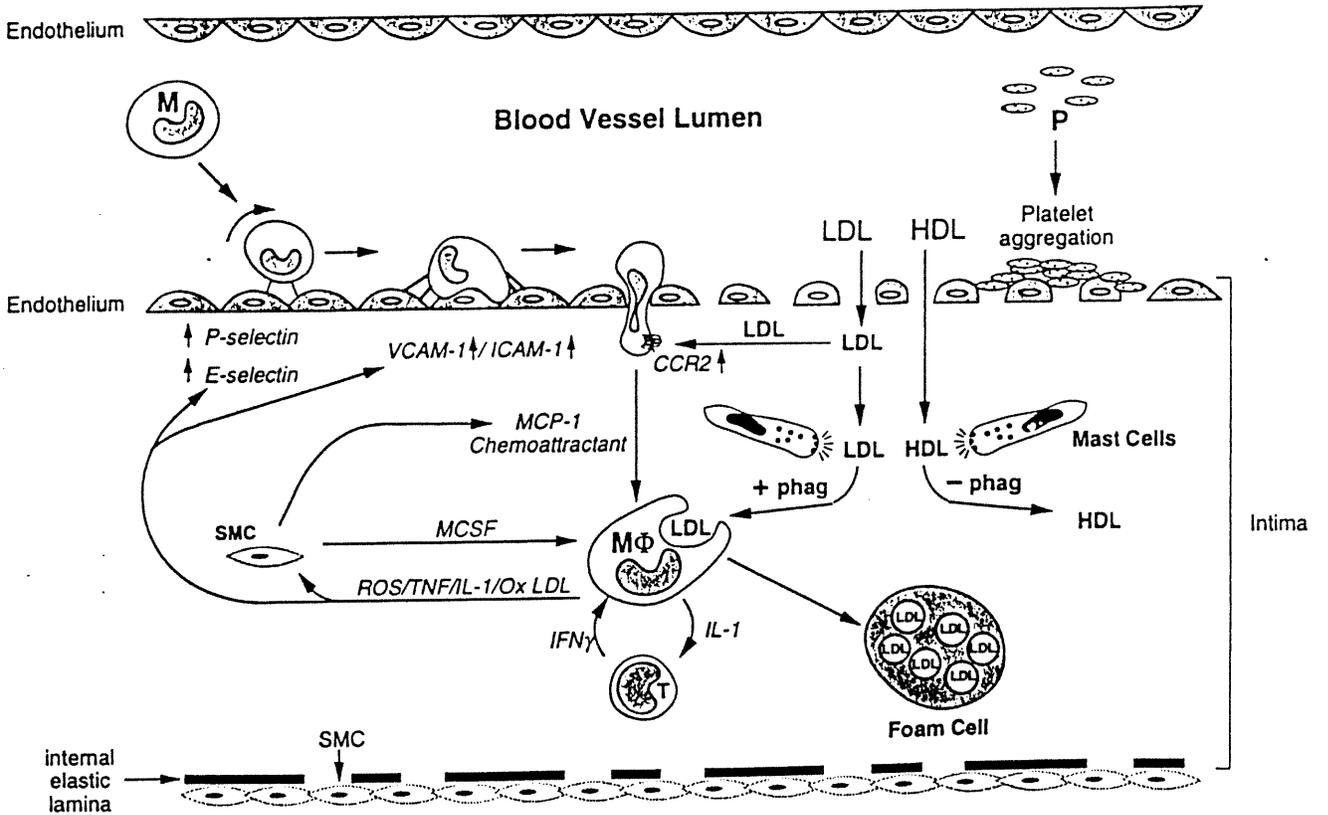


Fig. 1. Endothelial dysfunction and fatty streak formation [Sullivan et al 2000].

necrosis factor α (TNF- α), and interleukin-1(IL-1). Later these cells are joined by various numbers of smooth muscle cells (SMCs). SMC migration is stimulated by PDGF, fibroblast growth factor-2 (FGF-2) and transforming growth factor β (TGF- β) [Boring et al. 1997, Boisvert et al. 1998]. Platelet adherence and aggregation are also observed and are stimulated by integrins, P-selectin, fibrin, thromboxane A₂, and tissue factor [Ross 1999] (**Figure 1**).

I.I.2.3. Advanced, complicated lesion of atherosclerosis

As fatty streaks progress to intermediate and advanced lesions, they tend to form a fibrous cap that walls off the lesion from the lumen. This represents a type of healing or fibrous response to the injury. This fibrous cap covers a necrotic core containing leukocytes, lipid, and debris [Ross 1999].

I.I.2.4. Unstable fibrous plaques in atherosclerosis

Macrophages release metalloproteinases and other proteolytic enzymes at sites of thinning of the fibrous cap. These enzymes cause degradation of the matrix, which leads to hemorrhage from the vasa vasorum or from the arterial lumen, resulting in thrombus formation and arterial occlusion [Ross 1999]. Recent studies have shown that activated T cells stimulate metalloproteinase production by macrophages in the lesions promoting plaque instability [Schönbeck et al. 1997]. Erosion and rupture of the fibrous cap often occur at the shoulders of the lesion, where macrophages preferentially accumulate [Davies

1990]. Plaque rupture and thrombosis are notable complications of advanced lesions that lead to unstable coronary syndromes or myocardial infarctions.

I.I.3. Risk factors

I.I.3.1. Hypercholesterolemia and dyslipoproteinemia

High plasma levels of cholesterol and pro-atherogenic lipoproteins represent major risk factors for cardiovascular diseases. In particular, increased levels of circulating LDL is considered as a major risk factor of coronary heart disease and one of the earliest events in atherogenesis is the accumulation of LDL in the vessel wall. Retention and modification of LDL are key factors in lesion formation. LDL can be modified by several mechanisms, including oxidation, glycation, aggregation, association with proteoglycans, or incorporation into immune complexes [Steinberg et al. 1997, Khoo et al. 1998, Khoo et al. 1992, Navab et al. 1996]. Progressive oxidation of LDL takes place during the process of LDL particle trapping in arteries. OxLDL is internalized by macrophages through surface scavenger receptors [Steinberg et al. 1997, Khoo et al. 1992, Navab et al. 1996, Griendling et al. 1997, Han et al. 1997]. The uptake of oxLDL by macrophages results in intracellular cholesterol ester accumulation and foam cell formation. Macrophage-derived foam cells are present in all stages of atherogenesis and play a key role in the development and progression of atherosclerosis. Lipoprotein (a) (Lp(a)) closely resembles LDL in its content of cholesterol and apolipoprotein B-100 but differs by the presence of an attached glycoprotein, known as apoprotein (a). The involvement of Lp(a) in

the pathogenesis of atherosclerosis was strongly suggested by the presence of Lp(a) in human atherosclerotic lesions [Rath et al. 1989, Jurgen et al. 1993]. Numerous cross-sectional and prospective studies have also revealed associations between high plasma levels of Lp(a) and atherosclerotic vascular diseases, such as coronary heart disease and stroke [Utermann 1995, Djurovic et al. 1997]. The effect of high plasma levels of Lp(a) in development of atherosclerosis has also been well-studied in transgenic animal models [Lawn et al. 1992, Fan et al. 2001]. Although the importance of high LDL cholesterol as a risk factor for coronary artery disease is well established, the role of hypertriglyceridemia as an independent risk factor for the development of vascular diseases is still controversial. Various factors associated with hypertriglyceridemia, including dyslipoproteinemia, alterations of hemostatic processes, obesity and hypertension may account for the deleterious effect of high triglyceride levels on the atherosclerotic process [Malaguarnera et al. 2000]. Although, the meta-analysis of Austin and Hokanson, 1998 has recently suggested that hypertriglyceridemia is an independent risk factor for cardiovascular diseases, many investigators still believe that triglyceride-rich lipoproteins cannot migrate through the vascular endothelium [Faegerman, 1998]. Recently it has been suggested that postprandial hypertriglyceridemia may cause endothelial dysfunction via enhanced oxidative stress [Bae et al. 2001].

I.I.3.2. Hypertension

The renin-angiotensin system (RAS) plays an important role in the pathogenesis of cardiovascular disease. Angiotensin II, the principal product of the RAS, regulates numerous cellular responses. For example, angiotensin binds to specific receptors on SMC, eliciting the activation of phospholipase C (PLC) and leading to increased intracellular calcium concentrations and SMC hypertrophy [Gibbons et al. 1992]. Angiotensin II also decreases NO production, increases oxidative stress [Yanagitani et al. 1999] and induces the activation of NF- κ B [Kranzhöfer et al. 1999], protein kinase C (PKC) [Henrion et al. 1996] and mitogen activated protein kinases (MAPK) [Haendeler and Berk, 2000]. This factor also leads to increased expression of adhesion molecules, such as vascular cell adhesion molecule-1 (VCAM-1) and intercellular adhesion molecule-1 (ICAM-1) [Conzalez et al. 2000] contributing thereby to the accumulation of inflammatory cells in the vessel wall. High angiotensin II levels in hypertensive patients favors atherogenesis by stimulating the growth of SMC [Chobanian et al. 1996].

I.I.3.3. Diabetes

Patients with diabetes are at high risk of cardiovascular diseases [Garcia et al. 1974]. Several risk factors associated with diabetes including dyslipidemia, obesity, hypertension, hyperglycemia and hyperinsulinemia contribute to the accelerated atherosclerosis in human diabetes. Recent studies suggest that hyperglycemia is a major risk factor for the development of diabetic

macrovascular complications (UK Prospective Diabetes Study, 1998). Multiple biochemical alterations including the polyol pathway, advanced glycation end products (AGEs), oxidative stress, PKC activation seem to be involved in the development of diabetic vasculopathies.

I.I.3.4. Homocysteine

Homocysteine is a non-protein-forming sulfhydryl amino acid derived from methionine metabolism. Hyperhomocystinemia is considered to be a novel risk factor for atherosclerotic disease in the coronary, cerebral, and peripheral arterial circulation. Hyperhomocystinemia seen in general adult populations is associated with cystathionine synthase (CS) and methylenetetrahydrofolate reductase (MTHFR) deficiencies [McCully 1996, Mudd et al. 1985, Nehler et al. 1997, Nyard et al. 1997, Malinow 1995]. Mild homocysteine increase occurs in 20-30% of patients with atherosclerotic disease and usually, treatment with folic acid returns plasma homocysteine concentrations to normal [Yarnell 1991]. Ongoing trials are actually assessing the effect of folate treatment on outcomes.

Several mechanisms have been proposed to explain the atherogenic properties of homocysteine. These mechanisms include endothelial dysfunction [Brattström 2000], oxidative damage [Wall et al. 1980, Starkebaum et al. 1986], SMC proliferation [Tsai et al. 1994], activation of the PKC/c-fos signalling pathway [Dalton et al. 1997], platelet aggregation [Durand et al. 1997] and activation of the coagulation pathway [Welch et al. 1997].

I.I.3.5. Coronary artery calcification

Ectopic vascular calcification occurs commonly in atherosclerosis. Its presence and location in coronary arteries have been examined by ultrafast computed tomography scanning, providing interesting new information in patients [Fallavallita et al. 1994, Janowitz 2001]. The recent finding that TNF- α promotes, through the cyclic adenosine monophosphate (cAMP) pathway, osteoblastic differentiation of vascular cells [Tintut et al. 2000] suggests a role of pro-inflammatory cytokines in the vascular calcification process.

I.I.3.6. Family history, age and gender

It is clear that positive family history, advanced age and male gender increase the risk of developing coronary artery disease [Sianiko et al. 1990]. Numerous studies have shown that individuals with a family history of coronary heart disease (CHD) are at higher risk of atherosclerosis. For example, Pankow et al. [1997] investigated family CHD risk scores and found higher traditional CHD risk factors in individuals with a family history of heart disease.

Because of protection by female hormones, the onset of CHD tends to be delayed in women by about 10 years with some catch-up after menopause [Matthews et al. 1989]. This is the rationale for the administration of estrogens to post-menopausal women.

I.I.3.7. Obesity and smoking habit

The relationship between being overweight and cardiovascular disease was a matter of debate for many years. Obesity, especially visceral obesity, is associated with a cluster of metabolic complications increasing the risk of type 2 diabetes and CHD. For example, obese patients with visceral obesity show increased glycemic and insulinemic responses to an oral glucose load compared to normal weight individuals or compared to obese individuals with low visceral adiposity [Kothari et al. 1998]. Viscerally obese patients are also characterized by an unfavourable plasma lipid profile which includes elevated triglyceride and apolipoprotein B concentrations, reduced high density lipoproteins (HDL)-cholesterol levels as well as increased proportion of small, dense LDL particles [Despres et al. 2000].

Despite the epidemiological evidence linking cigarette smoking with cardiovascular disease, the precise components of cigarette smoke responsible for this relationship and the mechanisms by which they exert their effect have not yet been fully elucidated. Cigarette smoke is a complex mixture and only a few components have been extensively studied. Nicotine and carbon monoxide are much less damaging than is whole smoke. There is considerable evidence that cigarette smoking can result in both morphological and biochemical endothelial disturbances both *in vivo* and *in vitro* [Michael Pittilo 2000].

I.I.3.7. Infection

Herpes viruses and *Chlamydia pneumoniae* are two main types of infectious microorganisms that have been shown to correlate with the incidence of atherosclerosis [Libby et al. 1997, Hendrix et al. 1990, Jackson et al. 1997]. Both organisms have been found in atheromatous lesions in coronary arteries [Hendrix et al. 1990, Jackson et al. 1997]. The role of infectious agents in the pathogenesis of atherosclerosis is discussed in the following section.

I.I.4. Pathogenesis of atherosclerosis

I.I.4.1. Endothelial dysfunction hypothesis

As mentioned above, the vascular endothelium is an unicellular layer acting as a semi-permeable membrane between blood and tissues. It has been demonstrated that the endothelium performs a large range of important biological functions, participating in several metabolic and regulatory pathways.

The endothelium retains a reduced vasomotor tone, prevents leukocyte and platelet adhesion, and inhibits the proliferation of vascular SMCs under physiological conditions. Conversely, endothelial dysfunction plays a pathogenic role in the initial development of atherosclerosis [Ross 1993, Choen 1995, Schwartz et al. 1981]. Abundant evidence has proven that endothelial dysfunction precedes the development of atherosclerotic lesions [McLenachan et al. 1990, Harrison et al. 1987, Fish et al. 1988].

Ludmer et al. [1986] demonstrated that atherosclerotic coronary arteries contracted in response to intracoronary infusion of acetylcholine, whereas normal

coronary arteries became dilated. Later, Celermajer et al. [1992] documented endothelial dysfunction in children and otherwise healthy young adults with risk factors for atherosclerosis.

Besides locally increased antagonists that can reduce endothelium-derived vasodilators, two other factors involved in endothelial dysfunction have been well-studied. NO has been frequently considered to be the major cause of endothelial dysfunction in various clinical conditions. It has been established that NO released from the endothelium is decreased in patients with coronary atherosclerosis [Ludmer et al. 1986, Vita et al. 1989]. Diminished NO production leads to decreased endothelium-dependent vasodilation, increased platelet aggregation and adhesion of monocytes to the endothelium, and enhanced vascular SMC proliferation.

Another mechanism involved in endothelial dysfunction is the elevation of endothelin-1. High plasma endothelin-1 concentrations have been reported in myocardial infarction, cardiogenic shock, unstable angina pectoris, coronary artery disease in general, cardiac failure, and essential hypertension [Cernacek et al. 1989, Shichiri et al. 1990].

I.I.4.2. Lipid infiltration hypothesis

In the early 19th century, von Rokitansky [1852] found that the most characteristic feature of atherosclerosis is cholesterol accumulation in the intima. Much later, the lipid infiltration hypothesis was supported by the studies of Deng et al. [1993] demonstrating the presence of atherosclerotic lesions in rabbits fed

a cholesterol-enriched diet. The lipid infiltration hypothesis states that increased circulating levels of LDL lead to their infiltration in the vessel wall and thereby to the development of atherosclerosis. This hypothesis has been reinforced over the past years by clinical studies showing a direct correlation between plasma cholesterol levels and CHD and demonstrating a reduction of cardiovascular events by normalization of plasma lipid levels [Castelli et al. 1990, Lipid Research Clinics Program 1984, Brown et al. 1990].

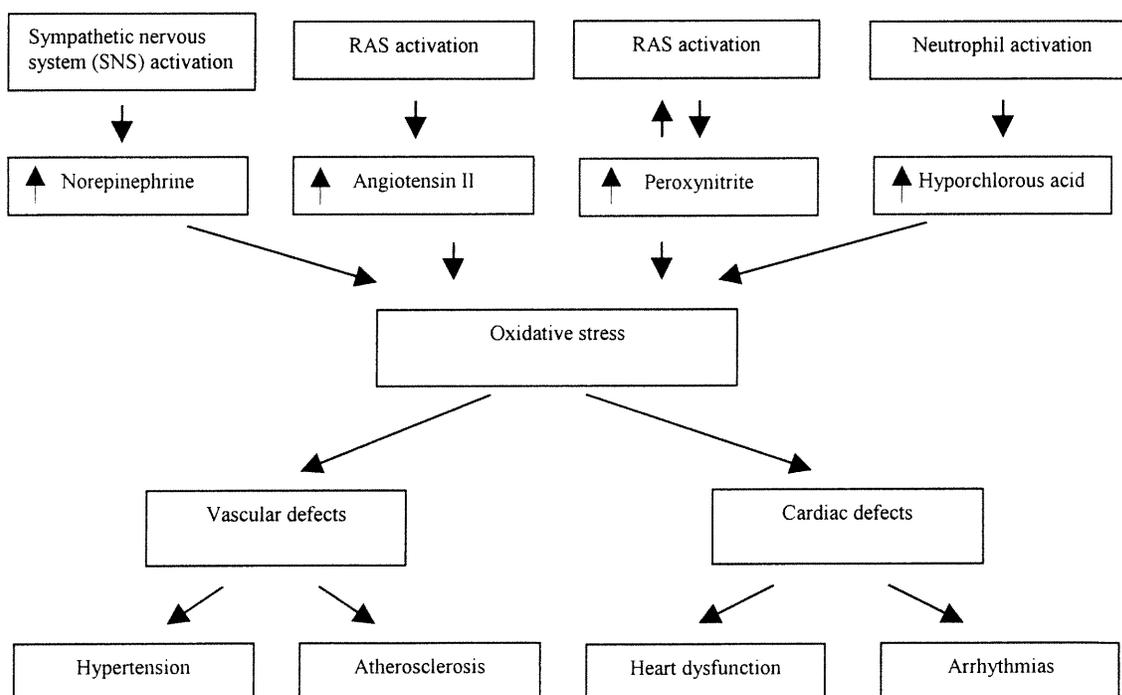
The lipid infiltration theory alone does not explain everything. Indeed, high cholesterol levels and inflammation appear to be two essential components in the pathogenesis of atherosclerosis and both components seem to play a key role in the formation of the atherosclerotic lesion. OxLDL particles are carriers of cholesterol into arterial wall macrophages [Brown et al. 1983, Steinberg et al. 1989], and macrophages in turn become activated by these particles [Wick et al. 1995].

I.I.4.3. Oxidative stress hypothesis

This hypothesis proposes that many pathogenic mechanisms in atherogenesis may result from increased oxidative stress resulting from increased reactive oxygen species (ROS) production. ROS are reactive chemical entities that can be classified into two categories: free radicals, and non-radical derivatives [Kukreja et al. 1994]. ROS have been implicated in the genesis of vascular abnormalities and subsequent cardiovascular tissue injury [Kukreja et al. 1992, 1994]. It has been suggested that ROS may contribute to endothelial

dysfunction in patients with atherosclerosis and that antioxidants such as probucol and ascorbic acid may improve endothelium-dependent relaxation in these subjects [Anderson et al. 1995]. Oxidative inactivation of NO by the superoxide anion (O_2^-) has also been proposed as a plausible explanation for endothelial dysfunction [Harrison 1997]. Finally, oxidation of NO by O_2^- may also play a role in the oxidation of lipoproteins [Beckman et al. 1990].

Because oxLDL plays a key role in atherosclerosis, treatment with antioxidants might be beneficial in preventing or retarding its progression. However, data from randomized intervention trials are still controversial [Aviram 1999] and therefore do not allow for the time being any population-wide recommendations regarding antioxidant supplementation for prevention of cardiovascular disease. A schematic diagram depicting the role of extra-cardiac and extra-vascular systems in the genesis of oxidative stress and development of cardiovascular alterations is presented below. Fig.2 [Dhalla et al. 2000].



I.I.4.4. Hypothesis of infection

There is reasonable evidence suggesting that infection may contribute to the pathogenesis of atherosclerosis. Several studies have addressed the possible role of infectious agents in the development of atherosclerosis. One interesting candidate is *Chlamydia pneumoniae* (*C.pneumoniae*), a human respiratory pathogen, which has been linked in both sero-epidemiological and immunohistochemical studies with CHD [Saikku et al, 1998, Elkind et al, 2000, Schmidt et al, 2000]. Results of animal experiments and preliminary intervention trials with antibiotics [Gurfinkel et al 1999] further suggest a role of this pathogen in atherogenesis. A second infectious agent is *Helicobacter pylori* (*H. pylori*), a pathogen involved in peptic ulcer [Danesh et al. 1997]. *H. pylori* DNA is evident in a considerable number of atherosclerotic plaques, but is absent in healthy vascular walls [Farsak et al. 2000].

These infectious processes could begin in early childhood and only become manifest with aging. An immunological imbalance could develop gradually when defense mechanisms begin to deteriorate as a result of advancing age and accompanying diseases.

I.I.4.5. Hypothesis of inflammation

Atherosclerosis is an inflammatory disease. Several studies have firmly established that immune mechanisms play a key role in the pathogenesis of atherosclerosis. In fact, atherosclerotic lesions can best be described as an

inflammatory disease because they represent a series of highly-specific cellular and molecular responses [Ross et al. 1973, 1986, *Idem* 1976].

Atherosclerosis is a chronic inflammatory response that causes activation of resident macrophages, mast cells, and T lymphocytes with recruitment of leukocytes and their precursors. There is evidence of subpopulations of activated and non-activated macrophages [Galis et al. 1994, Falkenberg et al. 1998] and T cells [de Boer et al. 1997] within plaques. Most studies that relate to inflammation and atherosclerosis focus on macrophages, the obvious reason being that these cells play an important role not only as lipid scavenger cells but also as immunocompetent cells secreting pro-inflammatory cytokines and growth factors. Indeed, activated macrophages are a major source of various molecules, such as PDGF and (interleukin-6) IL-6, which induce SMC migration and proliferation within the neointima of developing plaques [Jang et al. 1993, Hansson et al. 1994]. Macrophages affect endothelial-dependent vasoconstriction/vasodilation via the release of non-oxidative and oxidative products [Marceau 1996]. More than 85% of macrophages within atherosclerotic lesions express the lymphocyte function-related antigen-1 (LFA-1), [Watanabe et al. 1998], a monocyte/macrophage ligand for ICAM-1. This adhesion molecule plays an important role in atherosclerosis lesion formation by inducing monocyte binding to endothelium and monocyte/macrophage retention in the vessel wall.

Lymphocytes are present in each phase of the atherosclerotic process. Although T cells are not as common as macrophages in the atherosclerotic lesion, they could play an important regulatory role in atherogenesis because of

their capacity to control macrophage activity and inflammation. Among the cytokines that resting T cells secrete, interferon- γ (IFN- γ) is the major priming signal for macrophage activation. It leads to the production of macrophage-derived cytokines, such as IL-1 and TNF- α , as well as to the secretion of matrix metalloproteinases (MMP) [Moon et al. 1988. Advanced human plaque, which is dominated by T cells of the Th1 type, i.e. INF- γ -producing CD4⁺ T cells, is possibly due to the local vascular production of IL-12 [Uyemura et al. 1996]. T cells within atherosclerotic lesions could also react with self-antigens and thus generate an autoimmune response with inflammatory changes characteristic of these lesions. Recently, it was proposed that a significant proportion of plaque CD4⁺ T cells recognize oxLDL as an HLA-D^R-dependent antigen [Stemme et al. 1995]. This indicates that oxLDL not only activates, and is internalized by, macrophages but is also recognized as a local antigen by immune cells of the plaque.

Recent studies have provided evidence that mast cells are present in various stages of atherosclerotic lesions. Mast cells can assist in the recruitment of monocytes and lymphocytes into vascular tissues, thereby propagating the inflammatory response. Mast cell enzymes might activate pro-metalloproteinases, destabilizing atheromatous plaques via the secretion of pro-inflammatory cytokines. Mast cells can also facilitate foam cell formation by promoting cholesterol accumulation.

Inflammatory cells infiltrate vascular tissues by releasing cytokines and proteases. They also induce ROS and trigger vasoconstriction/vasodilation

[Peitzman et al. 1995], thrombus formation [Lassila et al. 1993, Nielsen et al. 1998], neointimal growth [Hansson et al. 1994, Wilensky et al. 1995], angiogenesis, and tissue remodeling [Wilensky et al. 1995, Mach et al. 1999].

Overall, the inflammatory response and cell-mediated immunity could initially be protective in atherogenesis, but persistent and excessive inflammatory responses will favor progression of the disease. Continued inflammation results in enhanced cycles of accumulation of mononuclear cells that proliferate in the plaque and induce the growth of SMC that become intermixed with the area of inflammation to form an intermediate lesion. The formation of fibrous tissue leads to further restructuring of the lesion, so that a fibrous cap, the so-called advanced and complicated lesion, covers it.

I.II. Lipoprotein lipase (LPL)

I.II.1. General

LPL is the major enzyme responsible for the hydrolysis of triglycerides (TG) in chylomicrons and very low-density lipoproteins (VLDL). Studies have shown that inhibition of the enzyme by antisera leads to the accumulation of TG in plasma [Ma et al. 1991, Kyte et al. 1982]. Patients with type 1 hypertriglyceridemia, a rare heritable disease, have decreased plasma LPL activity, with high plasma TG and low HDL concentrations. LPL is mainly synthesized by adipose and skeletal muscle tissues. However, it is also produced by many other tissues including heart, lung, mammary gland, kidney, adrenal gland, testes, ovaries, brain, liver and macrophages. LPL synthesized by these

tissues, is secreted to the cell surface, and transported, by an unknown mechanism, to the capillary endothelial surface where it binds to heparan sulfate proteoglycans (HSPG) [Enerbäck et al. 1987, Cheng et al. 1990]. In the body, LPL plays a directive function, such as fatty acid flux to given tissues, reflecting its activity on the capillary bed of these tissues [Parkin et al. 1982].

I.II.2. LPL properties

I.II.2.1. LPL gene organization

The human LPL gene [Kirchgessner et al. 1989, Deeb et al. 1989] is approximately 30 kb pairs with 10 exons in the mRNA-specifying sequence. Exons 1-9 are 105-276 bp in size, whereas exon 10 with the specific entire 3' noncoding sequence is 1,948 bp in length. The organization of human LPL gene is shown in **Figure 3**.

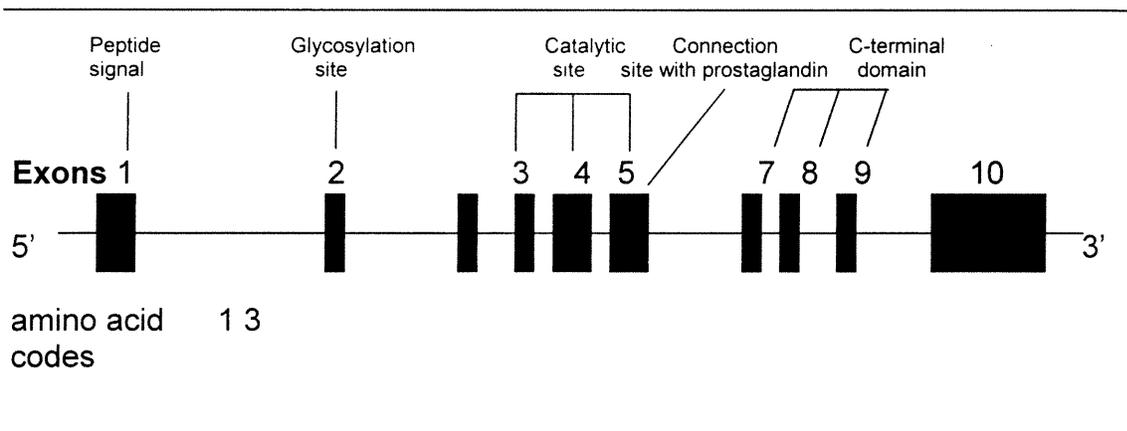


Figure 3. Diagrammatic representation of the LPL gene and its structure-function relationship. [Kirchgessner et al. 1989, Deeb et al. 1989].

I.II.2.2. Structural and functional domains of LPL

I.II.2.2.1 Tertiary structure

At present, the LPL crystal structure is not known. The crystal structure of hepatic lipase [Winkler et al. 1990] can serve as a good model for the crystal structure of LPL. The LPL molecule is folded into two domains. The large N-terminal domain comprises residues 1-336, a typical α/β structure dominated by a central β -sheet. The C-terminal domain is the β -sandwich type with four anti-parallel strands, formed by two layers of the β -sheet. The α -carbon backbone of the molecule is highlighted with the β -structures and disulfide bonds. The N-terminal domain forms a nearly spherical, globular structure, whereas the smaller C-terminal domain is elongated like a bent cylinder, which is attached to the spherical N-terminal domain.

I.II.2.2.2. Apolipoprotein CII (ApoCII)-binding site

Activation of LPL by apoCII is required for maximal LPL activity [Flier et al. 1989]. Under X-ray crystallography of hepatic lipase, the N-terminal peptide appears as part of a cleft structure. Further mapping is required to determine whether the corresponding cleft of LPL is the apoCII-binding site. Because of competitive inhibition of the charged carboxyl terminal tetrapeptide of apoCII [Cheng et al. 1990], the site could also include regions of high positive charge, such as heparin-binding sites [Martin et al. 1988]. This is consistent with the

finding that heparin is a competitive inhibitor of apoCII in LPL activation [Posner et al. 1983].

I.II.2.2.3. Heparin-binding domain

Many studies have shown the importance of the N-terminal domain of the LPL molecule for its binding to HSPG expressed on endothelial cell surfaces [Wong et al, 1991, Santamarina-Fojo et al, 1994]. The heparin-binding domain is located in exon 6 of the human LPL gene [Deeb et al. 1989]. In contrast, the role of the C domain in LPL binding to HSPG is still controversial [Wong et al, 1991, Santamarina-Fojo et al, 1994, Ma et al, 1994].

I.II.2.2.4. Glycosylation sites

Glycosylation is required for the maturation of LPL and the secretion of an active enzyme. There are three N-glycosylation sites in LPL: Asn-43, Asn-257, and Asn-359 [Semb et al. 1989, Semenkovich et al, 1990]. However, only Asn-43 is important for the secretion and the functional activity of the enzyme [Semenkovich et al. 1990], while substitution of Asn-257 and Asn-359 does not appreciably affect LPL activity.

I.II.3. Structure and function of apoCII

I.II.3.1. Active site domain of apoCII

The presence of apoCII increases basal LPL activity. The active-site domain of apoCII for LPL activation has been studied either with proteolytic fragments or synthetic apoCII-peptides. Based on cDNA sequencing, the human apoCII sequence contains 79 amino acids [Jackson et al. 1984, Myklebost et al. 1984]. ApoCII has two methionine residues. One is located at position 9, and the other at position 60. Both the N-terminal (apoCII₁₋₉) and the center fragments (apoCII₁₀₋₆₀) have no effect on LPL activation. Only the C-terminal peptide (apoCII₆₁₋₇₉) causes a four-fold increase in LPL activity.

I.II.3.2. ApoCII gene mutation

A deficiency of apoCII induces reduction of LPL activity, leading to hyperchylomicronemia, a rare genetic syndrome, described in 1978 by Breckenridge et al. [Breckenridge et al, 1978].

I.II.4. Role of LPL in lipid metabolism

While dietary lipids are transported in the bloodstream as chylomicrons, VLDL are synthesized in the liver. These TG-rich lipoproteins must be enzymatically processed to release free fatty acids (FFA), which are either re-esterified and stored in adipocytes or metabolized as energy sources in peripheral tissues [Robinson 1963, Ladu et al. 1991]. LPL plays a central role in the metabolism of chylomicrons and VLDL.

I.II.5. Mechanisms of LPL regulation

I.II.5.1. Transcriptional regulation

Several studies have demonstrated that *cis* elements present in the promoter of the LPL gene are involved in the transcriptional control of LPL. These elements include the octamer-1 (Oct-1), the glucocorticoid responsive element (GRE), the fat specific element (FSE), the thyroid responsive element (TRE), the activated protein -1 and 2 (AP-1, -2), the stimulatory protein1 (SP1) and the lipoprotein (LP) elements [Enerbäck et al. 1993]. The role of these elements in the regulation of the LPL gene has been examined by in vitro protein/DNA-binding analyses and by transient transfection assays [Hua et al. 1991, Previato et al. 1991, Enerbäck et al. 1992, Currie et al. 1992]. It has been demonstrated that Oct-1 binding to the promoter of the LPL gene is required for the transcription of the gene. Moreover, it has been reported that a transcriptional factor named *NF-Y* binds specifically to the CAAT motif located at position -65 relative to the transcriptional start site [Currie et al. 1992]. *Trans*-acting factors have also been shown to bind to the *cis*-element LP- α (-702 to -666) and LP- β (-468 to -430) [Enerbäck et al. 1992]. These *trans*-acting factors recognize a DNA element in common with the *fork head*/hepatic nuclear factor-3 (HNF-3) family of transcription factors [Lai et al. 1991].

Some experiments have used anti-sense DNA methods to provide evidence of transcriptional regulation of LPL expression. Two transcriptional DNA-binding proteins that play a role in controlling adipogenesis have been examined in this manner. They are c-fos, which is a component of the AP-1

complex [Barcellini-Couget et al. 1993], and the CCAAT-enhancer-binding protein or C/EBP [Samuelsson et al. 1991, Umek et al. 1991, Lin et al. 1992]. Recently, Sartippour et al. [1998] have reported that exposure of macrophages to high glucose sequentially induces PKC activation and its well-known target, *c-fos*, which, by interacting with the AP-1 sequence, leading to increased transcription of the LPL gene.

In transfection studies, deletion constructs have served to determine that both positive and negative regulatory elements exist within the 5' flanking region of the LPL promoter [Previato et al. 1991, Enerbäck et al. 1992]. In stable transfection experiments, it has been found that linkage of either the LP- α or LP- β sequence to a constitutively expressed promoter is sufficient to increase the reporter gene expression [Enerbäck et al. 1992].

Recently it has been demonstrated that activators of peroxisome proliferator-activated receptors (PPAR) alpha (α) and gamma (γ) regulate the transcription of the LPL gene in adipocytes [Schoonjans et al. 1996a]. This effect results from the formation of PPAR/retinoid X receptor (RXR) heterodimers and the binding of this complex to the cis-acting regulatory PPAR response element (PPRE) localized in the LPL promoter [Schoonjans et al. 1996b].

I.II.5.2. Post-transcriptional regulation

I.II.5.2.1 Stability of LPL mRNA

Little is known about the stability of LPL mRNA. White et al have reported that lipopolysaccharide (LPS) decreases the stability of human monocyte/macrophage LPL mRNA [White et al, 1988]. IFN γ also decreases by 50 % the stability of LPL mRNA in human monocytes/macrophages [Jonasson et al, 1990]. Recently, Ranganathan et al have demonstrated that translation of adipocyte LPL is regulated by a catecholamine-activated protein that binds to the 3' untranslated region of the LPL mRNA [Ranganathan et al, 1997]. PKC-induced phosphorylation of this protein has been suggested to be involved in the control of LPL translation [Ranganathan et al, 1998].

I.II.5.2.2. Glycosylation

There are three putative sites for N-linked glycosylation (Asn-X-Ser/Thr) located at Asn-43, Asn-257, and Asn-359 in the cDNA sequences of human, murine, and guinea pig LPL [Semb et al. 1989]. Glycosylation of LPL at the first N-linked glycosylation site is essential for catalytic activity and secretion [Semenkovich et al, 1990]. A number of studies have demonstrated the importance of glycosylation using inhibitors of glycosylation and inhibitors of glycoprotein transfer from the rough endoplasmic reticulum (RER) to the Golgi [Ben-Zeev et al. 1992, Simsolo et al. 1992, Casroll et al. 1992, Masuno et al. 1992].

I.II.5.2.3 Heparin-binding activity

An additional post-translational regulatory site is provided by the interaction of secreted LPL with cell surface HSPG. This pathway, with LPL bound on the cell surface, then either released into serum or internalized and degraded within the lysosomal compartment of the cell, provides a rapid mechanism for modulating plasma LPL levels [Cisar et al. 1989]. Binding of LPL to endothelial cells is heparin-sensitive indicating thereby that HSPG mediate this interaction [Shimada et al. 1981, Friedman et al. 1982]. There are two proteins, which may be responsible for the binding and transport of LPL within endothelial cells. One is a HSPG of 220 KD with a protein core of 50 kDa [Saxena et al. 1991], the other is a 116 kDa heparan releasable protein with a high affinity for both LPL and proteoglycans [Sivaram et al. 1992]. Evidence has recently been provided that transcytosis of LPL across endothelial cells requires both HSPG and the VLDL receptor [Obunike et al. 2001].

I.II.6. Physiological regulators

I.II.6.1. Nutrients

It is well-known that nutritional status is the first physiological regulator of LPL activity in the adipose and muscle tissues. In contrast, there are few data at present on the effects of fasting and refeeding on macrophage LPL control.

It has been demonstrated that in normal or lean subjects within 20% of ideal body weight, adipose LPL levels decrease up to 75% with caloric restriction [Taskinen et al. 1979, Lithell et al. 1978, Farese et al. 1991, Iverius et al. 1985].

In contrast, muscle LPL activity increases in the fasting state [Farese et al. 1991, Olivecrona et al, 1995]. In the post-prandial state, adipose LPL activity increases whereas muscle LPL activity decreases. Regulation of LPL in the fasting and post-prandial states has been postulated to involve post-translational mechanisms.

Glucose is a nutritional factor that modulates the expression of macrophage LPL expression. Indeed, Sartippour et al. [1998] reported that macrophages cultured in the presence of high glucose concentrations overproduce LPL. The regulation of macrophage LPL gene expression by glucose is exerted at the transcriptional level and implies the activation of PKC and the protooncogene c-fos [Sartippour et al. 1998].

LPL generates fatty acids by its hydrolytic action and evidence has been provided that LPL binds fatty acids [Edwards et al, 1994]. High level of fatty acids in the plasma facilitates the dissociation of LPL from its connection sites [Karpe et al. 1992, Peterson et al. 1990] and thereby regulates the release of LPL from the endothelium. Fatty acids are significant energy substrates for macrophages [Yin et al. 1997, Newsholme et al. 1987] and may therefore regulate macrophage LPL expression. This hypothesis has been supported by the findings that omega-3 fatty acids decrease the expression and production of LPL by murine macrophages [Renier et al. 1993] and that saturated and unsaturated fatty acids directly regulate murine macrophage LPL expression, both at the gene and protein levels [Michaud et al. 2001]. This effect was found to involve PPARs.

I.II.6.2. Hormones

I.II.6.2.1. Steroids

The in vitro effect of steroid compounds has been examined on both adipocyte and macrophage LPL expression. It has been shown that, in primary cultures of murine macrophages and in the macrophage-like J774 cell line, dexamethasone inhibits LPL activity [Goldman 1990, Goldman et al. 1989] and LPL secretion [Behr and Kraemer, 1986]. In vivo studies suggest that LPL levels are higher in female than in male rats. Sex steroids could account for this difference [Eisenbäck and Gimble, 1993]. Progesterone administration to female rats increases adipocyte LPL activity, while estrogens decrease this parameter [Gray and Wade, 1980, Pedersen et al, 1992].

I.II.6.2.2. Insulin

Insulin infusion is associated with increased adipose tissue LPL levels in normal subjects [Sadur et al. 1982]. The effect of insulin on adipocyte LPL seems to be exerted at the post-transcriptional level. Indeed, several studies have shown that insulin increases LPL protein synthesis by 42-48%, but has no influence on either total LPL mRNA levels or the LPL transcription rate [Samuelsson et al. 1991, Semenkovich et al. 1989]. The effect of insulin on macrophage LPL regulation has also been evaluated. Behr et al. [1988] found that insulin does not exert a direct effect on LPL secretion by macrophages, although these authors demonstrated that insulin deficiency causes a profound decrease in macrophage LPL secretion. In our laboratory we have obtained

evidence that hyperinsulinemic subjects overproduce macrophage LPL [Sartippour and Renier, 2000]. These observations are in contrast with those of Dobrian et al. [2000] demonstrating that macrophages from non-insulin-dependent-diabetes-mellitus patients display a decrease of LPL mRNA expression with a reduction of secreted LPL activity.

I.II.6.2.3. Growth hormone (GH)

Post-heparin plasma LPL activity decreases in hypophysectomized rats, and this effect is reversed by GH therapy. GH transiently activates c-fos gene expression by a PKC-dependent pathway and modulates the expression of the LPL gene in Ob1771 adipose cells [Pradines-Figuères et al. 1990].

Ottosson et al. [1995] found that GH counteracts the potent stimulatory effect of glucocorticoids on LPL activity without affecting LPL mRNA levels. Therefore, they suggested that the inhibition of LPL activity by GH probably occurs during translation and/or post-translational processing of the enzyme.

I.II.6.3. Pro-inflammatory cytokines

The regulation of LPL by cytokines is of potential crucial importance in determining the levels of LPL in the arterial wall and thereby the development and/or progression of the atherosclerotic lesions.

I.II.6.3.1. TNF- α

Accumulating evidence suggests that TNF- α affects circulating lipids as well as vascular wall biology and exerts potent pro-atherogenic effects. Indeed, TNF- α has been shown to stimulate new vessel formation [Leibovich et al. 1987] and to induce hemorrhagic necrosis [Watanabe et al. 1988], features characteristic of evolving atheroma. In addition to favoring leukocyte adhesion to endothelial cells [Gamble et al. 1985], this cytokine also promotes tissue factor-like procoagulant activity and suppresses endothelial cell surface anticoagulant activity [Bevilacqua et al. 1986]. It is expressed by macrophages in human atheroma [Barath et al. 1990, Rus et al. 1991] and plays a critical role in the induction of insulin resistance, a condition associated with increased vascular risk. This cytokine has been found to diminish LPL gene expression and activity in J774 macrophages. A maximal inhibitory effect of this cytokine on macrophage LPL expression was observed in presence of IFN γ [Tengku-Muhammad et al. 1996, 1998]. In contrast, no effect of TNF- α on human macrophages was observed [White et al. 1998]. Because this cytokine suppresses adipocyte LPL expression, it has been postulated that decreased LPL expression in animals

with visceral obesity may result from increased levels of TNF- α . [Hikita et al. 2000].

I.II.6.3.2. IL-1

IL-1 is a prominent pro-inflammatory cytokine in a multitude of systemic inflammatory states. Studies aimed at determining the role of IL-1 on LPL expression demonstrate that IL-1 decreases murine macrophage LPL expression [Tengku-Muhammad et al. 1996, 1999]. In contrast, no effect of this cytokine was reported on human macrophage LPL activity [Querfeld et al. 1990].

I.II. 6.3.3. IFN- γ

Accumulating evidence demonstrates that IFN- γ inhibits adipocyte and macrophage LPL activity [Patton et al. 1986, Ogawa et al. 1989, Beutler et al. 1985, Price et al. 1986, Grégoire et al. 1992]. In human monocytes/macrophages, IFN- γ causes a decrease of LPL activity [Querfeld et al. 1990, Jonasson et al. 1990]. Tengku-Muhammad et al. [1996, 1998, 1999] demonstrated that this effect is exerted at the level of LPL mRNA metabolism (decreased transcription or RNA stability) and that co-exposure of macrophages to IFN- γ and LPS or TNF- α results in a synergistic suppression of LPL activity.

I.II.6.3.4. IL-6

IL-6 is a potential mediator of the lipogenic effects of TNF- α [Grunfeld et al. 1990]. It is released systemically in response to TNF- α , IL-1, or LPS. IL-6 has been documented to reduce tissue LPL activity and may play a role in inducing cancer cachexia [Greenberg et al. 1994]. It also has been found that administration of IL-6 to mice in vivo resulted in a 50% decrease in adipose tissue LPL activity [Grunfeld et al. 1990]. In contrast no effect of IL-6 on macrophage LPL activity or LPL mRNA levels was found [Tengku-Muhammad et al. 1996].

I.II.6.3.5. Leukemia inhibitory factor (LIF)

LIF, a cytokine released by tumor cells, was initially identified on the basis of its ability to induce differentiation in a monocytic leukemia cell line [Hilton et al. 1991]. In vitro research has established its ability to decrease LPL activity in murine 3T3-L1 adipocytes [Mori et al. 1989, Kawakami et al. 1991]. This cytokine has no effect on macrophage LPL activity or LPL mRNA levels [Tengku-Muhammad et al. 1996].

I.II.6.3.6. IL-11

The original IL-11 cloned from bone marrow stromal cells had the ability to stimulate the proliferation of an IL-6-dependent plasmacytoma (B-cell) clone [Paul et al. 1990]. It has since been demonstrated that IL-11 inhibits LPL activity

in adipocytes [Kawashima et al. 1991, Ohsumi et al. 1994]. The effect of IL-11 on macrophage LPL has been studied in the murine J774.2 cell line [Tengku-Muhammad et al. 1996, 1998, 1999]. These authors found that IL-11 exerts an inhibitory effect on macrophage LPL expression.

I.II.6.3.7. LPS

LPS inhibits in vivo adipocyte LPL activity. This effect may be exerted at the post-transcriptional level [Gouni et al. 1993]. The suppressive effect of LPS on adipose LPL activity could involve the secretion of cytokines by macrophages including IL-1, IL-6, IFN- γ and TNF- α [Cornelius et al. 1988, Greenberg et al. 1992]. This possibility is supported by the findings that LPS inhibits both murine and human macrophage LPL activity in vitro [White et al. 1988, Sopher et al. 1987]. Recently, Tengku-Muhammad et al. [1999] used J774.2 macrophages to demonstrate that both the tyrosine kinase and phosphatidylinositol-3'-kinase signaling pathways are involved in the inhibitory effect of LPS and cytokines on macrophage LPL expression.

I.II.6.4. Prostaglandins (PGs)

PGs are produced in multiple cell types, including adipocytes, through arachidonic acid metabolism via the cyclo-oxygenase pathway. PGF₂ α alone in either primary rat adipocytes or murine pre-adipocytes inhibits LPL mRNA expression [Serrero et al. 1992]. In macrophages, an inhibitory effect of PGE₂ has been reported on macrophage LPL mRNA levels, mass and activity [De

Sanctis et al. 1994]. This effect is mediated by an increased production of cAMP. PGs have also been found to mediate LPS-induced inhibition of macrophage LPL expression [De Sanctis et al. 1994]. Recently, Obunike et al. [2000] have reported that enhanced LPL gene expression results in increased PG production.

I.II.7. LPL in diabetes

Diabetes is an independent risk factor for cardiovascular disease. LPL, a potential atherogenic protein, has been found to undergo significant functional alterations in the diabetic state.

Non-insulin-dependent diabetic patients have higher plasma TG and lower HDL cholesterol concentrations compared to normal subjects. This diabetic dyslipidemia is associated with low plasma LPL activity [Murata et al. 1988, Ishibashi et al. 1989, Rapp et al. 1994]. Whereas diabetes has been repeatedly shown to decrease adipose LPL activity, LPL activity in skeletal muscle of diabetic patients has been found to be either decreased or unchanged [Farese et al. 1991]. It is well-documented that LPL regulation is tissue- and cell-specific [O'Brien et al. 1994]. Upregulation of macrophage LPL secretion has been found in diabetes-prone mice [Corey et al. 1997] and in type II diabetic patients [Sartippour et al. 2000]. It has been proposed that the increase in macrophage LPL in human diabetes could be due to peripheral factors such as high glucose and fatty acids [Sartippour et al. 1998, Michaud and Renier, 2001].

I.II.8. LPL in atherosclerosis

LPL, which is synthesized by adipose cells, SMC, and macrophages [O'Brien et al. 1992] plays a central role in lipid metabolism. Depending on its location, LPL has been suggested to play a dual role in atherogenesis [Williams et al. 1992, Mead et al. 1999, Santamarina-Fojo et al. 2000].

I.II.8.1. Pro-atherogenic effect of LPL

The contribution of LPL to atherogenesis is significantly influenced by the balance between plasma LPL activity and vessel wall protein. Indeed, it has been demonstrated that LPL activity in plasma decreases vascular risk while LPL produced by macrophages in the vascular wall promotes atherosclerosis. Evidence for a pro-atherogenic role of macrophage LPL has been provided on the basis primarily of in vitro and ex vivo studies. It has been shown that LPL is synthesized by macrophages in the atherosclerotic lesion [Yal-Herttuala et al. 1991, O'Brien et al. 1992] and that macrophage LPL expression is positively associated with atherosclerotic susceptibility in inbred mice [Renier et al. 1993]. LPL content in the arterial wall has also been reported to increase with the progression of the lesion [Corey et al. 1977] and a correlation has been documented between its accumulation in the arterial wall and that of cholesterol ester [Zilversmit 1979]. LPL also functions as a ligand, associating with lipoproteins and promoting their binding to specific receptors expressed on cell surface. It may promote atherogenesis by increasing the binding and retention of LDL by proteoglycans of the subendothelial matrix [Lindqvist et al. 1983,

Ishibashi et al.1990, Eisenberg et al.1992, Rumsey et al. 1992, Beisiegel et al.1991, Mulder M et al.1992, Williams et al. 1992, Nykjaer et al.1993, Chappell et al. 1993, Saxena et al.1992, Williams and Tabas 1995]. The atherogenic ligand function of LPL is increased by LDL oxidation [Auerbach et al. 1996, Kaplan et al. 1997, Makoveichuk et al. 1998]. LPL also exerts its pro-atherogenic effects by acting as a monocyte adhesion protein [Obunike et al 1997, Mamputu et al. 1997]. Finally, LPL-mediated hydrolysis of VLDL produces LDL, a major contributor to the development of atherosclerotic lesions [Brown et al. 1983, Steinberg et al. 1989]. Recently, the pro-atherogenic effect of macrophage LPL has been confirmed in vivo [Babaev et al 1999, 2000, Van Eck et al. 2000].

I.II.8.2. Anti-atherogenic effect of LPL

Accumulating evidence supports the view that plasma LPL plays an anti-atherogenic role. Firstly, Benlian et al. [1996] have recently reported that several LPL-deficient patients develop relatively advanced atherosclerosis. Additionally, it has been found that individuals who are heterozygous for LPL mutations that reduce LPL enzymatic activity are predisposed to premature atherosclerosis [Henderson et al. 1999]. Conversely, a variant of LPL that is associated with increased plasma activity has been found to protect against atherosclerosis [Gagne et al, 1999]. Recently, pharmaceutical interventions intended to elevate HDL resulted in increased plasma LPL expression and protected against atherosclerosis [Tsutsumi et al. 1995, 1997]. Furthermore, in the liver, it has been demonstrated that LPL overexpression can normalize the atherosclerotic

lipoprotein profiles of both apoE-deficient and LDL receptor-deficient mice, and protect wild-type mice against diet-induced hyperlipidemia [Shimada et al. 1993, 1996, Zsigmund et al. 1997, Yagyu et, 1999].

I.III. PPARs

I.III.1. General

PPARs belong to the steroid/thyroid/retinoid receptor superfamily. They represent nuclear lipid-activated receptors that control a variety of genes involved in several pathways of lipid metabolism, such as fatty acid transport, intracellular binding and activation, as well as catabolism (β -oxidation and omega-oxidation). PPARs also influence cellular proliferation, differentiation and apoptosis and play a role in the control of inflammation.

I.III.1.1. PPAR structure and function

PPARs are compact molecules. Human PPAR α has 468 amino acid residues compared with 441 for PPAR β/δ and 479 for PPAR γ . PPARs have five or six structural regions (A-F) in four functional domains. The C domain is DNA-binding (DBD), and the E/F domain is ligand-binding, which plays a key role in transduction of the hormonal signal into transcriptional activation. Intramolecular communication takes place between the A/B NH₂-terminal and the DBD carboxy-terminal, where hormones bind to PPAR γ . Activation of PPAR γ can be depressed by phosphorylation of a seryl residue in A/B, mediated by MAPK [Shao et al.

1998], whereas phosphorylation of PPAR α positively affects receptor/ligand affinity [Shalev et al. 1996]. Phylogenetic studies indicate that the E domain in PPARs has evolved three times faster than in thyroid and trans-retinoic acid (RAR) receptors [Dreyer et al. 1993]. Perhaps this may explain PPAR α and γ differences and opposing metabolic pathways.

I.III.1.2. Molecular mechanism of action of PPARs

PPARs constitute a nuclear receptor subfamily. Three isoforms of PPARs, termed α , β (also called δ or NUC1) and γ , are each encoded by a separate gene and expressed by distinct tissues [Braissant et al. 1995, Auboeuf et al. 1997, Granneman et al. 1998]. Their developmental distribution patterns [Braissant et al. 1998] also have been described. PPARs are ligand-activated transcription factors, binding upon heterodimerization with RXRs to PPRE in the promoter of target genes [Schoonjans et al. 1996]. PPAR consensus PPRES consist of a direct repeat of nuclear receptor hexameric AGGTCA recognition sites (DR-1 and DR-2) [Gervois et al. 1999]. The DR-1 pattern is specific to the PPAR/RXR heterodimer (**Fig. 4**). DR-1 is clearly different from DR-3 (estrogen receptor, vitamin D receptor), DR-4 (thyroid hormone receptor) and DR-5 (RAR S- γ RAR), which are response elements of other nuclear receptors.

Recently, it has been shown that PPARs can also repress gene transcription by a combination of protein-protein interactions and cofactor squelching without binding to PPRES. PPARs can negatively interfere with the NF- κ B, STAT and AP-1 signaling pathways in a DNA-binding independent manner

[Chinetti et al. 1998, Ricote et al. 1998, Stael et al. 1998, Zhou et al. 1999, Delerive et al. 1999]. Furthermore, PPARs interact with AP-1 and NF- κ B proteins, including c-Jun [Sakai et al.1995] and P65 [Delerive et al. 1999], interfering with their target sequences [Delerive et al. 1999, Marx et al. 1999]. PPARs also interfere negatively with retinoic acid and GC receptors, which are also nuclear receptor family members [Kamei et al. 1996].

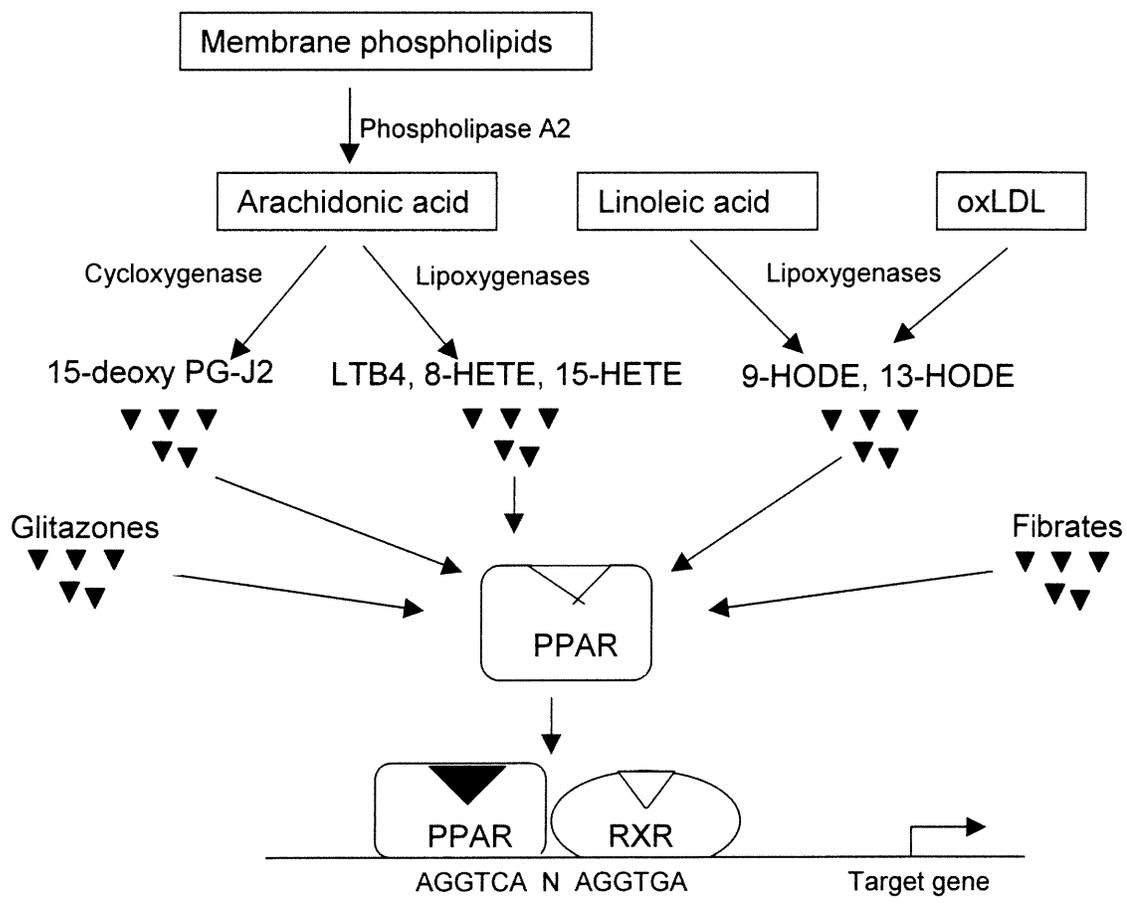


Fig. 4. Peroxisome proliferator-activated receptors : ligands and transcriptional activation [Chinetti et al. 2000].

I.III.1.3. Tissue distribution of PPARs

Studies of PPARs tissue distribution have been restricted to the analysis of its mRNA distribution. PPAR α is predominantly expressed in liver, heart, kidney and brown adipose tissue. PPAR β is abundantly expressed in various tissues, in almost the same distribution as PPAR α . PPAR γ 1 and PPAR γ 2 are expressed in a tissue-specific manner. PPAR γ 1 exhibits a distribution pattern reminiscent of PPAR α . PPAR γ 2 is predominantly expressed in adipose tissue. The differential tissue distribution of PPARs has been well-documented (**Table 1**).

Table 1. Relative tissue expression of PPAR isoforms

Tissue	PPAR α	PPAR β	PPAR γ 1	PPAR γ 2
Heart	+++	+++	+++	++
Liver	+++	+/-	+++	+/-
White adipose tissue	-	++	-	++++
Brown adipose tissue	+++	++	-	-
Lung	-	+++	+	++
Spleen	-	+++	+/-	++
Kidney	+++	++	+++	+
Brain	-	+++	+	+
Intestine	+	+++	-	-
Adrenal	-	+++	-	-
Muscle	+	+++	+	+
Thymus	+	-	-	-
Testis	+	+/-	+	-
Pancreas	-	-	-	-

I.III.1.4. Main characteristics of PPAR α and PPAR γ (Table 2)

Table 2. PPAR α	PPAR γ
Mainly liver (also present in other tissues)	Mainly adipose tissue and colon
Stimulation of β -oxidation . LPL metabolism	Stimulation of fat storage
Inflammation (stimulates breakdown of inflammatory fatty acids)	Glucose and lipid metabolism
Leukotriene B4, 8-S-HETE, and fibrates	Fat formation
	Prostaglandin J2 and thiazolidinediones

I.III.1.5. Natural and synthetic ligands of PPARs

PPARs can be activated by a number of ligands, which include natural and synthetic groups. There is firm evidence that fatty acids are PPAR natural ligands interacting directly with the nuclear receptor for at least part of their PPAR-dependent transcriptional activity. Polyunsaturated fatty acids bind to all three PPAR isoforms with varying affinities, though saturated fatty acids preferentially bind PPAR α (**Table 3**).

Synthetic ligands include some hypolipidemic and anti-diabetic agents. For example, clofibrate and WY-14643 belong to the hypolipidemic fibrate group binding preferentially to PPAR α . Thiazolidinediones (TZDs), which include troglitazone, pioglitazone, and BRL49653 (rosiglitazone), are a class of antidiabetic drugs that are structurally derived from clofibric acid but selectively bind PPAR γ [Lehmann et al. 1995, Berger et al. 1996] (**Table 4**).

Table 3. PPAR natural ligands

Natural ligands	PPAR α				PPAR β				PPAR γ			
	SABA or COBA	LIC	CARLA	DPSA	SABA or COBA	LIC	CARLA	DPSA	SABA or COBA	LIC	CARLA	DPSA
Unsaturated fatty acids												
ω 3-PUFAs												
α -Linolenic C18:3	+	+	+		+/-	+/-	+		+			+
γ -Linolenic C18:3	+	+			+				+			
Eicosapentaenoic C20:5(EPA)	+	+	+		+	+/-	+		+			+
Docohexaenoic C22:6 (DHA)		+	+			+/-	-					+
ω 6-PUFAs												
Linoleic C18:2	+	+	+		+/-	+			+			+
Dihomo- γ -linolenic C20:3	+				+				+			
Arachidonic C20:4	+	+	+		+	+			+			+
ω 9-mUFAs												
Palmitoleic C16:1	+				+				+			
Oleic C18:1	+		+		+				+			-
Elaidic C18:1trans									-/+			-
Erucic C22:1	-	-	-/+		-				-/+			-
Nervonic C24:1		-	-						-/+			-
ω 2-mUFA												
Petroselinic C18:1	+		+						-/+			+
Saturated fatty acids												
Capric C10:0	-				-							-
Lauric C12:0	-	+/-			-							-
Myristic C14:0	+	+/-			-/+							-/+
Palmitic C16:0	+	+			+							-
Stearic C18:0	+				+							-
Arachidic C20:0	-				-							-
Behenic C22:0	-				-							-
Dicarboxylic fatty acids												
Dodecanedioic C12				-								-
Eicosanoids												
\pm 8-HEPE(hydroxyeicosapentaenoic)		+										
\pm 8-HETE		+							-			
8S-HETE	+	+	+						+/-			-/+ -/+
8R-HETE	-	-	+/-						-			- -
8(9)-EpEtrE		-										
\pm 8-HETrE (hydroxyeicosatrienoic)		-/+										
12-HETE		-										
Leukotriene B4		-	+									
9-HODE(9-hydroxyoctadenoic acid)												+
13-HODE												+
15-Deoxy-12, 14-PGJ2		-	-						-	-		+

Direct interaction between natural and synthetic compounds and PPARs was analyzed by the following approaches : saturation binding assay (SABA), Competition binding assay (COBA), PPAR :RXR-DNA ligand –induced complex formation (LIC), coactivator-dependent receptor binding assay (CARLA), and differential protease sensitivity assay (DPSA). +, binding detected easily; +/-, weak binding; -/+, very weak binding detected; -, compound tested but no binding detected. [Desvergne et al. 1999]

Table 4. PPAR synthetic ligands

Synthetic ligands	PPAR α				PPAR β				PPAR γ			
	SABA or COBA	LIC	CARLA	DPSA	SABA or COBA	LIC	CARLA	DPSA	SABA or COBA	LIC	CARLA	DPSA
Prostaglandin 12 analogs												
Carbaprostacyclin (cPGI)		+										
Iloprost		+										
Cicaprost		-										
Leukotriene B4 analogs												
Trifluoromethyl leukotriene B4				+								
ZK 151657				+			+/-					-
ZK 158252				+			-					-
Leukotriene D4 antagonist												
Ly 171883		+	+									
Hypolipidemic agents												
Clofibrac acid		+	+	+								
Ciprofibrac acid		+	-									+
Bezafibrac acid(xPPARs)			-				+					-
Fenofibrac acid			-				-					-
Pirinixic acid (Wy-14643)		+	+				-					-
GW 2331 (fibrate analog)	+									+		
GW 2433 (fibrate analog)	+					+						
Eicosatetraynoic acid (ETYA; Arachidonic analog)				+	+			+				
Hypoglycemic agents (thiazolidinediones)												
Rosiglitazone (BRL 49653)	-	-	-				-	-		+		+
AD-5075										+		+
Troglitazone										+		
Hypolipidemic and hypoglycemic agents (nonthiazolidinedione)												
L-165041							+			-/+		
L-165461							+			+/-		
L-783483							+			+/-		
L-796449							+			+		
Nonsteroidal antiinflammatory drugs (NSAIDs)												
Indomethacin										+		
Flufenamic acid										+		
Fenoprofen										+		
Ibuprofen										+		
Carnitine palmitoyl transferase I (CPT1) inhibitors												
Ly-171883		+			+							
2-Bromopalmitate (2Br-C16)		+										
Tetradecylglycidic acid (TDGA)		+										
Fatty acyl-CoA dehydrogenase inhibitors												
Orlythiopropionic acid (OTP)		+										
Tetradecylthiopropionic acid (TTP)		+										
Nonylthioacetic acid (NTA)		+										
Tetradecylthioacetic acid (TTA)		+										

I.III.1.6. Regulation of PPAR expression by cytokines

It is known that PPAR expression is under the control of a wide variety of inflammatory cytokines. A recent study has shown that treatment with different glitazones can reverse the inhibitory effect of PPAR γ expression induced by TNF α , IL-1 α , IL-1 β , and IL-6 in mature rat adipocytes [Tanaka et al. 1999]. Conversely, IL-4, which exerts an anti-inflammatory action through macrophage inactivation, induces PPAR γ 1 expression in monocytes and macrophages [Huang et al. 1999]. In addition, 9- and 13-HODE, which are pro-inflammatory mediators derived from oxLDL increase PPAR γ mRNA levels in human macrophages [Tontonoz et al. 1998].

I.III.2. Role of PPARs in lipid-glucose metabolism and inflammation

Since the first characterization of PPARs [Issemann et al. 1990], their importance in metabolic regulation has become clear. It has been established that treatment with clinical hypolipidemic drugs (fibrates) efficiently decreases plasma triglyceride levels and increases HDL cholesterol concentration in diabetic patients [Staels et al. 1998b]. In the liver and in cultured hepatocytes, fibrates activate PPAR α , enhancing fatty acid β -oxidation, decreasing apoC-III production, and lowering TG and VLDL secretion [Schoonjans et al. 1996a, 1996b, 1997]. Recently, the role of PPAR α in HDL and triglyceride metabolism as well as in the hepatic regulation of apolipoprotein and fatty acid β -oxidation enzyme expression has been further demonstrated unequivocally [Peters et al.

1997, Aoyama et al. 1998]. Peters et al. [1997] has demonstrated that administration of the fibrate Wy 14,643 to wild-type mice results in marked depression of hepatic apolipoprotein C-III mRNA and serum triglycerides compared with untreated controls. Aoyama et al. [1998] has showed that PPAR α modulates constitutive expression of genes encoding several mitochondrial fatty acid-catabolizing enzymes in addition to mediating inducible mitochondrial and peroxisomal fatty acid beta-oxidation, thus establishing a role for the receptor in fatty acid homeostasis.

In contrast, PPAR γ ligands (glitazones), which are antidiabetic agents, enhance triglyceride catabolism, resulting in decreased plasma TG and FFA levels by the induction of LPL gene expression in adipose tissue [Lefebvre et al. 1997]. Glitazones also regulate important proteins involved in glucose utilization and insulin resistance/tolerance of adipose tissue [Kubota et al. 1999].

In addition to their effects on extracellular lipid metabolism, PPARs act as regulators of cellular fatty acid uptake and control their intracellular fate. Fatty acid transport protein (FATP) [Martin et al. 1997] and fatty acid translocase (FAT/CD36) [Tontonoz et al. 1998, Abumrad et al. 1993] regulate the import and export systems of intracellular fatty acid concentrations. Expression of long chain fatty acid transporters is induced in a tissue-dependent fashion in the liver by PPAR α and in adipose tissue by PPAR γ activators [Martin et al. 1997, Motojima et al. 1998]. Fibrates also enhance the effect of acyl-CoA synthetase (ACS), a key enzyme in fatty acid esterification which prevents fatty acid efflux from cells of this enzyme in the liver and kidney [Martin et al. 1997, Schoonjans et al. 1993].

Furthermore, PPAR α activators enhance carnitine palmitoyltransferase type I (CPT-I), a key enzyme in mitochondrial fatty acid catabolism, which contains a PPRE in its promoter region [Brandt et al. 1998, Mascaro et al. 1998].

PPAR α plays also an important role in the enhanced degradation of lipid-derived inflammatory mediators through β -oxidation pathways. This is consistent with the observation that inflammatory response to leukotrienes B₄ (LTB₄) is prolonged in mice with targeted disruption of the PPAR α gene [Devchand et al. 1996].

I.III.3. Role of PPARs in atherosclerosis

Formation of atherosclerotic lesions entails the recruitment and activation of different vascular cell types, such as monocyte/macrophages, endothelial cells, SMC, and T lymphocytes, in the intima of arteries. It has been shown that atherosclerotic lesions and macrophage foam cells express PPAR α and γ [Marx et al. 1998, Tontonoz et al. 1998, Ricote et al. 1998b, Staels et al. 1998a, Chinetti et al. 2000], suggesting that PPARs may affect the atherosclerotic process.

PPAR α plays an important role in the metabolism of fatty acid, lipids, and lipoproteins. Decreased plasma TG levels in response to fibric acids involve increased expression of genes involved in fatty acid- β oxidation, including LPL and apoC-III [Fruchart et al. 2001].

Experimental evidence implicates this PPAR isoform in inflammation and atherogenesis. Indeed, evidence has been provided that PPAR α -deficient mice exhibit a prolonged inflammatory response as compared to control mice

[Devchand et al. 1996] and that PPAR α activation inhibits the transcription of several inflammatory response genes. Although an anti-atherogenic effect of PPAR α is suggested by the finding that treatment with PPAR α activators reduces the progression of atherosclerotic lesions [Frick et al. 1997, Ericsson et al. 1996, Saitoh et al. 1995], evidence that PPAR α activation induces macrophage apoptosis [Chinetti et al. 1998] and enhances LPS-induced plasma TNF- α concentrations [Hill et al. 1999] also suggest possible pro-atherogenic effects of this PPAR isoform.

In recent years, many studies have focused on the role of PPAR γ in atherosclerosis. It has been found that PPAR γ is a crucial component of the innate immune system. Indeed, although PPAR γ is barely present in undifferentiated resting monocytes [Tontonoz et al. 1998, Greene et al. 1995, Ricote et al. 1998b], its expression increases strongly during macrophage differentiation [Tontonoz et al. 1998, Ricote et al. 1998b]. The strong expression of PPAR γ in macrophage foam cells and atherosclerotic lesions [Ricote et al. 1998b, Marx et al. 1998] suggests that PPAR γ may exert pro-atherogenic activity. Several pro-atherogenic effects of PPAR γ have been described. For example, it has been shown that activation of the PPAR γ /RXR heterodimer enhances macrophage differentiation [Tontonoz et al. 1998] and the uptake of oxLDL by macrophages [Tontonoz et al. 1998, Nagy et al. 1998]. Increased expression of ICAM-1 by PPAR γ has also been documented [Chen et al. 1999] and induction of this isoform by LPS has been reported [Leininger et al. 1999]. In contrast, PPAR γ may act as an anti-atherogenic factor. This possibility is supported by the

observations that PPAR γ inhibits the expression of activation- and differentiation-dependent genes in macrophages [Tontonoz et al. 1999, Ricote et al. 1998b, Jiang et al. 1998], interferes with vascular SMC proliferation [Li et al. 2000] and inhibits the expression of MMP-9 and of various pro-inflammatory cytokines in human macrophages [Marx et al. 1998, Su et al. 1999, Thieringer et al, 2000]. Moreover, it has been shown that the PPAR γ -specific agonists rosiglitazone and GW7845 strongly inhibited the development of atherosclerosis in LDL receptor-deficient male mice, despite increased expression of the CD36 scavenger receptor in the arterial wall [Li et al. 2000] and that the PPAR γ agonist troglitazone decreases intimal thickness in human carotid arteries [Law et al. 1998].

I.III.3.1. Effect of PPARs on vascular endothelial cells

Vascular endothelial cells contribute to the release of anti-atherogenic mediators in large blood vessels. Endothelial damage or dysfunction is considered to be one major mechanism for the development of atherosclerosis. It has been well-documented that vascular endothelial cells express PPAR α , PPAR δ , and PPAR γ [Inoue et al. 1998, Bishop-Bailey et al. 1999] but the role of PPAR δ in endothelial cells has not been well determined yet.

PPAR α inhibits the AP-1 signaling pathway, which is involved in thrombin-induced activation of endothelin-1 production by human endothelial cells [Delerive et al. 1999]. In addition, PPAR α activators suppress TNF- α -induced VCAM-1 expression partly through inhibition of the NF- κ B pathway in human

endothelial cells [Marx et al. 1999]. Recently, PPAR α has been shown to repress monocyte recruitment to early atherosclerotic lesions by inhibiting TNF- α -induced VCAM-1 expression [Marx et al. 1999c]. Moreover, it has been demonstrated that activation of PPAR α by the synthetic ligand WY14,643 stimulates the synthesis of IL-8 and MCP-1 by human aortic endothelial cells [Lee et al. 2000].

The role of PPAR γ in modulating endothelial function has been well-documented. It has been shown that PPAR γ activators inhibit the endothelial cell release of endothelin-1 [Sato et al. 1999, Delerive et al. 1999], a potent vasoconstrictor and vascular smooth muscle cell mitogen [Ruschitzka et al. 1997]. In contrast, these agonists have also been found to increase plasminogen activator inhibitor-1 (PAI)-1 expression [Loskutoff et al. 1997], a well known risk factor of myocardial ischemia and thrombosis. Finally, PPAR γ activators can inhibit angiogenesis by inducing apoptosis through a caspase-3-mediated process [Bishop-Bailey et al. 1999] and reducing the vascular endothelial growth factor (VEGF) receptors Flt-1 and Flk/KDR on the endothelial cell surface [Xin et al. 1999].

I.III.3.2. Effect of PPARs in vascular SMC

Vascular SMC also express PPAR α , PPAR γ , and PPAR δ [Staels et al. 1998, Marx et al. 1998, Ricote et al. 1998]. PPAR α ligands repress the NF- κ B signaling pathway, resulting in the inhibition of inflammatory responses in vascular SMC [Staels et al. 1998]. This mechanism, may explain the inhibitory

effect of fenofibrate and WY-16,463 on IL-1-induced IL-6 production and inducible cyclo-oxygenase (COX-2) expression in vascular SMC [Staels et al. 1998]. Clinical observations demonstrate that hyperlipidemic patients treated with fenofibrate have reduced circulating IL-6 and acute phase proteins [Staels et al. 1998].

Studies of PPAR γ in rat vascular SMC have shown that troglitazone inhibits the degradation of inducible NO synthase (iNOS) mRNA in a PPAR γ -independent manner [Hattori et al. 1999]. In contrast, in aortic SMC expressing PPAR γ , the PPAR γ activators, PGJ2 and 9-HODE, induce type II-secreted phospholipase A2 (type II sPLA2) expression [Couturier et al. 1999]. Because type II sPLA2 increases lipoxygenase-induced HODE production [Neuzi et al. 1998], it has been postulated that type II sPLA2-induced HODE synthesis may constitute a positive autocrine loop in the aorta during inflammatory states. Troglitazone has also been shown to inhibit, in vascular SMC, the induction of c-fos and serum response element-induced transcriptional activation [Law et al. 1996]. Finally, PPAR γ activation has been reported to inhibit PDGF-BB-induced SMC migration [Marx et al. 1998].

Both PPAR α and γ appear to have protective effects on the activity of vascular SMC. PPAR α ligands may reduce the inflammatory response within the vessel wall by at least interfering with NF- κ B signaling. PPAR γ ligands may specifically inhibit SMC migration, by interfering with processes involved in degradation of the extracellular matrix.

I.III.3.3. Effect of PPARs on vascular monocytes/macrophages

It has been well-demonstrated that macrophages are the predominant inflammatory leukocytes in a number of chronic inflammatory diseases, including atherosclerosis [Ross 1999]. Chinetti et al. [1998] have shown that PPAR α and PPAR γ are both expressed in differentiated human macrophages (**Fig. 5**).

Although PPAR γ has been postulated to promote monocyte-macrophage differentiation and to favor the uptake of oxLDL by macrophages [Tontonoz et al. 1998, Nagy et al. 1998], both natural and synthetic PPAR γ have been found to inhibit the transcriptional activity of iNOS, MMP-9 and scavenger receptor A genes by interfering with AP-1, NF- κ B and STAT-1 transcription factors [Ricote et al 1998]. Jiang et al. [1998] have also shown that incubation of human monocytes with the natural PPAR γ ligand PG-J2 or synthetic agonists inhibits, at the transcriptional level, the production of several pro-inflammatory cytokines, such as TNF- α , IL-1 β , and IL-6. The most pronounced effects are observed with PG-J2, which may not be very selective for PPAR γ and may also act through PPAR-independent mechanisms [Spiegelman et al. 1998, Petrova et al. 1999]. Recently evidence has been provided that PG-J2 may exert anti-inflammatory activities through the inhibition of I κ B kinase [Castrillo et al. 2000, Rossi et al. 2000]. In contrast, the findings that the natural PPAR α ligands LTB₄ and 8(S)-HETE stimulate nitrite accumulation in RAW 264.7 murine macrophages suggest that these compounds may act as pro-inflammatory molecules [Colville-Nash et al. 1998].

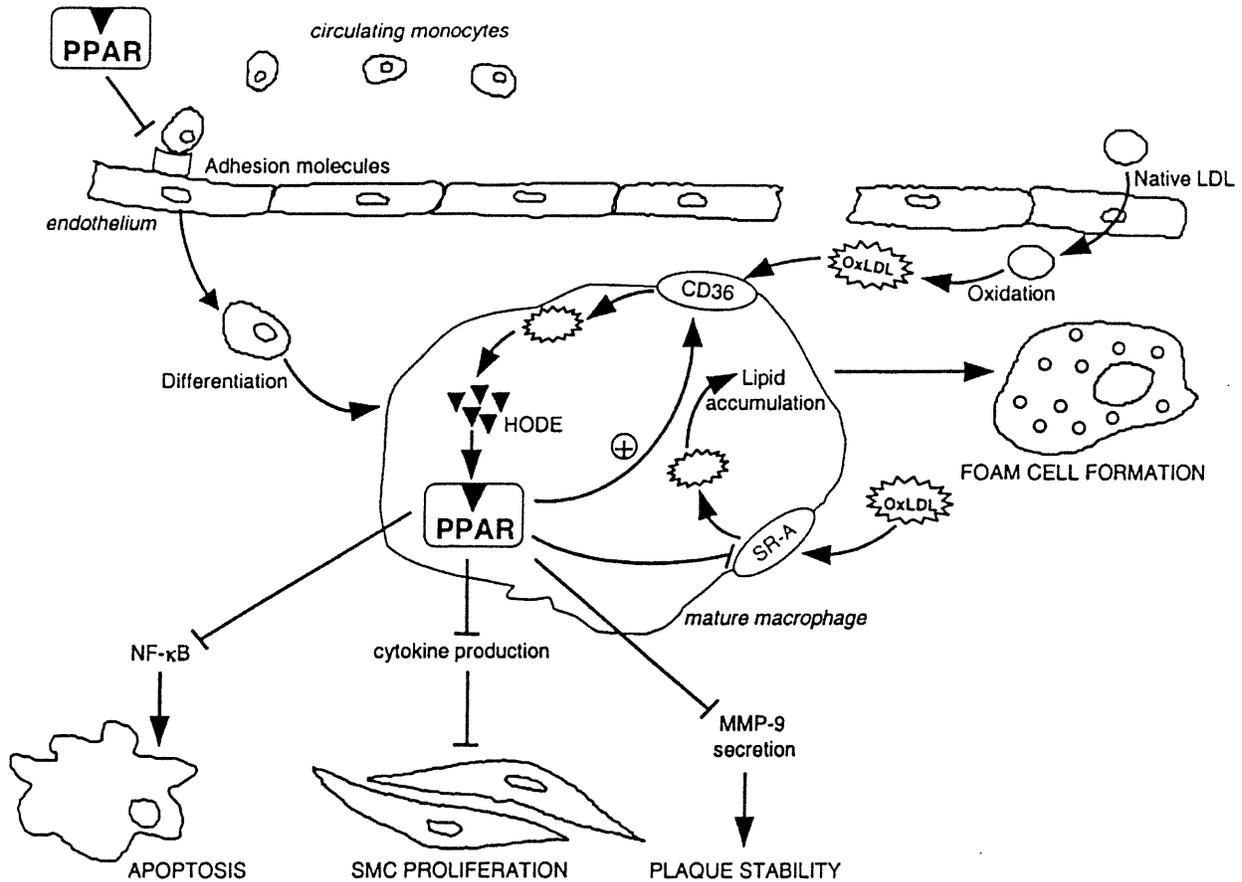


Fig. 5. PPARs control macrophage functions during atherosclerosis development [G. Chinetti et al. 2000]. PPAR activation controls the expression of genes implicated in monocyte adhesion, lipid accumulation (such as CD36 and SR-A), apoptosis, vascular inflammation (cytokines) and plaque stability (MMP-9), thus modulating atherosclerotic lesion development.

II. ARTICLE

**Peroxisome proliferator-activated receptor α and γ agonists upregulate
human macrophage lipoprotein lipase expression.**

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ABSTRACT

Peroxisome proliferator-activated receptors (PPARs) are transcriptional factors which mediate pleiotropic effects including regulation of genes involved in lipid metabolism and control of inflammation. In the present study, we measured the in vitro effects of PPAR α and γ ligands on macrophage lipoprotein lipase (LPL) expression. Human monocyte-derived macrophages (MDM) were cultured for 1 to 3 days in the presence of PPAR α and γ ligands. At the end of these incubation periods, extracellular LPL immunoreactive mass/activity and LPL mRNA levels were measured. Incubation of human MDM with PPAR α and γ ligands stimulated, in a time- and dose-dependent manner, human MDM LPL mass and activity. These agents also significantly increased macrophage LPL mRNA expression. In THP-1 cells treated with PPAR α and γ ligands enhanced nuclear protein binding to the peroxisome proliferator responsive element (PPRE) of the human LPL promoter was observed. Furthermore, in these cells, a decreased rate of decay of LPL mRNA was documented. Overall, these results demonstrate that PPAR α and γ activators increase macrophage LPL secretion. Given the proatherogenic effect of macrophage LPL in the vascular wall, better understanding of the biological role of PPARs in the regulation of macrophage LPL expression could lead to the development of new approaches in the prevention and treatment of atherosclerosis.

Keywords: Peroxisome proliferator-activated receptors, macrophage, lipoprotein lipase.

INTRODUCTION

Peroxisome proliferator-activated receptors (PPARs) are members of the superfamily of nuclear hormone receptors.¹⁻³ Members of this family include PPAR α , PPAR β , and PPAR γ . While PPAR α is expressed preferentially in the liver and is an important regulator of lipid metabolism,⁴⁻⁵ PPAR γ is adipose tissue specific and plays a key role in adipocyte differentiation and glucose homeostasis.⁶⁻⁷ PPARs function as ligand-dependent transcription factors, which upon heterodimerization with the 9-cis-retinoic acid receptor, bind to a specific response element termed peroxisome proliferator responsive element (PPRE) in the promoter of various genes. Several agents, including fatty acids, fibrates, eicosanoids and synthetic thiazolidinedione drugs activate PPARs.

It has been recently suggested that PPARs may play a key role in the pathogenesis of atherosclerosis. Indeed, it has been reported that principal participants in the atherosclerotic process namely monocytes/macrophages and macrophage-derived foam cells express PPARs.⁸⁻¹¹ Recent findings showing that PPAR α and γ regulate genes implicated in the inflammatory response and modulate the differentiation process of macrophages into foam cells further support this possibility.^{9, 12-13}

Macrophages present in the atherosclerotic vessel secrete lipoprotein lipase (LPL), a key enzyme in the metabolism of triglyceride-rich lipoproteins.¹⁴⁻¹⁵ Arguments that point to macrophage LPL as a principal participant in atherogenesis include its ability to promote lipid accumulation within lesion macrophages, to induce monocyte/macrophage activation, to enhance monocyte binding to the endothelium and to stimulate vascular smooth muscle cell growth.¹⁶⁻²³ Despite evidence showing that PPAR agonists induce the transcriptional activation of the LPL gene through a PPRE located in the promoter of the LPL gene,²⁴⁻²⁵

the effect of PPAR ligands on macrophage LPL expression has not been studied yet. Given the potential key role of PPARs in atherogenesis, we investigated in the present study the effect of PPAR α and γ ligands on human macrophage LPL gene expression, secretion and activity.

MATERIALS AND METHODS

Reagents

Fetal calf serum (FCS) was purchased from Hyclone Laboratories. RPMI 1640 medium, Hank's balanced salt solution, lymphoprep, penicillin-streptomycin, phorbol 12-myristate 13-acetate (PMA), glycine, sodium dodecyl sulfate (SDS) and TRIzol reagent were obtained from Gibco BRL (Burlington, Ontario, Canada). WY-14643, eicosatetraenoic acid (ETYA) and clofibrate were provided by Biomol. BRL-49653 and troglitazone were kindly provided by Parke Davis. Prostaglandin J₂ (PGJ₂) and GI-251929X were obtained from Calbiochem and Glaxo Wellcome, respectively. Formaldehyde solution was obtained from Fischer (Fair Lawn, NJ). [³²P] dCTP (specific activity 3,000 Ci/mmol) was provided by ICN Biochemicals (Costa Mesa CA).

Human macrophages

Human monocytes were isolated as previously described.²⁶ Briefly, peripheral blood mononuclear cells were isolated from healthy control subjects by density centrifugation using Ficoll, allowed to aggregate in the presence of FCS, then further purified by the rosetting technique. After density centrifugation, highly purified monocytes (85-90%) were recovered, as assessed by flow cytometry (FACScan, Becton Dickinson). Differentiation of monocytes into macrophages was achieved by culturing the freshly isolated monocytes (2×10^6 /ml) in RPMI 1640 medium containing 20% (vol/vol) autologous serum for 8 days. The cells were incubated at 37°C in a humidified 5% CO₂, 95% air atmosphere. The culture medium was changed at days four and eight.

Human monocytic THP-1 cells were obtained from American Type Culture Collection and cultured in RPMI 1640 medium supplemented with 25 mmol/L HEPES buffer, 10% (vol/vol) FCS and 1% (vol/vol) penicillin-streptomycin (Flow, McLean, VA). THP-1 monocytes were differentiated into macrophages by treatment with 1 μ mol/L PMA for 2 days.

THP-1 differentiated macrophages and human monocyte-derived macrophages (MDM) were treated for 1 to 3 days with PPAR α (WY-14643, ETYA, clofibrate) or PPAR γ ligands (PGJ₂, BRL-49653, troglitazone, and GI-251929X). Culture media containing DMSO or methyl acetate were used as controls.

Analysis of LPL mRNA expression

-Northern Blot Analysis:

7X10⁶ THP-1-derived macrophages were plated in plastic petri dishes (100x20mm) (Falcon). Following treatment with appropriate agents, macrophages were lysed with guanidine isothiocyanate. Total RNA was purified by centrifugation through a cesium chloride gradient.²⁷ Twenty-five μ g of total RNA were separated on a 1.2 % agarose gel containing 2.2 mol/L formaldehyde.²⁸ The blots were prehybridized for 8h with prehybridization buffer. The mRNA expression was analyzed by hybridization with [³²P] dCTP-labeled human LPL and GAPDH cDNA probes. Hybridization was detected by autoradiography. mRNA expression was quantified by high-resolution optical densitometry.

-Polymerase Chain Reaction:

Expression of the LPL gene in human MDM was performed by the polymerase chain reaction (PCR) technique. Total RNA for use in the PCR reaction was extracted

from 2×10^6 human MDM by an improvement of the acid-phenol technique of Chomczynski.²⁹ Briefly, cells were lysed with TRIzol reagent and chloroform was added to the solution. After centrifugation, the RNA present in the aqueous phase was precipitated and resuspended in diethyl pyrocarbonate water. cDNA was synthesized from RNA by incubating total cellular RNA with 0.1 μg oligodT (Pharmacia) for 5 min at 98°C then by incubating the mixture with reverse transcription buffer for 60 min at 37°C . The cDNA obtained was amplified by using 0.8 $\mu\text{mol/L}$ of two synthetic primers specific for human LPL (5'-GAGATTTCTCTGTATGGCACC-3') (5'-CTGCAAATGAGACACTTTCTC-3') and human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (5'-CCCTTCATTGACCTCAACTACATGG-3') (5'-AGTCTTCTGGGTGGCAGTGATGG-3'), used as internal standard in the PCR reaction mixture. A 277-base pair human LPL cDNA fragment and a 456-base pair human GAPDH cDNA fragment were amplified enzymatically by 22 and 25 repeated cycles, respectively. An aliquot of each reaction mixture was then subjected to electrophoresis on 1% agarose gel containing ethidium bromide. The intensity of the bands was measured by an image analysis scanning system (Alpha Imager 2000, Packard Instrument Company).

Electrophoretic mobility shift assay.

The isolation of the nuclei was performed as previously described.³⁰ Briefly, 5×10^7 THP-1 MDM were collected, washed with cold phosphate-buffered salt solution (PBS), and lysed in 1 ml ice-cold buffer A (15 nmol/L KCL, 2 mmol/L MgCl_2 , 10 mmol/L HEPES, 0.1 % phenylmethylsulfonyl fluoride (PMSF), and 0.5% Nonidet-P-40). After a 10-min incubation on ice, lysed cells were centrifuged, and the nuclei were washed with buffer A without Nonidet P-40. The nuclei were then lysed in a buffer containing 2 mol/L KCL, 25 mmol/L HEPES, 0.1 mmol/L EDTA, and 1 mmol/L dithiothreitol (DTT). After a 15-min incubation period, a dialysis buffer (25 mmol/L HEPES, 1 mmol/L DTT, 0.1 % PMSF, 2 $\mu\text{g/ml}$ aprotinin, 0.1 mmol/L EDTA, and 11% glycerol) was added to the nuclei

preparation. Nuclei were collected by centrifugation for 20 min at 13,000 rpm. Aliquots (50 μ l) of the supernatants were frozen at -70°C , and protein concentration was determined. DNA retardation (mobility shift) electrophoresis assays were performed as previously described by Fried and Crothers.³¹ Briefly, 5 μ g nuclear extracts were incubated for 15 min in the presence of 5 X binding buffer (125 mmol/L HEPES, pH 7.5, 50 % glycerol, 250 mmol/L NaCl, 0.25 % Nonidet P-40, and 5 mmol/L DTT). End-labeled double-stranded consensus sequences of the LPL promoter PPAR-enhancing element (20 000 cpm per sample) were then added to the samples for 30 min. Samples were analyzed on a 4 % nondenaturing PAGE containing 0.01% Nonidet P-40. The specificity of the nuclear protein binding was assessed by incubating the nuclear proteins isolated from THP-1 macrophages with a labeled DNA probe in the presence of a 1,000-fold molar excess of unlabeled DNA probe.

DNA probes

The cDNA probes for detection of human LPL were prepared by the polymerase chain reaction technique. cDNA was obtained from total RNA using a reverse transcription reaction. Two synthetic primers spanning bases 255-287 and 1117-1149 of the LPL cDNA were used to enzymatically amplify a 894-bp region of the LPL probe. The cDNA probes for GAPDH were purchased from American Type Culture Collection. A 20-mer double-stranded oligonucleotide containing the peroxisome proliferator-responsive element (PPRE) consensus sequence of the human LPL gene promoter²⁴ (sense : 5'-CGTCTGCCCTTTCCCCCTCT-3'; antisense : 5'-GAGAAGAGGGGGAAAGG-3') was synthesized with the aid of an automated DNA synthesizer. After annealing, the double-

stranded oligonucleotide was labeled with [γ - 32 P] ATP using the Boehringer-Mannheim 5' end-labeling kit (Indianapolis, IN).

Determination of LPL immunoreactive mass and activity

2×10^6 human MDM and THP-1 macrophages were cultured for 1 to 3 days with PPAR α or γ ligands. One hour before the end of the incubation period, heparin (100 U/ml) was added to the medium. The amount of LPL immunoreactive mass in the supernatant was measured by enzyme-linked immunosorbent assay (ELISA) using the Markit-F-LPL kit.³² Extracellular LPL activity was determined in the supernatants using the Confluolip kit.³³ Levels of LPL immunoreactive mass and activity were normalized to total cell protein levels and expressed as percentages of basal values.

Determination of total protein concentrations

Total protein content was estimated according to the Bradford method³⁴ by using a colorimetric assay (Bio-Rad, Mississauga, Ontario, Canada), and bovine serum albumin as standard.

Determination of cell viability

Cell viability following treatment with the PPAR agonists was assessed by trypan blue exclusion. Although cell viability was consistently found to be higher than 85%, a decrease in this parameter was observed in macrophages treated with high concentrations (1 μ mol/L) of troglitazone.

Statistical Analysis

All values were expressed as the mean \pm SEM to the mean. Data were analyzed by one-way analysis of variance (ANOVA) followed by the Tukey test or the Dunn test. A P value less than 0.05 was considered statistically significant.

RESULTS

Effect of PPAR α and γ agonists on LPL secretion by human MDM.

To assess the effects of activators of PPARs on human macrophage LPL secretion, human MDM were incubated for 1 to 3 days in the presence of both natural and synthetic PPAR α and γ ligands. Incubation of human MDM with PPAR α (WY-14643 (10 μ mol/L), ETYA (20 μ M), clofibrate (100 μ mol/L)) or PPAR γ agonists (PGJ₂ (1 μ mol/L), BRL-49653 (20 nmol/L), troglitazone (0.01 μ mol/L), GI-251929X (1 μ mol/L)) led to a time-dependent increase in LPL mass and activity produced by these cells. Significant stimulation of LPL secretion into the medium was observed after a 2-day incubation period. Levels of MDM LPL mass and activity in response to PPAR α and γ agonists are illustrated in Fig.1A and B and Fig.1C and D, respectively.

Dose-dependent effects of PPAR α and γ agonists on LPL secretion by human MDM.

To identify the optimal concentration of PPAR α and γ agonists required to stimulate macrophage LPL secretion, human MDM were cultured with various concentrations of PPAR α and γ agonists for 2 days. As shown in Fig 2, PPAR α and γ agonists increased extracellular LPL immunoreactive mass and activity in a dose-dependent manner. The levels of LPL mass and activity in response to increasing concentrations of WY (1-10 μ mol/L) and clofibrate (10-100 μ mol/L), are illustrated in Fig.2A and B. Both agents, at a concentration of 10 μ mol/L, exerted similar and maximal stimulatory effect on LPL mass. In contrast, maximal effects of WY and clofibrate on

LPL activity occurred at 1 $\mu\text{mol/L}$ and 100 $\mu\text{mol/L}$, respectively. PPAR γ agonists also stimulate in a dose-dependent manner the secretion of LPL mass and activity into the culture medium (Fig.2C and D). Maximal effect of troglitazone and GI on LPL mass and activity occurred at 1 $\mu\text{mol/L}$ and 10 $\mu\text{mol/L}$, respectively.

Effect of PPAR α and γ ligands on human MDM LPL mRNA expression.

To determine the effects of PPAR agonists on human MDM LPL gene expression, PCR analysis was performed. Our results demonstrated a sustained increase in LPL mRNA expression following treatment of human MDM for 1 to 3 days with both PPAR α and γ ligands (Fig.3A and B). The effect of PPAR ligands on LPL gene expression was specific as reflected by the lack of modulation of the mRNA expression of the housekeeping gene GAPDH (Fig.3A and B). LPL mRNA levels, normalized to the levels of GAPDH mRNA are presented in Fig. 3A and B.

Molecular mechanisms involved in the stimulatory effect of PPAR α and γ ligands on macrophage LPL gene expression.

On the basis of our observation that PPAR agonists upregulate human MDM LPL gene expression, we next determined whether incubation of macrophages in the presence of PPAR α and γ agonists might induce changes at the level of the LPL gene promoter binding PPAR protein and LPL mRNA half-life. As part of a setup for subsequent gel-shift and mRNA stability data, LPL gene expression and protein levels in human MDM THP-1 cells exposed to these ligands were first determined.

Incubation of THP-1 macrophages with PPAR α ligands for 2 days increased LPL mRNA levels (Fig.4A). A similar effect was observed when these cells were treated with PPAR γ agonists (Fig.4D). In THP-1 cells exposed to PPAR α and γ agonists, a significant increase in extracellular LPL mass (Fig.4B and E) and activity (Fig.4C and F) was also observed.

Incubation of THP-1 macrophages with clofibrate and GI increased the binding of nuclear proteins to the PPRE consensus sequence of the LPL promoter (Fig. 5A). This binding was specifically competed in the presence of a 1,000-fold molar excess of the unlabeled PPRE oligonucleotide (Fig, 5A).

To investigate the possibility that PPARs agonists might affect the mRNA half-life of macrophage LPL, the half-life of LPL mRNAs was measured in THP-1 cells treated with clofibrate and GI after the addition of D-actinomycin. As shown in Fig. 5B, decreased rate of decay of LPL mRNA was observed in both clofibrate- and GI-treated cells.

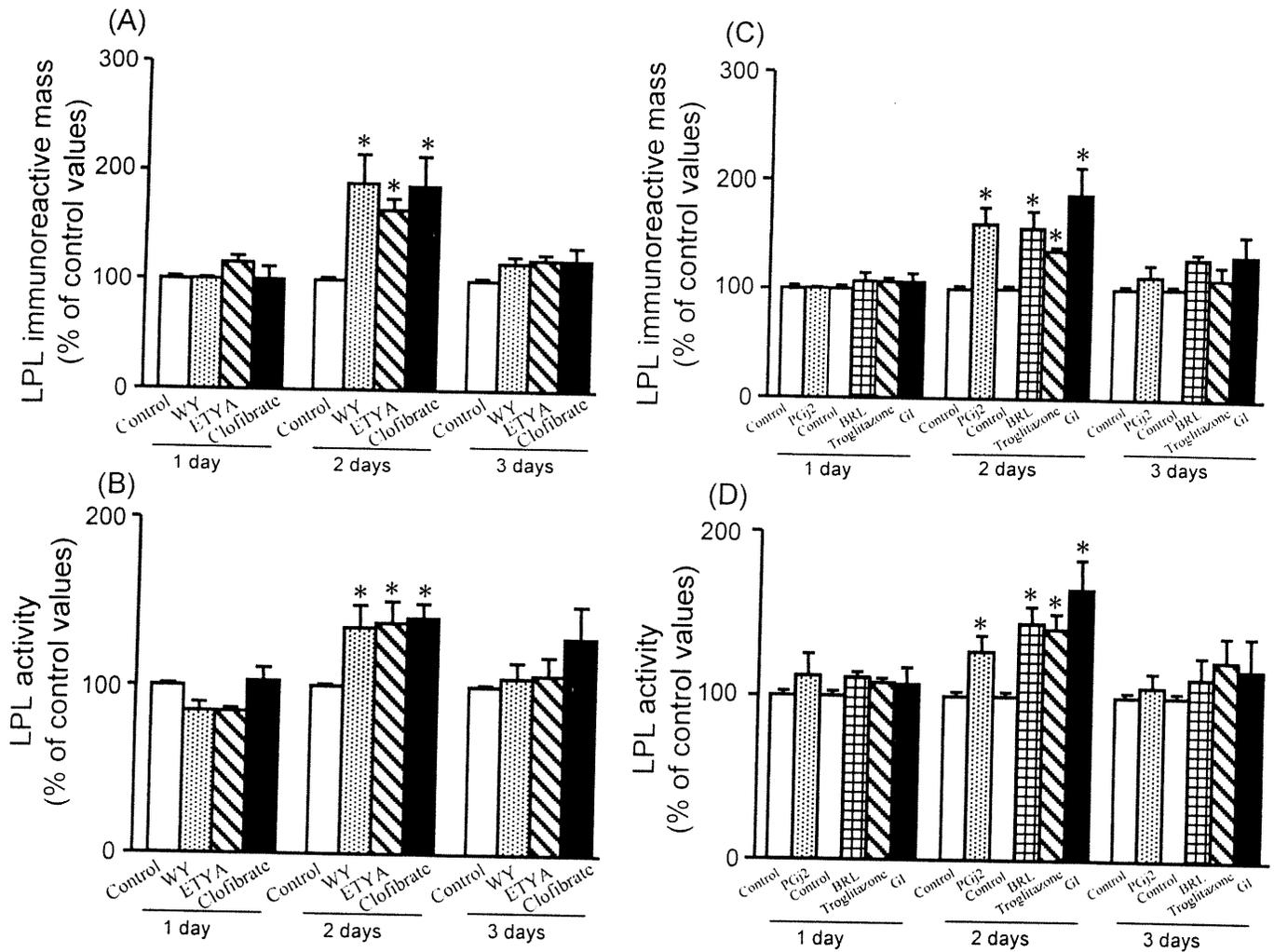


Figure 1. Effect of PPAR α and γ ligands on LPL immunoreactive mass and activity in human MDM. Human MDM were cultured for 1 to 3 days in presence of PPAR α ligands (WY-14643 (20 μ mol/L), ETYA (10 μ mol/L), clofibrate (100 μ mol/L) or PPAR γ ligands (PGJ₂ (1 μ mol/L), BRL-49653 (20 nmol/L), troglitazone (0.01/ μ mol/L), GI-251929X (1 μ mol/L)). At the end of the incubation periods, LPL immunoreactive mass (panels A, C) and activity (Panels B, D) were determined in the culture medium. Data represent the mean \pm SEM of 4 experiments, *, P < 0.05.

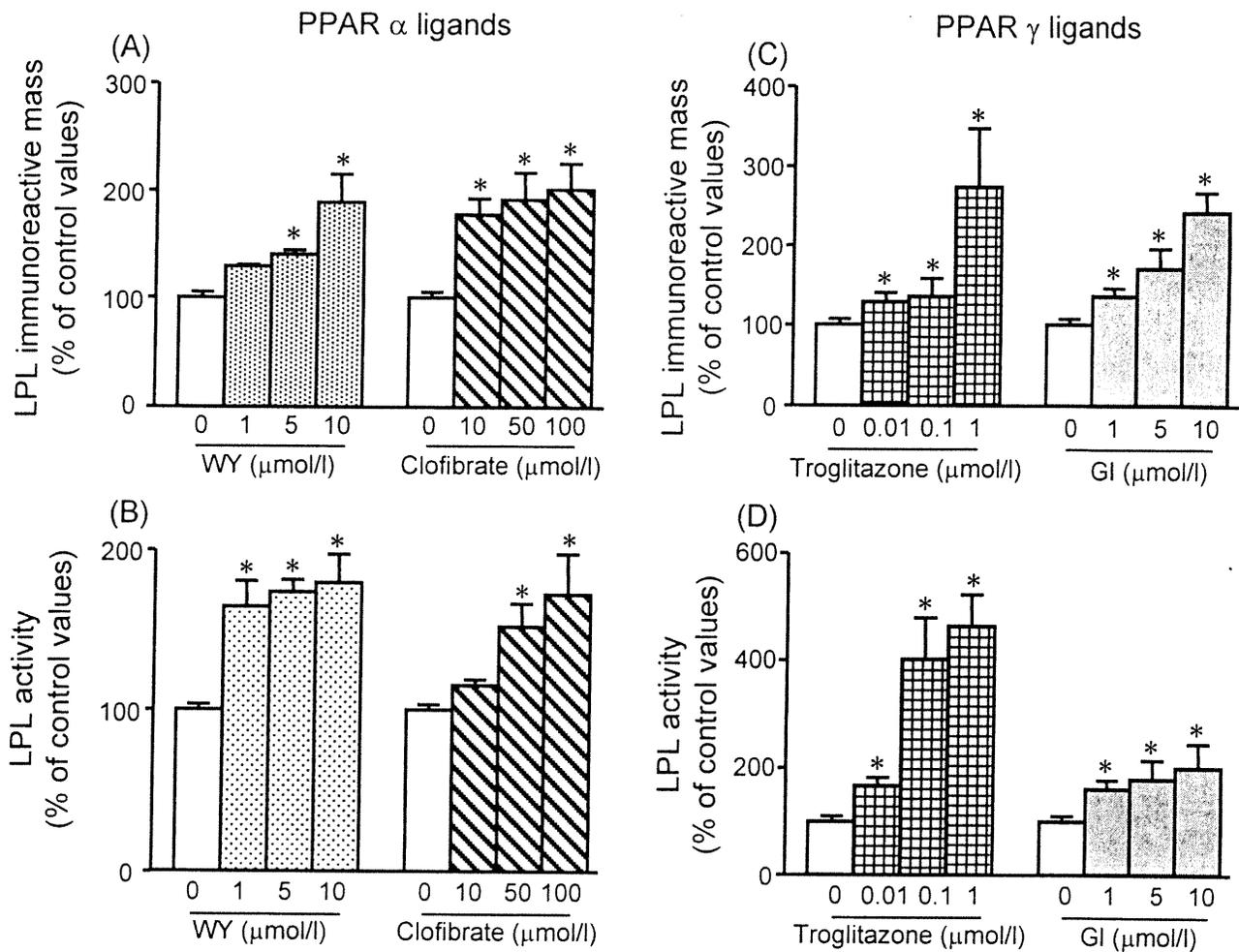


Figure.2. Dose-dependent effect of PPAR α and γ ligands on human MDM LPL immunoreactive mass and activity. Human MDM were treated for 2 days with increasing concentrations of PPAR α ligands or PPAR γ ligands. At the end of the incubation period, LPL immunoreactive mass (Panels A, C) and activity (Panels B, D) were determined in the culture medium. Data represent the mean \pm SEM of 5 experiments, *, $P < 0.05$.

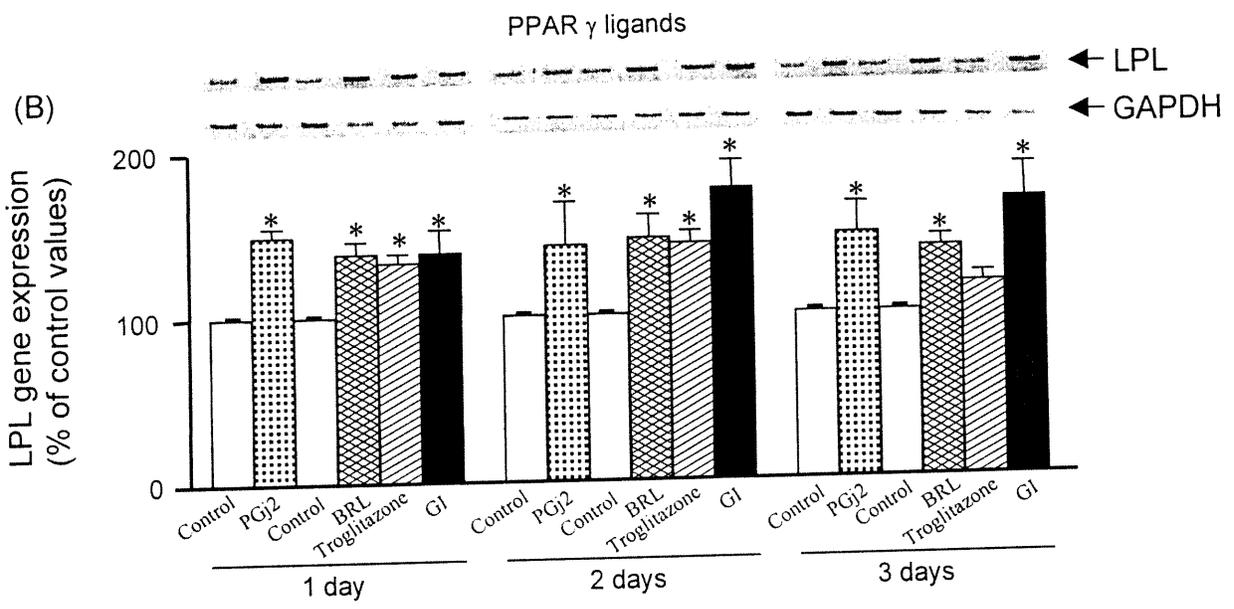
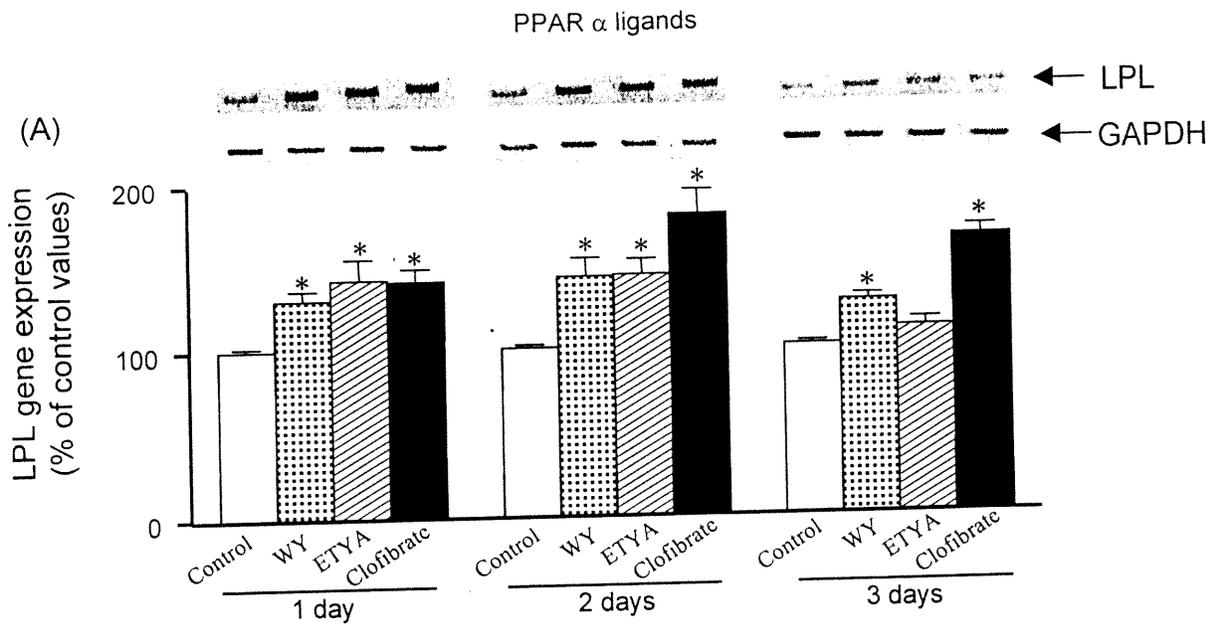


Figure.3. Effect of PPAR α and γ ligands on human MDM LPL mRNA levels. Human MDM were cultured for 1 to 3 days in presence of PPAR α ligands (Panel A) (WY-14643 (20 μ mol/L), ETYA (10 μ mol/L), clofibrate (100 μ mol/L) or PPAR γ ligands (Panel B) (PGJ₂ (1 μ mol/L), BRL-49653 (20 nmol/L), troglitazone (0.01 μ mol/L), GI-251929X (1 μ mol/L)). At the end of the incubation periods, human MDM were lysed. LPL and GAPDH mRNA expressions were analyzed by RT-PCR. Graphs represent the levels of LPL mRNA normalized to the levels of GAPDH mRNA. Data represent the mean \pm SEM of 5 experiments, *,P<0.05.

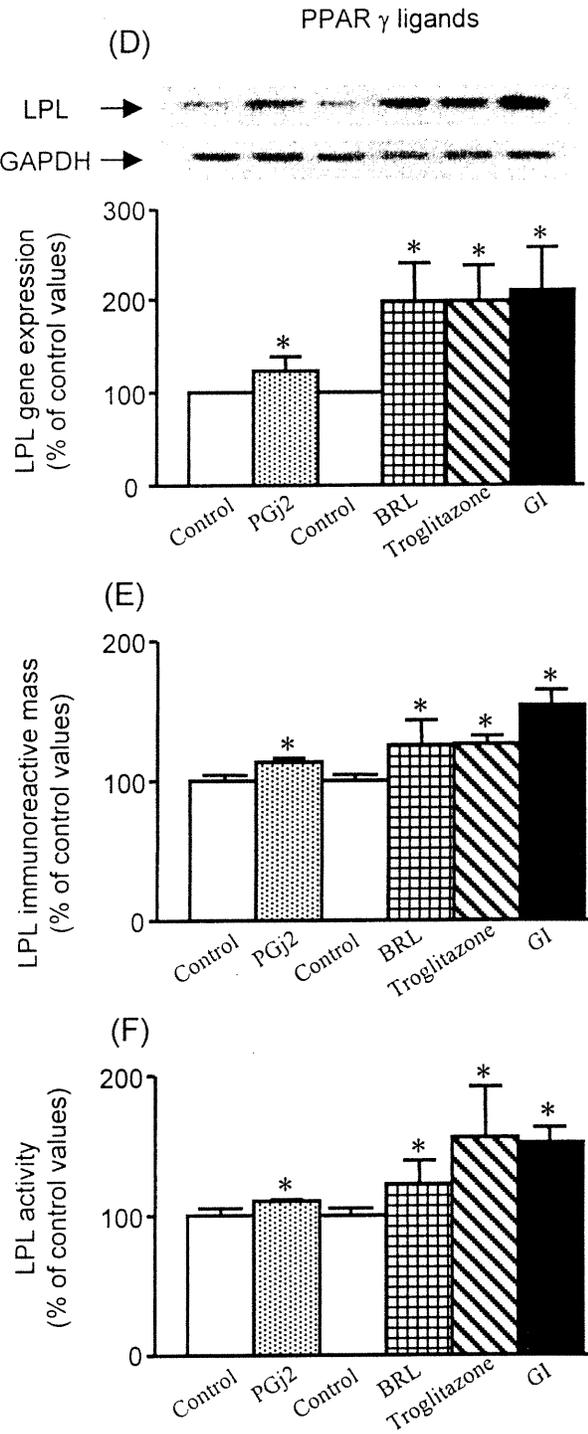
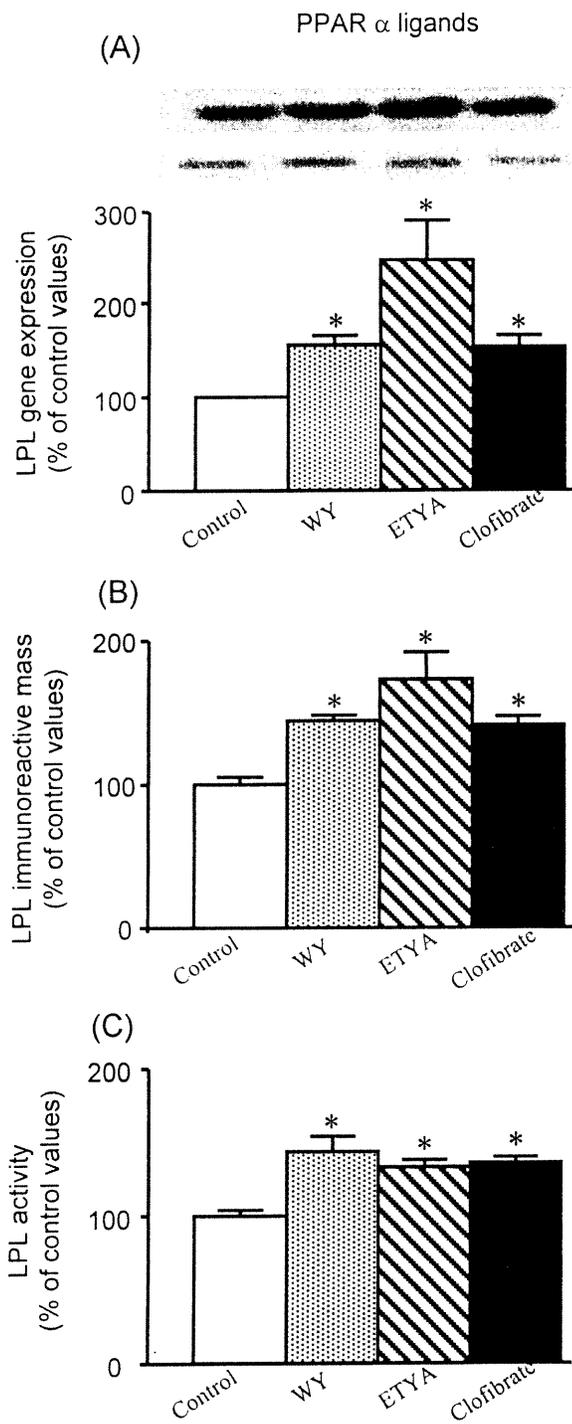


Figure. 4. Effect of PPAR α and γ ligands on LPL mRNA levels, mass and activity in THP-1 macrophages. THP-1 macrophages were treated for 2 days with PPAR α ligands (Panels A-C) (WY-14643 (20 μ mol/L), ETYA (10 μ mol/L), clofibrate (100 μ mol/L)) or PPAR γ ligands (Panels D-F) (PGJ₂ (1 μ mol/L), BRL-49653 (20 nmol/L), troglitazone (0.01 μ mol/L), GI-251929X (1 μ mol/L)). At the end of this incubation period, THP-1 macrophages were lysed. LPL and GAPDH mRNA expressions were analyzed by Northern blot analysis (Panels A,D). LPL immunoreactive mass (Panels B, E) and activity (Panels C, F) were determined in the culture medium. Data represent the mean \pm SEM of 5 experiments, *,P<0.05.

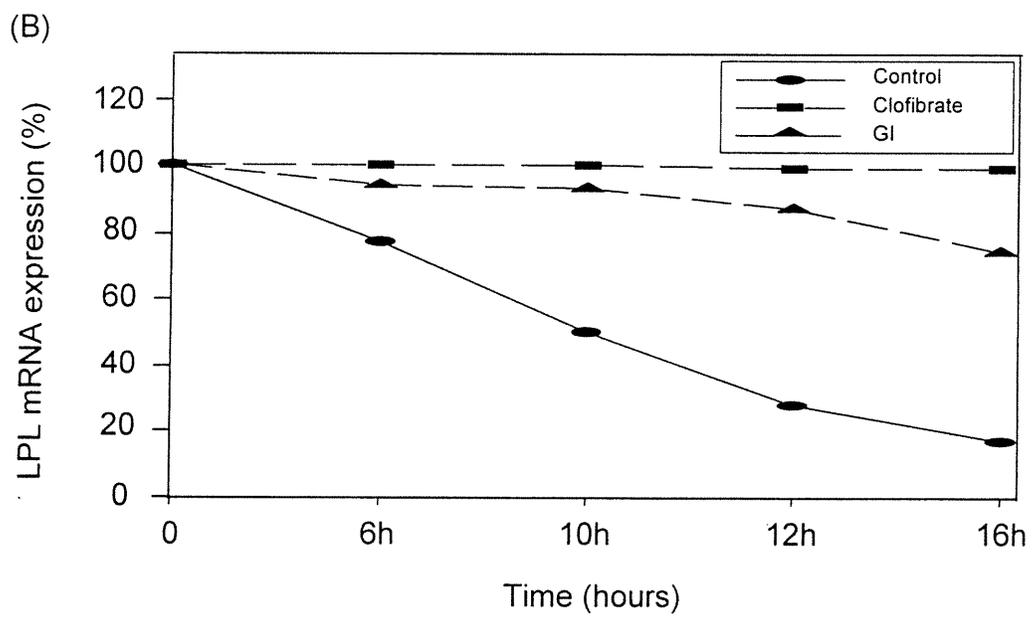
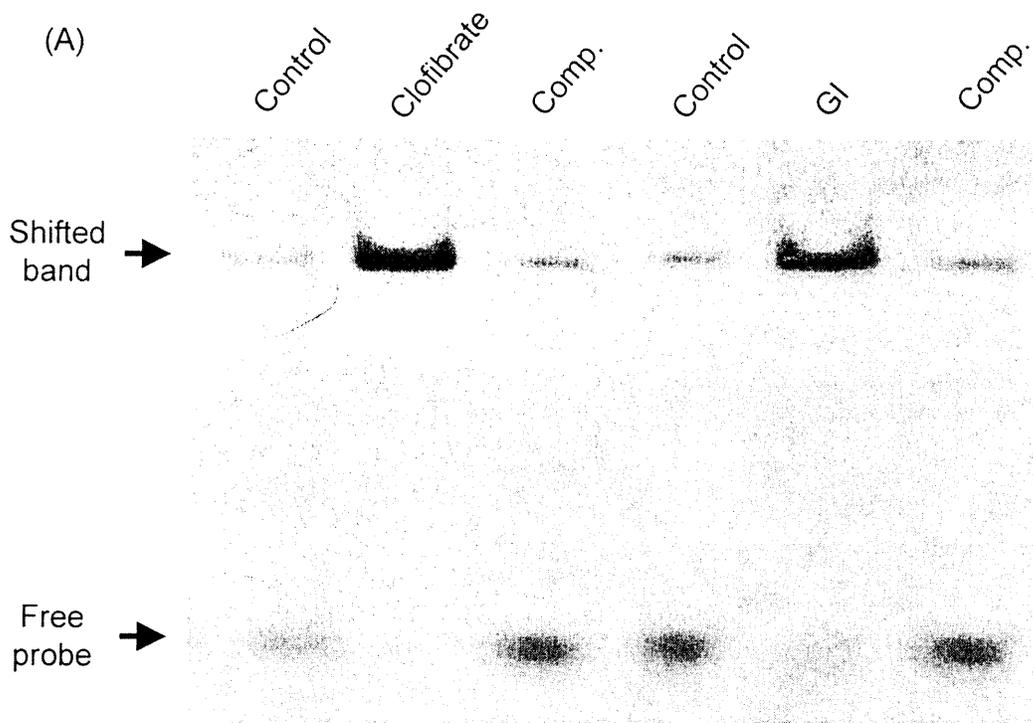


Figure. 5. Panel A: Effect of PPAR α and γ ligands on the binding of nuclear proteins to the regulatory PPRE sequence of the LPL gene promoter (A). THP-1 macrophages were cultured for 2 days in the presence of clofibrate (100 μ M) or GI (1 μ M). At the end of this incubation period, nuclear proteins were isolated from the cells and incubated with end-labeled double-stranded consensus sequences of the LPL promoter PPAR-enhancing element. Retardation was assessed by gel electrophoresis in 4% PAGE. Data are the results of one representative experiment out of three.

Panel B: Effect of PPAR α and γ ligands on the half-life of macrophage LPL mRNA. THP-1 macrophages were cultured for 2 days in the presence of clofibrate (100 μ M) or GI (1 μ M). Levels of LPL mRNA expression after 6, 10, 12, and 16 hours of actinomycin D treatment were calculated and plotted as a percentage expression compared with 100% of LPL mRNA extracted from cells exposed to these agents. Data represent the results of one representative experiment out of three.

DISCUSSION

The present study demonstrates for the first time that PPAR α and γ ligands increase human macrophage LPL expression, both at the mRNA and protein level. Our data showing that PPAR agonists upregulate macrophage LPL mRNA levels identify unequivocally the macrophage LPL gene as a response gene for PPAR action. Previous observations have demonstrated that PPAR α and γ activators induce LPL mRNA in liver and adipose tissue.²⁴⁻²⁵ Inducibility of LPL by these compounds was correlated with the distribution of the respective PPAR isoforms: an adipocyte-restricted expression of PPAR γ and a predominant expression of PPAR α in liver.²⁴ Our findings that PPAR α and γ ligands increase human MDM LPL mRNA expression is in accordance with previous results showing that human MDM express both PPAR α and γ ^{5,35} and that well characterized PPAR α and γ ligands, such as fatty acids, exert a direct modulatory effect on macrophage LPL gene expression.³⁶

The regulatory effect of PPAR agonists on human macrophage LPL gene expression may theoretically involve both transcriptional and/or post-transcriptional mechanisms. Our data which show that PPAR α and γ ligands increase the level of binding of nuclear proteins to a PPRE sequence element support the possibility that PPAR ligands may direct a transcriptional activation of the LPL gene via a PPRE sequence element. This possibility is supported by previous results demonstrating that a PPRE element present in the human LPL promoter mediates the functional responsiveness to fibrates and thiazolidinediones.²⁴ The hypothesis that PPAR ligands enhance the binding activity of the PPRE sequence in a PPAR-dependent manner awaits further studies aimed at evaluating the role of these agonists in LPL transcription

and reporter construct analysis. Alternatively, transcriptional activation of the macrophage LPL gene by PPAR agonists may occur through interference of activated PPARs with other transcription factor pathways, involved in LPL gene regulation such as stimulating protein-1.³⁷⁻³⁸ Future studies are required to determine whether LPL transcriptional activation by PPAR agonists may involve this mechanism.

Determination of the levels of LPL mass/activity in the culture media of human MDM clearly demonstrates that PPAR α and γ ligands lead to the production of increased amounts of catalytically active LPL. Although not very dramatic, the increased LPL secretion was observed with each of the agents used in the study. Because we tested a vast array of natural and synthetic PPAR ligands and used them at concentrations corresponding to their specific PPAR α or γ binding affinities, our data suggest that induction of macrophage LPL secretion in response to these agents involves PPAR activation. However, because PPAR ligands have many PPAR-independent effects,^{5,39-41} other mechanisms cannot be ruled out.

It is well known that LPL expression is controlled at both the transcriptional and post-transcriptional levels. Whereas adipocyte LPL regulation in response to PPAR γ ligands has been proposed to take place mainly at the post-transcriptional level⁴², our results suggest that regulation of macrophage LPL in response to PPAR agonists may involve both transcriptional and post-transcriptional events. The earliest point where post-transcriptional regulation can occur is at the level of LPL mRNA stability. Hattori et al recently demonstrated that troglitazone enhances nitric oxide synthase mRNA levels in vascular smooth muscle cells by prolonging its half-life.⁴³ In accordance with this observation, we found a decreased rate of decay of LPL mRNA in THP-1 cells exposed

to either PPAR α or γ ligands. These data indicate that PPAR α and γ ligands exert their stimulatory effect on macrophage LPL gene expression, at least partly, by enhancing LPL mRNA stability.

Data generated by time course and dose response experiments provide additional evidence that macrophage LPL expression in response to PPAR agonists may involve post-transcriptional events. One hand, results of time course experiments clearly indicate that induction of LPL secretion in response to PPAR agonists is transient despite a sustained increase of LPL mRNA levels from 1 to 3 days. This uncoupling between LPL gene expression and secretion suggests that regulation of macrophage LPL secretion in response to PPAR agonists occurs at the post-transcriptional level. On the other hand, treatment of human MDM with very low concentrations of PPAR agonists demonstrates increased secretion of inactive LPL but isolated activation of LPL activity in human MDM treated with clofibrate and WY, respectively. Such differential effect of PPAR activators on LPL mass and activity further suggest a regulation of macrophage LPL secretion in response to these agents at the post-translational level.

The discovery that PPARs are expressed in human atherosclerotic lesions and macrophage foam cells ⁸⁻¹¹ has raised many questions about their role on atherogenesis. While evidence has been provided that PPAR agonists modulate vessel wall function ^{9-13,35,44-48}, conflicting results have been generated about the role of PPARs in foam cell formation.^{9, 49-50} Although the findings that PPAR α and γ agonists lower the progression of atherosclerosis in humans and animals ⁵¹⁻⁵³ suggest a net in vivo anti-atherogenic effect of PPAR activation, Tordjman et al recently demonstrated that high-

fat-fed PPAR α -null mice develop less atherosclerosis.⁵⁴ Interestingly, these authors also documented higher levels of aortic mRNA for LPL in PPAR α $^{+/+}$ vs in PPAR α $^{-/-}$ mice. Based on the key role of macrophage LPL in atherosclerosis in vivo⁵⁵⁻⁵⁸, results of this study raise the possibility that decreased arterial wall LPL expression may represent a mechanism for less atherosclerosis in PPAR α $^{-/-}$ mice. These findings and our observations that PPAR α ligands increase macrophage LPL secretion in vitro further stress the crucial role of these agents in the regulation of vascular wall LPL expression.

Resolving the question whether PPAR ligands favor or inhibit atherogenesis in humans is of major clinical interest, especially for diabetic patients who are at high risk of accelerated atherosclerosis and are treated with PPAR agonists. The relevance of this question is further emphasized by our recent findings that human type 2 diabetes is associated with altered macrophage PPAR gene expression⁵⁹ and increased LPL secretion.⁶⁰ Detailed understanding of the role of PPARs in the regulation of vascular LPL expression and development of novel PPAR ligands that dissociate pro- and antiatherogenic properties will offer new strategies in the treatment of atherosclerosis.

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III. DISCUSSION

Cardiovascular diseases are the main cause of morbidity and mortality in diabetes. The high prevalence of these complications in diabetes results from accelerated atherosclerosis in diabetic patients.

LPL, an enzyme known to undergo significant functional alterations in the diabetic state, acts as a proatherogenic protein in the vessel wall. Indeed multiple studies indicate that LPL produced by macrophages in the vascular wall favors the development of atherosclerosis by promoting lipid accumulation within atherosclerotic lesions [O'Brien et al. 1992, Yla-Herttuala et al. 1991, Mattsson et al. 1994, Van Eck et al. 2000, Santamarina-Fojo et al. 2000].

PPARs, like LPL, are key factors in atherogenesis [Fruchart et al. 1999, Sartippour et al. 2000, Plutzky et al. 2000]. PPARs are transcriptional factors that regulate the expression of several genes encoding proteins involved in lipid metabolism, including LPL. For example, PPAR α activation increases apoA1 and apoAII transcription and interferes with HDL-mediated reverse cholesterol transport [Vu-Dac et al. 1994, 1995]. This PPAR isoform also stimulates LPL expression [Schoonjans et al. 1996] and inhibits the expression of apoCIII [Staels et al. 1995]. PPAR γ also regulates lipid metabolism and acts as a regulator of adipocyte differentiation [Fajas et al. 1998, Spiegelman et al. 1997, Rosen et al. 1999].

The present study investigated LPL gene expression in human and THP-1 macrophages in response to PPAR ligands. We showed that PPAR α and PPAR γ ligands directly enhanced macrophage gene expression in both THP-1 and human MDM. It is well known that the regulation of LPL gene expression is controlled by several *cis*- and *trans*-acting factors, such as PPRE, AP-1 and SP-1 regulatory elements, present in the LPL promoter [Enerback et al. 1993]. Schoonjans et al. [1996] have demonstrated that PPAR α and PPAR γ ligands induce in vivo LPL mRNA levels selectively in the liver and adipose tissue, respectively. PPAR γ ligands have also been shown to increase LPL mRNA levels in adipocytes [Ranganathan and Kern, 1998].

Evidence has been provided that transcriptional activation of the LPL gene by PPAR α and γ ligands is mediated by the interaction of PPAR-RXR heterodimers with PPRE in the LPL promoter [Schoonjans et al. 1996]. This possibility has been supported recently by Sartippour et al. [2000], who reported that anti-PPAR α decreases glucose-induced enhancement of nuclear protein binding to the PPRE regulatory domain of the LPL gene. It has also been established that PPAR can repress gene transcription by a combination of protein-protein interaction and co-factor squelching without binding to PPRE. For example, promoter studies have revealed that PPAR γ inhibits the transcriptional activity of iNOS, MMP-9 and scavenger receptor A genes by interfering with AP-1, NF- κ B and STAT-1 transcription factors [Ricote et al. 1998]. Krey et al. [1995] also demonstrated that the PPAR/RXR heterodimer interacts with SP-1 on the native TATA-less acyl-coenzyme-A (ACO) promoter. Based on such findings,

one may postulate that PPAR ligands may interfere positively with these transcriptional factors to regulate LPL gene expression. Further studies are necessary to delineate which transcriptional factor is responsible for PPAR signaling on LPL gene expression.

The selective affinity of PPAR α and PPAR γ ligands for PPARs has been well-documented [Lin et al. 1999, Lehmann et al. 1995, Forman et al. 1995, Willson et al. 1996], but their effect on human macrophage LPL expression was investigated for the first time in our experiments. Our data demonstrated unequivocally that both PPAR α and PPAR γ ligands increase macrophage LPL gene expression.

Although our data showed a similar magnitude of LPL mRNA changes upon exposure of macrophages to PPAR α or PPAR γ ligands, we found a temporal difference of LPL mRNA expression in PPAR α - and PPAR γ -ligand-treated THP-1 MDM (data not shown). Indeed, our results demonstrated that in THP-1 MDM, PPAR γ ligands induced LPL gene expression by day 1, whereas PPAR α ligands heightened LPL gene expression by day 2. These results are consistent with those of Schoonjans et al. [1996] which demonstrate that the PPAR γ ligand, BRL 49653, induces preadipocyte LPL mRNA levels much quicker than the PPAR α ligand, fenofibrate [Schoonjans et al. 1996]. The mechanisms responsible for the slower kinetics of LPL mRNA induction after PPAR α ligand treatment are unknown.

Our data also showed that the response of LPL gene expression to various PPAR agonists is not consistent. For example, among the PPAR α

ligands, clofibrate is most potent in human MDM, but a maximal increase in THP-1 MDM is observed with ETYA. In addition, among the PPAR γ agonists, the synthetic ligands, BRL, troglitazone, and GI are more potent than the natural ligand PGJ2 in inducing THP-1 MDM LPL gene expression, whereas similar responses are observed in response to all these ligands in human MDM. While species specificity in ligand recognition has been well documented between human and mouse, these results further suggest that specificity in ligand recognition may also occur in different human macrophage model systems. Whether specific characteristics of the transformed THP-1 macrophages are responsible for such differences is presently unknown.

Overall, our results demonstrate that both PPAR α - and PPAR γ -ligands are potent inducers of LPL mRNA levels in human macrophages. Because LPL expression is controlled at both the transcriptional and post-transcriptional levels, the amounts of LPL mass and activity secreted by human macrophages in response to PPAR α and γ agonists were next determined.

Several studies are consistent with LPL regulation in a tissue- and cell-specific manner [Eckel et al. 1989, Ding et al. 2000], notably in different macrophages [Behr et al. 1986, Hulten et al. 1996]. In 1983, Robinson et al. suggested that LPL could exist in the cell as an inactive precursor that required for its activation the presence of apoCII. Vannier et al. [1986] have shown that LPL is localized mainly in the Golgi, thereby establishing that the enzyme is a secretory protein. Today it is well established that LPL, in its active form, plays a central role in the overall lipid metabolism of the body. Specifically, the major role

of this enzyme in hydrolyzing TG-rich lipoproteins such as chylomicrons and VLDL and directing triglyceride-fatty acid traffic to fulfill the energy requirements of peripheral tissues is well documented [Robinson et al. 1983, Borensztajn et al. 1987, Ladu et al. 1991].

Both the hydrolytic and structural properties of LPL are involved in the regulatory effect of this enzyme on lipid metabolism. Indeed, LPL has been demonstrated to increase the cell association of lipoproteins by its bridging function [Goldberg et al. 1996] and recent experiments in transgenic mice expressing catalytically inactive LPL have provided evidence for LPL bridging in vivo [Merkel et al. 1998].

Alterations of LPL regulation have been associated with several disorders such as hypertriglyceridemia [Eckel et al. 1989] and atherogenesis [Babaev et al. 1999, 2000]. Because of the major role of LPL in both physiological and pathological states, there has been recently a great interest in studying the regulation of LPL (mass and activity) secretion by different cells and under various experimental conditions.

Relevantly, the present investigation demonstrates for the first time that both PPAR α and PPAR γ ligands increase the amount of extracellular LPL immunoreactive mass and activity in THP-1 and human MDM. Despite the fact that both cell types release more LPL in response to PPAR agonists, their response to these agents also differs in many ways: Firstly, the amount of LPL protein secreted upon exposure of these cells to PPAR ligands is significantly higher in human macrophages than in THP-1 MDM. In addition, in contrast to

human MDM, PPAR ligands only moderately enhance LPL mass and activity in THP-1 cells, thereby leading to the production of small amounts of catalytically active LPL. The response of LPL to the various PPAR ligands also differs between the THP-1 cells and human MDM. Among the PPAR α ligands, ETYA is most potent in THP-1 MDM while a maximal increase in human MDM is observed with WY and clofibrate. Differential response of THP-1 and human MDM to PPAR agonists may be linked to preferential binding affinity of these compounds for either cell types. Alternatively, involvement of differential signal transduction pathways and/or molecular events may explain, at least partly, the specific response of these cells to the different compounds tested in our study. This hypothesis is supported by recent results showing the involvement of several signal transduction pathways, such as protein tyrosine phosphatase activity [Maegawa et al. 1995] and calcium fluxes [Buchanan et al. 1995] in the effect of PPAR ligands.

It is well-established that LPL gene expression is controlled at both the transcriptional and post-transcriptional levels. Our results which demonstrate that PPAR ligands induced parallel changes in macrophage LPL mRNA levels, mass and activity at day 2 suggest that macrophage LPL regulation in response to these agents occurs at least partly at the transcriptional level. While this possibility is supported by the finding that fibrates regulate apoCIII and LPL at the transcriptional level [Stael et al. 1992, 1995], it is in contrast with other results showing that treatment of preadipocytes with PPAR γ ligands increase LPL mRNA levels but inhibit LPL activity [Ranganathan and Kern, 1998]. These results which

demonstrate differential regulation of macrophage and adipocyte LPL in response to PPAR agonists further stress the complex and cell-specific regulation of LPL. Our result also suggest that regulation of macrophage LPL in response to PPAR agonists may involve post-transcriptional events. Indeed, results of time course experiments clearly indicate that induction of LPL secretion in response to PPAR agonists is transient despite a sustained increase of LPL mRNA levels from 1 to 3 days. This uncoupling between LPL gene expression and secretion suggests that regulation of macrophage LPL secretion in response to PPAR agonists occurs at the post-transcriptional level. On the other hand, treatment of human MDM with very low concentrations of PPAR agonists demonstrate increased secretion of inactive LPL but isolated activation of LPL activity in human MDM treated with clofibrate and WY, respectively. Such differential effect of PPAR activators on LPL mass and activity further suggests a regulation of macrophage LPL secretion in response to these agents at the post-translational level.

PPAR ligands may induce macrophage LPL mRNA levels by altering mRNA stability. Previous studies have demonstrated that LPS and IFN γ decrease LPL mRNA stability [White et al. 1988, Jonasson et al. 1990]. Moreover, Ranganathan et al have demonstrated that adipocyte LPL translation is regulated by a catecholamine-activated protein that binds to the 3' untranslated region of the mRNA [Ranganathan et al. 1997]. Recently, Hattori et al [1999], demonstrated that troglitazone enhances nitric oxide synthase mRNA levels in vascular smooth muscle cells by prolonging its half-life. To evaluate the

possibility that PPAR ligands may affect macrophage LPL gene expression by altering LPL mRNA stability, we measured the half-life of LPL mRNA in THP-1 MDM exposed to PPAR ligands. In accordance with this observation, we found a decreased rate of decay of LPL mRNA in THP-1 cells exposed to either PPAR α or γ ligands. These data further establish that macrophage LPL is controlled both at the transcriptional and posttranscriptional levels by PPARs ligands.

It has been well documented that many PPAR agonists exhibit, when used at high concentrations, activity towards both PPAR α and PPAR γ . For example, ETYA which fully activates PPAR α at a concentration of 1 μ M, with an ED 50 of 200nM, [Keller et al. 1993] also activates PPAR γ at high concentrations. Conversely, PGJ2 which is specific for PPAR γ at low concentrations acts as a PPAR α ligand at high concentrations. Examination of the ligand specificities of PPARs is complicated by the need to physically separate protein-bound and free ligands for measurement of equilibrium dissociation constants (K_d). Determination of the K_d s for the formation of PPAR ligand-receptor complexes indicates that the formation of ligand-protein complexes is in the range of 10-50 μ M in vitro, which is higher than the ligand concentration of 5-60 nM in vivo [Lin et al. 1999]. The concentrations of the PPAR agonists used in our study have been chosen according to the estimated K_d of each compound. For example most of the thiazolidinediones have been found to have affinities for PPAR γ between 30 nM (BRL49653) and 700 nM (troglitazone), while WY14643 exhibits high specificity for PPAR α at a K_d value of 10 μ M. It should be noted that normal therapeutic doses of troglitazone result in blood levels that exceed its K_d for the

receptor. Given that full and specific agonist activity on PPAR α or PPAR γ will ultimately depend on its concentrations, we chose to use these compounds at concentrations that do not exceed their K_d s. This careful experimental approach allows us to strongly suggest that the observed stimulatory effect of the PPAR agonists tested in our study on macrophage LPL expression are mediated through PPAR activation and to relate these effects to PPAR α or γ activation. Dose response studies have also resulted in identification of optimal concentration of each ligand. Results of these studies demonstrate that both PPAR α and γ ligands induce human macrophage LPL mass and activity in a dose-dependent manner. They also establish a differential stimulatory effect of low concentrations of PPAR α ligands on LPL mass and activity, indicating a posttranslational control of this enzyme by these agents.

It has been well documented that the different PPAR isoforms are characterized by distinct tissue- and cell-specific expression patterns and exhibit distinct activation by various ligands. These observations suggest highly specific functions for each of these PPAR subtypes. While PPAR α is mostly present in tissues characterized by high rates of fatty acid catabolism, such as the liver and plays a key role in lipid metabolism [Kliwer et al. 1994, Braissant et al. 1996], PPAR γ is adipose tissue selective and is implicated as a mediator of adipocyte differentiation and regulation of glucose homeostasis [Chawla et al. 1994, Tontonoz et al. 1995].

Recent findings demonstrate that PPARs are also expressed in vascular cells. Indeed expression of both PPAR α and PPAR γ has been documented in

endothelial cells [Delerive et al. 1999, Marx et al. 1999, Inoue et al. 1998, Chinetti et al. 2000, 1998, Xin et al. 1999], SMCs [Staels et al. 1998, Iijima et al. 1998, Marx et al. 1998, Law et al. 2000] and monocytes/macrophages [Chinetti et al. 1998, Ricote et al. 1998, Tontonoz et al. 1998, Marx et al. 1998]. In contrast to PPAR α which is already expressed by human monocytes, PPAR γ is not detectable in human monocytes but is strongly induced upon differentiation of monocytes into macrophages [Chinetti et al. 1998].

LPL is also induced during the differentiation of monocytes [Chait et al. 1982]. Various lines of evidence have suggested that LPL secreted by macrophages and by macrophage-derived foam cells in the vessel wall [Yla-Herttuala et al. 1991, O'Brien et al. 1992] favors foam cell formation and atherosclerosis in vivo [Babaev et al. 1999, idem 2000, Semenkovich et al. 1998, Van Eck et al. 2000]. Macrophage LPL may promote atherosclerosis through a variety of mechanisms, including 1) monocyte recruitment and retention in the artery wall [Saxena et al. 1992, Mamputu et al. 1997, Obunike et al. 1997], 2) promotion of lipoprotein uptake by macrophages [Lindqvist et al. 1983, Aviram et al. 1987, Valdimir et al. 1999], and 3) increased retention of lipoproteins in the extracellular matrix through LPL-mediated bridging with proteoglycans [Saxena et al. 1992, Susanne et al. 2000].

LPL and PPARs share many features. Both factors play a key role in lipid metabolism and are expressed by macrophages in the arterial wall. Both also exhibit a parallel induction during the differentiation process of monocytes into

macrophages and have been shown to play a key role in arterial lipid metabolism and foam cell formation [Babaev et al. 1999, Tontonoz et al. 1998].

Our finding that PPAR ligands upregulate human macrophage LPL expression further supports the possibility that PPAR expressed in the arterial wall may regulate the production of macrophage LPL at vascular sites. Based on the key role of macrophage LPL in foam cell formation and on previous observations showing that PPAR γ activators may favor influx of lipids in macrophages, one may postulate that induction of LPL may represent one mechanism involved in PPAR-induced lipid uptake in macrophages. Future experiments aimed at comparing cholesterol influx in macrophages that are LPL $^{-/-}$ vs LPL $+/+$ in response to PPAR ligands will be conducted to evaluate this possibility.

Evidence that PPAR ligands stimulate macrophage LPL secretion further supports the possibility that PPARs are important modulators of atherosclerosis development. Despite the accumulating evidence showing that PPARs affect vascular cell function, there is still a considerable debate regarding the role of these compounds in atherogenesis. Indeed, many studies have demonstrated that PPARs may exert both pro- and anti-atherogenic effects. When considering the role of PPAR α agonists in atherogenesis, several studies have demonstrated the potential of these compounds to regulate the inflammatory processes in the arterial wall. Activation of PPAR α has been found to potentiate TNF- α -induced human macrophage apoptosis [Chinetti et al. 1998] and to increase CLA-1/SR-BI expression [Chinetti et al. 1999]. Both effects may result in reduced foam cell

content and activity in atherosclerotic lesions. Activation of PPAR α has also been documented to inhibit IL-6 secretion from mouse vessel wall ex vivo [Delerive et al. 1999], monocyte binding to human aortic endothelial cells and VCAM-1 expression on the endothelial cell surface [Jackson et al. 1999, Marx et al. 1999]. This latter effect has been suggested to result from the negative cross-talk between PPAR α and the transcription factor, NF- κ B [Marx et al. 1999]. Such inhibition is consistent with the recent findings of Delerive et al showing that fibrates inhibit the vascular inflammatory response via PPAR α by interfering with NF- κ B and AP-1 transactivation capacity [Delerive et al. 1999]. It has also been reported that PPAR α ligands repress thrombin-induced expression of endothelin-1 (ET-1), a potent vasoconstrictor peptide and inducer of SMC proliferation [Delerive et al. 1999]. Activation of PPAR α has also been shown to inhibit inflammatory responses in vascular SMC. Indeed evidence has been provided that PPAR α ligands inhibit cytokine-induced IL-6 production and cyclooxygenase-2 expression in these cells [Staels et al. 1998]. The anti-inflammatory effects of PPAR α agonists on vascular SMC appear to be mirrored in vivo as suggested by the reduction of plasma levels of IL-6 following administration of fenofibrate to patients with hyperlipidemia [Satels et al. 1998]. Further support for the anti-atherosclerotic effects of PPAR α agonists comes from recent studies showing that fenofibrate decreases atherosclerotic plaque formation [Saitoh et al. 1995, Fruchart et al. 2001].

In contrast, several reports suggest some pro-inflammatory effects of PPAR α . For example, it has been reported that the natural PPAR α ligands LTB₄

and 8(S)-HETE stimulate nitrite accumulation in monocytes/macrophages, suggesting that these agonists may exert some pro-inflammatory properties in the arterial wall [Colville-Nash et al. 1998]. Hill et al. [1999] found that in mice, fibrates markedly increase plasma TNF- α levels. Recently, Hans et al. [2000] demonstrated that PPAR α plays a role in mediating the effects of oxidized phospholipids on endothelial cell synthesis of the monocyte chemoattractants, MCP-1 and IL-8. Finally, Sartippour et al. [2000] recently suggested that PPAR α could mediate the stimulatory effect of high glucose on macrophage LPL gene expression.

Many studies have also examined the influence of PPAR γ in atherosclerosis. Studies aimed at examining the role of PPAR γ activators on macrophage function have shown that these agents promote macrophage apoptosis [Chinetti et al. 1998] and favor the differentiation of human monocytes and the uptake of oxLDL by macrophages through the induction of the oxLDL receptor CD36 [Tontonoz et al. 1999]. It has also been reported that constituents of oxLDL and products of 15-lipoxygenase activity promote foam cell formation and macrophage gene expression through PPAR γ activation [Nagy et al. 1998]. Moreover, it has been documented that constituents of oxLDL and products of 15-lipoxygenase activity promote foam cell formation and macrophage gene expression through PPAR γ activation [Nagy et al. 1998]. Another study from Huang et al also reported that IL-4 mediates CD36 expression via the induction of PPAR γ [Huang et al. 1999]. Based on these results it has been proposed that oxLDL and PPAR γ are involved in a positive feedback loop in which oxLDL

induces PPAR γ expression leading to increased CD36 expression which increases oxLDL uptake, subsequently reinforcing the positive feedback cycle. If these effects are reproduced in vivo, then activation of PPAR γ could contribute to the development of foam cells. An explosion of new information has led to the concept that PPAR γ ligands affect both the influx and efflux of cholesterol and oxidized lipids in macrophages, stimulating cholesterol removal from macrophages through downregulation of SR-A scavenger receptor [Moore et al. 2001] and stimulation of the ABCA1 pathway [Chinetti et al. 2001]. Recent observations showing that treatment of low density lipoprotein receptor-deficient or apoE knockout mice with PPAR γ ligands inhibits fatty streak lesion formation seem to support a net in vivo anti-atherogenic effect of PPAR γ activation in foam cells [Li et al. 2000, Chen et al. 2001]. PPAR γ has also been found to inhibit macrophage activation as demonstrated by the reduction of gelatinase B, inducible nitric oxide synthase activity/expression and TNF- α , IL-1 β , and IL-6 production. [Ricote et al 1998, Tontonoz et al. 1998]. Some of these effects have been related to the inhibitory effect of PPAR γ ligands on the activity of pro-inflammatory transcription factors including AP-1, STAT and NF- κ B. PPAR γ agonists also reduced the secretion and gelatinolytic activity of the metalloproteinase MMP-9 [Marx et al. 1999, 1998]. This anti-inflammatory effect of PPAR γ could be beneficial in the treatment of atherosclerosis. PPAR γ ligands also modulate endothelial cell function. For example, both inhibitory and stimulatory effects of these agents on plasminogen activator inhibitor-I release have been reported [Kato et al. 1999, Marx et al. 1999] and the ability of PPAR γ

agonists to inhibit secretion of ET-1 has been reported [Sato et al. 1999, Delerive et al. 1999]. These ligands also inhibit monocyte adhesion and the expression of the endothelial cell adhesion molecule, VCAM-1 [Jackson et al. 1999]. Furthermore, they could reduce monocyte recruitment into the artery wall by inhibiting endothelial cell production of MCP-1 [Mura et al. 1999]. It has also been reported that the PPAR γ activators pioglitazone and troglitazone inhibit in experimental models neo-intimal thickening, hypertrophy and hyperplasia [Dubey et al. 1993, Law et al. 1996, Igarashi et al. 1997, Shinohara et al. 1998]. While the ability of PPAR γ agonists to inhibit SMC proliferation has been well documented [Dubey et al. 1993, Law et al. 1996, Morikang et al. 1997], these compounds also reduce SMC migration [Marx et al. 1998] and calcium entry in these cells [Zhang et al. 1994, Song et al. 1997, Asano et al. 1999]. Recently, it has been shown that PPAR γ ligands reduce carotid artery intima and media thickness in patients with type 2 diabetes [Minamikawa et al. 1998] and inhibit development of atherosclerosis in LDL receptor-deficient mice [Li et al. 2000]. Interestingly, Sartippour et al. [2000] reported a reduction of PPAR γ mRNA expression in MDM isolated from patients with type 2 diabetes. A similar alteration was observed in human macrophages exposed in vitro to high glucose concentrations [Sartippour et al. 2000].

Overall, these data indicate that PPAR agonists may directly modulate vessel wall function and that these agents are likely important modulators of atherosclerosis development. Whether our results showing the ability of PPAR activators to stimulate macrophage LPL expression indicates a pro- or an anti-

atherogenic effect of PPAR α agonists is presently unknown. While such an effect may be considered as “protective” in the early stage of atherogenesis, it may also contribute later to increased foam cell formation and activity in atherosclerotic lesions.

IV. PERSPECTIVES AND CONCLUSION

IV.1. Perspectives

Although we have demonstrated that PPARs increase macrophage LPL expression both at the gene and protein levels, the functional relevance of the upregulation of macrophage LPL by PPARs remains unclear. To address this question, we propose to conduct future studies aimed at examining macrophage foam cell formation in LPL^{-/-} vs LPL^{+/+} mice in response to PPAR agonists. These studies will also allow to identify the role of LPL in PPAR-induced foam cell formation.

Experiments aimed at determining the molecular mechanisms involved in the induction of macrophage LPL gene expression by PPARs will also be conducted. In particular the possibility that these agents may regulate this gene by interacting with other nuclear factors, such as stimulating protein-1, will be evaluated.

Finally, we propose to further investigate the mechanisms involved in the differential regulation of macrophage PPAR expression in human type 2 diabetes [Sartippour et al. 2000]. Decreased macrophage PPAR γ expression in diabetes may theoretically involve TNF- α . Indeed it has been shown that high glucose stimulates TNF- α secretion [Morohoshi et al. 1995] and that this cytokine, in turn, exerts a suppressive effect on PPAR γ expression [Xing et al. 1997, Zhang et al. 1996]. Because advanced glycation end products accumulate in the blood and tissues of patients with diabetes and that these products increase the production of human monocyte and macrophage TNF- α [Morohoshi et al. 1996, Sartippour et al. 1998] and induce PPAR expression in mesangial cells [Iwashima et al.

1999], it will also be of major interest to characterize in the future the modulatory effect of these factors on macrophage PPAR expression.

IV.2. Conclusion

The present study provides the first evidence of a direct regulatory effect of PPAR agonists on human macrophage LPL gene expression and secretion. Our data showing that PPARs control macrophage LPL expression further stress the crucial role of these factors in the regulation of arterial lipid metabolism. The finding that PPARs agonists increase macrophage LPL production suggests a new mechanism by which these agents may favor foam cell formation and influence atherosclerosis. A detailed understanding of the role of PPARs in the regulation of vascular biology and the development of novel PPAR ligands that dissociate pro- and anti-atherogenic properties will offer new strategies in the treatment of atherosclerosis.

V. REFERENCES

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