

Université de Montréal

**Modulation of Endothelin-1 and Insulin-like Growth Factor
Type 1-induced Signaling by Curcumin in A-10 Vascular
Smooth Muscle Cells**

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Ce mémoire intitulé :

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Résumé

Les maladies cardio-vasculaires (MCV), telles que l'hypertension et l'athérosclérose, s'accompagnent de modifications structurales et fonctionnelles au niveau vasculaire. Un fonctionnement aberrant de la migration, l'hypertrophie et la prolifération des cellules musculaires lisses vasculaires (CMLV) sont des évènements cellulaires à l'origine de ces changements. L'endothéline-1 (ET-1) contribue à la pathogénèse des anomalies vasculaires, notamment via l'activation des protéines MAPK et PI3-K/PKB, des composantes clés impliquées dans les voies prolifératives et de croissance cellulaires. Il a été suggéré que le stress oxydant jouerait un rôle intermédiaire dans les effets pathophysiologiques vasculaires de l'ET-1. En conséquence, une modulation de la signalisation induite par l'ET-1 peut servir comme éventuelle stratégie thérapeutique contre le développement des MCV. Il apparaît de nos jours un regain d'intérêt dans l'utilisation des agents phyto-chimiques pour traiter plusieurs maladies. La curcumine, constituant essentiel de l'épice curcuma, est dotée de plusieurs propriétés biologiques parmi lesquelles des propriétés anti-oxydantes, anti-prolifératrices et cardio-protectrices. Cependant, les mécanismes moléculaires de son effet cardio-protecteur demeurent obscurs. Dans cette optique, l'objectif de cette étude a été d'examiner l'efficacité de la curcumine à inhiber la signalisation induite par l'ET-1 dans les CMLV. La curcumine a inhibé la phosphorylation des protéines IGF-1R, PKB, c-Raf et ERK1/2, induite par l'ET-1 et l'IGF-1. De plus, la curcumine a inhibé l'expression du facteur de transcription Egr-1 induite par l'ET-1 et l'IGF-1, dans les CMLV. Ces résultats suggèrent que la capacité de la curcumine à atténuer ces voies de signalisation serait un mécanisme d'action potentiel de ses effets protecteurs au niveau cardiovasculaire.

Mots-clés : CMLV, Curcumine, Egr-1, ERK1/2, ET-1, IGF-1, IGF-1R, PKB.

Abstract

Cardiovascular diseases (CVDs), including hypertension and atherosclerosis, are associated with vascular functional and structural changes. Some of the cellular events underlying these processes include aberrant vascular smooth muscle cell (VSMC) proliferation, hypertrophy and migration. Endothelin-1 (ET-1) has been implicated in the pathogenesis of vascular abnormalities through the hyperactivation of key components of growth promoting and proliferative signaling pathways, including MAPKs and PI3-K/PKB. Vascular oxidative stress has also been suggested to play an intermediary role in mediating ET-1-induced pathophysiological effects. Interference with ET-1-induced signaling may therefore serve as a potential therapeutic strategy against the progression of cardiovascular disorders. There is presently a surge of interest in the use of plant-derived phytochemicals for the treatment of various diseases. Curcumin, the main constituent of the spice turmeric, exhibits multiple biological properties, amongst them, antioxidant, anti-proliferative and cardioprotective properties. However, the molecular mechanisms of its cardiovascular protective action remain obscure. Therefore, in the present studies, we investigated the effectiveness of curcumin to inhibit ET-1-induced signaling events in VSMC. Curcumin inhibited ET-1-induced as well as IGF-1-induced phosphorylation of IGF-1R, PKB, c-Raf and ERK1/2, in VSMC. Furthermore, curcumin inhibited the expression of transcription factor early growth response-1 (Egr-1) induced by ET-1 and IGF-1, in VSMC. In summary, these results demonstrate that curcumin is a potent inhibitor of ET-1 and IGF-1-induced mitogenic and proliferative signaling events in VSMC, suggesting that the ability of curcumin to attenuate these effects may contribute as potential mechanism for its cardiovascular protective response.

Keywords: Curcumin, Egr-1, ERK1/2, ET-1, IGF-1, IGF-1R, PKB, VSMC

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Liste des abréviations, sigles et acronymes

ANF	atrial natriuretic factor
Ang II	Angiotensin II
ANP	atrial natriuretic peptide
AP-1	activator protein 1
ApoE	apolipoprotein E
AT1R	Angiotensin II type 1 receptor
BAD	Bcl-2 associated death promoter
Bcl-2	B-cell lymphoma 2
bFGF	basic fibroblast growth factor
BNP	brain natriuretic peptide
Ca ²⁺	calcium
cGMP	cyclic guanosine monophosphate
CHF	chronic heart failure
COX-2	cyclooxygenase-2
CSF	colony-stimulating factors
CVD	cardiovascular disease
DAG	diacylglycerol
DOCA	deoxycorticosterone acetate
ECE	endothelin converting enzyme
EGF	epidermal growth factor
EGF-R	epidermal growth factor receptor
Egr-1	early growth response-1
eNOS	endothelial nitric oxide synthase
ERK	extracellular signal-regulated kinase
ET	endothelin
ET _A	endothelin receptor type A
ET _B	endothelin receptor type B
FGF	fibroblast growth factor

G protein	guanosine nucleotide binding protein
GDP	guanosine diphosphate
GPCR	guanosine nucleotide binding protein-coupled receptor
GPx	glutathione peroxidase
Grb2	growth factor receptor-bound protein 2
GSK-3	glycogen synthase kinase 3
GSH	glutathione
GST	glutathione-s-transferase
GTP	guanosine triphosphate
H ₂ O ₂	hydrogen peroxide
HAT	histone acetyltransferase
HDL	high density lipoprotein-cholesterol
HIF	hypoxia inducible factor
HO-1	heme oxygenase-1
IGF-1	insulin-like growth factor type 1
IGF-1R	insulin-like growth factor type 1 receptor
IL	interleukin
iNOS	inducible nitric oxide synthase
ISO	L-isoproterenol
IR	insulin receptor
IRS	insulin receptor substrate
IP ₃	inositol triphosphate
JNK	c-Jun N-terminal kinase
kDa	kiloDalton
LDL	low-density lipoprotein-cholesterol
L-NAME	N ^o -nitro-L-arginine methyl ester
LOX	lipoxigenase
LOX-1	oxidized low density lipoprotein receptor 1
MAPK	mitogen activated protein kinase
MEF2	myocyte enhancer factor 2

MEK	mitogen extracellular regulated kinase
MI	myocardial ischemia
MMP	matrix metalloproteinase
mTOR	mammalian target of rapamycin
NADPH oxidase	nicotinamide adenine dinucleotide phosphate oxidase
NF-1	nuclear factor 1
NF- κ B	nuclear factor kappa-light-chain-enhancer of activated B cells
NO	nitric oxide
(O ₂ ^{·-})	superoxide anion
(OH [·])	hydrogen radicals
(ONOO ⁻)	peroxynitrite
p53	tumor protein 53
p70 ^{s6k}	p70 ribosomal S6 kinase
p90 ^{rsk}	p90 ribosomal kinase
PDGF	platelet derived growth factor
PDGF-R	platelet derived growth factor receptor
PDK	phosphoinositide-dependent kinase
PH	pleckstrin homology
PI3-K	phosphatidylinositol 3-kinase
PI	phosphatidylinositol
PI (4,5)P ₂	phosphatidylinositol 4, 5 triphosphate
PI (3, 4,5)P ₃	phosphatidylinositol 3, 4, 5 triphosphate
PLC β	phosphoinositide-specific phospholipase C β
PKB	protein kinase B
PKC	protein kinase C
PTK	protein tyrosine kinase
PTPase	phosphatase
PYK-2	proline-rich tyrosine kinase
R-PTK	receptor protein tyrosine kinase
ROS	reactive oxygen species

SH2	src homology 2
Shc	src homology collagen
SHR	spontaneously hypertensive rat
SHP-2	SH2 domain-containing tyrosine phosphatase-2
SOD	superoxide dismutase
SOS	son of seven less
STAT	signal transducer and activator of transcription
TNF- α	tumour necrosis factor- α
TGF- β	transforming growth factor- β
VSMC	vascular smooth muscle cell

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CHAPITRE 1

INTRODUCTION

Cardiovascular diseases (CVDs), including hypertension, atherosclerosis and heart failure, are among the most encountered pathologies that affect developed countries. Even though significant advances in diagnosis and treatment have been introduced, CVDs remain one of the leading causes of mortality and morbidity. Many pathways are implicated in the regulation of cardiovascular homeostasis and a variety of factors can contribute to the onset of CVDs. Among those factors are two important vasoactive peptides, endothelin-1 (ET-1) and angiotensin II (Ang II), that play an important physiological role in regulating vascular tone and blood pressure. Alterations in the regulation of these vasoactive peptides can contribute to the pathogenesis and progression of numerous CVDs. High levels of ET-1, associated with increased activation of growth promoting and proliferative signaling, are present and implicated in several CVDs, including hypertension, atherosclerosis and heart failure. Therefore, targeting the ET-1 system may be helpful for the management of these conditions and their associated complications. In this regard, the last decade has witnessed a surge of interest in investigating the potential role of various plant derived substances, such as curcumin that exhibit cardiovascular protective effects. Therefore, the objective of this section is to provide a brief overview on the aspects of the ET-1 system and its contribution to the pathophysiology of CVDs, as well as a brief overview on curcumin and its mechanism of action at the molecular level, with particular interest to its role in the cardiovascular system.

1.1. Endothelin

Endothelin (ET), discovered by Dr. Yanagisawa's group in 1988 (1), is one of the most prominent known vasoconstrictors that also exhibits inotropic, chemotactic and mitogenic properties, influences salt and water homeostasis, and stimulates the renin-angiotensin-

aldosterone as well as the sympathetic nervous systems (1, 2). ET plays a crucial role in cardiovascular physiology. The overall physiologic action of ET is to increase vascular tone and blood pressure (2). Alteration of this system has been associated with several CVDs (3). These events establish ET as a potentially important mediator in the pathogenesis of cardiac, vascular and renal abnormalities such as hypertension, atherosclerosis, hypertrophy, and restenosis (4). ET exerts its physiological action through the activation of several signal transduction pathways linked to cellular hypertrophy, migration and proliferation in several cell types, including vascular smooth muscle cells (VSMC) (5).

1.2 Structure of endothelins

ET exists as three 21 amino acid isopeptides named ET-1, ET-2 and ET-3. Three independent genes, located on chromosome 6, 1, and 20, respectively, encode the three structurally and pharmacologically distinct isopeptides (6). A proposed fourth member was later shown to be rodent homologue to human ET-2, rather than a truly novel isoform (7). ETs possess a great sequence homology with four further peptides, known as sarafotoxins, extracted from the venom of a snake, *Atractaspis engaddensis* (8). All ET isopeptides share a common cyclic structure that consists of two disulfide bridges joining the cysteine amino acids (positions 1-15 and positions 3-11) at the N-terminal end, a cluster of three polar charged side chains on amino acid residues 8-10 and a hydrophobic C-terminus containing an aromatic indole side chain at Trp²¹ (Figure 1.1). The C-terminal end contains amino acids that bind to the ET receptor while the N-terminal determines peptide affinity to the receptor (9). ET-2 contains two amino acid substitutions and shares 90% sequence homology with ET-1. ET-3 contains six amino acid substitutions and shares 71% sequence

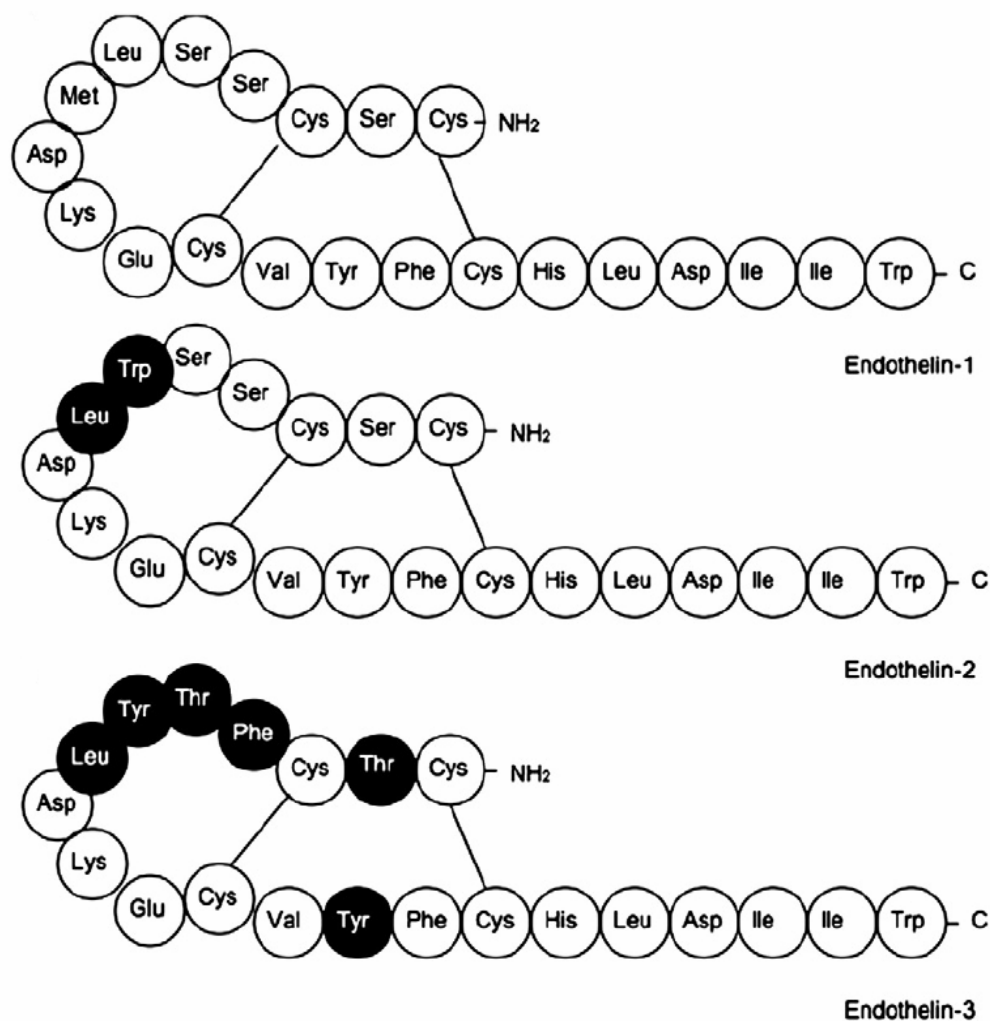


Figure 1.1 Structure of the isoforms of endothelin (ET).

Endothelin (ET) is a 21 amino acid cyclic peptide with two disulphide bridges joining the cysteine residues at positions 1-15 and 3-11. The amino acids highlighted in black represent the differences in between ET-2 and ET-3 compared to ET-1. (Khimji AK : *Cellular Signalling* 22: 1615-1625, 2010).

homology with ET-1 and ET-2. Amongst the three ETs, ET-1 is regarded as the most prominent isoform synthesized by the vasculature (1) and accounts for the majority of the pathobiological effects exerted by the ETs (10).

1.3 ET-1 regulation of generation and sites of generation

The regulation of ET-1 production is achieved at the transcriptional level of the preproET-1 gene (11). ET-1 expression is regulated at the promoter region (5') of the preproET-1 gene where there are binding sites for activator protein 1 (AP-1) and nuclear factor 1 (NF-1) transcription factors, which mediate the induction of mRNA for ET-1, through regulation by Ang II and transforming growth factor- β (TGF- β), respectively (12-14). Further post-transcriptional modulation occurs through selective destabilization of the preproET-1 mRNA via adenine-uracil-rich sequences, present in the non-translated 3' region, accounting for its selectively short biological half life of 15-20 minutes (15). ET-1 mRNA is upregulated by various stimuli, including vasoactive hormones, growth factors, hypoxia, low vascular shear stress, lipoproteins, free radicals, endotoxin and cyclosporin (16). However, ET-1 production is downregulated by high shear stress and by compounds that increase intracellular levels of cyclic guanosine monophosphate (cGMP), such as endothelium-derived nitric oxide (NO), nitrovasodilators, natriuretic peptides, heparin and prostaglandins (Figure 1.2) (16).

Vascular endothelial cells are the main site of ET-1 synthesis (6), which also correlates with the high expression levels of mRNA for ET-1 precursor molecule preproET-1 and its converting enzyme. VSMC also express ET-1 mRNA, but its production is 100 fold less than that of endothelial cells (15). Even in very low concentrations, ET-1 is also

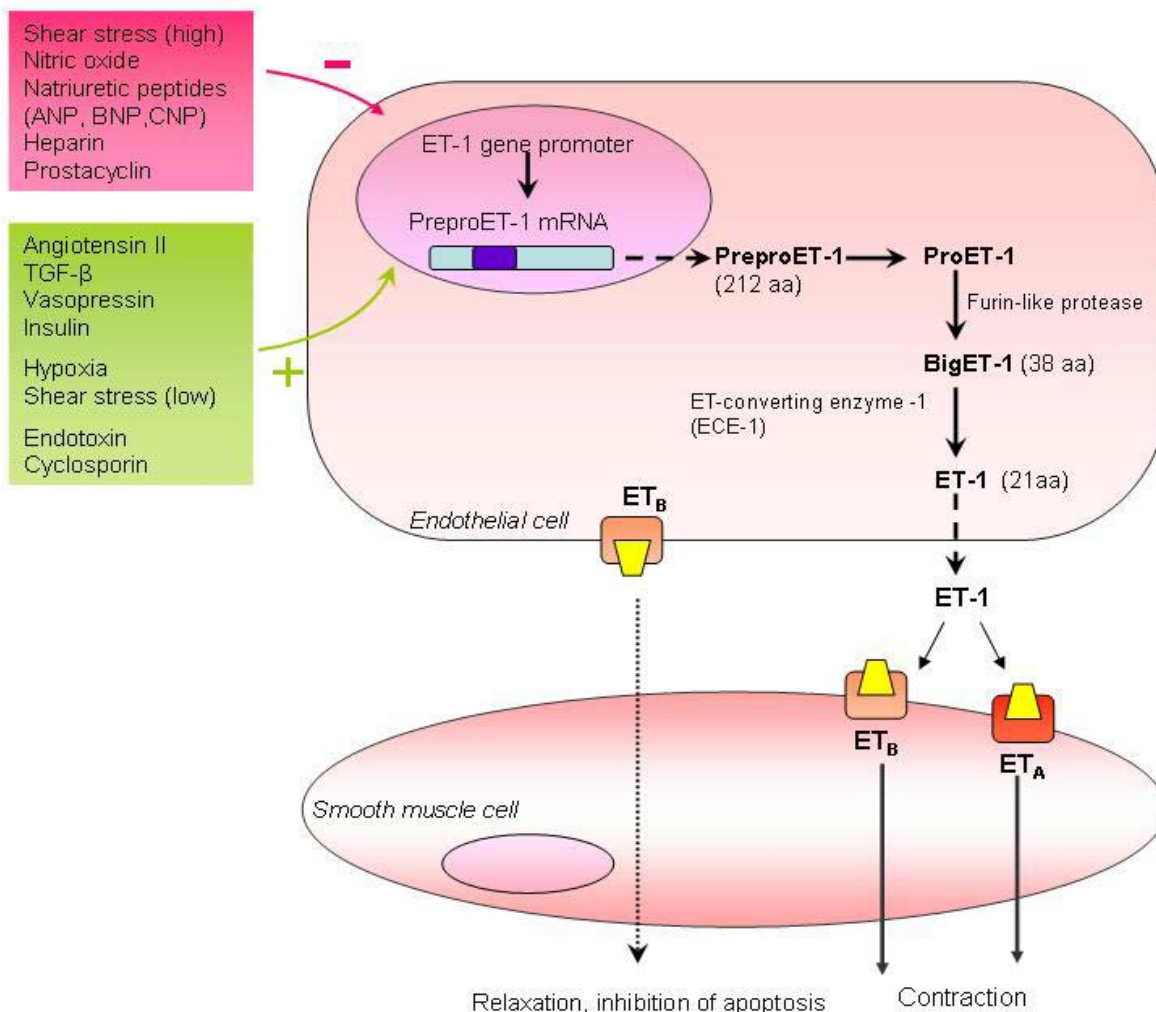


Figure 1.2 Factors regulating ET-1 synthesis, pathway of ET-1 generation and ET receptor-mediated actions on smooth muscle cells.

ET-1 synthesis is regulated by multiple factors; stimulators are highlighted in green and inhibitors in red. The synthesis of ET-1 begins with the transcription product preproET-1 (212 aa), which is cleaved to form proET-1. Pro-ET-1 undergoes cleavage by a furin-like protease to form bigET-1 (38aa) that is converted to mature ET-1 (21 aa) by endothelin converting enzyme-1 (ECE-1). ET type-A (ET_A) receptors are found in vascular smooth muscle cells and mediate vasoconstriction and cell proliferation, while ET_B receptors reside on endothelial and smooth muscle cells and mediate vasodilatation. ANP, atrial natriuretic peptide; BNP, brain natriuretic peptide; CNP, C-type natriuretic peptide; TGF- β , transforming growth factor β . (Remuzzi et al: *Nature Reviews Drug Discovery* 1: 986-1001, 2002).

produced by the heart, kidney, lung, posterior pituitary and central nervous system (10, 16, 17). In the cardiovascular system, ET-2 and ET-3 are expressed at very low levels.

1.4 Biosynthesis of ET-1

Several processing steps are required before the mature ET-1 peptide is formed (Figure 1.2). ET-1 synthesis begins with the transcription of the preproET-1 gene. The translation of the preproET-1 mRNA yields a large 212 amino acid precursor molecule, preproET-1. The latter is converted to proET-1 through the removal of its signal sequence and secreted into the cytoplasm (2). ProET-1 then undergoes a proteolytic cleavage at dibasic sites by a furin-like protease to form a biologically inactive 38 amino acid peptide, bigET-1 (18). BigET-1 is cleaved between Trp²¹ and Val²², in the rate limiting step in ET-1 synthesis, by the ET-converting enzyme-1 (ECE-1) metalloproteinase to yield the mature 21 amino acid bioactive ET-1 peptide (9). ET-1 has been known to be synthesized in a constitutive *de novo* manner and mature ET-1 is directly released into the bloodstream (11). Evidence suggests that in certain cells it is also secreted via pathways involving secretory granules (19). In fact, secretory vesicles containing both mature ET-1 and ECE have been identified in endothelial cells (20). ET-1 secretion by endothelial cells occurs in a polar manner, where most of ET-1 is secreted on the basal side, resulting in 100 fold higher concentrations within the vascular wall compared to plasma levels (21). Thus, under normal physiological conditions, ET-1 is not a circulating hormone but rather a locally-acting autocrine/paracrine factor (10).

1.5 Bioavailability and clearance of ET-1

In healthy subjects, the circulating concentrations of ET-1 in venous plasma are in the range of 1-10pmol/L (15). Circulating concentrations of ET-1 are lower than those which cause

vascular constriction *in vitro* and *in vivo*, although concentrations at the interface between an endothelial cell and VSMC are likely to be higher (15). Indeed, endothelial cells secrete substantially more ET-1 towards VSMC than they do lumenally (21). Thus, the circulating level of ET-1 might not directly reflect the full physiological impact of ET-1. Venous plasma ET-1 concentrations of bigET-1 and C-terminal fragments, when they are cleaved by ECE-1, appear to reflect generation of ET-1 more accurately (22). The low plasma levels of ET may be related to rapid elimination from the bloodstream.

ET levels are controlled by continuous metabolism/clearance. Clearance of ET-1 from circulation is very rapid, and its biological half life is about 1 minute, owing to its efficient extraction in the pulmonary and renal vascular beds (23). This extraction involves binding to the cell surface ET_B receptors, followed by internalization and degradation, probably within lysosomes (24). ETs are also degraded by neutral endopeptidases found in kidney proximal tubules (24). The liver is also a site of ET-1 clearance (25). On the contrary to its rapid elimination, its biological effects last considerably longer, possibly due to the almost irreversible binding of ET-1 to its receptor (26). For instance, its pressor effects are sustained for up to an hour (27) and it has been shown that ET-1 remains associated with ET receptor up to two hours after endocytosis (28).

1.6 ET-1 receptors

ET-1 exerts its biological effects in a paracrine/autocrine fashion through the activation of its receptors. Two main ET receptor subtypes, ET_A and ET_B, have been cloned in humans (29, 30). These receptors belong to the rhodopsin class A of seven transmembrane guanine nucleotide-binding protein-coupled receptors (GPCRs), which stimulate cellular events by

activation of heterotrimeric guanine nucleotide binding proteins (G proteins). They contain seven transmembrane domains of 22-27 hydrophobic amino acids in their estimated 400-amino acid sequences with an N-terminal extracellular region and C-terminal intracellular region (29, 30). Each receptor is capable of coupling to different G protein families. ET_A and ET_B receptors share 59% polypeptide sequence identity and are encoded by distinct genes located on chromosomes 4 and 13, respectively (31, 32). ET-1 receptors have different molecular and pharmacological characteristics and exhibit somewhat different physiological roles based on their location. ET_A receptors contain 427 amino acids (31) and are predominantly expressed in VSMC but are also found in cardiomyocytes, fibroblasts, hepatocytes, adipocytes, osteoblasts and brain neurons (29, 33), and exhibit higher affinity for ET-1 and ET-2 than for ET-3 (29). ET_B receptors contain 442 amino acids (31) and are predominantly expressed in endothelial cells, however, a relatively low level of expression in other cells including VSMC, cardiomyocytes, hepatocytes, fibroblasts, osteoblasts, different types of epithelial cells and neurons has been reported (30). ET_B receptors have equal subnanomolar affinities for all ET peptides (30).

Stimulation of ET_A and ET_B receptors elicits diverse physiological responses. ET-1 binding to ET_A and ET_B receptors on VSMC produces vasoconstriction, cell growth and cell adhesion (18). Conversely, ET-1 binding to endothelial ET_B receptors causes vasorelaxation through the release of vasodilators acting on VSMC, prevents endothelial cell apoptosis, inhibits ECE-1 expression within endothelial cells and is involved in ET-1 clearance (18). Thus, the net effect produced by ET-1 on the vasculature is determined on the receptor localization and the balance between ET_A and ET_B receptors.

1.7 Biological actions of ET-1 in the cardiovascular system

In the vasculature, ET-1 is involved in the basal vascular tone regulation. It induces a biphasic response represented by a transient vasodilatation followed by a sustained vasoconstriction. Endothelial cell ET_B receptors mediate vasodilatation through the production of endothelium-derived vasodilators, such as NO and prostacyclin, before the development of sustained vasoconstriction. Vasoconstriction is mediated by ET-1 activation of ET_A and ET_B receptors located on VSMC. The prolonged vasoconstriction is not dependent on ET-1 plasma levels but rather on the slow dissociation from its receptors (34). The vasoconstrictor effect is selective for some vascular beds. In animals, the coronary and renal vascular beds exhibit higher vasoconstriction to systemic administration of ET-1 (35). Systemic administration of ET-1 in humans induces sustained vasoconstriction in coronary vessels (36), but also causes renal and splanchnic vasoconstriction (37, 38). The differences among beds may be related to the balance between ET_A and ET_B-mediated effects.

ET-1 has been also shown to increase blood pressure *in vivo* in both animals and humans. In animals, bolus administration and intravenous infusion of ET-1 increased arterial pressure and this effect lasted for at least one hour before arterial pressure returned to base-line levels (39). In humans, intravenous infusion of ET-1 increased blood pressure in healthy volunteers (36, 40). Bolus administration of ET usually causes a preceding transient hypotension, which is mostly marked for ET-3 (6) and is mediated by endothelin ET_B receptors. This does not occur when ET concentrations rise more slowly, which is more likely to represent physiological conditions (39).

ET-1 is also synthesized in the heart by cardiomyocytes, cardiac fibroblasts and cardiac endothelial cells (41). The reported biological effects of the ET system on the healthy heart are

mainly positively inotropic in association with a negative lusitropic effect (33), positively chronotropic and hypertrophic (42). However, the ET system is upregulated in chronic heart failure, and ET-1-induced sustained coronary vasoconstriction may result in the deterioration of cardiac function causing myocardial ischaemia leading to fatal ventricular arrhythmias and cardiac hypertrophy (43, 44). Under such conditions, ET-1 exerts systemic and coronary vasoconstriction leading to increased afterload and reduced cardiac output (45). ET-1 induces cardiac hypertrophy, through its mitogenic properties, as an adaptational mechanism to stresses such as pressure overload (46-48).

ET-1 also exerts long-term effects in the vasculature, such as vascular remodeling, by promoting smooth muscle proliferation (49), protein synthesis (50), and production of a variety of cytokines (51) and growth factors (52). ET-1 also potentiates the mitogenic effects of growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF) and basic fibroblast growth factor (bFGF) and is considered as a co-mitogen with these growth factors (53).

1.8 Role of ET-1 in cardiovascular diseases

Dysregulation of the ET system is significantly involved in the development of cardiovascular pathologies, such as hypertension, atherosclerosis, cardiac hypertrophy, congestive heart failure and coronary artery disease, as well as CVDs linked to diabetes, pulmonary hypertension, pulmonary fibrosis, kidney failure and other important processes. ET-1 is believed to play a role in vascular remodeling associated with experimental and human hypertension (54). ET receptor antagonists that have been developed help to investigate the role of ET-1 in CVDs (48).

1.8.1 ET-1 in hypertension

1.8.1.1 ET-1 in experimental hypertension

Evidence of pressor action of ET-1 has led to the speculation that ET-1 is involved in the pathogenesis of hypertension (1). In fact, ET-1 plasma levels are found to be significantly increased in certain animal models of hypertension (55). Deoxycorticosterone acetate (DOCA) salt-hypertensive rats, DOCA salt-treated spontaneously hypertensive rats (SHR), Dahl salt-sensitive rats, Ang II-induced hypertension, 1-kidney 1-clip Goldblatt hypertensive rats, and stroke-prone SHR are all experimental models of hypertension that exhibit an increase in systemic levels of ET-1. The increased production of vascular ET-1 in these hypertensive models is associated with hypertrophic remodeling of resistance arteries, and a response to both selective and mixed ET receptor antagonism resulted in a reduction in blood pressure as well as a regression of vascular growth (55). ET-1 has been shown to activate nicotinamide adenine dinucleotide phosphate (NADPH) oxidase and increase reactive oxygen species (ROS) production in VSMC, in blood vessels and in hypertensive rats (56, 57). The growth-promoting remodeling action of ET-1 may be partly mediated by this increase in ROS production (58). In aldosterone-induced hypertension, systolic blood pressure, ET-1 plasma levels, systemic oxidative stress, and vascular NADPH activity in association with small artery hypertrophic remodeling was increased (59). However, all these aberrant parameters were normalized in this model by treatment with ET_A receptor antagonist (59).

ET-1 is involved in renal and cardiac target organ damage in hypertension. An increase in renal ET-1 in hypertensive rats is involved in renal fibrosis through the activation of growth factors and by inducing inflammation (60). These events were normalized when treated with a selective ET_A receptor antagonist, and kidney function was restored (60). Rats made hypertensive

through exogenous ET-1 infusion showed changes in renal function, and signs of oxidative stress that were reduced by a free radical scavenger further imply a role of ROS in this process (61). In the heart, ET_A receptor (62), ET_A/ET_B receptor (63) and ECE antagonists (64) prevented target organ damage in hypertensive animal models. Blockade of the ET system in transgenic mice with inducible malignant hypertension prevented an increase in cardiac ET-1 concentrations, suggesting that ET receptor blockade may provide as a protecting tool against hypertensive cardiac damage (65). It should, however, be noted that all animal hypertensive models are not the same, and that different hypertensive diseases have different etiologies in which ET-1 plays a different role within each form of hypertension.

1.8.1.2 ET-1 in essential hypertension

The hallmark of hypertension is an increase in peripheral vascular resistance displayed by increased vascular tone of small arteries and vascular remodeling (66, 67). In comparison to normotensive patients, there is no significant change in plasma concentrations of ET-1 in hypertensive patients from studies that have investigated the role of ET-1 in essential hypertension (54). As such, plasma concentrations of ET-1 do not reflect the presence of essential hypertension, presumably due to the fact that ET-1 is generated and is biologically active in a paracrine and/or autocrine manner. Increases in ET-1 levels seem to be related to age, smoking and renal dysfunction rather than to hypertension (68). However, in certain ethnic groups, such as African American hypertensive subjects, increased plasma ET-1 levels have been observed (69). Interestingly, increased preproET-1 is found in the endothelium of small arteries of patients with moderate-to-severe hypertension (70) and enhancement of ET-1 generation plays a role in hypertrophic signaling in these patients (70). Increased ET-1 messenger and protein levels in VSMC cause the formation of larger elastic and muscular arteries of hypertensive

patients (71). Increased ET system activity has been suggested in patients with hypertension in comparison to normotensive patients. This is based from studies where ET_A receptor antagonism causes vasodilation in forearm vessels of essential hypertensive patients compared with normotensive subjects (72). Conversely, ET_B receptor antagonism induced vasoconstriction on forearm resistance arteries in normotensive patients (73) and is shown to have a vasodilator action on hypertensive subjects (73), indicating a vasoconstricting effect of ET_B receptors in hypertensive but not in normotensive states. African Americans appear to have an increased expression of VSMC ET_B receptors that might mediate the ET-1 response (69). Other studies have investigated a long-term antihypertensive effect of ET receptor antagonism. A four-week treatment with ET_A/ET_B receptor antagonist, bosentan, significantly lowered diastolic pressure in a study with 293 patients with mild-to-moderate essential hypertension (74). Darusentan, a selective ET_A receptor antagonist, also significantly reduced systolic and diastolic blood pressure in human hypertension (75).

1.8.2 ET-1 in atherosclerosis

In addition to its effects on blood pressure, ET-1 is pro-inflammatory and is implicated in the development of atherosclerosis (76). Evidence supporting a role for the effect of ET-1 in the pathogenesis of atherosclerosis comes from data supporting that ET-1 and its receptor levels are elevated in experimental models of atherosclerosis (77, 78), and in human coronary artery atherosclerotic plaques (79). Additionally, ECE-1 has been shown to be upregulated in VSMC and in macrophages from atherosclerotic plaques (80). Further evidence is demonstrated in experiments showing that ET_A receptor antagonism inhibits the formation of early atherosclerotic lesions in hyperlipidaemic hamsters, by decreasing the number and size of macrophage-foam cells (81), suggesting a pro-inflammatory role of ET_A activation. ET_A receptor antagonism also

reduced the development of atherosclerosis in apolipoprotein E (ApoE) deficient mice, an animal model for atherosclerosis (82). Bosentan inhibited neointimal development in collared carotid arteries of rabbits, another known model of atherosclerosis (83). Bosentan also significantly attenuated the development of graft atherosclerosis in rat cardiac allografts (84). In humans, infusion of selective ET_A receptor antagonist BQ123, improves coronary vascular function in patients with atherosclerosis (85).

ET-1 has been associated with the development of atherosclerosis mainly through its actions on VSMC. ET-1 stimulates VSMC proliferation (86), migration (87), contraction (88), matrix remodeling (89), synthesis of extracellular matrix (90) and the expression of other pro-atherogenic growth factors such as PDGF and TGF- β (91).

1.8.3 ET-1 in heart failure

Circulating ET levels have been shown to be increased in both experimental and human heart failure (92, 93). ET-1 is proposed to contribute to acute and chronic increases in vascular resistance, ventricular and vascular remodeling, inflammation, and arrhythmogenesis in models of heart failure (94). ET-1 stimulates the secretion of other neurohormones and potentiates their effects, resulting in long-term effects on the heart and contribution to the progression of chronic heart failure (CHF) (47). The gene expression of ET-1 precursor and ECE-1 is up-regulated four and three-fold respectively, in the failing human heart (95). This increase is attributed to the production from cardiac as well as extra-cardiac tissues such as the lungs (93). The increased levels of ET-1 correlate with haemodynamic severity and symptoms (96, 97). Evidence is accumulating mostly from animal studies, that ET receptor antagonism can ameliorate the deleterious haemodynamics and structural changes associated with heart failure.

ET_A receptor antagonism in hamsters with CHF and in rat coronary ligation models improves their survival (98, 99). In heart failure in dogs, bosentan decreased aortic pressure and increased stroke volume (100). Dual ET receptor antagonist TAK-044 and ET_A receptor antagonist FR 139317 also decreased cardiac pressures, and increased cardiac output (101). In a pig model of CHF, combined Ang II receptor blockade with bosentan resulted in greater improvement of ventricular function (102). Recently, it has been shown in an acute model of rat heart failure that myocardial contractility was restored and cardiac relaxation significantly improved after application of PP36, an inhibitor of ECE, suggesting a crucial role of ET production in this pathophysiological state (103).

In clinical trials, short term administration of bosentan or ET_A receptor antagonist LU135252 exhibited beneficial haemodynamic effects of patients suffering with CHF (104-106). In another clinical trial, intravenous infusion of the dual ET receptor antagonist tezosentan rapidly and effectively improved haemodynamics in patients suffering from acute decompensated heart failure (107). Despite these results and the clear rationale for the use of ET antagonists in heart failure, human clinical trials have generally not been proven to be very effective. The beneficial haemodynamic effects have been found to be short lived and treatment with ET antagonists has been associated with adverse side effects, including hypotension and abnormal liver function (108, 109).

1.9 ET-1-induced signaling in vascular smooth muscle cells

ET-1 exerts its physiological actions through the activation of multiple signaling pathways which include the PLC/DAG/IP₃, MAPKs and PI3-K/PKB pathways. Receptor and non-receptor tyrosine kinases also play a role in mediating ET-1-induced signaling events. The

cellular events triggered by the activation of these pathways are involved in regulating cellular growth, proliferation, contraction and survival of VSMC (110).

1.9.1 Activation of the phosphoinositide cascade by ET-1 in VSMC

The binding of ET-1 to its receptor induces a conformational change in the heterotrimeric G protein, that consists of an α , β and γ -subunit (111). In its inactive form, the α -subunit is ligated to guanosine diphosphate (GDP) but when activated, GDP is exchanged for guanosine triphosphate (GTP), causing the α -subunit to dissociate from the $\beta\gamma$ dimer complex, while they all remain associated to the membrane (111). Activation of the $G\alpha$ subunit following ET-1 binding to its receptor initiates downstream G-protein signaling. This leads to the activation of phosphoinositide-specific phospholipase C β (PLC β), which then hydrolyzes the membrane phospholipid phosphatidylinositol-4'-5'-biphosphate (PIP₂) to generate two second messengers: hydrophobic diacylglycerol (DAG), and soluble inositol-1',4',5'-triphosphate (IP₃) (112). IP₃ stimulates the release of calcium (Ca²⁺) from intracellular stores, which plays an important role in regulating the contractile response of the cell (113). DAG, together with Ca²⁺, activate the phosphatidylserine-dependent protein kinase, protein kinase C (PKC) (114) (Figure 1.3).

PKC is a family of serine/threonine kinases, comprised of 12 currently identified isoforms (114) that translocate from the cytosol to the cell membrane, where they become activated and phosphorylate several cytosolic proteins (115). Many studies have implicated PKC in deleterious vascular effects of several pathologies including diabetes and hypertension (116). Growing evidence suggest that ET-1-induced activation of PKC in VSMC leads to protein synthesis (117), cellular proliferation (115, 118) and contraction (119). Thus, ET-1-induced activation of PKC and its downstream effects appears to be important in regulating vascular function.

1.9.2 ET-1-induced activation of MAPK cascade in VSMC

Downstream of PKC, ET-1 receptor activation also results in stimulation of mitogen activated protein kinase (MAPK) cascades. MAPK are a family of serine/threonine protein kinases which are classically associated with cell growth, proliferation, differentiation, death, and contraction (120, 121). Extracellular signal-regulated kinase 1 and 2 (ERK1/2), p38 MAPK and c-Jun N-terminal kinases (JNK) are the main groups of MAPKs. These MAPK all follow a similar system of sequential activation by several upstream signaling components, in which a stimulus activates a MAPKKK, which will then phosphorylate and activate a MAPKK, which will at last phosphorylate Thr and Tyr residues in the activation loop of the final effector, MAPK, leading to its activation and hence cellular response. ET-1 activates JNK and p38 cascades but to a lesser degree than ERKs in VSMC (122). Signals from GPCR to ERK1/2 are transmitted via Ras, a small membrane-bound GTP-binding protein. Ras cycles between an active GTP-bound conformation and inactive-GDP-bound

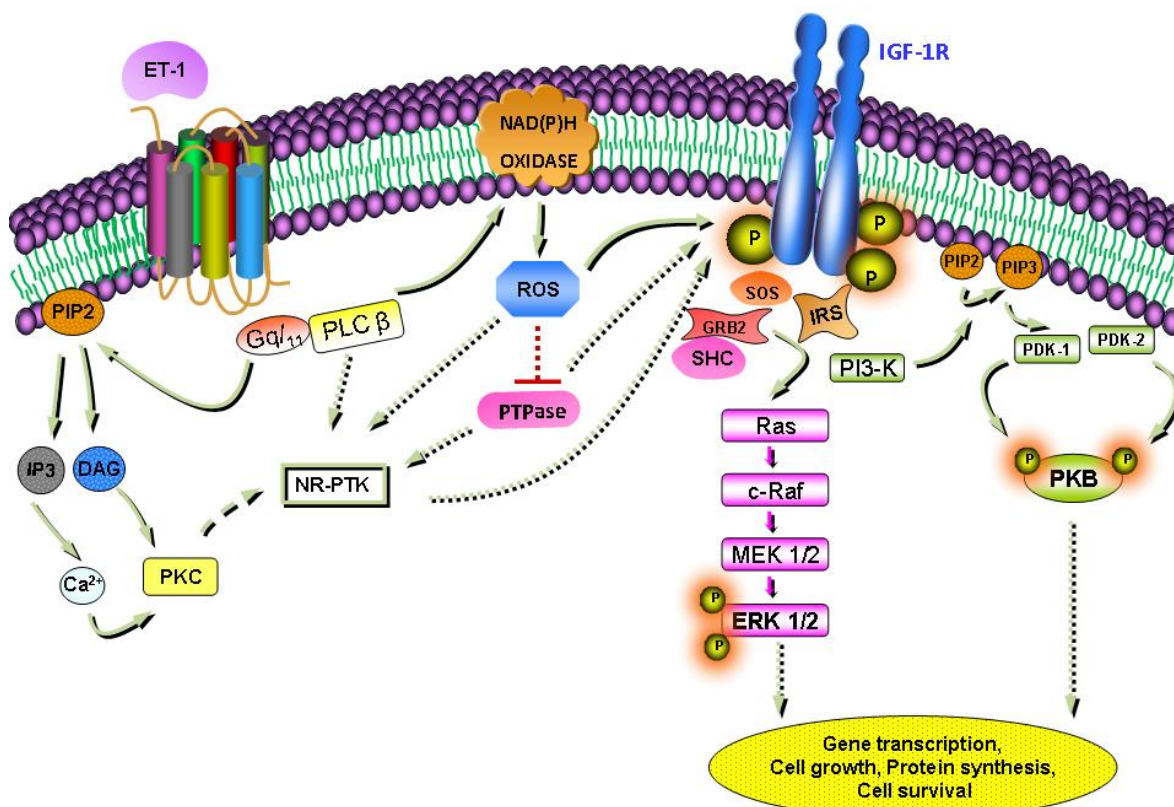


Figure 1.3 Schematic model showing the activation of ERK1/2 and PI3-K/PKB signaling pathways through IGF-1R phosphorylation by ET-1 in VSMC.

ET-1 receptor stimulation leads to both $Gq\alpha$, as well as $\beta\gamma$ activation, which in turn activate PLC β . PLC β converts PIP2 to IP3 and DAG. IP3 is responsible for elevating intracellular Ca^{2+} concentrations. DAG activates PKC. Through the activation of several downstream intermediates, Ca^{2+} alone or in partnership with PKC or other intermediates triggers the activation of NR-PTKs, by inducing their phosphorylation on target tyrosine residues. Activation of these PTKs leads to the phosphorylation of docking proteins, such as IRS-1, which serve as docking sites for Grb-2/SOS. The latter can lead to activation of Ras/Raf/MEK/ERK1/2 pathway. Phosphorylated IRS-1 activates PI3-K which goes on to catalyze the phosphorylation of PIP2 to PIP3, allowing PKD-1/2 recruitment to the plasma membrane, where PDK-1/2 will phosphorylate PKB on threonine and serine residues. ET-1 also increases ROS generation by activating NADPH oxidase, through an unknown mechanism, in VSMC. Endogenously produced ROS are able to inhibit PTPases through the oxidation of cysteine residues in its catalytic domain. Inhibition of these PTPases favours tyrosine phosphorylation of NR-PTKs and R-PTKs, resulting in the ligand-independent activation of R-PTK, such as IGF-1R, that act upstream of Ras/Raf/MEK/ERK1/2 and PI3-K/PKB pathways. Activation of ERK1/2 and PKB signaling cascades plays a role in mediating various cellular responses such as gene transcription, protein synthesis, cell growth and cell survival.

form (120). Activated Ras recruits and activates Raf, a MAPKKK, that phosphorylates MEK, a MAPKK, at specific serine/threonine residues, which in turn phosphorylates ERK1/2 in threonine and tyrosine residues (120). Chen et al. have reported an implication of PKC in ET-1-induced ERK activation through ET_A receptors in human VSMC (123). Activation of ERK1/2 leads to the phosphorylation of downstream cytosolic target substances on serine and threonine residues. ERK1/2, along with other MAPK family members, can also be translocated from the cytosol to the nucleus where they can phosphorylate and activate several transcription factors which lead to the activation of genes involved in cell growth and differentiation (120) (Figure 1.3).

Several reports have demonstrated that ET-1 activates ERK1/2 signaling pathways in cardiomyocytes (124), fibroblasts (125), glomerular mesangial cells (126) and VSMCs (5). Activation of ERK1/2 can potentially result to an increased proliferation and hypertrophy of VSMC in response to ET-1 given that inhibition of its upstream mediator, MEK1/2, resulted in inhibition of ET-1-induced DNA and protein synthesis (127, 128).

1.9.3 ET-1-induced phosphatidylinositol-3-kinase cascade activation in VSMC

Phosphatidylinositol-3-kinases (PI3-K) are a family of lipid kinases that have emerged as important effectors of ET-1 action (110). PI3-K phosphorylates the 3' position of the inositol ring of the membrane-bound phosphoinositides, phosphatidylinositol (PI), PI 4-phosphate, and PI 4,5-phosphate. This reaction generates biologically active lipids PI 3-P, PI 3,4-biphosphate (PI(3,4(P₂)) and PI(3,4,5)triphosphate (PI(3,4,5)P₃), respectively (129). These phospholipids act as second messengers to activate several protein kinases such as PI(3,4,5)P₃ dependent protein

kinase (PDK), protein kinase B (PKB) and 70kDa ribosomal protein S6 kinase (p70^{S6K}) (129) (Figure 1.3).

PI3-Ks are divided into three classes based on their substrate specificity, molecular structure and mode of regulation (129). Class I PI3-Ks generates PI(3)P, PI(3,4)P₂, PI(3,4,5)P₃ and are activated by receptor protein tyrosine kinases (R-PTK) and GPCRs (129). Class II PI3-Ks generate PI(3)P, PI(3,4)P₂, and possess a lipid binding domain, whereas, class III PI3-Ks only generate PI(3,4,5)P₃ (129). Class I PI3-Ks are further subdivided into class IA and IB PI3-Ks and are heterodimeric proteins composed of a catalytic and regulatory subunit. Class IA proteins consist of a 110 kDa (p110) catalytic subunit and an associated 85 kDa (p85) regulatory subunit. Class IA has three isoforms of the catalytic subunit, p110 α , p110 β and p110 δ , and several isoforms of the regulatory subunit, p85 α , p55 α , p50 α , p85 β and p55 γ . In contrast to class IA, class IB has only one catalytic member, p110 γ , and one form of the regulatory subunit, p101. The class IA PI3-Ks are activated by R-PTK, while class IB is activated by GPCR (130).

The PI3-K pathway plays a pivotal role in cell migration, differentiation, proliferation and survival (130). Several studies have reported an involvement of PI3-K as an upstream mediator of several ET-1 induced responses. However, except for rat glomerular mesangial cells, where ET-1-induced PI3-K activation is necessary for hypertrophy (131), no direct activation of PI3-K by ET-1 in VSMC has been documented. However, the PI3-K inhibitor wortmannin has been shown to have an inhibitory effect on ET-1-stimulated cell proliferation and protein synthesis in A-10 VSMC (127, 128).

1.9.4 ET-1-induced PKB activation in VSMC

Several downstream targets of PI3-K have been documented, the most studied being PKB, also known as Akt (a product of akt proto-oncogene). PKB is a 57 kDa serine/threonine kinase with three identified isoforms in the mammalian system, PKB α /Akt1, PKB β /Akt2 and PKB γ /Akt3 (132). All isoforms possess an N-terminal pleckstrin homology (PH) domain that binds to phospholipids generated by PI3-K, a central catalytic kinase domain with specificity for serine or threonine residues on substrate proteins, and a C-terminal regulatory domain containing a hydrophobic motif (132). Full activation of PKB is a sequential two step process where the lipid products generated from PI3-K are recognized by the PH domain of PKB, translocating it to the plasma membrane, where it then gets phosphorylated on Thr308 by PDK-1 and on Ser473 by a putative kinase termed PDK-2 for its complete activation (133) (Figure 1.3). Phosphorylation of both sites is mitogen-and PI3-K-dependent (133).

PKB has been shown to promote a variety of cellular responses including inhibition of apoptosis and promotion of cell survival, regulation of cellular proliferation, metabolism and hypertrophy (132). PKB substrates include members of cell survival and apoptosis cascade such as Bcl-2, BAD (134, 135), caspase-9 (136) and glycogen synthase kinase-3 (GSK-3) (137), as well as regulators of protein synthesis and cell growth such as mammalian target of rapamycin (mTOR) (138). ET-1 has been shown to activate PKB in cardiomyocytes (139), myofibroblasts (140), human umbilical vein endothelial cells (141) and A-10 VSMC (5, 127, 128).

1.10 ET-1-induced growth factor transactivation

Recent findings suggest that ET-1 and other vasoactive peptides, such as Ang II, whose receptors belong to GPCR family, stimulate intracellular signaling pathways through

transactivation of R-PTK, and thereby mediate the ERK1/2 and PKB signaling events. Among the main growth factor receptors implicated in this process, epidermal growth factor receptor (EGF-R), insulin-like growth factor type 1 receptor (IGF-1R) and platelet derived growth factor receptor (PDGF-R) have been investigated in some detail. EGF-R has been studied in some detail in response to Ang II and ET-1 (142, 143), as has PDGF-R in response to Ang II (144). However, only a few recent studies have investigated the involvement of IGF-1R.

1.10.1 Role of IGF-1R

The IGF-1R is a member of the tyrosine kinase class of growth factor receptors that shares structural and functional homology with the insulin receptor (IR). Human IGF-1R is a ubiquitously expressed product of a single-copy gene located on chromosome 15 (145). The IGF-1R is a transmembrane heterotetrameric structure that is comprised of two extracellular ligand-binding α -subunits that are linked by disulfide bonds to each other and to the two transmembrane β -subunits that contain intrinsic tyrosine kinase activity, which is believed to be essential for most of the receptors biological effects (145). Binding of the ligand to the α -subunit induces a conformational change, leading to the activation of the protein tyrosine kinase (PTK) domain of the IGF-1R β subunit that responds by *trans*-autophosphorylation of a cluster of tyrosine residues within the IGF-1R β to provide docking sites for effector proteins (145). Once these residues become phosphorylated, the intrinsic PTK activity of IGF-1R is enhanced, thus leading to the phosphorylation of several adaptor/scaffolding proteins, including insulin receptor substrate (IRS-1 or IRS-2) and Src homology collagen (Shc) (146). IRS-1 contains multiple tyrosine phosphorylation sites that recognize and bind to SH2 domain-containing signaling molecules, such as Grb2, Nck, the p85 subunit of PI3-K, and the SH2 domain-containing tyrosine phosphatase-2 (SHP-2) (147). Of these, the binding of Grb2 associated with SOS, a guanine

nucleotide exchange factor, to the tyrosine-phosphorylated IRS-1 activates Ras and initiates sequential phosphorylation that leads to the activation of ERK1/2 (148). Shc can also interact with IGF-1R, in an IRS-1-independent manner (149), to recruit the Grb2/Sos complex and activate Ras/Raf/MEK/ERK pathway (148). IGF-1R activation also leads to the activation of PI3-K/PKB pathway. Tyrosine-phosphorylated IRS-1 interacts with the p85 subunit of PI3-K, leading to the activation of the catalytic p110 subunit and to the subsequent activation of the downstream substrate PKB (reviewed in (150)).

In VSMC, a requirement of IGF-1R activity has been recently shown in ET-1-induced PKB phosphorylation. These studies demonstrate that ET-1 was able to phosphorylate tyrosine residues on IGF-1R β subunit and that use of AG1024, a selective pharmacological inhibitor of IGF-1R-PTK activity, attenuated IGF-1R and PKB phosphorylation, as well as protein and DNA synthesis induced by ET-1 (151). These results suggest an important role of IGF-1R in mediating PKB phosphorylation, as well as hypertrophic and proliferative responses induced by ET-1 in VSMC. The mechanism by which ET-1 induces IGF-1R transactivation is not fully understood. However, a potential role of ET-1-induced ROS generation in this process has been suggested since H_2O_2 and subsequent inhibition of PTPase have shown to contribute to the activation of IGF-1R-PTK in VSMC further resulting in activation of PKB (152, 153) (Figure 1.3).

1.11 ROS and ET-1 signaling

ROS are very small, rapidly diffusible, highly reactive molecules that take part in physiological reactions and signal transduction but an excessive synthesis can overcome antioxidant mechanisms and generate deleterious effects, often resulting in the development of CVDs (11). This is in part due to their physicochemical properties which allow them to disrupt

biological macromolecules such as lipids, DNA, carbohydrates and proteins. Hydrogen radicals (OH^\cdot), superoxide anions ($\text{O}_2^{\cdot-}$), hydrogen peroxide (H_2O_2), reactive nitrogen radicals and its derivative peroxynitrite (ONOO^\cdot) are amongst the most important ROS. They are generated both enzymatically and non-enzymatically by nearly every cell type including VSMC and endothelial cells (11).

ROS are potent stimulators of ET-1 synthesis in endothelial cells (154) and in human VSMC (155). Alternatively, studies demonstrate that ROS can be generated in response to ET-1. In fact, ET-1 has been shown to activate NADPH oxidase within several cell types, including VSMC (5, 156) and that *in vivo*, free radicals generated by ET-1 play important roles in mineralocorticoid-induced hypertension (57, 157). Both the pressure and vasoconstrictive effect of ET-1 were diminished in parallel with the normalization of $\text{O}_2^{\cdot-}$ levels after treatment of DOCA-salt rats with ET_A receptor antagonist (57).

Increased ROS generation promotes cell growth and proliferation, and is therefore associated with a variety of cardiovascular pathologies, including hypertension and atherosclerosis (158). The elevated levels of ET-1 during hypertension and atherosclerosis lead to excessive production of oxidative stress and a decrease in antioxidant status (159). The involvement of ROS in ET-1-induced activation of MAPKs including JNK, p38mapk and ERK1/2 has been demonstrated in cardiac fibroblasts (125). Moreover, a role of ROS in ET-1-induced activation of ERK1/2 and PKB signaling has been demonstrated in VSMC (5) (Figure 1.3).

1.12 Plant-derived cardiovascular protection

ET-1 is a key player in cardiovascular homeostasis through the activation of the previously mentioned signaling pathways, and though this activation is a physiological cellular event, aberrant signaling has been implicated in the development and progression of pathophysiological events. For instance, upregulation of ET-1-induced signaling through MAPK and PI3-K/PKB pathways, particularly in VSMC, is linked to vascular changes observed during CVDs such as atherosclerosis and hypertension (160, 161). Many pharmacological interventions that have been introduced to target this system failed to show optimal efficacy in diseases other than pulmonary hypertension, therefore, interventions are needed to directly target the cellular mechanism in order to prevent the effects of ET-1 on VSMC in the development of CVDs. In this regard, natural derived products have been extensively researched during the last few decades, due to their reported beneficial diverse biological and pharmacological activities on the cardiovascular system. Knowledge of traditional medicine has allowed us to identify plants and plant-derived substances believed to exhibit such health promoting effects. Plants produce a large and diverse array of bioactive substances, known as phytochemicals. These are non-nutritive substances that possess health-protective benefits (162). Some of these compounds have been shown to exhibit cardiovascular protective effects. Among them, the main constituent of the spice turmeric, curcumin, has attracted the attention of scientists and been the subject of their investigations. The putative therapeutic properties of curcumin are mainly attributed to its antioxidant, anti-inflammatory and anti-carcinogenic properties (163-165).

1.13 Historical aspects of curcumin

Curcumin is the main ingredient of the spice turmeric which is an ancient gold-coloured spice commonly used in Asiatic countries, mainly India and China, as a culinary ingredient for

food flavouring and preservation, as a yellow textile colouring agent, and as a natural remedy for medicinal purposes. Turmeric is derived from the rhizomes of the perennial plant *Curcuma longa* Linn, belonging to the Zingiberaceae family, which is distributed in tropical and subtropical regions of the world (Figure 1.4). Turmeric contains a wide variety of phytochemicals including curcuminoids, a group of polyphenolic compounds that have been shown to deliver beneficial effects on health and on events that help in preventing certain diseases. Curcuminoids are mainly comprised of three bioactive analogs, curcumin (curcumin I), demethoxycurcumin (curcumin II), and bisdemethoxycurcumin (curcumin III) (166) (Figure 1.4). They have all been isolated and differ in their methoxy substitution on the aromatic ring. Curcumin is the most active and abundant constituent of turmeric. It is estimated that approximately 2 to 5% of turmeric is composed of curcumin (167), while the remainder is made up of mineral matter, carbohydrates, proteins, fat and moisture (168). The isolation of pure curcumin is very tedious; consequently, the commercially available extracts consist of a combination of the three curcuminoids with curcumin as the main constituent (75-81%). Curcumin is responsible for the characteristic yellow pigmentation of turmeric and is now acknowledged as being responsible for most of its therapeutic effects (167).

In folk medicine, turmeric and natural curcuminoids have been applied for centuries in therapeutic household remedies throughout many parts of the world, particularly in the Orient, where it is widely consumed. Its therapeutic use can be traced back to ancient

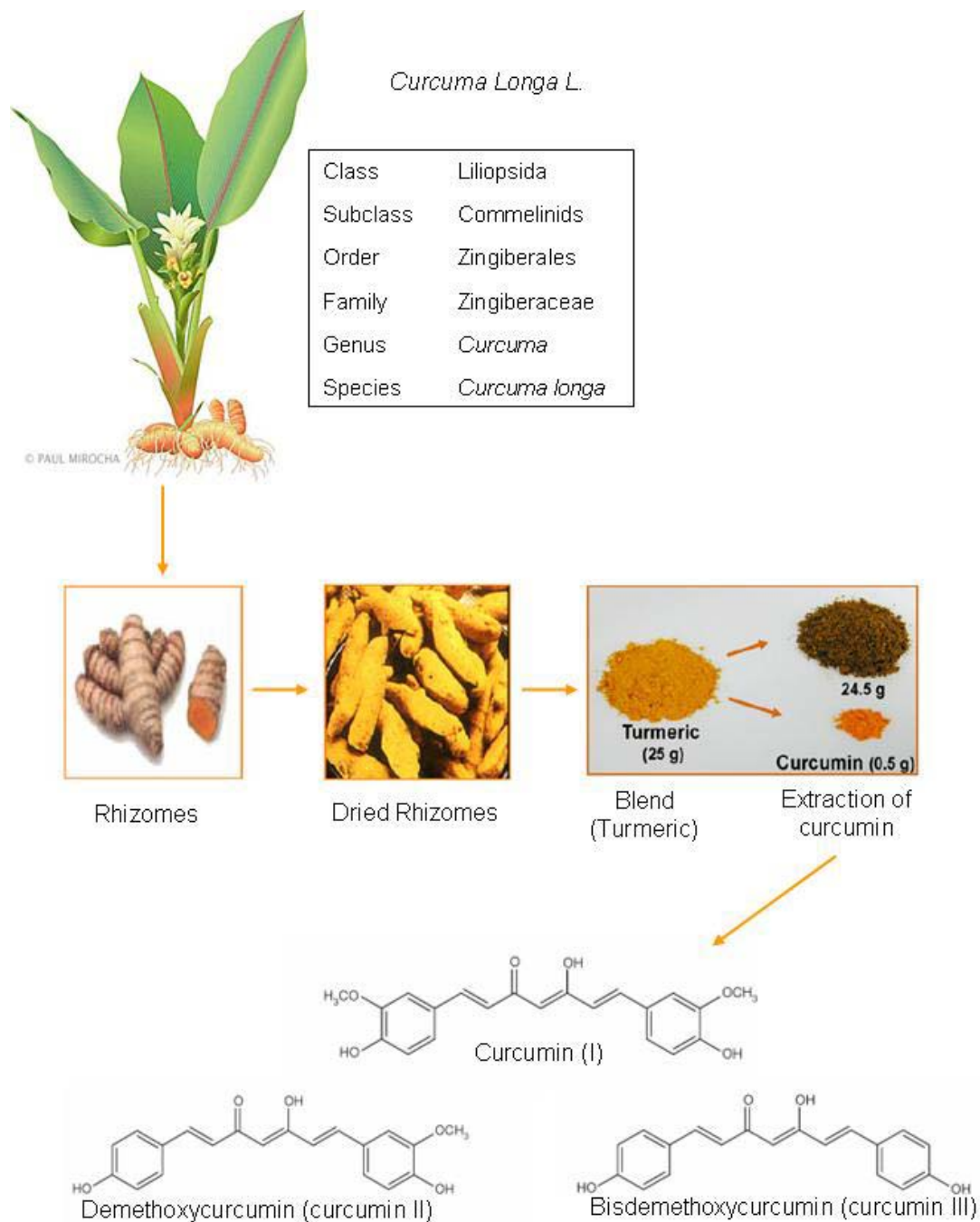


Figure 1.4 Taxonomic position of *Curcuma Longa Linn* and isolation, extraction and structure of parent curcuminoids. (Based on ref (169) and Chattopadhyay et al: *Current Science I*: 44-53, 2004).

Indian and Chinese medicines, where it was used as an anti-inflammatory agent to treat ailments associated with abdominal pain, inflammation and pain caused by injury (170). In Ayurvedic medicine, it was used against pulmonary disorders, liver disorders, anorexia, rheumatism, diabetic wounds, runny nose, cough and sinusitis (171).

1.14 Chemical properties of curcumin

Curcumin was first isolated from turmeric in 1815 by Vogel and Pelletier, obtained in crystalline structure and identified as 1,6-heptadiene-3,5-dione-1,7-bis(4-hydroxy-3-methoxyphenyl)-(1E,6E) or diferuloylmethane in 1870 by Daube (169). The hydrophobic polyphenol feruloylmethane skeleton was later elucidated and synthesized in 1910 by J. Milodedzka and V. Lampe (169). In chemical terms, it is bis- α , β -unsaturated β -diketone, a linear diarylheptanoid compound, where two oxy-substituted aryl moieties are linked together through a seven carbon chain (172) (Figure 1.4). The aryl rings may be substituted by hydroxy or methoxy groups to produce analogues of curcumin or curcuminoids. It exhibits keto-enol tautomerism and in solution it exists predominantly in the enolic form, which is the more stable form (173). In neutral and acidic aqueous solutions, the keto form dominates (174). Curcumin has a molecular weight of 368.37g/mol, a melting point of 183°C, and its molecular formula is C₂₁H₂₀O₆. It is insoluble in water or aqueous solvents but soluble in organic solvents such as dimethyl sulfoxide, methanol, ethanol and acetone. Spectrophotometrically, curcumin has a maximum absorption in methanol at 430nm and it absorbs maximally at 415 to 420nm in acetone, and a 1% solution of curcumin has 1650 absorbance units (175). It has a bright yellow colour at pH 2.5 to 7 and takes a red hue at pH higher than 7 (175).

1.15 Curcumin bioavailability, metabolism, biotransformation and pharmacokinetics

The bioavailability of curcumin is limited by a number of factors, which may be an obstacle to its utility as a therapeutic agent. Once absorbed, polyphenolic compounds can directly undergo conjugation reactions, predominantly methylation, glucuronidation, and sulfation (176). Based on animal studies, poor gastrointestinal absorption, poor water solubility, molecular instability, and rapid and efficient metabolism, mainly by the liver and intestine into metabolites that are rapidly excreted, are a combination of reasons that contribute to the notion that curcumin exhibits poor systemic bioavailability (177, 178). In order to enhance its bioavailability, the co-administration of curcumin with piperine or its complexation with phospholipids, liposomes and micelles has been proposed. Adjuvant co-administration prevents its rapid metabolism by interfering with enzymes that catalyze the metabolism of curcumin, while liposomes, micelles and phospholipid complexes can reduce the hydrophobicity of curcumin and increase the permeability of membrane barriers (166). Other strategies include employing nanoparticle technology providing easier penetration through membrane barriers because of their small size (166).

Data on the pharmacokinetics, metabolites, and systemic bioavailability of orally administered curcumin in humans, provided from trials mainly conducted on cancer patients, showed that after oral administration of curcumin, no curcumin excretion was detected and that serum concentration peaks observed at one to two hours were undetectable at twelve hours (179). However, most curcumin conjugates produced by *in vivo* human metabolism are detectable in plasma at greater concentrations than free curcumin with a peak after four hours of dosing (180). Although, it has not yet been established if these metabolites are as bioactive as their parent

compound, some curcumin metabolites, such as the reduction metabolite tetrahydrocurcumin, have been shown to be biologically active in some systems (163).

An important feature of curcumin is that despite being consumed daily for centuries, it has not been shown to cause any toxicity (172). Clinical trial results show that curcumin is well tolerated, even at high doses, where it appears non-toxic to animals or humans (179, 181). In human trials, only minor side effects of curcumin, namely diarrhoea, have been reported (182). These trials however have examined the short term outcome. There is some evidence that long-term high-dose curcumin administration in rodents can be tumourigenic (183). It has also been shown that curcumins predominant activity changes from antioxidant to pro-oxidant with increasing concentration (184).

1.16 Biological actions of curcumin

Curcumin has been demonstrated to have a wide range of beneficial effects through its most pronounced properties which encompass its anti-inflammatory, antioxidant and anti-carcinogenic activities (177). Modern science has revealed that curcumin is a highly pleiotropic molecule that mediates its effects by modulation of several important molecular targets, including transcription factors, enzymes, growth factors and their receptors, cell cycle proteins, cytokines, cell surface adhesion molecules, and genes regulating cell proliferation and apoptosis (185). However, the cellular and molecular mechanisms of the favourable effects of curcumin on human health are not fully understood.

1.16.1 Anti-inflammatory properties of curcumin

Most chronic illnesses are believed to be caused by dysregulated inflammation (186). For instance, inflammation is involved in cancer, cardiovascular diseases, pulmonary diseases, metabolic diseases and neurological diseases (187-191). Although, the mechanism of its anti-inflammatory action remains unclear, curcumin has been shown to negatively modulate several pro-inflammatory responses. Several studies have demonstrated that curcumin was able to modulate the production of various inflammatory cytokines, thereby exhibiting potent anti-inflammatory activity. It has been shown to downregulate nuclear factor- κ B (NF- κ B), a transcription factor that plays a critical role in the induction of many pro-inflammatory mediators involved in chronic and acute inflammatory diseases and various cancers (186). Aggarwal and Singh were the first to demonstrate that curcumin suppressed NF- κ B activation induced by different inflammatory stimuli (192), resulting in the suppression of NF- κ B-dependent gene products that suppress apoptosis and mediate proliferation, invasion, and angiogenesis (186). The downregulation of NF- κ B by curcumin results in a decrease in the expression of TNF- α , interleukin-1 (IL-1), interleukin-6 (IL-6) (169). Therefore, inhibition of pro-inflammatory cytokine production by regulation of transcription factors, such as NF- κ B, is a potential strategy for controlling inflammatory responses. In addition, curcumin has been reported to inhibit the activities of cyclooxygenase-2 (COX-2) and lipoxygenase (LOX) enzymes that are involved in generating lipid mediators intimately implicated in inflammation, thereby indicating that the anti-inflammatory actions of curcumin can also modulate arachidonic acid metabolism (193).

The nuclear transcription factor early growth response-1 (Egr-1) is implicated in the regulation of a number of genes involved in inflammation as well as growth and development, and is also a target of curcumin. Egr-1 regulates several pathophysiologically relevant genes in

the vasculature that are involved in differentiation, wound healing and blood clotting (194). It has been shown that curcumin suppressed the induction of Egr-1 in endothelial cells and fibroblasts, thereby modulating the expression of Egr-1-regulated genes in both these cell types (195). A recent study also showed that curcumin inhibits the inflammatory response and chemotaxis of monocytes by inhibiting Egr-1 (196).

Curcumin also downregulates MAPK pathways, which are activated by many inflammatory stimuli (194). Curcumin can contribute to the protection against the adverse vascular effect of the pro-inflammatory response through the suppression of TNF- α -stimulated ROS generation, monocyte adhesion, phosphorylation of JNK and p38 MAPK, and signal transducer and activator of transcription (STAT)-3 in endothelial cells (197). *In vitro* studies are somewhat contradictory since other investigators paradoxically show an activation of MAPK by curcumin (198, 199). The mechanism is unexplained, nevertheless; in both cases its final effects appear to be anti-inflammatory (172).

Curcumin thus exerts a protective role against inflammatory responses, through modulation of inflammatory mediators, and may therefore represent a therapeutic agent targeting the cardiovascular system since the inflammatory process plays a crucial role in the pathogenesis of some cardiovascular diseases, mainly atherosclerosis and acute coronary syndrome (200).

1.16.2 Antioxidant activity of curcumin

The antioxidant activity of curcumin was reported as early as 1975 (201). Oxidative stress associated with overproduction of ROS plays a major role in the pathogenesis of various diseases, including CVDs (158). Even though the antioxidant properties of curcumin have been shown to have several therapeutic advantages, its antioxidant mechanism remains poorly

understood. It has been shown to be a potent scavenger of a variety of ROS, including $O_2^{\cdot -}$ (174), OH^{\cdot} (202), nitrogen dioxide radicals (203) and non-free radical species such as H_2O_2 (174). Curcumin has also been shown to enhance the activity of antioxidant enzymes and to counteract the activity of ROS generating enzymes (170, 204). Sreejayan and Rao first claimed that the presence of phenolic groups in the structure of curcumin was fundamental in its ability to eliminate ROS (205). Recent literature proposes that the phenolic and methoxy groups on the phenyl ring and the 1,3-diketone system are important structural features that contribute to the antioxidant effects. Evermore so, the antioxidant activity increases when the phenolic group with a methoxy group is at the ortho position (206). A more recent study concluded that the H-atom donation from the phenolic group is responsible for the strong antioxidant properties of curcumin (174). Curcumin can also indirectly increase the endogenous cellular antioxidant defenses through alternative antioxidant mechanisms. Heme-oxygenase-1 (HO-1) is a widely distributed mammalian enzyme that is one of the most prominent protective genes proven to be effective in ameliorating cardiovascular problems associated with increased oxidative stress (158), and is yet another target of curcumin (207). Curcumin has been shown to protect against oxidative stress through an increase in HO-1 production in endothelial cells (206).

Curcumin has the ability to protect lipids and DNA against oxidative degradation by scavenging free radicals and inhibiting free radical generation (203, 208, 209). Lipids are the most susceptible macromolecules to oxidative stress (203) and lipid peroxidation consists of a series of free radical-mediated chain reaction processes that leads to the damage of cell membranes. Many studies demonstrate the potential of curcumin to reduce lipid peroxidation, a key process in the onset and progression of many diseases, including atherosclerosis, heart diseases and cancer (210-213). Curcumin has been shown to reduce lipid peroxidation by

augmenting the activities of antioxidant enzymes, such as superoxide dismutase (SOD), catalase, glutathione (GSH), glutathione-s-transferase (GST) and glutathione peroxidase (GPx) (170).

Curcumin also exhibits a protective role against oxidative ischemic injury through inhibition of free radical propagation with subsequent inhibition of ROS generating enzyme activity, resulting in decreased ROS production (214).

Although the exact mechanism by which curcumin promotes these effects remains to be elucidated, *in vivo* and *in vitro* studies suggest that its antioxidant properties appear to underlie its pleiotropic biological activities.

1.16.3 Anticarcinogenic effects of curcumin

In vivo and *in vitro* studies have demonstrated the ability of curcumin to inhibit carcinogenesis at three stages: tumour initiation, promotion and metastasis (215). Its anti-carcinogenic effect has been studied in gastrointestinal, liver, lung, blood, breast, oral, prostate and skin cancers. The molecular basis of the anti-carcinogenic and chemopreventive effects of curcumin is attributed to its effect on several targets including transcription factors, growth regulators, apoptotic genes, angiogenesis regulators and cellular signaling molecules (215). Cancer cells are able to evade apoptosis and grow in a rapid and uncontrolled manner. Curcumin has been shown to suppress the proliferation of tumor cells through the activation of caspases, the induction of tumor suppressor genes, such as *p53*, the upregulation of proapoptotic proteins and the downregulation of anti-apoptosis proteins (216, 217). Curcumin has been shown to induce *in vitro* and *in vivo* apoptosis of various tumour cell lines such as breast cancer cells, lung cancer cells, human melanoma cells, human myeloma cells, human leukemia cells, human neuroblastoma cells, oral cancer cells and prostate cancer cells (reviewed in (215)). Besides

inducing apoptosis, curcumin also inhibits the expression of PI3-K and the phosphorylation of the pro-survival kinase Akt/PKB (217).

Curcumin has also been shown to suppress growth factor-induced actions on human cancer cell growth. Recent *in vitro* studies have shown that treatment of cancer cells with curcumin can inhibit the intrinsic EGF-R tyrosine kinase activity, EGF-R ligand-induced activation, as well as the expression of EGF-R (218). Curcumin has been shown to inhibit human colon cancer cell growth by suppressing gene expression of EGF-R through reducing the activity of transcription factor Egr-1 (219). Recent data further demonstrate that curcumin also inhibits the expression and activation of the IGF-1R tyrosine kinase, thereby reversing the IGF-1-induced cell growth and apoptosis resistance (220). Moreover, curcumin inhibits PDGF-R-induced proliferation and PDGF-induced ERK1/2 phosphorylation of pancreatic stellate cells, through the induction of HO-1 gene expression (221). Additional growth factor pathways modulated by curcumin include TGF- β , fibroblast growth factor (FGF), hypoxia-inducible factor (HIF)-1 α , and colony-stimulating factors (CSFs) (reviewed in (175)).

MAPK signaling is a major pathway used by growth factors to trigger cell proliferation and differentiation. In tumor cells, curcumin, through inhibition of JNK phosphorylation, was shown to effectively block AP-1 and NF- κ B signaling pathways (222). Furthermore, curcumin strongly repressed tumor promoter-induced phosphorylation of ERK, JNK and p38 MAPK in brain tumor cells (223). Curcumin inhibition of gene expression of Egr-1 also requires interruption of ERK MAPK signal pathway (219). Several ongoing clinical trials still remain inconclusive, yet curcumin appears to have therapeutic potential for both prevention and treatment of cancer. Pharmacologically, it is safe in humans but its limited bioavailability interferes with its therapeutic potential.

1.17 Curcumin and cardiovascular diseases

Most of the earlier studies on curcumin focussed on its beneficial effects in various models of cancer, however, its anti-inflammatory and antioxidant properties have generated interest to investigate if this compound can also exert cardiovascular protective effects. Even though the underlying mechanism of action is not fully understood, evidence that curcumin exerts protective effects on the cardiovascular system has been previously described and its use as a therapeutic agent to mitigate CVDs is currently being investigated. Evidence indicates that curcumin exhibits protective effects against cardiovascular pathologies such as atherosclerosis, cardiac hypertrophy and heart failure.

1.17.1 Curcumin and atherosclerosis

Atherosclerosis is the most common form of heart disease. It is considered a chronic and progressive disease arising from the inflammatory processes and oxidative stress within the vessel wall (224). Curcumin has been shown to exhibit anti-atherosclerotic action through inhibition of platelet aggregation (225), protection against inflammation and oxidation, and modulation of cholesterol homeostasis. Several lines of evidence strongly suggest that curcumin may prevent atherosclerosis by regulating some elements in cholesterol homeostasis. Studies have reported that curcumin is beneficial in lowering low-density lipoprotein-cholesterol (LDL) and raising high-density lipoprotein-cholesterol (HDL) while reducing lipid peroxidation. Animal studies conducted in experimental atherosclerotic rabbits reported that curcumin effectively inhibited LDL oxidation, and decreased cholesterol and triglycerides levels (211). Supplementation with curcumin also demonstrated a significant prevention of early atherosclerotic lesions in thoracic and abdominal aorta, through reduction in oxidative stress and decreased lipid peroxidation, resulting in reduction of aortic fatty streak formation, in

experimental model of atherosclerosis where rabbits were fed a high cholesterol diet for 30 days (226). Orally administered curcumin also decreased the formation of atherosclerotic lesions by 20% in apoE and LDL receptor-double knockout mice model, an animal model developed for experimental atherosclerotic research (227). In a recent study, Liao et al. demonstrated that curcumin induced a 50% reduction in atherosclerotic lesion reduction in apoE knockout mice and inhibited oxidized-LDL-induced cholesterol accumulation in cultured VSMC (228). Curcumin has also proven to be an effective antioxidant through the prevention of oxidation and modification of LDL, and the subsequent restoration of prostacyclin release in human endothelial cells, thereby indicating a protective role in preventing pathological conditions related to oxidative stress and the development of atherosclerosis (229).

In humans, a study involving the administration of 500 mg of curcumin for 7 days to 10 healthy volunteers revealed a 29% increase in HDL cholesterol, a 12% decrease in total serum cholesterol and a 33% decrease in serum lipid peroxidases (230). The administration of curcumin also reduced total and LDL cholesterol levels in patients with acute coronary syndrome (231). Another study showed that 10 mg of curcumin given twice daily during 30 days significantly lowered the serum LDL levels and increased the serum HDL levels in healthy patients (232). The same group reported that 10 mg of curcumin administered twice daily for 15 days significantly lowered plasma fibrinogen levels in humans with atherosclerosis (233).

Abnormal proliferation of VSMC and mononuclear cells also contributes to the progression of cardiovascular diseases, including atherosclerosis. Curcumin suppressed mitogen-induced proliferation of human blood mononuclear cells, inhibited neutrophil activation and mixed neutrophil reaction, and also inhibited serum-induced as well as PDGF-dependent proliferation of rabbit VSMC (234). VSMC migration and collagen synthesis are also key events

involved in the pathological changes occurring with atherosclerosis. Curcumin has potent inhibitory effects on PDGF-induced VSMC proliferation, migration and collagen synthesis (235). This inhibitory effect on vascular remodeling is attributable to the attenuation by curcumin of PDGF-induced PDGF-R, ERK1/2 and Akt signaling in VSMC (235). Using an animal arterial balloon-injury model characterized by PDGF-R upregulation to substantiate the *in vitro* results, curcumin significantly inhibited neointima formation, collagen synthesis, cell proliferation and the overexpression of PDGF-R (235). Curcumin also decreased cholesterol-induced proliferation of aortic rat VSMC and suppressed the phosphorylation of ERK1/2 as well as its translocation to the nucleus (236). The vascular anti-proliferative effect of curcumin has also been demonstrated through the induction of HO-1 expression in rat and human VSMC (237). Curcumin's potential role in the prevention of atherosclerosis is further supported through its inhibitory effect on VSMC migration (238). This inhibitory effect was observed on TNF- α -induced migration that was mediated by decreasing TNF- α -induced ROS production, leading to suppression of matrix metalloproteinase 9 (MMP-9) activation and protein expression through the downregulation of NF- κ B (238). Synthetic curcuminoids have also been shown to exert anti-proliferative effects on cell growth. Dehydrozingerone, a biosynthetic structural analogue of curcumin, inhibited PDGF-stimulated VSMC migration, proliferation, collagen synthesis, and PDGF/H₂O₂-stimulated phosphorylation of PDGF-R and downstream Akt (239). HO-3867, another synthetic curcuminoid, significantly inhibited the proliferation of serum-stimulated VSMC (240). Hydrazinocurcumin, yet another synthetic curcumin derivative, potently inhibited the proliferation of bovine aortic endothelial cells (241). These studies support the notion that curcumin confers protection against pathological remodeling of blood vessels, a contributory mechanism of atherosclerosis.

Since atherosclerosis is a chronic inflammatory disease associated with increased oxidative stress in VSMC, it would be possible that the anti-atherogenic effects of curcumin are attributable to its antioxidant and anti-inflammatory properties (238). Curcumin modulates several targets that mediate an anti-atherosclerotic effect but the detailed anti-atherosclerotic mechanisms of curcumin still remain to be elucidated.

1.17.2 Curcumin effects on the heart

The effect of curcumin on cardiac hypertrophy and myocardial ischemia (MI) has been studied in both *in vivo* and *in vitro* models. Cardiac hypertrophy is an adaptive enlargement of the myocardium in response to a variety of stresses, such as an increased workload or myocardial infarction, and is characterized by an increase in the size of the individual cardiomyocytes and the whole heart (242). Cardiac remodeling plays a critical role in the progression of pathologic cardiac hypertrophy to heart failure and death (242). Hypertrophic stimuli initiate several subcellular signaling pathways and these signals reach the nuclei of cardiomyocytes and activate a subset of hypertrophy-responsive transcription factors that change the pattern of the gene expression. Activation of these transcription factors is mediated, in part, through post-transcriptional modifications, such as acetylation by histone deacetylases and an intrinsic histone acetyltransferase (HAT), p300 (243). Nuclear acetylation by p300 is a critical event during cell hypertrophy. Activation of p300 is not only required for pathological myocyte growth but also for normal myocardial development and differentiation. p300 also induces the expression of genes encoding atrial natriuretic factor (ANF), ET-1, and β -myosin heavy chain (β -MHC), which are well established markers of myocardial cell hypertrophy (244-246). Curcumin was reported to be an inhibitor of p300-HAT and was found to repress the p300 induced hypertrophic responses in cultured neonatal cardiomyocytes, including the expression of both ANF and β -MHC genes

(247). It also inhibited the p300 HAT activity and thereby prevented the development of heart failure in two different heart failure models *in vivo*, a hypertensive heart disease in salt-sensitive Dahl rats and in a surgically-induced myocardial infarction in rats (247).

Heart failure is a process of systemic inflammation with overexpression of local inflammatory cytokines including TNF- α (248). Recent reports have shown that TNF- α contributes to the process of myocardial remodeling in evolving heart failure (249). Orally administered curcumin improved left ventricular function in rabbits exhibiting heart failure-induced by pressure overload that resulted from the inhibition of myocardial collagen remodeling associated with suppression of TNF- α expression (250).

As previously mentioned, curcumin also behaves as a free radical scavenger and antioxidant, inhibiting lipid peroxidation and oxidative DNA damage. Puvanakrishnan et al. reported that curcumin plays a protective role against isoproterenol-induced myocardial necrosis in rats and that this protective effect is attributed to its antioxidant properties (214). L-Isoproterenol (ISO) is a synthetic catecholamine that causes myocardial damage when administered in large doses. Orally administered curcumin (200mg/kg) protected against ISO-induced oxidative myocardial injury in rats through enhancement of the antioxidant defense and thereby exhibited cardioprotective activity against ISO-induced cardiotoxicity (251). Furthermore, Venkatesan observed a protective effect of orally administered curcumin against cardiotoxicity produced by adriamycin in rats, showing a reduction in the parameters that indicate lipid peroxidation (252). Moreover, curcumin suppressed neutrophil infiltration into the human injured myocardium (164). Neutrophils are a major source of free radicals that characteristically invade the myocardial tissue during ischemia (164).

Ang II can play a critical role in the genesis of cardiac hypertrophy in hypertension and MI (253). Cardiac hypertrophy in response to Ang II is initiated through activation of its receptors, which results in marked oxidant stress via NADPH oxidase and NF- κ B activation (254, 255). Downstream of NADPH oxidase lies the major redox-sensitive transcription factor NF- κ B, which is perhaps the most critical transcription factor in mediating the transcription of a host of pro-inflammatory, pro-oxidant, and pro-growth genes, in response to Ang II (256). Freund et al. demonstrated the requirement of NF- κ B in Ang II-mediated cardiac hypertrophy *in vivo* (257). Curcumin attenuates Ang II-mediated ROS generation, and the expression of NADPH oxidase and NF- κ B in cardiomyocytes (253). Attenuation of the redox state by curcumin results in the abrogation of Ang II-mediated cardiomyocyte growth as well as the expression of the hypertrophic markers, ANP and BNP. Oxidized-LDL receptor-1 (LOX-1) upregulation has a central role in cardiomyocyte hypertrophy response to Ang II (253). Curcumin reduced the Ang II-mediated upregulation of Ang II type 1 receptor (AT1R) and LOX-1 expression and activation which translates into a strong inhibition of redox signaling resulting in a marked inhibition of cardiomyocyte growth (253).

1.17.3 Curcumin and hypertension

The effect of curcumin on hypertension has not been explored in detail, yet a recent study revealed for the first time, under *in vivo* conditions, that curcumin attenuated the development of hypertension in NO-deficient hypertensive rats (163). Curcumin suppressed blood pressure elevation, decreased vascular resistance and restored vascular responsiveness in rats with *N*^o-nitro-L-arginine methyl ester (L-NAME)-induced hypertension, through an antioxidant mechanism (163). Curcumin has also been shown to induce vasorelaxation on isolated porcine coronary arteries through its antioxidant capacity to promote NO release (258). Moreover,

curcumin supplementation showed significant attenuation of mean arterial blood pressure in streptozotocin-induced diabetic rats (259). In humans, oral turmeric supplementation decreased systolic blood pressure in patients with kidney disease, lupus nephritis (260). Curcumin supplementation may therefore be beneficial in improving vascular function and preventing cardiovascular complications.

1.17.4 Curcumin and diabetic cardiovascular complications

A pilot study done in 1972 reported that curcumin lowered blood sugar levels in human diabetic subjects (261). Since then, the modulation of curcumin has been extended to elucidate the molecular basis for obesity and obesity-related metabolic diseases, including type 2 diabetes and cardiovascular diseases. The anti-diabetic effects of curcumin are also linked with the inhibition of inflammatory and oxidative markers. Increased oxidative stress has been associated with the pathogenesis of chronic diabetic complications, including cardiomyopathy (262). It has been suggested that NO pathway is involved in augmenting oxidative stress (263). Many studies have shown the implication of eNOS and iNOS in the pathogenesis of cardiovascular complications in diabetes (264). In a study where myocardial tissue from diabetic rats exhibited increased levels of eNOS and iNOS mRNA, curcumin treatment prevented this NOS mRNA upregulation leading to a decrease in the oxidative DNA damage in association with a reduction in the expression of transcription factors NF- κ B and AP-1 (265).

Diabetic cardiomyopathy eventually leads to heart failure (186). Transcriptional co-activator p300 and its interaction with myocyte enhancer factor 2 (MEF2) play a role in diabetes-induced cardiomyocyte hypertrophy. Curcumin treatment prevented diabetes-induced

upregulation of these transcripts, suggesting a protective mechanism in glucose-induced cardiomyocyte hypertrophy in diabetes (266).

NF- κ B, TNF- α and Egr-1 have been closely linked with the induction of insulin resistance, a key feature in type II diabetes mellitus. Curcumin has been shown to downregulate these biomarkers (195, 267-270), suggesting a putative mechanism in overcoming insulin resistance as demonstrated by several animal studies (271-273).

Hyperglycemia leads to increased oxidative stress resulting in endothelial dysfunction. A randomized 8 week-study was performed on 72 patients with type II diabetes to evaluate the effects of curcumin on endothelial dysfunction in association with reductions in inflammatory cytokines and markers of oxidative stress. Patients receiving 150 mg of curcumin twice daily showed an improvement of endothelial function and significant reductions in the levels of malondialdehyde, ET-1, IL-6, and TNF- α (274). Curcumin supplementation also improved diabetes-induced endothelial dysfunction in streptozotocin-induced diabetic rats through decreased PKC expression and decreased ROS production (259).

The precise mechanism by which curcumin improves vascular homeostasis remains unclear. However, the ability of curcumin to ameliorate pathophysiological states, such as atherosclerosis, cardiac remodeling and myocardial ischemia, through antioxidant and anti-inflammatory properties, have been suggested to contribute to this response.

1.18 Goal of this study

The broad biological activity of curcumin, including antioxidant and anti-inflammatory effects, influences key cellular signal transduction pathways in multiple diseases. Curcumin has proven to be beneficial in studies within the cardiovascular system involving atherosclerosis,

ischemia-induced diseases, diabetic-induced cardiovascular complications, cardiac hypertrophy and myocardial infarction. However, very little is known regarding the molecular mechanisms involved in mediating these responses.

ET-1 is a very potent active molecule that plays an important role in health and disease through its ability to regulate various cardiovascular functions. ET-1 activates multiple signaling pathways including MAPK and PI3-K/PKB which mediate the hypertrophic and proliferative responses in VSMC. An important role of oxidative stress generation in mediating the effect of ET-1 has been demonstrated. Moreover, ROS are produced and act as second messengers as part of the signaling of receptor protein tyrosine kinases, which are activated after vascular injury. Curcumin has been shown to suppress ROS generation and to inhibit several of the mediators involved in the ET-1 signaling pathway in several cellular lines. Curcumin has also been shown to inhibit cell proliferation, arrest cell cycle progression and induced cell apoptosis in VSMC (275). However, the effect of curcumin in ET-1-induced signaling in VSMC has not been investigated. Therefore, the present study aims at examining the effect of curcumin on ET-1-induced phosphorylation of ERK1/2, c-Raf, PKB and IGF-1R. Since ET-1 action requires IGF-1R transactivation we have also investigated if curcumin modulates IGF-1-induced signaling in VSMC. In addition, we tested if the transcription factor Egr-1 is also a target of curcumin in response to ET-1 as well as IGF-1.

CHAPITRE 2

ARTICLE

*Attenuation of Endothelin-1 and Insulin-like-Growth-Factor 1-induced
Signaling by Curcumin in A-10 Vascular Smooth Muscle Cells*

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Attenuation of Endothelin-1 and Insulin-Growth-Factor Type 1-induced Signaling by Curcumin in A-10 Vascular Smooth Muscle Cells

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Abstract

Despite recent advances, mortality from cardiovascular disease remains high, highlighting the requirement for improved therapies. Several studies have demonstrated a correlation between cardiovascular disease and an increased activation of ET-1-induced signaling in vascular smooth muscle cell (VSMC), including protein kinase B (PKB) and extracellular signal-regulated kinase 1 and 2 (ERK1/2) pathways, as well as an increase in ET-1-mediated VSMC hypertrophy and proliferation. Oxidative stress has been suggested to play an intermediary role in mediating ET-1-induced cardiovascular pathophysiological effects. Curcumin (diferuloylmethane), a major component of the spice turmeric, has been shown to exhibit cardiovascular protective effects mainly through its antioxidant and anti-inflammatory properties. The current study was undertaken to examine the effectiveness of curcumin to inhibit ET-1-stimulated signaling events in A-10 VSMC. ET-1 (100nM) produced a marked phosphorylation of PKB, ERK1/2, c-Raf and insulin-like growth factor type 1 receptor (IGF-1R), in VSMC, that was dose dependently inhibited by pretreatment with curcumin. Curcumin also attenuated IGF-1-induced phosphorylation of PKB, ERK1/2 and c-Raf as well as phosphorylation of IGF-1R. Furthermore, curcumin also inhibited ET-1 and IGF-1-induced expression of early growth response-1 (Egr-1), a transcription factor downstream of ERK1/2 that plays a regulatory role in several cardiovascular pathological processes. In conclusion, these data provide evidence that curcumin is a potent inhibitor of ET-1 and IGF-1-induced mitogenic and proliferative signaling responses in A-10 VSMC and suggest that the ability of curcumin to attenuate these events may contribute as a potential mechanism for its cardiovascular protective effects.

Key words: Curcumin, Early growth response-1, Endothelin-1, Extracellular signal-regulated kinase 1 and 2, Insulin-like growth factor type 1, Insulin-like growth factor type 1 receptor, Protein kinase B, Vascular smooth muscle cells

Introduction

Endothelin-1 (ET-1) is a potent vasoconstrictor peptide that has been shown to exhibit mitogenic and hypertrophic responses in vascular smooth muscle cells (VSMC) (1, 2). A potential role of ET-1 in promoting the pathophysiology of cardiovascular diseases such as coronary artery disease (3), hypertension (4), heart failure (4) and vascular remodeling (atherosclerosis and restenosis) (5) has been suggested. VSMC play a critical role in the structural and functional characteristics of the vessel wall, including growth, repair and remodeling (6). ET-1 mediates its effects on VSMC through interaction with its two subtypes of heterotrimeric G protein coupled receptors (GPCR), ET_A and ET_B (1, 2). This leads to the activation of multiple signaling pathways, including growth promoting mitogen-activated protein kinases (MAPK), of which extracellular signal-regulated kinase 1 and 2 (ERK1/2) is the most well characterized, and phosphatidylinositol 3-kinase (PI3-K)/protein kinase B (PKB) pathways (1, 2). An intermediary role of transactivation of growth factor receptor protein tyrosine kinases (R-PTK) in transducing ET-1-induced signaling events has been proposed (7). In this regard, we have recently shown that insulin-like growth factor type 1 receptor (IGF-1R) plays a critical role in mediating ET-1-induced PKB activation, as well as hypertrophic and proliferative responses induced by ET-1 in VSMC (7). Although the mechanism of action responsible for R-PTK transactivation is not yet fully understood, several factors are suggested to be implicated in this process. Amongst them, the generation of reactive oxygen species (ROS) which has been shown to play an important role in inducing the activation of ERK1/2 and PKB signaling in VSMC in response to ET-1 (8), has also been shown to contribute to the activation of IGF-1R-PTK in VSMC (9). IGF-1R is classically activated by its growth factor ligand, insulin-like growth factor type 1 (IGF-1). IGF-1 can be synthesized and secreted in cultured VSMC (10), and has been shown to act as a potent mitogen for VSMC *in vitro* (11, 12). ERK1/2 and PI3-K/PKB signaling promotes IGF-1-induced

mitogenic and proliferative responses respectively, in VSMC (13, 14). Accordingly, inhibition of ET-1 and IGF-1-stimulated VSMC signaling pathways may serve as a potential therapeutic intervention to attenuate cellular manifestations associated with the progression of many vascular diseases.

Curcumin, a natural polyphenolic compound found in the spice turmeric (*Curcuma Longa*), has recently attracted much attention as it has been shown to exhibit a vast array of biological activities, including antioxidant, anti-proliferative, anti-tumour and anti-inflammatory properties (15). Several studies have suggested that curcumin may play a role in the protection against certain cardiovascular diseases, including arterial disease (16), atherosclerosis (17), cardiac hypertrophy (18-20), heart failure (20), and damage caused by myocardial ischemia (21-23). The precise mechanisms responsible for the cardiovascular protective effect remains obscure however, curcumin has been shown to exert its effects on several signaling pathways linked to growth, proliferation and gene expression (24-29). It has been shown to inhibit serum-induced and platelet-derived growth factor (PDGF)-dependent mitogenesis in VSMC (26). In a recent study, curcumin attenuated PDGF-induced signaling in VSMC through inhibition of PDGF receptor, ERK1/2 and PKB phosphorylation (25). Since curcumin exhibits anti-proliferative effects and has potent antioxidant properties with its ability to scavenge ROS (30-32), and ET-1 exerts its effects through the generation of ROS with an intermediary role of IGF-1R transactivation (7, 8), the purpose of this study was to investigate the effect of curcumin on ET-1 and IGF-1-mediated proliferative and hypertrophic signaling responses in VSMC. Therefore, we examined the effect of curcumin on ET-1 and IGF-1-induced phosphorylation of IGF-1R, c-Raf, ERK1/2 and PKB, key mediators involved in growth-promoting, proliferative and hypertrophic responses. In addition, we have also investigated the effect of curcumin on early growth response

(Egr)-1, a transcription factor which is a downstream target of ERK1/2 and is implicated in multiple cardiovascular pathological processes (33).

Materials and Methods

Antibodies and reagents:

Cell culture reagents were procured from Invitrogen Corp. (Grand Island, NY). ET-1 was purchased from American Peptide Inc. (USA). IGF-1 was purchased from Peprtech Inc. (USA). Monoclonal phospho-specific-Tyr²⁰⁴ ERK1/2, polyclonal ERK1/2, anti-IGF-1R, Egr-1 and GAPDH antibodies, as well as horseradish peroxidase-conjugated goat anti-mouse immunoglobulin were from Santa Cruz Biotech (Santa Cruz, CA). The phospho-Ser⁴⁷³-specific-PKB, anti-PKB, phospho-Ser³³⁸-specific-c-Raf, anti-c-Raf and anti-rabbit antibodies were from Cell Signaling (Beverly, MA). Curcumin was procured from Calbiochem (San Diego, CA). Anti-phosphospecific IGF-1R (phospho-Tyr^{1158/1162/1163}) antibody was obtained from Biosource. Hoechst 33342 (10mg/ml) was obtained from Invitrogen. The enhanced chemiluminescence (ECL) detection kit was from Amersham Pharmacia Biotech (Baie d'Urfé, Qc, Canada).

Cell culture:

VSMC are derived from embryonic rat thoracic aorta A-10 cells and were maintained in culture with Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum (FBS) and 1% penicillin + streptomycin, at 37°C in a humidified atmosphere of 5% CO₂. Cells were grown to 80-90% confluence in 60mm plates and incubated in serum-free DMEM 20 hours prior to treatment. They were passaged twice a week by harvesting with Trypsin/EDTA.

Immunoblotting:

Cells incubated in the absence or presence of various agents were washed twice with ice-cold PBS and lysed in 200µl of buffer (25mM Tris-HCl, pH 7.5, 25mM NaCl, 1mM Na orthovanadate, 10mM Na fluoride, 10 mM Na pyrophosphate, 2 mM benzamide, 2 mM ethylenebis (oxyethylenitrilo)-tetraacetic acid (EGTA), 2mM ethylenediamine-tetraacetic acid (EDTA), 1 mM phenylmethylsulphonyl fluoride (PMSF), 10 µg/ml aprotinin, 1% Triton X-100, 0.1% sodium dodecyl sulfate (SDS) and 0.5 µg/ml leupeptin) on ice. The cells were scraped, collected and clarified by centrifugation at 12,000g for 10 minutes at 4°C to remove insoluble materials. Protein concentrations were measured using Bradford assay. Equal amounts of protein were subjected to 7.5% SDS-polyacrylamide gel (SDS-PAGE), transferred to polyvinylidene difluoride (PVDF) membranes (Millipore, MA, USA). The membranes were blocked 1 hour with PBS-Tween 20 containing 5% non-fat dry milk at room temperature and then incubated overnight at 4°C with respective primary antibodies (Monoclonal phospho-specific-Tyr²⁰⁴ ERK1/2 antibody (1:4000), phospho-Ser³³⁸-specific-c-Raf (1:2000), phospho-Ser⁴⁷³-specific-PKB antibody (1:2000), phospho-Tyr^{1131/1135/1136}-specific-IGF-1R (1:000), Egr-1 (1:1000), anti-PKB (1:2000), polyclonal ERK1/2 (1:4000), anti-c-Raf (1:2000), anti-IGF-1R (1:1000) and GAPDH (1:2000)). The antigen-antibody complex was detected by horseradish peroxidase-conjugated second antibody (1:4000), and protein bands were visualized by ECL. The intensity of the bands was quantified by densitometric analysis using Quantity One imaging and Graphpad Prism 5 software programs.

Nuclear extraction protocol

Cells incubated in the absence or presence of various agents were washed twice with ice-cold PBS and collected in 500 μ l of buffer solution containing 10mM Hepes, 10mM KCl, 0.1mM EDTA, 0.1mM EGTA, 1mM PMSF, 1mM protease cocktail inhibitor and 1mM Na orthovanadate. Lysates were incubated in ice for 15 minutes before the addition of NP40 10% detergent and then they were vortexed for 10 seconds at highest setting before being centrifuged at 13000RPM for 4 minutes at 4°C. The supernatant (that corresponds to the cytoplasmic fraction) was saved and transferred in a clean tube. The pellet was resuspended in 60 μ l, by pipeting up and down several times, in buffer containing 10mM Hepes, 400mM NaCl, 0.1mM EDTA, 0.1mM EGTA, 1mM PMSF, 1mM protease cocktail inhibitor and 1mM Na orthovanadate. Lysates were sonicated by performing 6 cycles at 10 seconds per cycle with 30 second intervals and then centrifuged at 13000RPM for 5 minutes at 4°C. Pellet was discarded and the supernatant, which corresponds to the nuclear fraction, was collected. Protein concentrations were measured using Bradford assay.

Apoptosis assay

Curcumin-induced apoptosis was monitored by the extent of nuclear fragmentation. Nuclear fragmentation was visualized by Hoechst 33342 staining of apoptotic nuclei. Hoechst 33342 is a fluorescent bisbenzimidazole that stains DNA and penetrates membranes of dead cells. It is excited by ultraviolet light of 350nm and emits blue light of 461nm wavelength. After treatment with varying concentrations of curcumin for 30 minutes cells were treated with 2% paraformaldehyde (diluted in PBS) in 2000 μ L basal medium. The adhered cells were then stained with 2.5 μ L of Hoechst 33342 (10mg/ml Invitrogen) in 2500 μ L medium and incubated at room temperature in the dark for 15 minutes. The cells were imaged under an Olympus BH-2 fluorescence microscope

using 350nm stimulation and 460nm emission. Triplicates samples were used for each treatment. Under our assay the treatment of A-10 VSMC for 30 minutes at 50 μ M did not cause any significant cell death (data not shown).

Statistics:

Statistical analysis was performed by one-way, repeated-measures analysis of variance (ANOVA) followed by a Tukey *post hoc* test. All data are reported as means + SE. the differences between means were considered significant at $P < 0.05$.

Results

Curcumin inhibits ET-1- and IGF-1-induced phosphorylation of PKB in A-10 VSMC

PKB activation has been shown to contribute to hypertrophic responses in VSMC (reviewed in (1)). Therefore, we investigated the effect of curcumin on PKB phosphorylation induced by ET-1 and IGF-1. As shown in Fig. 1 both ET-1 and IGF-1 enhanced the phosphorylation of PKB 3 fold and 15 fold, respectively. However, pretreatment of A-10 VSMC with curcumin for 30 minutes dose-dependently attenuated both ET-1 and IGF-1-induced phosphorylation of PKB. The attenuating effect of curcumin could be detected at 5 μ M but was more prominent at higher concentrations and at 25 μ M almost complete inhibition of ET-1-induced PKB phosphorylation was observed (Fig. 1A). Similarly, curcumin also inhibited IGF-1-induced phosphorylation of PKB in these cells but appeared to be slightly less potent as compared to its effect on ET-1-induced response (Fig. 1B).

Curcumin inhibits ET-1- and IGF-1-induced phosphorylation of c-Raf and ERK1/2 in A-10 VSMC

Activation of ERK1/2 signaling has been implicated in mediating hypertrophic and proliferative effects of ET-1 (34, 35). Therefore, we next investigated the effect of curcumin on ERK1/2 signaling (Fig 2). Treatment with ET-1 and IGF-1 increased ERK1/2 phosphorylation in A-10 VSMC (Fig. 2). However, pre-treatment of the cells with curcumin prior to stimulation with either ET-1 or IGF-1 resulted in a significant inhibition in ERK1/2 phosphorylation induced by both ET-1 and IGF-1 (Fig. 2). Curcumin had no effect on the expression of ERK1/2 protein (Fig. 2).

ERK1/2 activation requires sequential activation of Ras, Raf and MEK upstream signaling components (1). Therefore, we examined the effect of curcumin on the activated c-Raf levels by measuring the phosphorylation level of the c-Raf protein at serine 338 in A-10 VSMC treated with ET-1 and IGF-1. As shown in Fig. 3, curcumin pretreatment markedly inhibited the phosphorylation of c-Raf stimulated by both agents in a dose-dependent manner without altering the levels of this protein. The inhibitory effect of curcumin on both ET-1 and IGF-1-induced phosphorylation of c-Raf was quite significant at 25 μ M and became even more prominent at 50 μ M, where almost complete inhibition was observed (Fig. 3). These data indicate that curcumin inhibits the phosphorylation and hence the c-Raf kinase activity of this upstream component of ERK1/2 signaling pathway and thereby inhibits ET-1 and IGF-1-induced phosphorylation of ERK1/2 in A-10 VSMC.

Attenuation of ET-1- and IGF-1-induced tyrosine phosphorylation of IGF-1R β subunit by curcumin in A10-VSMC

Since, we have previously reported that ET-1 is capable of increasing tyrosine phosphorylation of IGF-1R β subunit, which is required for its activation, and that IGF-1R-PTK is involved in mediating ET-1-induced PKB activation in A-10 VSMC (7), we next tested the effect of curcumin on the ET-1-mediated phosphorylation of IGF-1R. As shown in Fig. 4A, when compared with ET-1 alone, curcumin inhibited ET-1-induced phosphorylation of IGF-1R. A pronounced attenuating effect was detected at 5 μ M whereas almost complete inhibition of IGF-1R phosphorylation was observed at 25 μ M (Fig. 4A). In order to distinguish this ET-1-induced transactivation of IGF-1R with the ligand-dependent activation of IGF-1R, we investigated the effect of curcumin on IGF-1-induced phosphorylation of IGF-1R. As expected, IGF-1 increased

IGF-1R phosphorylation and curcumin dose-dependently attenuated this effect with a marked attenuation observed at 25 μ M and an almost complete inhibition observed at 50 μ M (Fig. 4B).

Inhibition of ET-1- and IGF-1-induced upregulation of Egr-1 by curcumin in A-10 VSMC

It has been suggested that Egr-1 plays a regulatory role in multiple cardiovascular pathological processes (33). It has a low basal level expression in normal vessels but is rapidly and transiently expressed in VSMC and endothelial cells in response to injury (36). Egr-1 protein is biologically active and has exerts profound chemotactic and mitogenic effects in injured vascular cells, which may contribute to the structural remodeling that typically occurs in the pathogenesis of vascular diseases (36). Therefore, we wished to determine if ET-1 or IGF-1 will upregulate Egr-1 expression in A-10 VSMC. We observed that Egr-1 protein expression was upregulated within 30 minutes and peaked at 60 minutes of ET-1 and IGF-1 exposure of A-10 VSMC (Fig. 5). Since Egr-1 gene expression has been shown to be dependent on ERK1/2 signaling (33), and curcumin exerts an inhibitory effect on the ERK1/2 pathway, we were further interested in investigating the effect of curcumin on ET-1 and IGF-1-induced Egr-1 expression in A-10 VSMC. As shown in Fig. 6, pre-treatment of VSMC with curcumin prior to stimulation with either ET-1 or IGF-1 inhibited the expression of Egr-1 induced by these two vasoactive agents.

Discussion

Curcumin has been suggested to exert cardiovascular protective effects in a variety of experimental models. However, the precise molecular mechanism responsible for this response remains poorly understood. ET-1 and IGF-1 are important vasoactive peptides with a key role in the pathogenesis of vascular disease. The current study has assessed the effect of curcumin, the major active ingredient of turmeric (*Curcuma Longa*) spice, on ET-1 and IGF-1-induced signaling events. Here, we demonstrate that curcumin treatment attenuated ET-1 and IGF-1-induced phosphorylation of IGF-1R, ERK1/2, c-Raf and PKB in VSMC. We also show that curcumin treatment also inhibited the expression of zinc finger transcription factor Egr-1 by these vasoactive agents.

There is growing evidence that curcumin has a potential role in the protection against cardiovascular diseases. It was reported that curcumin improved the development of cardiac hypertrophy, through deactivation of hypertrophic signaling, and heart failure in animal models (18, 20). A recent study demonstrated that curcumin attenuated the development of hypertension, improved hemodynamic status and restored vascular function in nitric oxide-deficient hypertensive rats through alleviation of oxidative stress (37).

Although, curcumin has been shown to attenuate the response of several growth factors and their signaling pathways in cancerous cell lines (24), there are only limited studies on its effect in VSMC. Yang et al. have reported an inhibitory effect of curcumin on PDGF signaling and PDGF-stimulated VSMC proliferation, migration, and collagen synthesis (25). They demonstrated that curcumin inhibits PDGFR phosphorylation as well as the PDGF-induced phosphorylation of ERK1/2 and PKB (25). Dehydrozingerone, a structurally half-analog and biosynthetic intermediate of curcumin, also elicited a similar inhibition of PDGF-stimulated

phosphorylation of PDGFR, PKB and ERK1/2 in VSMC, leading to the inhibition of VSMC migration, proliferation and collagen synthesis (38). However, our work represents the first study to demonstrate that curcumin antagonizes both ET-1 and IGF-1-induced IGF-1R phosphorylation, as well as their ability to stimulate the phosphorylation of c-Raf, ERK1/2 and PKB in VSMC. Given that an upregulated ET-1 system has been linked to hyperproliferation in VSMC from SHR (39), it may be suggested that curcumin-induced attenuation of ET-1 signaling might serve as one of the mechanisms by which curcumin exerts anti-hypertrophic effects. Since curcumin is an antioxidant and ET-1 as well as IGF-1-induced signaling requires ROS generation (8, 40), it may be possible that the ability of curcumin to reduce ROS formation may be one of the mechanisms by which curcumin exerts its attenuating effect on these signaling events.

The zinc finger transcription factor Egr-1 plays an important role in vascular biology. The Egr family includes Egr-1, Egr-2, Egr-3, and Egr-4. Among the family members, the best characterized is Egr-1. Following activation, Egr-1 is primarily expressed in the nucleus and is capable of regulating the transcription of several genes implicated in the development of vascular disease (41). Egr-1 is weakly, if at all, expressed in normal vessel wall but has been shown to be highly expressed in response to acute injury (36, 42) and vasoactive agents, such as angiotensin II (Ang II) (43). It is highly expressed in VSMC of atherosclerotic lesions (44) and plays critical roles in regulating VSMC growth and intimal thickening after vascular injury (45). ERK1/2 plays a prominent role in activating Egr-1 expression in endothelial cells (46) and VSMC (43, 47). Studies have shown that attenuation of Egr-1 gene expression inhibits VSMC migration and proliferation (48-51). Thus, it may be suggested that curcumin-induced attenuation of Egr-1 expression may attribute to its cardiovascular protective role. This notion is further supported by studies in which antisense nucleotides against Egr-1 were found to block ET-1-induced cardiac protein synthesis, a marker of cardiac hypertrophy (52).

The antioxidant activity of curcumin was reported as early as 1975 (53). Oxidative stress associated with the overproduction of ROS plays a major role in the pathogenesis of various cardiovascular diseases, including hypertension and atherosclerosis (54). The antioxidant activities of curcumin may be attributable to many factors, including the ability to scavenge ROS, the increase in NO bioavailability, and the enhancement of the antioxidant defense system. Curcumin has been proven to be a potent scavenger of a variety of ROS including superoxide anion radicals (O_2^-) (30), hydroxyl radicals (OH^\cdot) (31), nitrogen dioxide radicals (32) and non-free radical species such as hydrogen peroxide (H_2O_2) (30). It has also been shown to enhance the activity of antioxidant enzymes (55) and to counteract the activity of ROS generating enzymes (56). In human endothelial cells, curcumin was shown to abolish ROS production and attenuate NADPH oxidase activity (57). In cardiomyocytes, attenuation of the redox state by curcumin resulted in the abrogation of Ang II-mediated cardiomyocyte growth (19). In synergy with its anti-inflammatory properties, curcumin prevented VSMC migration through its ability to suppress ROS generation (58). Moreover, curcumin has been shown to inhibit H_2O_2 -stimulated phosphorylation of PDGF receptor in VSMC (38). As previously mentioned, ET-1 has been shown to increase the production of ROS in VSMC and this ROS generation has been shown to be a critical mediator in ET-1-induced signaling events linked to growth-promoting proliferative and hypertrophic pathways in VSMC (8). Our earlier studies have also shown that tyrosine phosphorylation of β -subunit IGF-1R is an important step in transducing the effect of H_2O_2 on the phosphorylation of ERK1/2 and PKB in VSMC (9, 59). Since both ERK1/2 and PKB signaling pathways play a critical role in mediating hypertrophic and cell survival responses (1), it is reasonable to suggest that the ability of curcumin to inhibit the IGF-1 and ET-1-induced activation of these pathways may be due to its antioxidative properties. In light of these findings,

it may be suggested that curcumin-induced inhibition of both PKB and ERK1/2 signaling, and Egr-1 expression, may at least, partially contribute to the vascular protective effect of curcumin.

In summary, this is the first report demonstrating that curcumin attenuates the signaling responses of ET-1 and IGF-1 in A-10 VSMC. We demonstrated that curcumin attenuated both IGF-1 and ET-1-stimulated increase of PKB, c-Raf, ERK1/2 and IGF-1R activation and Egr-1 expression in A-10 VSMC. Since ERK1/2, PKB and Egr-1 play a key role in mediating VSMC growth and hypertrophy, it may be suggested that the ability of curcumin to attenuate these pathways may serve as a potential mechanism by which it counteracts the biological response of IGF-1 and ET-1 and exerts a vascular protective effect.

Acknowledgments

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Figure Legends

Figure 1. Curcumin attenuates ET-1 and IGF-1-induced PKB phosphorylation in A-10

VSMC. A. Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 100nM of ET-1 for 5 minutes. **B.** Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 6.5nM of IGF-1 for 5 minutes. Cell lysates were immunoblotted by phospho-specific-Ser⁴⁷³-PKB antibody (top panels of each section). Blots were also analyzed for total PKB (middle panels of each section). Bottom panels (bar diagrams) represent average data quantified by densitometric scanning of protein bands shown in the top panel. Values are the means \pm SE of 6 distinct western blots from 3 independent experiments that were performed in duplicate, and are expressed as fold increase over basal phosphorylation, which is taken as 1. No results were excluded. $P < 0.05$ considered as statistically significance versus ET-1 or IGF-1 alone. * indicates that $P < 0.05$, ** indicated that $P < 0.005$, and *** indicates that $P < 0.0005$.

Figure 2. Curcumin attenuates ET-1 and IGF-1-induced ERK1/2 phosphorylation in A-10

VSMC. A. Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 100nM of ET-1 for 5 minutes. **B.** Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 6.5nM of IGF-1 for 5 minutes. Cell lysates were immunoblotted by phospho-specific -Tyr²⁰⁴ERK1/2 antibody as shown in the top panels of each section. Blots were also analyzed for total ERK1/2 (middle panels of each section). Bottom

panels (bar diagrams) represent average data quantified by densitometric scanning of protein bands shown in the top panel. Values are the means \pm SE of 6 distinct western blots from 3 independent experiments that were performed in duplicate, and are expressed as fold increase over basal phosphorylation, which is taken as 1. No results were excluded. $P < 0.05$ considered as statistically significance versus ET-1 or IGF-1 alone. * indicates that $P < 0.05$, ** indicated that $P < 0.005$, and *** indicates that $P < 0.0005$.

Figure 3. Curcumin attenuates ET-1 and IGF-1-induced c-Raf phosphorylation in A-10

VSMC. A. Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 100nM of ET-1 for 5 minutes. **B.** Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 6.5nM of IGF-1 for 5 minutes. Cell lysates were immunoblotted by phospho-Ser³³⁸-specific-c-Raf antibody as shown in the top panels of each section. Blots were also analyzed for total c-Raf (middle panels of each section). Bottom panels (bar diagrams) represent average data quantified by densitometric scanning of protein bands shown in the top panel. Values are the means \pm SE of 6 distinct western blots from 3 independent experiments that were performed in duplicate, and are expressed as fold increase over basal phosphorylation, which is taken as 1. No results were excluded. $P < 0.05$ considered as statistically significance versus ET-1 or IGF-1 alone. * indicates that $P < 0.05$, ** indicated that $P < 0.005$, and *** indicates that $P < 0.0005$.

Figure 4. Curcumin attenuates ET-1 and IGF-1-induced IGF-1R tyrosine phosphorylation

in A-10 VSMC. **A.** Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 100nM of ET-1 for 5 minutes. **B.** Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 6.5nM of IGF-1 for 5 minutes. Cell lysates were immunoblotted by phospho-specific IGF-1R (phospho-Tyr^{1158/1162/1163}) antibody as shown in the top panels of each section. Blots were also analyzed for total IGF-1R (middle panels of each section). Bottom panels (bar diagrams) represent average data quantified by densitometric scanning of protein bands shown in the top panel. Values are the means \pm SE of 6 distinct western blots from 3 independent experiments that were performed in duplicate, and are expressed as fold increase over basal phosphorylation, which is taken as 1. No results were excluded. $P < 0.05$ considered as statistically significance versus ET-1 or IGF-1 alone. * indicates that $P < 0.05$, ** indicated that $P < 0.005$, and *** indicates that $P < 0.0005$.

Figure 5. Egr-1 is upregulated by ET-1 and IGF-1 in A-10 VSMC.

A. Serum-starved quiescent A-10 cells were treated without or with 100nM ET-1 for the identified time periods. **B.** Serum-starved quiescent A-10 cells were treated without or with 6.5nM of IGF-1 for the identified time periods. Nuclear fractions of the cell lysates were immunoblotted by Egr-1 antibody as shown in the top panels of each section. Blots were also analyzed for protein loading, using GAPDH (middle panels of each section). Bottom panels (bar diagrams) represent average data quantified by densitometric scanning of protein bands shown in the top panel. Values are the means \pm SE of 6 distinct western blots from 3 independent experiments that were performed in duplicate, and are expressed as fold increase over basal phosphorylation, which is taken as 1. No

results were excluded. $P < 0.05$ considered as statistically significance versus control. * indicates that $P < 0.05$.

Figure 6. Curcumin downregulates Egr-1 in response to ET-1 and IGF-1 in A-10 VSMC.

A. Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 100nM of ET-1 for 60 minutes. B. Serum-starved quiescent A-10 cells were pretreated without or with the indicated curcumin concentrations for 30 minutes, followed by 6.5nM of IGF-1 for 60 minutes. Nuclear fractions of the cell lysates were immunoblotted by Egr-1 antibody as shown in the top panels of each section. Blots were analyzed for total nuclear protein by GAPDH (middle panels of each section). Bottom panels (bar diagrams) represent average data quantified by densitometric scanning of protein bands shown in the top panel. Values are the means \pm SE of 6 distinct western blots from 3 independent experiments that were performed in duplicate, and are expressed as fold increase over basal phosphorylation, which is taken as 1. No results were excluded. $P < 0.05$ considered as statistically significance versus ET-1 or IGF-1 alone. *** indicates that $P < 0.0005$.

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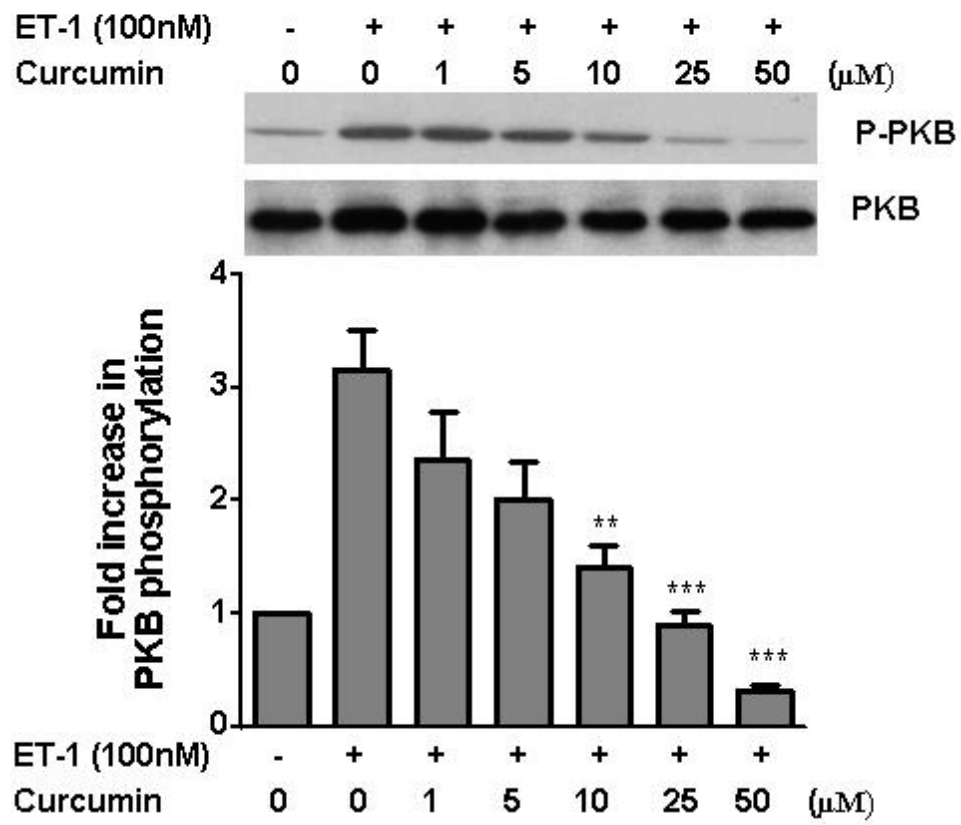


Figure 1

B.

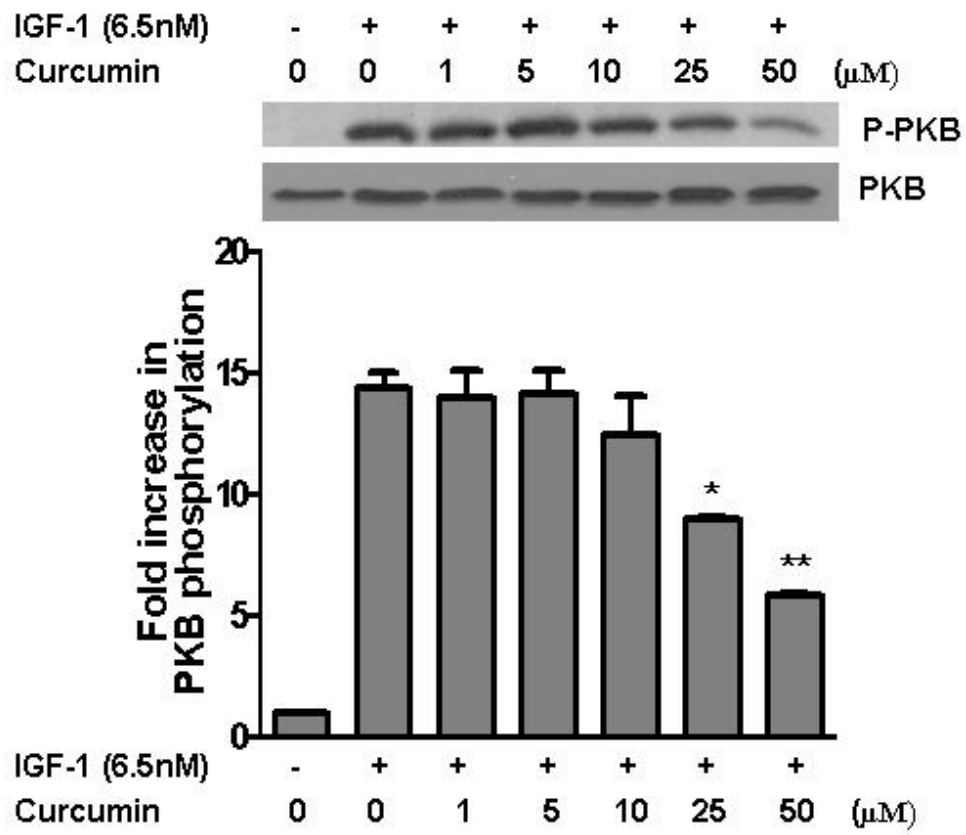


Figure 1

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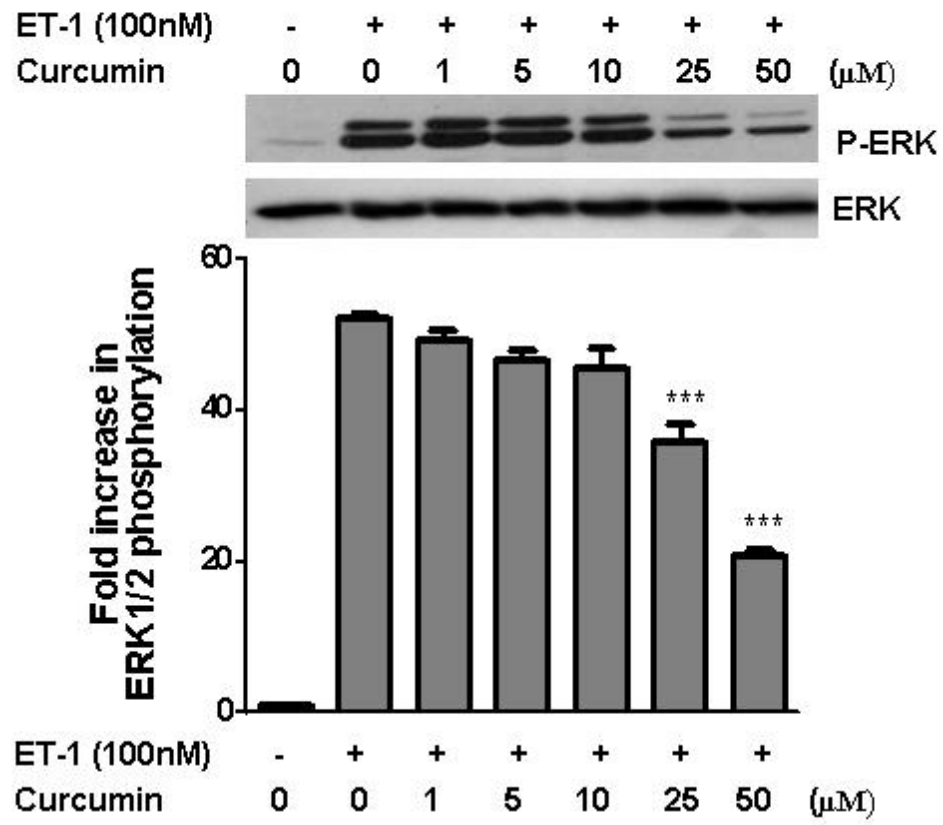


Figure 2

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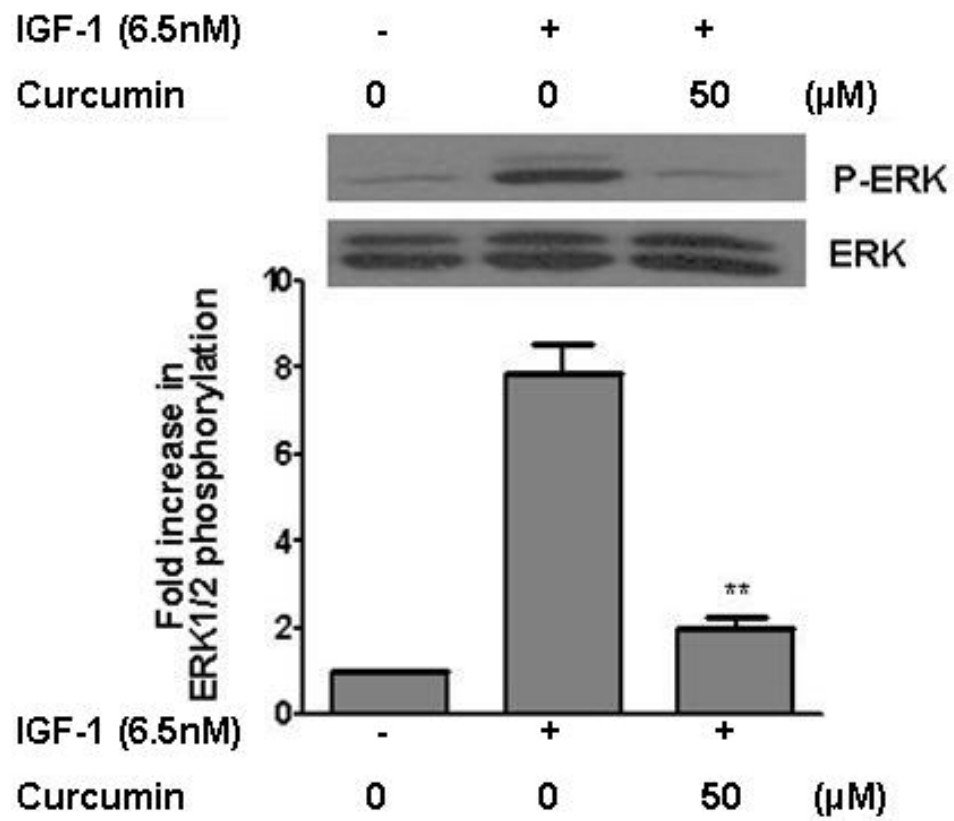


Figure 2

A.

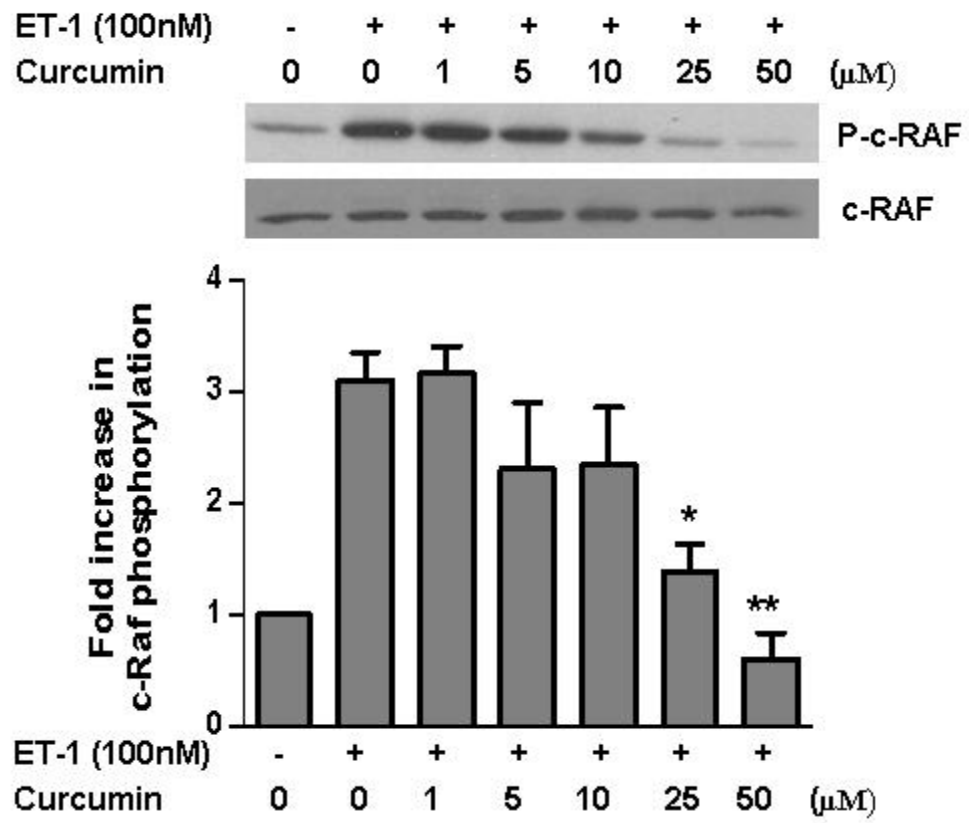


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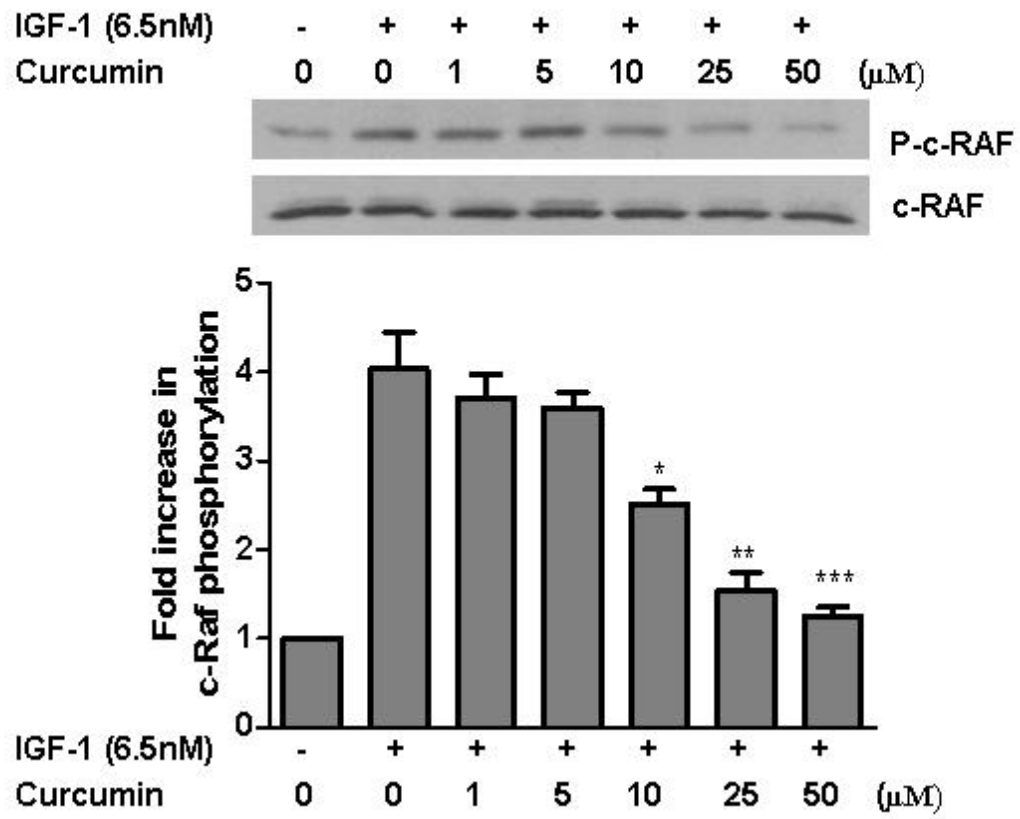


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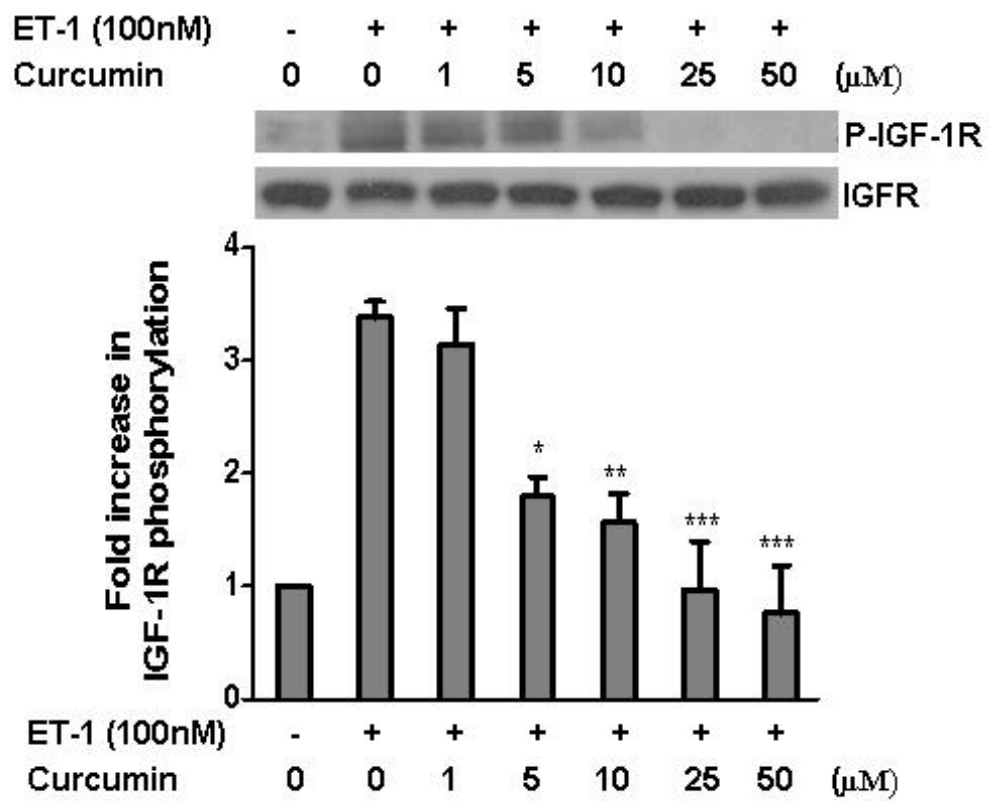


Figure 4

A.

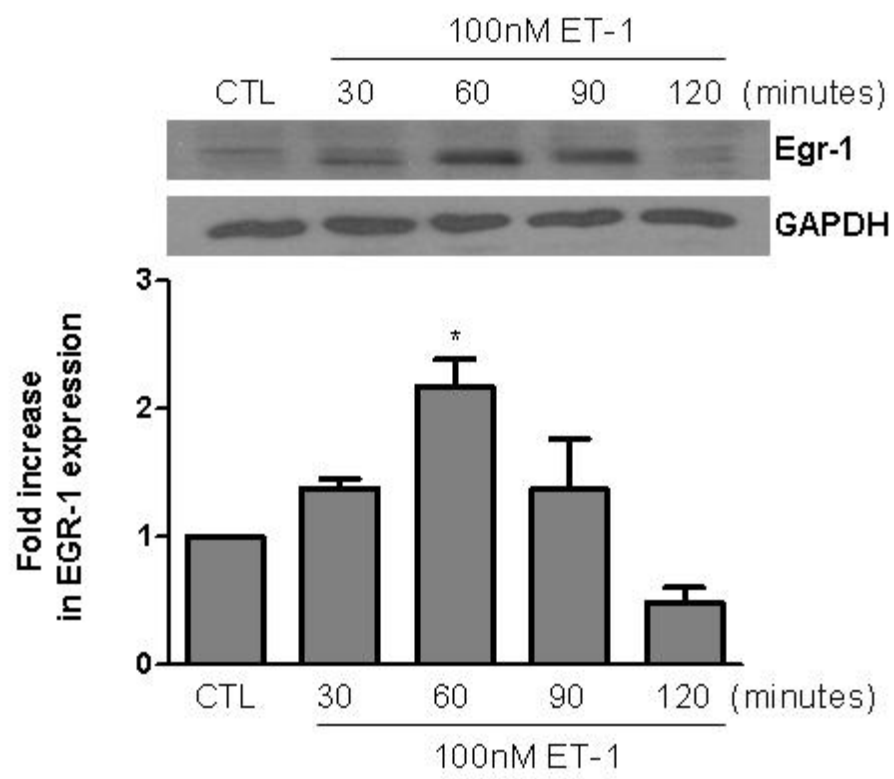
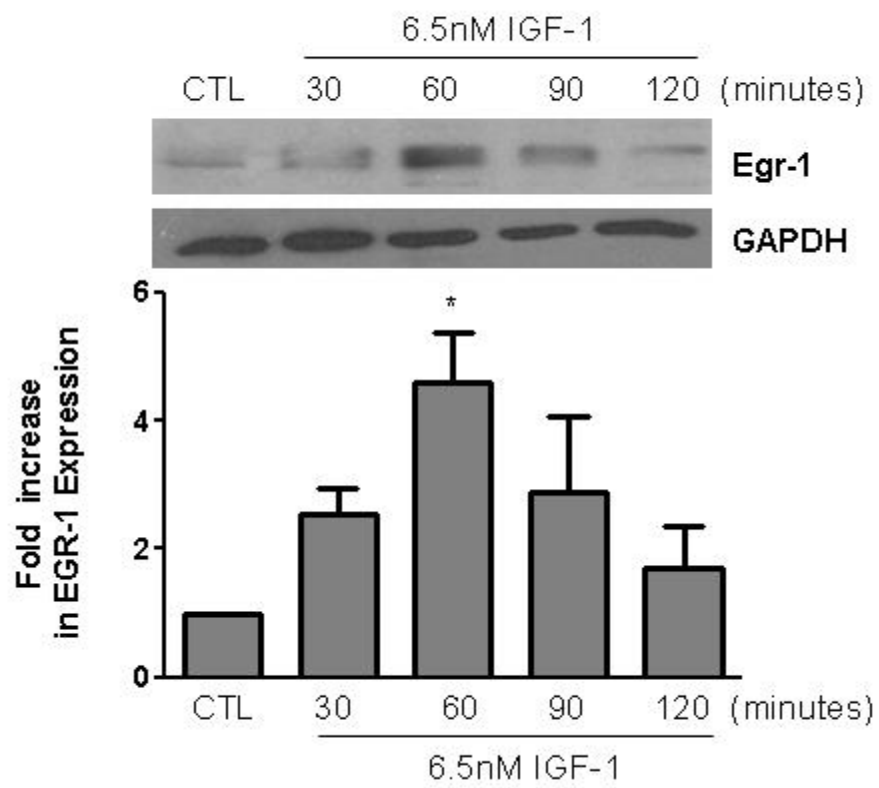


Figure 5

B.

**Figure 5**

A.

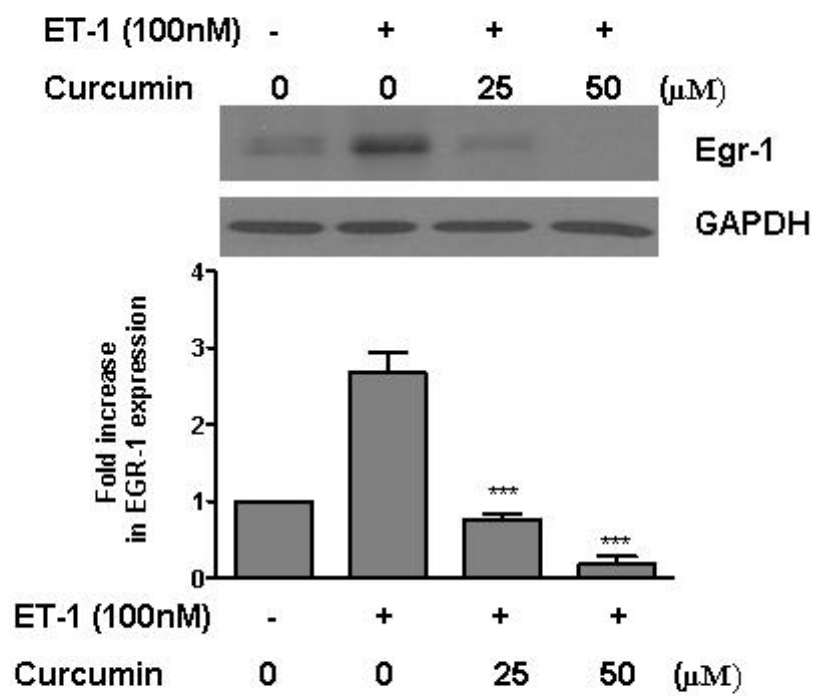


Figure 6

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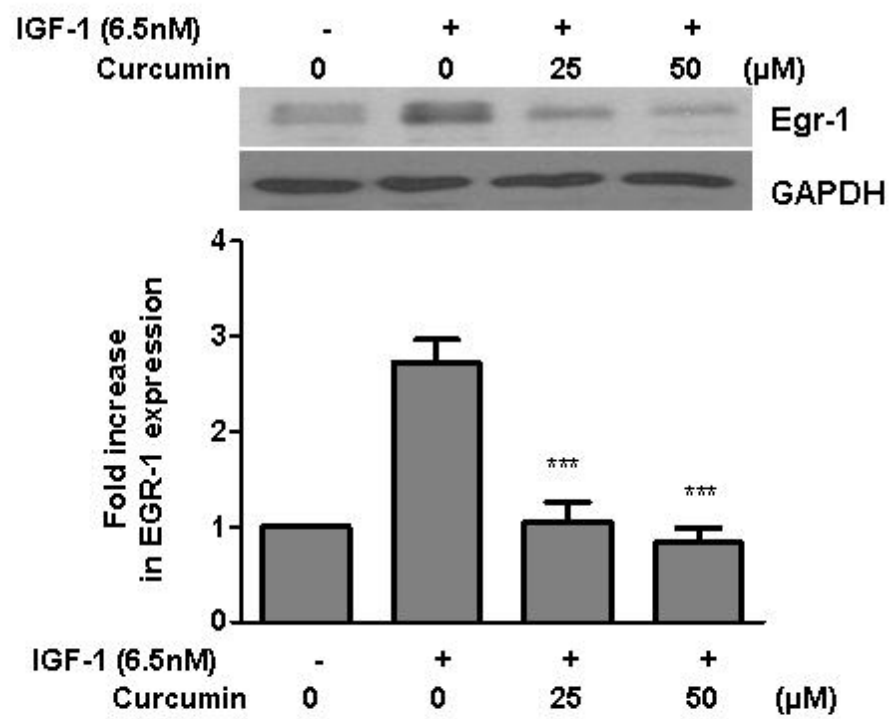


Figure 6

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CHAPITRE 3

DISCUSSION GÉNÉRALE

The discovery of endothelin (ET), the potent vasoconstrictor, surfaced only two decades ago and the endothelin peptide family has now evolved into an intricate system. Endothelin-1 (ET-1) is the most predominant isoform synthesized by the vasculature, mainly by the vascular endothelium and smooth muscle cells, and is accountable for the majority of the pathobiological effects exerted by the endothelin peptide family. In the vascular system, ET-1 mainly exerts a basal vascular tone regulation. A long term upregulated ET-1 system has been suggested to contribute to the deterioration of vascular function that leads to the development of vascular diseases. ET-1 exerts its action through the activation of its endothelin receptors, ET_A and ET_B, but ET_A is mainly responsible in the contribution of ET-1 to the pathogenesis of vascular abnormalities, such as hypertension, atherosclerosis, restenosis, and other cardiovascular diseases. Based on recent research, ET-1 receptor antagonists exhibit inhibition of ET-1-induced functional and structural alterations in the vasculature. Nevertheless, ET-1 mediates its pleiotropic actions through the activation of several signaling pathways and further investigation is required to provide a better knowledge of these ET-1 signal transducing pathways for designing specific therapeutic agents directed against critical components of the signaling systems implicated in pathological contribution of ET-1-induced vascular remodeling.

ET-1 elicits its biological effects in a paracrine-autocrine manner through the activation of its G-protein-coupled receptors (GPCR). This leads to the activation of multiple signaling pathways including mitogen-activated protein kinase (MAPK) and phosphatidylinositol 3-kinase/protein kinase B (PI3-K/PKB) pathways that promote cellular growth, proliferation, hypertrophy and survival, and these are all key processes involved in vascular cell remodeling often encountered in ET-1 triggered pathophysiological states. Once ET-1 activates its receptor, the latter recruits Ras, a small G-protein that leads to the activation of MAPK, including

extracellular signal-regulated kinase 1/2 (ERK1/2), c-jun-NH₂-terminal kinase (JNK), and p38mapk (276). In parallel, ET-1 also activates PI3-K (131) and several downstream targets of PI3-K have also been documented, the most studied being protein kinase B (PKB), also known as Akt (a product of akt proto-oncogene) (5). Activation of receptor and non receptor protein tyrosine kinases (PTK) has been proposed to be implicated in transducing ET-1-induced signaling events. Epidermal growth factor receptor (EGFR) (277, 278), c-Src (278, 279), and Ca²⁺ dependent PYK2 (278-280) are amongst the PTK that are activated by ET-1. We have recently shown a requirement of insulin-like growth factor type 1 receptor (IGF-1R) in ET-1-induced PKB activation in VSMC (151). However, the precise molecular mechanism responsible for this transactivation still remains unresolved. A possible contribution to this mechanism might be mediated through ROS generation. Several studies have demonstrated that ROS play a key role in propagating growth factor and vasoactive peptide signaling. The high levels of ET-1 observed in hypertension and atherosclerosis lead to excessive production generation of ROS and in a decrease in the antioxidant status (159). At physiological concentrations, ROS generated within the vasculature are important signaling molecules. However, an excessive synthesis of ROS can overcome antioxidant mechanisms and generate deleterious effects often seen in cardiovascular disorders (11). The involvement of ROS in ET-1-induced activation of MAPKs including JNK, p38mapk and ERK1/2 has been demonstrated in cardiac fibroblasts (125). Moreover, a role of ROS in ET-1-induced activation of the redox-sensitive ERK1/2 and PKB signaling pathways has been demonstrated in VSMC (5). In this context, several studies have investigated the possible vascular protective effect of antioxidants. A surge of interest has recently erupted around the use of naturally-occurring compounds with antioxidant capacity. Medicinal plants are rich in phytochemicals that possess several therapeutic effects, including antioxidative properties. Curcumin, the main constituent of the spice turmeric that is extracted

from the rhizomes of the *Curcuma Longa* L. herb, is an ancient known phytochemical that exhibits a vast spectrum of biological properties, amongst them, antioxidant and anti-inflammatory properties. It has mainly been investigated for its effects against cancer. Recent studies though have demonstrated that curcumin also exhibits cardiovascular protective effects and its actions are pleiotropic and appear to involve the regulation of transcription factors, growth factors, cytokines, protein kinases and others (185). Curcumin has been shown to suppress ROS generation (174, 202, 203) and to inhibit several of the mediators involved in the ET-1 signaling pathway in several cellular lines. However, the therapeutic efficacy of curcumin in ET-1-induced signaling has yet to be reported. Therefore, these studies were undertaken to investigate the effect of curcumin on ET-1-induced signaling of the redox-sensitive ERK1/2, PKB pathways which are believed to be key players in ET-1-induced proliferative and hypertrophic responses. In an attempt to understand the mechanism, we studied the effect of curcumin on ET-1-stimulated IGF-1R, PKB, c-Raf and ERK1/2 signaling in A-10 VSMC.

Our results are the first to report an inhibitory effect of curcumin on ET-1-stimulated hypertrophic and proliferative signaling in VSMC. In the first part of this study, we observed a dose-dependent inhibitory effect of curcumin on ET-1 stimulation of IGF-1R, PKB, c-Raf and ERK1/2 phosphorylation in A-10 VSMC. Given that ET-1 requires IGF-1R transactivation, we further investigated the effect of curcumin on IGF-1-induced signaling in VSMC. A similar dose-dependent inhibitory effect was observed on the IGF-1-induced IGF-1R, PKB, c-Raf and ERK1/2 phosphorylation in A-10 VSMC. Moreover, we tested if transcription factor early growth response-1 (Egr-1), a downstream component of ERK1/2 that is a key player in multiple cardiovascular pathological processes (281), is a target of curcumin in response to ET-1 as well as IGF-1. Curcumin attenuated ET-1 and IGF-1-induced expression of Egr-1 in VSMC.

Taken together, we demonstrate that curcumin inhibits ET-1 and IGF-1-stimulated increase in the phosphorylation state of IGF-1R, PKB, c-Raf and ERK1/2, as well as Egr-1 expression in A-10 VSMC. Since ERK1/2, PKB and Egr-1 play a crucial role in mediating VSMC growth and hypertrophy, it may be suggested that the ability of curcumin to attenuate these pathways may serve as a potential mechanism by which curcumin counteracts the biological responses of ET-1 and thus exerts a cardiovascular protective effect.

CHAPITRE 4

CONCLUSION

The results presented here demonstrate for the first time a negative modulatory effect of curcumin on ET-1-stimulated signaling components: PKB, c-Raf, ERK1/2 and IGF-1R, in A-10 VSMC. Given the fact the curcumin exhibits a significant inhibitory effect on ET-1-induced IGF-1R phosphorylation, we expanded our studies to investigate its effect on IGF-1-induced signaling and highlighted an inhibitory effect of curcumin on IGF-1-induced phosphorylation of PKB, c-Raf, ERK1/2 and IGF-1R, in A-10 VSMC. Our work also demonstrates that curcumin inhibits the expression of ET-1 and IGF-1-induced transcription factor Egr-1 in VSMC (Figure 4.5).

Thus, the findings in the present study have uncovered curcumin as a potent antagonist of ET-1 action in VSMC. Provided that curcumin exhibits such profound inhibitory effects on ET-1-induced signaling events that have been shown to promote mitogenic and hypertrophic actions in the vasculature, it may be suggested that curcumin may be beneficial in attenuating vascular remodeling associated with several cardiovascular diseases. However, due to its vast array of biological properties, curcumin is able to interfere with numerous signaling pathways and it is suggested that a single site of action is possibly not enough to represent all the effects of this substance.

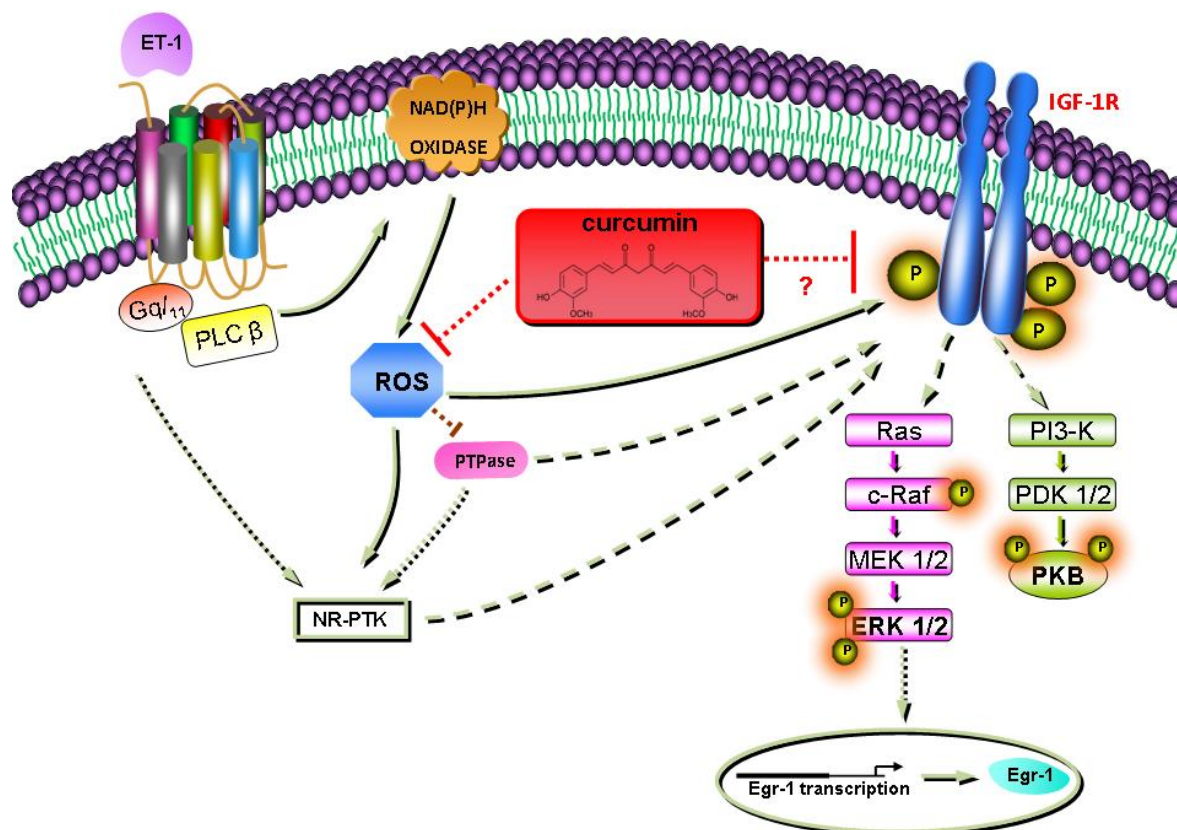


Figure 4.5 Schematic hypothetical model summarizing the potential interaction of curcumin with ET-1 signaling pathways in VSMC.

The ability of curcumin to inhibit ET-1-induced IGF-1R β phosphorylation and downstream phosphorylation of PKB, c-Raf and ERK1/2, along with the expression of Egr-1 suggests that curcumin might act upstream of IGF-1R in mediating this inhibitory effect. Curcumin may also inhibit oxidative stress generation thereby turn off ET-1-induced signaling in VSMC.

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