# David Abraham · Clive Handler Michael Dashwood · Gerry Coghlan Editors

# Translational Vascular Medicine

Pathogenesis, Diagnosis, and Treatment



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Pathogenesis, Diagnosis, and Treatment



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### Preface

This is the third volume in the series of books on translational medicine gleaned from the annual vascular biology and clinical medicine workshop held at the Royal College of Physicians. The chapters are invited papers presented by internationally recognized basic science and clinical experts. The aim of the workshop is to bring basic scientists and clinicians together to discuss their work and perspectives in areas of cardiovascular medicine and biology. We ask them to address the areas which are likely to be important in the future and the associated challenges.

Our previous books, *Vascular Complications in Human Disease* (2008) and *Advances in Vascular Medicine* (2010), both also published by Springer, have dealt with other key and developing areas of basic science and its clinical applications. This volume covers new and exciting advances in cardiovascular medicine. As before, we have tried to explore the bi-directional and integrated approaches of translational cardiovascular medicine, linking basic science to patient care.

The chapters in this book span a number of translational themes in cardiovascular medicine. There is a section on surgery and non-pharmacological treatments for atherosclerotic disease of the aorta. Pulmonary arterial hypertension is a rapidly evolving area following recent discoveries of some of the molecular pathways implicated in its pathogenesis which have led to some promising drug development and clinical optimism. Some of the trials underpinning clinical guidelines are described. Other chapters include "Cytoprotective Mechanisms in the Vasculature," "Potassium Channels Regulating the Electrical Activity of the Heart," and "Novel Molecular Mediators Regulating the Cardiovascular System." We are particularly pleased to include a chapter on "The Broken Heart Syndrome" by our friend and colleague, Professor Larry Cohen, from Yale University School of Medicine, with which UCL has recently established a collegiate and collaborative relationship.

We hope that this book, a formal record and reference of our annual workshop, is a useful way to transmit the information from the excellent papers presented at the meeting to a wider readership. Our authors provide their expert insight into important areas of translational cardiovascular medicine and key bibliographies for the reader. We hope that this book, like its predecessors, is a useful contribution to the literature in this fascinating field.

> David Abraham Clive Handler Michael Dashwood Gerry Coghlan

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# **Abbreviations**

5-HT	Serotonin
5-HTT	Serotonin transporter
AGM	Aorta-gonad mesonephros
ALK-1	Active-like kinase type-1
AMP	Adenosine monophosphate
bHLH	Basic helix-loop-helix
BL-CFC	Blast colony-forming cells
BMP	Bone morphogenetic protein
BMPR2	Bone morphogenetic protein receptor II
CADASIL	Cerebral arteriopathy with subcortical infarcts
	and leukoencephalopathy
cAMP	Cyclic adenosine monophosphate
cGMP	Cyclic guanosine monophosphate
CSL	CBF1 Suppressor of Hairless Lag-1
DAPT	<i>N</i> -[(3,5-Difluoro phenyl)acetyl]-L-alanyl-2-phenyl]glycine-1,
	1-dimethylethyl ester
Dll	Delta-like ligand
DMOG	Dimethyl-oxalylglycine
E	Embryonic day
EC	Endothelial cell
ECE-1	Endothelin converting enzyme-1
ECGS	Endothelial cell growth supplement
eNOS	Endothelial nitric oxide synthase
ET	Endothelin
ET-1	Endothelin-1
ET-2	Endothelin-2
ET-3	Endothelin-3
ETA	Endothelin receptor type A
ETB	Endothelin receptor type B
FAK	Focal adhesion kinase
FGF	Fibroblast growth factor
FIH	Factor inhibiting HIF

GLUT4	Glucose transporter type 4
HGF	Hepatocyte growth factor
HIF	Hypoxia-inducible factor
HSC	Hematopoietic stem cell
IPAH	Idiopathic pulmonary arterial hypertension
IPC	Ischemic preconditioning
IR	Ischemia-reperfusion
Jag	Jagged
KO	Knockout
Kv1.5	Voltage-gated potassium channels subunit 1.5
MAGP-1	Microfibril-associated glycoprotein-1
MAPK	Mitogen-activated protein kinases
mmHg	Millimeters of mercury
mPAP	Mean pulmonary artery pressure
MSC	Mesenchymal stem/stromal cell
NEP	Neutral endopeptidase
NG2	Neuron glial 2
NICD	Notch intracellular domain
NO	Nitric oxide
PAH	Pulmonary arterial hypertension
PDE-5	Phosphodiesterase type
PDGF	Platelet-derived growth factor
PGI <sub>2</sub>	Prostacyclin
PH	Pulmonary hypertension
PHD	HIF prolyl hydroxylases
PVR	Pulmonary vascular resistance
Rbpj	Recombination signal binding protein for immunoglobulin kappa
10	J region
RGD	arginine-glycine-aspartic acid
RGS-5	Regulator of G protein signaling 5
RV	Right ventricle
RVH	Right ventricular hypertrophy
SERT	Serotonin transporter
SSc	Systemic sclerosis
SSRI	Selective serotonin reuptake inhibitor
TGF-β	Transforming growth factor
TRPC6	Transient receptor potential cation channel subfamily C, member 6
VEGF	Vascular endothelial growth factor
VEGFR	Vascular endothelial growth factor receptor
VegfR2	Vascular endothelial growth factor receptor 2
VHL	von Hippel–Lindau tumor suppressor
VIP	Vasoactive intestinal peptide
VSMC	Vascular smooth muscle cells
vWF	von Willebrand factor

Section I

**Hot Topics in Vascular Biology** 

# Pericytes: Adaptable Vascular Progenitors

1

Gareth D. Hyde and Ann E. Canfield

#### 1.1 General Introduction

The existence of perivascular cells associated with capillaries was first reported by Eberth and Rouget in the late nineteenth century. Since then, these cells have been given a variety of names, including Rouget cells, mural cells, deep cells, adventitial cells, perivascular cells, and periendothelial cells. Zimmermann introduced the name "pericyte" (*peri*=around; *cyte*=cell) in 1923, and it is this term which is still used most frequently.

In this chapter, we will discuss the morphological characteristics of pericytes, their frequency and distribution within the vasculature, the markers that can be used to identify pericytes, and the theories about the origin of these cells. In addition, we shall discuss pericyte function and review the evidence that pericytes are adaptable vascular progenitor cells with potential therapeutic use. Readers are referred to other excellent recent reviews for information on additional pericyte functions, including regulating microvascular blood flow, and pericyte involvement in diseases such as cancer, hypertension, and diabetic retinopathy [1–3].

#### 1.2 Pericyte Morphology, Frequency, and Distribution

Although pericytes are an extremely heterogeneous population of cells, they can be characterized by several morphological properties. For example, pericytes are typically elongated, stellate-shaped cells with multiple processes that extend along the length and, sometimes, the circumference of the vessel. In addition, pericytes often

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**Fig. 1.1** Transmission electron micrograph of a capillary. A ring of endothelial cells (*EC*) forms the lumen of the capillary which contains several erythrocytes. On the abluminal surface of the capillary, a pericyte can be seen. The pericyte has several characteristic features including a large heterochromatic nucleus (*HN*), and an elongated cellular process containing large amounts of rough endoplasmic reticulum (*RER*) (Image kindly provided by Dr. C. Jones, University of Manchester)

possess a heterochromatic nucleus, large numbers of plasmalemmal vesicles, and contractile microfilament bundles (see Fig. 1.1).

Interestingly, the actual shape and size of pericytes can vary markedly depending on their anatomical location. The relative frequency of pericytes also varies between vessel type, developmental stage, and species. For example, the human retina has been shown to have a higher pericyte to endothelial cell ratio than rats (1:1 and 1:3 respectively) [4] and retinal microvessels have been reported to contain a higher ratio (1:1) compared to those in striated muscle (1:100) [5]. It is also noteworthy that alterations in pericyte frequency and distribution can contribute to the development and progression of several pathologies, including diabetic retinopathy (loss), myopathy (gain), fibrosis, and cancer (distribution) [1].

In arterioles, capillaries, and venules, pericytes are closely associated with endothelial cells and are embedded within a shared basement membrane. Via their long processes, pericytes can make contact with multiple endothelial cells, resulting in the partial coverage of the abluminal surface, and can also connect vessels within the microcirculation. Pericytes are frequently found adjacent to endothelial cell junctions and themselves form multiple connections with endothelial cells via peg and socket arrangements, adherens junctions, gap junctions, and tight junctions.

Pericyte or pericyte-like cells have also been identified in larger vessels by immunohistochemistry using the 3G5 antibody [6–8] which recognizes a cell surface ganglioside present on pericytes but not on endothelial cells, smooth muscle cells, or fibroblasts [9]. Using this antibody, pericytes have been shown to be present in the subendothelial layer of the intima; in the media and in the vaso vasora of the adventitia; in large, medium, and small arteries and veins. Furthermore, the pericyte-like cells identified in these locations were shown to contact each other via their processes forming a subendothelial network in the vascular bed [6].

5	1 5	
Marker	Description	Example References
Alpha-smooth muscle actin	Cytoskeletal contractile protein	[10–13]
Aminopeptidase A+N	Zinc-dependent peptidase	[14–16]
Desmin	Intermediate filament protein predomi- nantly expressed in muscle cells	[17, 18]
Nestin	Intermediate filament protein predomi- nantly expressed in nerve cells	[14]
Neuron glial 2 (NG2) (HMWMAA)	Chondroitin sulfate proteoglycan	[19–21]
Platelet-derived growth factor (PDGF) receptor-beta	Transmembrane receptor tyrosine kinase	[22]
Regulator of G protein signaling 5 (RGS-5)	GTPase-activating protein	[23, 24]
3G5	Cell surface ganglioside	[6, 9]

Table 1.1 Most commonly used pericyte markers

#### 1.3 Pericyte Markers

The heterogeneous nature of pericytes has made the identification of cell markers difficult. Indeed, the identification of a marker exclusively expressed by pericytes and expressed by all pericytes at all times remains elusive. In the absence of such a maker, many other antigens have been used (see Table 1.1).

It should be stressed that the expression of these markers by pericytes is species, tissue, developmental stage, and disease dependent. For example, NG2 is present on the surface of arteriolar and capillary pericytes but is absent in venular pericytes [19]. Alpha-smooth muscle actin is absent in pericytes in many tissues but is present in pericytes isolated from chick embryonic brains [25] and appears to be upregulated in pericytes within tumors [21, 26].

#### 1.4 Pericyte Origin

One reason for the heterogeneity in pericyte marker expression may be their differing origins. As with vascular smooth muscle cells (VSMCs) [27], pericytes have been proposed to arise from multiple embryonic and cellular progenitors. Pericytes are often thought of as having a mesenchymal origin. However, studies using avian embryos have shown that the pericytes of the face and forebrain develop from the neural crest, whereas the endothelial cells are mesoderm-derived [28]. It has also been reported that perivascular mural cells (pericytes and VSMC) and endothelial cells can both develop from Flk1-positive embryonic stem cells [29]. As Flk1 is a marker of the embryonic lateral plate mesoderm, this work suggests that both endothelial and perivascular cells have a common mesodermal origin. These two theories are not mutually exclusive, and it is therefore possible that in the face and forebrain, pericytes arise from the neural crest, while in other parts of the body they develop from a more mesodermal progenitor that can also give rise to endothelial cells.

The study that proposed a common ontogeny for both perivascular mural cells and endothelial cells went on to show that Flk1-positive embryonic stem cell differentiation into these cell types is dependent on PDGF-BB and vascular endothelial growth factor (VEGF) respectively. As a result of this, and many other studies, it is now well known that PDGF-BB and its receptors are critical for pericyte differentiation, recruitment to endothelial tubes, and normal vessel morphogenesis and function [30–33].

In addition to having multiple embryonic origins, it has also been suggested that pericytes can be derived from several adult cell types. These include VSMC [34], endothelial cells [35], and bone marrow–derived cells [36–39]. Pericyte progenitor cells have also been isolated from the rat aorta using suspension culture. This method led to the isolation of an anchorage-independent population of cells that formed spheroidal colonies in suspension and that expressed several pericyte markers [40].

#### 1.5 Pericyte Function

Pericytes have multiple functions within the vasculature. These include:

- · Giving structural rigidity to the vessel wall
- Regulating the contractile ability, blood flow, and permeability of the vessel
- Regulating endothelial cell proliferation and differentiation
- Maintaining the functional integrity of the blood-brain barrier
- · Phagocytic and antigen-presenting functions

For further details on these functions, readers are referred to other recent excellent reviews [1, 3]. This chapter will focus on pericyte function as vascular progenitor cells.

#### 1.5.1 Pericytes as Progenitor Cells: An Historical Perspective

In 1927, Maximov described pericytes as "resting wandering cells" and "primitive mesenchymal cells" [41]. After Maximov's ideas of the 1920s, the concept that pericytes could act as progenitor cells failed to receive much attention until the early 1980s. At this time, it was proposed that pericytes could give rise to immature adipocytes in response to thermal lesions in the rat inguinal fat pad [42], and that pericytes were the target of bone morphogenetic protein (BMP) signaling during cranial bone regeneration, resulting in pericyte differentiation into osteoprogenitor cells [43]. These early analyses of animal injury models generated the first data indicating that pericytes had the ability to differentiate into other cell types.

In a series of elegant studies performed in the early 1990s, Diaz-Flores and colleagues labeled vascular cells with Monastral Blue and monitored their fate in vivo. Their studies investigating neochondrogenesis in grafted perichondrium [44] and periosteal osteogenesis [45] indicated that pericytes could differentiate down the chondrogenic and osteogenic lineages, respectively. Subsequent ultrastructural studies during post-injury bone formation supported these conclusions [46, 47].



**Fig. 1.2** Pericytes cultured in vitro deposit a calcified matrix. Immunocytochemical detection of alpha-smooth muscle actin (**a**) and the cell surface ganglioside recognized by the 3G5 monoclonal antibody (**b**) in pericytes isolated from bovine retinal microvessels. Scanning electron micrograph of a multicellular nodule formed by bovine retinal pericytes during in vitro culture (**c**). Transmission electron micrographs showing matrix calcification in sections cut through pericyte nodules (**d**–**f**). Areas of dense calcification can be seen in many sections (**d**–**e**). In addition, matrix vesicles (*arrowed*) and needle-like crystals of hydroxyapatite are apparent (**f**) (Figures **a** and **b** are reproduced from Farrington-Rock et al. [49]. Figures **c**–**f** are reproduced from Schor et al. [48])

The first direct evidence that pericytes could undergo osteogenic differentiation was published in 1990, when it was demonstrated that isolated bovine retinal pericytes could deposit a calcified matrix which resembled bone in vitro [48]. After reaching confluence, pericytes cultured on either plastic or a collagen substratum formed multilayered areas that retracted away from each other, leading to the formation of multicellular nodules containing needle-like crystals of hydroxyapatite (see Figs. 1.2 and 1.3). Furthermore, the cells within these nodules expressed markers of the osteoblastic lineage including bone sialoprotein, osteocalcin, osteonectin, and osteopontin [50].

In addition to undergoing osteogenic differentiation, cultured pericytes were shown to be able to differentiate along the chondrogenic and adipogenic lineages. When grown as pellets in chondrogenic medium, pericytes deposited an extracellular matrix rich in sulfated proteoglycans and expressed the chondrogenic markers Sox9, aggrecan, and type II collagen (see Fig. 1.3). In adipogenic medium, pericytes



**Fig. 1.3** Pericytes can undergo osteogenic, chondrogenic, and adipogenic differentiation in vitro and in vivo. In vitro differentiation of pericytes (**a**–**c**). Pericytes grown in monolayer in vitro form multicellular nodules that stain positive with alizarin red, indicating the presence of calcium deposits (**a**). Pericytes grown as a pellet in chondrogenic medium produce type II collagen that can be detected immunohistochemically (*brown staining*) (**b**). Pericytes cultured in adipogenic medium accumulate intracellular lipid droplets (**e**). In vivo differentiation of pericytes (**d**–**f**). Pericytes inoculated into diffusion chambers and implanted into athymic mice could be seen to form mineralized bone (**d**), cartilage and mineralized cartilage that stained with Von Kossa indicating the presence of mineral (**e**), and adipocyte-like cells (**f**) (Figures **b**, **e**–**f** are reproduced from Farrington-Rock et al. [49])

accumulated oil red O positive lipid droplets and expressed the adipocyte transcription factor proliferator-activated receptor-gamma [49].

Direct evidence that pericytes could undergo multi-lineage differentiation in vivo was generated when isolated pericytes were inoculated into diffusion chambers and implanted into athymic mice. When recovered, the chambers containing pericytes were found to contain tissue resembling bone, mineralized cartilage, fibrocartilage, non-mineralized cartilage with lacunae containing chondrocytes and small clusters of cells that resembled adipocytes [49, 50] (see Fig. 1.3).

There is now evidence that in addition to being able to differentiate along the "classical" osteogenic, chondrogenic, and adipogenic lineages, pericytes can also

differentiate into VSMCs [51], Leydig cells [52], fibroblasts [53], myoblasts [54], myofibroblasts [55, 56], odontoblasts [57], and neuronal cell types [58], suggesting that these cells have enormous therapeutic potential.

#### 1.5.2 Regulation of Pericyte Differentiation

Aberrant pericyte differentiation has been implicated in multiple disorders including chondro/osteoblastic differentiation in calcific vasculopathies [7] and myofibroblastic differentiation in kidney fibrosis [55], dermal scarring [53], spinal cord scarring [59], and systemic sclerosis [56]. Understanding what regulates pericyte differentiation would not only be of potential therapeutic use in these conditions but would also be of use in tissue regeneration and engineering strategies that use pericytes as a source of progenitor cells.

Despite the potential value of understanding how pericyte differentiation is regulated, little is currently known. One signaling pathway that has been implicated in pericyte differentiation is the canonical Wnt pathway [60]. In these studies, Wnt signaling was activated by the addition of either Wnt3a or LiCl, or inhibited (by adenovirus mediated overexpression of dominant negative TCF-4) during pericyte in vitro differentiation. Using this approach, it was demonstrated that Wnt signaling promoted pericyte chondrogenic differentiation, and inhibited pericyte adipogenic differentiation [60]. In support of this finding, it has been demonstrated that endothelial cells repress the adipogenic potential of adipose stromal cells (which have a functional and phenotypic overlap with pericytes [61, 62] by the secretion of Wnt ligands [61]. Recent studies have also shown that Wnt signaling regulates the osteogenic differentiation of pericytes, although this effect is highly dependent upon the stage at which Wnt signaling is activated (Canfield and Brennan, unpublished information). BMPs and fibroblast growth factors (FGFs) have also been implicated in pericyte differentiation. BMP signaling has been suggested to promote the osteogenic differentiation of pericytes [43] whereas basic FGF has been shown to promote the neuronal differentiation of central nervous system-derived pericytes [58].

In addition to secreted signaling molecules, dexamethasone, a synthetic glucocorticoid, has been shown to downregulate pericyte expression of calcification inhibitor molecules and thereby promote pericyte osteogenic differentiation [63]. Similarly, dexamethasone has been shown to stimulate odontoblastic differentiation of pericytes isolated from human dental pulp [57]. However, it is clear that we still have much to learn about what regulates pericyte differentiation, both in disease states and in potential tissue regeneration strategies.

#### 1.6 Progenitor Cells and the Perivascular Niche

The perivascular niche is a 3-dimensional microenvironment that includes the progenitor cells, their neighboring differentiated cells, the extracellular matrix, and soluble secreted molecules. It is proposed that residing within this specific niche allows adult progenitor cells to retain their multi-lineage potential and self-renewal capacity. Many studies have suggested that in different tissues and organs, adult progenitor cells or mesenchymal stromal/stem cells (MSCs) reside within a perivascular niche. These include: bone marrow [64, 65], dental pulp [66], periodontal ligament [67], aorta [7, 68], umbilical cord Wharton's jelly [69], skeletal muscle [54], adipose tissue [62, 70], neural tissue [71], infrapatellar fat pads [72], chorionic villi [73], bone [74], and saphenous vein [75]. Indeed, it has now been established that MSCs reside in a perivascular niche in virtually all postnatal tissues and organs [71, 76, 77].

In many of these cases, the population of adult stem cells isolated from the tissue or organ has been found to express markers of pericytes. For example, dental pulp stem cells were found to be positive for alpha-smooth muscle actin and the cell surface ganglioside recognized by the 3G5 antibody [66]. Skeletal muscle progenitors were shown to express NG2 and alkaline phosphatase [54], adipose-derived stem cells have been shown to express the 3G5 epitope [70] and other pericyte markers [62], and stem cells in human placental chorionic villi [73] and infrapatellar fat pads [72] were shown to express the 3G5 epitope. Indeed, adult stem cells have been isolated from many human tissues on the basis of the expression of pericyte markers [66, 67, 76, 77].

In addition to adult stem cells being shown to express pericyte markers, pericytes have been shown to express markers normally associated with mesenchymal stem cells, such as STRO-1 [50, 66, 77]. Furthermore, pericytes isolated from multiple human tissues have been shown to have clonal multi-lineage potential during long-term culture [77], and such data has led Caplan to ask the question: "are all MSCs pericytes?" [78] In 2008, Covas and colleagues performed gene expression profiles and other characterizations on MSCs isolated from adult and fetal human tissues, differentiated cell types, and retinal pericytes [79]. A comparison of the gene expression profiles demonstrated that MSCs and pericytes are very similar, more similar then pericytes and smooth muscle cells or fibroblasts, for example [79]. Taken together, these data demonstrate that pericytes and adult mesenchymal stem cells have many common characteristics including their perivascular location, their distribution throughout the body, their cellular phenotype, and their differentiation potentials.

#### 1.6.1 Therapeutic Potential of Pericytes

Several groups have started to explore the potential of using pericytes or pericyte-like cells as a source of progenitor cells for tissue regeneration and repair. Promising results have been achieved using human skeletal muscle–derived pericytes for the treatment of Duchenne muscular dystrophy [54]. In this study, human skeletal muscle–derived pericytes were inoculated into a murine model of Duchenne muscular dystrophy and their fate, effect on muscle regeneration and functional consequence, was analyzed. The implanted pericytes where shown to colonize host muscle, generate muscle fibers containing human dystrophin, and to result in partial but significant functional recovery as judged by frequency of falling and treadmill exhaustion tests.

Another group has also demonstrated that in addition to being able to repair dystrophic muscle, human pericytes derived from either muscle, placenta, or pancreas can regenerate cardiotoxin-injured muscle [77]. The same group has also

reported that human skeletal muscle–derived pericytes improve cardiac function in acutely infarcted mouse hearts, and they suggested that this improvement may be due to increased angiogenesis and reduced fibrosis [80, 81]. These suggestions are consistent with recent studies demonstrating that pericyte-like progenitor cells increase neovascularization in a mouse model of muscle ischaemia [75] and improve repair of infarcted mouse hearts through pro-angiogenic and anti-fibrotic programs [82].

Beyond muscle regeneration, there is evidence for pericyte therapeutic potential in bone fracture repair. Over twenty-five years ago, pericytes were suggested to be the target of BMP signaling and the source of osteoprogenitor cells during cranial bone regeneration; much more recently, it was shown that inoculation with human umbilical cord perivascular cells (a cell population with many similarities to pericytes [69]) increases the rate of bone and cartilage regeneration in mice. A recent study has also shown that pericytes can promote epidermal tissue renewal by modifying the extracellular microenvironment of epithelial stem cells, suggesting that these cells may also be of therapeutic use in skin regeneration [83].

The potential use of pericytes for therapeutic tissue engineering is also starting to be explored [84]. He and colleagues seeded human pericytes onto bi-layered tubular, elastomeric, biodegradable scaffolds and implanted them into rats as aortic interposition grafts. Interestingly, the grafts initially seeded with pericytes had a higher patency rate than unseeded controls. There was evidence of extensive tissue remodeling, together with the deposition of collagen and elastin, and the presence of cells expressing VSMC and endothelial cell markers. Intriguingly, these cells appeared to originate from the host tissue, rather than from the pericytes themselves [84], which suggests that pericytes may improve the patency of vascular grafts by promoting the recruitment of host progenitor cells through the secretion of specific growth factors.

#### 1.7 Conclusion

That pericytes closely resemble MSCs and are adaptable progenitor cells with great potential for tissue regeneration and repair is without question. The therapeutic potential of these cells may result from their ability to differentiate along multiple lineages, but it may also be due to their ability to evoke a host response, by releasing specific growth factors, cytokines, or matrix proteins, or by inducing angiogenesis [75, 80, 83]. However, as uncontrolled differentiation of pericytes can also contribute to calcific vasculopathies and fibrosis (for example), it is important that long-term follow-up studies are performed when the therapeutic potential of these cells is evaluated in vivo.

Several key questions remain to be resolved. For example: Do all pericytes have multi-lineage potential? What is the nature of the perivascular niche? How is the stemness of pericytes maintained and controlled in vivo? How are pericytes liber-ated from their niche? How is pericyte differentiation regulated? Do pericytes really contribute to repair and regeneration in vivo and, perhaps most importantly, do these cells have therapeutic potential in humans? The answer to all of these questions is eagerly awaited.

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# Benefits and Risks of Manipulating the HIF Hydroxylase Pathway in Ischemic Heart Disease

Tammie Bishop and Peter J. Ratcliffe

#### 2.1 Introduction

Ischemic heart disease is a major cause of morbidity and mortality in the Western world. It occurs when oxygen delivery cannot meet the metabolic needs of the heart, as observed in patients with stable coronary artery disease as well as those experiencing acute myocardial infarction. Although conditions leading to myocardial injury have been well studied, and physical means of revascularization by stenting or coronary bypass surgery are well developed, there remains a need to define treatments that limit damage in the acute phase or promote revascularization by medical means. In particular, mechanisms that preserve cellular function during ischemia remain poorly understood.

Experimental models of myocardial ischemia in rodents have demonstrated that prior exposure to sublethal cycles of ischemia-reperfusion (I/R) protects tissues such as the heart from subsequent ischemia. There is compelling evidence that this ischemic preconditioning (IPC) is, at least in part, conferred through hypoxic activation of the transcription factor: hypoxia-inducible factor (HIF). HIF is a master regulator of oxygen homeostasis that induces the expression of hundreds of genes in response to hypoxia, including those that stimulate glycolysis, angiogenesis, and erythropoiesis. These changes help the organism adapt to oxygen deprivation at both the cellular and tissue levels. Pharmacological modulators of HIF are consequently being pursued as therapeutic targets for myocardial (as well as more general tissue) ischemia.

HIF is an  $\alpha/\beta$  heterodimeric transcription factor, whose  $\alpha$  subunit is regulated through posttranslational modification by HIF prolyl hydroxylases (PHDs, prolyl hydroxylase domain): PHD1, 2 and 3 (reviewed in Kaelin and Ratcliffe [1]).

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**Fig. 2.1** Dual regulation of HIF-alpha subunits by prolyl and asparaginyl hydroxylation. In the presence of oxygen, active HIF prolyl hydroxylases (*PHDs*), as well as factor inhibiting HIF (*FIH*), downregulate and inactivate HIF $\alpha$  subunits. PHDs hydroxylate prolyl residues to promote von Hippel–Lindau tumor suppressor (*VHL*)–dependent proteolysis of HIF $\alpha$  subunits. FIH, on the other hand, hydroxylates an asparaginyl residue, which blocks p300 co-activator recruitment from activating HIF $\alpha$ -subunit transcriptional activity. In hypoxia, HIF hydroxylases (*PHDs* and *FIH*) are inactive and these processes are suppressed, which allows the formation of a transcriptionally active HIF complex

These non-heme Fe(II) and 2-oxoglutarate-dependent dioxygenase PHD enzymes are now widely regarded as cellular oxygen sensors that transduce the oxygen status to the cell via posttranslational hydroxylation of HIF $\alpha$ . In the presence of oxygen, PHD hydroxylates two proline residues within a central degradation domain in HIF-1 $\alpha$  and -2 $\alpha$ . This promotes their binding to von Hippel–Lindau tumor suppressor (VHL) E3 ubiquitin ligase, leading to proteasomal degradation. A second point of regulation involves asparaginyl hydroxylation by another non-heme Fe(II) and 2-oxoglutarate-dependent dioxygenase termed FIH (*factor inhibiting HIF*). During hypoxia, reduced PHD and FIH activity allows HIF $\alpha$  subunits to escape proteolysis and assemble into an active  $\alpha/\beta$  heterodimer that induces a broad range of target genes (Fig. 2.1).

A substantial body of work indicates that despite this dual control system, activation of HIF can be achieved through inhibition of the PHD/VHL degradation pathway alone. Indeed, several PHD inhibitory drugs are in development to test whether pharmacological modulation of the HIF hydroxylase system to activate HIF protects from subsequent ischemic insult. This type of intervention may have effects in the short term through enhanced cellular metabolism (for example, stimulation of glycolysis, glucose metabolism, and reduced mitochondrial oxygen consumption) as well as in the medium to longer term through increased perfusion (for example, by stimulation of angiogenesis), giving potential applications both in the acute phase as well as in chronic ischemic heart disease.

The safety of long-term PHD inhibition/HIF activation, however, remains unclear. Given the ubiquitous distribution of the HIF hydroxylase system and wide range of processes affected by HIF, it seems unlikely that all consequences of HIF activation will be beneficial to treating myocardial ischemia; some may even impinge normal physiological function in the heart or other tissues. We consider in this review evidence relating to the benefits and risks of manipulating the HIF hydroxylase system as a therapeutic means of treating myocardial ischemia.

#### 2.2 Benefits

#### 2.2.1 Genetic Manipulation of HIF-1 $\alpha$

Evidence for the essential role of HIF-1 $\alpha$  in IPC was obtained from transgenic mouse models, wherein haploinsufficiency of *HIF-1* $\alpha$  is sufficient to ablate the protective effect conferred by IPC on myocardial infarction [2, 3]. This result is similarly present in mice treated with intraventricular infusion of *HIF-1* $\alpha$  siRNA [4].

In agreement with this, overexpression of HIF-1 $\alpha$  in the myocardium of mice attenuates infarct size and improves cardiac function several weeks (but not 24 h) after coronary artery occlusion [5]. This delayed protective effect is thought to be conferred, at least in part, through increased capillary density in the infarct and peri-infarct zones via transcriptional activation of pro-angiogenic HIF target genes such as vascular endothelial growth factor (VEGF) and angiopoietin-2. Together with the predicted vasodilation from HIF-mediated stimulation of inducible nitric oxide synthase, these changes are postulated to help restore delivery of blood to the heart. It should be noted that the overexpressed HIF-1 $\alpha$  in these mice would be subject to normoxic degradation, thus limiting upregulation of the pathway in the cells that are best oxygenated. The long-term effects of more complete HIF-1 $\alpha$ activation from blockage of the degradation pathway, therefore, cannot be readily deduced from this study.

Further, overexpression of a stable form of HIF-1 $\alpha$  in the epidermis of mice has been shown to induce hypervascularity (in line with the predicted induction of pro-angiogenic HIF target genes) [6]. Interestingly, in contrast to transgenic mice overexpressing myocardial VEGF, in which rapid stimulation of dysregulated angiogenesis leads to fragile and immature vessel formation [7, 8], HIF-1 $\alpha$  overexpression induces blood vessel formation without any leakage or inflammation. Most probably this is because of multiple, coordinated actions on the angiogenic process. It is also possible that effects of HIF activation at sites remote from the site of ischemia may have protective actions (for instance, by increasing circulating endothelial progenitors). This might conceivably assist perfusion of distant tissues and may underlie remote ischemic preconditioning effects, whereby IPC of, for example, the kidney can result in cardioprotection [9].

#### 2.2.2 Pharmacological Inhibition and Genetic Manipulation of PHD Enzymes

Small molecule inhibitors of the PHD enzymes potently activate the HIF response both *in vitro* and *in vivo*. Thus, it has been proposed that administration of PHD inhibitors could mimic, at least in part, the protective effects of exposure to hypoxia. Indeed, PHD inhibition likely results in greater HIF activation than the submaximal levels achieved through ischemic insult.

Initial studies using cobalt chloride and the iron chelator desferrioxamine to inhibit PHD enzymes (by displacement of their Fe(II) center or decreasing Fe(II) availability in solution) suggested that PHD inhibition acts similarly to IPC in providing protection against myocardial infarction [10, 11]. However, such inhibitors would be predicted to target other Fe(II)-containing enzymes and likely result in side effects from dysregulation of non-HIF hydroxylase pathways.

Subsequent studies have applied more specific inhibitors of PHD activity, dimethyl-oxalylglycine (DMOG) and FG2216, to rodent models of myocardial ischemia. DMOG is a 2-oxoglutarate analogue that inhibits the 2-oxoglutarate-dependent-dioxygenase family of enzymes (which includes the PHD enzymes); FG2216, on the other hand, is a more selective analogue which is proposed to specifically target the PHD enzymes, making it attractive for therapeutic use. Both DMOG and FG2216 have been reported to minimize tissue damage 24 h to several weeks after myocardial infarction [4, 12–14].

Genetic manipulation of PHD activity has also been shown to protect from myocardial I/R. Although all three isoforms of PHD (1, 2, and 3) can hydroxylate and regulate HIF $\alpha$  in vitro, the ubiquitously high level of PHD2 protein across a range of cell lines is thought to account for its dominant role in setting low steady-state levels of HIF in normoxia [15]. In keeping with this, intraventricular infusion with *PHD2*, but not *PHD1* or 3, siRNA reduced post-ischemic infarct area [4, 16, 17]. Similar results were obtained with PHD2 silencing using intramyocardial injection of *PHD2* shRNA [18].

Genetic deletion of *PHD2* (but not *PHD1* or *3*) in mice results in embryonic lethality [19]. It has been reported, however, that transgenic mice containing hypomorphic alleles for *PHD2* are viable with no obvious cardiac abnormalities. These mice have improved functional recovery, coronary flow rate, and reduced infarct size following I/R in the isolated mouse heart [20], in agreement with the dominant role of the PHD2 isoform in HIF regulation.

Interestingly, *PHD1*—— mice, which survive until adulthood with no obvious heart defects, have also been reported to show significant protection from myocardial I/R [21]. Further, this protection against ischemic insult is observed in *PHD1*—— skeletal muscle [22] and liver [23], indicating that the mechanisms involved are not restricted to the heart. Although the latter phenotypes are thought to involve HIF-dependent pathways, it is curious that the other hallmarks of HIF activation such as polycythemia and angiogenesis are not observed in *PHD1*—— mice. Indeed, PHD1 has been reported to have HIF-independent functions in regulating cellular proliferation [24] and it is possible that these may contribute to the ischemic protection. Alternatively, it may be

that PHD1 loss induces HIF to a lesser extent than loss of PHD2, such that there is sufficient HIF to provide protection from ischemia without activating erythropoiesis or angiogenesis. Whatever the mechanism, the findings raise the interesting possibility that PHD isoform-specific inhibitors (which have yet to be developed) could provide more targeted drug intervention.

Overall, these studies provide evidence that short-term (or mild chronic) activation of HIF, by either pharmacological inhibition of PHD enzymes or genetic manipulation of PHD/HIF, can be beneficial against myocardial I/R. The protection conferred may occur shortly after HIF induction via changes in cellular metabolism (for example, enhanced glucose uptake and metabolism through activation of HIF target genes such as GLUT-1, pyruvate dehydrogenase kinase, and 6-phosphofructokinase 1) and vasodilation (for example, by induction of nitric oxide synthases). In addition, activation of HIF may confer delayed protection via angiogenesis and vascular remodeling.

Long-term HIF activation, for example, through genetic manipulation of the HIF hydroxylase system, however, has potential detrimental effects. These are outlined below.

#### 2.3 Risks

#### 2.3.1 Genetic Manipulation of HIF $\alpha$

Evidence for the detrimental effects of sustained HIF $\alpha$  activation are obtained from recent studies, whereby overexpression of a stable form of either HIF-1 $\alpha$  or HIF-2 $\alpha$  in cardiomyocytes results in cardiomyopathy [25, 26].

#### 2.3.2 Genetic Manipulation of PHD Enzymes

The effects of chronic PHD inhibitor exposure are largely unknown and existing data derives from *PHD* knockout mice which may not accurately mimic the effects of catalytic inhibition (for example, because of loss of additional non-catalytic effects of the enzyme protein). It is worth noting, however, that supplementation of a certain brand of Canadian beer with cobalt sulfate was identified as a contributing etiological factor in the so-called Quebec beer-drinker's cardiomyopathy (with associated polycythemia) of the late 1960s [27]. This hints at protracted PHD inhibitor usage being potentially detrimental to cardiac function – a possibility that is supported by genetic manipulation of the PHD enzymes in mice.

Widespread, conditional inactivation of *PHD2* in adult mice results in severe polycythemia and hyperactive angiogenesis/angiectasia, in line with the predicted induction of HIF $\alpha$ , pro-angiogenic HIF target genes, and erythropoiesis-promoting HIF target gene erythropoietin. However, these mice also suffer from dilated cardiomyopathy and premature mortality [28–31]. The latter phenotypes may occur either as an indirect consequence of polycythemia and/or as a direct action of *PHD2* loss in cardiomyocytes. Further studies demonstrate that, in fact, cardiac-specific loss of *PHD2* is sufficient to induce dilated cardiomyopathy and premature mortality in adult mice, which is exacerbated when on a *PHD3*-/- background [25]. Thus, sustained PHD2 inactivation/HIF activation in the heart itself is detrimental to cardiac function and may even play a causal role in the pathogenesis of ischemic cardiomyopathy [25].

Aside from the risks of dysregulated erythropoiesis and angiogenesis, loss of PHD activity in other noncardiac tissues may also pose risks to both cardiovascular and other tissue functions. For instance, *PHD3*–/– mice, though viable and with no obvious cardiac abnormalities, suffer from abnormal sympathoadrenal development that is likely to be the cause of the observed reduced catecholamine secretion and systemic hypotension [32]. In humans, activating mutations in HIF-2 $\alpha$  have been associated with pulmonary hypertension [33]. Systemic administration of PHD inhibitors may therefore result in a range of side effects from HIF activation in tissues other than the heart.

#### 2.3.3 Genetic Manipulation of VHL

As both VHL and PHD negatively regulate HIF, and assuming a lack of divergence in the PHD/HIF/VHL oxygen-sensing pathway, one might predict loss of VHL to phenocopy loss of PHDs (in particular PHD2, given its dominant role in HIF regulation). Indeed, *VHL*-/- mice, like *PHD2*-/- mice, are embryonic lethal due to placental defects [34]. Cardiac-restricted ablation of *VHL* in adult mice leads to dilated cardiomyopathy, lipid accumulation, myocyte loss, fibrosis, and even malignant transformation, in a HIF-1 $\alpha$ -dependent manner [35]. The cardiac phenotype after *VHL* loss is therefore more severe than observed after combined *PHD2/PHD3* inactivation, possibly because of residual PHD1 activity and/or a contribution from PHD and HIF-independent functions of VHL. However, the findings again suggest that long-term, high-level upregulation of HIF pathways is likely to entrain significant side effects.

Overall, genetic studies demonstrate that extensive HIF activation in the heart is potentially deleterious to cardiovascular function. Thus, PHD inhibitors will probably require careful dose titration to achieve the desired risk/benefit profile and/or limitation of the duration of therapy.

#### 2.4 Summary

Current work has defined both benefits and risks associated with the manipulation of the HIF hydroxylase system as a therapeutic means of treating myocardial ischemia.

Short-term (or mild, chronic) activation of HIF, like IPC, is protective against ischemic insult. Although this has been determined using interventions that precede ischemia, two findings raise the possibility that PHD inhibitors could equally be

applied post-ischemia. First, HIF activation lasts several days following ischemic insult [36]. Second, cycles of I/R applied at the onset of, rather than preceding, ischemia are still able to confer protection (a process known as ischemic post-conditioning [37]). The ability to treat myocardial ischemia by post-event drug intervention would make PHD inhibitors particularly useful in the clinical setting.

Prolonged, excessive HIF activation, on the other hand, phenocopies ischemic cardiomyopathy and is deleterious to cardiovascular function. It may also have detrimental side effects in noncardiac tissues if applied in a systemic manner. Ablation of *PHD1* in mice induces hypoxia tolerance without effect on PHD2-/HIF-regulated pathways such as erythrocytosis. In this regard, a PHD1-specific inhibitor, though not yet available, may be beneficial.

In summary, PHD inhibitors that activate HIF are an attractive therapeutic option for minimizing tissue damage from myocardial ischemia or improving perfusion by medical means. However, care will be required to avoid side effects from uncontrolled activation of hypoxia pathways. This highlights the need for time, dose, tissue, and/or PHD isoform-specific drug interventions in order to minimize the potential deleterious side effects of PHD inhibitors.

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# Cytoprotective Mechanisms in the Vasculature

Justin C. Mason

# 3.1 Introduction

The vascular endothelium forms an essential barrier, separating blood constituents and the extravascular tissues. For a long time considered an inert semipermeable membrane, the vascular endothelium is now recognized to be multifunctional, dynamic, and heterogeneous organ. In health, the endothelium contributes to the control of vasodilatation and permeability, while maintaining an anti-thrombotic, anti-inflammatory, anti-adhesive phenotype. This is an active process controlled by intrinsic gene expression and external stimuli. As a consequence specialized endothelium is found in the blood-brain barrier, lining fenestrated capillaries in the kidney, as sinusoidal endothelium in the liver and in lung alveoli to facilitate gas exchange. The endothelium is also highly adaptable, changing phenotype in response to specific stimuli and so facilitating hemostasis and regulating the response to inflammatory stimuli. In the latter, the endothelium regulates vascular permeability, expression of cellular adhesion molecules and recruitment of leukocytes. In addition, release of growth factors such as vascular endothelial growth factor (VEGF) and subsequent endothelial proliferation are important in tissue repair.

As a consequence of its anatomic location, the vascular endothelium is continuously exposed to potentially harmful factors such as endotoxin, cytokines, advanced glycation end-products, complement components, activated leukocytes, and oxidatively modified low-density lipoproteins (ox-LDL). If uncontrolled, these noxious stimuli predispose to endothelial dysfunction, predominantly driven by reduced expression of endothelial nitric oxide synthase (eNOS) [1].

Endothelial injury is the earliest detectable event in atherogenesis [2], and induces a local inflammatory response resulting in endothelial dysfunction, characterized by

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reduced NO biosynthesis, oxidative stress, increased permeability to lipoproteins, and monocyte recruitment [3]. Moreover, apoptosis occurs preferentially at sites of endothelial injury and atherosclerosis [4], where denudation of vascular endothelium enhances the risk of thrombosis. Thus, mechanisms that control endothelial inflammation and minimize vascular injury are essential for the maintenance of vascular integrity, initiation of repair, and resistance to atherogenesis. A detailed understanding of these molecular mechanisms may in turn reveal novel therapeutic targets which will help to prevent vascular injury and allow the maintenance of vascular endothelial homeostasis and integrity [5].

### 3.2 Accelerated Atherosclerosis

Heart attack and stroke as a consequence of atherosclerosis remain the leading cause of death in the western world. Moreover, certain disease groups are exposed to the risk of accelerated atherogenesis, with hyperlipidemia, the metabolic syndrome, and diabetes mellitus the best recognized. Over the last decade, the increased risk of accelerated atherogenesis in patients suffering from systemic inflammatory diseases has emerged as an intense area of research.

Prolonged systemic inflammation, such as that associated with rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE), may accelerate atherogenesis with cardiovascular disease responsible for 35–50% increased mortality in RA [6]. Importantly, the disease itself represents a specific risk factor [7]. Likewise, SLE is an independent risk factor and responsible for a 10–50 fold increase in myocardial infarction in a female population characteristically protected against cardiovascular disease [8]. Thus, although patients with chronic inflammatory disease commonly have more traditional risk factors than age- and sex-matched controls, these alone do not account for the increased cardiovascular risk. Additional mechanisms implicated include increased oxidative stress, pro-inflammatory cytokines, endothelial activation leading to enhanced leukocyte adhesion, and the deleterious effects of immune complexes, anti-phospholipid antibodies, homocysteinemia, hypercoagulability, CD4+CD28<sup>-</sup> T cells, and drug toxicity [6]. The significance of chronic systemic inflammation is reinforced by evidence of accelerated atherosclerosis in patients with vasculitides and other non-rheumatic inflammatory diseases.

A current challenge is to identify early the subgroup of patients with these diseases most at risk of developing accelerated atherogenesis. The advance in novel noninvasive imaging techniques is one approach that has been adopted in recent years. For example, high-resolution ultrasound can monitor intima-media thickness and demonstrate early disease [9]. Using positron emission tomography with oxygen-15-labeled water, we have demonstrated that the increase in myocardial blood flow in response to intravenous adenosine is significantly attenuated in some patients with RA and SLE. These patients were known to have normal or minimally diseased ( $\leq 20\%$  luminal reduction) coronary arteries and no significant difference in conventional cardiovascular risk factors when compared with age- and sexmatched controls [10]. Likewise, we have shown that an integrated method for cardiovascular magnetic resonance angiography (CMR) in patients with Takayasu's arteritis provides not only accurate delineation of arterial wall thickening, but can also identify early atherosclerotic plaques, demonstrate dynamic ventricular function and myocardial scarring [11]. These techniques may have the potential to identify patients most at risk of accelerated atherosclerosis, so allowing early preventative therapy.

However, current treatments for atherosclerosis are directed predominantly at established symptomatic lesions, with an outstanding need for new preventative therapies. Intensive management of inflammation combined with traditional risk factor modification is required to minimize cardiovascular risk in rheumatic diseases. Methotrexate and mycophenolate mofetil demonstrate anti-atherogenic effects, with methotrexate reducing cardiovascular mortality in RA by 70% [12, 13]. Anti-tumor necrosis factor- $\alpha$  therapy may enhance endothelial function, and the risk of myocardial infarction in patients with RA who respond to anti-TNF agents is significantly reduced when compared to non-responders [14]. An important additional approach is to target endothelial dysfunction, an end achieved to some extent by statins [15] and angiotensin-converting enzyme inhibitors [16], which also exert anti-inflammatory effects. However, efficacy needs to be established by prospective studies, and to optimize this approach, we need a detailed understanding of vascular endothelial cytoprotective signaling pathways and their downstream target genes.

# 3.3 Vascular Cytoprotection

Exogenous factors and intracellular mechanisms combine to control inflammatory responses, prevent bystander endothelial injury, and maintain the integrity of the vascular wall (Fig. 3.1). I will provide a brief overview of these mechanisms before dealing in more detail with some recent advances.

A variety of anti-inflammatory cytokines and growth factors play an important role in the maintenance of endothelial homeostasis, regulation of inflammation and reparative mechanisms including angiogenesis. The IL-1 receptor antagonist (IL-1ra) and soluble TNF receptors exert potent anti-inflammatory effects and are used clinically in the treatment of systemic inflammatory diseases including autoinflammatory disorders [17] and rheumatoid arthritis [18]. In murine models IL-1ra is atheroprotective, inhibiting early atherogenesis in ApoE-deficient mice [19], while IL-1ra knockouts suffer arterial inflammation and a low expressing polymorphism has been linked to coronary artery disease [20]. IL-10 is particularly important for its effects on macrophages, inhibiting pro-inflammatory cytokine synthesis and favoring a CD163hi anti-inflammatory phenotype [21]. Although its effects on vascular endothelium are less well understood, IL-10 is reported to inhibit NF- $\kappa$ B, vascular inflammation, and endothelial cell adhesion molecule expression [22].

Growth factors play an essential role in endothelial homeostasis with basic fibroblast growth factor (FGF-2) and VEGF (see below) capable of activating anti-apoptotic pathways. In addition to its mitogenic actions, FGF-2 induces expression of the antiapoptotic protein Bcl-2 [23]. It may also enhance protection against complementmediated injury through induction of decay-accelerating factor (DAF) [24], and exert



**Fig. 3.1** Cytoprotective mechanisms in the vasculature. The vascular endothelium is protected by exogenous anti-inflammatory and pro-survival factors including IL-10, Ang1, and VEGF. Induction of intrinsic cytoprotective genes via PKC and PI-3 K/Akt-dependent pathways results in enhanced protection against apoptosis, oxidative stress, thrombosis, and complement-mediated injury. *IL* interleukin, *IL-1RA* IL-1 receptor antagonist, *VE-Cad* VE-cadherin, *PKC* protein kinase C, *VEGF* vascular endothelial growth factor, *HO-1* heme oxygenase-1, *PGI*<sub>2</sub> prostacyclin, *DAF* decay-accelerating factor, *Ang1* angiopoietin 1

anti-thrombotic, anti-inflammatory effects [25, 26]. TGF- $\beta$  signals via two type 1 receptors, activin receptor-like kinases Alk-1 and Alk-5 which induce opposite effects, with Alk-1 driving pro-proliferative and pro-migratory gene expression, while Alk-5 signaling facilitates growth arrest, matrix synthesis, and formation of a stable vessel [27]. TGF- $\beta$  may also inhibit expression of E-selectin so reducing leukocyte adhesion. Angiopoietin-1 (Ang-1) has also emerged as an important vasculoprotective growth factor, signaling predominantly via Tie2, with its actions opposed by family member Ang 2. Ang1 may exert multiple protective effects in the vasculature including anti-inflammatory, anti-apoptotic, and anti-thrombotic actions [27, 28].

### 3.3.1 Cytoprotective Genes

Many of the vasculoprotective properties of exogenous mediators are facilitated through induction of intrinsic cytoprotective genes. In the vascular endothelium, these include endothelial nitric oxide synthase (eNOS), superoxide dismutases, A1, A20, B cell lymphoma protein (Bcl)-2, Bcl-xL, heme oxygenase-1 (HO-1) [5], and membrane-bound complement regulatory proteins DAF and CD59 [29, 30]. A20 is an inducible ubiquitin-editing anti-inflammatory protein that negatively regulates NF- $\kappa$ B-dependent gene expression. A20 is induced as a consequence of NF- $\kappa$ B activation and exerts a negative feedback on further activation acting at multiple levels within the NF- $\kappa$ B pathway [31]. The importance of A20 is well illustrated by the phenotype of the knockout mice which are markedly susceptible to TNF and develop severe widespread inflammation and cachexia [32].

Bcl-2, Bcl-xL, and A1 are members of the anti-apoptotic Bcl-2 family, which may also exert important anti-inflammatory and cytoprotective effects. The balance between the pro- and anti-apoptotic members of the Bcl-2 family is critical in determining cell fate [33]. Thus, if pro-apoptotic Bim, Bid, and Bad are present in sufficient amounts to bind to and overwhelm Bcl-2 and Bcl-X<sub>L</sub>, sequestered Bax and Bak are released allowing the escape of mitochondrial cytochrome *c*. This in turn results in the generation of the apoptosome, which cleaves and activates downstream apoptosis effector caspases 3, 6, and 7, [33]. We have recently reported that protein kinase C $\epsilon$  forms a signaling complex and acts co-operatively with anti-apoptotic kinase (Akt) to protect human vascular endothelial cells against apoptosis, through induction of Bcl-2 and inhibition of caspase-3 cleavage [30].

#### 3.3.2 Resistance to Complement

Mechanisms implicated in complement deposition on the EC surface include activation of the classical pathway by immune complexes, anti-phospholipid, and antiendothelial cell Abs, and through recognition of apoptotic cell blebs by C1q [34]. Induction of both CD59 and DAF on EC via distinct signaling pathways contributes significantly to the regulation of complement activity and protection against bystander injury [35, 36]. In particular, the propensity for DAF expression to be induced suggests it represents an important response to inflammation and injury and hence in the protection against vascular injury. We have shown DAF expression to be upregulated in response to TNF $\alpha$ , IFN $\gamma$ , thrombin, VEGF, and bFGF, while epidermal growth factor and PIGF failed to alter expression. The increase in DAF led to enhanced protection against complement-mediated injury (Fig. 3.2), which was



**Fig. 3.2** Induction of decay-accelerating factor (DAF) protects endothelial cells against complement. Exposure of human endothelial cells to certain growth factors and pro-inflammatory mediators for 24–48 h increases DAF expression on the cell surface and resistance to complement-mediated injury following opsonization with an anti-endoglin mAb and exposure to normal human serum. Data expressed as percent cell lysis versus untreated (UT) control. *EGF* epidermal growth factor, *PIGF* placenta growth factor, *VEGF* vascular endothelial growth factor, *bFGF* basic fibroblast growth factor, *TNF* tumor necrosis factor, *IFN* interferon- $\gamma$ 

reversed by inclusion of an inhibitory DAF mAb [24, 29, 35, 37, 38]. Moreover, DAF<sup>-/-</sup> and CD59<sup>-/-</sup> mice, when crossed with atherosclerosis prone strains, suffer accelerated disease [39–41].

## 3.3.3 Vascular Endothelial Growth Factor

In addition to their better known roles in vasculogenesis and angiogenesis, it is increasingly recognized that VEGFs are important in adult endothelial homeostasis [42]. The five main VEGF ligands, VEGFA-D, and placenta growth factor PIGF are also found as splice variants. Thus, the isoforms of human VEGFA are VEGFA121, VEGF145, VEGFA165, VEGFA189, and VEGFA206. The VEGFs signal via the receptor tyrosine kinases VEGFR1-3 and this signaling maybe modulated by co-receptors such as neuropilin and heparan sulfate proteoglycans (see ref. [43] for a detailed review). The ability of VEGFA to induce cytoprotective gene expression in vascular endothelium is well established and the cytoprotective actions of VEGFA include induction of the anti-apoptotic genes Bcl-2 and A1 [30, 44]. In addition, VEGF increases eNOS expression and NO release [45], induces expression of HO-1 [46], and contributes to the maintenance of an anti-thrombotic endothelial surface through induction of prostacyclin synthesis [45]. VEGF also enhances protection against complement-mediated injury via upregulation of DAF expression [47]. Recent elegant studies, in which mice with an inducible podocyte-specific deletion of vegfA were generated, have demonstrated endothelial cell swelling, local thrombosis, and subsequent proteinuria and hypertension [48]. These abnormalities may contribute to the side effects associated with the use of the anti-VEGFA mAb bevacizumab in disseminated colonic carcinoma, which include both hypertension and thrombosis [48, 49].

### 3.3.4 Heme Oxygenase-1

HO-1 is an inducible cytoprotective enzyme which degrades heme, generating carbon monoxide, bilirubin, and ferrous iron which is rapidly sequestered by intracellular ferritin [50, 51]. The cytoprotective properties of HO-1 are attributed to its products and include antioxidant, anti-apoptotic, anti-thrombotic, and anti-inflammatory actions [50] (Fig. 3.3). The importance of these cytoprotective actions are reflected in the severe sequelae of HO-1 deficiency, which include intravascular hemolysis, anemia, diffuse endothelial damage, and accelerated atherosclerosis [52]. We have recently reported an additional cytoprotective action of HO-1, the regulation of complement activation, mediated via induction of DAF. Analysis of cardiac EC isolated from  $Hmox1^{-/-}$  mice revealed a significant reduction in DAF expression as compared to  $Hmox1^{+/+}$  EC, while the  $Hmox1^{-/-}$  cells displayed enhanced sensitivity to complement-mediated lysis [53]. HO-1 expression is required for prolonged allograft survival, and both HO-1 expression and complement regulation are important in accommodation, the resistance of a transplanted organ to graft-specific antibodies and complement fixation [54]. Therefore, our data



**Fig. 3.3** Heme oxygenase-1-mediated degradation of heme. HO-1 catalyzes the breakdown of heme into equimolar amounts of carbon monoxide (CO), biliverdin, and free iron (Fe<sup>2+</sup>). Biliverdin reductase subsequently catalyzes the conversion of biliverdin to bilirubin. The increase in intracellular Fe<sup>2+</sup> induces expression of the iron-binding protein heavy chain-ferritin and the opening of Fe<sup>2+</sup> export channels. The products of heme degradation exert a variety of effects on endothelial cells which are protective against atherosclerosis. *ROS* reactive oxygen species, *I/R* ischemia reperfusion

linking the activity of HO-1 and expression of DAF is likely to be important in accommodation, resistance to post-transplant vasculopathy, and prolonged graft survival [55, 56]. HO-1 and its products may also protect against atherogenesis. Inhibition of VSMC proliferation, combined with its anti-inflammatory, antioxidant actions and anti-thrombotic actions, contributes to the protective role of HO-1 against atherogenesis and its ability to stabilize the vulnerable plaque. Furthermore, epidemiological studies suggest that a mildly raised serum bilirubin significantly protects against ischemic heart disease.

### 3.4 Vascular Cytoprotection and Shear Stress

The geometric nature of atherosclerosis within the arterial tree led to the study of blood flow patterns as an influence in atherogenesis. These studies suggest that a disturbed flow (DF) waveform, with low shear reversing flow patterns, such as that located at arterial branch points, is pro-atherogenic, whereas unidirectional pulsatile



**Fig. 3.4** Shear stress-induced vascular cytoprotection. Laminar shear stress is a critical component in the cytoprotection of arterial endothelium. Shear activates anti-thrombotic and cell survival genes including anti-apoptotic and antioxidant proteins. Nitric oxide exerts anti-adhesive, anti-thrombotic, and vasodilatory effects. In addition, release of nitric oxide and TGFβ inhibits vascular smooth muscle cell proliferation. *NO* nitric oxide, *PGI2* prostacyclin, *tPA* tissue plasminogen activator, *TM* thrombomodulin, *TNF* tumor necrosis factor, *HO-1* heme oxygenase-1, *MnSOD* manganese superoxide dismutase, *EC* endothelial cells, *VSMC* vascular smooth muscle cells

laminar shear stress (LSS) >10 dyn/cm<sup>2</sup> is atheroprotective [57]. This is reflected in the phenotype of EC exposed to LSS, typically characterized by enhanced endothelial nitric oxide synthase (eNOS) expression and nitric oxide (NO) biosynthesis, prolonged EC survival, and an anticoagulant, anti-adhesive cell surface [58, 59] (Fig. 3.4). In contrast, endothelium exposed to DF exhibits reduced levels of eNOS, increased apoptosis, generation of reactive oxygen species, permeability to LDL, and leukocyte adhesion [57].

## 3.4.1 Cytoprotective Transcription Factors

Considerable recent attention has been given to the investigation of LSS-inducible cytoprotective transcription factors, and in particular Kruppel-like factors (KLF) 2 and 4 and NF-E2-related factor-2 (Nrf2). KLF2 and KLF4 are members of a family of 17 zinc-finger transcription factors. In vitro, endothelial KLF2 is induced by LSS but not DF, while in vivo, KLF2 is differentially expressed in areas of the aorta exposed to LSS and DF [60]. Importantly, KLF2 activity has been shown to be an important regulator of cytoprotective genes including eNOS, thrombomodulin, and HO-1 [61–63]. An ERK5/myocyte enhancing factor 2 pathway has been identified upstream of KLF2 transcription, and this can be therapeutically activated by statins [64].

KLF4 activity has also been linked to the regulation of vasculoprotective genes including eNOS and thrombomodulin [65, 66]. A recent study has demonstrated that shear stress–induced KLF4 expression via MEK5/MEF2 pathway shared with KLF2 [66]. Subsequent microarray analysis demonstrated significant overlap in



target genes between the two transcription factors. Thus, further details of their precise relationship in the maintenance of endothelial homeostasis both in the resting vascular endothelium and during inflammation are awaited with interest.

Nrf2 is similarly an important flow-inducible cytoprotective transcription factor. Nrf2 is retained in the cytoplasm by kelch-like ECH-associated protein (Keap1). LSS results in dissociation of the Nrf2–Keap1 complex allowing Nrf2 translocation to the nucleus, where it controls expression of phase II detoxification enzymes and antioxidant proteins including HO-1, NAD(P)H:quinine oxidoreductase 1, ferritin heavy chain, glutathione reductase, and thioredoxin reductase 1 via the antioxidant response element [67, 68].

We have recently reported that LSS induces expression of CD59 in vascular EC via an ERK5/KLF2-dependent pathway, thereby preventing C9 insertion into the MAC and protecting against complement-mediated injury. We also demonstrated regional differences in CD59 in the murine aorta, with maximal expression of CD59 at atheroprotected sites [69]. These data combined with the observation of accelerated atherosclerosis in CD59/LDLR mice suggest CD59 contributes significantly to shear stress-mediated protection against atherosclerosis [40].

Recent data suggests that shear stress may influence endothelial responsiveness to exogenous factors including drugs. Thus, we have reported that atorvastatinmediated HO-1-dependent antioxidant effects [63] are enhanced by LSS, demonstrating that biomechanical signaling contributes to endothelial responsiveness to pharmacological agents. This synergistic relationship between LSS and statin involved Akt phosphorylation, activation of both KLF2 and Nrf2, eNOS induction, and prolonged HO-1 mRNA stability [68] (Fig. 3.5).

This observation has potentially important implications for statin efficacy in patients with ischemic heart disease, and for the increasing use of statins in prevention of accelerated atherosclerosis in patients suffering from systemic inflammatory diseases. The data emphasize the need for novel therapies to optimize vasculoprotection, and our recent report of sulforaphane-mediated activation of Nrf2 in atheroprone sites of the murine aorta offers hope in this regard [70].

## 3.4.2 Peroxisome Proliferator-Activated Receptors (PPARs)

PPAR $\alpha$ , PPAR $\delta$ , and PPAR $\gamma$ , members of the nuclear receptor family, are ligandactivated transcription factors which regulate energy balance. Transcriptional activation of their target genes requires ligand-induced heterodimerization with the retinoid X receptor and co-factor recruitment [71]. PPARs are activated by mediators including polyunsaturated fatty acids linoleic and docosahexaenoic acid, eicosanoids such as prostayclin and 15d-PGJ<sub>2</sub> and components of ox-LDL [71]. Expression of the PPARs in the vasculature and reported anti-inflammatory effects of synthetic ligands has led to significant interest therapeutically. PPAR $\alpha$  agonists (Fibrates) and PPAR $\gamma$  agonists (Thiazolidinediones) are in current clinical use for the treatment of hyperlipidemia and diabetes mellitus respectively, while PPAR $\delta$ agonists reduce abnormalities associated with the metabolic syndrome [72]. However, the relatively disappointing data to date as regards reduction of cardiovascular events with fibrates and thiazolidinediones suggests an improved understanding of PPAR biology and the actions of PPAR ligands is required [73].

Recent findings of note include the report that LSS induces expression of the PPAR $\gamma$  target gene CD36 via the PPAR $\gamma$ -responsive element in the CD36 promoter [74]. Release of endogenous PPAR ligands, particularly prostacyclin, is likely to be important in LSS-induced protective responses, and EC-derived prostacyclin has been shown to activate PPAR $\alpha$  and  $\delta$  in vascular smooth muscle cells [75]. PPAR $\delta$  appears to play a multifunctional role in the vasculature, including increased fatty acid oxidation, protection against apoptosis and antioxidant, anti-inflammatory actions such as suppression of VCAM-1 [76]. These actions may contribute to the atheroprotective effect of PPAR $\delta$  ligand treatment of ApoE<sup>-/-</sup> mice [77]. An additional important mechanism may be the ability of PPAR $\delta$  ligands to upregulate HO-1 in vitro, a response that requires the co-activator PGC-1 $\alpha$  and can be reproduced in vivo [78].

## 3.5 Therapeutic Manipulation of Vascular Cytoprotection

Therapeutic induction of cytoprotective genes in the vasculature has the potential to condition the vascular endothelium against injury, so minimizing or reversing endothelial dysfunction and preventing or slowing the progress of atherogenesis. This would be of particular benefit to patients known to be at particularly high risk, such as those with diabetes mellitus, hyperlipidemias, and systemic inflammatory diseases. Current immunosuppressive drugs may achieve this to some extent; however, therapies specifically targeting the vasculature are likely to be more effective.

Among these, biologic therapies such as those targeting  $TNF\alpha$  are of particular interest, and of note, these agents appear to reduce the rate of atherogenesis and myocardial infarction in patients with RA [18].

### 3.5.1 Statins

Perhaps the best studied drugs in this regard are the statins, 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase antagonists, which inhibit cholesterol synthesis and reduce serum LDL-cholesterol. This is turn reduces morbidity and mortality from ischemic heart disease. However, clinical trial data also demonstrates that the benefits of statins are rapid, extend to patients within the accepted normal LDL-cholesterol range [79] and exceed those of other lipid-lowering drugs, despite comparable falls in cholesterol [80]. These observations suggest that statins have pleiotropic effects above and beyond LDL-cholesterol lowering [81]. These cholesterol-independent actions of statins result in significant improvement in endothelial function in both hyper- and normocholesterolemic patients with atherosclerosis [82].

Statin-mediated inhibition of isoprenoid lipid production and subsequent protein prenylation and activity of signaling proteins such as the small GTPases underlie many of the LDL-cholesterol-independent actions [81, 82]. This mechanism, initially identified in vitro, has been supported by two recent studies in which a reduction in Rho-associated protein kinase (ROCK) activity and improved endothelial function was observed in patients treated with high-dose statins when compared to low-dose statins or ezetimibe (an alternative class of lipid-lowering agent) [83]. In vascular endothelium, statins increase eNOS mRNA stability and NO biosynthesis, leading to inhibition of leukocyte trafficking, an anti-inflammatory response that is lost in eNOS-deficient mice [84]. Statins also exert anti-thrombotic, antioxidant, and immunomodulatory effects in EC [81, 85–87]. We have identified an additional cytoprotective action of statins, the regulation of complement activation. At least in vitro, atorvastatin and simvastatin induce expression of DAF [88] and under hypoxic conditions, both DAF and CD59 [36] and we propose that this response may contribute to both their atheroprotective and anti-inflammatory actions.

#### 3.5.2 Heme Oxygenase-1

There is considerable interest in the therapeutic potential of HO-1 either through modulation of its expression or delivery of its products [50]. However, such an approach is not straightforward in light of the potential toxicity of CO, free iron, and bilirubin. In vivo animal models are encouraging and HO-1 induction favors long-term allograft survival [89] and protects against atherosclerosis [90]. Exogenous CO may substitute for HO-1, conferring protection against ischemia reperfusion [91], restenosis injury, and allograft rejection [92]. Although less well studied, biliverdin and bilirubin exert similar effects [92]. In the vascular endothelium, we and

others have demonstrated HO-1 induction in vitro following treatment with statins [63, 68, 93], celecoxib [94], rapamycin [95], and probucol [96]. PPAR $\alpha$ , PPAR $\gamma$ , and PPAR $\delta$  agonists have also been shown to induce HO-1 in vitro [78, 97]. Moreover, we have recently reported that treatment of mice with PPAR $\delta$  agonists increases aortic EC expression of HO-1 [78]. Thus, the development of approaches through which HO-1 can be induced or its products delivered safely, and subsequent clinical trials investigating the efficacy of such an approach, is awaited with interest.

# 3.6 Conclusion

Inflammatory reactions within the vasculature are tightly regulated, with dysregulation increasingly recognized as a significant contributory feature in a variety of disease states including atherosclerosis and chronic inflammatory auto-immune diseases. Vascular endothelial cell injury predisposes to endothelial dysfunction, a critical precursor to atherogenesis, and a potential target for preventative therapy. Significant progress has been made in dissecting the molecular mechanisms through which the vascular endothelium is protected against injury, and over the next decade, it is hoped that these insights will reveal novel cytoprotective targets that can be therapeutically manipulated. This in turn may allow early intervention in those patients known to be at particularly high risk.

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# Notch Signaling in Vascular Development

Shalini Jadeja and Marcus Fruttiger

# 4.1 Introduction

During vascular development, numerous cell fate decisions must occur. The hematopoietic, endothelial, and mural cell lineages are all derived from the mesoderm, and during early embryonic development precursor cells must "decide" which of the three lineages to enter. Also, within each of these lineages, more decision making is needed to generate additional sub-specification of cells. For instance, the vascular tree is split into different caliber vessels, arteries, veins, and capillaries; therefore, endothelial cells building this complex network are far from a uniform cell population. Instead they differentiate into vessel-specific and even tissue-specific phenotypes. The main function of the Notch signaling pathway is to generate cell diversity by mediating cell fate decision, and it is therefore no surprise that this signaling pathway participates critically on many levels throughout vascular development (Fig. 4.1).

# 4.1.1 Development of Hematopoietic and Vascular Cells

During early embryonic development, mesodermal progenitors give rise to blood cells and primitive vascular networks. In amniotes, this occurs in two areas: in the embryo proper and extra-embryonically, in the yolk sac. Fish and amphibians do not

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**Fig. 4.1** Notch signaling is implicated extensively in hematopoietic and vascular development, from the early mesoderm progenitor stage through to endothelial cell differentiation. *Blue coloring* indicates Notch signaling involvement

have a volk sac and therefore have no extra-embryonic source of vessels and blood. However, the precise lineage relationship of blood cells, vascular cells, and their mesodermal precursors is complex and only partially understood. During gastrulation, mesoderm cells emerge from the posterior primitive streak and migrate to the proximal region of the yolk sac [1, 2]. There they give rise to so-called blood islands containing hematopoietic and endothelial precursors. In mice by circa embryonic day (E) 7.5, the first blood islands can be detected in the yolk sac [3]. These morphologically distinct cell clusters segregate into blood cells and ensheathing endothelial cells, then remodel into smaller channels and eventually into blood filled vascular networks [4]. Due to the close spatiotemporal relationship between hematopoietic and endothelial precursor cells, the existence of a common mesodermal progenitor (the hemangioblast) has been proposed [5, 6]. Indeed, detailed mapping studies have shown that early mesodermal precursors are already committed to the hemangioblast lineage when they are still in the primitive streak [7]. Furthermore, genetic deletion of the Vascular endothelial growth factor receptor 2 (Vegfr2) in mice results in a lack of hematopoietic and endothelial cells and blood islands do not form [8]. However, it has also been suggested that, as the mesodermal precursors emerge from the primitive streak, allocation to the hematopoietic lineage may occur before, and independently of, the bulk of vascular commitment [9].

Furthermore, mesodermal precursor cells not only give rise to the blood and endothelial lineage, but they also generate smooth muscle cells; the cells that participate in building the vascular wall (therefore referred to as "mural" cells). *In vitro* experiments have shown that cell colonies cultured from the primitive streak have hematopoietic, endothelial, and smooth muscle potential [7]. It is also possible to generate endothelial and smooth muscle cells from embryonic stem cell-derived cells that are Vegfr2-positive [10, 11]. In addition, embryonic stem cell-derived embryoid bodies contain blast colony-forming cells (BL-CFC) that have the potential to generate hematopoietic, endothelial, and smooth muscle cells depending on culture conditions [5, 12]. Alternatively, the three lineages may simply be derivatives of ventral mesoderm that can give rise to a broader array of cell types [13]. It is therefore not entirely clear yet whether the three cell types are derived from a single common precursor or even whether the hemangioblast exists *in vivo*.

Once endothelial precursor cells (also known as angioblasts) have been generated, they migrate, coalesce, and differentiate into endothelial cells, which form a primitive vascular plexus de novo. This is the classic definition of "vasculogenesis" [14], the process responsible for forming blood vessels in the yolk sac and, intraembryonically, the endocardial tube, dorsal aortae, and cardinal veins. Subsequently, the primitive vessel networks recruit mural cells, remodel, and form further vessels in a process termed "angiogenesis" [15, 16].

# 4.2 Notch Signaling Mechanisms

In mammals, there are four Notch receptors (Notch1-4) and two types of ligands: The Delta-like ligands (Dll1, Dll2 and Dll4) and the Jagged ligands (Jag1 and Jag2). Flies only have one Notch receptor and two ligands, Delta and Serrate (homologue to Jagged). Receptors and ligands are both transmembrane proteins and as a result Notch signaling is mediated between neighboring cells. Ligand–receptor binding induces proteolytic receptor cleavage, first by the Adam metalloproteases, and then for a second time by a  $\gamma$ -secretase complex (containing Presenilin) to release the Notch intracellular domain (NICD), which then translocates to the nucleus. There it forms a complex with the transcription factor "Recombination signal binding protein for immunoglobulin kappa J region" (Rbpj, also known as CSL) and relieves the repression of downstream target genes. This mechanism is known as the "canon-ical" Notch pathway (reviewed by Kopan and Ilagan [17]). Non-canonical Notch signaling has also been observed [18, 19], but is not discussed here.

Despite the pleiotropic function of Notch signaling in numerous cell types in all metazoa, to date, only a few downstream target genes have been identified. The best characterized target genes are basic Helix-loop-helix (bHLH) transcription factors from the *Hes* and *Hey* gene families (in vertebrates) and the related *Hairy* and *E(spl)* genes (in Drosophila). In classic examples, in flies, it has been shown that these transcription factors are part of a feedback mechanism that allows initially identical (or very similar) neighboring cells to take on different identities [20, 21]. Notch signaling–mediated activation of the bHLH transcription factors causes increased expression of Notch receptor and decreased expression of Notch ligand. In the absence of the receptor. Such a bi-stable system amplifies small, initial differences and simultaneously forces neighboring cells into opposite states regarding Notch

expression. In this model, referred to as the "lateral inhibition model," a cell that expresses Notch ligand usually suppresses a particular differentiation outcome in its neighbors. However, some Notch signaling is also mediated by "lateral induction," where a ligand-expressing cell induces a specific cell fate in its neighbors [21, 22].

Superficially, the mode of action of the canonical Notch pathway appears relatively simple, but there is a remarkable array of posttranslational and biological processes that modulate signaling strength and add significant complexity to the system (reviewed by [22–24]). For instance, ligand expression in receptor positive cells may have inhibitory function under certain circumstances (so-called cisinhibition). Furthermore, in Drosophila, it has been shown that ubiquitination and subsequent endocytosis of Notch ligands is essential for their activity [23]. Similarly, Notch receptor function also critically depends on posttranslational modifications. Glycosylation of Notch receptors is initiated by *O*-fucosyl transferase by adding a fucose molecule. The carbohydrate chains are then extended by glycosyl transferases such as the Fringe family. This can modify the responsiveness of Notch receptors to specific ligands. For instance, Fringe-modified Notch becomes more responsive to Delta-like/Delta and less responsive to Jagged/Serrate ligands [25, 26]. It has also been shown that receptor endocytosis and subsequent trafficking can influence Notch activity. In addition, the multiple proteolytic cleavages and the various proteases involved to generate the NICD add more possibilities to regulate Notch signaling and complicate things further. The bewildering complexity of these regulatory mechanisms seems to suggest that Notch signaling is so fundamental and important for biological function that it requires sophisticated and tight regulation.

## 4.3 Vascular Notch Expression and Knockout (KO) Mice

Most Notch receptors and their ligands are expressed in the developing vasculature (Table 4.1), whereas in the adult vasculature, expression becomes more restricted. It is remarkable that in the developing mammalian vascular system, with the exception of Notch 2 and Dll3, all Notch receptors and ligands are expressed. Interestingly, endothelial cells are usually not polarized into receptor- and ligand-expressing cells (as during lateral inhibition) but often express Notch receptors and ligands simultaneously. In line with the prominent expression of Notch genes in the vasculature, most Notch gene deletions tend to cause embryonic lethality due to disturbed vascular and cardiac development (Table 4.1).

#### 4.3.1 Notch Receptors

Notch1 and 4 are expressed in endothelial cells. While Notch1 expression is widespread in numerous other cells types, Notch4 is largely restricted to the vascular endothelium [27, 28]. Genetic deletion of *Notch1* in mice is lethal by embryonic day (E)10.5. In these mice, development proceeds normally until E9.5 but subsequently somite condensation fails and cell death is apparent in the nervous

Gene	Expression	Knockout phenotype	Reference
Notch1	Endothelial cells (widespread in many other tissues)	Lethal by E10.5	[28]
		Defective remodeling of the vasculature	
Notch3	Smooth muscle cells	Viable	[37, 38]
		Artery differentiation defects in adults	
Notch4	Endothelial cells	Viable	[30]
Dll1	Endothelial cells (arterial)	Lethal at E12	[40]
		Segmentation defects	
Dll4	Endothelial cells	Embryonic lethal at E10.5	[43-45]
		Vascular development defects	
Jag1	Endothelial cells and smooth muscle cells	Lethal between E10.5 & E11.5	[51]
		Defects in remodeling yolk sac and embryonic vasculature	
Jag2	Endothelial cells and hematopoietic precursors	Perinatal lethal Craniofacial malformations	[53]

 Table 4.1
 Expression of Notch signaling mechanisms and mouse knockouts

systems. Although embryonic lethality was not attributed to primary defects in the vasculature, the vessels that did form were anastomosing [28]. Endothelial specific loss of *Notch1* results in embryonic death by E10.5, with severe vascular defects [29].

In contrast, *Notch4* KO mice are viable and fertile [30]. It is possible that Notch1 can compensate for the loss of Notch4 because compound knockouts for both *Notch1* and *Notch4* exhibit a more severe phenotype than the single *Notch1* KO embryos. In these *Notch1/4* double KO embryos, vascular remodeling and sprouting is disturbed, as in *Notch1* KO mutants; but whereas in the *Notch1* KO mutants, the dorsal aorta is collapsed with a closed lumen, in the *Notch1/4* double mutants, both the dorsal aorta and the anterior cardinal vein are collapsed [30]. Notch signaling is usually activated transiently with a high signal turnover. Switching on the expression of constitutively active *Notch4* in endothelial cells during early development also leads to severely abnormal vascular remodeling [31]. Overactive *Notch4* postnatally causes brain arteriovenous malformations resulting in hemorrhage, neurological damage, and perinatal death [32]. In summary, it appears that both under- and overactive Notch4 is redundant during embryonic development, it may still play a role in this process.

Notch3 is expressed predominantly in vascular smooth muscle cells late in development and in adults, with particular high levels in arteries [34–36]. Notch3 function is not needed for viability and fertility in mice [37], but adult *Notch3* KO mice display structural defects in arteries [38]. Vascular smooth muscle cells are recruited to the arteries in these KO mice but display abnormal differentiation and morphology, resulting in a thinner coating of the arteries with smooth muscle cells.

#### 4.3.2 Delta-Like Ligands

Dll1 is expressed in many tissues including the endothelium of major blood vessels during late development [39]; in the postnatal vasculature, its expression is limited to endothelial cells of arteries [40]. Dll4, on the other hand, is relatively vascular endothelium specific (apart from a few exceptions). It is most strongly expressed in developing arteries and is downregulated in mature vessels [30, 34, 41]. Both, *Dll1* and *Dll4* KO mice are embryonic lethal, due to severe hemorrhages, although the *Dll1* KOs also suffer from abnormal somite formation [42]. However, while heterozygous *Dll1* deletion results in only a minor vascular phenotype (impaired arteriogenesis in adults), heterozygous *Dll4* KO mutants also died in early embryogenesis [43–45]. Although, subsequent studies have shown that in certain genetic backgrounds heterozygous Dll4 KO mutants are viable and fertile [46–48].

### 4.3.3 Jagged Ligands

Jagged1 is found in blood vessels throughout development into adulthood, where it is expressed by endothelial cells, vascular smooth muscle cells, and other cell types (e.g., neurons in certain brain nuclei) [49, 50]. Null mutants exhibit early embryonic lethality due to hemorrhaging and defects in remodeling of the embryonic and yolk sac vasculature [51]. Endothelial cell–specific knockouts of *Jag1* exhibit the same phenotype with initial vascular patterning unperturbed, but remodeling of the blood vessels and vascular smooth muscle development affected [52]. In contrast to Jagged1, Jagged2 is expressed in virtually all postnatal neurons but appears only transiently in the developing vasculature [49]. Perhaps unsurprisingly, *Jag2* null mutants die perinatally with severe craniofacial defects, but they do not display vascular defects [53], suggesting that Jagged2 function in the vasculature is redundant.

# 4.4 Notch Signaling in Hematopoiesis

In zebrafish, it has been shown that Notch signaling influences the balance between the endothelia and hematopoietic lineage [54]. In mammals and birds, the situation is more complicated because in these animals, the first wave of hematopoiesis occurs in the yolk sac (termed "primitive hematopoiesis") and only generates primitive erythrocytes and some macrophage progenitors [3, 55]. Hematopoiesis then shifts to intraembryonic sites such as the aorta-gonad mesonephros (AGM) region where hematopoietic stem cells (HSC) bud off from the ventral wall of the dorsal aorta [56–58], giving rise to all hematopoiesis, where endothelial and blood cells may have a common mesodermal precursor, in the AGM the hematopoietic lineage is derived from endothelial cells. Deleting *Notch1* or *Rbpj* in mice severely impairs intra-embryonic hematopoiesis but, interestingly, has no effect on yolk sac hematopoiesis [59, 60]. Furthermore, deletion of *Jag1* (but not *Jag2*) also disrupts the generation of HSCs in the AGM [61], demonstrating that Jag1–Notch1 interactions are required for definitive hematopoiesis. Notch signaling also plays a major role in the immune system, where it is critically involved in T and B cell development and cell fate decisions in the myeloid lineage, which is reviewed elsewhere [62, 63].

## 4.5 Notch Signaling in Vascular Wall Development

As discussed previously, early ventral mesoderm does not only generate hematopoietic and endothelial precursors, but is also a source of vascular smooth muscle cells [64]. Notch signaling has been implicated by several studies in the specification of the vascular smooth muscle lineage. In vivo electroporation of chicken ventral mesoderm cells with constitutively active Notch1 led to a strong bias toward smooth muscle cell differentiation, whereas application of a Notch inhibitor N-[N-(3,5-Diffuorophenacetyl)-L-alanyl]-S-phenylglycine t-butyl ester (DAPT) skewed the balance toward the hematopoietic/vascular lineage [65]. Similarly, constitutively active Notch1 favoured the generation of mural cells from cultured embryonic stem cells [66]. This suggests that Notch signaling pushes mesodermal precursor cells toward the mural cell lineage.

Notch signaling has also been implicated in smooth muscle cell differentiation, which occurs later, once mural precursors have been generated, and when they start to invest primitive endothelial networks. At this stage, bi-directional signaling between mural and endothelial cells mediates vascular remodeling and initiates vascular network maturation. Signaling through Notch3 (among other signaling systems) is part of this cross-talk. This is demonstrated by the abnormal artery differentiation in *Notch3* KO mice (see above).

Similarly, human mutations in *Notch3* cause cerebral arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), which is an autosomal dominant disorder of small arterial vessels in the brain [67].

Jagged1 is a likely ligand for Notch3 signaling during artery differentiation and maturation, as endothelial-specific deletion of *Jag1* in mice causes deficits in vascular smooth muscle cell differentiation [52]. Co-culture experiments have also shown that endothelial cells can induce and activate Notch3 via a positive feedback loop that includes endothelial-derived Jagged1 [68]. The role of this pathway in mural cell differentiation is further supported by the observation that in vitro stimulation of a mesenchymal cell line (C3H10T1/2) with Jagged1 (but not with Dll4) induced multiple smooth muscle marker genes [69]. However, how the role of Notch in mural cell differentiation relates to its earlier function in mural cell generation is not fully understood yet.

### 4.6 Notch Signaling in Vasculogenesis

During early embryogenesis, the dorsal aortae and cardinal veins are formed de novo from migrating and coalescing angioblasts [14]. Although arteries and veins are structurally and functionally distinct, for many years, it was thought that

this distinction was due to differences in blood flow and pressure. However, it is now clear that endothelial cells start to express either arterial or venous markers before the onset of circulation, suggesting a genetic influence [70].

Lineage tracing in zebrafish has shown that individual angioblasts may already be restricted to an arterial or venous fate before the first embryonic vessels are fully established [71]. Angioblasts migrating toward the midline contribute either to the dorsal aorta or the cardinal vein. Exposure of these cells to Vascular endothelial growth factor (Vegf) activates Notch signaling and arterial specification [72]. Loss of Notch signaling leads to reduced arterial markers and ectopic expression of venous markers in the dorsal aorta [73]. In addition, the dorsal aorta fails to form in fish that lack the bHLH transcription factor gridlock (grl), the zebrafish orthologue of the mammalian Hey2 and a downstream target of Notch signaling [71, 74].

Between fish and mammals, the role of Notch signaling in vasculogenesis is remarkably well conserved. Transgenic overexpression of *Dll4* in mouse embryos leads to grossly enlarged dorsal aortae and embryonic lethality before E10.5 [75]. Conversely, mice lacking *Dll4* display reduced dorsal aorta calibers and increased endothelial cell migration away from the dorsal aorta [76]. Similarly, experiments using constitutively active *Notch4* have shown that overactive Notch signaling results in enlarged dorsal aortae and underdeveloped cardinal veins, whereas the opposite (small aortae and enlarged veins) was found in endothelial-specific *Notch1* KO mice [77].

Interestingly, this study also found that the overall number of endothelial cells was unchanged by the manipulation of Notch signaling, suggesting that Notch signaling reciprocally balances the size of the dorsal aortae and cardinal veins by modulating how angioblasts are allocated to either the developing aortae or the veins.

Dll4 and Jag1 are both expressed during early dorsal aorta vasculogenesis [39–41], but it appears that only Dll4 is essential for early arterial cell fate specification. In *Jag1* KO mice, the primitive vascular plexus is initially established but then fails to remodel properly [51], suggesting a non-essential role of Jag1 in vasculogenesis. Dll1 is not expressed in the vasculature until after the first blood vessels are formed and therefore also not required for vasculogenesis [78]. However, Dll1 is needed to stabilize arteries after they have formed and, in comparison to Dll4, seems to act at a later stage of artery differentiation [40, 78].

# 4.7 Notch Signaling in Angiogenesis

After the first blood vessels have been generated, the vascular system is further expanded by angiogenesis (vascular growth from existing vessels). For instance, the developing retinal vasculature in mice is formed by angiogenesis [79]. The mouse retina is avascular at birth and its vasculature develops in the first 3 weeks postnatally. During the first postnatal week, a primary vascular plexus emerges from the optic nerve head and uses a template of retinal astrocytes as a substrate to spread across the inner surface of the retina. Angiogenic sprouting activity occurs at the growing edge, and vascular remodeling and differentiation can be observed more centrally.

Furthermore, the plexus consists of radially alternating and easily identifiable arteries and veins. In the second week, a secondary, deeper plexus sprouts from the superficial, primary network into the retina; and in the third week, vessels fully mature. Because of its stereotypical development and its 2-dimensional topology in the first week, the developing mouse retinal vasculature has become a popular model system to study sprouting angiogenesis [80].

In particular, the so-called tip cells at the sprouting edge can easily be identified in the growing retinal vasculature. These specialized endothelial cells at the leading tip of angiogenic sprouts have pronounced filopodia and respond to angiogenic growth factors such as Vegf by migration. The endothelial cells that follow the tip cells are called "stalk cells" and proliferate in response to Vegf [81]. Endothelial cells can switch rapidly between the tip or stalk state and compete between each other for tip cell status [82]. This competition is mediated by a transcriptional feedback loop that is based on lateral inhibition via Dll4-Notch signaling and regulates the sensitivity of endothelial cells toward Vegf. High levels of Vegf in tip cells promote the expression of Dll4 and Vegfr2. The strong Dll4 expression in tip cells then activates Notch signaling and suppresses Dll4 and Vegfr2 transcription in adjacent stalk cells.

However, if stalk cells are exposed to high Vegf concentrations, they can upregulate Dll4 and Vegfr2 and turn themselves into tip cells [82]. Inhibition of Dll4-Notch signaling by chemical or genetic manipulation in mice or zebrafish disturbs the balance between tip and stalk cells and results in more tip cells and excessive vascular branching [46–48, 83, 84]. Interestingly, there is also a Notch ligand that can inhibit this signaling axis. This is based on the fact that glycosylation of Notch receptors leads to stronger binding of Delta-like ligands versus Jagged ligands. Experiments studying the retinal vasculature of *Jag1* KO mice have shown that Jag1 can compete with Dll4 for receptor binding/activation and therefore act as an endogenous Dll4 antagonist [85]. There are also other signaling pathways that can regulate Notch activity, such as the TGF $\beta$  or Wnt signaling pathways [86, 87]. How these signaling pathways precisely interact with Notch signaling is one of the current challenges in vascular biology.

### 4.8 Conclusions

In summary, Notch signaling plays a critical role at several, distinct stages of vascular development. Because a properly functioning vascular system is strictly required for the survival of embryos once they grow beyond the size of 1–2 mm, complete loss of function mutations in the Notch signaling pathway is therefore often embryonic lethal. This might explain, at least in part, why as yet only two genetic Notch mutations have been characterized in humans, the Alagille Syndrome (*JAG1*) and CADASIL (*NOTCH3*) [67, 88]. The fact that they are both autosomal dominant conditions further highlights the importance of Notch signaling in development. Because Notch signaling is used at multiple times throughout vascular development, it is usually difficult to interpret phenotypes in KO mice. Sophisticated model systems that allow for conditional mutations in a cell- and time-specific manner will therefore play a particularly important role in future research of Notch signaling in the vascular system.

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**Section II** 

Novel Molecular Mediators Regulating Cardiovascular System

# The Therapeutic Potential of Dimethylarginine Dimethylaminohydrolase-Mediated Regulation of Nitric Oxide Synthesis

James Leiper, Francesca Arrigoni, and Bierina Ahmetaj

# 5.1 Introduction

The establishment and progression of cardiovascular disease is associated with endothelial dysfunction. It is widely accepted that nitric oxide production from the vascular endothelium plays a key role in regulation of vascular function in normal health and during disease. Therefore, mechanisms that regulate vascular nitric oxide production have become the focus of significant attention from both vascular biologists and the pharmaceutical industry. The inhibition of nitric oxide synthase activity by endogenously produced competitive inhibitors has recently been linked to reduced nitric oxide synthesis in numerous animal models of disease and several human disease states. In this chapter, we will review the current literature describing these relationships and briefly focus on the pharmacological effects that some of the current therapies for treating these diseases might have on this pathway.

# 5.2 ADMA Synthesis

Asymmetric dimethylarginine (ADMA) is an amino acid that is constitutively produced following the posttranslational modification of Arginine residues. A complex process, this methylation is carried out by protein arginine methytransferases (PRMTs) that can catalyze monomethylation, producing mono-methylated Arginines such as L-NG-monomethyl Arginine (L-NMMA) [1]. The PRMTs themselves exist

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**Fig. 5.1** Structures of L-arginine and the endogenous methylarginines L-NMMA, ADMA, and SDMA. The methylarginines L-NMMA and ADMA are both inhibitors of NOS, whereas SDMA is not

as different isoforms, and are classified according to their enzyme activity (Type I enzymes and Type II enzymes) and substrate specificity. PRMT 1 produces ADMA and PRMT2 the symmetrical isomer, SDMA (Fig. 5.1) [2]. The activity of PRMT enzymes is regulated by many factors including cellular stresses [3–5].

As there is no evidence to suggest that ADMA can be made from the methylation of free arginines [6, 7], the proteolysis of methylated arginines appears to be the sole source of ADMA [8] that correlates with elevated levels of ADMA in induced cardiovascular diseases [3, 5].

The intracellular pool size of ADMA and other monomethylarginines is believed to be controlled predominantly by the hydrolysis of ADMA to citrulline and dimethylamine by dimethylarginine dimethylaminohydrolase (DDAH) [9, 10], while SDMA is left unhydrolyzed [10]. Alternative pathways can also metabolize DMAs into derivatives of alpha-ketoacids (renal dimethyl pyruvate transferase DPT) and acetylated metabolites; however, these low-capacity pathways are minor and not thought to provide any major metabolic changes [11].

The movement of the methylated arginines into and out of the cell is regulated by the cationic amino acid transporter family (CAT) [12]. These transport amino acids, which include ADMA and SDMA, into and out of the cell in a oneto-one exchange for another amino acid via an antiporter mechanism [13]. ADMA has a high affinity for both the CAT type 1 and 2 transporters [12, 14] demonstrating a greater affinity for them than L-arginine [15]; both ADMA and SDMA are considered to have an equal affinity to other members of the CAT transporter family such as the CAT2B isoform [12]. The overall effect of competition between methylated and non-methylated arginine at these transporters is not fully clear; however, at very high, superphysiological, concentrations, methylarginines may prevent the uptake of L-Arginine into the cell, and promote Arginine efflux [16]. Due to the cationic nature of the transporter, the potential across the cell membrane can regulate its activity, both positively and negatively [17]. This can provide a driving force of cationic amino acids into the cells so that by inducing membrane hyperpolarization, vasoactive agonists like Acetylcholine and Bradykinin can increase the driving force of CAT-mediated amino acid entry into the cell [18, 19], potentially altering cellular Arginine and ADMA uptake [17].

Following its export into the plasma, all the free methylated Arginines are ultimately cleared from the body by renal excretion and hepatic metabolism [7].

### 5.3 ADMA-Mediated Regulation of Nitric Oxide Synthesis

ADMA is a potent reversible inhibitor of all three Nitric Oxide Synthase (NOS) isoforms (nNOS, eNOS, iNOS) [20, 21] by behaving as an L-arginine analogue. L-Arginine is the substrate of the Nitric Oxide Synthase (NOS) enzyme family that produces Nitric Oxide (NO) and L-citrulline. The enzymes, eNOS (endothelial), iNOS (inducible), and nNOS (neuronal), coded by different genes [22] were originally classified according to their cellular distribution: in the endothelium, inducibly in most cells, and neuronally but this has since been shown not to be exclusive. The isoforms are classified according to their dependence on intracellular Ca<sup>2+</sup> [23], duration of action, and the fact that iNOS is inducible and nNOS and eNOS are constitutively produced [24, 25].

Optimal NOS activity requires the presence of a number of cofactors including NADPH and BH4, substrate L-Arginine, and, depending on the isoform, Ca<sup>2+</sup>. NO diffuses from the cell of origin into the target cells. NO reversibly binds to the heme group in soluble guanylate cyclase to form nitrosyl complexes in the target tissue that leads to cGMP production [26]. cGMP in turn activates Protein Kinase G (PKG) [27] that in the smooth muscle lowers intracellular Ca<sup>2+</sup>, resulting in the dephosphorylation of myosin light chains causing a decrease in vascular tone. The actions of cGMP are terminated upon hydrolysis by a family of phosphodiesterases or prolonged pharmacologically by phosphodiesterase inhibitors [28].

When produced in large enough quantities, such as following the induction of iNOS, NO can feedback negatively to inhibit NOS activity by s-nitrosylating the enzyme [29, 30].

Other end products of NOS activity include nitrate and nitrite that can be reduced to NO, a reactive oxygen species, under conditions of low oxygen tension. If it reacts with superoxide, peroxynitrite (ONOO) forms, leading to cellular damage and death [31]. Other actions of peroxynitrite that will affect NO production are thought to occur indirectly through tyrosine nitration of the CAT transporters [32] that may lead to increases in intracellular ADMA and reductions in L-arginine [33].

As a result of its actions, Nitric Oxide (NO) is involved in a wide variety of regulatory mechanisms that in the cardiovascular system include: the maintenance of vascular tone, anti-thrombotic effects, control of smooth muscle cell proliferation, leukocyte adhesion, endothelial cell proliferation, motility and survival [34–37], the
promotion and expression of VEGF and pro-angiogenic factors [37, 38], and the inhibition of anti-angiogenic factors [34].

Consequently, a reduction in NO bioavailability in vivo and in vitro results in numerous alterations in vascular function. The endothelial dysfunction that is directly linked to a decrease in the production of NO from eNOS is a risk factor associated with atherogenesis.

All NOS isoforms are inhibited by ADMA [20, 21, 39, 40] with IC<sub>50</sub> values ranging from 1 to 10  $\mu$ m [41] depending on the prevailing substrate concentration. Inhibition of eNOS by methylated Arginine analogues has been comprehensively measured by Cardounel and colleagues [15]. For endothelial NOS, the K<sub>m</sub> for eNOS = 3.14  $\mu$ mol/l. The Ki for eNOS by ADMA is 0.9  $\mu$ mol/l and by L-NMMA is 1.1  $\mu$ mol/l. Under normal physiological conditions, these methylated arginine levels inhibit only 10% of eNOS activity [15].

Under pathophysiological conditions with plasma concentrations of ADMA increasing threefold to ninefold, cellular NO output can be inhibited by 30–70% [7, 42, 43]. This effect may be amplified by the action of CAT transporters that are able to concentrate methylarginines by up to 10× more inside than outside the cell. Some of these transporters have a higher affinity for methylarginines than arginine and would therefore tend to increase the intracellular methylarginine:arginine ratio [15]. Thus, small changes in plasma levels of ADMA can result in large changes intracellularly [14].

Other effects of increasing intracellular ADMA levels is the uncoupling of eNOS, which leads to superoxide production and subsequent increases in oxidative stress [44, 45] that underlie the pathologies of many cardiovascular diseases [44, 46, 47].

In healthy humans, the plasma levels of ADMA range from 0.35 to 0.7  $\mu$ mol/l [17, 20, 21, 48]. These levels are due to the PRMT activity, hydrolysis by DDAH, and removal from the plasma by the kidneys [49].

The selective nature of the metabolism of ADMA by DDAH means that ADMA/ SDMA ratios effectively demonstrate DDAH metabolism since the CAT transporters are not selective for DMAs. Consequently, SDMA levels are determined by PRMT activity and renal clearance and may therefore be a useful marker of renal function [50]. Indeed, SDMA correlates with creatinine clearance, while ADMA levels do not correlate with glomerular filtration rate [51–53] as a consequence of metabolism by DDAH.

# 5.4 DDAH-Catalyzed ADMA Hydrolysis

In mammals, there are two DDAH isoforms encoded by different genes [54, 55]. While ADMA is ubiquitously expressed in all cells, DDAH is selectively expressed to varying degrees in different organs, cellular and subcellular structures with some similarities to NOS isoforms. DDAH-1 is expressed in the pancreas, forebrain, aorta, peritoneal neutrophils and macrophages [55, 56], and in the liver and kidney at sites of NOS expression [57–59]. Using murine DDAH-1 knockouts, decreased expression of DDAH-1 independent of DDAH-2 can be found in skeletal muscle, lung, brain, and heart [60].

DDAH-2 expression is high in fetal tissue, vascular endothelium (in cytosol), smooth muscle, heart, placenta, spleen, thymus, peripheral leukocytes, lymph nodes, and bone marrow [55]. In the kidney, the selective structural distribution of DDAH includes the proximal tubule [61], macula densa, distal convoluted tubule, the thick ascending limb of the loop of Henle, and the collecting ducts of the cortex and the medulla [61].

DDAH isoforms are highly conserved at the amino acid level particularly in residues important for substrate binding and hydrolysis. Across species, DDAH isoforms are highly conserved with homology in the murine, bovine, and human gene sequences of DDAH-1 (92%) and DDAH-2 (95%).

DDAH catalyzes the metabolism of one molecule of ADMA to one molecule of Dimethylamine and L-Citrulline and does not hydrolyze SDMA [62]. The  $K_m$ for ADMA metabolism by DDAH is 180 µmol/l [62]. Interestingly, recombinantly expressed DDAH-2 has a greater  $K_m$  for L-NMMA of 0.51 mmol/l compared to 0.36 mmol/l for rat DDAH-1 [62].  $K_m$  values for ADMA and L-NMMA have been reported ranging from 69 to 170 µmol/l and 53.6 to 90 µmol/l respectively for native and recombinant DDAH1 [63, 64]. All investigations have demonstrated that the  $K_m$  values for DDAH are greater than intracellular concentrations of ADMA, which suggests that the DDAH enzyme active site is never fully saturated, allowing ADMA metabolism to be proportional to its concentration.

It has been estimated that more than 70% of ADMA can be metabolized by DDAH [65] with global heterozygous deletion of DDAH1 in the mouse increasing ADMA in the plasma, brain, and lung by 20% [60].

There are a wide variety of factors that regulate DDAH activity and expression, some are isoform specific. DDAH can be competitively inhibited by L-Arginine, although the required Ki is relatively high (Ki of 2.5 mM). This causes inhibition of ADMA metabolism in HepG2 liver cells increasing intracellular ADMA levels [66, 67]. This may explain not only the inability of supplemental L-Arginine to improve vascular function but also the adverse effects that have been observed following administration [68].

NO itself also regulates DDAH activity and expression. It is known that excess NO production found following iNOS stimulation often leads to inhibition of activity of constitutively expressed NOS isozymes by s-nitrosylation [29, 30]. NO can also reversibly inhibit recombinant DDAH in vitro and in mammalian DDAH extracts in a similar fashion via s-nitrosylation of cys-249 in the DDAH active site. This occurs after cytokine induced expression of the inducible NOS isoforms [69]. Interestingly, in IL-1 $\beta$ -stimulated smooth muscle cells, the induction of iNOS is associated with increased DDAH activity and expression, causing ADMA levels to decrease [40]. One can assume that any consequence of nitrosylation of the enzyme that occurs with high NO is negligible in this case, and further investigations into the precise mechanisms of DDAH regulation need to be undertaken. One putative mechanism might be via a cGMP-dependent pathway that can increase expression of the DDAH-2 isoform following increases in NO levels [70] maintaining intracellular levels of NO.

Other regulators of DDAH are: estradiol that increases DDAH activity [71] and expression [72]; insulin that increases DDAH activity [73], by inducing SIRT-1, an enzyme associated with the prevention of premature senescence [74]; and all-trans-retinoic acid that can influence angiogenesis and is a transcriptional regulator of DDAH2. All-trans-retinoic acid targets the promoter region of the DDAH-2 gene, which also contains the PPAR/RXR site, [65] and various PPAR ligands have been shown to increase the expression and activity of DDAH [74, 75].

DDAH activity can be downregulated by factors that induce reactive oxygen species as part of their mechanistic actions. These include: CF6, a component of mitochondrial ATP synthase that inhibits phospholipase A2 [76], LPS [77, 78], and TNF  $\alpha$  [73, 77]. Sensitive to oxidation, peroxynitrite, and H<sub>2</sub>O<sub>2</sub> [63], DDAH has been reported by some to be less sensitive to in vitro inactivation by the potent oxidizer H<sub>2</sub>O<sub>2</sub> [64], because the active site may be protected from direct oxidation [79], perhaps because of the high pKa of the active site [64].

# 5.5 ADMA, DDAH, and the Regulation of Vascular Function

Increased plasma ADMA concentrations as a consequence of the regulatory mechanisms described above are linked to numerous vascular diseases alongside new and classical cardiovascular risk factors and are all associated with low NO output and endothelial dysfunction [80–84]. Patients with pro-atherogenic cardiovascular diseases such as hypercholesterolemia, hyperhomocystinemia, and hypertriglyceridemia demonstrate reduced endothelium-dependent flow-mediated vasodilatation in association with elevated plasma ADMA and reduced L-Arginine/ADMA ratios [85–87].

The contribution of DDAH to NO-mediated dilatation has been demonstrated using experimental models in DDAH1<sup>+/-</sup> mice, where in vitro vasorelaxation to Acetylcholine (ACh) and the calcium ionophore is reduced [60]. Using small inhibitory RNA (siRNA) constructs targeted to DDAH-1 and DDAH-2 in rats, Wang and colleagues demonstrated that while DDAH-1 appeared to be responsible for regulating serum levels of ADMA, NO-mediated vasodilatation was regulated primarily through the DDAH-2 isoform [88].

The angiogenic capabilities of endothelial cells are also affected by DDAH, improving following transfection of DDAH-2 by enhancing VEGF mRNA expression [9, 89]. Overexpression of DDAH1 increases neovascularization of tumor cells in vivo [90] and results in improved endothelial regeneration following femoral artery injury in DDAH1 transgenic mice [91].

Conversely, in DDAH1<sup>+/-</sup> mice, with elevated levels of ADMA, endotheliummediated angiogenesis is inhibited [89, 92, 93]. These pro-apoptotic and antiproliferative effects of ADMA are thought to occur via an increase in reactive oxygen species (ROS) and a p38 MAPK pathway in endothelial cells [44] that induces apoptotic responses [94]. Increased levels of ADMA in patients with stable angina have also been shown to be associated with a decrease in myeloid endothelial progenitor cell number [95], suggesting a role for DDAH in vascular repair mechanisms of the endothelium.

# 5.6 Nitric Oxide Synthase–Independent Actions of Methylarginines

Not all actions of L-Arginine analogues are related directly to the activity of NOS and NO production. Other effects of L-Arginine analogues include: inhibition of cytochrome C [96], antagonism of muscarininc ACh receptors [97], impairment of the urea cycle [98], and induction of cytokines [99]. Rats overexpressing DDAH suppress the gene and protein expression of the cytokine TGF- $\beta$  in a rat model of chronic kidney disease [100].

The importance of ADMA in non-NO-related pathology is demonstrated in eNOS<sup>-/-</sup> mice, where following long-term administration of ADMA, coronary vascular lesions are found, typified by medial thickening and a perivascular fibrosis in the coronary microvessels [101, 102]. As this group found no expression of iNOS or nNOS in the thickened microvessels, the lesions occurring as a consequence of ADMA inhibition of other NOS isoforms were ruled out. Indeed, while NOS triple knockout mice are viable, homozygous null mice for DDAH-1 are embryonically lethal [60] supporting the proposition of significant non-NO-dependent effect of ADMA.

Several studies have investigated the NO-independent relationship of ADMA with angiotensin. Angiotensin II is used to artificially induce hypertension and renal injury, and in these cases, ADMA is elevated perhaps as a result of increased PRMT synthesis [5]. The augmented levels of ADMA further upregulate angiotensin-converting enzyme [47, 102] that converts angiotensin I to angiotensin II.

Angiotensin II can however reduce ADMA levels by acting on AT-1 receptors, causing an increase in the mRNA expression of arginases, DDAH-2 [103] and CAT transporter expression and activity in the healthy kidney of angiotensin II hypertensive rats [103, 104]. This feedback system may consequently contribute to the paradoxically stable ADMA levels observed in rat models of angiotensin II hypertension when the kidneys are healthy [5].

# 5.7 ADMA Clearance: The Liver and Kidneys

Free methylarginines are cleared from the plasma by renal excretion and hepatic metabolism [7, 105].

Hepatocytes take up large amounts of particular amino acids from the hepatic circulation that include Arginine and ADMA [57, 58] and regulate the circulating levels of ADMA by expressing high levels of Arginases [57, 58] and DDAH [55]. Consequently, in liver failure, the plasma levels of Arginine, ADMA, SDMA, and other amino acids are elevated [57, 58, 106].

In the kidney, SDMA and ADMA are excreted equally. The kidney is also very sensitive to circulating levels of L-arginine and plays a major role in Arginine metabolism. ADMA can be both generated and metabolized by the kidney as ADMA is taken up from the circulation via CAT transporters [17].

In chronic kidney disease, there is reduced nitric oxide production [107] and increased ADMA and SDMA levels. SDMA levels are associated with high levels of creatinine, a marker of kidney dysfunction [108] and high SDMA levels are suggestive of an increased expression of PRMTs [109].

Relatively small increases in ADMA concentrations that occur in early-stage renal failure are associated with large increases in cardiovascular event rates. Dysfunctional kidneys excrete less ADMA, the severity of the renal disease correlating to increased ADMA concentration and reduced NO bioavailability [110]. High ADMA levels in turn cause a decrease in renal plasma flow contributing to further progression of kidney damage that will raise ADMA to pathophysiological levels [20, 21, 111] and contribute to the progression of cardiovascular dysfunction [107]. Experimentally induced chronic NOS inhibition can result in: systemic and glomerular hypertension; tubulointerstitial injury; proteinuria, glomerular ischemia, and glomerulosclerosis [112]; and chronic renal disease [113]. Consequently, plasma ADMA concentration is a strong independent predictor of disease progression in patients with kidney failure [111, 114] with elevated plasma ADMA strongly associated with mortality in patients with renal failure [84] and an increased morbidity and mortality in renal transplant patients [115]. Interestingly, in end-stage renal disease, the frequency of hemodialysis has very little effect on ADMA levels [116].

# 5.8 Associations Between DDAH/ADMA and Disease

Clearly, ADMA has the potential to exert significant effects on nitric oxide synthesis and DDAH is a key regulator of ADMA levels in vivo (Fig. 5.2). In the following sections, we will review the literature implicating dysregulation of ADMA levels in several major human diseases.

#### 5.8.1 Cardiovascular Disease

The pathologies of most patients with renal disease are characterized by cardiovascular morbidity and mortality due to complications and premature atherosclerosis [117].

Atherosclerosis is the leading cause of death and disability in North America [117], and in 2003, the World Health Organisation (WHO) estimated that approximately 16.7 million people die annually of cardiovascular disease [118].

Atherogenesis proceeds as a result of continuing endothelial dysfunction that is associated with cardiovascular risks. These include: aging, hyperhomocysteinemia, postmenopausal state, smoking, diabetes, hypercholesterolemia, and hypertension



**Fig. 5.2** The DDAH/ADMA/NOS pathway. The methylation of protein incorporated arginine by PRMTs and subsequent proteolysis of arginine methylated proteins leads to a production of the methylarginines ADMA, L-NMMA, and SDMA. ADMA and L-NMMA (but not SDMA) inhibit the enzyme NOS which is essential for the production of NO in the presence of tetrahydrobiopterin (BH<sub>4</sub>), NADPH, and Ca<sup>2+</sup>. NO is converted to nitrite (NO<sub>2</sub><sup>-</sup>) and nitrate (NO<sub>3</sub><sup>-</sup>) and under low oxygen conditions can be converted to the superoxide (SO•) to form the peroxynitrite (ONOO<sup>-</sup>), leading to cellular damage and death and the suppression of DDAH 1 and 2 expression. NO binds to, and activates, soluble guanylate cyclase (sGC) forming cGMP. cGMP may enhance DDAH expression/activity. The methylarginines ADMA and L-NMMA are converted to citrulline and dimethylamine (DMA)

[119] and can be assessed according to the Framingham Risk score [120], although the Framingham Risk currently underestimates event rates of chronic Kidney disease [121, 122].

The relationship between the progression of atherosclerosis and the NO pathway is a close one. Plasma ADMA is elevated in established atherosclerosis [81], peripheral vascular disease [85], and coronary artery disease [66, 67].

Behaving as an independent predictor of cardiovascular disease in patients with coronary artery disease [42, 123], elevated ADMA is associated with what are considered to be classical risk factors for cardiovascular disease that include: hypercholesterolemia [85, 124, 125], raised low-density lipoproteins [77], triglycerides [86], raised C-reactive protein [123], ageing [81], hypertension, pulmonary hyperten-

sion[126], diabetes, hyperlipidemia [124, 127–129], and hyperhomocysteinemia [130, 131]. High levels of homocysteine, which are associated with coronary and peripheral vascular disease [132], result in elevated oxidative stress and increased ADMA levels in both animal [124] and human experiments [133] by directly increasing ADMA accumulation [131, 134] causing endothelial dysfunction [130].

## 5.8.2 Hypertension

Hypertension involves an interaction of multiple underlying mechanisms that include: the renin-angiotensin system [135, 136], oxidative stress [137], and nitric oxide synthesis.

Nitric oxide plays an integral role in the regulation of vascular tone and blood pressure [138, 139], and in both human and animal experiments, there is an increasing body of evidence associating the development of hypertension with NO deficiency. Blood pressure is associated with plasma levels of ADMA in healthy subjects [81] and the infusion of ADMA into healthy subjects will moderately elevate blood pressure, offset by decreases in cardiac output and cardiac dysfunction [127]. In patients with essential hypertension, plasma ADMA has been reported by some groups to be elevated [140–143] and by others to remain unaffected [144, 145].

However, increased ADMA levels in hypertensive patients correspond with impaired flow-mediated vasodilatation [146] and experiments performed ex vivo on resistance vessels taken from patients with essential hypertension demonstrate elevated ADMA levels that correlate with endothelial dysfunction and a reduced NOS activity [147]. Experimentally increased plasma ADMA concentrations have been shown to result in hypertension. Genetic or pharmacological inhibition of ADMA metabolism causes elevated systemic and pulmonary pressures [60], while genetic overexpression of DDAH1 produces the opposite effects.

ADMA may also regulate blood pressure by affecting the kidney excretion of Na<sup>+</sup> ions. Mice lacking eNOS are salt sensitive [148] and the effects of endogenous NOS inhibitors can induce kidney-mediated salt-sensitive hypertension in rats [149].

## 5.8.3 Metabolic Syndrome

Metabolic syndrome is a cluster of the most dangerous risk factors, characterized by obesity, dyslipidemia, hypertension, and insulin resistance. It has reached epidemic proportions globally primarily due to an increased sedentary lifestyle and dietary habits. It is associated with an approximate twofold increased risk of cardiovascular morbidity and mortality in the European population [150]. This increased association is due in part to vascular complications contributing to an increase in cardiovascular risk [151, 152] with impaired NO-mediated vasorelaxation [153].

In rat models of metabolic syndrome, associations with either reduced NO [154] or endothelial dysfunction alongside oxidative stress [155] have been demonstrated.

Hypertension in the rat model of metabolic syndrome used by Roberts and co-workers was associated with NO downregulation and dysfunction of the pathway downstream from NO [156]. Patients with metabolic syndrome show correlations between NO and BMI, systolic blood pressure and triglyceride levels [157], and decreased vascular reactivity to ACh compared to age-matched healthy controls [158].

Decreased NO bioavailability in metabolic syndrome is associated with increased levels of ADMA [159]. Insulin resistance, which is pivotal to this syndrome [160], positively correlates with ADMA levels in nondiabetic, normotensive individuals [159]. Increased ADMA levels are most likely the result of a decrease in DDAH activity that is associated with obesity, hypercholesterolemia, and oxidative stress [161, 162] and an upregulation of PRMT1 expression that has been shown in the presence of low-density lipoprotein or oxidized LDL in cultured endothelial cells [2, 44].

#### 5.8.4 Diabetes

In approximately 70% of all deaths in patients with diabetes, cardiovascular disease is responsible [163, 164]. Insulin signaling pathways in the vascular endothelium share similarities with metabolic insulin signaling pathways in adipose tissue and skeletal muscle [165]. In skeletal muscle, insulin can stimulate an increase in NO production, resulting in increased blood flow [166]. In this situation, increased NO production is the result of eNOS phosphorylation and activation that is downstream of Akt signaling. [167, 168]. When insulin-mediated glucose uptake is defective, it has been suggested that the MAP-kinase pathway can also regulate insulin-dependent NO production [169, 170]. Insulin can also increase arginine bioavailability via improved CAT transport, upregulate eNOS expression and activity in cultured Human Umbilical endothelial cells (HUVEC) [171], and increase DDAH activity [73].

Predictably, in animal models of diabetes [172, 173] and in patients with impaired glucose tolerance [81], insulin resistance [159], and both type 1 and 2 diabetes [174–176], plasma ADMA levels are elevated.

## 5.8.5 Insulin-Resistant Type II Diabetes

Insulin resistance is typically defined as "decreased sensitivity and/or responsiveness to the metabolic actions of insulin that promote glucose disposal" [177]. Type 2 diabetes is strongly linked to the metabolic syndrome and cardiovascular disease [160], and obese patients with insulin resistance have higher plasma ADMA levels than obese patients without insulin resistance [178] with a decline in ADMA plasma levels reported only with weight loss in patients with insulin resistance and not those without insulin resistance [179].

Strong associations between the duration of the disease, smoking, nephropathy, and diabetic retinopathy were significantly associated with ADMA levels in a cohort

of 343 patients with type 2 diabetes [180]. Genetic variations in both DDAH-1 and DDAH-2 genes in this cohort associated with the elevated levels of ADMA [180].

Underlying the acquired insulin resistance present in type 2 diabetes is a degree of glucotoxicity, lipotoxicity, and inflammation which are responsible for the increased levels of oxidative stress and inflammatory molecules which contribute to endothelial dysfunction [181].

Elevation of intracellular glucose levels is associated with an increase in ADMA [182, 183] that is secondary to increased oxidative stress, reduced DDAH activity [3] and eNOS expression [183, 184], and increased PRMT activity [3]. Hyperglycemia has also been shown to downregulate DDAH activity in rat models of critical illness [182], cultured endothelial cells [185], and rat models of type 2 diabetes [172].

Further consequences of high plasma glucose levels and oxidative stress are the production of Advanced End Glycation (AGE) products that are associated with elevated plasma ADMA in both type 2 diabetes [186] and in hypercholesterolemia [187]. One putative mechanism for the action of AGE is via the inhibition of eNOS [184] and/or a decrease in DDAH activity that can attenuate NO-dependent vasore-laxation in rat aortic rings [189].

# 5.9 Pharmacotherapy of ADMA

The importance of ADMA as an independent marker of cardiovascular disease risk [81] and a marker for atherosclerotic change [190] [110] suggests that the outcomes of certain cardiovascular diseases might be improved by pharmacologically manipulating the ADMA/DDAH pathway. Here we discuss some of the more common therapies used in treatment of cardiovascular diseases that have been shown to modulate the activity of the ADMA/DDAH pathway (Table 5.1).

# 5.9.1 ACE and ARB Inhibitors

Numerous studies have shown a link between ADMA and the renin-angiotensin system (RAS). Angiotensin-converting enzyme inhibitors (ACEIs) and angiotensin AT<sub>1</sub> receptor blockers (ARBs) prevent eNOS uncoupling and oxidative stress via inhibitory effects on the activity of free radical–producing enzymes [87, 191, 192]. ACEIs work by inhibiting angiotensin II which increases ROS formation by vascular NADPH oxidase. The production of ROS leads to inactivation of DDAH and also upregulates activity of PRMTs, consequently contributing to increased levels of ADMA.

Delles et al. first demonstrated the link between an activated renin-angiotensin system and the ADMA pathway by showing that (independent of blood pressure lowering effects) the monotherapy or combination therapy of an ACEI and ARB reduced ADMA plasma concentrations in young, mildly hypertensive men [193]. The effects of such treatments were later confirmed by Suda et al., who revealed that vascular lesions and superoxide production in both wild-type and endothelial

Table 5.1 Pharmacological t	reatments and	their effects on ADMA le	evels, CAT/y <sup>+</sup> tr	ansport, L-arginine levels and DDAH activity and/or protein expression
Pharmaceutical reagents	ADMA	CAT/y <sup>+</sup> transport	L-arginine	DDAH activity and/or protein expression
ACEIs and ARBs				
Valsartan	$\rightarrow$	I	I	↑ DDAH 2 expression
Telmirsartan	$\rightarrow$	1	I	↑ DDAH 2 activity and expression via activation of PPAR $\gamma$
				signaling
Eprosartan	$\rightarrow$	I	I	1
Statins + LDLs				
Rosuvastatin	$\rightarrow$	I	Ι	1
Pravastatin	↑/ <del>-</del>	Ι	Ι	↓ Inhibition of DDAH activity
Simvastatin	$\rightarrow$	I	I	↑ DDAH 1 mRNA expression via the knockdown of SREBP2
Atorvastatin	Ι	I	I	1
Probucol	$\rightarrow$			↓ PRMT 1 expression/↑ DDAH activity
Antioxidants				
Kaempferol	$\rightarrow$	I	Ι	↑ DDAH 2 expression
Taurine	$\rightarrow$	I	←	↑ DDAH activity via reduction of lipid peroxidation
Vitamin E	$\rightarrow$	I	I	
Acetylcholine/Bradykinin	$\rightarrow$	¢	←	1
Anti-inflammatory Drugs				
Aspirin/Fenofibrates	$\rightarrow$	I	Ι	$\downarrow$ TNF $\alpha$
GW4046	$\rightarrow$	↑ CAT-1	I	1
Antidiabetics				
Rosiglitazone	↓/-	Ι	Ι	↑ PRMT 1 expression
Pioglitazone [194]	$\rightarrow$	I	I	↑ DDAH 2 expression
Metformin	$\rightarrow$	←	Ι	1
Insulin	$\rightarrow$	←	←	$\uparrow$ DDAH activity when induced by TNF $\alpha$ / Upregulates eNOS
				activity
L-arginine	←	I	←	UDAH activity
Vitamin A	$\rightarrow$	I	I	↑ DDAH 2 mRNA and protein expression

NOS-deficient mice were caused by chronic treatment with ADMA, and treatment by either ACEI or ARBs prevented these changes [102].

In addition, treatment with Telmisartan, an ARB commonly used in the management of hypertension as well as a selective modulator of PPAR-γ, delayed endothelial cell senescence, decreased oxidative stress, and upregulated the activity and protein expression of DDAH II. Importantly, Telmisartan was also shown to decrease the concentration of ADMA in endothelial cells, thereby inducing NO synthesis [74]. Studies comparing Telmisartan to another ACEI (Valsartan) in hypertensive patients with type 2 diabetes and overt nephropathy have shown renoprotection but no significant difference in ADMA levels over a course of 12 months [195].

While a significant number of data indicates the positive effects of ACEIs and ARBs on lowering ADMA, the effects of these agents on PRMT activity and (methyl)-arginine transport remain unclear [196].

#### 5.9.2 Statins

Statins are commonly prescribed for adults with clinical evidence of cardiovascular disease. Different statin types exist and are prescribed on an individual basis according to their difference in ability to reduce cholesterol levels. These Hydroxymethylg-lutaryl Co-enzyme A reductase inhibitors decrease plasma cholesterol but can also inhibit platelet and leukocyte adherence to the endothelium, block proliferation of vascular smooth muscle, and stimulate eNOS expression [197]. They also improve oxidative shear stress by reducing the activity and/or expression of NAD(P) oxidase that leads to a reduction in vascular superoxide production [198].

The suggestion that native or oxidized-LDL may cause ADMA accumulation via increases in PRMT activity or by oxidative inhibition of DDAH activity [2] has meant that the effects exhibited by drugs such as statins might potentially lead to improvement of endothelial dysfunction.

However, studies investigating the effects of statins have shown an improvement in endothelial function in cardiovascular diseases independently of ADMA levels and the L-arginine/ADMA ratio [199]. Young and co-workers showed that a doubleblinded, placebo-controlled crossover study of 40 mg Atorvastatin administered once daily for 6 weeks on patients with non-ischemic left ventricular dysfunction did improve lipid profiles, and endothelium-dependent vasodilatory responses of both the microvascular and macrovascular circulation, however, did not influence ADMA levels [199].

Similarly, a 24-month study in patients with mild-to-moderate Chronic Kidney Disease (CKD) showed that plasma ADMA concentrations, which did not alter over time, were not influenced by Pravastatin, or homocysteine-lowering therapy [200].

Of the major trials involving statins, the treatment of patients with hypercholesterolemia by the administration of Rosuvastatin (10 mg/day for 6 weeks) was the only one shown to decrease plasma ADMA levels significantly. Reduction in ADMA levels and low-density lipoprotein cholesterol corresponded with increases in flowmediated dilatation [162]. Rosuvastatin has also been shown to be potent in lowering plasma cholesterol levels in patients with hypercholesterolemia [201] as well as decreasing vascular endothelial NO production in mice subjected to myocardial ischemia reperfusion injury [202]. Interestingly, recent experiments on cultured endothelial cells have shown that another statin, Simvastatin, decreases ADMA concentration by increasing DDAH1 mRNA expression via an SREBP2-dependent mechanism [203]. Overall, the effects of statins on ADMA levels remain unclear, dependent on the specific Statin prescribed and the type of cardiovascular disease.

# 5.9.3 Antioxidants and DDAH

Cardiovascular disease is linked to inflammation and oxidative stress [137, 204], induced by elevating levels of superoxide anions and peroxynitrite [205, 206] which are known to inhibit DDAH and induce ADMA [161, 162]. Numerous synthetic antioxidants have been shown to reduce the formation of ADMA and prevent a decrease in DDAH activity. Probucol, a potent antioxidant drug which inhibits the oxidation of cholesterol in LDL, significantly reduces levels of ADMA and improves endothelium-dependent relaxation by inhibiting PRMT 1 expression and enhancing the activity of DDAH [44, 207].

Studies on the sulfur-containing semi-essential amino acid Taurine, which has shown to be a potent antioxidant with the potential to inhibit lipid peroxidation and lower production of oxidant free radical [208, 209] significantly decreased ADMA levels in vivo by increasing DDAH activity via the reduction of lipid peroxidation [210].

More recently, Xiao et al. [211] showed that Kaempferol, a naturally occurring flavonoid with antioxidant properties, increased DDAH2 expression, decreased plasma ADMA levels, and increased plasma NO in ApoE<sup>-/-</sup> mice. This effect was accompanied by a significant decrease in ROS production levels [211].

In patients with mild-to-moderate Chronic Kidney Disease (CKD) administration of Vitamin E decreased plasma ADMA concentrations, perhaps as a result of improved DDAH activity [210], but neither Pravastatin nor other antioxidant therapy that included vitamin B6, B12, and folic acid affected ADMA levels [200]. This suggests that not all antioxidant therapies produce the same anti-inhibitory mechanisms for DDAH. The variations of the antioxidant effects on DDAH activity could in part be due to the protection of the active site by oxidized proteins that release zinc ions [212].

# 5.9.4 Antidiabetic Drugs

The rise in obesity in developed countries has led to an increase in the prevalence of associated diseases such as type 2 diabetes and metabolic syndrome. These diseases are closely associated to hypercholesterolemia as well as oxidative stress which lead to increased plasma ADMA levels by reducing DDAH activity [161, 162]. Pharmacological antidiabetic drugs include PPAR- $\gamma$  agonists, sulfonylureas, insulin mimetics, and biguanides.

#### 5.9.5 PPAR Agonists

Thiazolidinediones (TZDs) are PPAR- $\gamma$  agonists which have shown beneficial effects for the glycemic management of type 2 diabetes mellitus. By acting directly on the vascular wall and peripheral tissues, they are thought to improve vascular structure and function, improve flow-mediated dilation, and have antiatherogenic effects among others [213, 214, 215]. Disadvantages in the use of TZDs have been shown to be an increased risk of fractures, particularly in women aged 65 years and over, particularly as individuals with type 2 diabetes are prone to rapid bone loss and the TZDs decrease bone formation; thus, therapy must be tailored appropriately to suit the patient's requirements [216].

Studies of the effects of the TZD Rosiglitazone have shown a variety of effects, with some studies showing positive ADMA-lowering effects by up to 30% in seven insulin-resistant patients with hypertension [159] as well as reduced plasma ADMA levels in patients with metabolic syndrome [217]. However, a recent study in a mouse model of high cardiovascular risk has shown that although Rosiglitazone can prevent carotid remodeling, a subsequent increase in superoxide and ADMA production and oxidative stress impairs endothelial dilatation of carotid arteries in response to ACh [218].

A randomized 6-month study comparing Rosiglitazone with Glyburide, a commonly prescribed sulfonylurea used to treat type 2 diabetes mellitus, showed that compared to Glyburide, Rosiglitazone significantly decreased c-reactive protein, c-peptides, improved arterial flow mediators, and showed trends toward improvements in carotoid artery distension. However, ADMA levels and other markers of oxidative stress remained unchanged in both groups, suggesting that ADMA was not associated with the improvements obtained by Rosiglitazone in this study [219]. This was confirmed by Richer et al. [220] and Mittermayer et al. who showed no effect in ADMA lowering by Rosiligtazone in critically ill patients [220, 221].

#### 5.9.6 Biguanides

Metformin is a biguanide antidiabetic drug which can be transported to cells by the CAT transporter system due to its similar structure to ADMA [222] and unlike other antidiabetic drugs does not cause hypoglycemia. Asagami et al. [223] first looked at the effect of Metformin, either as monotherapy or in combination with sulfonylurea treatment, on ADMA, glucose, and L-Arginine levels in patients with type 2 diabetes. The study revealed that metformin (1–2 g/day for 3 months) decreased plasma ADMA concentrations by 30% in association with improved glycemic control in patients and this occurred regardless of single or combination use. Metformin did not have any effect on L-arginine levels [223]. Several other studies have confirmed this by showing that metformin treatment in women with polycystic ovaries (PCOS) reduced plasma ADMA levels as well as improved hormonal and metabolic parameters [224, 225].

## 5.9.7 Insulin

In 2007, Eid et al. showed that co-stimulation of HUVECs and HCAECs with insulin (10 nM) or adiponectin (20  $\mu$ g/ml) for 48 h inhibited dose-dependent TNF-induced ADMA. A reduction in ADMA was a result of an increase in DDAH activity [73]. A study on young people with type 1 diabetes confirmed these findings by showing that ADMA levels were not affected by acute change in glycemia but were significantly reduced by insulin infusion [226]. Insulin sensitivity was shown to be augmented by a decrease in ADMA and an overexpression of DDAH [227].

## 5.9.8 L-Arginine Supplementation

The supplementation of L-arginine should in theory provide increased substrate for NOS and therefore increase the levels of NO released by cells. In patients with hypertension [228, 229], diabetes [220], and hypercholesterolemia [230, 231], short-term effects of L-arginine infusion do demonstrate improvements in vasodilation and lower levels of ADMA.

However, in 17 human studies on oral L-arginine supplementation, five of them have demonstrated no benefits at all [232].

Two studies by Blum showed that oral L-arginine supplementation (9 g/daily for one month) did not enhance NO synthesis and release in postmenopausal women [233, 234], or improve NO bioavailability in coronary artery disease patients [233, 234]. Chin-Dusting and colleagues [235, 236] measured forearm blood flow and showed that in normal healthy patients, endothelial function was not improved by oral L-arginine supplementation (20 g/day for 28 days) [235], as was the case in patients with heart failure [236] and in some cases was associated with their death [68]. Such results could be explained by the fact that L-arginine supplementation leads to increases in intracellular levels of L-arginine and ADMA and consequently impairs activity of DDAH which is required for the metabolism of ADMA [237].

Increasing evidence associates cardiovascular disease with endothelial dysfunction and dysregulation of the DDAH/ADMA/NO pathway. A number of currently used cardiovascular drugs reduce plasma ADMA concentrations and enhance NO-mediated vascular function. A greater understanding of the regulation of DDAH gene expression and enzyme activity may provide novel therapeutic opportunities for the treatment of cardiovascular diseases.

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# Potassium Channels Regulating the Electrical Activity of the Heart

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# 6.1 Introduction

The potassium conductance in cardiac myocytes governs repolarization during the action potential, sets the resting membrane potential, and responds to hormonal and metabolic changes. Since the 1950s, the use of electrophysiological techniques has led to an appreciation of the large diversity of these currents and the reconstruction of their role in cardiac physiology using mathematical models [1, 2]. The Na<sup>+</sup>\K<sup>+</sup> ATPase is largely responsible for establishing the ionic gradients underlying excitability, but it is the temporally coordinated flux through sodium, calcium, and potassium ion channels that determines the trajectory and properties of the action potential in a myocyte. Ion channels are protein pores in the membrane that allow a high flux of ions down their electrochemical gradients and often show high selectivity between different ions. Cloning efforts revealed the molecular species underlying these proteins in the 1990s. During this time, it also became clear that genetic defects in these proteins were responsible for human cardiac disease. In this chapter, we are going to discuss this interface between human disease and basic potassium channel biology. In particular, we will focus on the molecular pathogenesis of diseases that have been associated with potassium channel defects, and the implications for therapeutics in both hereditary and the commoner nonhereditary cardiac pathology.

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**Fig. 6.1** A schematic of the ventricular cardiac action potential present in man. The fast upstroke seen in *phase 0* is generated by the activation of a sodium current ( $I_{Na}$ ). The following downward deflection/notch, *phase 1*, is then formed by the activation and rapid inactivation of a K<sup>+</sup> current  $I_{lo}$ . After *phase 1*, the action potential enters a plateau phase, early *phase 2*, which is maintained by the entry of Ca<sup>2+</sup> ions through L-type Ca<sup>2+</sup> channels ( $I_{Ca,L}$ ) and a small amount of late sodium current ( $I_{Na,L}$ ). Three K<sup>+</sup> currents,  $I_{Kr}$ ,  $I_{Ks}$ , and  $I_{K1}$ , then act in a concerted fashion to repolarize the heart, *phases 2* and *3*. In *Phase 4*,  $I_{K1}$  and  $I_{KATP}$  act to set the membrane potential. *Blue arrows* indicate an inward flow of ions. *Red arrows* indicate an outward flow of ions

# 6.2 The Human Cardiac Action Potential and Three Repolarizing K<sup>+</sup> Currents

The starting point for discussion is the action potential in human ventricular cardiac myocytes. The initial depolarization is mediated by Na<sup>+</sup> entry via the sodium channel, and the subsequent plateau and repolarization is shaped by Ca2+ entry and outward K<sup>+</sup> currents as illustrated in Fig. 6.1. The action potential waveform actually varies within different regions of the heart and even between the endocardium and epicardium of the same chamber. For example, in the SA (sinoatrial) node, there are several unique currents such as the hyperpolarization-activated cation current responsible for pacemaker depolarization, the G-protein-gated inwardly rectifying K<sup>+</sup> current (GIRK/ $I_{KAch}$ ), and the initial action potential depolarization is mediated by  $Ca^{2+}$  entry with little contribution from sodium currents [3]. In particular, we are going to focus on three K<sup>+</sup> currents responsible for the terminal repolarization of the ventricular cardiac action potential namely  $I_{\kappa r}$ ,  $I_{\kappa s}$ , and  $I_{\kappa 1}$ . In the ventricular myocytes of large mammals, including man, there is a K<sup>+</sup> current that characteristically activates with a delay ("delayed rectifier") and this was originally assumed to be a single current (" $I_{\kappa}$ "). In contrast, in smaller mammals, such as the rat, terminal repolarization is determined by a transient outward K<sup>+</sup> current [4]. The use of E-4031 refined the picture of  $I_{\kappa}$  leading to the pharmacological separation of two currents namely  $I_{Kr}$  and  $I_{Ks}$  [5].  $I_{K1}$  is the classical strong inward rectifier first identified by Weidmann in sheep Purkinje fibers and subsequently in other species [6].

Potassium channels are oligomeric complexes consisting of pore-forming alpha subunits often in complex with beta subunits that can critically alter trafficking and function of the alpha subunit. The alpha subunits of voltage-gated channels ( $K_v$ ) and inwardly rectifying channels ( $K_{ir}$ ) are tetramers while twin pore channels ( $K_{2p}$ ) are dimers [7]. The alpha subunits underlying  $I_{Kr}$  (HERG, Kv11.1) and  $I_{Ks}$  (KCNQ1, KvLQT1, Kv7.1) are members of the voltage-gated family of K<sup>+</sup> channels and have six transmembrane domains. In contrast, the pore-forming subunits of the  $I_{K1}$  are members of the inward rectifier family and have two transmembrane domains.

# 6.2.1 I<sub>кr</sub>

The use of E-4031 allowed the separation of  $I_{K}$  into two components. The drugsensitive component was labeled  $I_{Kr}$  as it activated relatively rapidly compared to the drug-insensitive fraction (see below) [5]. The current is inwardly rectifying, and in contrast to the classical inward rectifiers, this arises from fast inactivation and not block by Mg<sup>2+</sup> or polyamines [8, 9]. HERG was originally cloned from a brain cDNA library but its' significance in cardiac electrophysiology was not truly appreciated until it was linked with the long QT syndrome [10, 11]. The properties of HERG after heterologous expression are similar but not identical to the native  $I_{Kr}$ current [12, 13]. It has been proposed that HERG channels have a beta subunit, KCNE2, in a fashion similar to  $I_{Ks}$  (see below) and that defects in this protein can rarely lead to the long QT syndrome [14]. However, this has been disputed [15] and it is clear that KCNE2 can interact with a number of other ion channels [16–19].

# 6.2.2 I<sub>Ks</sub>

The E-4031-insensitive current has exceptionally slow activation (and deactivation) kinetics and steady-state current amplitude is only achieved after seconds of depolarization [5]. These properties have led to the designation of  $I_{K^uslow^u}$  abbreviated to  $I_{Ks}$ . However, this behavior is also physiologically important as it means that it is important late in repolarization and the current progressively accumulates during increases in heart rate as deactivation is incomplete.

 $I_{ks}$  is composed of the pore-forming KCNQ1 and the auxiliary subunit KCNE1 [20, 21].  $I_{ks}$  is thought to be a complex of four alpha KCNQ1 subunits and probably two beta KCNE1 proteins [22]. In the absence of coexpression of KCNE1, KCNQ1 expression gives rise to smaller K<sup>+</sup> selective currents that also activate rapidly and inactivate upon prolonged depolarization. When the two subunits are expressed, currents are substantially enhanced compared to those occurring with expression of KCNQ1 alone. Furthermore, the activation and deactivation kinetics are markedly slowed, inactivation is lost, and the steady-state activation curve is shifted rightward to more depolarized potentials [20, 21]. The native current in cardiac myocytes is similar to that occurring after coexpression of the two subunits; however, it is also possible that there is some KCNQ1 that is not complexed with KCNE1. Secondly,

it is known that during adrenergic beta receptor activation, the current is increased. This is important as increased Ca<sup>2+</sup> entry through L-type Ca<sup>2+</sup> channels would otherwise prolong the action potential duration during sympathetic activation. The underlying molecular mechanism by which this occurs is also unusual. The activation is mediated through protein kinase A but involves an anchoring protein known as yotiao [23]. This occurs both through direct channel phosphorylation by PKA which is dependent on the A-kinase anchoring abilities of yotiao but also seems to involve a direct effect of PKA phosphorylated yotiao on channel function [24].

# 6.2.3 I<sub>K1</sub>

 $I_{K1}$  in ventricular myocytes has the biophysical properties of a classical strong inward rectifier namely that inward currents are more prominent than outward ones and the rectification properties are dependent on the membrane potential and potassium reversal potential. The isolation of the first member of the Kir2.0 family of inward rectifier (Kir2.1) was achieved using expression cloning [25]. Using homology approaches, the family now has six members [26, 27]. The exact isoforms and nature of the current in the heart are controversial. There is no dispute that Kir2.1 is of central importance in most species. For example, in the mouse, global genetic deletion of Kir2.1 leads to a complete loss of the current in ventricular myocytes [28]. Furthermore, genetic defects in the gene (KCNJ2) lead to Andersen–Tawil syndrome in man: a component of which is a prolonged QT interval (see below) [29–31]. However, a case has been made for a component of  $I_{K1}$  being constituted by Kir2.2, Kir2.3, Kir2.4, and heteromultimers of these isoforms with Kir2.1 [32, 33]. It is possible there are species differences and developmental changes.

# 6.3 K<sup>+</sup> Current Channelopathies Affecting the Heart

The main channelopathies affecting the heart involve the molecular counterparts underlying  $I_{\kappa r}$ ,  $I_{\kappa s}$ , and  $I_{\kappa 1}$  and proteins that regulate these currents.

#### 6.3.1 Long QT Syndrome

Long QT syndrome is characterized by prolongation of the rate-corrected QT interval on the ECG and this predisposes the individual to torsade-de-pointes (TdP) and subsequent sudden arrhythmic death due to ventricular fibrillation. The commonest correction is Bazett's  $(QTc=QT/(R-R))^{0.5}$  but other corrections have been proposed. Probably the most accurate approach in a research setting is to examine the behavior of QT interval with heart rate on a beat-by-beat basis and compare this to normal individuals. It is also worth appreciating that it may not be the QT interval per se that is important. It is not solely the increase in action potential duration that is proarrhythmic and in fact all other things being equal this may well be antiarrhythmic [34–36]. Instead the proarrhythmic potential depends on three other factors: (1) the spatial dispersion of the corrected QT interval, (2) that early repolarization is delayed leading to an action potential with a more triangular shape, and (3) that the action potential duration becomes unstable with varying heart rates predisposing to ventricular alternans [37]. Two clinical syndromes are distinguished in the hereditary disease. In the Romano–Ward syndrome (RWS), inheritance occurs in an autosomal-dominant pattern, while in the rarer autosomal-recessive Jervell and Lange-Nielsen syndrome (JLNS), there is profound hearing loss in addition to the prolonged QT interval and predisposition to sudden death [38, 39]. Numerous genetic studies have shown that approximately 90% of hereditary diseases are due to defects in K<sup>+</sup> channel alpha subunits in KCNQ1 (LQT1) and HERG (LQT2) [40].

A variety of mutations have been identified in KCNQ1 in LQT1. These are widely distributed throughout the protein with some evidence that mutations might cluster in the transmembrane and pore regions [40]. This is not surprising as these regions are responsible for the voltage sensor and the pore architecture. Much more rarely, the beta subunit, KCNE1, is affected in LQT5 [41, 42]. Mutations in KCNQ1 and KCNE1 can result in both RWS and JLNS. In an analogous fashion, mutations in HERG underlie LOT2 and the mutations are similarly widely distributed throughout the coding sequence. It has been proposed that mutations in KCNE2 underlie LOT6, and this subunit is a potential beta subunit of HERG. This interaction is however still controversial, and it is clear that the KCNE subunits are promiscuous in interacting with a number of K<sup>+</sup> and other channels (see above). Both missense and nonsense mutations can occur in the coding sequence and other genetic mechanisms can also be operative (see below). A mutation has also been identified in yotiao in one patient and the mutant A-kinase anchoring protein fails to mediate normal sympathetic modulation to the  $I_{\kappa_{e}}$  current [43]. And ersen-Tawil syndrome (LQT7) is a rare syndrome characterized by periodic paralysis, cardiac arrhythmia, and dysmorphic features. It has an autosomal-dominant inheritance, and a number of mutations in Kir2.1 have been identified [29–31].

Clinically, the commonest cause of LQTS is the administration of drugs. A whole variety of pharmacophores developed for a wide range of diseases can prolong the QT interval and this has caused a major issue in drug development and post-marketing surveillance [44, 45]. There is considerable debate as to the most appropriate safety screening strategy (see [36]). Intriguingly the major molecular mechanism seems to be block of the HERG K<sup>+</sup> channel linking the acquired and hereditary causes of the disease (see below).

#### 6.3.2 Short QT Syndrome

This is an intriguing syndrome in which the QT interval is dramatically shortened (QTc <320 ms) and there is a predisposition to sudden death. In addition, the ECG shows a virtual absence of the ST segment and tall peaked T-waves [46]. There seems to be some overlap with hereditary atrial fibrillation as these patients are also predisposed to this disease. Mutations that cause short QT syndrome have been identified in HERG, KCNQ1, and Kir2.1 [47–49].

## 6.3.3 Hereditary Atrial Fibrillation

Though rare as a cause of atrial fibrillation, hereditary disease is particularly interesting from a mechanistic point of view. In a number of families, a single gene mutation has been linked with the disease. With regard to the K<sup>+</sup> channels discussed here, mutations that cause atrial fibrillation have been described in KCNQ1, KCNE2, and Kir2.1 [50–52].

# 6.4 Disease Mechanisms

At the simplest level, a number of potential mechanisms might be operative. In the long QT syndrome, the ECG abnormality implies that the normal repolarizing  $K^+$  currents are reduced, leading to an increase in the action potential duration (APD). This could occur because the protein is not transcribed and/or translated effectively, or alternatively a mutant protein is made that interferes with the normal cellular function of the protein. The short QT syndrome and hereditary atrial fibrillation represent the flip side of the coin. Under these circumstances, one would expect an increase in K<sup>+</sup> currents such that the QT interval is shorter and/or the atrial action potential duration and effective refractory period are reduced. In this case, one might envisage a gain-of-function effect in the K<sup>+</sup> channel proteins such that currents were increased under physiological conditions.

## 6.4.1 Genetic Issues

As discussed above, the protein may simply not be made but what type of genetic mechanisms underlies this? Aberrant splicing will interfere with the generation of a mature mRNA. Such mutations occur in about 5–7% of cases [40]. A second and less appreciated mechanism is nonsense-mediated decay [53]. This refers to degradation of mRNA containing a premature stop codon by cellular quality control mechanisms. Both frame-shift and nonsense mutations have the potential to do this and these occur in approximately 10–15% of cases. Recently, there has been a study describing such a mechanism in long QT with HERG mutations (W1001X and R1014X) [54]. It is also worth bearing in mind that compound mutations are relatively common in the long QT syndrome (~8% of probands). In addition, they lead to severe disease and are associated with a poor prognosis [55].

In hereditary LQTS, mutations show variable penetrance [56]. For example, Priori et al. studied nine families and estimated penetrance in these families to be 25% [57]. In view of this low penetrance, it has been suggested that sporadic cases of LQTS, for example, such as those induced by drugs, could in fact be a *forme fruste* of hereditary LQTS [58–60]. It is apparent that drug-induced long QT syndrome only occurs relatively rarely in patients given a particular pharmacophore and might only attract regulatory attention during post-marketing surveillance. In a study of 16 patients with acquired LQTS [61], only 1 patient had an identifiable

mutation in the *HERG* gene. The remaining 15 patients showed no detectable mutations in *KCNQ1*, *KCNE1*, *KCNE2*, and *HERG* genes. Polymorphisms in KCNE2 (T8A) and the sodium channel SCN5A (S1102Y) in African Americans have been associated with a propensity to drug-induced LQTS [59, 60]. Finally, in a more recent study, 20 patients were tested with drug-induced disease and 40% were found to have mutations in long QT-related genes while the ascertainment rate in the hereditary disease was 52% [62]. Therefore, the prevalence of mutations leading to abnormal protein expression or function in the drug-induced syndrome remains an open question.

A related hypothesis is that individuals have a variable degree of cardiac ventricular repolarization reserve [63, 64]. In other words, it is possible that some individuals tolerate a diminution of repolarizing currents without physiological and clinical sequelae. The degree of such reserve may differ among individuals and contribute to the predisposition to drug-induced LQTS. Genome-wide association studies have been used to investigate heritability in long QT. Ten genetic loci were isolated, and some of these were predictable, for example, the K<sup>+</sup> channel and Na<sup>+</sup> channel genes. However, for others, such as the nitric oxide synthase 1 adapter protein, the association was unexpected. Subsequent functional studies revealed a role in action potential repolarization [65–67]. However, there were loci for which the link with cardiac excitability was opaque. For example, one SNP lay in the 3' UTR of RNF207 a ring finger protein of unknown function, another in LITAF which is a DNA-binding protein and another group close to NRDG4/GINS3/CNOT1/SETD6 complex of genes.

## 6.4.2 Protein Function

If a mutant protein is translated, how might it generate pathophysiology? The majority of hereditary LQTS occurs as an autosomal-dominant syndrome (i.e., RWS). It is important to appreciate that in the cases occurring with K<sup>+</sup> channel alpha subunits, a dominant negative mechanism is likely to be operative [68]. As mentioned before, both KCNQ1 and HERG are tetrameric proteins and the dominant negative effect arises most prominently when the presence of a single mutant in a tetramer can inactivate or modify the function of the complex. In contrast, in the autosomalrecessive form of the disease (i.e., JLNS), the heterozygotes are asymptomatic. In JLNS, it is therefore unlikely that dominant negative mechanisms play a role, indicating that a simple loss of function is the predominant mechanism. Our own in vitro studies using heterologous expression largely bear out this generalization [63].

In LQTS, the mutations in the K<sup>+</sup> channel subunits most commonly lead to a loss of function [69, 70]. However, there are mutations that impair channel gating such that repolarizing currents are reduced. For example, in KCNQ1, the steady-state activation may be shifted due to slowing of voltage-dependent activation or an acceleration of deactivation at a given potential [63, 71–73]. Some of these mutations occur in RWS and it is important to consider how a single mutant subunit might influence the behavior of the wild-type subunit in a heteromultimeric complex. In contrast, in the short QT syndrome and hereditary atrial fibrillation, there is a predicted increase in repolarizing current. The V307L mutation in KCNQ1 in the short QT syndrome leads to a pronounced shift in the half maximal activation potential and an acceleration in the activation kinetics [48]. The S140G mutation described in a family with hereditary atrial fibrillation leads to an increase in current with instantaneous activation and deactivation and a linear current–voltage relationship [50].

In Andersen's syndrome, the disease mechanisms have not been as comprehensively investigated though many of the same principles apply [74]. One particularly interesting study correlated mutations in this channelopathy with known residues affecting the binding of phospatidylinositol bisphosphate ( $PIP_2$ ) to the channel [75]. A number of common residues existed and the disease mutants were resistant to the activating actions of  $PIP_2$  addition, potentially explaining the loss of channel function in cell membranes.

# 6.4.3 Cellular Mechanisms

The loss of function in hereditary LQTS was originally ascribed to the presence of non-functional channel complexes at the plasma membrane. However, it soon became apparent that other mechanisms could play a role in LQTS. Of these, the aberrant trafficking of channel complexes appears to play a major role in both LQT1 and LQT2 disease pathogenesis. The various trafficking checkpoints and cellular controls that may be important are illustrated in Fig. 6.2. Defects in the trafficking of HERG and KCNQ1 to the cell surface have been reported for a variety of LQT1 and 2 mutations [76–84]. In fact, in LQT2, it has been suggested that most mutations act to reduce  $I_{kr}$  current density through defects in trafficking [85]. Whether this is also the case for LQT1 is less well established [76, 79, 80, 82, 83].

Of the mutations in HERG or KCNQ1 that cause defective trafficking the vast majority result in retention of the channel protein in endoplasmic reticulum (ER) [77, 79, 82]. In Fig. 6.3, we show a typical example of ER retention of a mutant KCNQ1. In general, it is thought that such mutations act to disrupt protein folding or complex assembly and can be found throughout both channels' structures. However, for HERG, it does appear that when mutations occur in regions that contain a highly ordered structure, e.g.,  $\alpha$ -helices or  $\beta$ -sheets, the dominant cause of loss of function is defective delivery to the plasma membrane [85]. This also appears to be the case for KCNQ1, although the majority of mutations appear to cluster in three regions, the S2–S3 linker, the pore, and the C-terminus [76, 79, 80, 82, 83, 86]. Although the location of mutations that affect trafficking is diverse, specific focus on mutations that occur in certain domains has helped to establish how these domains are involved in channel biogenesis in the secretory pathway. In HERG and KCNQ1, mutations that occur in the C-terminus have been extensively investigated [81, 83, 87–89]. In HERG, two nonsense C-terminal mutations, Q725X and R1014X, result in the formation of truncated proteins. Both proteins traffic abnormally, but only R1014X is able to form a tetrameric complex with wild-type HERG and suppress current in a dominant negative fashion [88]. In addition, it has been shown that the last 147 amino acids of the C-terminus of HERG act



**Fig. 6.2** Processing of normal and mutant  $K^+$  channels in the secretory pathway. (1) Mutations lead to defects in transcription and translation and channel proteins are not synthesized. (2) Mutations lead to aberrant folding of the channel complex. Complexes that are incorrectly folded tend to be retained in the endoplasmic reticulum (*ER*) and are recognized as abnormal by chaperone and ER resident proteins that act to target these complexes to the proteasome for degradation. (3) If the mutant channels manage to pass cellular quality control in the ER, they can still be recognized as abnormal or fail to associate with golgi resident proteins, important for sorting and packaging, and be retranslocated back to the ER or targeted for degradation. (4) Mutations could affect the exocytosis and endocytosis of channel containing vesicles to and from the cell surface. (5) Normally processed channels. **X** = a block in the trafficking pathway

to mask an ER retention motif (RXR) located at position 1005–1007. Intriguingly, the surface delivery of this HERG deletion construct (HERG<sub> $\Delta 147$ </sub>) can be rescued by the coexpression of a 100-amino-acid peptide, as an ER targeted mini-gene, that spans the region containing the ER retention motif [89]. In KCNQ1, the C-terminal mutations, R518X, Q530X, T587M, and R594Q all cause significant ER retention [82, 83]. R518X and Q530X cannot act in a dominant negative manner and it is thought that the loss of the last ~150 amino acids impairs assembly through the removal of a tetramerization domain [63, 81, 82, 90]. A small C-terminal region of KCNQ1 has also been identified, residues 610–620, that is required for efficient trafficking to the cell surface. This region does not contain an ER retention motif, as is seen in HERG, but does provide a structural coiled coil domain that appears critical [91]. A putative ER retention motif (RXR) does however exist in the N-terminus and S2–S3 linker region of KCNQ1, and this motif is important for cell



**Fig. 6.3** An example of ER retention of a mutation in KCNQ1 causing LQT1. The LQT1 mutation E261K disrupts trafficking by acting to promote retention of the channel complex in the endoplasmic reticulum (*ER*). (a) Confocal images of Chinese hamster ovary (CHO)-K1 cells transfected with either wild-type KCNQ1-GFP or the LQT1 mutant E261K-KCNQ1-GFP in the presence of KCNE1 and the ER marker DsRed2-ER. Images are shown for GFP alone, DsRed2-ER alone, and the merged image. Colocalization between GFP and DsRed2-ER appears as yellow. Scale bar indicates 10  $\mu$ m. (b) Mean data showing the proportion of wild-type and mutant channel ER colocalization. Data are presented as means ±SE. \* *P*<0.05 compared with control (KCNQ1-GFP+KCNE1) (analysis made using a one-way ANOVA with Bonferroni post hoc test for multiple comparisons) [82]

surface delivery [86]. The LQT1 mutation, L191P, is located in the middle of this ER retention signal, and although it does not affect channel activation or deactivation kinetics, it does affect surface expression. In KCNQ1, there are two clusters of mutations that cause intracellular retention in the N-terminus, indicating that this region may also be important for trafficking [76]. Indeed, a structural motif has been identified, between residues 106 and 114, which based on structure prediction forms a short helix. Mutations in this region, Y111C and L114P, that may disrupt the structure of this short helix prevent normal trafficking of KCNQ1 and promote intracellular retention of the channel [76].

#### 6.4.3.1 Beta Subunit Related Disease

Both KCNQ1 and perhaps HERG are thought to require the coexpression of  $\beta$ -subunits to reconstitute I<sub>Ks</sub> and I<sub>Kr</sub>: KCNE1 for KCNQ1 (MinK, IsK) and more controversially KCNE2 (MIRP1), for HERG [14, 20, 21]. Mutations in KCNE1 and KCNE2 account for LOT5 and LOT6 respectively. Mutations in KCNE1 act in general to cause a reduction in  $I_{K_{e}}$  current density [92]. Polymorphisms in KCNE2, T8A and Q9E, cause an increase in the sensitivity of HERG channels to druginduced arrhythmia by LOTS-causing drugs [14, 59]. The mechanisms by which mutations/polymorphisms in KCNE2 cause disease are unclear. In comparison, several studies have investigated whether LQT5 mutations cause disease through defective trafficking. In general, these studies highlight that mutations in KCNE1 can promote defective trafficking of the  $I_{K_s}$  complex, for example, the mutations L51H, R98W, and T58P/L59P. However, in our opinion, the effects of defective trafficking in LQT5 do not appear to be as severe or as common as those seen for mutations in HERG or KCNQ1 [93–95]. The role of defective trafficking in LQT5 and LQT6 may also be complicated by the fact that KCNE1 and KCNE2 appear to exhibit promiscuity in alpha subunit interaction (as described above). For example, both subunits have been shown, in vitro, to modulate the biophysical properties of both HERG and KCNQ1 [96].

#### 6.4.3.2 Mechanisms That Underlie the Defects in Trafficking

Mutations in HERG and KCNQ1 can result in trafficking defects but how do they act to reduce surface expression if they do not affect small peptide motifs? Before surface delivery occurs, proteins must first overcome cellular quality control. This occurs in the ER and golgi compartments, and here a large number of proteins can recognize if proteins are correctly folded and assembled (see [97]). Incorrectly folded proteins are targeted for degradation in an effort to prevent the passage of incorrectly folded complexes to the cell surface and/or the formation of toxic aggregates [97]. A number of studies have investigated whether mutant channels interact differentially with cellular quality control systems.

In the early stages of channel complex biogenesis, chaperones, which normally aid and promote the folding of proteins, have been shown to interact abnormally with mutant HERG and KCNQ1 channels. For example, the chaperones Hsp 70 and 90 interact with wild-type HERG and the specific Hsp90 inhibitor geldanamycin inhibits maturation and increases proteasomal degradation of wild-type HERG.
For the HERG mutations, R725W and G601S, the interaction with Hsp70 and Hsp90 is increased and these mutants remain tightly associated in the ER [98]. The Hsp40 type 1 chaperones, DJA1 and DJA2, also modulate HERG degradation and overexpression of both reduces HERG trafficking efficiency. The DJAs reduce HERG protein stability and the overexpression of DJA2 can reduce the partial rescue of trafficking seen for G601S when incubated at 26°C (discussed later) [99]. Another chaperone, FKBP38 (38-kDa FK506-binding protein), promotes HERG trafficking. FKBP38 immunoprecipitates and colocalizes with HERG in the ER and knockdown of FKBP38 causes a reduction of HERG trafficking. Interestingly, the overexpression of FKBP38 can partially rescue the mutant F805C [100].

Whether Hsp40, Hsp70, or Hsp90 plays a role in the trafficking of KCNQ1 or KCNQ1 mutants has not yet been investigated. However, the assembly and function of KCNQ1 is blocked by mutations that disrupt interaction with calmodulin (CaM). CaM is an obligate subunit for many ion channels and appears to act as a type of chaperone as it contributes to the control of channel assembly. CaM orchestrates the Ca<sup>2+</sup>-controlled regulation of channel assembly. The formation of KCNQ1 tetramers requires CaM interaction with the C-terminus and mutations in IQ motifs; S373P (IQ1) and R518X (truncates the channel before IQ2) disrupt interaction of the channel with CaM [101, 102].

Mechanisms that regulate the rate of protein turnover are also altered by the presence of mutations in HERG or KCNQ1. A study by Gong et al. identified that degradation of the HERG mutant, Y611H, is enhanced in comparison to wild-type HERG and that this degradation is inhibited by the proteasomal inhibitors N-acetyl-L-leucyl-L-leucyl-L-norleucinal and lactacystin but not by the lysozyme inhibitor leupeptin. Inhibition of the proteasome also leads to the accumulation of polyubiquitinated HERG channels, indicating that the degradation of HERG is mediated by the cytosolic proteasome in a process that involves mannose trimming, polyubiquitination, and deglycosylation of mutant channels [103]. In a similar fashion, the LOT1 (N-terminal) mutants Y111C, L114P, and P117L are retained in the ER. All three exhibit reduced expression levels compared to wild-type KCNO1 and radiolabeled pulse-chase experiments highlight that the reduced expression is not because of reduced rate of synthesis. Specifically, Y111C is in fact ubiquitinated and degraded in the proteasome more rapidly. The degradation of Y111C is also not dependent on Derlin 1, an ER resident protein implicated in the retrotranslocation of the cystic fibrosis transmembrane conductance regulator (CFTR) from the ER to the cytosol [104].

Mutations that cause defects in trafficking also appear able to disrupt/alter interactions with proteins that are involved in channel trafficking distal to the ER. For example, HERG normally interacts with the golgi resident protein, GM130, that plays a role in the packaging and sorting of specific vesicles. Trafficking-deficient mutations in the C-terminus of HERG, V822M, S818P, and R823W, located in the cyclic-nucleotide-binding domain, disrupt interactions with GM130 [105].

It is also possible that mutations in HERG or KCNQ1 may increase endocytosis (and degradation), reduce recycling, or decrease the rate of exocytosis. However, membrane levels of channel complexes are tightly regulated [106]. Indeed, the membrane density of KCNQ1 is regulated by Nedd4-2. Nedd4/Nedd4-like proteins

bind to and ubiquitylate certain channels that contain a PY motif  $(L/PPxYxx\Phi)$ in their intracellular C-terminus. Overexpression of a catalytically inactive form of Nedd4-2, that is able to antagonize the action of endogenous Nedd4-2, results in an increase of  $I_{\mu_{e}}$  current density in guinea pig cardiomyocytes. In HEK293 cells, the overexpression of Nedd4-2 increases ubiquitylation of KCNQ1 and reduces current density [107]. For HERG, channel density at the membrane appears to be strongly regulated by the concentration of extracellular K<sup>+</sup>. Guo et al. have found that low extracellular K<sup>+</sup> promotes ubiquitination of the HERG channel-enhanced endocytosis and finally increased degradation of the channel [108, 109]. Additionally, the four and a half LIM domain protein 2 (FHL2) interacts with and regulates both  $I_{Kr}$ and I<sub>ve</sub> [110, 111]. Coexpression of FLH2 with HERG increases current density and results in a faster deactivation of the tail current [111]. FHL2 also appears to be able to regulate  $I_{K_s}$  and the expression of an antisense FHL2 construct reduces  $I_{K_s}$  current density [110]. It also appears that signals from the stress-axis can regulate  $I_{\nu_{e}}$  function. The expression of SGK1 (Serum and Glucocorticoid inducible Kinase 1) is regulated by cortisol and in vitro SGK1 stimulates I<sub>Ks</sub>. SGK1 appears to increase I<sub>Ks</sub> current density by phosphorylating PIKfyve which in turn promotes an increase in the exocytosis of KCNQ1/KCNE1 channels to the membrane via a Rab11-dependent pathway [112]. Intriguingly, a gain-of-function mutant in SGK1 is associated with shortening of the QT interval [113].

#### 6.4.3.3 Trafficking and Acquired LQTS

Originally, it was thought that drugs that prolong the APD do so by acting as pore blockers, reducing HERG channel current density. However, a number of the drugs also inhibit the trafficking of HERG. In a thorough study, the ability of 100 compounds to inhibit HERG trafficking, 50 blockers and 50 non-blockers, was screened in a high-throughput system. This study identified that 40% of the HERG blockers studied were also able to inhibit trafficking [114]. Interestingly, some drugs not thought to block HERG directly, such as pentamidine or probucol, are able to affect trafficking without causing a direct block of  $I_{kr}$  function [115, 116]. Importantly, these effects could be missed without screening for pharmacophores that reduce  $I_{kr}$  through this mechanism. It is unclear as to how important these observations might be for drug development, but the implications are disconcerting.

It is surprising that the majority of cases of acquired LQT are due to drug interactions with  $I_{Kr}$  and not due to other repolarizing currents in the heart. The binding site for drugs that functionally block HERG has been identified by mutagenesis and has been modeled computationally. These studies have identified that the high-affinity drug-binding site compromises the amino acids G648, Y652, F656 in the S6 transmembrane domain and residues T623 and V625 of the pore helix [117, 118]. In particular, the antihistamine terfenadine, a drug removed from market due to proarrhythmia, interacts with residues Y652 and F656 [117]. The aromatic residues Y652 and F656 are unique to eag/erg K<sup>+</sup> channels, and this may explain why drugs that block HERG do not in general appear to affect the function of other channels that control APD [117].

#### 6.4.3.4 Pharmacological Rescue of Trafficking Defects

Several methods have been developed for the rescue of trafficking defects in HERG. These methods, discussed in detail below, are varied and involve the use of reduced temperature incubation or nonspecific or specific pharmacological chaperones.

The concept that HERG trafficking could be rescued by incubation at reduced temperature came from the observation that the surface expression of the CFTR mutation  $\Delta$ F508 could be increased by reducing temperature to 26°C [119]. At 37°C, the HERG mutations, N470D, R752W, and G601S, are retained in the ER, but when incubated at 26°C, all are able to fold correctly and traffic normally [78, 120, 121]. Interestingly, once at the membrane, these mutations appear to function normally. It is thought that a reduction in temperature provides more time for correct folding to occur which in turn reduces the level of targeted degradation [78, 120, 121]. We have tried to rescue the trafficking defect for mutations in KCNQ1 by reducing temperature. However, none of the trafficking defects for the mutations tested (R243H, E261D, L273F, R518X, Q530X, 1008delC, or R594Q) could be rescued [82]. A variety of low-molecular-weight compounds, that are believed to act as "nonspecific" chemical chaperones, such as dimethylsulfoxide (DMSO) and glycerol can also rescue trafficking for certain HERG mutants [78, 121]. Whether these agents can promote rescue of trafficking for KCNQ1 mutants has not been determined.

The use of specific pharmacological chaperones to aid/rescue trafficking has been particularly successful for a number of HERG mutants. Specific blockers of HERG channels, such as E-4031, are able to restore trafficking for N470D but not for all HERG mutations, for example, R725W is not rescued by E-4031 [78, 121]. In contrast, the specific  $I_{Ks}$  channel blockers and activators, Chromanol 293B and HMR-1556 respectively, are not able to rescue the trafficking defect seen for the KCNQ1 mutants R243H or E261D [82]. For HERG, the ability of pharmacological chaperones to rescue trafficking of the mutant G601S varies directly with their blocking potency. Ficker et al. have identified a binding site in the hydrophobic inner vestibule of HERG and have established that the ability for rescue was related to hydrophobicity and cationic charge [122]. In addition, they show that the mutants F805C and R823W could not be rescued. These data imply that rescue is domain limited and that mutations that occur in the pore are more readily rescued by poreblocking pharmacological chaperones.

### 6.5 Therapeutic Considerations

For LQT1, drug therapy with beta-blockers is known to be effective; however, there have only been a few attempts to target drug therapy to the underlying channel mutation and/or disease mechanism [70]. The possibilities for mutation-specific therapy are actually quite broad. For LQT2, specific biophysical defects in HERG can be paradoxically overcome by increasing the extracellular K<sup>+</sup> concentration and there is evidence that K<sup>+</sup> supplementation is beneficial [123]. Nonsense mutations might be overcome by agents known to promote readthrough

and one such agent is in use in clinical trials in other diseases [124]. Specific agents in LQT5, such as fenamates and stilbenes, might be efficacious [125]. Finally, gain-of-function mutations in Na<sup>+</sup> channels in LQT3 and in KCNQ1 and HERG in short QT and atrial fibrillation might be managed with agents known to block these channels [126, 127].

Whether the rescue of the function of mutants that are trafficked abnormally is feasible in the clinical situation remains a subject of debate [128]. There are two problems in a clinical setting. The first is that a lot of the techniques used, for example, low temperature, toxic chemicals, and channel-blocking agents cannot be used therapeutically. However, agents that rescue trafficking but do not cause channel block have been identified for HERG. Fexofenadine can rescue channel trafficking for N470D and G601S at concentrations that are ~350 fold lower than those that cause half maximal channel block [129]. In addition, thapsigargin, a sarcoplasmic/ endoplasmic reticulum Ca<sup>2+</sup> ATPase inhibitor, can also rescue the function of G601S without causing channel block [130]. A second practical point is that each mutation responds differently to a selected form of therapy and this means that clinical intervention would have to be mutation specific.

### 6.6 Conclusions

Potassium channels in the heart govern repolarization of the cardiac action potential. It has also become clear that they are involved in human disease and their abnormal function underlies hereditary and acquired disorders of cardiac rhythm. In one of these disorders, the long QT syndrome, abnormal trafficking of the KCNQ1 and HERG proteins, seems to be of major pathophysiological significance.

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# Free Radicals, Oxidative Stress, and Cardiovascular Disease

K. Richard Bruckdorfer

## 7.1 Introduction

The evolution of cardiovascular disease occurs over many decades and has several phases associated with it. It is a process of two parts, one which involves the development of atherosclerotic plaque and the other the formation of thrombi most typically, but not exclusively, in the later stages of the disease. The association of free radicals and oxidative stress with some stages of this process is widely considered to be most relevant to the inflammatory elements of the disease. The principal phases leading to the formation of stable and unstable plaque are outlined in Table 7.1.

The purpose here is to examine the role of free radicals in cardiovascular disease and of antioxidants as prophylactic agents. The following questions will be considered:

Are free radicals always harmful?

What is the evidence that they play a role in the development of atherosclerosis?

Which radicals or reactive species are involved?

Do dietary antioxidants offer an effective means of therapy to prevent oxidation?

# 7.2 Free Radicals in Normal Physiology

There is a widespread assumption that free radicals and non-radical oxidizing species are always damaging to living cells and must always be suppressed. This is far from the truth, as is the common impression that they are of equivalent oxidizing power under all conditions and that they can be suppressed in the same way by all antioxidants.

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Structural and Molecular Biology, Faculty of Life Sciences, University College London, London, UK e-mail: k.bruckdorfer@ucl.ac.uk Table 7.1 Sequence of events in the development of atherosclerotic plaque

Endothelial injury

Recruitment of monocyte/macrophages

Lipid deposition from lipoproteins into macrophages and their transformation into foam cells Formation of a fibrotic plaque over the lipid layers by proliferation of smooth muscle cells in their fibroblastic phenotype

Further evolution to become vulnerable plaques linked to serious clinical events Angiogenesis, calcification, fissuring, and thrombosis

Reactive oxygen species, a term which covers free radical and non-radical oxidants, are produced as by-products of normal metabolic processes. Cells have excellent endogenous antioxidant mechanisms which regulate their reactivity and these species have specific physiological purposes not least in primary defense mechanisms against microorganisms. It is only when their production becomes excessive, as is the case in inflammation, do they contribute to pathologies such as atherosclerosis and other inflammatory conditions. It was perhaps not until the discovery of the enzyme super-oxide dismutase [1], and the realization that substantial amounts of free radicals are produced normally in the body, that this was fully understood.

In normal exercising muscle, free radicals are formed in tandem with increased mitochondrial respiratory activity. This evokes a protective response at gene level. Antioxidant enzymes such as hemoxygenase-1, other chaperone proteins, and antioxidant enzymes are induced to prevent damage to muscle protein [2]. Regular exercise promotes lasting antioxidant protection in response to the greater production of free radicals.

The main free radical produced through metabolic activity is superoxide anion, a by-product of mitochondrial oxidative phosphorylation, and the activity of NADPH oxidase. This has been estimated to be of the order of 1 kg per annum for a healthy individual [3]. Macromolecules can be also be radicalized and this may be an important step in the regulation of the activity of enzymes and other proteins where sulfy-dryl, histidyl, and tyrosyl residues are particularly vulnerable to radicalization. The main product of superoxide anion catabolism is the non-radical oxidant hydrogen peroxide, which is also formed during the metabolism of lysine. The peroxide is believed to have an important physiological role in the relaxation of the free radical nitric oxide, biosynthesized from L-arginine, as an important vasodilator released from the endothelium of larger blood vessels [5]. Furthermore, free radicals have an important role in the normal life cycle of the cell by initiating apoptosis [6].

## 7.3 Discoveries Leading to an Understanding of the Role of LDL Oxidation in the Development of Atherosclerosis

Low-density lipoproteins (LDLs) are implicated in the development of cardiovascular disease, but also have an essential role in normal physiology. They transport much of the cholesterol from its site of biosynthesis in the liver or in the diet to peripheral

tissues, where the sterol is required for the assembly of cell membranes and, in some cases, the formation of steroid hormones and bile salts. LDLs carry not only cholesterol, but dietary polyunsaturated fatty acids required for biosynthesis of longer chain fatty acids and membrane phospholipids and eicosanoids. Polyunsaturated fatty acids are found in the phospholipid and cholesterol ester fractions of LDL in amounts that are disproportionately large compared to the normal dietary intake of polyunsaturated fat. However, their double bonds are susceptible to oxidative attack by free radicals.

LDL transports a high proportion of dietary fat-soluble antioxidants, particularly tocopherols and carotenoids, which are delivered to the periphery. These are normally sufficient to protect the LDL from oxidation. Furthermore, water-soluble vitamin C accepts electrons from tocopheryl radicals formed during oxidative attack, thereby suppressing the propagation of fatty acid oxidation. LDLs are readily oxidized in the presence of transition metal ions through the formation of hydroxyl radicals generated in the presence of the traces of hydrogen peroxide (Eq. 7.1). These free radicals attack LDL polyunsaturated fatty acids peroxyl radicals, aldehydes, and other derivatives [7]. The formation of Schiff's bases with the ε-amino groups of lysine residues on apolipoprotein B100 impairs its recognition by LDL receptors. Incubation of LDL with cultured macrophages or endothelial cells leads to similar change in these lipoproteins [8] which become oxidized, more electronegative and are recognized by the scavenger receptors on macrophages SRA-1 and CD36. The macrophages arise in the artery by diapedesis of monocytes and transformation into the phagocytotic form subsequent to endothelial damage by hypercholesterolemia, smoking, or hypertension. The macrophages become foam cells as they engorge with lipid droplets of cholesterol esters derived from oxidatively modified LDL. These macrophage receptors also remove apoptotic cells and cell debris from the tissues as part of the normal senescence and repair process. In the presence of cytotoxic oxidized LDL, macrophage/foam cells cannot leave the atherosclerotic plaque and return the circulation as monocytes. Ultimately cell death ensues and cholesterol is released as cholesterol ester droplets or crystalline nonesterified cholesterol.

Formation of hydroxyl radicals:

$$Fe^{2+} + H_2O_2 \rightarrow OH + OH^- + Fe^{3+}$$
(7.1)

## 7.4 Oxidants in Atherosclerotic Plaque

Attention has been given in recent years to the nature of the reactive species produced by macrophages. It is widely accepted that superoxide anions are not directly responsible for the oxidation of LDL. Hazen and colleagues have shown that myeloperoxidase in activated macrophages leads to the release of hypochlorous acid [9] which is a two-electron oxidant but not a free radical (Eq. 7.2). The enzyme contributes to the primary defense mechanisms against microorganisms. This oxidant chlorinates tyrosine residues on LDL and these are taken into the cells via a scavenger receptor mediated process.

The formation of hypochlorite catalyzed by myeloperoxidase:

$$H_2O_2 + Cl^- + H^+ \rightarrow HOCl + H_2O \tag{7.2}$$

Furthermore, another two-electron oxidant, peroxynitrite, is formed by the action of this enzyme using nitrite ions as the substrate (Eq. 7.3). The heme moiety of myeloperoxidase is essential for this conversion in its higher oxidation state and activates the formation of the nitrogen dioxide radical – a powerful oxidant.

Mechanisms leading to formation of nitrogen dioxide radicals from nitrite catalyzed by myeloperoxidase:

$$MPO - heme (III) + H_2O_2 \rightarrow MPO - heme (IV^*)$$
$$MPO - heme (IV^*) + NO_2^- \rightarrow NO_2 + MPO - heme (IV)$$
(7.3)

The nitrogen dioxide radical nitrates susceptible tyrosyl residues in LDL and other proteins to 3-nitrotyrosine. Peroxynitrite may also be formed more directly by the reaction of nitric oxide and superoxide anion, both of which are produced in large amounts in activated macrophages as part of the primary defense mechanisms against infection (Eq. 7.4). Peroxynitrite readily decomposes at physiological pH to yield nitrogen dioxide radical and hydroxyl radical. The myeloperoxidase activity leaves a fingerprint of chlorinated and nitrated proteins in areas of plaque rich in macrophages. These findings have been extended to show that HDL is also capable of modification by hypochlorite and peroxynitrite [10]. This has profound effects on the ability of this lipoprotein to remove cholesterol from the macrophages through the ABC-A1 receptor and the enzyme phospholipid cholesterol acyltransferase (PCAT) which promotes cholesterol esterification in HDL. These proteins are integral to the reverse cholesterol transport system for the return of cholesterol to the liver and its excretion. Therefore, these oxidants inhibit the removal of cholesterol from plaque and enhance its deposition. Other relevant molecules may be modified by peroxynitrite. For example, nitration of fibrinogen may render this molecule more thrombotic by decreasing the stability of clots and increasing the risk of microthrombi [11]. A pro-thrombotic state is therefore induced by posttranslational modification of fibrinogen. Similarly, plasmin activity is impaired by nitration [12].

The formation of peroxynitrous acid from nitric oxide:

$$NO + O_{2^{--}} \rightarrow ONOO- + H^{+} \rightarrow ONOOH$$
$$ONOOH \rightarrow NO_{2} + OH.$$
(7.4)

## 7.5 Consequences of Lipoprotein Oxidation and Its Effects on Arterial Function

The products of lipoprotein oxidation are important to events than the formation of foam cells because of the formation of a wide range of oxidation products from polyunsaturated lipids. Many of these products are cytotoxic and genotoxic. Lysophosphatidylcholine is a potent detergent that damages the endothelium [13]. Lysophosphatidic acid is an activator of platelets [14] which, in concert with the diminished synthesis of endothelial nitric oxide a platelet inhibitor, is pro-thrombotic. Cholesterol oxides at low concentrations activate genes for chaperones and antioxidant enzymes which are protective for the endothelium, through the nuclear transcription factors LXR and RXR [15], thus providing some protection against the effects of oxidation. However, at higher concentrations, they are cytotoxic. Isoprostanes formed from the oxidation of polyunsaturated fatty acids are potent vasoconstrictors. The elevated plasma concentrations of isoprostanes are excellent markers for lipid oxidation in vivo [16].

### 7.6 Antioxidants and Cardiovascular Disease

Over the last 20 years, epidemiological studies pointed to a link between dietary antioxidants and cardiovascular disease. There was evidence of an independent inverse link between the consumption of fruit and vegetables and mortality from cardiovascular disease (see below). This allowed many to make the assumption that it resulted from the presence of antioxidants in these foods, although there are alternative explanations for such an association.

Esterbauer found that if  $\alpha$ -tocopherol (but not  $\beta$ -carotene) was added exogenously to the LDL, or by oral doses to healthy subjects, these lipoproteins became much more resistant to oxidation [7]. The first endogenous material to become oxidized in the presence of cupric ions is  $\alpha$ -tocopherol before the lipids oxidize. However, the susceptibility of the LDL to oxidation ex vivo was independent of the amount of *endogenous*  $\alpha$ -tocopherol in LDL isolated from the cohort of donors. In the original experiments, the oral dosage of  $\alpha$ -tocopherol was well in excess of the dietary norm. However, smaller amounts of the vitamin also increased resistance to oxidation [17]. Ascorbate also increases the resistance to oxidation: Electrons pass from the tocopherol in the LDL to ascorbate, limiting the oxidation of polyunsaturated fatty acids [18].

Experimental evidence in vitro showed that  $\alpha$ -tocopherol has a number of inhibitory effects on processes which lead to the formation of atherosclerotic plaque, but it was not clear that these were due to its antioxidant function. Effects of  $\alpha$ -tocopherol were even found in healthy individuals on platelet function which was attenuated by the vitamin [17] even at oral doses of 75 i.u. per day, much less than had been used in many trials, but still well above the intake from non-supplemented foods. These findings suggested that antioxidants, at least  $\alpha$ -tocopherol, may have an effect on thrombosis which is a key concomitant to myocardial infarction. These effects were minor compared with the actions of aspirin on platelet function which reduces the risk of infarction by about 20%.

The existence of antibodies to oxidized LDL in the plasma seemed to add supportive evidence for the oxidation hypothesis. The association of the concentration of these antibodies with extent of atherosclerosis in patients with cardiovascular disease was weak [19]. Indeed it has been suggested that the formation of these antibodies may be a protective response since dietary intervention to reduce oxidative stress increased the titer of circulation antibodies [20]. Indeed oral supplements of  $\alpha$ -tocopherol increased the titer of circulating antibodies to oxidized LDL [21]. The autoimmune response to oxidized LDL is also associated with the contribution of bacterially derived antigens and the participation of Toll-like receptors in macrophages of atherosclerotic plaques [22]. Furthermore platelets express CD66 which links their activation to the presence of oxidized LDL in the circulation [23].

## 7.6.1 Epidemiological Studies on Antioxidants and Cardiovascular Disease

The experimental studies and the established inverse relationship between the consumption of fruit and vegetables and cardiovascular disease elicited a number of new studies on patients and populations which, for the most part, seemed to reinforce the central role of antioxidants as protective nutrients.

Coronary Heart Disease rates were known to be higher in areas where fruit and vegetable consumption was lowest [24]. In countries where consumption of fruit and vegetables was high, rates of CHD were lower [25]. Furthermore, vegetarians have lower rates of CHD [26]. The diets of over 75,000 nurses and nearly 39,000 male health professionals were compared showing a 31% reduction in the risk of stroke in the quintile eating the most fruit and vegetables compared with the quintile eating the least [27].

The Lyon Diet Heart Study on M.I. patients found that those who followed a "Mediterranean" diet had a significant reduction in the re-occurrence of myocardial infarction after 4 years [28]. Higher fruit and vegetable intakes lower the cardiovascular disease risk factors, blood cholesterol and blood pressure [29, 30]. These studies were the basis for further studies. More recent evaluations of the benefits of fruit and vegetables reinforce this view, but suggest that the evidence is not always strong [31] and that controlled nutritional prevention studies are scarce [32].

These and other findings led researchers to investigate whether the active factor in the fruit and vegetables could indeed be attributed to their antioxidant content. The MONICA study showed a north-south gradient in cardiovascular disease risk across Europe inverse to the gradient for plasma concentrations of vitamin E. These findings were supported by the results of case-control studies [33, 34]. Further studies demonstrated a lower risk of cardiovascular disease with a higher dietary intake of antioxidant nutrients [35, 36]. The European Prospective Investigation of Cancer (EPIC) study found a relationship between high levels of ascorbate and reduced risk of cardiovascular disease [37].

Prospective studies have investigated the contribution of vitamin supplements. In "The Nurses' Health Study" [35], where women in the highest (fifth) quintile of  $\alpha$ -tocopherol consumption, many used supplements of vitamin E and had a 44% lower risk of CHD compared to those in the lowest quintile of intake of this vitamin. Those in the fourth quintile for dietary intake of vitamin E (mainly dietary vitamin rather than supplements) also had a lower risk (26% lower than the first quintile). In a cohort of men [33], the risk was also lower with higher  $\alpha$ -tocopherol intakes. A total of 34,000 postmenopausal women in the Iowa Women's Health Study showed an inverse association between dietary vitamin E intake and deaths from CHD and stroke [38, 39]: Here vitamin E supplementation was not associated with protection from cardiovascular disease.

Intake of antioxidant flavonoids was shown to be inversely associated with CHD risk in several studies. The Iowa Women's Study found that increased intake of flavonoids was associated with a decreased risk of death from CHD [40]. A recent study from within the Iowa cohort showed a strong inverse association between CHD and intake of some types of catechins.

Selenium is important to the activity of certain antioxidant enzymes, particularly glutathione peroxidase. Patients with MI had low plasma selenium concentrations [41], but not all studies show an inverse relationship between plasma selenium concentrations and cardiovascular disease. Selenium is a micronutrient for which a significant proportion of the population of the UK and other countries has a marginal deficiency [42].

In other studies, the intake of fruit and vegetables has been associated with changes in markers for cardiovascular disease or in measurable physiological changes in arterial function. Many studies have looked at the relationship to these markers and the level of antioxidants in the diet or to measurements in the plasma. Plasma C-reactive protein is used as an index of inflammation, but also has been correlated strongly to the incidence and mortality from cardiovascular disease [43]. CRP plasma levels, in a prospective population study of 3,258 men aged 60–79, were also correlated inversely with plasma ascorbate concentrations and dietary vitamin C, even after adjustment for other confounding factors [44]. Another marker for endothelial dysfunction, the tissue plasminogen activator – 1, was also inversely correlated to these two parameters.

LDL and, to a greater extent and more permanently, oxidized LDL inhibit endothelium-dependent relaxation of arteries, a process mediated by the generation of nitric oxide. Organ bath studies with rabbit aortic rings showed that ascorbate reversed the actions of high concentrations of LDL but not that of oxidized LDL [45] In endothelial cell cultures, increasing concentrations of ascorbate within the physiological range could enhance the synthesis of nitric oxide [46], probably by increasing the biosynthesis of one of the co-factors for NO-synthase, tetrahydrobiopterin. Arterial dilatation, in response to acetylcholine in the human coronary artery, improved endothelial responses with pre-treatment with antioxidants using angiographic procedures. Relaxations of the brachial artery were measured using plethysmography or ultrasound techniques. Large oral doses of vitamin C (2 g) or direct infusion of the vitamin could improve these responses if they had been impaired by atherosclerosis or hypercholesterolemia [47].

### 7.7 Intervention Trials

The stage was set for intervention studies to determine whether antioxidants had an important therapeutic value alongside the statins.

In the last decade, a number of intervention studies have been completed: Many of them very expensive to run. In most cases, the antioxidants used were in quantities many fold greater than those found in any diet and at a level where their action would be considered pharmacological rather than fulfilling any nutritional requirement. There have been both primary and secondary intervention trials, some with a matrix design, so that the effects of single antioxidant, a combination of antioxidants with a statin, or a single antioxidant and fish oils could be tested [48, 49]. With a small number of exceptions where benefit was indicated, the majority of trials showed that antioxidant therapy did not decrease risk of cardiovascular disease. No benefit was demonstrated whether the antioxidants, mainly  $\alpha$ -tocopherol, β-carotene, and ascorbic acid, were used individually or in combination. Indeed some, but not all of the trials, indicated negative effects especially among smokers [50-54]. The assessment of the major studies suggests that positive effects are only seen in patients who were experiencing oxidative stress [55]. Meta-analysis of these studies indicated that there is no real discernible benefit for antioxidant therapy [56].

One study found that  $\alpha$ -tocopherol supplementation suppressed restenosis in surgically induced atherosclerosis [57]. The most recent reviews conclude that, though more work may be required, the future of antioxidants as therapeutic agents is bleak [58, 59]. Despite this, the sale of over-the-counter antioxidants and other dietary supplements remains a multi-billion dollar industry. In the food industry, they are frequently used for the preservation of foods. It is hard for consumers to avoid them.

The MRC/BHF Heart Protection Study was a large trial that examined the effects of a cocktail of antioxidant vitamins over 5 years (600 mg vitamin E, 250 mg vitamin C, and 20 mg  $\beta$ -carotene) or placebo in 20,536 UK adults (aged 40–80) with coronary disease, other occlusive arterial disease, or diabetes mellitus [48]. The supplements increased the blood levels of antioxidant vitamins, but without any significant reduction in mortality from vascular disease or cancer. The protection given by treatment with a cholesterol-lowering statin was evident and contrasted with the ineffectiveness of the antioxidant supplements. The GISSI-Prevenzione trial examined both the effects of vitamin E and dietary fish oils. The latter reduced the risk of death, non-fatal myocardial infarction, or stroke, but vitamin E supplementation (300 mg daily for 3.5 years) did not augment this effect [49].

### 7.8 What Could Be the Explanation?

An analysis of a large cohort of women aged between 60 and 79 years selected for the British Women's Heart and Health Study was performed in which plasma  $\alpha$ -tocopherol and ascorbate concentrations were measured [60]. There was a strong associated with socioeconomic position indicators: the lower the social status, the lower the plasma concentration of these vitamins. Lower socioeconomic status is also strongly related to a higher incidence of cardiovascular disease. Tunstall-Pedoe demonstrated that social deprivation is a factor that is often neglected. [61]. These studies also exposed very low levels of plasma vitamin C in some individuals in the lowest socioeconomic groups [62]. Low levels of vitamin C are associated with smoking which may in turn affect food choice. These issues open the question whether the major intervention trials included only a small proportion of socially deprived individuals. This group may benefit from antioxidant therapy or nutritional advice to increase their plasma antioxidant levels. Low levels of ascorbate were also found in a study of the elderly and associated with an increased risk of cardiovascular disease and other diseases [63]. Genetic mutations which lead to impairment of the intestinal ascorbate cotransporter were found to have a small but significant lowering effect on blood ascorbate levels [64].

Antioxidants are not the sole nutritional factor in a diet rich in fruit and vegetables. An increased intake of these foods will lead to a beneficial decrease in other food components, particularly saturated fats. An increase in dietary fiber lowers blood cholesterol and improves glucose tolerance: Salt intakes are likely to be lower. There would also be an increase in the intake of polyunsaturated fatty acids with a concomitant decrease in LDL cholesterol.

The antioxidant content of the artery wall does not change significantly during the evolution of the atherosclerotic plaque. Only at the most advanced stage of the lesion is a reduction in the amount of  $\alpha$ -tocopherol evident [65]. Plaque lipoproteins contained  $\alpha$ -tocopherol alongside lipid oxidation products. Either the antioxidants do not function or they are radicalized in this environment. Antioxidants become pro-oxidants in the presence of metal ions as indicated above and are cyclically depleted and repleted through these radical forms.

The studies that showed hypochlorite and peroxynitrite were key oxidants in atherosclerosis were published after the main intervention studies had begun. The footprints of these oxidants are found in atherosclerotic plaque (Fig. 7.1) but also in other inflammatory diseases such as rheumatoid arthritis, Alzheimer's disease, and diabetes. The nitration and chlorination of proteins arises by the action of the enzyme myeloperoxidase in macrophages [9]. Serum myeloperoxidase levels have been associated with the future risk of coronary artery disease [66]. There is evidence that  $\gamma$ -tocopherol is a more effective antioxidant against peroxynitrite than  $\alpha$ -tocopherol and that the flavonoid epi-gallocatechin or its gallate is yet more effective. These catechins are found in large amounts in green tea, chocolate, red wine, and fruit such as apples. Glutathione peroxidase, an antioxidant enzyme containing selenium, reduces peroxynitrite [67].



Fig. 7.1 The role of peroxynitrous acid and hypochlorous acid in the oxidation of low-density and high-density lipoproteins and its relevance to the development of atherosclerosis

Under experimental conditions, epi-gallocatechin gallate, at concentrations as low as 2  $\mu$ M, inhibits protein nitration during the activation of blood platelets [68]. Although large amounts of these compounds may be consumed, levels in the plasma are low. The maximum concentration for this compound found in the plasma is 1  $\mu$ M: The intracellular concentrations are unknown. Catechins are metabolized and eliminated in the form of glucuronides: Some of these products may have antioxidant activity. No major intervention studies have been attempted using these compounds, despite the current enthusiasm for them. The biological availability of potential antioxidants is important. A cocktail of these compounds and metabolites may have important collective antioxidant actions.

One of the key roles of the free radical nitric oxide released from the endothelium is to prevent the proliferation of smooth muscle cells and to maintain them in their contractile state, inhibiting differentiation into a fibroblastic phenotype. The fibroblastic phenotype biosynthesizes collagen and is abundant in fibrous plaque. Ascorbate is essential for the biosynthesis of collagen, specifically the hydroxylation of proline. NO has an inhibitory effect on collagen biosynthesis [69] whereas ascorbate opposes the inhibitory action of NO on collagen biosynthesis in skin fibroblasts [70]. These studies have been extended now to show that epi-gallocatechin gallate enhances the inhibitory action of NO. The role of catechins and other polyphenols in prevention of cardiovascular disease has not been established [71].

The upregulation of genes in response to oxidative stress leads to the increased synthesis of protective proteins. These include the enzyme hemoxygenase-1, which catalyzes the formation of the endogenous antioxidant bilirubin and is a chaperone. These actions are mediated through nuclear transcription factors, some of which are sensitive to the reduction/ oxidation status of the cell which can be changed by oxidation stress. Some of these proteins are regulated by NO through its interactions with sulfydryl groups on the transcription factors which are themselves proteins, e.g., NFkB, Nrf-2, and HIF-1. These factors operate through antioxidant response elements on the chromosome near regions where these antioxidant proteins are expressed. Siow and colleagues showed that polyphenols augment gene expression for antioxidant enzymes, chaperones, and increase NO biosynthesis through NFkB and Nrf-2 [72].

Jackson and co-workers [73] investigated the action of antioxidant vitamins on the expression of protective genes following muscular exercise. Changes were observed in the proteins of lymphocytes and skeletal muscle in untrained human subjects with and without supplementation with ascorbate (0.5 g/day for 8 weeks). There was an increase in lymphocyte superoxide dismutase, catalase activity, and the cellular content of HSP60 and HSP70 chaperone proteins in response to a low concentration of hydrogen peroxide, without ascorbate supplementation. After supplementation, the basal activity or content of the cellular proteins was slightly increased, but the cells gave an attenuated response to the peroxide. In muscle post exercise, there was a rise in HSP60 and HSP70 was diminished by supplementation with ascorbate, at least for HSP60.

### 7.9 Conclusions

A survey of the progress over 40 years of research into oxidative stress, free radicals, and the role of dietary antioxidants as therapeutic agents shows that it had its high points and distinctive low points. It is clear that there is more to do to understand the complex effects of dietary antioxidants and how they influence signaling mechanisms that respond to oxidative stress. Not all free radicals and reactive species are suppressed by the same dietary antioxidants. The simple "free radicals bad – antioxidants good" slogan is simply not adequate to comprehend how they may contribute to the lifelong process of atherosclerosis. It is clear that oxidative stress is important to its evolution. However, pharmacological doses of antioxidants do not prevent these pathological changes. It does seem that a diet rich in fruit and vegetables is beneficial and family resources may be better spent on them rather than expensive and ineffective supplements.

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Section III

Clinical Aspects of Cardiovascular Disease

# The Takotsubo (Broken Heart Syndrome)

Lawrence S. Cohen

### 8.1 Introduction

An interesting syndrome was reported from Japan close to 20 years ago [1-5]. It had a varying nomenclature but the name takotsubo syndrome or apical ballooning syndrome was used frequently. More recently, the descriptive name, "broken heart" syndrome has been used. Also recently, the syndrome has been reported in patients from the United States and Europe [6-10].

The syndrome is found predominantly in postmenopausal women. It is sometimes mistaken for an acute myocardial infarction. The patient usually presents with chest pain or extreme weakness, has electrocardiographic changes mimicking an acute myocardial infarction, may have some elevation of cardiac biomarkers, and may present with hypotension or cardiogenic shock. Coronary arteriography reveals normal epicardial coronary arteries. Cardiac supportive therapy is usually successful in getting the patient through the acute event. Takotsubo cardiomyopathy is most often characterized by transient regional contractile dysfunction with hypokinesis or akinesis of the left ventricular apical segments and hyperkinesis of the basal segments. The term "takotsubo" was used by the original Japanese investigators as the left ventriculogram of a patient with the syndrome resembled a takotsubo, or Japanese octopus fishing pot (Fig. 8.1). In Japanese, "takotsubo" means "fishing pot for trapping octopus." These traps have a round bottom with a narrow neck. When

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**Fig. 8.1** A takotsubo or "Japanese fishing pot." These traps have a round bottom with a narrow neck. When the octopus enters the takotsubo, it is trapped

the octopus enters the takotsubo, it is often trapped while the fisherman pulls the device to the surface. The other feature of the syndrome is that it most often is initiated by a severe emotional or psychological life event. These may include violent arguments, domestic abuse, death of a relative, learning of a catastrophic medical event in oneself or a close relative, or financial or gambling losses.

## 8.2 Case History

P.O. is a 68-year-old woman who had no cardiac history until May 2005 when she was 65 years of age. She had a history of surgical removal of uterine fibroids and the resection of a benign breast cyst. She was 10 years postmenopausal and had a lifelong history of Raynaud's phenomenon.

During a routine yearly checkup in April 2005, an electrocardiogram was totally normal. In early May 2005, she had a severely emotional and stressful afternoon at her mother's funeral. She had no chest pain but felt extremely weak and unwell. She was seen by her physician on May 19, 2005, where an electrocardiogram was quite abnormal. It revealed deep coved T waves in I, II, III, Avf, V3-V6. The QTc was 484 ms (Fig. 8.2).

On June 16, 2005, the T wave coving was less and the QTc was 450 ms (Fig. 8.3). On July 7, 2005, the abnormalities were starting to abate. The QTc was 445 ms (Fig. 8.4). By September 22, 2005, the ECG was virtually normal with no T wave abnormalities. The QTc was 412 ms (Fig. 8.5).

### 8.3 Epidemiology and Prevalence

Since first being described, the number of cases reported has increased. It is estimated that up to 2% of patients presenting with an acute coronary syndrome may actually be presenting with the takotsubo syndrome. This number of cases



Fig. 8.2 ECG – May 19, 2005 – Deeply coved T waves. QTc 484 ms



Fig. 8.3 ECG – June 16, 2005 – T wave coving improving. QTc 450 ms



Fig. 8.4 ECG – July 7, 2005 – T wave coving improving. QTc 445 ms



Fig. 8.5 ECG – September 22, 2005 – T waves normal. QTc 412 ms

has been reported both in the United States and in Europe. There is a strong predominance of postmenopausal women. The reasons for this are not clear but as will be discussed later, it is likely that sex hormones exert important influences on the sympathetic neurohumoral axis as well as on coronary vasoreactivity.

## 8.4 Clinical Presentation

Takotsubo cardiomyopathy is characterized by the acute onset of chest pain, dyspnea, and at times syncope. It is predominantly seen in postmenopausal women in their 50s or 60s. There is usually a severe emotional or physical event in the antecedent period leading up to the clinical presentation. News of an unexpected death or other such emotional trauma is common. The patient may be hypotensive and may require circulatory pharmacologic support. Similarly the patient may present with severe dyspnea and at times pulmonary edema. With appropriate hemodynamic support which at times may require an intra-aortic balloon pump, the immediate prognosis is favorable.

## 8.5 The Electrocardiogram

The electrocardiogram may mimic closely that of an acute anterior wall myocardial infarction. There is ST-segment elevation which may evolve into deeply coved T waves after the ST segment approaches baseline. There is usually a prolonged QT (QTc) interval which returns to normal somewhat more quickly then pathologic precordial Q waves if present.

## 8.6 Echocardiogram

The initial left ventricular ejection fraction is most often markedly depressed, at times as low as 20%. The typical contractile pattern demonstrates preserved basal function, moderate-to-severe dysfunction in the mid-ventricle, and apical akinesis or dyskinesis. Within a week's time, the left ventricular ejection fraction is usually improved and the mid-ventricular and apical segments are only mildly hypokinetic.

## 8.7 Cardiac Biomarkers

There is frequently a mild elevation of troponin T or troponin I levels. This elevation is by no means invariable and the biomarkers often remain normal. Similarly creatine kinase or creatine kinase MB levels may be normal or only minimally elevated.

## 8.8 Coronary Angiography and Ventriculography

Coronary angiography usually displays normal epicardial coronary arteries. At times there may be spasm recognized particularly in the left anterior descending coronary artery. The left ventriculogram usually displays typical apical ballooning and hypercontraction of the basal segments.

### 8.9 Pathogenesis

The etiology of the takotsubo syndrome is unclear. The most common explanation is that excessive catecholamine secretion and catecholamine cardiotoxicity are important. In support of this thesis, patients reported by Wittstein et al. had plasma levels of catecholamines (i.e., epinephrine, norepinephrine, and dopamine) on hospital day 1 or 2 two to three times higher than patients with Killip class IV myocardial infarction. Plasma levels of metanephrine and normetanephrine were also increased among patients with stress cardiomyopathy [10]. Further support for the thesis that a massive catecholamine discharge is relevant in this pathogenesis of the "broken heart" syndrome comes from the neurologic literature where patients with subarachnoid hemorrhage have been reported to develop profound electrocardiographic changes characterized by deep symmetrical T wave changes across the anterior precordium [11].

The mechanism underlying the association of catecholamine excess and electrocardiographic changes is not clear. One possibility is that catecholamine excess may lead to epicardial coronary artery spasm. Soufer and colleagues [12] have demonstrated that mental stress is a powerful initiator of a process that activates cerebral and adrenal pathways that lead to increased myocardial oxygen demand and simultaneously leads to coronary and peripheral vasoconstriction or spasm.

An alternative mechanism related to the above may be spasm of the myocardial microvasculature. The coronary microvasculature system is very responsive to sympathetic stimulation and may under periods of stress alter the delivery of oxygen to the myocardial muscle.

The idea of myocardial stunning was enunciated in an early paper addressing the effects of transient ischemia on myocardial contractility. Braunwald and Kloner [13] put forth the idea that transient coronary occlusion with reopening before necrosis occurs could lead to stunning or hibernation of the affected myocardium. With time, often up to a week or two, full function could be achieved. This phenomenon certainly mimics what is seen in women who develop the takotsubo syndrome. Lyon et al hypothesize that takotsubo cardiomyopathy is a form of myocardial stunning but with a different cellular effect than that secondary to myocardial ischemia. They believe that high levels of circulating epinephrine trigger a switch in intracellular signal trafficking in ventricular cardiomyocytes [14].

In addition, the fact that the overwhelming incidence of takotsubo cardiomyopathy occurs in women obviously raises the question of whether estrogen, or the lack thereof, plays a role in the pathogenesis of this syndrome. There is considerable experimental evidence that estrogen lack may also contribute. The fact that most patients with takotsubo cardiomyopathy are postmenopausal women is very suggestive. It has been shown that in postmenopausal women, estrogen supplementation enhances nitric oxide release and attenuates norepinephrine-induced vasoconstriction. The evidence is very strong that postmenopausal women who develop takot-subo cardiomyopathy are estrogen deficient. Further it is clear that the precipitating event causes an increase in norepinephrine and other catecholamines. The postmenopausal estrogen-deficient female may likely develop profound epicardial coronary artery vasoconstriction. The 17-beta-estradiol therapy lessens angina in postmenopausal women with normal coronary arteries [15]. In an experimental rat model, it has been shown that estrogen supplementation partially reversed the cardiac changes brought about by laboratory-induced stress [16].

Therefore patients with takotsubo cardiomyopathy clearly have exaggerated sympathetic activation. It is a hypothesis yet to be proved that the catecholamine excess associated with grief reacts on a coronary artery system primed for spasm and stunning due to estrogen lack.

The weight of evidence points to a multifactorial pathogenesis in patients who develop the takotsubo syndrome. It is akin to a physiologic perfect storm. An extreme emotional event unleashes a catecholamine surge. The postmenopausal estrogen-deficient female is particularly susceptible to the actions of the catecholamine surge. It is likely that a catecholamine-induced combination of vasoconstriction of the epicardial coronary arteries, constriction of the coronary microvasculature, and a direct effect on cardiomyocytes lead to a stunning effect on the left ventricular myocardium. With time, these changes resolve and the syndrome abates. Recognition of this syndrome leads to more rational and effective therapy.

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# Lymphatic Vessels in Health and Disease

9

Elisabetta Weber, Francesca Sozio, Erica Gabbrielli, and Antonella Rossi

What made the long neglected lymphatic vessels an interesting aspect of vascular biology are two important discoveries: a lymphatic-specific growth factor, VEGF-C, and its receptor, VEGFR-3, and an excellent marker, D2-40.

# 9.1 The Discovery of VEGF-C and Its Receptor VEGFR-3

In 1995, the group of Alitalo in Helsinki found a specific receptor: Flt4, subsequently re-named vascular endothelial growth factor receptor-3 (VEGFR-3), which is initially expressed by blood and lymphatic developing vessels and later becomes restricted to lymphatic endothelium [1]. The year later the same group isolated and cloned from human prostatic carcinoma cells the ligand for VEGFR-3: vascular endothelial growth factor-C (VEGF-C), the first growth factor specific for lymphatic vessels [2]. Transgenic mice overexpressing VEGF-C have hyperplastic lymphatic vessels [3]. Defective VEGFR-3 signaling due to missense mutations has been reported in the congenital hereditary form of lymphedema: Milroy's disease [4, 5]. In this disease, lymphatic vessels are absent and lymphedema of the lower extremities is already present at birth and increases with age.

# 9.2 Lymphatic Markers

Research on lymphatic vessels has long been hampered by the difficulty to recognize them in common histological sections particularly when they are collapsed as they very often do. Lymphatic vessels are also easily confused with venules. A number of

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Fig. 9.1 Immunostaining of human dermal lymphatic microvascular endothelial cells in culture with lymphatic markers: (a) LYVE-1, (b) Prox-1, (c) VEGFR-3, (d) D240



**Fig. 9.2** Human lung: lymphatic vessels (*arrows*) stained in black by D240 around an artery

lymphatic markers have been proposed, but they had to be used in combination because a single marker often missed part of the lymphatic vessels present in a given tissue [6]. The most commonly used lymphatic markers besides VEGFR-3 are: Prox-1, the homologue of the Drosophila homeobox gene; Prospero, a master gene in specifying lymphatic fate [7, 8] – it is a nuclear marker; and LYVE-1 [9], the receptor for
hyaluronan, homologue of CD44 for blood vessels. The immunostaining of cultured human lymphatic endothelial cells with these markers is illustrated in Fig. 9.1. But the ideal marker, reliable and strongly expressed in all lymphatic vessels, is D2-40 [10] (Fig. 9.2), a monoclonal antibody that recognizes podoplanin [11]. The role of podoplanin in lymphatic vessel biology is not well understood, but podoplanin knockout mice have defects in lymphatic vessels with congenital lymphedema and dilation of skin and intestinal lymphatic vessels [12].

# 9.3 Development of Lymphatic Vessels

How do lymphatic vessels develop has been the subject of a long debate. A very old theory by Sabin [13] said that lymphatic vessels arise from veins. Recent experimental evidence provided support to this theory: Primitive lymphatic vessels indeed bud from the cardinal vein at embryonic day 9 [14]. Some endothelial cells in the wall of the vein start expressing Prox-1 [7]; this gene determines lymphatic commitment. Prox1 null mice fail to develop any lymphatic vasculature. Prox1expressing cells migrate and form primitive lymph sacs. Sprouting from primitive lymph sacs is made possible by VEGF-C stimulation. Homozygous deletion of VEGF-C in mouse embryos leads to the complete absence of the lymphatic vasculature, whereas heterozygous mice display severe hypoplasia [15]. Maturation of lymphatic vessels is controlled by several different factors including angiopoietins, FOXC2, Ephrin B2, Podoplanin. During maturation, the wall of lymphatic collecting vessels becomes provided with smooth muscle cells and valves are formed. In the absence of the forkhead transcription factor FOXC2, valves are inefficient and lymph flows back leading to a hereditary form of lymphedema with late onset, known as lymphedema-distichiasis because patients also have a double row of eyelashes [16].

# 9.4 Postnatal Lymphangiogenesis

Once lymphatic vessels are formed, several growth factors may promote postnatal lymphangiogenesis acting on receptors present in lymphatic endothelial cells. VEGFR-3 binds not only VEGF-C but also VEGF-D [15]. VEGF-D is dispensable during development but, when exogenously added, it rescues the impaired vascular sprouting in VEGF-C null mice. Lymphatic endothelial cells also have VEGFR-2, which binds VEGF-A. In adult lymphangiogenesis, VEGFR-2 and VEGFR-3 have cooperative and redundant roles of signaling [17]. This has important implications in therapy: Combined inhibition of both receptors may be more efficient in reducing tumor lymphangiogenesis than the inhibition of either receptor alone. Hepatocyte growth factor (HGF) is a novel potent lymphangiogenic factor that promotes lymphatic vessel formation and function independently from VEGFR-3 [18]. HGF receptor may be an interesting new target for inhibiting pathological lymphangiogenesis.

In the cornea, which normally is avascular, during inflammation, new lymphatic vessels are formed [19]. These newly formed lymphatics do not originate from the preexisting ones of the limbus but they rather arise in the center of the cornea due to the transdifferentiation of CD11b-positive macrophages that express lymphatic markers, Prox1, podoplanin, and LYVE-1. Macrophages have also been shown to be in vitro able to form lymphatic capillaries in matrigel.

# 9.5 Lymphatic Vessels and Tumors

The role of lymphatic vessels in tumor spreading has been extensively studied and is beyond the objectives of this chapter. Of particular interest is however the recent report that VEGF-A binding to VEGFR-2 in tumors not only induces angiogenesis but also tumor and sentinel lymph node lymphangiogenesis, promoting lymphatic metastasis. Non-metastatic sentinel lymph nodes have been shown to contain increased numbers of enlarged LYVE-1-positive sinusoids [20], confirming the old seed and soil hypothesis: Tumor cells prepare the soil (the lymph node) where they are going to be seeded during metastatic diffusion.

# 9.6 Lymphatic System Organization

Initial lymphatic vessels arise bluntly in the interstitium where they drain fluids and macromolecules escaped from blood capillaries and venules. Initial lymphatic vessels, improperly known as capillaries, are larger than blood capillaries, with a characteristically tortuous, irregular profile. Their wall is extremely thin, made only by endothelial cells without pericytes. They may contain valves. ECs of initial lymphatic vessels are large, oak-leaf shaped, with overlapping flaps sealed by "buttons" that contain, like the "zippers" of collecting vessels, VE-cadherin and tight junction–associated proteins [21]. Buttons may open and close without disrupting junctional integrity to allow fluid entrance.

From initial lymphatic vessels, lymph flows into larger vessels, provided with valves, precollectors, whose wall has an alternation of thinner tracts made solely by endothelial and thicker tracts in which the endothelium is irregularly surrounded by smooth muscle cells [22, 23]. Precollectors drain into collecting vessels, characterized by larger dimensions and a continuous wrapping of smooth muscle cells. Their course is interrupted by lymph nodes. The largest lymphatic vessels, the thoracic duct and the right lymphatic duct, eventually convey lymph into the large veins at the base of the neck.

Under transmission electron microscopy, lymphatic vessels are characterized by a discontinuous basement membrane, which may be for long tracts absent, and anchoring filaments (Fig. 9.3) which connect the abluminal membrane of endothelial cells with the surrounding extracellular matrix [24].



# 9.7 Anchoring Filaments

Anchoring filaments have long been postulated to favor interstitial fluid drainage by pulling apart interendothelial junctions in edema [25]. They are made of fibrillin [26], a large (approximately 350 kDa) and ancient molecule [27], present even in jellyfish. In those animals that have a circulatory system, fibrillin during development forms a track for the deposition of elastin, the protein that confers elasticity to blood vessels. This is called the "structural" role of fibrillin. Fibrillin also has an "instructive" role due to its capacity to sequester transforming growth factor- $\beta$  (TGF- $\beta$ ) and bone morphogenetic protein complexes in the extracellular matrix [28].

Around skin initial lymphatic vessels, fibrillin microfibrils, establish a connection with elastic fibers forming a fibrillo-elastic apparatus [29] that, under the mechanical solicitations of the surrounding connective tissue, dilates lymphatics favoring lymph formation and then allows the lymphatic to resume the original dimensions.

Fibrillin is produced by several types of cells; it was first found in the cell culture medium of fibroblasts [30], but it is also deposited in the extracellular matrix. We found that cultured bovine lymphatic endothelial cells obtained from the largest lymphatic vessel, the thoracic duct, also produce fibrillin (Fig. 9.4) [31] and the related protein microfibril-associated glycoprotein-1 or MAGP-1 [32].

Based on literature and personal data, we have recently proposed [33] that the role of fibrillin-containing anchoring filaments in lymphatic vessels might be much more sophisticated than previously thought. A schematic diagram is illustrated in

Fig. 9.4 An irregular web of fibrillin microfibrils deposited by cultured lymphatic endothelial cells in the underlying matrix FOCAL ADHESIONS Mechanical signals **Biochemical signals** Fibrili Growth factors ECM αvβ3 integrins Intermediate molecules Cytosol FAK MAPK ERK1/2 Metabolism Permeability Movement Shape Transcription Strong connection Proliferation and cytoskeletal rearrangement Nucleus

Fig. 9.5 Schematic representation of signal transduction at focal adhesions

Fig. 9.5. Briefly, fibrillin contains an RGD (arginine-glycine-aspartic acid) motif capable of binding to integrins at focal adhesions [28]. Focal adhesions are the molecular devices responsible for the transduction of mechanical signals from the extracellular matrix into biochemical signals inside the cytoplasm [34]. They are formed by clusterings of integrins. Since integrins have no enzymatic activity, many

of the signaling functions of focal adhesions rely on the phosphorylation on tyrosine of an associated molecule: focal adhesion kinase (FAK). FAK phosphorylation triggers a cascade of phosphorylations that causes actin and cytoskeletal rearrangement so that cells may strongly connect with the matrix and modify their shape [35]. Molecular cascades triggered by FAK are also directed toward the nucleus. The short duration signals of tyrosine phosphorylation are converted into long-lasting serine-threonine phosphorylations by mitogen-activated protein kinases (MAPK). On MAPK converge not only mechanical stimuli acting on focal adhesions but also biochemical signals acting on receptors, for instance, growth factors contained in serum or in cell culture medium. MAPK isoforms ERK1-(44 kDa) and ERK2-(42 kDa) are phosphorylated, leave the cytoplasm and enter the nucleus [36], where they act on the promoter of genes for transcriptional modulation. Thus, a number of cell activities, including metabolism, proliferation, and permeability, may be modulated [37, 38].

We applied static stretching to bovine thoracic duct segments and lymphatic endothelial cells cultured on elastic membranes and evaluated the expression of ERK1/2 by Western blotting [33]. The stretching of isolated thoracic duct segments and lymphatic endothelial cells cultured on elastic membranes activated the expression of MAPK ERK1/2. ERK1/2 activation occurs also in cells deprived of growth factors and grown with only 0.1% serum. The cells exposed to 20% serum with endothelial cell growth supplement (ECGS) express ERK1/2 independently from mechanical stimulation via the receptorial route of activation of ERK1/2. Signal transduction may thus occur in lymphatic endothelial cells in response to mechanical stimulation of focal adhesions or via receptor activation by growth factors. Lymphatic endothelial cells would respond to these stimuli modifying their permeability. Lymph formation would so be precisely and continuously adapted to functional requirements.

# 9.8 Lymphatic Vessels in SSc Skin

Vascular involvement is frequent in scleroderma, but the role of the lymphatic vasculature is poorly known. Interestingly, systemic sclerosis (SSc) patients have no clinical evidence of lymphedema in spite of the profound alterations of their skin, which might potentially affect lymphatic circulation. In the skin of SSc patients, angiogenesis is insufficient despite severe hypoxia which is a major pro-angiogenic stimulus. VEGF-A is strongly overexpressed in the skin and serum of SSc patients [39], and serum levels of VEGF correlate with the development of fingertip ulcers [40] Prolonged exposure to VEG-A leads however to formation of a chaotic vessel network with megacapillaries and reduced blood flow, resembling the disturbed vessel morphology of SSc patients [41, 42]. Circulating levels of VEGF-C and local expression of its lymphatic receptor VEGFR-3 in the skin have been reported to be also increased in patients with scleroderma [43].

The only report on lymphatic vessels in the skin of SSc patients is a fluorescence microlymphography study by A.J.Leu et al. [44] showing that in SSc, the clinically

**Fig. 9.6** (a) Only one lymphatic vessel (*arrow*) is present in this micrograph of the reticular dermis of a patient affected by SSc. (b) The density of lymphatic vessels in the reticular dermis of patients affected by SSc is significantly lower than in controls (P < 0.05)



affected areas have a pattern of lymphatic microangiopathy, characterized by increased length of the visualized lymphatic capillaries and cutaneous backflow or even the complete absence of stained microlymphatics.

We sought to determine whether lymphatic vessels are affected in SSc [45] postulating that they might be decreased in number as in other fibrotic diseases due to inhibition of lymphangiogenesis by overexpression of TGF- $\beta$ 1 [46, 47] or dilated as in conditions of chronic lymphostasis [48] and in other autoimmune diseases [49, 50]. Forearm skin biopsies of SSc patients (4 with the diffuse and 5 with the limited form) and healthy volunteers were fixed in formalin and embedded in paraffin. Double immunolabeling was performed with the lymphatic marker D2-40 followed by a panendothelial antibody to von Willebrand factor (vWF). Lymphatic and blood vessels were so easily recognized by their different staining, brown and red, respectively. Both in controls and SSc biopsies, the density of lymphatic and blood vessels



in the papillary dermis resulted markedly greater, and their mean area conversely smaller, than in the reticular dermis. In SSc, in the reticular dermis, the density of lymphatic vessels was significantly lower than in controls, and a similar trend (although not reaching statistical significance) was observed in the papillary layer (Fig. 9.6).

Interestingly, periglandular lymphatic vessels were preserved in scleroderma (Fig. 9.7). To assess whether this could be due to local production of lymphangiogenic factors, we stained some sections with a polyclonal antibody to VEGF-C and we found that the epithelial cells of glands were strongly immunoreactive for VEGF-C.

Although the mean outer area was similar in the two groups, in the reticular dermis, the percentage of inner luminal area (Fig. 9.8), which can be considered a sign of dilation, was significantly greater in SSc with respect to controls (p < 0.05). This difference was mainly due to the dilation of periglandular lymphatics. Lymphatics not associated with glands were similar in the two groups.

In conclusion, in SSc lymphatic vessels decrease in number due to diminution of the lymphatic vessels of the reticular dermis not associated with glands. Periglandular



**Fig. 9.8** Percentage of dilation in periglandular and not periglandular lymphatics in SSc and in controls. Periglandular lymphatic vessels only are dilated in SSc

lymphatics are in fact spared in SSc, possibly due to VEGFC produced by the epithelium of glands and dilated, interpretatively as a compensatory mechanism.

# 9.9 Perspectives for the Future

Experimental evidence suggests possible perspectives in therapy: congenital lymphedema might be treated by manipulation of VEGFR-3 signaling [51] or alternatively other lymphangiogenic factors like HGF. Inhibition of VEGFR-3 might be exploited to prevent lymphatic spreading of tumors. Inhibition of VEGFR-2 signaling by a well-known anti-angiogenic drug, Avastin, may also be useful to prevent lymphangiogenesis induced by VEGF-A through VEGFR-2 in regional lymph nodes [17, 20]. Also the opposite is true: tumoral angiogenesis is stimulated also via VEGFR-3. Blockade of this receptor, which is normally restricted to lymphatic endothelium, but is upregulated in tumors, has been shown to suppress angiogenic sprouting in a mouse model [52]. Targeting VEGFR-3 may thus provide additional efficacy for anti-angiogenic therapies in cancer.

As to secondary lymphedema, which is most often caused by surgical ablation of lymph nodes particularly in breast cancer, a new approach has been recently proposed:





Axillary Reverse Mapping [53]. A blue dye is injected dermally or subcutaneously in the arm and reaches the axillary nodes. The resulting blue lymph nodes that drain the upper arm can, in most cases, be preserved except when too close to or coincident with the sentinel lymph node. It has been shown that even when most axillary nodes are metastatic, the blue ones are not. This simple technique has proved safe and effective and, if one considers the burden of a life-long invalidating condition as lymphedema, it seems reasonable that axillary reverse mapping should enter standard surgical procedures as the sentinel lymph node one. Since also collectors are colored in blue, this technique also facilitates performing lymphatico-venous anastomoses [54].

# 9.10 Tissue Engineering of Lymphatic Vessels

Tissue-engineered blood vessels have been successfully implanted in humans, particularly in children with congenital vascular malformations [55]. The tissue-engineered vessel grew with the child with no need of re-intervention. Tissue-engineered vessels can be made with autologous endothelial cells taken from a peripheral vein, expanded in culture, and seeded onto a reabsorbable polymer or with autologous bone marrow cells [56].

Research on tissue engineering of lymphatic vessels is still in its infancy. Due to the fragility of their wall, it is unfeasible that the same approaches that have led to pioneer successful implants of tissue-engineered blood vessels in man may be applied to lymphatics. Basic research is needed to understand the strategies that can be useful for lymphatic vessel tissue engineering. Under this respect, micropatterned surfaces with different geometries based on the alternation of hyaluronan domains that prevents cell adhesion and aminosilanized glass ones that promote it have been proved effective in orienting lymphatic endothelial cell growth [32, 57, 58]. Cells may be induced to align along the desired direction and also actin cytoskeleton is accordingly oriented (Fig. 9.9). Fibrillin deposition is also influenced by the

geometry of the substrate. Being able to condition cell growth, orientation, and metabolic activities may help in designing tissue-engineered vessels capable of adapting to the functional requirements of the environment.

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# Importance of Subtype Selectivity for Endothelin Receptor Antagonists in the Human Vasculature

10

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# 10.1 Endothelin Pathway in the Human Vasculature

The endothelins (ETs) are a family of three endogenous peptides: ET-1, ET-2, and ET-3 that are structurally similar in being comprised of 21 amino acids [1, 2]. In man, ET-2 differs from ET-1 by only two amino acids and both isoforms mediate their action via two G-protein-coupled receptors,  $ET_A$  [3, 4] and  $ET_B$  [5]. In contrast, ET-3 differs by six amino acids, representing more substantial changes, and is the only isoform that can distinguish between the two receptor subtypes, having a similar potency at the  $ET_A$  receptor as ET-1 and ET-2 but much lower affinity for the  $ET_B$  subtype [6, 7]. The deleterious actions of ET are mainly mediated by the  $ET_A$  receptor, whereas  $ET_B$  activation results in many of the beneficial effects of the peptide, frequently acting as a regulatory counterbalance [7].

Two distinct therapeutic strategies have emerged to block the unwanted action of ET in pathophysiological conditions: receptor antagonists [8] and inhibitors of the endothelin-converting enzymes (ECE-1 [9] and ECE-2 [10]), the major synthetic pathway in the human vasculature [11]. Bosentan (Tracleer) was the first ET antagonist to be introduced into the clinic for the treatment of pulmonary arterial hypertension (PAH [12]) and is a mixed  $ET_A/ET_B$  antagonist blocking both receptors. This was followed by ambrisentan (Letairis, Volibris) in 2007, reported to display modest  $ET_A$  selectivity [13], and the more  $ET_A$ -selective antagonist sitaxentan (Thelin)

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A.P. Davenport (⊠) Clinical Pharmacology Unit, University of Cambridge, Centre for Clinical Investigation, Addenbrooke's Hospital, Cambridge, UK e-mail: apd10@medschl.cam.ac.uk [14, 15]. While mixed  $ET_A/ET_B$  and  $ET_A$ -selective antagonists have become established as having therapeutic benefit in PAH [16, 17], the relative merits of the two classes continue to be debated [18–20]. To date both  $ET_A/ET_B$  or modest  $ET_A$ selective antagonists are thought to have little or no efficacy in chronic heart failure and further trials with more ET<sub>A</sub>-selective antagonists are unlikely [21]. More promising clinical uses are in chronic kidney disease where the ET system is increasingly recognized as an important pathway [22-27] and where efficacy has been demonstrated with experimental ET<sub>A</sub>-selective antagonists in acute trials [28]. ET receptors are also emerging as new therapeutic targets in autoimmune disorders of the vasculature such as scleroderma [29] and remarkably in cancer [30-32], particularly the treatment of refractory cancer of the prostrate by the ET, -selective antagonist ZD4054 [32]. This is notably the first G-protein-coupled receptor in Family A to be targeted for the treatment of cancer. Inhibitors of ECE are represented by SLV-306 (Daglutril). This compound is an orally active mixed enzyme inhibitor of both ECE and neutral endopeptidase (NEP) and a Phase II trial has been completed in 2010 by Solvay for the treatment of essential hypertension and congestive heart failure [33–35]. It is not yet clear whether lowering levels of endogenous ET changes the ratio of ET-1:ET-3 which could then impact on the relative activation of the two receptor subtypes. Significantly, ET antagonists represent a spectrum of selectivity that has the potential to be exploited for extending the therapeutic targets for this class of compound. The objective of this review is to consider the importance of subtype selectivity for ET receptor antagonists in the human vasculature.

# 10.1.1 ET-1

ET-1 is the most abundant isoform in the human cardiovascular system and is one of the most powerful constrictors of human vessels discovered [7]. ET-1 plays a major physiological role in regulating vascular function in most, if not all, organs systems including heart, kidney, lungs, and liver. Overproduction in pathophysiological conditions may lead to vasospasm, particularly where there is endothelial cell dysfunction and associated loss of opposing vasodilators such as nitric oxide, prostacyclin, and endothelium-derived hyperpolarizing factor. The peptide is thought to stimulate proliferation in multiple cell types, including vascular smooth muscle cells, as well as contributing to fibrosis and inflammation – processes associated with vascular remodeling.

# 10.1.2 Dual Synthetic Pathway in Endothelial Cells and Interaction with ET<sub>A</sub> and ET<sub>B</sub> Receptors

The primary source of ET-1 within vessels is the endothelial cells although other cell types that synthesize the peptide could also modulate vascular reactivity. These include perivascular neurons in the periphery, perivascular astrocytes in the CNS, and, under pathophysiological conditions such as atherosclerosis, macrophages and

monocytes. ET is synthesized in a three-step process. Initially pre-pro-ET-1 is cleaved by a signal peptidase to proET-1, which is in turn cleaved by a furin enzyme to an inactive precursor big ET-1 which is subsequently transformed to the mature, biologically active peptide by the action of the pathway-specific ECE-1. ECE-1 is present within the small secretory vesicles of the constitutive pathway from where ET-1 is continuously released to maintain normal vascular tone. A second enzyme, ECE-2, is also present within the vesicles and functions at an acidic pH [6] that may occur under pathophysiological conditions associated with ischemia. Unusually for vasoactive peptides, ET-1 is also synthesized by ECE-1 and stored in specialized Weibel-Palade bodies within endothelial cells until released following an external physiological or pathophysiological stimulus (the regulated pathway) to produce further vasoconstriction [11, 36].

# 10.1.3 ET Receptors and Vasoconstriction

In the human vasculature, ET-1, released by these two distinct exocytotic pathways, can potentially interact with the  $ET_A$  receptors that predominate on the underlying smooth muscle.  $ET_A$  receptors are widely expressed on vascular smooth muscle cells throughout the human cardiovascular system and mediate vasoconstriction. Under pathophysiological conditions,  $ET_A$  activation may contribute to proliferation, apoptosis, and fibrosis within the vessel wall. In some, but not all, human vessels, a small population of  $ET_B$  receptors (usually <15%) are present and these may also mediate constriction [37, 38]. Haynes and Webb [39] were the first to report that infusion of an  $ET_A$ -selective peptide antagonist, BQ-123, into healthy volunteers via the brachial artery using venous occlusion plethysmography caused progressive vasodilatation. This is consistent with ET-1 being continuously released by the constitutive pathway to cause vasoconstriction and is unusual as antagonists of other vasoconstrictors, such as angiotensin II, do not alter blood flow in normotensive individuals.

# 10.1.4 ET<sub>R</sub> Receptors and Vasodilatation

ET-1 also interacts with endothelial cell  $\text{ET}_{\text{B}}$  receptors. Although representing about 1% of the weight of the vessel wall, endothelial cells line the vasculature of every organ and tissue in the body that receives blood supply and have a combined mass comparable to some endocrine glands. Infusion of an  $\text{ET}_{\text{B}}$  selective antagonist, BQ788, caused systemic vasoconstriction in healthy volunteers, showing that the main consequence of activation of endothelial  $\text{ET}_{\text{B}}$  receptors by tonically secreted ET-1 was the physiological basal release of nitric oxide [40]. The interaction of ET-1 feeding back onto endothelial receptors to release nitric oxide not only limits  $\text{ET}_{\text{A}}$ -mediated vasoconstriction by stimulation of vascular cyclic GMP, but also limits further ET-1 release, emphasizing the importance of  $\text{ET}_{\text{B}}$  receptors as a counterregulatory pathway.

In agreement, and importantly, where different concentrations of ET-1 have been compared, infusions of low doses of exogenous ET-1 into the brachial artery caused vasodilatation, but this was followed by sustained vasoconstriction of the forearm vascular bed at higher doses [41]. Initially, it was surprising to find in studies, knocking out the ET-1 gene, that ET-1+/- heterozygous mice (which produced lower levels of ET-1 in plasma and lung tissue than wild-type) developed elevated blood pressure and mild hypertension, rather than the fall in blood pressure that might have been expected [42]. These results suggest that ET-1 has an essential physiological role in cardiovascular homeostasis. Low levels promote vasodilatation, whereas higher and pathophysiological concentrations of ET-1 increase blood pressure and total peripheral vascular resistance. Interestingly, renal and pulmonary circulations are particularly sensitive to the vasoconstrictor effects of ET-1. Thus, in the vasculature, nitric oxide and other dilators are crucial in balancing the ET system, but these may be reduced and absent in pathophysiological conditions. Furthermore, alternative pathways for ET-1 synthesis from big ET-1 by vascular smooth muscle (see Sect. 2.1) result in ET-1 binding immediately to ET<sub>A</sub> receptors without activation of the endothelial ET<sub>p</sub> feedback pathway to oppose vasoconstriction.

# 10.1.5 ET<sub>R</sub> Clearing Receptors, Diuresis, and Natriuresis

In addition to releasing vasodilators, the ET<sub>B</sub> receptor also functions as a "clearing receptor," to internalize the ligand-receptor complex and remove ET-1 from the circulation [43–45]. As a result, the plasma half-life of ET-1 is comparatively short. In the human heart, when the ratio of  $ET_A:ET_B$  receptors is measured,  $ET_A$  receptors are more abundant (>60%). In marked contrast, while autoradiography reveals  $ET_{A}$ receptors also predominate on the smooth muscle of the vasculature in human lung, kidney, and liver, these organs are characterized by particularly high densities of the  $ET_{p}$  subtype, reflecting that they are rich in endothelial cells [46]. For example, the lungs have one of the highest densities of ET receptors (~9,600 fmol/g protein) compared with other peripheral tissues and even higher than the brain (~5,000 fmol/g protein). In lung, ET<sub>B</sub> receptors are present on airway smooth muscle (and mediate bronchoconstriction), epithelial cells, and vascular smooth muscle cells, but the majority are present on the endothelium. Similarly, in human kidney, ET<sub>B</sub> receptors comprise 70% of the ET receptors in both the cortex and medulla.  $ET_{\rm p}$  receptors localize to endothelial cells throughout the renal vasculature consistent with their roles in endothelium-dependent vasodilatation and as clearing receptors, removing ET-1 from circulation [47, 48].  $ET_{p}$  receptors are also present on epithelial cells throughout the tubular epithelium, particularly the inner medullary collecting duct cells where the major action of ET-1 is to promote beneficial diuresis and natriuresis [47, 48]. As a result, evidence is emerging that  $ET_{A}$ -selective antagonists might be superior to mixed blockade, as antagonism of ET<sub>B</sub> receptors may be undesirable.

ET-1 is also a very potent and sustained vasoconstrictor of the hepatic vasculature [49], and preclinical in vivo studies have suggested that ET antagonists could be new therapeutic agents in the treatment of portal hypertension [50]. Interestingly, the isolated perfused liver avidly extracts proportionately more ET-1 than the lungs, with 80% uptake in a single pass. This is hypothesized to occur mostly through binding to ET<sub>p</sub> receptors on hepatic stellate cells and is reduced in conditions such as cirrhosis [51]. Portal hypertension remains a major cause of morbidity and mortality in patients with cirrhosis of the liver, but only about a third of patients respond to current therapies and new treatments are urgently needed. In human cirrhosis, plasma levels of ET-1 are enhanced and elevated concentrations in the liver are thought to be a consequence of both increased synthesis and decreased clearance [52]. Bosentan has been tested in a single patient and shown to beneficially reduce hepatic venous gradient over time [53]. The cellular expression of ET subtypes has not been studied in detail in human liver, and the precise identity of cells expressing ET<sub>B</sub> receptors is unclear. A small number of animal studies have addressed whether ET<sub>A</sub> receptor-selective antagonists provide an advantage over nonselective agents in ameliorating the effects of portal hypertension; the majority of these data indicate that selective antagonists may be sufficient [54, 55]. Thus, animal studies and a single clinical observation support a role for ET-1 in portal hypertension, but there are as yet insufficient human data to draw conclusions regarding optimum receptor selectivity for therapeutic ET receptor blockade in this condition.

The rapid clearance of ET labeled with the positron-emitting isotope [<sup>18</sup>]F from the circulation can be visualized in vivo using positron emission tomography in animal models [56]. In these studies, the distribution of ET into all major organs can be measured and confirms that the major sites for clearance of circulating [<sup>18</sup>F]-ET-1 are the lungs, the liver, and the kidney, with little uptake by other tissues. Binding could not be displaced with BQ788 administered *after* infusing the radioligand, in agreement with the proposed internalization of ET-1 by ET<sub>B</sub> receptors and degradation in the lysosome. In contrast, infusion of BQ788 prior to injecting [18F]-ET-1 significantly reduced clearing in lung and kidney by 85%, although importantly the amount of [<sup>18</sup>F]-ET-1 significantly increased in the liver as the label was no longer cleared by ET<sub>B</sub> receptors and now bound to the ET<sub>A</sub> subtype. Surprisingly, binding of [18F]-ET-1 could not be visualized to receptors within the heart in the control animal, but binding was detected in this organ when ET<sub>B</sub> receptors were blocked by the antagonist. These results show that clearance of ET-1 was mediated by the  $ET_{\rm B}$ receptor in the lung, kidney, and to a certain extent by the liver, and crucially, this prevents binding of ET-1 to the heart. This mechanism is important in limiting the detrimental vasoconstrictor effect caused by upregulation of ET-1 in the vascular system associated with disease.

 $ET_{B}$  receptors are expressed by a number of cell types in addition to endothelial cells including epithelial and smooth muscle cells. Currently, there are no antagonists that distinguish between these receptors, but endothelial  $ET_{B}$  receptors have been selectively deleted in mice [57, 58]. This did not alter the remaining  $ET_{B}$  (or  $ET_{A}$ ) receptor expression which was confirmed by radioligand binding and autoradiography. As expected, clearance of an intravenous bolus of labeled ET-1 was impaired in these knockout animals compared with controls. An  $ET_{B}$  antagonist

reduced clearance in controls but not in the knockout mouse providing clear evidence that endothelial  $\text{ET}_{\text{B}}$  receptors are mainly, if not exclusively, responsible for ET clearance from the circulation.

# **10.2** Alternative Pathways for ET Synthesis

# 10.2.1 Tissue-Specific Conversion of Big ET-1 by Non-endothelial Cell ECE and Effect of ECE/NEP Inhibitors

A key question will be to determine what effect (if any) the lowering of ET levels by inhibiting synthesis has on ET receptors (Fig. 10.1). Some big ET-1 circulates in plasma but does not bind to vascular ET receptors until cleaved to ET-1 by converting enzymes present on smooth muscle [59]. Interestingly, ECE activity is increased in endothelium-denuded human vessels with atherosclerosis [60] suggesting that



**Fig. 10.1** ET pathway in the human cardiovascular system. All three ET isoforms are synthesized by a three-step process. For ET-1 and ET-2, this consists of an initial proteolytic cleavage of the signal peptidase of preproET-1, a second cleavage of proET-1, to big ET-1-by a furin-like enzyme. Transformation to the mature, biologically active peptides is mainly by the action of ECE-1 but also by ECE-2 within endothelial cells. Further processing may occur by smooth muscle ECE or via alternative pathways catalyzed by chymase for ET-1. ET-3 is synthesized by a similar pathway but not by the endothelium. Following release from endothelial cells, ET-1 interacts predominantly with  $ET_A$  receptors on the underlying smooth muscle. In some, but not all, human vessels, a small population of  $ET_B$  receptors to act as a feedback mechanism to limit the constrictor response by the release of vasodilators such as nitric oxide. Low levels of ET-1 can also be detected in the plasma thought to be the result of overspill from the endothelium.  $ET_B$  receptors present in organs that are rich in this subtype, the kidney and lungs, remove ET-1 from the circulation by internalization followed by lysosomal degradation. Targets for therapeutic intervention are currently ECE and by blocking the ETA or both subtypes by antagonists

nonendothelial ECE may contribute to increased plasma/tissue ET levels in disease. To date, orally active dual inhibitors of both NEP and ECE have been developed, rather than purely ECE selective [61, 62]. These have the potential advantage over selective ECE inhibitors of reducing plasma ET and increasing plasma concentrations of the atrial and brain natriuretic peptides, both beneficial vasodilators. The first study has been carried out on the acute effect of single oral doses of the NEP/ ECE inhibitor SLV 306 [63]. This measured, in 15 normotensive volunteers, the blood pressure response to infused big ET-1 at doses, determined in pilot studies, likely to lead to a rise in mean arterial pressure of approximately 20 mmHg. SLV 306 dose dependently attenuated the rise in blood pressure after big ET-1 ratio in a concentration-dependent manner consistent with systemic ECE inhibition, preventing metabolism of the enzyme substrate, big ET-1, to its active metabolite, ET-1. Plasma atrial natriuretic peptide levels also increased as predicted.

This process of big ET-1 conversion can be imaged in the living animal by infusion of [18F]-big ET-1 to quantify tissue-specific conversion to [18F]-ET-1 which immediately binds to  $ET_{A}$  receptors on the vascular smooth muscle [64]. Infused  $[^{18}F]$ -big ET-1 was rapidly cleared from the circulation with a half-life (t<sup>1</sup>/<sub>2</sub>) of less than 3 min. Whole body images showed highest uptake of radioactivity in two major organs, the liver and lungs, which could be significantly reduced using phosphoramidon, an inhibitor of ECE and NEP, consistent with inhibition of enzyme conversion and subsequent reduction of [18F]-ET-1 receptor binding. The ET<sub>A</sub> antagonist, FR139317, did not alter half-life of [18F]-big ET-1 (t1/2=2.5 min) in the plasma, but radioactivity uptake was reduced in all tissues consistent with binding of the cleavage product [ $^{18}$ F]-ET-1 to this subtype rather than to ET<sub>B</sub> receptors. Plasma levels of big ET-1 are also elevated in pathophysiological conditions such as PAH. It is significant that the lungs were an important site for big ET-1 conversion, suggesting that overexpression of big ET-1, with subsequent cleavage to ET-1 and binding to ET, receptors, is an additional source of peptide in PAH. Plasma levels of ET-1 are also elevated in renal failure. Interestingly in the kidney, in marked contrast to liver and lungs, there was no binding to renal ET receptors reflecting excretion of [<sup>18</sup>F]-big ET-1 unchanged without conversion to ET-1. In agreement with animal studies, big ET-1 can be detected in urine of normal human subjects [65] and levels are increased in patients with acute myocardial infarction, chronic renal failure, essential hypertension, and vasospastic angina pectoris. These results suggest that excretion of unmetabolized big ET-1 by the kidney may be an important mechanism for removal of the precursor and, although not yet tested, may be a site of removal of increased plasma big ET-1 in volunteers treated with NEP/ECE inhibitors.

#### 10.2.2 Non-ECE Pathways: The Serine Protease Chymase

One of the unexpected findings of Yangisawa and colleagues [66] was the presence of significant amounts of ET-1/ET-2 in the ECE-1/ECE-2 double knockout mouse embryos, suggesting other proteases must be significantly involved in the tissue

production of mature ET-1 and ET-2. This study has important implications for the action of NEP/ECE inhibition on the ET pathway and has led to the search for alternative synthetic pathways to ECE.

The serine protease chymase, which is present in mast cells, can mediate an additional conversion pathway by cleaving the Tyr<sup>31</sup>–Gly<sup>32</sup> peptide bond of big ET-1 to generate ET-1(1-31), which is in turn converted to the mature peptide by cleaving the  $Trp^{21}$ -Val<sup>22</sup> bond [67, 68]. Importantly, ET-1(1-31) was equipotent compared with big ET-1 in causing vasoconstriction in human isolated vessels, including coronary arteries, and this was associated with the appearance of measurable levels of ET-1 in the bathing medium, consistent with conversion to the mature peptide. ET-1(1-31)competed for specific [ $^{125}$ I]-ET-1 binding to ET<sub>A</sub> and ET<sub>B</sub> receptors in human heart with a single affinity, indicating little or no selectivity for the subtypes. Vasoconstriction was fully blocked by ET, -selective antagonists, reflecting the predominance of the  $ET_{A}$  receptor on vascular smooth muscle [69]. The precise physiological role of mast cells within the human blood vessels is unclear, but following degranulation, which may occur under pathophysiological conditions, the mast cell chymase is associated with interstitial spaces with the potential to convert circulating big ET-1 and provide a further source of ET-1. Mast cell expression is increased in cardiovascular disease, for example, in atherosclerotic lesions. In pathophysiological conditions, it is possible that the contribution of this pathway within the vasculature, leading to overexpression of ET-1, may be underestimated particularly in conditions of endothelial malfunction where opposing levels of endogenous vasodilators may be reduced. It is unclear whether under conditions of NEP/ECE inhibition, the rising levels of big ET-1 would favor increased conversion by the serine protease pathway, thus increasing the pressor effect via ET<sub>A</sub> receptors or whether excretion of unmetabolized big ET-1 by the kidney would be sufficient to remove the elevated levels of precursors.

## 10.3 ET-2: The Forgotten Isoform

ET-2 remains the least studied of the endothelin isopeptides and much less is known of its function and location than for ET-1 and ET-3. Messenger RNA encoding ET-2 [70] together with the peptide [71] is present in the human cardiovascular system including failing hearts. Both mRNA [71] and the precursor big ET-2 are detected in the cytoplasm of endothelial cells [72] and ET-2 may also be released from these cells in addition to ET-1. Intriguingly, big ET-2 levels are higher in normal human plasma than big ET-1 [73] and plasma levels of ET-2 are detectable, with an average value in 40 volunteers of  $0.9\pm0.03$  pmol/l. ET-2 differs from ET-1 by only two amino acids and binds with a similar affinity as ET-1 to both receptor subtypes [74] and it is as potent a vasoconstrictor of isolated vessels as ET-1 ([37].

Recently, a global knockout of ET-2 revealed a distinct phenotype exhibiting growth retardation and changes in energy homeostasis. Importantly, given the current therapeutic targets of ET antagonists, changes in lung morphology and function were also observed [75]. While the importance of the ET-2 signaling pathway is not yet clear, big ET-2-like immunoreactivity has been detected in human lungs [76] and some of the alternatively spliced variants for ET-2 mRNA contain sites for the

posttranscriptional processing of preproET-2 into mature ET-2 and posttranscriptional processing may be disrupted or altered in these variants [70]. A detailed investigation into the specific contribution, if any, of ET-2 to human diseases such as PAH has not yet been carried out.

#### 10.4 ET-3: The Receptor Subtype Selective Isoform

ET-3 and its precursor big ET-3 circulate in the human plasma although at lower concentrations than ET-1 [73] and ET-3 is present in other tissues including the heart [71]. Endothelial cells do not synthesize ET-3, but alternative sources may be from the adrenal gland [77] with conversion of big ET-3 to the mature peptide within the vasculature [78]. ET-3 is the only endogenous isoform that distinguishes between the two subtypes with at least 100-fold lower affinity at the ET<sub>A</sub> receptor.

# 10.5 Is There a Shift Toward ET<sub>B</sub>-Mediated Vasoconstriction in Human Disease?

In human coronary artery disease, there is no functional evidence for an upregulation in  $\text{ET}_{\text{B}}$  receptors. Variable responses to the  $\text{ET}_{\text{B}}$  agonist sarafotoxin S6c were obtained in control vessels (n=15) and diseased coronary arteries containing atherosclerotic lesions (n=16) with 40% and 50% of arteries not responding to S6c, respectively. While S6c contracted the remaining vessels, there was no significant difference in the maximum response to S6c observed between the two groups. In agreement, there was no significant alteration in medial  $\text{ET}_{\text{B}}$  subtype density observed in diseased vessels compared to control, with  $\text{ET}_{\text{A}}$  receptors still comprising over 90% of the total ET receptor population in both diseased and control arteries. These results imply that there is no increase in the importance of the constrictor  $\text{ET}_{\text{B}}$  receptor in human coronary artery disease [79].

These results from in vitro experiments are supported by a substantial clinical study on the effect of ET antagonists in 39 patients with coronary atherosclerosis, or risk factors for coronary artery disease, undergoing cardiac catheterization. In agreement with forearm blood flow studies in healthy volunteers, selective  $ET_{\rm B}$  receptor antagonism in this group caused coronary microvascular constriction, without affecting epicardial coronary tone or endothelial function. Treatment with combined  $ET_{\rm A}$  and  $ET_{\rm B}$  blockade dilated coronary conduit and resistance vessels and improved endothelial dysfunction of the epicardial coronary arteries. This evidence therefore suggests that ET-1 acting predominantly via  $ET_{\rm A}$  receptors contributes to basal constrictor tone and in disease to endothelial dysfunction.  $ET_{\rm B}$  activation mediated beneficial coronary vasodilatation in these patients indicating that selective  $ET_{\rm A}$  blockade may have greater therapeutic potential than nonselective agents, particularly for treatment of endothelial dysfunction in atherosclerosis [80].

In human pulmonary resistance arteries with an internal diameter of  $150-200 \,\mu\text{m}$ , ET-1 caused the expected sustained vasoconstriction, but the responses to low concentrations of peptide could be blocked by ET<sub>B</sub> antagonists. In contrast, higher

concentrations above 1 nM were blocked by an  $ET_A$  but not an  $ET_B$  antagonist, suggesting that at levels of ET-1 in the pathophysiological range,  $ET_A$  receptors will be activated [81]. Davie and colleagues [82] carried out an extensive study on the distribution of ET receptors in pulmonary arteries with an internal diameter of about 500–1,000 µm from pulmonary hypertensive patients versus control subjects, using in vitro autoradiography, so that the ratio of the two subtypes could be quantified in the small arteries. ET receptor density in distal arteries and lung parenchyma was twofold greater in these patients compared with controls. Although distal arteries possessed a higher proportion of medial smooth muscle  $ET_B$  receptors than proximal arteries, there was no change in any vessel in the ratio of the two subtypes in patients compared with controls and therefore no shift toward increased  $ET_B$  expression. These results are consistent with  $ET_B$ -mediated constrictor responses at low ET concentrations, but in the absence of an upregulation in receptor density, it is unlikely there would be increased  $ET_B$  constrictor response in this patient group.

# 10.6 Endothelin Antagonists and Receptor Selectivity

# 10.6.1 Rationale for ET-1 Receptor Blockade: How Do We Define Selectivity?

The definition of selectivity depends on the measurement of the affinity (the equilibrium dissociation constant or  $K_D$ ) of each compound at the two receptor subtypes and the comparison of these affinities to give a ratio of selectivity [6, 7]. This classification of antagonists will crucially depend on how affinities were measured and this varies between investigators. Many of the reported affinities for endothelin receptor antagonists are based on assays using cloned receptor subtypes each expressed in separate cell lines. Artificially expressed receptors may not reflect and correspond to the affinities measured in native tissues for a number of reasons, such as differences in posttranslational modifications and expression at much higher densities than is encountered in native human tissue. Affinities for antagonists should ideally be measured in competition binding assays from their ability to compete for the binding of radiolabeled ET-1 since this is the predominant endogenous ligand that needs to be blocked in the clinic. However, in some cases, selectivity is calculated using radiolabeled ET-1 to identify  $ET_A$  receptors but radiolabeled ET-3 to identify  $ET_B$ .

ET receptor antagonists are classified as either selective for one subtype or alternatively as mixed antagonists that block both receptors. The classification is usually made by the manufacturer (Fig. 10.2) but there is no agreed definition and there are anomalies. We have proposed that antagonists that are  $ET_A$ -selective should display more than 100-fold selectivity for the  $ET_A$  subtype and those that block both  $ET_A$ and  $ET_B$  (mixed antagonists) should demonstrate less than 100-fold  $ET_A$  selectivity. The rationale for this is shown in Fig. 10.3. The Langmuir isotherm for the theoretical occupancy of ET receptor subtypes is shown for an  $ET_A$ -selective compound that has an affinity of 1 nM for the  $ET_A$  receptor but 100 nM for the  $ET_B$ , that is 100-fold  $ET_A$  selectivity. Occupancy is calculated using the formula  $L^*/(K_D + L^*)$ , where



**Fig. 10.2** Reported degree of selectivity of ET receptor antagonists for  $ET_A$  receptors versus classification by manufactures as either mixed or ETA-selective



Fig. 10.3 Langmuir isotherm for a compound with 100-fold selectivity for  $ET_A$  over  $ET_B$  receptors

L\*=free ligand concentration (M) and  $K_D$  is the affinity constant (M). At a concentration of 10 nM, 90% of  $ET_A$  receptors are predicted to be blocked but less than 10% of the  $ET_B$ .

Compounds displaying 100-fold selectivity are therefore useful, at least in vitro where an ET<sub>A</sub>-selective concentration can be accurately achieved. However, 100fold selectivity is likely to represent the minimum that can be used in vivo to achieve selective ET<sub>A</sub> receptor blockade. An increase in the concentration of such an antagonist by only one log unit results in a significant (50%) occupancy of ET<sub>B</sub> receptors (Fig. 10.3). In practice, if selective  $ET_{A}$  blockade is desired, then compounds of higher selectivity are needed for testing in vivo in animal models or in clinical trials and experimental medicine to be certain that there is no significant activation of  $ET_{p}$ receptors. Ideally, compounds of greater than a 1,000-fold selectivity are needed for in vivo studies to ensure ET<sub>A</sub> selectivity. Fortunately, the most widely used compounds for preclinical as well as clinical studies, that are also commercially available, are the very highly selective peptide antagonists, FR139317, BQ-123 (both  $ET_{A}$ -selective), and BQ-788 ( $ET_{B}$ ). In addition, subtype selective radiolabeled ligands for the pharmacological characterization of receptors, [125I]-PD151242 or  $[^{3}H]$ -BQ123 (ET<sub>A</sub>) and  $[^{125}I]$ -BQ3020 or  $[^{125}I]$ -IRL1620 (ET<sub>B</sub>), also display a high degree of selectivity. If these pharmacological tools have been used in studies, the results can be interpreted with confidence that the expected subtype is blocked without affecting the other [6, 7].

The situation is more complex for nonpeptide antagonists. In Fig. 10.2, examples of the selectivity of compounds used in clinical trials have been calculated from data published by the manufacturer when characterizing the compounds for the first time and using the manufacturer's own classification as to whether they considered the compound mixed or ET<sub>A</sub> selective. The figure includes the three antagonists currently available for the treatment of PAH: bosentan, sitaxentan, and ambrisentan. The selectivity spectrum ranges from bosentan, the first mixed antagonist to be introduced clinically, to the markedly ET, -selective sitaxentan to ZD4054, that is in Phase III clinical trial for refractory prostate cancer, that remarkably is reported to have no affinity for ET<sub>R</sub> receptors. For compounds that display marginal selectivity, such as ambrisentan, the interpretation of results is less clear as it is difficult to be certain whether, in particular studies, the antagonist has been used at a concentration that blocked both receptors or just the ET<sub>A</sub> receptor. Additional confusion arises as some compounds that have similar marginal  $ET_A$  selectivity such as enrasenatan and darusentan were reported by their manufactures to be a mixed antagonist and an ET<sub>A</sub>-selective antagonist respectively.

# 10.6.2 Measuring Selectivity

One approach toward measuring selectivity is to compare the affinity constants for a particular antagonist measured from its ability to compete for the binding of [<sup>125</sup>I]-ET-1 in the same assay to both native receptors using human tissue, the therapeutic



target, rather than using artificially expressed human receptors or animal tissues. ET receptor subtypes are present in left ventricle of the human heart in a ratio of about 60% ET<sub>A</sub> to 40% ET<sub>B</sub> which is ideal for accurately measuring affinity constants for antagonists against both receptors in the same tissue. Having determined the K<sub>D</sub> of radiolabeled ET-1 for the target receptors in a saturation assay, this information is used to determine the ability of unlabeled antagonists, tested over a much wider concentration range (typically 10 pM–100  $\mu$ M), to compete for the binding of a fixed concentration of [<sup>125</sup>I]-ET-1 in human left ventricle. An example of a competition curve is shown in Fig. 10.4, visualized by plotting the amount of [<sup>125</sup>I] ET-1 bound as a percentage of total specific [125I] ET-1 binding (specific binding in the absence of competitor) against the log<sub>10</sub> of the molar concentration of the competing ligand. A steep competition curve is usually indicative of binding to a single population of receptors. However, increasing concentrations of unlabeled FR139317 inhibited the binding of [125]-ET-1 biphasically. Computer-based programs such as LIGAND are used to mathematically model the curve and to measure whether a two-site fit is statistically a better fit than a one-site model. In this case, a two-site fit was preferred, consistent with FR139317 binding with high affinity to the  $ET_{A}$  site but with low, micromolar affinity to the  $ET_{R}$  receptors, giving >200,000 fold selectivity for the  $ET_{A}$  receptor ([83], Table 10.1).

# 10.6.3 Comparison of the Selectivity of ET Antagonists Determined in Human Tissues Versus Cloned Human or Animal Receptors

A crucial question is therefore how do values of antagonist affinity obtained from either cloned human receptors or animal tissues relate to those obtained in human tissues that express both receptor subtypes and which are the intended target for endothelin antagonists clinically, specifically the heart, lungs, kidney, and vasculature? We have identified a number of antagonists, belonging to different structural classes (Fig. 10.5) that have a spectrum of reported ET receptor affinity and selectivity, and have pharmacologically characterized their activity at ET receptors in these human tissues. Table 10.1 shows the literature reported selectivity of compounds determined for human cloned receptors or in cells/animal tissues that endogenously express only (or predominantly) one or other receptor subtype. Those antagonists that we have investigated belonging to the peptide, sulfonamide, or

, i i i i i i i i i i i i i i i i i i i	Cloned receptors <sup>a</sup>	Human left ventricle					
Antagonist	Reported ET <sub>A</sub> selectivity	K <sub>D</sub> ET <sub>A</sub>	K <sub>D</sub> ET <sub>B</sub>	ET <sub>A</sub> selectivity			
Peptides							
BQ123	653 [ <b>85</b> ]	0.73±0.22 nM [86]	$24.3 \pm 2.0 \ \mu M$ [86]	33,288 [86]			
FR139317	7,300 [87]	1.20±0.28 nM [88]	287±93 μM [88]	239,167 [88]			
PD151242	ND	7.21±2.80 nM [89]	104±23 μM [89]	14,424 [89]			
PD142893	1.7 [ <b>90</b> ]	$0.30 \pm 0.03 \ \mu M^{b}$	$1.17 \pm 0.14 \ \mu M^{b}$	4 <sup>b</sup>			
Sulfonamides							
Ro-462005	1.5 [91]	One site fit $50.3 \pm 9.5$	μM [88]	Non-selective [88]			
Bosentan	20 [92]	One site fit $77.6 \pm 7.9$	nM [88]	Non-selective [88]			
Sitaxentan	7,000 [93]	$1.65 \pm 0.80 \ nM^{b}$	$327 \pm 134 \ \mu M^{b}$	198,182 <sup>ь</sup>			
BMS 182874	1,042 [94]	$590 \pm 100 \text{ nM}^{\text{b}}$	Not detectable <sup>b</sup>	>10,000 <sup>b</sup>			
Carboxylic acids							
SB209670	34 [95]	One site fit 0.67±0.14 nM [96]		Non-selective [96]			
PD156707	2,600 [97]	0.92±0.38 nM [98]	13.3±2.1 μM [98]	14,457 [ <b>98</b> ]			
L-749329	65 [ <b>99</b> ]	One site fit $303.5 \pm 34$	4.3 nM <sup>b</sup>	Non-selective <sup>b</sup>			
Myceric acids							
50235	>1,000 [100]	162±61 nM [88]	$171 \pm 42 \ \mu M \ [88]$	1,056 [88]			
S97-139	1,000 [101]	$45.3 \pm 25 \text{ nM}^{b}$	$47.6 \pm 9.9 \ \mu M^{b}$	1051 <sup>b</sup>			

 
 Table 10.1
 Receptor subtype binding affinity and selectivity of endothelin antagonists determined in model systems and human left ventricle

ND Not determined

<sup>a</sup>Or cells/animal tissues that endogenously express one receptor subtype exclusively or predominantly

<sup>b</sup>Unpublished data

#### Peptide antagonists



BQ123





FR139317

PD151242

#### Sulphonamides







Bosentan

Sitaxentan

BMS182874

#### **Carboxylic Acids**



SB209670

PD156707

Myceric Acids



Fig. 10.5 Structures of the most widely used ET peptide antagonists and examples of structures from the families of nonpeptide antagonists

carboxylic acid groups comprise both reported  $ET_A$ -selective and mixed antagonists. From our human data, it is apparent that for these groups of compounds, the degree of selectivity for the  $ET_A$ -selective compounds is markedly increased from 800 to 8,000 fold in model cell/tissue systems to more than 10,000 fold in the human left ventricle binding assay. As expected, those that are reported to be mixed antagonists do not distinguish between the two receptors in human heart and a one-site fit is statistically preferred by data analysis. Interestingly, the myceric acid derivatives have about 1,000-fold  $ET_A$  selectivity in both the model receptor assays and in human cardiac tissue.

The binding experiments in human heart are carried out in the presence of bovine serum albumin (BSA) to more closely reflect in vivo conditions, as some of these compounds are known to show appreciable binding to plasma proteins [84]. Indeed, in the absence of BSA, the potency of, for example, sitaxentan for both the  $ET_A$  and  $ET_B$  receptor is increased and  $ET_A$  selectivity is maintained (unpublished data  $ET_A$   $K_D$  0.06 nM;  $ET_B K_D$  13  $\mu$ M;  $ET_A$  selectivity >230,000 fold). However, there are differences in the binding assays between the model systems and the human tissues that may account for some of the observed discrepancies in selectivity. Where animal tissues or cells have been employed, species differences in the ET receptors may need to be considered when comparing reported antagonist data to data obtained in human tissues. In some cases, the different radioligands, [<sup>125</sup>I]-ET-1 and [<sup>125</sup>I]-ET-3, are used to label  $ET_A$  and  $ET_B$  receptors respectively in both cloned/animal tissue experiments, whereas [<sup>125</sup>I]-ET-1 is used to label both populations of receptor subtypes in the human left ventricle.

If selective blockade of the vascular ET<sub>A</sub> receptor is clinically desirable, how predictable of functional potency is the affinity of an antagonist determined in a receptor binding assay? To address this question we have carried out an additional study to measure how well the ET<sub>A</sub> affinity of selective and mixed antagonists, determined in binding experiments, reflects their potency as functional antagonists at the ET<sub>A</sub> receptor in vitro. We carried out Schild analysis of data obtained from the antagonism of ET-1-induced vasoconstriction in human isolated coronary artery and/or saphenous vein (an ET<sub>A</sub> response [37, 38]) for representative antagonists from each structural group and compared the Schild-derived affinity values (ET<sub>A</sub>  $K_{B}$  to the  $ET_{A}$  affinity ( $K_{D}$ ) determined in binding experiments in the same vascular tissue. The resulting data were expressed as a  $K_{\rm p}/K_{\rm p}$  ratio (Table 10.2) and it can be seen that for most of the antagonists tested, their ability to block ET-1 vasoconstriction was 10–1,000 fold less than predicted by their binding affinity determined in the same tissue. The degree of  $K_{p}$  to  $K_{p}$  discrepancy did not appear to relate to structural class, although the peptide antagonists were particularly less effective as functional antagonists than predicted by their binding affinity. To what extent these data can be extrapolated to the clinical setting is unclear, but it may be that for some antagonists, such as bosentan, the concentration required to achieve sufficient receptor occupancy in vivo for clinical efficacy may be much greater than predicted by in vitro binding assays. While this is not necessarily a problem for compounds that are either nonselective or have a very marked ET, selectivity, it may mean that those compounds that have a more marginal  $ET_A$  selectivity may have to be administered at doses at which ET<sub>B</sub> occupancy will become apparent and so these compounds will not behave as selective  $ET_A$  antagonists at clinically effective doses.

		Binding	Functional					
Antagonist	Vascular preparation	$ET_A K_D$	$ET_A K_B^{\ a}$	$K_B/K_D$				
Peptides								
BQ123	Saphenous vein	0.55±0.17 nM [102]	141 nM [ <b>37</b> ]	256				
	Coronary artery	0.85±0.03 nM [102]	91 nM [37]	107				
FR139317	Saphenous vein	$0.56 \pm 0.01 \text{ nM}^{b}$	87 nM [37]	156				
	Coronary artery	0.41±0.13 nM [74]	126 nM [37]	307				
PD151242	Coronary artery	0.51±0.07 nM [103]	1.1 μM [ <mark>103</mark> ]	2,157				
Sulfonamides								
Ro-462005	Saphenous vein	$0.15\pm0.01~\mu M^{\rm b}$	1.4 μM <sup>b</sup>	9				
	Coronary artery	$0.19 \pm 0.04 \ \mu M$ [74]	$2.4 \ \mu M^{b}$	12				
Bosentan	Saphenous vein	$32.2 \pm 3.2 \text{ nM}^{b}$	1.6 μM <sup>b</sup>	50				
	Coronary artery	2.94±0.95 nM [74]	2.9 μM <sup>b</sup>	967				
BMS 182874	Saphenous vein	$580 \pm 40 \text{ nM}^{\text{b}}$	219 nM <sup>b</sup>	0.4				
Carboxylic acids								
SB209670	Saphenous vein	$11.2 \pm 1.4 \text{ nM}^{b}$	12 nM <sup>b</sup>	1.1				
PD156707	Saphenous vein	0.5±0.13 nM [98]	2 nM [98]	4				
	Coronary artery	0.15±0.06 nM [98]	8 nM [98]	40				
L-749329	Saphenous vein	$66.7 \pm 7.5 \text{ nM}^{\text{b}}$	6.5 nM <sup>b</sup>	0.1				
Myceric acids								
50235	Coronary artery	6.8±2.9 nM [104]	1.1 μM [ <mark>104</mark> ]	157				

**Table 10.2** Comparison of  $ET_A$  receptor affinity for endothelin antagonists determined in binding and functional assays in human coronary artery and saphenous vein

 ${}^{a}K_{B}$  derived from Schild data with slope constrained to one or from Gaddum-Schild equation  ${}^{b}$ Unpublished data

# 10.7 Conclusions

The differential distribution and function of ET receptor subtypes provides the rationale for using two distinct pharmacological strategies, mixed or  $ET_A$ -selective antagonism. To exploit this difference for selective compounds, it is essential to be able to achieve concentrations where  $ET_A$  receptors are blocked, but there is no significant  $ET_B$  receptor occupancy. While this can be achieved in vitro with >100-fold selectivity, in vivo antagonists such as sitaxentan which display at least 1,000-fold selectivity may be the minimum to resolve this hypothesis.

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# Non-Pharmacological Treatment of Peripheral Vascular Disease

11

Janice Tsui and George Hamilton

# 11.1 Introduction

Peripheral vascular disease (PVD) due to atherosclerosis of the lower limb arteries is an increasing problem in Western societies. Epidemiological studies suggest that the prevalence of asymptomatic PVD is approximately 7–15% in the middle-aged and elderly population [1]. About 15% of these patients develop lower limb symptoms within 5–7 years [2], with 1 in 2,500 of the population developing critical limb ischemia each year [3].

Risk factors for PVD are those of atherosclerosis: smoking, diabetes, hypertension, hyperlipidemia, hypercoagulable states, and sedentary lifestyle. While aggressive control of risk factors, smoking cessation, antiplatelet and statin therapy, and physical exercise are important in patients with PVD whose cardiovascular risks are significantly increased [4], this chapter provides an overview on non-pharmacological therapy in the treatment of lower limb symptoms in these patients.

# 11.2 Treatment Aims in PVD

Patients with symptomatic PVD present with either intermittent claudication (IC) or critical limb ischemia (CLI). IC describes pain in affected muscle groups on exercise. In CLI, patients suffer from pain at rest and may develop ulcers and gangrene. The viability of the limb is threatened with a significant risk of limb loss. The treatment aims and strategies are different for these two modes of presentation.

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# 11.2.1 Intermittent Claudication

Patients with IC experience pain on exercise when the blood supply to the lower limb muscles is unable to meet metabolic requirements. The muscle groups affected depend on the arterial lesions present and the pain occurs at consistent walking distances with rapid relief on resting. While the lower limb outcomes of these patients are generally good, with less than 10% deteriorating sufficiently to merit revascularization over time [5], they are at significantly higher risks of cardiovascular complications due to atherosclerosis in other vascular territories [6]. The treatment aims in these patients are therefore to reduce their risks of cardiovascular events and to improve quality of life by increasing walking distance. Aggressive risk factor management is crucial to reduce cardiovascular events, but despite available evidence, risk factors generally remain suboptimally monitored and managed in patients with PVD [7–9]. Exercise therapy in the form of supervised exercise training programs is effective in improving walking ability and functional outcomes but long-term compliance is a problem [10, 11]. As interventions are not without risks, in this group of patients where limb viability is not threatened, intervention is only considered for patients with disabling symptoms which are significantly affecting their day-to-day life.

# 11.2.2 Critical Limb Ischemia

In CLI, patients suffer from pain at rest, which is worse on elevation. Patients describe relentless pain particularly at night and may resort to sleeping in a chair. The viability of the limb is threatened and ulceration and/or gangrene may occur. Revascularization by endovascular, surgical, or a combination of techniques is required to prevent limb loss.

# 11.3 Revascularization Procedures in PVD

Non-pharmacological treatments of PVD are mainly divided into endovascular and surgical revascularization procedures. Since most patients who require intervention have CLI, the treatment options related to this group of patients will be discussed. The goal of revascularization is to re-establish in-line flow to the foot. In CLI, this generally involves treating multiple arterial segments; inflow disease is addressed prior to treating outflow lesions. While treating proximal lesions may improve symptoms, establishment of uninterrupted flow in at least one infrapopliteal vessel to the foot is usually required where tissue loss is present [12].

### 11.3.1 Endovascular Treatment of CLI

Many institutions have a strategy of using endovascular intervention as the initial choice of treatment since most patients with CLI have significant comorbidities and high short-term mortality [12, 13]. Endovascular procedures are generally less prolonged than surgical bypasses and can be performed under local anesthetic in high-
risk patients. In addition, prior endovascular procedures do not preclude subsequent surgery and in patients with diseased distal vessels and lack of suitable conduit for bypass, endovascular treatment may be the only option for limb salvage.

Recent evidence from the BASIL trial, however, suggests that surgery is the more durable option and should be considered as initial treatment in some patients. In this trial, 452 patients with CLI due to infrainguinal disease were randomized to either surgery first (n=228) or angioplasty first (n=224). At 5.5-year follow-up, 248 (55%) patients were alive without amputation, 38 (8%) were alive with amputation, 36 (8%) were dead after amputation, and 130 (29%) were dead without amputation. After 6 months, there was no significant difference in amputation-free survival or health-related quality-of-life measurements between the two treatment arms. However, hospital costs were higher in the surgery first group than the angioplasty first group [14]. Beyond 2 years however, the surgery first group did better, suggesting that for patients who have a life expectancy of 2 years or more, surgery may be the more durable option. Moreover, surgical outcomes were worse after an initial failed angioplasty [15].

#### 11.3.1.1 Suprainguinal Intervention

Endovascular procedures to improve inflow include percutaneous transluminal angioplasty (PTA) with or without stenting of the iliac arteries. In CLI, stent placements improve the success rates of treating iliac stenoses and occlusions compared to PTA alone, with primary patency rates of 90%, 74%, and 69% at 1, 3, and 5 years respectively. Women and patients with chronic renal insufficiency had poorer outcomes [16].

#### 11.3.1.2 Infrainguinal Intervention

For infrainguinal lesions, PTA with or without subintimal angioplasty or adjunctive stenting is associated with reasonable rates of limb salvage. In subintimal angioplasty, the wire is intentionally directed subintimally and then redirected within the true lumen, enabling long diffuse stenoses or occlusions to be crossed and treated [17, 18].

In the femoral and popliteal arteries, PTA is associated with lower patency rates than for iliac arteries. In one study of femoro-politeal angioplasty with provisional stent placement in patients with CLI, patency rates at the end of 2 years were 65% but with limb salvage rates of 97% [19]. A meta-analysis of 19 studies reported 3-year patency rates of 30–43% following angioplasty and 60–65% following additional stent placement [20].

Angioplasty of infrapopliteal vessels in CLI is reported to have limb salvage rates of between 92% and 95% [21] (Fig. 11.1). In a series of 235 patients with CLI, tibio-peroneal angioplasty had an overall success rate of 92% with limb salvage rate of 95% at 5 years [22]. Bare metal stents have been used successfully in infrainguinal vessels but with similar success rates to angioplasty alone [23]. Drug-eluting stents are also under investigation to reduce restenosis rates [24].

As increasingly challenging lesions are treated, different approaches have been described including retrograde puncture of pedal vessels and combined antegrade and retrograde approaches [25]. Long-term outcomes of these procedures from large studies are awaited.

#### 11.3.1.3 Adjunctive Endovascular Devices

While the overall technical success rates of angioplasty and stents in the treatment of lower limb arterial lesions are relatively high, immediate failure is most commonly related to lesions that are difficult to cross or dilate, or difficulty in re-entering the distal lumen, due to long lesions, total occlusions, calcified vessels, and diffuse distal disease. Several devices have been developed to try and overcome these problems. These include cutting balloon catheters with embedded atherotomes on the exterior of the balloon aimed at treating heavily calcified arteries which are difficult to dilate; laser-assisted angioplasty devices which aim to debulk atheromatous plaques which are difficult to cross; and directional atherectomy catheters which allow plaque to be excised and removed. Currently, there is inadequate evidence of their efficacy and cost-effectiveness in the treatment of CLI [26].

Late failure occurs due to intimal hyperplasia leading to restenosis of the native vessel as well as in-stent restenoses. A cryoplasty balloon catheter was developed with the aim of delivering cold thermal energy to the vessel wall to induce apoptosis and reduce restenosis, but again, there is little evidence to support its use in CLI. Other adjunctive devices include self-expandable stents which may be useful in the superficial femoral arteries or tortuous or tapering arteries; drug-eluting stents based



**Fig. 11.1** Infrapopliteal angioplasty. (a) Tight stenoses at origins of the right infrapopliteal arteries with subsequent occlusion of the posterior tibial artery (*arrow*). (b) Angioplasty of the anterior tibial artery. (c, d) Following successful angioplasty of the anterior tibial and peroneal arteries, in-line flow is restored to the foot



Fig. 11.1 (continued)

on their use in the coronary circulation; covered stents and bioabsorbable stents [26]. While some of these warrant further investigation, they are currently not recommended for routine use in CLI.

#### 11.3.1.4 Complications of Endovascular Procedures

Endovascular procedures are not without complications, particularly in patients with CLI who have calcified vessels and multilevel disease [27].

Puncture site complications are the most common with reported incidence of 2–6% [28]. These include bleeding, hematoma, false aneurysms, arteriovenous fistulae formation, and infection. Bleeding complications usually resolve with conservative

management but may require surgical intervention and may be life-threatening such as in cases of massive retroperitoneal hematomas. False aneurysms at the groin can usually be treated with thrombin injection [29].

Complications related to the target vessel include vessel rupture, local dissection, thrombosis, and distal embolization. These are uncommon and can mostly be treated endovascularly with covered stents, further balloon inflations, and local thrombolysis, but may require surgical intervention. Serious complications leading to limb loss have been reported to occur following 2.2% of angioplasties for CLI [27].

In addition, with increasing use of devices, device-specific complications such as device migration and deployment failure may occur.

# 11.3.2 Surgical Treatment of CLI

In many centers, surgical revascularization is reserved for patients with lesions that are deemed unsuitable for endovascular treatment or for those where endovascular treatment has failed. Younger patients with prolonged life expectancy are more commonly considered for surgical revascularization due to its more durable results, particularly in light of recent evidence from the BASIL trial as discussed above.

#### 11.3.2.1 Suprainguinal Procedures

Aortoiliac disease is treated with either aortic reconstruction or with an extra-anatomical bypass (e.g., axillofemoral, axillobifemoral, femorofemoral bypass). While aortobifemoral bypasses have good patency rates of 80% and 72% at 5 and 10 years respectively, operative mortality is on average 3.3%, rising to 8% in patients with significant comorbidities [30]. For patients who are less fit, extra-anatomical bypasses using externally supported Dacron or PTFE grafts are alternatives with 5-year limb salvage rates of 60–90% [31].

# 11.3.2.2 Infrainguinal Procedures

Infrainguinal procedures include common femoral endarterectomy and profundaplasty which may used to improve inflow prior to an infrainguinal bypass procedure. However, there is evidence that isolated common femoral endarterectomy is sufficient to salvage limbs in some patients with CLI [32].

Infrainguinal bypass procedures are usually taken from the common femoral artery to the above- or below-knee popliteal artery or to the tibial or peroneal arteries. Autologous vein rather than synthetic grafts should be used where possible, particularly in infrageniculate bypasses. A meta-analysis had shown primary patencies of 66% for vein at any level compared to 47% for above-knee PTFE and 33% for below-knee PTFE at 5 years [33]. While the long saphenous vein is the most commonly used autologous conduit, the short saphenous vein, arm veins, and deep leg veins can be used. Different strategies have been used to try and improve the outcome of vein grafts [34], but the lack of a suitable autologous conduit is usually the problem. Vein cuffs performed at the distal anastomosis or less commonly formation of an arterio-venous fistula to an adjacent vein at the distal anastomosis have been used to improve

patency of infrageniculate bypasses using synthetic grafts [35, 36]. With advances in the fields of biomaterials and tissue engineering, novel grafts exploiting these innovative technologies are likely to be the solution to improved outcomes of these procedures [37, 38].

# 11.3.3 Hybrid Procedures in CLI

Hybrid procedures combining endovascular and open procedures are increasingly used to revascularize patients with CLI. These may offer less extensive procedures, reduced perioperative complications, and better outcomes [39, 40]. For example, iliac angioplasty and stenting may be combined with an infrainguinal bypass procedure; angioplasty of an iliac stenosis may then allow a femorofemoral crossover graft to treat bilateral iliac disease; superficial femoral artery (SFA) angioplasty of a focal lesion may enable a shorter SFA-distal bypass graft to be performed particularly where availability of vein is limited. The procedures can be done as staged procedures or increasingly commonly as concomitant procedures [41] (Fig. 11.2).



**Fig. 11.2** Iliac angioplasty and femorofemoral crossover graft in a 70-year-old man with CLI. (a) Gangrenous ulcer on dorsum of right foot at presentation. A left-to-right femorofemoral crossover graft was initially performed which failed 2 weeks later due to inadequate inflow (diseased left iliac artery) and poor outflow (occluded right superficial femoral artery). (b) A left iliac angioplasty, crossover graft thrombectomy, and femoro-distal bypass were successfully performed. (c) Ulcer healing following revasuclarization. (d) Residual ulcer of approximately 1 cm in diameter

#### Fig. 11.2 (continued)



# 11.4 Other Treatment Strategies

In patients with CLI who have non-reconstructable disease, other treatment strategies are offered in an attempt to avoid or delay amputation. They aim to reduce ischemic rest pain, promote ulcer healing, and prevent further deterioration.

#### 11.4.1 Sympathectomy

Lumbar sympathectomy may be offered to patients with non-reconstructable disease. Open surgical sympathectomy has largely been replaced by percutaneous chemical sympathectomy [42] or the laparoscopic approach [43]. These techniques have been shown to be of some benefit in terms of pain relief and limb salvage in patients with CLI [44].

# 11.4.2 Spinal Cord Stimulation

Spinal cord stimulation employs low-voltage electrical impulses from a subcutaneous pulse generator which are delivered to the epidural space by electrodes placed at the L3/4 level. The exact mechanism of action is unknown but is thought to improve microcirculatory blood flow. Early controlled studies suggested a benefit in pain control although there was no improvement in ulcer healing, limb salvage, or mortality rates [45, 46]. However, most of these studies had small patient numbers and a recent systematic review found no significant benefit of the technique above best medical therapy [47]. Moreover, spinal cord stimulation is more expensive [48].

#### 11.4.3 Therapeutic Angiogenesis

Therapeutic angiogenesis using gene- and cell-based therapies to stimulate new vessel formation has been investigated over the past decade. While initial preclinical studies were promising [49], clinical trials have been less convincing. A meta-analysis identified six phase II randomized, controlled trials in therapeutic angiogenesis for PVD: four in patients with IC and two in CLI [50]. While the meta-analysis of the pooled data from these studies concluded that therapeutic angiogenesis was beneficial in patients with CLI with only a slight increase in side effects of edema, hypotension, and proteinuria, this was mainly due to the results of two of the trials. The TRAFFIC trial showed that intra-arterial recombinant basic fibroblast growth factor (bFGF) improved peak walking time in patients with IC [51] while the TACT trial demonstrated that autologous bone marrow mononuclear cell implantation significantly improved rest pain in CLI patients [52]. Since then, the TAMARIS trial which was a randomized controlled study designed to evaluate the efficacy of NV1FGF, a non-viral plasmid-based gene delivery system for FGF-1, in CLI patients has failed to meet its primary endpoint of prevention of major amputation or death at 12 months [53]. Overall, the results of these studies are disappointing and probably reflect the complexity of angiogenesis which is unlikely to be easily manipulated by the administration of single factors.

# 11.5 Amputation

Major amputation may be required in patients where no revascularization option is available or where treatment has failed. In some patients, primary amputation may be considered due to an unsalvageable limb, fixed flexion contractures of the leg or in patients who are already bed-bound due to comorbidities. The goals of amputation are pain relief, removal of nonviable or infected tissue, and the formation of a well-healed stump that maximizes chances of rehabilitation. The level of amputation therefore depends on healing and rehabilitation potential as well as prosthetic considerations.

# 11.5.1 Levels of Amputations

In patients with PAD, minor amputations, i.e., amputations of the foot, are generally performed only following successful revascularization to remove necrotic and/or infected tissue. Without revascularization, minor amputations are unlikely to heal and the patient is then faced with multiple procedures with increased risks and delayed rehabilitation.

The commonest levels of amputation in PAD patients are perigeniculate: belowknee (transtibial), through-knee (knee disarticulation and Gritti–Stokes amputation), and above-knee (transfemoral) amputations. In patients who are likely to achieve prosthetic walking, the knee joint should be preserved if possible and a below-knee amputation performed if healing at this level is likely. If healing is likely to be compromised, an above-knee amputation still allows prosthetic fitting. In patients who are likely to remain chair- or bed-bound, through-knee amputations avoid development of fixed flexion contractures and subsequent difficulties with transfers while providing longer lever lengths and larger surface areas for improved balance. Patients who have already developed a fixed flexion deformity of the knee, an above-knee amputation is more realistic.

Hip disarticulation and hindquarter amputations are extensive procedures which fortunately are rarely performed [54].

In order to provide these patients with optimal care, the involvement of a dedicated multidisciplinary team including specialist physiotherapists, occupational therapists, pain specialists, prosthetists, and social workers, from preoperative planning stages through to rehabilitation, is essential [55, 56].

# 11.6 Prognosis of Patients with PVD

As mentioned above, lower limb outcomes for patients with IC are generally good. About 50% of patients will remain stable or experience some improvement in their symptoms over a 5-year period; 25% will deteriorate and only 1-2% will require major amputation. However, 2-4% of these patients will have a non-fatal cardio-vascular event within the first year of diagnosis with a 1-3% annual incidence

thereafter. Overall, patients with PAD have a 25% greater mortality risk than those without [57].

In patients with CLI, overall long-term prognosis is poor with amputation rates of 10–40% and mortality rates of 20% at 1 year and 40–70% at 5 years [58]. While there is data from Denmark [59]and Finland[60] showing reduced amputation rates with more aggressive revascularization policies, the number of major amputations performed each year in the UK for vascular diseases has remained at approximately 3,000 from 2000 to 2007 [54]. In 1999, Dormandy et al. reported that within 2 years, 15% of below-knee amputees required a contralateral major amputation and 30% were dead [61]. More recently, Dillingham et al. reported similar figures: 10% of below-knee amputees had a contralateral amputation and over a third died within 1 year [62].

# 11.7 Conclusions

In conclusion, PVD is a prevalent disease and with an aging population and an increase in cardiovascular diseases, it will continue to be a challenging healthcare issue. In order to improve the outcomes of these patients, they must be managed by vascular specialists within multidisciplinary teams who are able to combine endovascular and surgical techniques to revascularize threatened limbs and to reduce the impact of their overall cardiovascular risks. Novel therapeutic therapies are urgently required particularly to improve the quality of life of patients with disease that is not amenable to revascularization and also as adjuncts to improve the results of currently available treatment options.

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# Surgical Approaches to Abdominal Aortic Aneurysm Repair

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# 12.1 Introduction

In the last decade, there have been dramatic changes to the management of abdominal aortic aneurysms (AAA) in the UK, and further progress is likely in the next few years. The central strategy in managing abdominal aortic aneurysms is to detect these lesions before they rupture and perform an elective repair with low morbidity and mortality. Rupture of an abdominal aortic aneurysm is a catastrophic event which carries a community mortality in excess of 90%.

Historically, the UK has one of the worst mortality rates for aneurysm surgery in the world. The reasons for this are multi-factorial but involve late diagnosis, high rates of comorbidity, low uptake of endovascular technology, and fragmented service organization. This chapter will focus on three specific aspects of abdominal aortic aneurysm surgery which will have a major impact on UK practice in the next few years: the introduction of a national screening program, the use of endovascular techniques to reduce operative mortality, and the urgent need for centralization of aortic surgery.

# 12.2 Screening for AAA

Community-based ultrasound screening is a noninvasive, cheap, and accurate method of detecting AAA. Large-scale population screening trials have shown that it is effective in men aged 65–75 years [1], and reduces the rate of aneurysm rupture and aneurysm-related mortality. On this basis, the UK Secretary of State for Health announced a UK national screening program for abdominal aortic aneurysms in

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January 2008. The primary aim of the program is to reduce AAA-related mortality by providing a systematic population-based screening program for the male population during their 65th year, and on request for men over 65.

There are still many other practical aspects relating to screening programs that require further work. These include techniques to optimize the uptake of screening, whether to use internal or external aortic diameters, cost-effective surveillance intervals, and the management of anxiety and cardiovascular risk factors within the screened population with small aneurysms. The national quality assurance framework and audit processes in place within the UK screening program may help to clarify some of these issues in due course.

The UK program is being rolled out in a staged process. The first six centers commenced screening in 2009 as "early implementation sites," namely St Georges London, Leicester, Manchester, South Devon, Gloucester and West Sussex. By 2012/13, the aim is to have 60 centers operational around the country covering a population of 270,000 men aged 65. Sites are based on a minimum 800,000 total screening population, working within established vascular networks and able to demonstrate acceptable perioperative aneurysm mortality through submission to the National Vascular Database.

Subjects will receive an invitation to a single ultrasound scan during their 65th year, performed within community healthcare facilities. If the aorta measures less than 3 cm, no further recall scans will be arranged. For aortas measuring 3.0–4.4 cm, a follow-up scan will be arranged for 1 year, and for aortas measuring 4.5–5.4 cm, a further scan is arranged for 3 months. Above this size, an automatic referral is generated to the screening center or local network hospital.

Currently, internal aortic diameters are used though there has been debate about the use of external diameters. Ultrasound has high sensitivity and specificity if performed with adequate quality assurance, particularly for internal diameters. Ultrasound can reliably image the aorta in 99% of subjects. If the aorta is not visualized, the subject should be rescanned by an experienced sonographer. The incidence of false-positive scans is uncertain but is small and of little clinical consequence.

The decision to introduce a national program was based on four randomized trials, namely the Chichester trial in the UK [2], the Viborg trial in Denmark [3], the Western Australia trial [4], and the UK Multi-centre Aneurysm Screening Study (MASS) [1]. In each study, individuals were randomized either to an offer of aneurysm screening, or to no offer of screening. In all four trials, screening was shown to reduce aneurysm-related mortality for men. In the MASS trial, the screening group demonstrated a 43% reduction in overall mortality from aneurysm disease. Overall the odds ratio in favor of screening for men was 0.60 [95%CI 0.47–0.78]. The individual characteristics of the trials are summarized in Table 12.1.

There is no good evidence to support aneurysm screening in women. In the only screening trial conducted in women, there was no reduction in the incidence of aneurysm rupture at 5 or 10 years [5]. Smoking and family history are important independent risk factors for aneurysm development, and though not specifically targeted within the program, these increased risks should be highlighted. Within the UK program, there exists the opportunity for lifestyle advice and cardiovascular risk factor assessment, particularly for those with small aneurysms. For example,

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	Chichester	Viborg	MASS <sup>a</sup>	Western
Trial	UK	Denmark	UK	Australia
Number randomized	15,775	12,628	67,800	41,000
People	Men and women	Men	Men	Men
Age (years)	65-80	65–73	65–74	65–79
Dates recruited	1988–90	1994–8	1997–9	1996–8
Date published	1995	2002	2002	2004
% accepting screening	68	76	80	70
Detection rate	4% (7.6% in men)	4%	4.9%	7.2%
Intervention policy	At 6 cm	At 5 cm	At 5.5 cm	None
Mean follow-up (months)	30.5	61	49	43
AAA-mortality, odds ratio	0.59 (men only)	0.31	0.58	0.72
Screened vs. not (95%CI)*	(0.27–1.29)	(0.13-0.79)	(0.42–0.78)	(0.39–1.32)
All-cause mortality, odds ratio	1.07 (men only)		0.97	0.98
Screened vs. not (95%CI)**	(0.93-1.22)		(0.93-1.02)	(0.91 - 1.04)

Table 12.1 Summary of the population-based randomized screening trials

\*Pooled odds ratio over all four trials is strongly in favor of screening, OR 0.57 (0.45–0.74), with a halving of the incidence of aneurysm rupture in screened populations

\*\*Pooled odds ratio trend in favor of screening, OR 0.98 (0.95–1.02)

<sup>a</sup>The MASS trial recently published 10-year follow-up, demonstrating the cost-effectiveness of screening and a significant all-cause mortality benefit, but a rising incidence of AAA rupture in the screened group

statins may reduce aneurysm growth rates by about 50% and smoking cessation appears to reduce growth rate by 20–30%.

While the benefits of screening are clear from the population-based studies, the possibility of causing harm must also be considered. Detection of a small aneurysm with the potential for unpredictable expansion and rupture is likely to create anxiety. Both the MASS and Viborg trials demonstrated a decreased quality of life for a short period after positive screening, though the effects resolved within a few months [6]. More importantly, there is the mortality risk associated with intervention. If screening is to be conducted safely, the referral centers must have an audited low mortality for both open and endovascular repair. For elective open repair, the operative mortality should be less than 5%, as in the Chichester, Viborg, and MASS trials, and for EVAR less than 2%. The early advantage of EVAR is unlikely to result in a greater survival advantage for population screening if the "catch-up" in all-cause mortality demonstrated in the EVAR trials is sustained in contemporary practice [7]. Again, the effectiveness of a national program has been based on the available trial data, though the UK program has set an upper limit perioperative mortality of 7% as the standard for screening centers. The current UK mortality for aneurysm surgery is higher than other European countries, and there is a drive from the Vascular Society of Great Britain and Ireland to reduce this by 50%.

It should be noted that in all studies, an age range up to 75 or 80 was screened. Calculations and projections on the benefits and cost-effectiveness of a national program have been based on these data. The initial detection rate in the UK program is likely to be lower due to the lower age at screening. Self-invitation in the 65–75-year age group has been estimated to only recruit around 2% of the target popula-

tion, while the trials demonstrate a 68–80% acceptance rate from formal invitation. Early figures from the early implementation centers within the UK national program suggest that screen uptake rates will be below 80%. There is also some concern about late aortic ruptures in men screened early from the MASS trial [8]. Further detailed analysis will be required to see how the decision to limit invited screening to 65-year olds, and the effect of an aging UK male population, influences the success of the national program.

# 12.3 Endovascular Aneurysm Repair

Since its inception in the early 1990s, endovascular repair of AAA has assumed an increasingly important role in the management of elective and ruptured AAA. It might be argued now that endovascular repair might be considered the first-line therapy for the treatment of AAA, with many units reporting that over 90% of infrarenal aneurysms are treated with this technology.

Endovascular aneurysm repair involves the exclusion of an aneurysm from the circulation using a stent graft that is delivered to the aneurysm via the femoral arteries – often using a totally percutaneous approach (Fig. 12.1 a,b). Most endovascular grafts are designed as a modular reconstruction that is assembled within the aneurysm sac. Standard endovascular aneurysm repair can only be performed if there is an adequate fixation zone between the renal arteries and the start of the aneurysm to allow adequate anchorage of the stent. Most series report that 50–70% of AAA are anatomically suitable for endovascular repair, but this percentage has increased in recent years with newer stent graft systems and the advent of fenestrated and branched endografts (Figs. 12.2 and 12.3).

The potential advantages of endovascular aneurysm repair relate to the minimally invasive nature of the procedure with both a laparotomy and aortic cross clamping being avoided. The reduction in operative severity leads to a reduction in physiological stress with cardiac, respiratory, metabolic, and renal parameters being improved in comparison to conventional surgical procedures. It was hoped that the reduction in physiological stress associated with endovascular repair would translate to a reduction in the mortality and morbidity of elective aneurysm repair.

Endovascular aneurysm repair has arguably evolved into the first-line therapy for patients with infra-renal abdominal aortic aneurysms. The evidence for this position has been derived from a number of sources. At present, there is a substantial body of evidence that suggests an endovascular first strategy is reasonable. Data from the randomized clinical trials has demonstrated that endovascular repair has a significant advantage over an open strategy with regard to operative mortality rates. Data from the randomized trials comparing endovascular with open surgery (EVAR-1 [7], DREAM [9] and OVER [10]) (Table 12.2) suggest an odds ratio for endovascular repair in the order of approximately 0.3 [11]. These data are backed up by large population-based registry figures, which suggest a similar advantage for endovascular repair over all age ranges [12]. It might be expected that as the technology improves, endovascular repair might be performed with a mortality of less than 1%, in contrast to open surgery, which will still most likely have a mortality of 3–5%.

**Fig. 12.1** (a) 3D reconstruction of an infra-renal abdominal aortic aneurysm with a good landing zone between renal arteries and start of the aneurysm. (b) 3D reconstruction of an infra-renal abdominal aortic aneurysm repaired using an endovascular stent graft



**Fig. 12.2** 3D reconstruction of a juxta-renal aneurysm that has been repaired with a fenestrated endograft. In these cases, the endograft is manufactured with fenestrations that are designed to individual patient anatomy. In the illustrated case, the graft has three fenestrations, one each for the renal arteries and the superior mesenteric artery



**Fig. 12.3** 3D reconstruction of thoracoabdominal aneurysm that has been repaired with a branched endograft. In these cases, the endograft is manufactured with branches designed to individual patient anatomy. In the illustrated case, the graft has two fenestrations for the renal arteries and two branches for the visceral vessels



Table 12.2Mortality rates for openand endovascular surgery (EVR) inthree randomized trials

	30-d mortality EVR	30-d mortality open
EVAR-1	1.7	4.7
DREAM	1.2	4.6
OVER1.7	0.2	2.3

Recently performed patient preference studies have also demonstrated that patients express a preference for endovascular repair over open procedures. Winterborne et al. [13] demonstrated that in a population of screened patients, 84% would prefer EVR. Postoperative mortality and morbidity were more important than need for surveillance or long-term problems with EVR. Similarly, Reise et al. [14] demonstrated a clear patient preference for endovascular repair in a cohort of patients given information regarding both procedures.

In the current healthcare climate, preferences for new technology need to be underpinned by a cost-effectiveness analysis. In the UK, the National Institute for Health and Clinical Excellence has recently concluded "endovascular stent grafts are recommended as a treatment option for patients with unruptured infra-renal abdominal aortic aneurysms, for whom surgical intervention is considered appropriate. The decision on whether endovascular aneurysm repair is preferred over open surgical repair should be made jointly by the patient and their clinician after assessment of a number of factors including, aneurysm size and morphology, patient age, general life expectancy and fitness for open surgery, the short and long term benefits and risks of the procedures including aneurysm related mortality and operative mortality." This decision was based on an economic analysis that estimated the incremental costeffectiveness ratio of endovascular procedures to be in the range of £12,000. Despite the positive data presented above, endovascular procedures are associated with some disadvantages. Most reports suggest that aneurysm-related reinterventions after endovascular procedures are significantly greater than open repair. It must also be remembered that endovascular procedures are not applicable to all aneurysms, and that the percentage of patients treated by current commercially available endografts may be as low as 40%, if the indications for use are followed.

Endografts have continued to evolve since their inception and there is evidence from several studies that the newer generation of endografts perform better than early generations [10, 15]. In designing new endografts, several features have become increasingly desirable:

- The ability to treat a higher proportion of patients with infra-renal aneurysms. In
  particular designs need to incorporate features to allow fixation and seal in difficult proximal neck anatomy and narrow, tortuous iliac access
- An ability to reduce intraoperative complication rate should be incorporated with less reliance on adjunctive procedures which are known to affect outcome [16, 17]
- A reduction in the postoperative intervention rate with a reduction in endoleak and limb thrombosis rates

The evolution of endovascular aneurysm repair has been rapid and now approaches the treatment of first choice for many patients with AAA. Improvements in the design and follow-up protocols remain likely over the next few years.

# 12.4 Centralization of Aortic Surgery

It seems a paradox that, in the modern healthcare climate, vascular professionals and commissioners continue to debate whether complex surgical interventions with high morbidity and mortality should be performed in centers of proven excellence with an adequate caseload, or whether they should remain in a greater number of more local, low-volume providers with little proof of safety. The evidence for centralization appears robust and incontrovertible, but aortic services in the UK have not been rationalized into large volume centers.

# 12.4.1 The Volume–Outcome Relationship for Elective Aneurysm Repair

There is a strong evidence base that suggests that mortality from elective aneurysm surgery is significantly less in centers with a high caseload than in units that perform a lower number of procedures. A meta-analysis of the existing literature [18] reviewed studies containing 421,299 elective aneurysm repairs and reported a weighted odds ratio of 0.66 in favor of higher volume centers dichotomized at 43 cases per year. This result echoes meta-analyses of most complex surgical interventions and should be regarded as definitive and highly informative.

However, although robust, meta-analyses can be criticized due to publication bias, heterogeneity, and the predominance of data from certain countries. Additional information may be gathered by analyzing national administrative data. A typical "volume–outcome" curve is illustrated in Fig. 12.4 [19] for elective aneurysm repair in the UK between 2001 and 2005. These data demonstrated that the mean mortality for an elective repair was 7.4%, and that 80% of all aneurysm repairs were carried out in units performing less than 33 cases annually (Table 12.3). Importantly, the mortality rate in the units with lowest caseload was 8.5% as compared to the 5.9% reported by units with a higher workload. Even more worrying are the many small volume centers where the elective mortality may often exceed 20% (region A in Fig. 12.4). These data provide the strongest possible inditement of the organization of vascular services.

Individual hospital performance from administrative datasets can be assessed by safety plots [20]. In a safety analysis of UK data, 30 of 410 hospitals performing elective aneurysm surgery had a mortality rate significantly above the national



**Fig. 12.4** Figure demonstrating mortality plotted against number of aneurysm repairs over a 5-year period (2000–2005)

<b>Table 12.3</b>	Organization	of elective	aneurysm	services as	s derived	from HES	data for th	ne years
2000-2005								

Quintile	Quintile volume	No. of cases	No. of deaths	Mortality (%)	No. of hospitals
1	0-7.2	3,149	269	8.5	272
2	7.3–12.6	3,070	234	7.6	60
3	12.7–19.4	3,126	225	7.2	38
4	19.5–32	2,943	227	7.7	25
5	>32	3,227	190	5.9	15

average. All of these units with high mortality rates were at the low end of the volume spectrum. Additionally, to statistically demonstrate a record of safe surgery (below the national average), an annual volume of at least 39 elective cases was required with a mean national mortality of 7.4%. If the national mean mortality were to be lower (as might be expected with EVAR or different service configuration), then a greater number of cases would be needed in order to prove safety.

Data from alternative sources [21, 22] confirms that elective and ruptured aneurysm repair is performed with lower mortality rates in units with a large caseload, that services are currently inappropriately organized in a mass of small volume centers, and that units with low volumes cannot demonstrate evidence of safety.

Vascular surgery has been curiously reluctant to recognize the importance of the volume–outcome relationship, with an attendant excess mortality under current service configurations, and centralize aneurysm services. A number of theoretical objections to centralization have been raised which will be discussed below.

# 12.4.2 Is the Magnitude of Absolute Difference in Mortality Sufficient to Justify Centralization?

It might be argued that the 3–4% absolute mortality difference between the lowest volume and highest volume units does not justify centralization of aneurysm services. Irrespective of the absolute mortality differences in elective surgery, the mortality differences in the emergency setting are more dramatic. In a study of ruptured AAA in the UK between 2003 and 2008, the absolute mortality differences between hospitals in the lowest and highest volume quintiles reached 24% [23].

In addition, relying on operative mortality will minimize differences in outcome, as case mix and patients considered "unfit" for surgery must also be considered. In these areas, there is evidence to suggest disparate practices, with no surgical intervention being offered to over 50% of emergency patients in lowest quintile units as compared to approximately 20% in the highest volume centers [23].

# 12.4.3 What About Low-Volume Centers with No Mortality?

In any volume–outcome plot, there are a number of relatively low-volume units that have an elective aneurysm mortality of 0% (region B in Fig. 12.4). It is tempting to speculate that these units should not be part of any centralization due to their apparent good results. This zero mortality paradox was investigated by Dimick and Welch [24] who studied hospitals that had reported a zero mortality between 1997 and 1999. When the outcomes for these hospitals in 2000 were compared with the rest of the Medicare data, the "zero mortality" hospitals had a lower caseload (4 vs. 13) and higher mortality (6.3% vs. 5.8%). The finding of zero mortality in this study was therefore not reflective of superior results, just a function of low case volume. None of these hospitals would be able to demonstrate statistical evidence of safety.

# 12.4.4 Are Volume–Outcome Data Applicable to the Endovascular Era?

The majority of data investigating the effect of caseload on elective aneurysm surgery have been derived by analysis of patients undergoing open repair. Clearly, the advent of endovascular surgery will change this relationship. Two recent studies have investigated the effect of endovascular repair on the volume–outcome relationship for elective aneurysm surgery. The studies demonstrated that:

- The volume–outcome relationship was maintained for endovascular surgery, open surgery, and the combined cohort [25]. There was a significant difference between endovascular mortality between the lowest and highest quintile providers (6.88% vs. 2.88%), and a 77% reduction in mortality was observed for every 100 endovascular repairs performed.
- Higher volume hospitals were more likely to adopt endovascular therapy (44% in high-volume hospitals vs. 18% in low-volume hospitals) [21].
- · Hospital volume was an independent predictor of mortality.
- Results were defined by the total aneurysm caseload rather than either endovascular or open cohorts alone, i.e., hospitals with a large, predominantly endovascular, caseload also reported better than average results from open aneurysm repair.

The data from both studies suggested that, if anything, the relationship between hospital caseload and outcome becomes even more important if endovascular technology is incorporated into the analysis.

# 12.4.5 Travel Times and Patient Preferences

The most important aspect defining the provision of aneurysm (or any other) services must be the acceptability to patients. There is a clear trade-off between the advantages associated with a high-volume center and the difficulties caused by prolonged travel times for both patients and relatives. In a modeling exercise, Holt et al. [26] defined the increased travel times that would be associated with a centralized model of care for aneurysm surgery in the UK. If aneurysm surgery was performed in centers with a record of demonstrable safety and a relatively low-volume threshold of 33 procedures per year, the number of hospitals performing aneurysm repair fell from 242 to 48 and travel times increased by 28 min relative to the nearest hospital.

The acceptability of increased travel times was assessed in a study of 262 patients [27]. Patients were asked to complete a questionnaire that was calibrated against the time an individual was willing to travel to access specific attributes of an aneurysm service. Approximately 92% of individuals stated a willingness to travel for at least 1 h beyond their nearest hospital in order to access services with a lower perioperative mortality, lower nonfatal complication rates, a high annual caseload of aneurysm repairs, and routine availability of endovascular repair. This study demonstrated that patients' preference to access safe, modern surgery in a high-volume center outweighed their concerns over travel.

# 12.4.6 Centralization Implies Poor Surgeon Performance in Low-Volume Units

Undoubtedly, discussion of centralization has been made more difficult by the feeling that stopping aneurysm surgery at an institution implies that surgeons in these centers are performing poorly. While there is a relationship between individual surgical caseload and outcome [28], it is the institutional experience which is the most important facet of delivering good quality care. The importance of the institutional component was recently emphasized by Ghaferi et al. [29] who studied 84,730 inpatients undergoing vascular or general surgery. The study reported that complication rates after surgery were not different between high- and low-volume institutions but that mortality following major complications was much higher in the low-volume units (21.4% vs. 12.5%). This study gives credence to the impression that outcomes may be defined by the institutional facilities, protocols, and familiarity with challenging management of complex interventions.

The data presented above would imply that aneurysm services should be performed in high-quality, high-volume providers with a proven record of safety. There appear to be no convincing arguments for maintaining aneurysm repair in low-volume hospitals.

Perhaps the most pertinent unresolved question is how to define high- and lowvolume centers. The available literature utilizes differing thresholds according to study design with many studies merely dividing caseload data into quartiles or quintiles to demonstrate the nature of the relationship. Exact volume thresholds will differ in various healthcare systems where there is disparate organization of services. However, it is important to note that the volume–outcome relationship is continuous with improvements in outcome seen with increasing volume. Clearly a pragmatic approach to defining an appropriate threshold is mandated. It might be suggested that aneurysm repair should not be undertaken in centers performing less than 50 cases per year, and ideally the annual caseload.

# 12.5 Concluding Remarks

The UK has been notoriously poor in managing patients with abdominal aneurysms with mortality rates inferior to most international comparators. Initiatives from commissioning bodies to centralize services will continue the trends toward better management that have been stimulated in recent years by the adoption of modern technology and institution of screening programs.

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**Section IV** 

Clinical and Translational Aspects of Pulmonary Vascular Disease

# Understanding the Pathobiology of Pulmonary Vascular Disease

13

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# 13.1 Introduction

Pulmonary arterial hypertension (PAH) is characterized by a progressive increase in pulmonary arterial pressure in association with variable degrees of pulmonary vascular remodeling, vasoconstriction, and in situ thrombosis. This leads to increased pulmonary vascular resistance and eventual right heart failure and death. A greater understanding of the complex pathobiology of PAH is essential for the future development of new therapeutic options. The following is a brief review of this pathobiology.

# 13.2 What Is Normal?

Normal pulmonary arteries have a thin media of circular muscle whose thickness is less than 5% of the diameter of the vessel [1] (Fig. 13.1). Consequently, under physiological conditions, the pulmonary circulation is characterized by low pressure and low vascular resistance. An exhaustive systemic review of the literature [2] that included data from 1887 healthy individuals enrolled in 47 studies from 13 countries revealed that the mean pulmonary artery pressure (mPAP) at rest was  $14.0 \pm 3.3$  mmHg, and this was independent of sex and ethnicity and only slightly influenced by age (<30 years:  $12 \pm 3.1$  mmHg, >50 years:  $14.7 \pm 4.0$  mmHg).

Therefore, if the upper limit of normal is defined by the mean plus two times the standard deviation, then the upper limit for the mPAP at rest in healthy subjects is 20.6 mmHg; this is considerably lower than the established definition for pulmonary hypertension of >25 mmHg. This same systematic review [2] showed that the mPAP

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Fig. 13.1 Normal pulmonary arteriole (Van Giesen elastic stain) flanked by a normal bronchiole (the latter at the 11 o'clock position) courtesy of Ellen Reimer, M.D., J.D., Assistant Professor of Pathology and Laboratory Medicine, Medical University of South Carolina.



with exercise was dependent on age, exercise type, and exercise intensity, making it difficult to establish a threshold value that would accurately define exercise-induced pulmonary hypertension. As a result, the former exercise criterion (>30 mmHg) was abandoned during the Fourth World Symposium on Pulmonary Hypertension in Dana Point [3]. Although modestly elevated mPAPs in the setting of chronic lung diseases are often associated with a poor prognosis [4–7], the significance of a "borderline" mPAP (20–25 mmHg) in subjects that are otherwise healthy remains unclear. This highlights the importance of the clinical assessment and the need for early biomarkers as compared to a focus on hemodynamics alone, especially since these data suggest that the prevalence of individuals with an mPAP >25 mmHg will be substantially higher than the known prevalence of PAH [2, 8].

# 13.3 The Pathologic Lesion

The histologic findings in PAH are characterized by variable intimal hyperplasia, medial hypertrophy, adventitial proliferation, and fibrosis culminating in concentric obliterative lesions (Fig. 13.2) that occur in close proximity to plexiform lesions (Fig. 13.3). The plexiform lesion results from neo-intimal proliferation and progresses from a cellular to fibrotic lesion with advanced disease [9]. It is made up of a predominance of endothelial cells in different stages of vascular organization. The endothelial cells in a plexiform lesion express growth factors typically seen in angiogenesis (vascular endothelial growth factor and hypoxia inducible factor). Therefore, the disease state might represent an abnormal form of angiogenesis [10]. Pulmonary vascular remodeling has also been associated with in situ thrombosis and infiltration by inflammatory and progenitor cells [9, 11]. In idiopathic PAH (IPAH), these histologic abnormalities are heterogeneous in their distribution and prevalence within the

Fig. 13.2 Concentric obliterative lesion characteristic of PAH. There is intimal proliferation with encroachment on the lumen. Note a plexiform lesion to the left of the artery (at the 9 o'clock position) (Van Giesen elastic stain. 40× objective) courtesy of Russel Harley, M.D., Professor of Pathology and Laboratory Medicine, MUS and Chairman, Dept. of Pulmonary and Mediastinal Pathology, AFIP





Fig. 13.3 Plexiform lesions characteristic of PAH (Van Giesen elastic stain, 10× objective) courtesy of Russel Harley, M.D., Professor of Pathology and Laboratory Medicine, MUS and Chairman, Dept. of Pulmonary and Mediastinal Pathology, AFIP

lungs and typically spare the airway, veins, bronchial circulation, capillaries, and systemic vasculature [12].

# 13.4 PAH is a Disease of Resistance Resulting in Right Heart Failure

As the vascular pathology progresses, the pulmonary vascular resistance (PVR) increases and pulmonary artery pressure rises in concert in order to maintain cardiac output. As long as the right ventricle is able to compensate for the resistance, the pressure continues to increase as the PVR increases. When the contractile reserve of the right ventricle (RV) is exhausted, right ventricular systolic failure ensues. A varying degree of right ventricular diastolic dysfunction is also present in pulmonary hypertension and is related to RV muscle mass and after-load and correlates with parameters of disease severity. The combination of reduced RV output and diastolic dysfunction enhances diastolic interdependence, severely impairing left ventricular filling and ulti-

mately resulting in hemodynamic deterioration [13]. Consequently, prognostic indicators are generally related to right ventricular function and include: clinical and echocardiographic findings of right ventricular failure/dysfunction, exercise tolerance, functional class, serum concentrations of B-type natriuretic peptide, and hemodynamics (right atrial pressure, cardiac index) [14].

With longstanding PAH, the right ventricle attempts to revert to the fetal/neonatal phenotype and becomes hypertrophied (RVH) allowing for ejection against an increased pulmonary vascular resistance. For example, in RVH, phosphodiesterase type-5 (PDE-5), which was expressed in the fetal RV, is selectively reexpressed [15]. In addition, there appears to be a metabolic switch to glycolysis with increased expression of the glucose transporter type 4 (GLUT4) and increased activation of adenosine monophosphate (AMP)–activated protein kinase and pyruvate dehydrogenase kinase [16].

# 13.5 Classification

Pulmonary hypertension was previously classified into two categories: primary pulmonary hypertension or secondary pulmonary hypertension, depending on the absence or the presence of identifiable causes or risk factors. The diagnosis of primary pulmonary hypertension was one of exclusion after ruling out all other causes for PH. Subsequent classification schemes have attempted to create categories of PH that share pathologic and clinical features as well as similar therapeutic options. These classification schemes have allowed investigators to conduct clinical trials in well-defined groups of PAH patients with a shared underlying pathogenesis resulting in nine approved therapies. The more inclusive category of PAH has also afforded increased opportunities for treatment of some rare forms of PAH that were previously too rare for individual treatment studies. The most recent classification scheme was a product of the 4th World Symposium on PH held in 2008 in Dana Point, California [17] (Table 13.1).

Unfortunately, a limitation of these classification schemes is the fact that the many patients with PH have "multifactorial pulmonary hypertension." The clinician is thus faced with treating PH patients with a variety of clinical scenarios that often include features from more than one of the WHO groups. For example, there may be some elevation of pulmonary venous pressures, some obstructive or restrictive lung diseases, or some valvular heart disease that under usual clinical presentations would not account for PH severity. These "out of proportion" PH patients are not included in clinical trials; therefore, there is a paucity of data pertaining to the safety and efficacy of conventional PAH therapies in this population. There are also different survival curves for different types of PAH. For example, patients with congenital heart disease typically have an improved survival compared to patients with IPAH, whereas patients with connective tissue disease have a worse survival [18]. This highlights another limitation of the classification scheme. Although the different types of PAH share similar pathobiology, there are key differences that include different responses of the right ventricle (congenital heart disease), differences in the pathologic lesion (absence or reduced presence of the plexiform lesion seen in the connective tissue diseases), concomitant left Table 13.1 Updated clinical classification of pulmonary hypertension

1. Pulmonary arterial hypertension (PAH)

```
1.1 Idiopathic PAH
  1.2 Heritable
     1.2.1 BMPR2
     1.2.2 ALK1, endoglin
     1.2.3 Unknown
  1.3 Drug or toxin-induced
  1.4 Associated with
      1.4.1 Connective tissue diseases
      1.4.2 HIV infection
     1.4.3 Portal hypertension
     1.4.4 Congenital heart diseases
     1.4.5 Schistosomiasis
      1.4.5 Chronic hemolytic anemia
  1.5 Persistent pulmonary hypertension of the newborn
1'. Pulmonary veno-occlusive disease and/or pulmonary capillary hemangiomatosis
2. Pulmonary hypertension owing to left heart disease
3. Pulmonary hypertension owing to lung disease and/or hypoxia
4. Chronic thromboembolic pulmonary hypertension (CTEPH)
5. Pulmonary hypertension with multifactorial mechanisms
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Adapted from Simonneau et al. [17]

ventricular diastolic dysfunction and/or pulmonary fibrosis (commonly seen in scleroderma), differing response to vasodilatation, hyperdynamic/high flow states (congenital heart disease, portopulmonary hypertension, and chronic hemolysis), and other comorbidities seen in all of the "associated" forms of PAH. Unfortunately, what is known about the pathobiology of PAH largely stems from research on patients with IPAH or animal models that are meant to represent IPAH.

# 13.6 Pathobiology

The pathobiology of PAH is thought to result from a multiple-hit hypothesis [19] involving the interaction of a predisposing state interacting with an inciting stimulus. This results in the alteration of various pathways and mediators (Table 13.2) that lead to vascular constriction, cellular proliferation, and a pro-thrombotic state, ultimately leading to the pathologic lesion of PAH and its clinical sequelae.

# 13.6.1 Genetics

Several genotypes have been associated with heritable PAH. These include mutations in bone morphogenetic protein receptor II (BMPR2), active-like kinase type-1 (ALK-1), and endogolin [20].

BMPR2 mutations are seen in 70–80% of patients with heritable PAH, but are relatively uncommon in patients with associated PAH [20, 21]. Fortunately, pene-

Table 13.2Mediators andpathways in PAH	Increased activity	Decreased activity	
	Endothelin-1	Prostacyclin	
	Serotonin	Prostacyclin synthase	
	Thromoxane A <sub>2</sub>	Nitric oxide	
	Angiopoietin-a	Nitric oxide synthase	
	Plasminogen activator inhibitor-1	Vasoactive intestinal peptide	
	Growth factors	Voltage-gated potassium channels	
	Oxidant stress	Fibrinolysis	
	Inflammation		

trance is low, and only approximately 25% of carriers will go on to develop PAH [22]. The mechanism of BMPR2 mutations is felt to be largely a result in defective SMAD signaling, which results in vascular proliferation and suppression of apoptosis.

Like BMPR2, Activin-like kinase type-1 and endogolin are also members of the transforming growth factor-beta (TGF- $\beta$ ) super-family and are located on endothelial cells. Mutations in ALK-1 and/or endogolin are associated with the autosomal dominant disorder hereditary hemorrhagic telangiectasia and PAH [23].

Research into epigenetic mechanisms (gene methylation) and single nucleotide polymorphisms with a current focus on the serotonin transporter (SERT) [24], voltage-gated potassium channels (Kv1.5) [25] and TRPC6 (Transient receptor potential cation channel, subfamily C, member 6) [26] is currently underway with hopes to explain other forms of heritable PAH and/or enhanced disease susceptibility.

# 13.6.2 Cellular Mediators and Pathways

PAH results from an imbalance that favors vasoconstriction, thrombosis, and mitogenesis; restoration of this balance by inhibition of endothelin and thromboxane or augmentation of nitric oxide and prostacyclin forms the basis of today's current therapies. Ongoing research of other mediators and pathways (Table 13.2) promises new targets for novel therapies.

# 13.6.2.1 Prostacyclin

Prostacyclin ( $PGI_2$ ) is a product of endothelial cells as a result of the action of prostacyclin synthase on arachidonic acid. Prostacyclin relaxes smooth muscle by increasing intracellular cyclic AMP (cAMP). It is also an inhibitor of platelet aggregation and smooth muscle cell proliferation. Patients with PAH have increased excretion of urinary metabolites of thromboxane and decreased excretion of urinary metabolites of prostacyclin when compared with normal controls [27]. Likewise, there is reduced prostacyclin synthase activity in patients with PAH [28].

# 13.6.2.2 Endothelin

Endothelin-1 (ET-1) is synthesized and secreted by endothelial cells and is metabolized in the normal lung. It is a potent acute vasodilator and chronically stimulates cellular proliferation and fibrosis. Patients with PAH have increased plasma levels of endothelin-1 and decreased clearance when compared to normal controls; furthermore, levels of ET-1 correlate with severity of PAH and prognosis [29, 30]. Endothelin-1 immunoreactivity is increased in pulmonary arteries of all sizes in subjects with PAH [31] and acts on two different endothelin-1 receptors: ETA and ETB. Both receptors are located on vascular smooth muscle cells. ETB is also expressed on the endothelial cell. Both ETA and ETB receptors mediate vascular smooth muscle proliferation. ETA receptors also mediate vasoconstriction, whereas ETB receptors may have a role in either vasoconstriction via actions on smooth muscle receptors or vasodilation and clearance via actions on endothelial cells [31].

# 13.6.2.3 Nitric Oxide

Nitric oxide (NO) is a potent vasodilator that is produced by endothelial cells from arginine by nitric oxide synthase and acts on the vascular smooth muscle cells via cyclic guanosine monophosphate (cGMP). Phosphodiesterase-5 degrades cGMP, thus counteracting this vasodilatory pathway. Patients with PAH have decreased plasma levels of nitric oxide metabolites [32]; likewise, endothelial nitric oxide synthase (eNOS) expression is reduced in the pulmonary arteries [33].

# 13.6.2.4 Serotonin

Serotonin (5-HT) is a smooth muscle mitogen that is transported into cells primarily via serotonin transporter (SERT, 5-HTT). Elevated plasma levels of serotonin and increased SERT function [34, 35] have been observed in patients with PAH. Administration of the selective serotonin reuptake inhibitor (SSRI) fluoxetine, which inhibits SERT uptake of serotonin, results in a decrease in serotonin uptake when compared to controls indicating that the increased uptake of serotonin is through the SERT pathway [34]. The expression of the serotonin receptors is also increased in PAH and mediates vasoconstriction and vascular proliferation [35].

# 13.6.2.5 Ion Channels

Downregulation of the expression and activity of voltage-gated potassium channels, especially Kv1.5, is common in PAH, particularly in the resistance arteries that are the major site of pathology. Not only do these channels regulate the resting membrane potential important for controlling vascular tone, but through the regulation of intracellular potassium, these channels also affect proliferation and apoptosis and thus vascular remodeling [12]. These channels are inhibited by a number of stimuli including chronic hypoxia and dexfenfluramine, both of which have been implicated in the development of PAH [12].

#### 13.6.2.6 Coagulation

As a result of endothelial dysfunction, abnormalities of the coagulation cascade, and disordered platelet function, a number of procoagulant alterations in patients

with PAH have been identified. These include increased levels of von Willebrand factor, plasma fibrinopeptide A, plasminogen activator inhibitor-1, serotonin, and thromboxane and decreased levels of tissue plasminogen activator, thrombomodulin, NO, and PGI<sub>2</sub> [14].

# 13.6.2.7 Vasoactive Intestinal Peptide

Vasoactive intestinal peptide (VIP) is a member of the glucagon-growth hormonereleasing super-family and increases cardiac output, scavenges oxygen free radical species, inhibits platelet activation, is a potent vasodilator and inhibits the proliferation of pulmonary artery smooth muscle cells [12]. Reduced serum and lung levels of VIP associated with increased VIP receptor expression and receptor-binding affinity in pulmonary artery smooth muscle cells in patients with PAH compared with controls suggests that VIP may be an important mediator [36].

#### 13.6.2.8 Inflammation

There is increasing evidence for the role of inflammation in the pathogenesis of PAH. This includes the presence of perivascular inflammation as well as inflammatory cells within plexiform lesions, autoantibodies to endothelial cells and fibroblasts, and raised cytokine (interleukin-1 $\beta$  and interleukin-6) and chemokine levels [12, 37].

# 13.7 In Conclusion

In conclusion, PAH is a panvasculopathy that begins in the lumen of the pulmonary artery and extends through the adventitia. The pathobiology includes excesses of vasoconstriction, thrombosis, and mitogenesis, resulting in concentric obliteration of pulmonary arteries, formation of the plexiform lesion, increased pulmonary vascular resistance, right heart failure, and death. PAH may occur as a result of genetic mutations or polymorphisms, coexisting disease, and/or environmental exposures. As a result of a better understanding of the pathobiology of PAH, and the interplay between multiple pathways, novel therapeutic targets and therapeutic strategies are under development that hopefully will lead to a cure.

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Figures 13.2 and 13.3 courtesy of Russel Harley, M.D., Professor of Pathology and Laboratory Medicine, MUS and Chairman, Dept. of Pulmonary and Mediastinal Pathology, AFIP.

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# Inflammation in Pulmonary Arterial Hypertension

14

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The pathophysiology of PAH is not fully elucidated and no curative treatment is yet available. However, the presence of inflammatory cells and the intense release of inflammatory mediators in pulmonary PAH lesions, associated with the high level of pro-inflammatory cytokines and of autoantibodies targeting vascular components in the sera of patients, raise the question of the involvement of inflammation and autoimmunity in the initiation, the perpetuation, and/or the worsening of the disease. This review covers PAH immunopathological aspects with a special emphasis on the role of inflammation on the pulmonary vascular remodeling, the potential immunopathological mechanisms of PAH, the relevance of inflammatory mediators as prognostic and predictive markers in PAH, and on the immunopathological to properties of current PAH therapies.

# 14.1 Introduction

Pulmonary arterial hypertension (PAH) belongs to a heterogeneous group of progressive precapillary diseases characterized by an increase in resting mean pulmonary arterial pressure above 25 mmHg. PAH occurs as a consequence of small pulmonary arterial obstruction that leads to an impaired blood flow in the pulmonary vascular bed. The increased pulmonary vascular resistances (PVR) result in a compensatory right ventricular hypertrophy (RV), followed by right cardiac failure in the late and symptomatic phase of this severe disease [1, 2].

PAH can be idiopathic (IPAH), heritable, or associated with other diseases and drugs (connective tissue diseases, congenital heart disease, human immunodeficiency virus (HIV) infection, portal hypertension, drug-induced anorexia, etc.) [3]. Germline mutations in the bone morphogenetic protein receptor type 2 (*BMPR2*) are detected in 10–40% of IPAH and in 58–74% of heritable PAH [4]. The current PAH therapies are essentially focused on decreasing the PVR by stimulating pulmonary vasodilation (prostacyclin analogues, inhibitors of the phosphodiesterase-5, and endothelin receptor antagonists) [2]. These treatments improve disease symptoms and the quality of life in a majority of PAH patients. Nevertheless, new treatments targeting other PAH pathophysiological mechanisms would be useful to slow down the disease progression. One of the novel pathways under evaluation is

represented by the tyrosine kinase inhibitors (TKI), such as imatinib and sorafenib, that have been shown to partially reverse PAH in different animal models [5, 6]. One of the beneficial effects of TKI relies on inhibition of the platelet-derived growth factor (PDGF) receptor, one of the signaling pathways linked to growth factors implicated in PAH pathophysiology [7]. Even though the use of TKI has been suggested to have beneficial effects in few clinical cases [8], it has clearly been shown that imatinib and sorafenib might induce cardiac toxicity, leading to serious safety problems in a disease characterized by underlying cardiac failure [9, 10].

Another therapeutic option would be to target PAH immunopathological component. Increasing evidences suggest that inflammatory mechanisms could play a role in human and experimental PAH genesis. Increased serum levels of pro-inflammatory cytokines and chemokines (cytokines involved in chemoattraction of leukocytes) have been measured in IPAH patients, without any underlying inflammatory, infectious, or recognized autoimmune disease by definition [11-13]. In IPAH, the pulmonary vascular lesions are sites of intense chemokine production often associated to inflammatory cells recruitment [14]. Circulating autoantibodies, in particular anti-endothelial cells and anti-fibroblasts, have been reported in 10-40% of IPAH patients [15, 16], suggesting a possible role of autoimmunity in the pathogenesis of PAH pulmonary vascular lesions. The importance of inflammatory mechanisms in PAH pathophysiology has also been highlighted by the kinetics of inflammatory patterns in standard experimental models, such as monocrotaline (MCT)-induced and hypoxia-induced PAH in rats. In these models, it has been clearly shown that inflammation precedes vascular remodeling and PAH. It has also been demonstrated, particularly in MCT-induced PAH, that immunosuppressive therapies prevent PAH development and reverse totally or partially PAH lesions [17-19]. Finally, immune mechanisms are obviously implicated in the etiology of PAH associated with autoimmune diseases or with HIV infection [14], in which PAH develops in a clear inflammatory context. In these cases, immunosuppressive or anti-inflammatory treatments significantly improve hemodynamic and clinical parameters [20, 21], highlighting the role of immune mechanisms in PAH genesis or progression.

This chapter covers PAH immunopathological aspects and their influence on pulmonary vascular remodeling.

#### 14.2 Inflammation and Pulmonary Vascular Remodeling

The classical form of arterial inflammation, that is arteritis with fibrinoid necrosis, as described in the Heath and Edwards' classification of PAH associated with congenital heart diseases, is less frequently observed nowadays [22]. Classical arteritic PAH lesions comprise transmural inflammatory cell infiltrates with focal vessel wall necrosis and fibrinoid insudation, a histological pattern which has been etiologically linked with particularly severe forms of PAH. The histological "inflammatory mark," which is much more frequent if not common, corresponds to perivascular inflammatory infiltrates, mainly constituted of T lymphocytes, of mast cells, and of macrophages [14]. Furthermore, it has been shown that immature dendritic cells are present within the perivascular infiltrates of idiopathic PAH lungs. These dendritic cells could contribute to the immune disorders observed in PAH [23]. Whether these inflammatory infiltrates are involved in the pathobiology of PAH or whether they are only epiphenomena linked to other pathologic mechanisms leading to pulmonary vascular remodeling is still unclear. However, according to the experience gained in our national reference center which gives us access to a large collection of heart-lung samples from severe PAH, inflammatory lesions seem more often associated to "active" and cellular arterial remodeling, rather than cicatricial-like fibrotic modifications, suggesting an early role of inflammation in disease progression.

In the recent past, there has been increasing scientific evidence for inflammatory involvement in the initiation of pulmonary vascular remodeling in pulmonary hypertension. In this field, animal models have demonstrated their efficiency in dissecting the kinetics of events leading to PAH. In the rat PAH model induced by monocrotaline (MCT), a potent vegetal toxin, an early endothelial injury is followed by a marked pulmonary vascular inflammation during the first 2 weeks post-injection. Subsequently, obliterative vascular remodeling and severe PAH are present at 3 weeks post-injection, leading to right heart failure 1 week later [24]. In this model, a number of immunosuppressive and anti-inflammatory approaches have been successful in treating or preventing the development of the disease [17-19, 25]. Hypoxiainduced PAH involves perivascular inflammatory infiltrates, as well, and the importance of this infiltration is proportional to the extent of pulmonary vascular remodeling [25]. PAH also develops spontaneously in transgenic mice overexpressing specifically in the lungs the pro-inflammatory cytokine IL-6 [26]. Knockdown of genes that are crucial for the integrity of the pulmonary vasculature reciprocally leads to perivascular inflammatory infiltration [27, 28]. More generally, pulmonary vasculature is sensitive to inflammation, and remodels frequently in inflammatory conditions, even though it does not necessarily lead to a recognized PAH. For instance, experimental allergic asthma is associated with pulmonary vascular thickening without PAH [29, 30], and infection of macaques with a chimeric viral construct containing the HIV nef gene in a simian immunodeficiency virus (SIV) backbone (SHIV-nef) [31], or injection of Schistosoma mansoni eggs into mice [32], induces pulmonary vascular lesions similar to those described in human explanted PAH lungs. However, this vascular remodeling is not associated with hemodynamic alteration in the analyzed time-course (which could have been too short). In this context, it seems that pulmonary vascular smooth muscle cell (SMC) proliferation is a physiological response to inflammatory stimuli. Indeed, it has been shown that these cells are able to proliferate and/or migrate in vitro, in response to some proinflammatory cytokines/chemokines [13, 33, 34]. When pulmonary inflammation is dysregulated, one can hypothesize that vascular remodeling switches from an adaptive and asymptomatic form to an obliterative and symptomatic condition. Chronicity and loss of tolerance seem to be key elements responsible for this imbalance. Swain et al. [35] have recently highlighted this point of view, showing that infection of immunocompetent mice with Pneumocystis pneumonia leads to a strong pulmonary inflammation associated with a transient PAH linked to a temporary thickening of the pulmonary vasculature. Conversely, when CD4 T cells are temporally depleted in *Pneumocystis*-infected mice, and then allowed to recover, the prolonged inflammation results in PAH that persists even after clearance of *Pneumocystis*. A genetic predisposition can also favor the switch from a transient and asymptomatic vascular remodeling to a fixed and symptomatic condition. Indeed, the pulmonary endothelial injury and inflammation caused by exposure to MCT combined with intratracheal instillation of replication-deficient adenovirus expressing 5-lipoxygenase (MCT + Ad5LO) has no hemodynamic effect in wild-type mice (it is known that mice are resistant to MCT-induced PAH) whereas it induced persistent PAH in heterozygous BMPR2-mutant mice [28]. Moreover, Hagen et al. [36] have demonstrated both in vitro and in vivo a complete negative feedback loop between IL-6 and BMP, suggesting that an important consequence of BMPR2 mutations may be poor regulation of cytokines and thus susceptibility to an inflammatory second hit. Hence, individual genetic predisposition associated to a switch from resolved to chronic uncontrolled inflammatory condition could result in persistent pulmonary vascular remodeling and may precipitate the occurrence of PAH.

#### 14.3 PAH Immunopathological Mechanisms

Besides inflammation in the broader sense, fine targeted immune mechanisms are characterized by a specific response to an antigen. These mechanisms are favored by an inflammatory background and refer to adaptive immunity. The effectors of the immune response are the T and B lymphocytes which are selected in the thymus and in the bone marrow, respectively, to react against the non-self antigens, and are activated only in the presence of foreign antigens from pathogens and/or different from self-antigens. When adaptive immunity attacks the self-antigens, there is a breakdown of self-tolerance, and, as a consequence, there is the development of an autoimmune response (i.e., directed against self-antigens) that can give rise to an autoimmune disease. The self-tolerance is controlled in the periphery by a particular population of T lymphocytes called regulatory T lymphocytes (Treg), which develops in the thymus and plays a role in the pathogenesis of several inflammatory and autoimmune diseases. Tregs are involved in the feedback control of the immune response and in the return to homeostasis. They are also known to dampen autoreactive responses and may delay the onset and progression of autoimmune disorders [37, 38]. Reduced Treg cell count and/or defective suppressor function has been observed in humans, namely patients with systemic lupus erythematosus, juvenile idiopathic arthritis, autoimmune type II polyglandular syndrome, and multiple sclerosis [39–44]. Interestingly, the BMPR2 pathway plays a role in T cell thymic development [45], which could contribute to an intrinsic defect in the function and/or number of Treg in PAH BMPR2 mutation carriers. Little is known about the role of Treg in pulmonary diseases, particularly in PAH. Two recent studies showed a Treg increase in peripheral blood in PAH patients [46, 47]. Although these studies raise new hypothesis in PAH physiopathology, the data remain descriptive and Treg identification needs to be better defined [48]. In PAH, the Treg function has not yet been explored. It also remains to investigate the presence of these cells in patients' lungs, which

	Incidence of PAH	References
Autoimmune disorders		
Scleroderma	7–12%	[49]
Mixed connective tissue disease	Rare, <1%	[50]
Systemic lupus erythematosus	Rare and often multifactorial, 0.5-14%	[51]
Sjögren syndrome	<50 reported cases	[52]
Sarcoidosis	5%, Often multifactorial (interstitial pathology, mediastinitis, pulmonary arterial compression)	[53]
Polymyositis/	Some cases reported	[54]
dermatopolymyositis		
Autoimmune thyroid disease	Frequent association, 30-50%	[55]
Systemic vasculitis	Rare	[56]
APECED syndrome	<10 cases described	[57]
Chronic infections		
HIV infections	0.1-0.5%	[58]
Bilharziosis	Frequent in severe hepatosplenic forms of the disease	[59]
Castleman's disease associated with HIV infection	Some cases reported	[60]

Table 14.1 Immune	disorders	linked t	o severe	PAH
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APECED syndrome: type-1 autoimmune polyendocrinopathy

represent an important inflammatory site where the self-tolerance breaks and autoimmunity can potentially take place.

The hypothesis that autoimmunity participates in PAH pathogenesis is still largely debated. According to current knowledge, it is particularly difficult to assess if such autoimmunity would be cause or effect of the disease. Nevertheless, since almost 50 years, it is recognized that severe PAH is associated with autoimmune disorders or chronic infections, leading to immunodeficiency (Table 14.1). One trait in common between these immune disorders is a confirmed or latent immunodeficiency that could lead to immune dysregulation and activation of pathogenic T and B cells. It is important to note that patients with an associated immune disorder present pulmonary lesions that cannot be discriminated from those encountered in patients with IPAH, and respond to the same treatments, indicating similar effector mechanisms. It is clear that T and B cells are present in vascular lesions [61], and that dendritic cells invade vascular lesions in both experimental PAH and human IPAH [23]. Immunoglobulin G deposits have even been detected – in and around – the plexiform lesions in patients with IPAH [45]. Hence, all the effectors of a local immune response are present around the remodeled vessels in patients with IPAH.

Little progress has been achieved in understanding how immune aggression could contribute in PAH pathogenesis. However, the search of autoantibodies in patients with IPAH, or with PAH associated with an autoimmune disease, has become a growing field of investigation. It is estimated that 30–40% of patients with IPAH present anti-nuclear antibodies, and 10–15% of these patients have anti-phospholipid antibodies [62]. The latter are able to bind to and activate endothelial cells [63]. It has been proposed that antibodies directed to vascular endothelium could promote



**Fig. 14.1** A model of disease progression in PAH. Different triggers intervening in susceptible subjects with genetic predisposition could lead to unresolved pulmonary vascular inflammation. As a consequence, autoantibodies against vascular components are raised and can initiate and/or perpetuate a vicious circle of vascular injury, inflammation, and autoimmunity, leading to endothelial and smooth muscle cell dysfunction. Inflammation and vascular dysfunction promote pulmonary vascular remodeling, increase in the pulmonary vascular resistances and compensatory right heart hypertrophy

endothelial cell apoptosis, and that endothelium aggression could initiate a dysfunction leading to uncontrolled proliferation [45, 64, 65]. Consequently, an altered communication between endothelial cells and smooth muscle cells would lead to the development of the typical vascular lesions found in PAH, to remodeling and vascular dysfunction. Figure 14.1 integrates such an autoimmune mechanism, as central in the pathophysiology of PAH. A similar mechanism could operate in experimental models of PAH using VEGF-R antagonists, which induce early endothelial cell apoptosis, then compensated and relieved by uncontrolled endothelial cell proliferation [66]. Antibodies to endothelial cells are detected in autoimmune diseases associated to PAH, such as lupus and scleroderma [67, 68]. The prevalence of anti-endothelial cell antibodies has recently been estimated to 82% in patients with PAH associated to connective tissue disease [69]. In PAH associated to lupus and to Sjögren syndrome, antibody and complement deposits were localized to the vascular wall [70, 71]. Another pretty favorable condition to local autoimmunity is the presence of mastocytes in and around vascular lesions [72, 73] as a source of IL-4 needed for local B cell expansion and as a link between immune and adaptive immune responses, namely within the context of autoimmunity [74]. All this is on top of the pro-inflammatory environment of PAH, with increased production of IL-1 and IL-6 [11], two proinflammatory cytokines involved in activation, proliferation, and differentiation of B cells. It is worth noting that patients with IPAH or with PAH associated to connective tissue disease do not present autoantibodies directed to BMPR-II or ALK-1, indicating that a mechanism based on autoantibody attack of the BMPR-II pathway does not contribute to PAH development [75].

More recently, systematic search of autoantibodies of the IgG type, directed against different components of the vascular wall (not only endothelial cells but also smooth muscle cells and fibroblasts), has been undertaken, as well as the search of the targets of these autoantibodies using proteomic approaches, in the purpose to identify biomarkers for the diagnosis and follow-up of PAH [15, 16, 76, 77]. Among the 21 targets recognized in the fibroblasts, keys actors involved in cell biology and the maintenance of homeostasis are represented [16]. It is important to note that this approach identifies not only autoantibodies against vascular wall components, but that the differential analysis which is performed reflects in addition pathophysiological changes of the different cell types brought into play. However, among all the autoantibody targets identified, it remains to define which ones are recognized by pathogenic antibodies that would influence the vascular function and/or play a role in remodeling. It is noteworthy that the proteomic approach using bi-dimensional gels does not favor the detection of targets present at the cell membrane, which does not exclude the potential pathogenic role of autoantibodies directed against cytoplasmic or nuclear components. Such autoantibodies would emerge following initial endothelial cell aggression through a toxic compound, inducing endothelial cell apoptosis and neoantigen exposure. Yet, a recent study has confirmed the prevalence of anti-endothelial cell autoantibodies that recognize cell surface components in patients with IPAH (62% prevalence) or associated PAH (prevalence 78%) [65]. The presence of these autoantibodies may indicate the possibility of humoral mechanisms in the pathogenesis of PAH. It remains that such autoantibodies should be considered as a circumstantial observation associated to the disease, and do not constitute a formal proof of autoimmunity. A direct demonstration of pathogenicity is required in experimental models of PAH, and by serum or cell transfer from human to animals.

# 14.4 Interest in Inflammatory Mediators as Prognostic and Predictive Markers in PAH

Previous chapters highlighted the likely involvement of inflammation and autoimmunity in the progression of PAH, favoring and accompanying pulmonary vascular remodeling, from early stages of disease development to late stages characterized by extensive vascular obstruction and right heart failure requiring lung or heart-lung transplantation.

In clinical practice, these observations find expression in several studies demonstrating a relationship between circulating levels of some inflammatory mediators and patient survival. Quark et al. [78] recently showed that circulating CRP levels were increased in chronic thromboembolic pulmonary hypertension (CTEPH) and PAH patients compared with those in control subjects, and that CRP levels were correlated with PAH severity and patient survival. In additional support to this observation of high CRP levels that could be interpreted as a marker of hemodynamic severity and right heart failure, Soon et al. [79] showed that the circulating levels of interleukin (IL)-1 $\beta$ , -2, -4, -6, -8, -10, -12p70 and TNF- $\alpha$  were increased in IPAH patients and that levels of IL-6, -8, -10, and -12p70 allowed the prediction of patient survival - high levels of these cytokines being associated with poor prognosis, without any correlation with hemodynamic data in these patients. These observations possibly reveal independent markers of right heart function, that are potentially involved in the pathobiology of IPAH. Circulating levels of LIGHT (Lymphotoxin-like Inducible protein that competes with Glycoprotein D for Herpesvirus entry mediator on T lymphocytes), a chemokine implicated in vascular inflammation [80], were also associated with PAH patient mortality [81], high levels predicting poor prognosis. In this study, the prothrombotic action of LIGHT on pulmonary vascular endothelium was also highlighted, that could explain the harmful effect of LIGHT on PAH vasculature. Another chemokine, CXCL10/Interferon gamma-induced protein 10 kDa (IP-10), which is important for the recruitment of activated T lymphocytes, is also increased in the serum of PAH patients [82]. However, patients presenting the highest circulating levels of CXCL10 do survive better than those with lower levels. As CXCL10 is known to hold anti-angiogenic properties, its rise could be beneficial to counterbalance the aberrant endothelial growth occurring in PAH.

# 14.5 Immunomodulatory Properties of Current PAH Therapies

Three therapeutic classes are currently used in the treatment of PAH: prostacyclin (epoprostenol) and its analogues (treprostinil, iloprost, beraprost), endothelial receptor antagonists (ERA) (bosentan, ambrisentan), and phosphodiesterase type 5 inhibitors (iPDE5) (sildenafil, tadalafil). These treatments target endothelial dysfunction and induce vasodilation. However, they may also hold immunomodulatory properties, which could contribute to their efficacy.

Prostacyclin and its analogues act on  $IP_2$  receptors, inducing vasodilation and inhibition of platelet aggregation. Moreover, anti-inflammatory properties of prostacyclin have recently been discovered. Iloprost reduces dendritic cell migration and recruitment, and epoprostenol prevents CD4+ Th2 cells' recruitment in animal models of asthma [83, 84]. Prostacyclin analogues inhibit also in vitro pro-inflammatory cytokines production by T lymphocytes [85] and alveolar macrophage activation stimulated by LPS through NF-kappaB [86]. Moreover, prostacyclin analogues diminish in vitro the adhesion between lymphocytes and endothelial cells, and decrease the expression of adhesion molecules and cytokines by a cAMPdependent mechanism [87]. Circulating levels of VCAM-1 were also decreased with a beraprost treatment in human diabetes mellitus [88]. Finally, treatment with epoprostenol significantly decreases MCP-1 serum levels in PAH patients, a chemokine known to be elevated in this population [89]. Circulating neutrophils of PAH patients release much more inflammatory mediators than those of the control population, and this production is reduced by iloprost treatment [90]. Moreover, endothelial cell activation is decreased in PAH patients treated by prostacyclin associated with ERA, which supports its immunomodulatory role. Indeed, anti-inflammatory properties of prostacyclin and its analogues could constitute an additional benefit in the treatment of PAH. However, due to these anti-inflammatory properties, immunosuppression is not excluded, and increased risk of infection with prostacyclin treatment needs to be considered [91, 92].

As a potent vasoconstrictor, endothelin-1 (ET-1) also holds pro-inflammatory effects through NF-kappaB activation [93], increasing vascular permeability and activation of neutrophils [94]. Dual ET-A and ET-B receptors antagonists bosentan reduces vascular permeability in animal inflammatory models [95]. Bosentan also decreases pro-inflammatory cytokine expression in bronchoalveolar lavages through NF-kappaB inhibition [96]. Moreover, bosentan exposition of CRP-pre-treated endothelial cells reduces significantly the expression of adhesion molecules and MCP-1 production [97]. A treatment with a selective antagonist to ET-A receptors, ambrisentan, decreases pro-inflammatory genes expression in ischemia/reperfusion models, leading to a cytoprotective effect on vascular and neuronal microcirculation [98, 99]. ET-1 receptor blockade leads to maturation defect and alteration of antigen-presenting capacity of dendritic cells [100]. In PAH patients, a recent study demonstrated that the reduction of ICAM-1 and of IL-6 plasmatic levels that occurred after bosentan treatment correlated with a hemodynamic improvement [101].

Immunomodulatory effects of iPDE-5 are linked to the cyclic GMP pathway. Treatment by sildenafil decreases inflammation, mucus production, and leukocyte infiltration in animal models of airway inflammation [102, 103]. Moreover, sildenafil restores antitumoral immunity through suppression of arginase 1 and NO synthase inducible expression – two enzymes required to activate immunosuppressor myeloid cells, the *myeloid-derived suppressor cells* (MDSCs) recruited by growing tumors [104]. No study on the immunomodulatory effects of iPDE-5 was reported in PAH patients. However, the potent anti-inflammatory properties of the others iPDE5 (mainly iPDE4), their antiproliferative properties, and restoration capacity of endothelial function support the use of iPDE-5 use as potential treatment for autoimmune disease [105].

The recent implication of PDGF signaling in the pathophysiology of PAH [7] focused attention to tyrosine kinase inhibitors (TKI) as a new therapeutic option in PAH management. Among these TKI, imatinib has anti-inflammatory properties, inhibiting in vitro monocyte/macrophage development from bone marrow progenitors [106], and affecting T lymphocytes and dendritic cells in their capacity to mount a

cytotoxic lymphocytic response [107, 108]. Imatinib also has antitumoral properties through activation of a specific type of dendritic cells recently identified as *interferon-producing killer dendritic cells* (IKDC) [109].

In conclusion, current therapeutics of PAH act all along the inflammatory process, blocking adhesion molecules expression on endothelial cells, inhibiting the release of pro-inflammatory cytokines and chemokines, and preventing the activation of effector cells such as lymphocytes and dendritic cells.

# 14.6 Conclusion

This chapter brings to light a unique sensitivity of the pulmonary vascular bed to inflammatory stimuli. A deregulated and unresolved pulmonary inflammation on the top of a genetic predisposition background could conduct to a persisting vascular remodeling leading to PAH. In this context, some mediators of inflammation are correlated to the survival of patients suffering from this severe condition. Whether autoimmune manifestations are cause or worsening consequence of PAH deserves further in-depth examination. Only circumstantial data on association between the presence of autoantibodies and the disease are currently available. A long road remains to be covered in order to assess the role of autoimmunity in PAH.

Several avenues could be explored:

- · A better characterization of inflammatory infiltrates in patients
- The search for deficient immunoregulation, for example, a defect in regulatory T cells
- The formal proof that a tolerance breakdown toward an autoantigen expressed by pulmonary vascular components could conduct to PAH
- The search of pathogenic autoantibodies, and the proof of their mechanism of action, with the possibility to transfer the disease from man to animal
- The discovery of novel experimental models of PAH, involving autoimmune mechanisms
- · The formal proof that autoimmunity influences vascular remodeling

In this line, a multifactor appraisal of the pathogenic process in PAH, in which inflammatory mechanisms, namely autoantibodies directed to vascular wall components, play a central role could be proposed (Fig. 14.2). The pulmonary environment being tolerogenic in nature, perturbation agents could act as triggering factors in a given genetic and environmental background. An initial acute inflammation that is normally expected to resolve with return to homeostasis would conduct to the production of autoantibodies against vascular wall components, and would shift to chronic persisting and chronic inflammation, endothelial barrier breakdown, infiltration by immune cells, local and chronic autoimmunity, and vascular remodeling culminating in PAH. Identification of the factors that could trigger this irreversible process remains a major challenge to understanding the mechanisms of PAH, and to the proposal of novel therapeutic targets.



**Fig. 14.2** Contribution of inflammatory mechanisms in vascular remodeling. Agents that interfere with the resolution of inflammation and return to homeostasis such as genetic predisposition and environment could favor chronic and persistent pulmonary inflammation, endothelial barrier breakdown, immune cell infiltration, breakdown of self-tolerance and autoimmunity, and vascular remodeling. Autoantibodies to vascular components may have a central role in perpetuating unresolved inflammation and a lung inflammatory environment

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# Endothelin Receptor Antagonists in Cardiovascular Medicine: Challenges and Opportunities

15

Matthias Barton

# 15.1 Endothelin: An Endothelium-Derived Vasoconstrictor

In 1980, Robert Furchgott made the seminal observation that endothelial cells modulate vascular tone by releasing a vasodilator factor [1], which was later identified as nitric oxide [2]. Only 1 year later, de Mey and Vanhoutte first reported endothelium-dependent vasoconstriction [3–5]. By the mid-1980s, several investigators independently reported a peptidergic vasoconstrictor activity released from cultured endothelial cells [3, 6–9]. After a combined effort of several Japanese groups led by Tomoh Masaki [10, 11], sequences of the gene and the peptide encoding for endothelin were published in *Nature* in March 1988 [12]. Today, endothelin still represents the most potent and long-lasting vasoconstrictor known in humans [13, 14], being 100-times more potent than noradrenaline [15, 16].

# 15.2 Molecular Biology and Biological Functions of Endothelin

# 15.2.1 The Endothelin Peptide Family

Endothelin-1 (ET-1) is a 21-amino acid peptide with a hydrophobic C terminus and two cysteine bridges at the N terminus and the main member of the endothelin peptide family [3, 17]. Two structurally related peptides differing by two and six amino acids were identified and termed endothelin-2 (ET-2) and endothelin-3 (ET-3), respectively; they were identified shortly after the discovery of ET-1 [17].

*ET-1* is produced by vascular endothelial [18] and smooth muscle cells, airway epithelial cells, macrophages, fibroblasts, cardiac myocytes, brain neurons, pancreatic islets,

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and also by other cells (reviewed in [15, 19]). Endothelial cell–specific overexpression of ET-1 in vascular endothelial cells causes hypertension-associated changes in the vasculature, including hypertrophy and inflammation [20–22]. In contrast, endothelial cell–specific deletion of the preproendothelin gene is associated with hypotension [18, 22]; this blood pressure–lowering effect of gene deletion is similar to that of vascular smooth muscle–specific deletion of the ET<sub>A</sub> receptor [18]. In endothelial cell–specific ppET-1 null mice, plasma levels of ET-1 are reduced by about 90%, indicating that endothelial cells are indeed the major source of circulating ET-1 [18]. Moreover, ET-1 tissue levels in organs such as the heart and the lung markedly reduced in these animals consistent with the notion that endothelial cells in these organs largely contribute to endothelin-1 production in tissue [18].

ET-2 is expressed in the ovary and in intestinal epithelial cells, and, among other functions, is involved in the regulation of lung alveolarization, thermoregulation, ovulation, and intestinal epithelial cell homeostasis, and thus possibly for inflammatory bowel disease [23–26].

*ET-3* is found in endothelial cells, brain neurons, renal tubular epithelial cells, and intestinal epithelial cells and mediates release of the vasodilators NO and prostacyclin, among others [19].

#### 15.2.2 Endothelin-Converting Enzymes

The endothelin-1 precursors are processed by two proteases to create the mature active forms [19, 27] (Fig. 15.1). The 212-residue preproendothelins are cleaved at dibasic sites by furin-like endopeptidase to form biologically inactive intermediates, namely 37- to 41-amino acid peptides termed pro- or big endothelins (big ETs) (Fig. 15.1). Processing is mediated by a family of membrane-bound zinc metallopro-teases from the neprilysin superfamily, termed endothelin-converting enzymes (ECEs) (reviewed in [19]). Depending on the cleaving enzyme (Fig. 15.1), 21-, 31-, or 32-amino acid isoforms with specific receptor activities are formed. In addition to these proteases, other enzymes such as vascular chymase [28–30] and non-ECE metalloproteinase [31] must contribute to the final processing step, since in mice lacking both ECE-1 and ECE-2, the levels of mature endothelin peptides are reduced by only one-third [32]. Recent studies suggest that carboxypeptidase A (cathepsin A) plays an important role in degradation of the ECE product endothelin-1 [33]. The role of ET-1 degradation in physiology and disease, however, remains yet to be studied.

#### 15.2.3 Endothelin Receptors

In humans, two seven-transmembrane domain, G protein–coupled endothelin receptors ( $\text{ET}_{A}$  and  $\text{ET}_{B}$ ) mediate the cellular activities of endothelins (reviewed in [34]) (Fig. 15.1). It is currently not clear whether receptor dimerization into homo- or heterodimers [35] plays a role of endothelin receptor activity and function in vivo such as endothelin effects on diuresis [23, 36], or whether receptor dimerization is



**Fig. 15.1** Biosynthetic pathways of endothelin peptides  $\text{ET-1}_{(1-21)}$ ,  $\text{ET}_{(1-31)}$ , and  $\text{ET}_{(1-32)}$  peptides following transcription of preproendothelin-1 mRNA. Enzymes are in *italics*. Prepro-ET mRNA is translated into preproET-1, a 203-amino acid peptide, which is cleaved by furin convertase to the 38-amino acid precursor, big ET-1<sub>(1-38)</sub>. Big ET-1 is processed to ET-1<sub>(1-21)</sub> by endothelin-converting enzymes (ECEs), mast cell and smooth muscle cell chymases, and a novel non-ECE metalloprotease (secreted soluble endopeptidase, SEP) (*left*). Two novel pathways involve mast cell chymase, yielding the 31-amino acid ET-1<sub>(1-31)</sub> (*middle*), and matrix metalloproteinase-2 (MMP-2), forming another vasoconstrictor peptide, ET-1<sub>(1-32)</sub> (*right*)

affected by drug treatment. The ET<sub>A</sub> receptor shows sub-nanomolar affinities for ET-1 and ET-2 and 100-fold lower affinity for ET-3 [19]. ET<sub>B</sub> has equal sub-nanomolar affinities for all endothelin peptides. The ET<sub>A</sub> receptor mediates constriction and growth, whereas the ET<sub>B</sub> receptor inhibits cell growth and vascular tone; the ET<sub>B</sub> receptor also functions as a "clearance receptor," as indicated by the ET<sub>B</sub>-dependent inhibition of the accumulation of intravenously administered, radio-labeled ET-1 in tissue [15, 19]. This ET<sub>B</sub> receptor–mediated clearance mechanism is particularly important in the lung, which clears about 80% of circulating ET-1 [15]. The ET<sub>A</sub> receptor can be considered the principal vasoconstrictor and growth-promoting receptor, whereas the endothelial ET<sub>B</sub> receptor generally inhibits cell growth and vascular beds expressing contraction-mediating ET<sub>B</sub> receptors in the media [15, 27]. The ET<sub>B</sub> receptor is important for embryonic development, and its deficiency is associated

with a phenotype consistent with Hirschsprung's disease, featuring aganglionosis and megacolon development [37–39]. The endothelial  $ET_{B}$  receptor also functions as a "clearance receptor," because  $ET_{B}$ -selective antagonists inhibit the accumulation of intravenously administered, radio-labeled ET-1 in tissue [15, 19, 40]. This  $ET_{B}$  receptor–mediated clearance mechanism is particularly important in the lung which clears about 80% of circulating ET-1 [41], which however is affected by chronic endothelin receptor antagonist (ERA) treatment distributing clearance to other organs such as the liver [40]. In animals lacking  $ET_{A}$  receptors specifically in vascular smooth muscle, a compensatory upregulation of vasoconstrictor  $ET_{B}$  receptors occurs [18]. In vast majority of tissues, the disease-promoting effects of ET-1 are mediated by activation of the  $ET_{A}$  receptor, and include activity such as inflammation, excessive cell proliferation, contraction, ROS formation, and coagulatory activation (Fig. 15.2) [27, 43, 44].



**Fig. 15.2** Effects of endothelin (ET-1) in vascular endothelial and smooth muscle cells. ET-1 is generated by endothelial and smooth muscle cells in response to lipoproteins, Ang II, and inflammatory stimuli. Activation of endothelial ET<sub>B</sub> receptors increases the release of nitric oxide (NO), whereas ET<sub>A</sub> receptors mediate cell proliferation, migration, and contraction. Endothelin induces expression of TNF-α and interleukins in monocytes and vascular adhesion molecule expression, and stimulates leukocyte adherence and platelet aggregation. Endothelin also enhances production and activity of other growth factors, and promotes DNA and protein synthesis and progression of the cell cycle. Abbreviations used in figure: *Ang II* angiotensin II, *ONOO*<sup>-</sup> peroxynitrite, *ET-1* endothelin-1, *ET<sub>A</sub>* endothelin ET<sub>A</sub> receptor, *ET<sub>B</sub>* endothelin ET<sub>B</sub> receptor, *NO* nitric oxide, *NOS* nitric oxide synthase, *MCP-1* monocyte chemoattractant protein-1, *ICAM-1* intracellular adhesion molecule-1, *VCAM-1* vascular cell adhesion molecule-1, *LDL* low-density lipoprotein, *oxLDL* oxidized low-density lipoproteins, *O*<sub>2</sub> superoxide anion; *LOX* oxidized LDL receptor, *IL-1* interleukin-1, *IL-6* interleukin-6, *IL-8* interleukin-8, *TNF-α* tumor necrosis factor-α, *TGF-β1* transforming growth factor-β1, *phox* NADPH oxidase, (+) stimulation, (-) inhibition (Reproduced from [42], with permission of the publisher and the American Heart Association)

#### 15.2.4 Biological Functions of Endothelin

Endothelins (ETs), of which ET-1 represents the predominant and biologically most relevant isoform [15, 19], can be considered ubiquitously expressed stress-responsive regulators working in a paracrine and autocrine fashion, with both beneficial and detrimental effects [19]. Endothelins exert a number functions during embryonic development and physiology [45], including neural crest cell development and neurotransmission (reviewed in [19]). In the vascular system, endothelin via activation of ET<sub>A</sub> receptors has a basal vasoconstricting role [46] and contributes to the development of vascular disease in hypertension and atherosclerosis [43, 47] (Fig. 15.2). Endothelins are involved in the regulation of myocardial contractility, [14], chronotropy [19], and arrhythmogenesis [48], as well as myocardial remodeling during congestive heart failure [49]. In the lung, the endothelin system regulates the bronchial tone [50] and proliferation of pulmonary airways blood vessels and promotes the development of pulmonary hypertension [51]. Endothelin also controls water and sodium excretion and renal acid-base balance under physiological conditions [27], and promotes the development of glomerulosclerosis [52–55]. In the brain, the endothelin system modulates cardio-respiratory centers and release of hormones [19] and regulates the growth guidance of developing sympathetic neurons (Makita et al. 2008). In addition, endothelins participate in physiologic and pathophysiologic functions of the immune system [44, 56, 57], the liver [58], muscle, adipose tissue, the reproductive system, and are involved in glucose homeostasis [58–60].

## 15.3 Role of Endothelin in Development and Therapy of Cardiovascular Disease

#### 15.3.1 Arterial Hypertension

The identification of endothelin as a vasoconstrictor [16] and the finding of its release from vascular endothelial cells suggested that this peptide is involved in the pathogenesis of hypertension and vascular disease [61]. Further support for this hypothesis came from case reports of hemangioendothelioma patients that presented with markedly elevated high levels of plasma ET-1 and hypertension and showed normalization of elevated ET-1 levels and blood pressure after tumor removal [62]. In contrast, ET-1 plasma levels are mostly normal in patients with essential hypertension; however, local ET-1 levels increase in the vascular wall in hypertension [63, 64]. In the 1990s, the role of endothelin and experimental hypertension due to high salt or angiotensin II was investigated in several laboratories, results demonstrating potent antihypertensive effects and end-organ protection of endothelin receptor antagonists (reviewed in [47, 64–67]). Endothelial cell–specific overexpression of endothelin in vascular endothelial cells causes hypertension-associated changes in the vasculature, including hypertrophy and inflammation, yet does not cause hypertension [20–22]. On the other hand, endothelial cell–specific deletion of the preproendothelin gene is associated with hypotension [18, 22]; this blood pressure–lowering effect of gene deletion is similar to that of vascular smooth muscle–specific deletion of the  $ET_A$  receptor [18]. In mice lacking endothelin in vascular endothelial cells, plasma levels of ET-1 are reduced by about 90%, indicating that endothelial cells are indeed the major source of circulating ET-1 [18]. In human hypertension, ET-1 plasma levels are mostly normal; however, ET-1 levels increase locally in the vascular wall in hypertension [47, 65, 66, 68].

The kidney expresses all components of the endothelin system [69]. Endothelins were shown to be involved in the regulation of renal blood flow, re-absorption of water and sodium, as well as in acid–base balance [23, 69]. The renal vasculature represents one of the most sensitive vascular beds contracting to endothelin concentrations in the picomolar range, and contraction is mainly mediated by ET, receptors [16, 70]. Renal endothelin has been linked to the development of salt-sensitive hypertension which may involve both the inflammatory NOS (iNOS) [43, 71], which is constitutively expressed in the kidney, [43, 71] and the ET<sub>B</sub> receptor [32]. Indeed, blockade of the endothelin system with an ET<sub>A</sub> receptor antagonist in genetically salt-sensitive hypertensive Dahl rats increases the abnormally low NO synthase activity in the kidney and markedly attenuates blood pressure induced by salt feeding [43]. Most recent work indicates that NOS also – at least in part – mediates endothelin-1-dependent sodium excretion in the collecting duct and blood pressure [72]. Interestingly, collecting duct-specific deficiency of endothelin abrogated the increase in activity of all three NOS isoforms in the inner medulla in response to sodium loading [72]. Also, genetic deficiency of the ET<sub>p</sub> receptor via conditional knockout results in sodium-sensitive hypertension that can be improved by blocking the luminal epithelial sodium channel using amiloride [32]. These studies indicate that salt sensitivity, a common feature of patients with resistant hypertension, involves several underlying pathomechanisms and that it may be particularly accessible to treatment with endothelin antagonists.

Preclinical data on hypertension have been underscored by clinical studies in humans with essential hypertension. Treatment with either the nonselective ET receptor antagonist bosentan [73] or the ET, receptor-selective antagonist darusentan [74, 75] causes substantial reductions of arterial blood pressure in patients with essential or resistant essential hypertension, darusentan even when added to existing therapy of at least three antihypertensives, including a diuretic [74, 76, 77]. It remains currently unclear whether selective antagonists provide an advantage over nonselective compounds. Selectivity appears to be a crucial issue as blockade of  $ET_{p}$  receptor-mediated effects may attenuate the pressure-lowering effect and interfere with endothelium-dependent dilation [78, 79]. In this regard, the reported selectivity and specificity data of drugs may depend on the assays and cells employed for the selectivity determination and appear to largely vary between drug companies. Indeed, recent studies indicate that selectivity profiles of several endothelin receptor antagonists from different pharmaceutical companies largely differ from the data in published literature depending on whether human or animal cell assays were used [80]. This also dictates caution with the interpretation of results from experimental studies regarding the selectivity of individual components. Resistant hypertension is frequently seen in African American and in obese patients, who are both at increased risk for cardiovascular and renal disease and show elevated plasma ET-1 levels

[81–83]. Long-term clinical studies are required to determine whether treatment with darusentan or other endothelin antagonists has the potential role to lower mortality in these patients, which might involve organ protection beyond that of the pressure-lowering effects of ET receptor blockade [84–86].

#### 15.3.2 Atherosclerosis and Coronary Artery Disease

Expression of endothelin and its receptors is increased in the atherosclerotic plaques of human coronary arteries [87, 88] and both endothelin-1 peptide and ET, receptors have been causally implicated in the development of atherosclerosis, as inhibition of this pathway inhibits formation of atherosclerotic plaque in animal models [43, 71, 89–91]; moreover, acute blockade of endothelin ET, receptors ameliorates myocardial ischemia and biochemical changes caused by infarction in mice with coronary atherosclerosis [92] and reduces lipid-induced macrophage activation [89]. Indeed, endothelin has strong growth-promoting activity in the vascular wall and both endothelin and its receptors are widely expressed in macrophages, vascular smooth muscle cells, and fibroblasts (reviewed in [15, 43]) (Fig. 15.2). A common observation made in almost all studies investigating effects of endothelin receptor blockade on vascular function in animal models of hypertension, hypercholesterolemia, or atherosclerosis was that chronic treatment improved endothelium-dependent, NO-mediated vasodilation [43, 71, 93, 94]. This improvement of NO-dependent vasodilation after endothelin ET<sub>A</sub> receptor blockade has also been observed in clinical studies and is blocked by  $ET_{p}$  antagonists [79]. Acute blockade of endothelin receptors of isolated internal mammary arteries in vitro obtained from in patients with coronary atherosclerosis improves endothelium-dependent vasodilation [95, 96], and similar findings have been reported from in vivo studies in humans with atherosclerosis [97-101]. A recent study of the effects of 6-month treatment with the ET<sub>A</sub> antagonist atrasentan in patients with coronary artery disease also reported improved coronary artery endothelium-dependent vasodilation [102, 103]. Although ACE inhibitors [104] and statins [105] inhibit endothelin expression in vitro, ACE inhibition and statin treatment surprisingly has no effect on the markedly elevated endothelin peptide expression in the mammary artery of patients with coronary atherosclerosis [106], suggesting the need for additional therapies. In contrast, ET, blockade is effective to completely normalize endothelin peptide levels in atherosclerosis, at least in experimental studies [63, 71].

Environmental cardiovascular risk factors such as cigarette smoking or air pollution have been only recently investigated. Smoking is one of the central risk factors contributing to many cardiovascular deaths [107]. Cigarette smoke enhances inflammatory airway responses [108] and induces ECE-1 peptide expression [21]. Correspondingly, contractile responses to ET-1 in arteries from patients with coronary artery disease are much stronger in smokers than in non-smokers [109]. Cox et al. described protective effects of ERA treatment after smoke inhalation–induced pulmonary injury [110], and preventive effects of ERA treatment on emphysema development, one of the long-term consequences of smoking and COPD, have been reported [111]. As with cigarette smoke, air pollution by car fumes, particularly

**Fig. 15.3** Vascular mRNA expression of bone morphogenetic protein (BMP) receptor II in mice with autoimmune diabetes. Chronic treatment with an  $ET_A$  receptor-selective ERA (BSF 431314, a follow-up compound of ambrisentan) for 6 weeks reduced BMP-receptor II expression by almost 80%, indicating its regulation through endothelin (Reproduced from [132], with permission of the publisher)



diesel exhaust, increases cardiovascular morbidity [112]. Exposure to diesel exhaust results in  $ET_{B}$  receptor dysfunction [113] and increases in vasoconstrictor responses to ET-1 [114]; car fumes have also shown to increase vascular endothelin in atherosclerosis [114, 115]. Effects of diesel exhaust on endothelin activation have also been observed in humans [116]. Fine particulate matter as part of air pollution has also been implicated in diseases such as hypertension and airway diseases [117] and causes inflammation [21]. Increases in carbon and particulate matter air pollution increases circulating ET-1 levels [118], and  $ET_A$  receptor expression [111, 119]. Importantly, air pollutants may also induce endothelin and endothelin receptors in the absence of any local or systemic inflammation [120].

Obesity is another independent risk factor for atherosclerosis [121, 122]. Six years ago, according to WHO estimates, 1.6 billion adults worldwide were overweight, and 400 million were obese. By 2015, the numbers are expected to increase further to 2.3 billion overweight and 700 million obese, respectively [123]. In both cases, these numbers do not include children and adolescents, in which obesity has also become a worldwide problem [121]. Obesity leads to insulin resistance and subsequently to diabetes, and is associated with activation of the renal but not the pulmonary reninangiotensin system in an ET<sub>a</sub>-dependent manner [121]. Antidiabetic and beneficial structural effects of ERA treatment have been reported in numerous preclinical studies [58, 124–127], and recent clinical data suggest that proteinuria in diabetes may be directly linked to endothelin activation [128–131]. In diet-induced obesity, renal activation of ACE occurs, which is regulated via ET<sub>4</sub> receptors, suggesting that under certain conditions ET<sub>A</sub> receptors may actually act as ACE inhibitors [43]. ET<sub>A</sub> receptors also regulate vascular expression of bone morphogenetic protein (BMP)-2 [132] (Fig. 15.3), an important regulator of vascular calcification and cell growth [133]. In obesity, endothelin and  $ET_{A}$  receptors are increased in the vasculature and kidney [43, 134, 135] ET-mediated vascular tone and metabolic function is abnormal in obesity and diabetes [59, 134–137]. In type 1-diabetes,  $ET_{A}$  receptor blockade also prevents



**Fig. 15.4** Effects of diabetes and ERA treatment on ECE-1 and ECE-2 gene expression in the arterial vasculature of control (CTL) and non-obese diabetic (NOD) mice, a model of type 1 diabetes. Diabetes increased expression of ECE-1 and ECE-2. This upregulation was completely prevented by concomitant endothelin receptor blockade using the orally active compound BSF/LU461314, indicating that ERA treatment has ECE-inhibitor-like effects under certain pathological conditions (Reproduced from [126])

upregulation of ECE-1 and ECE-2 isoenzymes [126] (Fig. 15.4). Endothelin also directly affects obesity development by regulating adipogenesis and lipolysis [138, 139], and stimulates the release of pro-inflammatory cytokines from adipocytes [25]. Thus, endothelin blockade may be particularly feasible to interfere with cardiovascular and renal disease in obese patients and possibly might also be suitable for treatment of obesity and its associated complications such as insulin resistance [58]. Endothelin inhibits insulin action [140], and accordingly, Pernow and coworkers have recently shown that insulin sensitivity or impaired skeletal muscle glucose uptake in insulin-resistant humans [59] is improved after ERA treatment [141]. Insulin, which facilitates glucose uptake in target tissues [59], not only stimulates endothelin [143], suggesting a positive feedback loop between these two pathways which may be of therapeutic importance regarding ERA treatment.

Endothelin blockade may thus be particularly feasible to prevent cardiovascular and renal disease in these patients and possibly might also be suitable for treatment of obesity and its associated complications such as insulin resistance [58]. Finally, endothelin contributes to glycemic control and glucose uptake [144–146] and development of type 1 diabetes [126], making metabolic diseases and obesity potential and attractive clinical targets for the application of endothelin receptor antagonists.

#### 15.3.3 Heart Failure

Congestive heart failure is a clinical syndrome with high mortality caused by different etiopathologies, hypertension and coronary artery disease being among the most important ones. In the heart, the endothelin system helps to maintain cardiac function, with ET-1 and the ET<sub>A</sub> receptor being the predominant signaling components of the endothelin system [147-149]. In the normal heart, endothelins contribute to inotropy, chronotropy, and arrhythmogenesis, as well as myocardial contractility [19]. Early studies have shown that impairment of cardiac function results in increases in circulating levels of ET-1 or big ET-1 [17] that are reliable prognostic indicators of survival in patients with heart failure [150, 151]. Elevated circulating levels of ET-1 in heart failure are thought to derive from pulmonary congestion, which impairs the clearance function of the lung [152]. The role of endothelin in the post-infarct heart remains controversial. Although a number of experimental prevention studies have demonstrated a benefit of chronic endothelin blockade on survival and left ventricular remodeling in animals of myocardial infarction [149, 153–155], there is currently no evidence for a protective effect of chronic endothelin antagonism in humans with heart failure [23, 156]. It is also important to note that in all experimental studies except for one [157] treatment was begun in animals without preexisting heart failure, i.e., before or immediately after inducing myocardial infarction. In chronic heart failure, i.e., in long-term survivors of experimental infarction, ET, receptor blockade more or less normalized hypertrophy of the right atrium and ventricle and reduced pulmonary congestion [157] (Fig. 15.5). Moreover, treatment was performed in models that had no ischemic myocardial damage due to coronary artery disease which is present in many heart failure patients. Thus, well-designed experimental studies are still lacking. Studies in humans showed that treatment with the nonselective ET receptor antagonist bosentan over 2 weeks reduced pulmonary and mean arterial pressures, pulmonary and systemic resistance between 10% and 30%, and caused a 13% increase of the cardiac index [158]. Similar effects were seen in heart failure patients who received the ET<sub>A</sub> receptor-selective antagonist BQ-123 where treatment reduced pulmonary and arterial pressures, decreased systemic (but not pulmonary) resistance, and increased cardiac index [159]. Although the results of these early studies looked promising, all long-term clinical trials investigating chronic endothelin receptor antagonist treatment in patients with acute or chronic congestive heart failure have been negative without exception [23, 55, 156, 160]. These studies include the ENABLE trial (bosentan), the HEAT-CHF trial (darusentan), the EARTH trial (darusentan), the ENCOR trial (enrasentan), and the RITZ-1 through RITZ-4 trials (tezosentan) [23]. A problem inherent to most of these studies is the fact that



**Fig. 15.5** Effects of chronic experimental heart failure and ERA treatment with darusentan on right atrial and ventricular remodeling and pulmonary edema measured by tissue weight. In rats which had survived acute myocardial infarction for 6 months, right atrial and ventricular weights were increased compared to sham controls (CTL), compatible with right heart hypertrophy. Similarly, lung weight, an indicator of pulmonary edema, was increased by approximately 35%. After darusentan treatment (50 mg/kg/d, DAR) of animals with chronic heart failure for 6 weeks, increased myocardial or pulmonary weights were reduced or even normalized. \*p<0.05 vs. CTL; †p<0.05 vs. CHF (Reproduced from [157], with permission of the publisher)

only the results of some of these studies were published and also that if published, not all data were included in the manuscripts or are otherwise available to the scientific community [161]. Also, due to FDA regulations study patients had to be maintained on standard heart failure therapy and received the endothelin antagonist on top of standard treatment, which could be one of the reasons for the disappointing results. It may well be possible that certain predisposing pathological conditions in heart failure patients may be determinants of therapeutic success or failure, such as development of peripheral edema, one of the most often encountered side effects seen in patients on endothelin blocker. In addition, drug dosages [23] and drug toxicity of sulfonamide-based ERAs in patients with heart failure may be a critical problem, particularly in those with right heart failure and subsequent hepatic congestion. Before these data have been fully analyzed and published, no definitive conclusion on whether endothelin antagonists on top of ACE or ARB treatment may be effective remedies in selected patients with heart failure is possible.

#### 15.3.4 Pulmonary Arterial Hypertension (PAH)

Both heart and lungs are important sources and targets of ET-1. Unlike normal subjects, patients with pulmonary hypertension have higher pulmonary arterial vs. venous plasma levels of ET-1, suggesting increased pulmonary ET-1 production and/or decreased lung clearance [19]. In the pulmonary vasculature, ET-1 induces  $ET_A$ -dependent vasoconstriction, and perhaps more importantly, acts as a growth factor leading to proliferation of pulmonary artery vascular smooth muscle cells

(Fig. 15.2) [51]. The inhibition of cell growth by ERAs is likely to be one of the important factors contributing to the long-term benefit of endothelin blockade in patients with pulmonary hypertension interfering with pulmonary artery remodeling [162]. Effectiveness of both  $ET_A$  receptor antagonists as well as nonselective ET receptor blockade with bosentan has been demonstrated to reduce pulmonary artery pressures, right ventricular hypertrophy, and remodeling of pulmonary arteries in a number of experimental studies [147, 162, 163]. In contrast,  $ET_B$ -selective antagonists administered to dogs with pulmonary hypertension increase pulmonary resistance and pressures [19]. This suggests that selective  $ET_A$  receptor antagonists might be advantageous in the treatment of pulmonary hypertension.

In the past two decades, the pharmaceutical industry has extensively tested pulmonary hypertension as a clinical target for ET antagonism, and first randomized clinical trials have demonstrated beneficial effects on clinical outcome and quality of life compared with placebo [164, 165]. In 2001, bosentan (Tracleer<sup>TM</sup>) was the first endothelin receptor antagonist ever to receive approval for the treatment of patients [166]. This historically important approval was granted for the treatment of primary pulmonary arterial hypertension (PAH), a severe disease with unfavorable prognosis often seen in patients with connective tissue disease, heart failure, or HIV infection [167, 168]. Meanwhile, another ET antagonist has been granted approval by the FDA or by Federal Health Agencies around the world for the treatment of PAH, the ET, receptor-selective antagonists ambrisentan (Letairis<sup>TM</sup>), a follow-up compound of darusentan. Whether selective antagonists are superior over nonselective ones in terms of clinical benefits, side effects, and survival in PAH patients is unknown, and the same holds true for the two different classes of endothelin antagonists (propionic vs. sulfonamide compounds); respective clinical trials are needed, and ongoing trials also include combination therapy of endothelin antagonists as with other pulmonary vasodilators such as sildenafil or prostacyclin [23]. A first study suggests superiority of bosentan over prostacyclin treatment in patients with cirrhosis and pulmonary hypertension [26]. Finally, new treatment options such as aerosol delivery of endothelin antagonists appear to be efficacious and can minimize side effects [169–172]. Endothelin antagonists have now become a standard part of pulmonary hypertension therapy to improve survival in these severely ill patients.

#### 15.3.5 Cardiac Transplantation and Allograft Rejection

Chronic allograft rejection after cardiac transplantation increases endothelin in the graft [173] but also increases the expression of endothelin system components in the host organs such as the liver [174] (Fig. 15.6). An immunomodulatory role of endothelin has also been shown in different models of acute or chronic rejection following solid organ transplantation. Even in the absence of standard immunosuppression from endothelin receptor,  $ET_A$  blockade was able to prevent upregulation of circulating interleukin and TNF  $\alpha$  levels [175] after cardiac allo-transplantation which again would be compatible with a direct role of endogenous endothelin contributing to the host's immune response. It is thus not surprising that treatment with



ERAs very effectively interferes with the development of graft atherosclerosis or the development of fibrosis or glomerulosclerosis-related to solid organ transplantation of the liver, lung, aorta, heart, or kidney, even in the absence of immunosuppression [154, 176–180]. Up to now, no clinical studies have been performed to investigate the therapeutic potential of endothelin receptor antagonists in transplantation medicine, which possibly could also lead to improved donor organ preservation by adding ET antagonists to the preservation solution [181] or to novel combination therapies. Possibly, this would also allow to reduce the amount of immunosuppressant drugs which are responsible for many of the unwanted side effects of solid organ transplantation, such as neurotoxicity [182, 183], development of kidney disease due to nephrotoxicity of drugs like cyclosporin, and secondary, drug-induced hypertension due to immunosuppressive therapy with cyclosporin [184, 185].

# 15.3.6 Proteinuric Renal Disease

Chronic renal disease and proteinuria are independent risk factors for atherosclerosis and coronary artery disease [52]; in fact, the majority of deaths of patients with renal disease is due to cardiovascular causes [52]. Work from several laboratories in the early 1990s has demonstrated that the endothelin system contributes to the pathological changes leading to glomerulosclerosis in models of hypertension or renal ablation (reviewed in [186-188]). This pro-sclerotic effect of endothelin in the kidney was confirmed by overexpressing human ET-1 in mice which develop glomerulosclerosis even without developing hypertension [54]. A large number of experimental prevention studies have investigated the effects of chronic endothelin blockade on the development of glomerulosclerosis due to hypertension, subtotal nephrectomy, chronic nitric oxide deficiency, diabetic nephropathy, focal segmental glomerulosclerosis, among others [55, 189]. The majority of these studies found pronounced nephroprotective effects that were either in part or even completely independent of systemic blood pressure [186, 190–194]. The mechanisms by which endothelin contributes to glomerular injury following damage of podocytes [192-194], which form the glomerular filtration barrier, include protein that induces endothelin in glomerular podocytes, which in turn causes reorganization of the podocyte actin cytoskeleton [195].



**Fig. 15.7** Proposed concept of renal disease regression after inhibition of endothelin action through blockade of endothelin  $ET_A$  receptors, RAAS-inhibition through blockade of angiotensin  $AT_1$  receptor blockers (ARBs) or ACE inhibitors, or statin therapy. *Left*: Glomerular renal injury with damage of podocytes (*dark green*) and formation of fibrotic, "sclerotic" tissue (*yellow*) resulting in proteinuria ("Injury"). *Right*: Glomerulosclerosis can be reversed by drug treatment if renal structural injury is less than severe. Disease regression is accompanied by improvements of glomerular architecture and structural improvement of podocytes (*dark green*) and the GBM of the glomerular capillary ("Regression") (Reproduced from [52], with permission of the publisher)

This effect is mediated by  $ET_A$  receptors [194, 196]. Interestingly, dietary protein aggravates renal injury by augmenting renal acid production and worsening proteinuria [197]. This effect can be blocked by the  $ET_A$ -selective antagonist darusentan but not by the nonselective antagonist bosentan [197], indicating a role for the  $ET_B$ receptor which is highly expressed in podocytes. Indeed, this hypothesis is supported by a most recent study indicating sera of patients with proteinuria increase glomerular formation of endothelin and shedding of the podocyte-specific protein nephrin, which can be prevented by an endothelin  $ET_A$  receptor antagonist [198]. These studies collectively and strongly indicate that glomerular protein loss, which is caused by and further aggravates podocyte injury, depends on mechanisms that are at least in part endothelin-mediated [52]. This appears to be even more important since proteinuria or albuminuria is a good predictor of future cardiovascular events [189, 199].

Only few studies have investigated the effects of endothelin receptor blockade in conditions in which renal disease was already established [52]. Studies have investigated the anti-proteinuric effect of endothelin receptor antagonists in normotensive or severely hypertensive animal models [192, 194, 200, 201]. In these studies, treatment not only a reversed proteinuria but also lead to a partial healing of the previously injured glomeruli and podocytes (Fig. 15.7). This suggested that renal disease is a particularly relevant area for the clinical application of ERAs with the

potential to reverse established glomerular disease [53, 194, 201], as has been demonstrated for experimental vascular disease [202, 203].

# 15.4 Endothelin Antagonists in Clinical Practice: Current Developments

Within only 4 years after the discovery of endothelin, its receptors were cloned and receptor antagonists had become available [204, 205]. Several hundred compounds are available today of which the majority is orally active [206]. The first clinical trial in patients with congestive heart failure was performed in Zurich, Switzerland, in the early 1990s and results were published in 1995 [158]. Nevertheless, it took a number of years and numerous unsuccessful clinical trials in heart failure patients until endothelin receptor blockade could be established as a new therapeutic concept in clinical medicine [55, 147, 207]. Ten years ago, bosentan ( $Tracleer^{TM}$ ) was the first endothelin receptor antagonist to receive approval for clinical application from the U. S. Federal Food and Drug Administration (FDA) [166]. Bosentan, which is a nonselective ET<sub>A</sub>/ET<sub>B</sub> receptor antagonist, was approved in 2001 for the treatment of patients with primary pulmonary arterial hypertension (PAH) [164, 165]. In 2007, ambrisentan (Letairis<sup>TM</sup>), an ET<sub>A</sub> receptor-selective antagonist, was also approved by the U.S. FDA for the same indication. A number of other receptor antagonists have been or are being evaluated in clinical studies for indications such as PAH, congestive heart failure-resistant hypertension, cancer, coronary artery disease, or proteinuric renal disease. The highly selective ET<sub>A</sub> receptor antagonist sitaxsentan (*Thelin*<sup>TM</sup>) had even approved for treatment of PAH in three continents; yet, after several cases of fatal liver failure, Pfizer withdrew Thelin<sup>TM</sup> from the market at the end of 2010 [208]. Two years earlier, Speedel announced the discontinuation of the development of avosentan after severe drug-related side effects including heart failure had occurred in diabetics with advanced proteinuric renal disease [208]. These studies will be briefly discussed below. The development of the ET<sub>A</sub> receptor antagonist darusentan as an antihypertensive with nephroprotective properties was abandoned by Gilead Sciences, Inc. after the completion of two phase III trials in patients with resistant hypertension at the end of 2009 [74, 76, 77, 208]. According to information available, issues such as short remaining patent life of darusentan and financial risks for further phase III trials were among the reasons for the discontinuation. In addition, ERAs have been evaluated in clinical trials for the treatment of coronary artery disease and atherosclerosis [95–103], cancer [23, 209–211], and autoimmune diseases such as scleroderma [51, 212–218]. More recently, proteinuric renal disease has been revived as target for endothelin antagonism [84, 208]. Treatment with a selective ET receptor antagonist atrasentan (Xinlay<sup>TM</sup>) for 12 weeks reduces proteinuria and blood pressure [219], and even more impressive reductions in albuminuria reduction were seen using the endothelin ET, receptor blocker avosentan in patients with diabetic nephropathy in the ASCEND trial [129, 130]. Interestingly, these effects were mostly independent of systemic blood pressure [129, 130]. In many of the patients with chronic renal disease participating in the ASCEND trial, fluid retention and heart

failure developed because of which the study was stopped prematurely [129]. It is noteworthy that the effects of proteinuria were seen despite the fact that patients are already receiving ACE inhibitors or AT, receptor antagonists, indicating additive and thus independent beneficial effects of both treatments. Thus, ERAs represent a new treatment option to halt and even reverse proteinuric renal disease (Fig. 15.7). Antiproteinuric effects of ERA therapy were also observed with the ET<sub>A</sub> receptor antagonist sitaxsentan [216, 220-223]. The ET, antagonist atrasentan was also recently reported to have anti-proteinuric effects in patients with diabetic nephropathy, without having major side effects [128]. It should be noted that most of the patients studied in randomized endothelin antagonist trials in hypertension and diabetic nephropathy were overweight or obese, conditions known to be associated with impaired renal sodium handling [224]. Thus, it is likely that the side effects of endothelin blockade will depend on the overall health status and comorbidities of the patient receiving the drug. Indeed, in patients with chronic renal disease and normal body weight receiving ET<sub>A</sub> receptor antagonists, edema rarely occured [216, 220-223].

# 15.5 Conclusion and Perspectives

Endothelin – acting predominantly through the ETA receptor – is now recognized as a multifunctional peptide with cytokine-like activity affecting almost all aspects of cardiovascular cell function. Although pharmaceutical companies had rapidly developed drugs blocking endothelin receptors within only a few years after the discovery of endothelin, clinical drug development has been complicated by the fact that both, pharmaceutical industry and clinical investigators, embarked in clinical trials without really knowing endothelin physiology in general and in humans in particular. Also, at the time, the relevance of the endogenous endothelin system in maintaining central organ function in disease (i.e., during heart failure) was not known. It came to no surprise that the largest part of clinical trials were negative, i.e., patient selection (comorbidity burden, stage/severity of disease), excessively high doses of ERAs used, liver toxicity of the sulfonamide-based ERAs in patients with liver comorbidities (hepatic congestion in heart failure, fatty liver disease in obese type II diabetics), and the FDA requirement to study ERAs only if given on top of standard therapy are some of the reasons why so many trials failed. Also, timing of therapy initiation appears to be a critical issue, as is evident from studies in patients with advanced form of cancer, which have been mostly negative [209]. Recent work from Theodorescu's laboratory has shown that endothelin plays a critical role in cancer metastasis [225], which may in part explain the inefficacy of ERA treatment in advanced forms of cancer [209, 210, 226]. It is therefore reasonable to assume that ERA treatment (with its controllable side effect fluid retention) will be effective only if disease is diagnosed early, as has been shown for moderate but not advanced renal failure [128–130].

Some of the clinical indications initially chosen for clinical studies such as heart failure have been not yet shown to benefit from ERA therapy on top of standard



treatment due to the lack of adequately designed studies and inadequate patient selection [227]. In contrast, therapeutic efficacy of ERA therapy had been shown in preclinical studies of PAH, which became the first clinical indication for ERAs [166]. Similarly, results from preclinical studies of diseases that are similarly associated with cell growth and/or inflammatory activation such as or resistant arterial hypertension and glomerulosclerosis or immune-mediated disease such as cancer, connective tissue diseases, chronic allograft rejection, or metabolic diseases such as obesity or diabetes (Fig. 15.8) suggest that these conditions could become new indications for endothelin antagonist therapy in the future [27, 208, 227]. Today, more than two decades after the discovery of endothelin and its receptors, only two compounds (bosentan and ambrisentan) are approved and in use for treatment of patients, and only for two indications (PAH and scleroderma-related ulcerations). It is well possible that factors such as the desire to be the first to publish results from clinical studies with these new drugs, lack of knowledge about limitations of patient suitability and disease severity, and perhaps hope for economic reward from the potential sales of "blockbuster" drug candidates pre-marketed to investors have contributed to the unsuccessful clinical drug development of ERAs [227]. Also, some drug companies dropped drug candidates after successful completion of phase III trials for which the remaining patent lives was only a few years. Several hundreds of ERAs have been developed [206], and well and carefully designed clinical studies in correctly selected patients are still warranted to test, verify, or disprove any therapeutic benefit of ERAs for cardiovascular medicine and related fields. That this is possible, without risking severe side effects using carefully selected patients, was recently demonstrated by Kohan and colleagues in patients with moderate proteinuric renal disease [128]. Hope remains that ERA treatment will be available for more than only two indications once the pharmaceutical industry realizes the potential of their drugs and supports investigators in performing correctly done clinical trials.

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