



# ROS signaling and redox biology in endothelial cells

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**Abstract** The purpose of this review is to provide an overview of redox mechanisms, sources and antioxidants that control signaling events in ECs. In particular, we describe which molecules are involved in redox signaling and how they influence the relationship between ECs and other vascular component with regard to angiogenesis. Recent and new tools to investigate physiological ROS signaling will be also discussed. Such findings are providing an overview of the ROS biology relevant for endothelial cells in the context of normal and pathological angiogenic conditions.

**Keywords** Reactive Oxygen Species · Redox signaling · Angiogenesis · Genetically-encoded sensors · Redox compartmentalization · Pathological angiogenesis

## Introduction

Reactive Oxygen Species, also known as ROS, are an important constituent of cellular physiology since they are normally produced in response to disparate exogenous and endogenous stimuli and they are continuously generated, transformed and consumed in tissues during the normal

metabolic activity [1, 2]. A growing body of evidence suggests the existence of an intricate balance between ROS-producing and ROS-scavenging systems that are tightly regulated over time and space and interact with the cellular redox-sensitive elements to shape and finely modulate downstream signaling events in a cell-specific and context-specific manner [3]. In this respect, endothelial cells (ECs), which form blood vessels and the circulatory system, are quite peculiar. Indeed, compared to other cells, they act as an interface between the tissues of different origin and circulating elements such as oxygen, metabolites, and fluid stress. Indeed ECs are constantly exposed to a different array of biochemical and mechanical stimuli and actively adapt their biological responses to preserve the homeostasis of the vascular function [4]. ROS might function as a double-edged sword in endothelial cells. A moderate increase of ROS may promote cell proliferation and survival. However, when the burden of ROS reaches a certain level (the toxic threshold), it may overwhelm the antioxidant capacity of the cell and trigger cell death. Under physiological conditions, normal endothelial cells maintain redox homeostasis with a low level of basal ROS by controlling the balance between ROS generation (pro-oxidants) and elimination (antioxidant capacity). Cells in normal vessels can tolerate a certain level of exogenous ROS stress owing to their 'reserve' antioxidant capacity, which can be mobilized to prevent the ROS level from reaching the cell death threshold. Although high levels or prolonged formation of ROS is generally associated to vascular dysfunctions such as diabetes, carcinogenesis atherosclerosis and aging due to DNA, protein and lipid damage, appropriate levels of ROS have been shown to be indispensable mediators of physiological processes and redox-regulated cellular signaling pathways in endothelial cells.

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## ROS signaling: principles, facts and locations

Despite the term ROS includes radicalic (e.g., hydroxyl radical, OH<sup>•</sup>) and non-radicalic (e.g., hydrogen peroxide, H<sub>2</sub>O<sub>2</sub>) molecules derived from incomplete reduction of oxygen (O<sub>2</sub>), it is important to recognize that different species possess distinct reactivity, half-life and molecular targets that influence their selectivity and dictate their biological relevance in a specific context [5]. Among the diverse ROS, hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) fulfills most if not all the prerequisites for serving as an intracellular second messenger and appears to be the evolutionarily selected ROS for redox signaling purposes. Indeed, this molecule is almost ubiquitously generated through direct activation of specific systems or alternatively by enzymatic conversion of other precursors (i.e., superoxide anion, O<sub>2</sub><sup>•-</sup>), has a relatively long half-life and can reach target molecules located far from the site of its generation, exerting short-term and prolonged effects in different signaling pathways [6, 7]. Understanding the chemistry of redox signaling is essential to define the specificity and the principles of downstream modifications that represent the real interface between ROS and redox-sensitive targets. It is now well established that under appropriate circumstances H<sub>2</sub>O<sub>2</sub> can react with and modify specific redox-reactive cysteine residues (with pKa values between 4 and 5) within target proteins, inducing a covalent modification that is able to influence the activity, stability or subcellular localization of a great variety of molecules, including enzymes, transcription factors, ion channels, cytoskeletal proteins, tyrosine kinase receptors, protein kinases and phosphatases [8–14]. It is important to mention that other amino acids such as methionine and histidine can be oxidized by ROS, but little experimental evidence has been provided and some of the underlying mechanisms as well as the biological consequences of their modifications in redox signaling are still largely unknown. Since the most extensively studied and predominant post-translational modification of redox-sensitive elements involves the reversible oxidation of cysteines, we will mainly discuss the general mechanisms and the potential implication of cysteine-based redox signaling in functional angiogenesis. Cysteine is one of the more readily oxidized amino acids though its relative high pKa values (8–9 at physiological pH) make it a slowly reacting nucleophile due to the prevalence of the protonated thiol form (-SH) in the sulfur atoms. Interestingly, the proximity of positively charged amino acids (Arg, His, Lys) in the local microenvironment of the protein can lower the pKa of specific cysteines (3–4 at physiological pH) greatly increasing their dissociation rate into the thiolate form (S<sup>-</sup>) and therefore their susceptibility to ROS-induced modifications [15–17]. Therefore,

it seems that only a limited group of reactive cysteines has been evolutionarily selected to participate in redox signaling events although the existence of additional determinants and mechanisms is under investigation and remains still elusive. It is, however, now well recognized that most of the biological oxidants, including H<sub>2</sub>O<sub>2</sub>, react exclusively with the thiolate anion form [15, 17, 18]. Mild oxidation of redox-sensitive cysteines generates reactive sulfenic acid (SOH) that can either form intramolecular/intermolecular disulfide bonds or undergo further oxidation to sulfinic (SO<sub>2</sub>H) or sulfonic (SO<sub>3</sub>H) acid forms [19]. With the exception of sulfonic acid formation, the sulfenic acid and to a lesser extent the sulfinic acid formation can be reversed by specific reducing systems including peroxiredoxins and thioredoxins [15], determining spatial and temporal control of the associated signaling event [3]. Therefore, in contrast with pathological alterations (pathological angiogenesis), the general principles that drive redox signaling events require the controlled, specific and reversible interaction between physiological amounts of ROS (i.e., H<sub>2</sub>O<sub>2</sub>) and an appropriate biologically relevant target (thiolate anion of a reactive cysteine residue) that should intercept the peroxide molecules avoiding the kinetic competition of highly efficient scavenging systems or the prolonged accumulation of potentially harmful byproducts [20].

## Redox compartmentalization

Different functions of the mammalian cells including the ECs are optimized by clear separation of compatible reactions and chemistries into defined subcellular compartments limited by lipid-containing membranes or even into specialized microdomains located within a certain cellular region [21]. Accumulating knowledge of redox processes in the cytoplasm, nucleus, mitochondria and the secretory pathway of mammalian cells indicates that peculiar redox features have co-evolved with specific residing elements that receive and transduce redox-related signals under tightly controlled spatiotemporal regulation. The emerging concept known as “redox hypothesis” assumes that different redox couples, in their thiol/disulfide forms, are confined in specific subcellular compartments and maintained at distinct steady-state redox potentials that confer them independent properties in terms of specificity and reactivity towards a defined redox event, promoting the regulation of multiple biological processes [22, 23]. Within compartments, the redox couples appear to be controlled by the opposing action of reductive (i.e., Thioredoxin and Glutathione systems) and oxidative systems (i.e., NADPH Oxidases and mitochondrial ETC) that ultimately dictate the redox state of the oxidizable thiols located within

susceptible proteins. Importantly, the redox signaling and control systems co-evolved in specialized redox environments that ensure optimal efficiency while disruption of these complex redox circuits can impair redox control and lead to oxidative stress [24]. Intuitively, defining the mechanisms through which the regulated/reversible oxidation of thiols is exerted within different subcellular compartments will provide a better comprehension of pathophysiological mechanisms associated with oxidative stress [2]. Despite the great relevance of this aspect, it has been historically difficult to achieve a comprehensive knowledge of the interrelation between the production of a certain ROS molecule and the functional modification of the major redox couples or sensitive proteins residing within a certain organelle. The detailed study of these processes would therefore require appropriate tools to investigate local and specific changes with high spatial and temporal resolution that only recently became available.

### Experimental approaches to investigate redox compartmentalization

To study the link between ROS formation and redox signaling, it would be desirable to identify the ROS molecule, the redox couple and the putative target proteins that participate to a certain biological process and define their relationship in a spatiotemporal context. A great variety of techniques have been developed to measure ROS generation, to study the redox status (i.e., redox potentials) of specific redox couples or to identify modifications of thiols groups within redox-sensitive proteins [21]. For example, small chemical probes have been extensively used to detect the generation of Superoxide anion ( $O_2^-$ ), Hydroxyl radical ( $OH^\cdot$ ),  $H_2O_2$  or less defined ROS-induced alterations (DCFH-DA) in different types of cells; similarly, high-performance liquid chromatography (HPLC) has been employed to estimate GSH/GSSG and NAD(P)H/NAD(P)<sup>+</sup> redox potentials while the combination of redox western blot, chemical labeling of thiols groups (ICAT) and mass spectrometry techniques has been exploited to gain information on the redox status of cysteines residing within proteins of interest [25]. Although widely used, these methods still suffer from general limitations and cannot provide conclusive or totally reliable information of a redox signaling event. In particular, even when sufficient specificity is achieved, the main pitfalls are related with the disruption of cell integrity that precludes dynamic measurements in intact cells and generates experimental artifacts with partial or complete loss of compartment-specific information. Conversely, when organelle-specific probes are employed in living cells, the lack of reversibility poses serious limitations for the temporal analysis of a

given process [26]. In the following section, some of the most common fluorescent probes, falling into the categories of chemical and genetically encoded molecules, will be briefly described.

### Chemical probes for ROS detection

Several small molecule fluorescent probes are currently available, though few of them can be targeted into specific subcellular organelles and possess sufficient sensitivity and selectivity for the detection of a definite ROS molecule generated at physiological levels. These molecules can be grouped into two main classes, “oxidant sensitive” or “non-redox” dyes. The former includes commonly used probes that become fluorescent after being oxidized while the latter comprises molecules wherein the nucleophilic attack by the oxidant releases a masked fluorophore. Probably the most widespread-used detection method for  $H_2O_2$  in cultured cells is based on the oxidation of dihydrochlorofluorescein ( $H_2DCFH$ ) to the fluorescent derivative dichlorofluorescein (DCF). However, artifactual oxidation of the probe can occur without the formation of  $H_2O_2$  and is more generally related to the activation of poorly defined oxidative processes [27–29] or the induction of apoptotic cell death leading to cytochrome c release from the mitochondrial inner membrane [30]. Other oxidant-sensitive indicators include MitoSOX Red, a hydroethidine derivative that is uptaken by actively respiring mitochondria and generates 2-hydroxiethium after reacting with superoxide, or the reduced MitoTracker CM- $H_2TM/XROS$  dyes, that become fluorescent, positively charged and readily accumulate into well-energized mitochondria upon oxidation by still undefined ROS molecules. However, the major drawback for the oxidant-sensitive class of sensors is a general lack of specificity, a low sensitivity and the absence of reversibility [31]. New generation of chemical probes with improved sensitivity and specificity such as Amplex Red (dihydroxyphenoxazine derivative), Peroxy Green1 or Peroxy Crimson1 (Boronate derivatives) was subsequently introduced allowing detection of physiological amounts of endogenous  $H_2O_2$  produced in response to growth factor stimulation [27, 32]. Importantly, the attachment of appropriate functional groups has enabled compartment-specific localization of peroxide generation as for the nuclear-Peroxy Emerald1 (nucPE1) [5], mitochondrial-Peroxy Yellow1 (MitoPY1) [33], or even measurement of redox events in living organisms as for Mito-Boronic acid B (MitoB) or SHP-Mito [34, 35]. Nevertheless, intrinsic limitations related to slow reaction rates, lack of reversible behavior and the inability to generate animal models with stable transgenesis raise important concerns on the applicability of these

compounds to signaling events and the correct interpretation of the experimental information provided by their use in living systems.

### Genetically encoded redox sensors

One of the most innovative, exciting and biologically relevant tools for rapid, real-time and reversible detection of specific redox events with high spatiotemporal resolution has been represented by the introduction of genetically encoded redox-sensitive proteins. Many of the limitations associated with the use of chemical probes were already overcome by the development of the first GFP-based redox-sensitive probes. By introducing reactive cysteines in strategic positions of either the GFP or YFP  $\beta$ -barrel scaffold, the groups of Jakob Winther and James Remington, respectively, created the redox-sensitive yellow fluorescent protein (rxYFP) [36] and the redox-sensitive GFP (roGFP) [37]. In these sensors, the redox status of the sensitive cysteines depends on the equilibration with the GSSG/GSSH redox couples through the thiol–disulfide exchange catalyzed by the enzyme glutaredoxin (Grx), while the fluorescent properties of the chromophore region are accordingly affected by redox events that modify the steady-state level of the oxidized or reduced susceptible cysteines. Although both allow specific and non-invasive analysis of the dithiol–disulfide equilibrium with the glutathione system, the rxYFP has quite limited dynamic range, is sensitive to pH and chloride anions and does not possess a clear ratiometric behavior. Moreover, its equilibration rate with the glutathione system depends on the availability or the activity of Grx isoforms. This limitation was partially overcome by fusing the rxYFP to Grx1 to eliminate the dependency on endogenous Grx (rxYFP-Grx1) [38]. In contrast, the roGFP class of sensors has two distinct excitation peaks around 400 and 480 nm with a single emission wavelength around 520 nm, that shift in opposite directions when the sensitive cysteines located on  $\beta$ -strands 7 and 10 exist in the dithiol or disulfide forms. When the vicinal cysteines are oxidized, the formation of a disulfide bridge induces several rearrangements in the  $\beta$ -strands and other conformational changes that ultimately influence the protonation status of specific phenolic groups residing within the chromophore region, producing divergent changes in the excitation peaks. This behavior can be exploited for ratiometric measurements that are insensitive to experimental artifacts related to different expression levels of the sensor, photobleaching or changes in the cellular morphology [26]. Further implementation and genetic engineering of the prototypical roGFP by the group of Tobias Dick led to the generation of additional variants (six so far), among which the roGFP2 is the most used and best characterized due to its pH insensitivity, its high dynamic

range and a suitable midpoint redox potential ( $-280$  mV) for measurement of redox events in most of the organelles of mammalian cells. By fusing redox-active enzymes with redox-sensitive roGFP2 moiety, the same group created redox-relay based sensors that are able to rapidly equilibrate with defined redox pairs such as GSSG/2GSH (Grx1-roGFP2) or  $\text{H}_2\text{O}_2/\text{H}_2\text{O}$  (roGFP2-Orp1) in a reversible, kinetically efficient and specific way [39–41]. Not surprisingly this class of sensors has been successfully employed to study redox changes in different subcellular compartments (cytosol, mitochondria, ER) and various experimental conditions in both cultured cells [22, 42–45] and living organisms [45–47].

Another  $\text{H}_2\text{O}_2$ -specific sensor, called HyPer, was developed by the group of Sergei Lukyanov by inserting a circularly permuted YFP (cpYFP) into the regulatory domain of the OxyR transcription factor from *E. coli* [48]. Similar to the roGFPs, HyPer exhibits submicromolar affinity for  $\text{H}_2\text{O}_2$ , can be targeted in different subcellular districts [49] or even into specialized intracellular microdomains [50] and allows ratiometric and reversible measurements. Engineered variants with expanded dynamic range (HyPer2) [51] or improved kinetic response (HyPer3) [52] have been introduced and successfully employed in intact cells [53] and model organisms [54]. However, as for other cpFPs, the HyPer excitation ratio is quite sensitive to pH fluctuations so that an independent method for monitoring the pH changes in a given experimental setting should be devised to avoid artifactual results [26, 55]. Similar limitations have been reported for another sensor named cpYFP that was initially targeted into the mitochondria and appeared to detect superoxide production derived from the mitochondrial electron transport chain activity [56]. However, the underlying chemistry was not sufficiently clarified and the presumed specificity of cpYFP for superoxide has been debated for a long time [57] leading to a passionate controversy that only recently was solved by showing that cpYFP responds to pH rather than superoxide changes [57, 58]. Another rapidly expanding class of redox sensors is based on fluorescent resonance energy transfer (FRET) that exploits structural changes induced by different redox states to modify the distance between a FRET donor and acceptor. Though quite limited experimental information is currently available on FRET-based redox sensors, novel variants such as rOHser [59] [60] or CY-RL7 [61] have been recently introduced and targeted to the cytosol, mitochondria, endoplasmic reticulum and nuclei of different cell types [62] or even fused to the dual oxidase activator (DuoxA1) for detection of redox events occurring at the level of the plasma membrane [63]. Despite the great advantages and the exceptional contribution provided by the genetically encoded biosensors in the study of redox events, it should



be recognized that intrinsic limitations are still present such as the restricted number of different fluorophores that are currently available or potential alterations of cell physiology (e.g., signaling pathways) that might derive from the introduction of the sensor in a living system [25]. For these reasons, care should be taken for the interpretation of the results and additional methods should be used to further support the experimental hypotheses under investigation.

### Mechanisms of ROS production and scavenging in endothelial cells

ECs form an active monolayer organ that enfolds the inner surface of the blood vessels in the cardiovascular system representing a natural barrier between the blood and the other tissues. ECs represent also an active platform of interaction with numerous cellular elements including leukocytes, vascular smooth muscle cells, pericytes and stem cells. ECs are metabolically active cells constantly exposed to different biochemical and biomechanical stimuli. They are very plastic in the way they adapt to these physiological conditions by preserving the integrity and homeostasis of blood vessels [64]. In several pathological conditions, this homeostasis is perturbed leading to vascular-related diseases [65]. Indeed, it is now well recognized that altered redox homeostasis plays a key role in the pathogenesis of endothelial dysfunctions including atherosclerosis [66], hypertension [67, 68] and diabetes [69], while the appropriate and controlled production of ROS is essential for the activation of signaling pathways involved in normal endothelial functions [70]. Indeed, ROS signaling in endothelial cells drives the formation of new vessels during development, a process called angiogenesis [71, 72]. Redox signaling events in the cardiovascular system rely on the precise, site-specific and reversible modifications of target proteins induced by either reactive oxygen (ROS) or nitrogen species (RNS). The principal mechanisms by which ROS and RNS generate specific biological effects in the endothelial cells include the post-translational modification of cysteine thiols within the active site or regulatory domains of target proteins, the oxidation of iron-sulfur cluster-containing centers and the S-glutathionylation or S-nitrosylation of protein thiolate anions (anionic forms of the sulfur atom contained in cysteine or methionine residues). In line of principle, a fine-tuned regulation of redox signaling depends on the complex interrelation between ROS/RNS production and their elimination exerted by scavenging systems or other regulators that control the intensity of ROS/RNS release or temporally regulate the effect of a certain modification associated to a biological event. The following section will describe the main ROS sources in the vascular system.

### NADPH oxidases

NADPH oxidases (NOXs) represent a large family of professional enzymes with oxidase activity that has evolved as specialized sources of ROS production and essential regulators of vascular function and dysfunction [73]. Since the discovery of the phagocytic NADPH oxidase (Nox2), six additional members have been so far identified (Nox1, Nox3, Nox4, Nox5, Duox1 and Duox2) and functionally characterized in mammals. Each of them possesses specific regulatory mechanisms, downstream targets and differential expression in tissues and cellular compartments [72].

All NOXs are membrane-spanning proteins with a core catalytic subunit (Nox1-5, Duox1-2) and a number of accessory subunits (i.e., p47phox, p67phox, p22phox, p40phox, Rac1-2, DuoxA1-2, NoxA1 and NoxA1) that facilitate the assembly of the functional enzyme. In response to specific upstream stimuli, the NOXs transfer electrons from the substrate NADPH to the molecular Oxygen, leading to either superoxide ( $O_2^-$ ) or  $H_2O_2$  production [74–77]. Importantly, ROS production from NADPH oxidases can occur either in the extracellular space or inside the cellular milieu, depending on the biological membrane wherein the enzyme is located, ranging from plasma membrane, endosomes, endoplasmic reticulum, nucleus, caveolae and mitochondria [77, 78]. Nox4 is the far most abundant isoform in the endothelial cells where in concert with Nox2 seems to be responsible for the basal tone of ROS derived from normal metabolic activity [79]. However, Nox1, Nox2, Nox4 and Nox5 have been shown to mediate physiological and pathological events in the vascular system [76]. Recent evidences suggest that NOXs regulate multiple redox-sensitive signaling pathways of the endothelial cells, including inhibition of tyrosine phosphatases [80], activation of specific transcription factors [81] and enzymes [82] or modulation of ion channels [83] in response to activating stimuli. Nox1 activity has been implicated in cell signaling, cell growth, cell motility and angiogenesis but also in pathologic alterations such as atherosclerosis, hypertension, inflammation and cancer [72, 84–86]. It has been recently demonstrated that NOX5 activation is required for stromal derived factor 1 $\alpha$  (SDF-1 $\alpha$ )-induced JNK3 activation and angiogenesis in bovine aortic endothelial cells [87].

It is known that Nox2-derived ROS are important mediators of p38 MAPK-dependent proliferation and VEGF-induced migration. Moreover, NOx2 activation appears to affect NO bioavailability and regulate the expression of adhesion molecules during angiogenesis and inflammation [76, 88, 89]. The precise role of NOX4 in physiological and pathological events is still controversial since under certain conditions this isoform was shown to promote oxidative stress and tumorigenesis [90] or positively regulate the

neovascularization process during oxygen-induced retinopathy [91], while evidence from Nox4<sup>-/-</sup> mice pointed out its protective role from ischemic and pro-inflammatory stress [79]. Similarly, Nox4 was shown to counteract hypertensive alterations [92] and promote angiogenesis through eNOS activation [82] or HIF1 $\alpha$  stabilization [93].

### Shear stress

ECs lining the lumen of the blood vessels are constantly exposed to blood flow that produces mechano-stress important to shape the vasculature and maintain ECs homeostasis. Interestingly, NOXs-derived ROS production has been shown to play a pivotal role in transducing the mechano signal, a process that modifies redox balance in response to altered mechanical load of the vascular system [94]. Depending on the pattern and the type of the stress, the activation of specific NOXs enzymes can be either beneficial or detrimental [95, 96]. Indeed, in some cases, NOXs-dependent ROS formation has been shown to promote cellular adaptation to physical forces and vascular protection during physiological mechano-stress (laminar shear stress) [8] while conversely disturbed blood flow (turbulent flow, oscillatory high rates) or extensive stretch has been associated to prominent ROS production due to NOXs overactivation (e.g., Nox1, Nox2), and subsequent oxidative damage [97, 98]. However, additional studies will be needed to better define the specificity of NOXs-dependent redox signaling in mechano-transduction events.

### Mitochondria

The mitochondria are considered the prominent sources of endogenous ROS under physiological conditions and deregulated mitochondrial ROS production is associated to many cardiovascular alterations [99]. The mitochondrial electron transport chain machinery (mETC), located in the inner mitochondrial membrane, is considered main responsible for mitochondrial ROS production. More specifically, NADH or FADH<sub>2</sub> molecules generated in the Krebs cycle are used as electron donors by four complexes in the mETC catalyzing the reduction of molecular oxygen to water through four single-electron transfer reactions. The controlled electrons flow is generally used to build up a chemiosmotic proton gradient across the inner mitochondrial membrane that ultimately drives ATP synthesis at the level of Complex-V (ATP synthase). At several sites along the respiratory chain, especially in the Complex I and III, the electrons can be diverted to reduce molecular oxygen or other electron acceptors and generate free radicals (e.g., O<sub>2</sub><sup>-</sup>). In addition to the inner membrane, ROS can be additionally produced in the intermembrane space

(IMS) by the cytochrome c interacting protein p66shc, in the matrix by metabolic enzymes such as aconitase, PDH,  $\alpha$ -KGDH, or even in the outer mitochondrial membrane (OMM) by the flavoprotein monoamine oxidases (MAO A and MAO B) [100].

A minor fraction of the superoxide derived from the mETC can leak into the cytosol through the pore-component VDAC, while the vast majority is enzymatically converted into H<sub>2</sub>O<sub>2</sub> by the Mn-SOD (SOD2). Since considerable amounts of peroxide can be generated during mETC activity, Catalase and Glutathione peroxidases cooperate to prevent excessive H<sub>2</sub>O<sub>2</sub> production and cellular toxicity, therefore shaping intensity and duration of peroxide levels for signaling purposes. Laminar shear stress was recently shown to promote mitochondrial ROS production and modulate the mitochondrial bioenergetic profile [101]; It was also shown that several cell types respond to acute hypoxia with a transient increase in mitochondrial superoxide that might be used to stabilize Hif1 $\alpha$  and contribute to preconditioning [102]; it has been recently proposed that mitochondrial ROS represent an important mechanism of eNOS activation during mitochondrial depolarization in isolated rat cerebral arteries [103]. Compelling evidence emphasized the role of mitochondria as master regulators of redox signaling through the use of ROS-dependent diffusible signals for inter-organellar communication [104]. Indeed, physical relocation of the mitochondrial network in a perinuclear cluster has been shown to promote hypoxia-induced transcription in the nucleus [105], while the use of mathematical models suggests that the dynamics of mitochondrial network might influence the production of intracellular ROS and the sensitivity to oxidative stress [106]. However, mitochondrial ROS can also be associated to detrimental conditions since hyperglycemia has been shown to increase mitochondrial ROS generation in cultured cells [107, 108] and in mice models of type2 diabetes [107, 109].

### Uncoupled eNOS

Nitric oxide (NO<sup>•</sup>) is a gaseous transmitter that stimulates vascular growth and remodeling. In mammals, three different isoforms of nitric oxide synthase have been described (NOS1-3). Among them, the endothelial (eNOS or NOS3) and the neuronal (nNOS or NOS1) enzymes mediate constitutive NO<sup>•</sup> production, while iNOS activity can be induced in response to pro-inflammatory or pro-angiogenic stimuli. NOSs are homodimeric oxidoreductases that upon activation transfer electrons from the NADPH to the heme iron leading to the oxidation of the guanidine group of L-arginine forming L-citrulline and NO<sup>•</sup> [110]. The presence of specific cofactors, such as BH<sub>4</sub>, L-

arginine and probably COQ10, is critical for keeping the enzyme activity coupled to NO production (coupled NOS) since their limited availability promotes the stabilization of a monomeric form with prevalent generation of  $O_2^-$  instead of  $NO^\cdot$  [111–113]. When uncoupled, eNOS can become a powerful source of  $O_2^-$  in the endothelium, leading to peroxynitrite formation (ONOO<sup>-</sup>) and dysfunctional alteration of the vascular system including hypertension or diabetes [114, 115]. However, controlled production of  $NO^\cdot$  regulates important processes of the vascular integrity and function such as vasodilation, endothelial cell proliferation and angiogenesis [71, 116]. Interestingly, the peculiar subcellular localization of the eNOS, located in the caveolae and the Golgi network membranes, might have important implications in redox signaling events [117, 118]. As for the reversible oxidation of cysteines to sulfenic acid, the formation of S-nitrosothiols is increasingly recognized as a post-translational modification that can alter structure and function of target proteins [119, 120]. Indeed, it has been shown that different endothelial cell lines activate eNOS in response to bradykinin leading to increased EGFR S-nitrosylation and subsequent activation of pro-angiogenic signaling [121]. Importantly, changes in the local redox potential can in turn induce reversible modification of eNOS activity through S-glutathionylation of specific cysteines [122] or dramatically affect  $NO^\cdot$  bioavailability [115, 123].

### Xanthine oxidoreductase

Xanthine oxidase (XO) and xanthine dehydrogenase (XDH) are convertible forms of the enzyme xanthine oxidoreductase (XOR) that catalyze the reduction of hypoxanthine to uric acid in the purine degradation pathway, generating  $H_2O_2$  and  $O_2^-$  as byproducts [124]. XDH is the predominant form in well-oxygenated tissues and is converted into XO by reversible thiol oxidation or proteolytic modification under pathological settings including ischemia, inflammatory states and hypoxia [125]. Though mainly expressed by epithelial cells in the liver, intestine and mammary gland, damaged cells can release XDH into the circulation where it can be converted into the XO form. Due to its high affinity for the glycosaminoglycans present on their cell surface, XO can bind to endothelial cells and promote vascular dysfunction [126] [127]. Early reports showed that hypoxia mediates the activation of XDH/XO in primary lung microvascular endothelial cells (LMVEC) through sequential activation of JAK-STAT pathway [128]. It has been recently shown that XO, activated in response to intermittent hypoxia, can promote HIF-2 $\alpha$  degradation through ROS-dependent activation of calpains [129]. Recent evidence also showed that XO-derived ROS

are required for mediating endothelial cell migration in response to the heparin-binding growth factor, pleiotrophin [130].

### Thioredoxin system

The Thioredoxin system includes two isoforms of thioredoxins (Trx1 and Trx2), an interacting protein with negative modulatory functions named Thioredoxin-interacting protein (TXNIP) and Thioredoxin Reductases (TrxR1, TrxR2, TrxR3) that use NADPH equivalents to regenerate the reduced form of thioredoxins once oxidized. Trxs are critical antioxidant enzymes protecting against non-radical oxidants through maintenance of an appropriate protein thiol–disulfide status. They both exert essential roles in vascular growth and remodeling through redox-dependent regulation of signaling events or cellular stress responses [131]. Trx1 is mainly localized in the cytoplasm but can translocate to the nucleus in a context-dependent way, while Trx2 is exclusively localized in the mitochondria [132] [133]. Using knockout mice and human microvascular cells (HME) silenced for TXNIP, it has been demonstrated that this protein is required for VEGF-mediated activation of VEGFR2 and angiogenesis both in vitro and in vivo [134]. It has been also shown that PARP1 inhibition in HUVEC induced TXNIP translocation to the plasma membrane, an event associated with VEGFR2 activation, suggesting that cellular relocalization of TXNIP can mediate nuclear-to-plasma membrane communication [135]. Similarly, it has been shown that TXNIP promotes Trx1 translocation to the plasma membrane leading to VEGFR2 transactivation in response to TNF- $\alpha$  induced ROS production [136]. TXNIP was also recently found to be essential for VEGFR2 internalization in Rab5 endosomes and subsequent activation of endothelial angiogenesis [136], confirming its role in normal vascular growth. Early reports evidenced a direct implication of Trx-1 in HIF1- $\alpha$  increased expression and activity during hypoxic conditions [137]. More recently, Takagi et al. [138] observed that Trx-1-dependent HIF1- $\alpha$  activation was associated with neoangiogenic events in human endothelial cells, suggesting a key role of Trx1 in the regulation of HIF1- $\alpha$ -dependent signaling related to pathological angiogenesis. On the other hand, however, Trx-1 might exert a beneficial effect promoting angiogenesis during tissue ischemia as evidenced by a recent study wherein adenoviral-mediated Trx1 overexpression in diabetic rats conferred protection against myocardial infarction [139]. In an earlier work, it was demonstrated that transgenic mice with increased expression of the mitochondrial Trx-2 isoform had enhanced arteriogenesis and angiogenesis compared to WT littermates, after femoral artery ligation-induced ischemia [140]. Interestingly, the mitochondrial thioredoxin reductase (TrxR2) has recently emerged as a central player in the control of

mitochondrial H<sub>2</sub>O<sub>2</sub> levels by functional interaction with the thioredoxin and peroxiredoxin axis [141]. In a recent work, it has been shown that TrxR2 deficiency prevented HIF1- $\alpha$  stabilization and decreased VEGF levels, ultimately impairing tumor growth and vascularization [142] [143]. Overall, these observations demonstrate that different members of the Thioredoxin system play an important role in vascular function and dysfunction, though the specific contribution of each component in physiological or pathological contexts still needs to be fully elucidated.

### Peroxiredoxins

The peroxiredoxin family includes six different members (Prx1-6) that catalyze the reduction of sulfenic acid residues to the corresponding thiols using either glutathione or ascorbic acid as reductants. Over-oxidation of the peroxidic cysteine in the active site of Prxs to sulfinic acid requires an ATP-dependent process wherein sulfiredoxin restores back the thiol form [144]. By exerting a tight control over intracellular peroxide levels and redox-sensitive target proteins, Prxs play an essential role in many signaling pathways related to cell growth and cell survival. Prx1 has been shown to positively regulate VEGFR expression in endothelial cells through TLR4-mediated HIF1- $\alpha$  activation [145]. [146, 147]. [148]. It is becoming increasingly clear that by controlling intracellular H<sub>2</sub>O<sub>2</sub> levels and their effects on sensitive target proteins, Prxs can act as sensors and fine regulators of the associated redox signaling events [149]. It has been recently reported that Prx-2 plays an important role in redox signaling events since its catalytic activity was shown to be necessary for preventing ROS-dependent VEGFR2 inactivation in endothelial cells [150]. Recent evidence suggests that Prx-1 [151] and Prx-2 [101] can be positively regulated by laminar shear stress, with important implications for the endothelial cell metabolism and redox balance. In another pathological context, Prx-1 was found to be overexpressed in human prostate cancer specimens and implicated in positive regulation of tumor growth via TLR4-mediated regulation of tumor vasculature [152]. [153]. [154]. In summary, depending on the redox state of the endothelial cells, Prxs might mediate positive or negative regulation over angiogenesis and attenuate or worsen potential vascular dysfunctions in a context-specific way accounting for the dynamic and complex regulation of the endothelial redox signaling and balance.

### Glutathione system

The glutathione system includes reduced (GSH) and oxidized (GSSG) forms of glutathione and additional components that regulate its synthesis, recycling and utilization in downstream

biological processes. Gamma-glutamyl cysteine ligase ( $\gamma$ -GCL) and glutathione synthetase (GS) are responsible for de novo glutathione synthesis, while glutathione reductase (GSR) and gamma glutamyl transpeptidase ( $\gamma$ -GGT) are the enzymes required for its regeneration and recycling, respectively [71]. A complex network of glutathione-dependent enzymes including glutathione peroxidases (GPXs) and glutathione s-transferases (GSTs) is directly involved in mechanisms of ROS detoxification, while other enzymes such as Glutaredoxins (Grxs) counteract oxidative damage or oxidative-induced modifications in redox-sensitive proteins by adding or removing glutathione equivalents from specific residues [155].

The tripeptide glutathione (GSH) and its metabolism represent the primary antioxidant system in cells and tissues and critically control several aspects of cellular functions including proliferation, survival and signaling events through direct post-translational modification (i.e., glutathionylation) of target proteins [156]. Given the importance of redox homeostasis in the vascular system, it is not surprising that altered glutathione metabolism or signaling can lead to severe dysfunctions of vascular growth, repair and remodeling. The existence of distinct GSH pools within the subcellular organelles supports an elegant mode for independent redox regulation of metabolic processes, including those that control cell fate [23, 156].

Recent studies started to investigate the potential mechanisms through which glutathione might regulate angiogenesis. It has been shown that ICAM-1 was able to promote VEGF-induced eNOS activity and angiogenesis, by increasing the glutathione levels [157]. Later studies evidenced that changes in the GSSG/GSH ratio were able to control HIF-1 $\alpha$  activity, since more oxidizing states of glutathione pool were associated to increased HIF-1 $\alpha$  stabilization and transactivation of target genes [158].

A direct involvement of S-glutathionylation in the regulation of endothelial cells function has been recently described in human microvascular endothelial cells (HME), wherein VEGF stimulation was able to induce S-glutathionylation of the LMW-PTP, promoting FAK activation and subsequent cell migration [159]. Using mice model of hind limb ischemia, it has been shown that Grx1 overexpression was able to increase the expression of soluble VEGFR1 (sFlt) through a direct NF- $\kappa$ B deglutathionylation, an event associated with decreased pathologic neovascularization [160]. Recent studies provided evidence of a direct mechanism through which glutathione status can affect NO bioavailability, since reversible s-glutathionylation of the eNOS was able to induce uncoupling of the enzyme acting as a redox-dependent switch that might regulate cellular signaling, endothelial function and vascular tone [122] [161]. Using HUVEC cells, it has been shown that BSO-induced glutathione



depletion was able to attenuate TNF- $\alpha$  induced endothelial activation triggering an adaptive response mediated by increased Nrf2 nuclear translocation and subsequent HO-1 and NQO1 transactivation [162]. In a recent work, the protective action of GSH on oxidative stress-induced damage was confirmed in brain endothelial cells. Here, GSH was able to attenuate H<sub>2</sub>O<sub>2</sub>-dependent generation of NO, ROS production and formation of oxidized 8-hydroxy-2'-deoxyguanosine (8-OHdG) [163]. It has been shown that human brain vascular endothelial cells (HBVEC) are protected from fatty acid-induced oxidative stress by high levels of GSH and this occurs through increased PI3K activation and Akt phosphorylation [164].

### Mediators of redox signaling in angiogenesis

It is increasingly recognized that tightly controlled ROS production can regulate several aspects of vascular function, including endothelial cell activation during inflammation, angiogenesis vascular growth and remodeling [165]. Compelling evidence indicates that local and controlled ROS production can positively or negatively modulate the expression or the activity of crucial angiogenic mediators, acting on specific signaling pathways. Potential mechanisms include direct activation of tyrosine kinase receptors (i.e., VEGFR2), modulation of functional regulators (i.e., kinases, phosphatases or other cofactors), modification of ion channels properties (i.e., SERCA pumps), regulation of enzymes (i.e., eNOS and sGC) and alteration of transcription factors activity (i.e., Nrf2 or NF- $\kappa$ B).

### Growth factor, cytokines and ROS signaling

VEGF is a prominent inducer and regulator of angiogenesis and vasculogenesis under physiological and pathological settings. Extensive research in the past decades has clarified that upon binding on VEGFR-1 and VEGFR2, this growth factor promotes endothelial cell migration, proliferation and survival, activating downstream effectors including protein kinase-C (PKC), c-Src, PI3K-Akt, phospholipase-C (PLC) MAPK/ERK1/2 cascade and p38-MAPK. Among the molecular mechanisms regulating VEGF-VEGFR axis functions, it has been recently reported that in B1647 leukemia cells, VEGFR2 physically interacts with caveolin-1 in caveolae/lipid rafts, leading to negative modulation of redox signal cascades linked to cell proliferation and glucose uptake [166]. It has also been reported that extracellular H<sub>2</sub>O<sub>2</sub> generated by SOD3 enzymes localized in caveolae/lipid rafts was able to sustain VEGF signaling through oxidative inactivation of PTP1B and DEP1 phosphatases in ischemic mice models [167]. Interestingly, the same group demonstrated that the adaptor

protein p66Shc is an important regulator of ROS-dependent VEGFR2 phosphorylation in caveolae/lipid rafts, since VEGF administration was able to induce p66Shc phosphorylation and downstream p38 MAPK activation promoting EC proliferation, migration and capillary tube formation [168]. In another study, VEGF signaling has been shown to induce ROS production through NOX2 and NOX4 activation, promoting leukemic cells survival from apoptotic cell death [169]. It has also been shown that VEGF was able to induce dimerization of the CD146 cell adhesion molecule in response to NOX4-dependent ROS production [170]. The importance of VEGF-NOX functional interaction was further confirmed in another study wherein NOX2- and NOX4-dependent ROS generation was able to induce reversible s-glutathionylation of SERCA and consequent Ca<sup>2+</sup> influx, a necessary event for VEGF-induced endothelial cell migration [171]. However, it has been recently reported that knockdown of NOX1 but not NOX2 or NOX4 impairs angiogenic processes in mice models [172]. Other experimental work indicates that in rat models of retinopathy NOX4 activation mediates VEGFR2-dependent neovascularization through ROS-dependent activation of STAT3 while in human ECs, the same molecular pathway induced cell proliferation [91]. According to recent evidence, NOX4 activation might also be an important protective mechanism against hypoxia/reoxygenation injury, leading to decreased apoptosis and increased endothelial cells proliferation and migration through upregulation of VEGF/HIF1- $\alpha$  signaling [173]. In another functional study, NOX4-derived ROS production was found to be necessary for HIF1- $\alpha$  and VEGF-mediated pro-angiogenic events induced by insulin administration in human microvascular endothelial cells (HMVEC) [93]. Increased NOX1-dependent ROS production has been shown to promote tumor angiogenesis and tumor growth in prostate cancer cells upregulating Akt and ERK1/2 pathways [174]. Other potential mechanisms of VEGF redox signaling have been recently explored. Compartment-specific ROS production has been proposed to play an important role in VEGF signaling. Indeed, intermittent high glucose stimulation of human retinal endothelial cells (HRECs) has been shown to increase mitochondrial ROS production from the mETC, a necessary event for increased VEGF expression and cell proliferation [175]. Further implication of mitochondrial ROS was more recently confirmed in a study wherein cultured HUVECs stimulated with physiological amounts of VEGF exhibited significant mitochondrial ROS production and increased cell migration [176]. It has also been shown that VEGF stimulation was able to induce localized formation of sulfenic acid residues in target proteins located at the leading edge of endothelial cells, promoting directional migration and post-ischemic angiogenesis [20]. Less conventional regulators

of VEGF functions have been also recently identified. Indeed, it has been evidenced that redox-mediated CD40/CD40L interactions were able to enhance VEGF-induced angiogenesis of HUVEC cells [177]. More recently, Murdoch et al. [160] reported that Grx-1 overexpression was able to attenuate the post-ischemic neovascularization in transgenic mice exposed to hind limb ischemia surgery through deglutathionylation of p65, enhanced activation of NF- $\kappa$ B and increased secretion of soluble VEGF receptor-1 (sFlt). Moreover, s-glutathionylation of LMW-PTP was also shown to be an important regulatory mechanism for VEGF-induced FAK activation and endothelial cell migration of human microvascular endothelial cells [159]. It has been recently reported that Thioredoxin-interacting protein (TXNIP) expression was required for VEGF-induced VEGFR2 activation and subsequent angiogenic response both in vitro and in vivo [134]. On the other hand, the activity of antioxidant enzymes has been shown to play an important role in VEGF signaling. In this context, recent studies demonstrated that Prx2 prevented the oxidative inactivation of VEGFR2 in response to H<sub>2</sub>O<sub>2</sub> in human aortic endothelial cells (HAEC) [150].

Another important soluble factor in causing ROS production and signaling in ECs is tumor necrosis factor alpha (TNF- $\alpha$ ), a pleiotropic inflammatory cytokine. TNF- $\alpha$  has been shown to both be secreted by endothelial cells and to induce intracellular ROS formation possibly via Rac/NADPH oxidase [178]. Alternatively, TNF- $\alpha$  can stimulate superoxide production in ECs, via CAPK (ceramide-activated protein kinase), XO and uncoupled eNOS. Importantly, TNF- $\alpha$  expression induces the production of ROS resulting in endothelial dysfunction in many pathological conditions [179].

### Protein tyrosine phosphatases (PTPs) and ROS signaling

The vast majority of cellular signaling events rely on the tight regulation between phosphorylation events of target proteins controlled by multiple protein kinases and dephosphorylation events catalyzed by specific protein phosphatases leading to positive or negative modulation of the kinase activity. Importantly, several lines of investigation suggest that many phosphatases can be regulated by reversible oxidation of sensitive cysteines located within their catalytic site, leading to efficient and temporally regulated kinase-dependent signaling [14, 180]. By virtue of a remarkably low  $pK_a$  (near 6.0 at physiological pH), the catalytic cysteines of protein phosphatases are prevalent in the thiolate form and therefore particularly susceptible to oxidative modification leading to sulfonic acid formation (Cys-SOH) [14]. Several studies have been aimed to clarify the processes involved in reactivation of oxidized

phosphatases and it is now becoming increasingly clear that irreversible inactivation of tyrosine phosphatases due to higher oxidative states is prevented by the rapid formation of a sulfenylamide species (as for PTP1B) or by direct conjugation with either glutathione (S-glutathionylation) [181] or nitric oxide (S-nitrosylation) [182]. Reactivation of PTP1B and PTEN has also been shown to occur via the Thioredoxin system [183]. Earlier studies reported that mitochondrial SOD2 activity was necessary to induce H<sub>2</sub>O<sub>2</sub>-dependent PTEN inactivation leading to increased expression of VEGF through PI3K-Akt pathway overactivation [184]. In a more recent report, SOD1 activity was found to be essential for H<sub>2</sub>O<sub>2</sub>-mediated inactivation of phosphatases during growth factor signaling [185]. The role of mitochondria-derived ROS was further confirmed in a recent study wherein p66Shc-induced ROS production in response to PDGF stimulation was found to be important for PTP1B, SHP-2 and DEP1 inactivation, promoting downstream signaling and cell proliferation [186]. It has also been shown that Trx1 selectively reactivated PTP1B but not SHP2 activity, potentiating PDGF- $\beta$  receptor-dependent signaling and promoting cell proliferation [187]. Recent evidence suggests that redox regulation of tyrosine phosphatases might play an important role in cell adhesion and migration [188]. A functional interrelation between NOXs and tyrosine phosphatases has been recently reported since siRNA-mediated down-regulation of NOX4 impaired cell growth and motility of U87 glioblastoma cells, while conversely NOX4-derived ROS promoted proliferation and migration through PTP1B oxidative inactivation [189]. Moreover, it has also been shown that TGF- $\beta$ -mediated EMT in pancreatic cancer cells is strongly dependent on NOX4-mediated ROS generation and subsequent PTP1B inactivation [190].

### Protein kinases (PKs) and ROS signaling

Protein kinases represent one of the largest families of enzymes in the higher organisms and essential components of most cell signaling pathways. In addition to indirect regulation derived from PTPs inactivation, functional regulation of both receptor and non-receptor tyrosine kinases can be mediated by direct oxidative modification on specific amino acidic residues. Oxidant sensing and signaling from kinase activation represents an important interface between oxidant signals and phospho-regulated pathways [191]. Early evidence for ROS-dependent regulation of kinase activity initially focused on the oxidation of c-Src tyrosine kinase on two specific cysteine residues, an event that was associated with increased Tyr416 phosphorylation and the induction of a super-activation state [192]. This observation has been further confirmed in a great variety of different models wherein c-Src has been shown to mediate cell

proliferation, adhesion, survival, cytoskeletal organization and migration through the regulation of Ras/MAPK, FAK and PI3K/Akt pathways [193–195]. Conversely, other reports provided evidence that H<sub>2</sub>O<sub>2</sub>-mediated oxidation of the conserved Cys277 induces c-Src inactivation through increased Tyr527 phosphorylation, suggesting that redox changes can exert opposing effects on c-Src activity in a context- and cell-dependent way [196]. It has been recently shown that hyperglycemia can potentiate IGF-1-mediated c-Src activation through NOX-4-dependent ROS generation in vascular smooth muscle cells [197], suggesting that different functional or dysfunctional states in the vascular system can regulate the activity of this tyrosine kinase. Compelling evidence suggests that redox events might also modify the activity of several members of the MAPK family, including JNK, ERK1/2 and p38 MAPK, whose tight regulation is critically important for cell growth and cell fate decision [198, 199]. Earlier reports demonstrated [200] that specific cysteines of the ERK2 kinase were susceptible to oxidation in presence of low H<sub>2</sub>O<sub>2</sub> doses associated with cell proliferation, while higher amounts were able to oxidatively modify the corresponding cysteines of JNK2 and p38MAPK, with different impacts on cell viability. Therefore, it seems likely that different MAPKs possess peculiar susceptibility to redox changes that might dictate the biological outcome downstream their ROS-induced activation. A recent study demonstrated that continuous activation of endothelial cells induced by TNF- $\alpha$  was able to promote the angiogenesis of endothelial cells as a consequence of sustained p38-MAPK activation induced by NOX-4-dependent ROS [201]. As a stress sensor, p38-MAPK can respond to altered redox states directly linked to endothelial dysfunction. Indeed, it has been shown that HUVECs stimulated with TGF- $\beta$  undergo significant apoptosis as a consequence of NOX-4-induced ROS production and subsequent p38 activation, an effect that was reverted by pharmacologic inhibition of p38 [202]. Additional Serine/Threonine kinases including protein kinases A/C/G, (PKA, PKC, PKG), JNK and Akt have been shown to undergo redox-dependent modification of their catalytic activity that can influence the related signaling pathways [203]. All 12 PKC isoenzymes contain cysteines in both the regulatory and catalytic domains, whose specific redox modification exerts either positive or negative effects on their enzymatic activity [204]. Although the precise mechanisms through which ROS can activate specific PKC isoforms are still unknown, the intensity, the duration and the localized production of oxidative bursts might play an important role. Recent evidence suggests that the oxidative modification of PKA and PKG on susceptible cysteines induces the formation of an intermolecular disulfide bridge, promoting the cyclic nucleotide-independent activation of the enzyme [205]. The redox regulation of Akt was initially proposed by

Ushio-Fukai et al. [206] as a positive regulator of its activity in VSMCs stimulated with Angiotensin-II or submicromolar amounts of H<sub>2</sub>O<sub>2</sub>. More recent studies, however, indicate that the functional consequence of Akt oxidation is rather an isoform specific event, since PDGF-induced ROS production was shown to be responsible for the direct oxidation of three cysteines in important domains of the Akt2 isoform, leading to kinase inactivation, whereas in the same conditions Akt1 and Akt3 remained active [207]. Recent studies suggest also that the kinase activity of JNK or Akt enzymes might be influenced by S-nitrosylation acting as a negative modulator of their enzymatic activity [208, 209].

Accumulating evidence from the last decade indicates that AMP kinase (AMPK) might represent a key regulator of important ROS-mediated cellular functions. Indeed, using HEK293 cells, it has been shown that H<sub>2</sub>O<sub>2</sub> can induce AMPK activation by oxidizing Cys299 and Cys304 residues located in the AMPK- $\alpha$  subunit, while cysteine to alanine mutation partially or totally abrogated the AMPK-enhanced activity, respectively [210]. By directly sensing changes in the energetic and redox balance, AMPK might act as a sensor that integrates metabolic cues and redox-dependent processes and trigger appropriate downstream pathways [211, 212]. A recent study showed that hypoxia can activate AMPK through ROS-dependent Ca<sup>2+</sup> release from the STIM1-CRAC channel [213], while Wang et al. [214] reported that treatment of bovine aortic endothelial cells (BAEC) with the glycolysis inhibitor 2-Deoxyglucose induces autophagy through mitochondrial ROS-dependent AMPK activation.

Among the most relevant receptor tyrosine kinases, the platelet-derived growth factor receptor (PDGFR), the insulin receptor (IRK), the VEGFR2, and the EGFR have been shown to undergo direct oxidation in specific cysteine residues [215]. Early studies performed on NIH3T3 fibroblasts reported that upon stimulation with PDGF, NOX-dependent ROS production promotes PDGFR autophosphorylation and downstream signaling [216], while more recent evidence suggests that PDGFR kinase activity might be important for controlled H<sub>2</sub>O<sub>2</sub> production in response to PDGF treatment [217]. Although the redox regulation of the IR seems to be mainly related to oxidative inactivation of PTP1B, PTEN or SHP2 phosphatases through NOX-4-dependent ROS production [218–220], the inactivation of Prx1 represents an additional regulatory mechanism [221]. However, further studies would be necessary to substantiate and better clarify the molecular mechanisms through which ROS induce direct IRK activation in different cellular and pathophysiological contexts.

It has been recently shown that exogenous H<sub>2</sub>O<sub>2</sub> or EGF administration can promote the oxidation of Cys797 located in the EGFR kinase active site and the consequent formation of a sulfenic acid residue [222], confirming that

direct redox regulation can contribute to propagate EGFR-dependent signaling. Among the three different RTKs that mediate the biological effects of VEGF (VEGFR1-3), the only form that appears too susceptible to redox regulation is the VEGFR2 [193]. Early studies demonstrated that H<sub>2</sub>O<sub>2</sub> was able to both increase VEGFR2 mRNA levels [223] and enhance its phosphorylation due to NOX-derived ROS [224] and inactivation of PTP1B phosphatase [225]. The presence of redox-active cysteines in the VEGFR2 kinase domain that might be responsible of its direct oxidation has also been described, though the specific residues were not identified [226]. A later study reported that H<sub>2</sub>O<sub>2</sub> administration can induce the formation of an intramolecular disulfide bridge between Cys1199 and Cys1209 exerting a negative effect on the VEGFR2 activity, rescued by the antioxidant enzyme PrxII [150]. Later studies evidenced that VEGFR2 can also be regulated by extracellular SOD (SOD3) activity leading to H<sub>2</sub>O<sub>2</sub> accumulation in lipid/caveolae rafts and increased VEGFR2 phosphorylation due to PTP1B and DEP1 inactivation [167]. More recent evidence suggests that the mitochondrial regulator p66shc plays an important role in mediating ROS-dependent VEGFR2 phosphorylation in caveolae lipid/rafts of endothelial cells stimulated with VEGF [168]. Similarly, using HCAEC cells, it has been shown that VEGFR2 can be modified and trigger downstream signaling pathways (i.e., Src-PI3K-Akt) as a consequence of VEGF-induced NOX-dependent ROS generation [194]. Finally, another study reported that FGFR1 oxidation on Cys277 might negatively modulate downstream signaling events, providing evidence of a complex and probably context-dependent regulation of RTKs by redox changes [227].

### Transcription factors (TF) and ROS signaling

Redox regulation of transcription factors such as HIF1, Ets-1, NF- $\kappa$ B and Nrf2 plays an essential role in vascular function and dysfunction. [228]. The hypoxia-inducible factors (HIFs) transcriptionally regulate several target genes in response to changes in the oxygen levels. HIF1 is a heterodimeric protein composed by an oxygen-regulated HIF-1 $\alpha$  and a constitutive oxygen-insensitive HIF-1 $\beta$  subunit. Under hypoxic conditions, HIF-1 $\alpha$  degradation is prevented, leading to heterodimerization with the HIF-1 $\beta$  subunit and functional activation of downstream targets. Among the disparate target genes, VEGF and VEGFR are the most relevant for the regulation of angiogenic processes [229]. Importantly, pro-inflammatory cytokines, RNS and ROS have also been shown to promote HIF1- $\alpha$  stabilization through oxygen-independent mechanisms. Earlier studies reported that HIF1- $\alpha$  can be S-nitrosylated at the level of Cys533 leading to enhanced stability and transcriptional

activity [230], an observation confirmed by a later study [231]. NOX-derived ROS have also been shown to promote HIF1- $\alpha$  stabilization under both hypoxic or normoxic conditions in endothelial cells [232] and prostate cancer cells [233]. Intriguingly, recent evidence indicates that mitochondria-derived ROS might induce HIF1- $\alpha$  stabilization in melanoma cells [234], while a later study from Calvani et al. [235] proposed a biphasic regulation of HIF-1 in melanoma cells survival wherein mitochondria-derived ROS mediated early HIF1 activation, while NOX-dependent ROS promoted its prolonged stabilization. Together these studies highlight the multifaceted and complex role exerted by redox changes and ROS on HIF1 regulation, with important implications for normal and pathologic angiogenesis.

NF- $\kappa$ B is another heterodimeric transcription factor that regulates the expression of genes involved in cell proliferation, cell survival, inflammation and angiogenesis. Under basal conditions, NF- $\kappa$ B is retained as a cytosolic inactive dimer due to the interaction with I $\kappa$ Bs inhibitors [236]. Stress conditions induce IKK-dependent I $\kappa$ B phosphorylation promoting its proteasomal degradation and the subsequent NF- $\kappa$ B translocation into the nucleus, where activation of target genes occurs. Redox regulation of NF- $\kappa$ B is intricate since oxidation of the Cys62 in the p50 subunit occurs in the cytosol leading to nuclear translocation while its reduction mediated by Trx1 or Ref1 is required for DNA-binding and gene transactivation [237, 238]. Exogenous addition of H<sub>2</sub>O<sub>2</sub> has been shown to promote alternative phosphorylation of I $\kappa$ B enhancing NF- $\kappa$ B activation in some cell systems while conversely the same modification can exert inhibitory effects in other experimental systems [237]. The IKK complex contains redox-sensitive cysteines (Cys178 in IKK $\alpha$  and Cys179 in IKK $\beta$ ) that mediate redox regulation of NF- $\kappa$ B activity and generally inhibit its activation [236], while in certain cell types the same modification seems to promote NF- $\kappa$ B activation [239]. Interestingly, both S-nitrosylation and S-glutathionylation modifications have been shown to negatively regulate the NF- $\kappa$ B activation, an effect reversed by either Grx1 or reducing agents [240]. In the endothelial cells, the NF- $\kappa$ B pathway has often been associated with pathological alterations such as atherosclerosis [241], pro-inflammatory states [242] and impaired vascular function in type2 diabetes [243]. In contrast, other recent reports suggest that increased NF- $\kappa$ B can attenuate the post-ischemic revascularization in mice models of hind limb ischemia [160] or positively contribute to vascular remodeling during angiogenesis and vascular regression through transcriptional modulation of pro-apoptotic (FasL) and anti-apoptotic (cFLIP) genes [244]. In summary, the functional interaction between ROS and the NF- $\kappa$ B pathway is intricate and context dependent, since



ROS can be generated and interact with different effector molecules leading to either activation or inhibition of the NF- $\kappa$ B signaling. Similarly, the biological outcome of ROS-dependent regulation appears to be strongly influenced by the duration of the oxidant stimulus and the specific cellular context. With this respect, further studies are required to elucidate the complexity of this process and its interrelation with normal or pathological angiogenesis.

The nuclear factor erythroid 2-related factor (Nrf2) is a master regulator of redox homeostasis that transcriptionally controls the expression of several antioxidant and phase-II enzymes in response to oxidative stress and inflammation. Under basal conditions, Nrf2 is sequestered in the cytosol by the negative regulator Kelch-like ECH-associated protein1 (Keap1) that promotes its proteasomal degradation and prevents the activation of target genes. Key cysteine residues in Keap1 (Cys151, Cys273, Cys288 and Cys613) can be susceptible to oxidative modification or conjugation with electrophiles, leading to Keap1–Nrf2 complex disruption, nuclear translocation of Nrf2 and association with Maf proteins culminating in the transactivation of ARE-containing genes [245]. Among the approximately 600 cytoprotective genes induced by Nrf2, the inducible heme oxygenase (HO-1), the catalytic subunit of glutamate–cysteine ligase (GCLC), NAD(P)H:quinone oxidoreductase 1 (NQO1) and glutathione *S*-transferase (GST) are the most relevant for the vascular system.

Earlier studies reported that Nrf2 activation conferred protection from H<sub>2</sub>O<sub>2</sub>-induced cytotoxicity and exerted anti-inflammatory effects in HAECs [246]. Another recent study confirmed the importance of Nrf2 in maintaining the functional integrity of the vasculature, since disruption of its signaling by siRNA-mediated knockdown severely impaired the angiogenic processes in human coronary arterial endothelial cells stimulated with VEGF [247]. Recent evidence suggests that Nrf2 pathway is an important regulator of angiogenesis in endothelial cells and bone marrow-derived progenitor cells (PAC), while its deficiency enhanced the muscle blood flow in a mice model of hind limb ischemia [248]. A recent report indicates that Nrf2 can positively regulate the ECs sprouting and vascularization by suppressing Dll/Notch4 pathway *in vitro* and *in vivo* [249]. Another study confirmed that Nrf2 is a potent regulator of hypoxia-induced angiogenesis in cardiac microvascular endothelial cells (CMECs) [250]. Interestingly, a functional crosstalk between the Nrf2 pathway and the unfolded protein response has been recently documented in several endothelial cells wherein oxidized phospholipids were able to induce ATF4 and VEGF upregulation through Nrf2-dependent activation [251]. Another recent study reported that Nrf2 activation can promote retinal vascular development and protect the retina from hyperoxia-induced oxidative stress in C57BL/6

mice models [252]. In the context of tumor angiogenesis and malignant progression, it has been recently shown that downregulation of Nrf2 can block the angiogenesis in glioblastoma cells through inhibition of the hypoxia-induced activation of HIF1- $\alpha$  [253]. Notably, this observation was partially confirmed by another study wherein shRNA-mediated Nrf2 knockdown in human colon cancer cells was able to impair tumor growth and tumor angiogenesis in mice xenografts [254]. Therefore, even the redox regulation of Nrf2-associated events seems to produce complex and opposite biological effects that largely depend on the cell type and the physiopathological context.

### Hypoxia

Short exposure to hypoxia/reoxygenation, either directly or indirectly, produces ROS that induce oxidative stress associated with angiogenesis or tumor vascularization. ROS can cause tissue injury on one hand and promote tissue repair on the other side by promoting angiogenesis [255]. It thus appears that after causing injury to the cells, ROS promptly initiate the tissue repair process by triggering angiogenic response. Recently, it has been reported that redox signaling may influence neovascularization that occurs during pathological conditions. Tumor angiogenesis is regulated by several growth factors (EGF, TGF- $\alpha$ , beta-FGF, VEGF). It has been clearly demonstrated that induction of VEGF by the tumor is triggered by tissue hypoxia. Hypoxia exerts its pro-angiogenic action through various angiogenic factors also in wound healing and tissue regeneration [256, 257].

### Redox signaling in endothelial pathologies

ROS signaling and its deregulation (e.g., oxidative stress) are often associated with endothelial dysfunction, with involvement in the pathogenesis of several vascular-related diseases such as hypertension, diabetes or atherosclerosis. Also neoangiogenesis-related pathologies ranging from tumorigenesis and eye diseases (e.g., retinopathies) are greatly characterized by oxidative stress conditions and altered ROS signaling.

The role of redox signaling in tumor angiogenesis is not yet completely characterized. Indeed, converse mechanisms are postulated about how ROS recruit new blood vessels for tumor progression by promoting VEGF secretion [258]. Therefore, analysis and characterization of molecules that sustain redox signaling is a new opportunity for setting up innovative strategies of anti-cancer therapy. In tumor vessel endothelial cells, the increase in ROS generation from metabolic abnormalities and oncogenic signaling may trigger a redox adaptation response, leading

to an upregulation of antioxidant capacity and a shift of redox dynamics with high ROS generation and elimination to maintain the ROS levels below the toxic threshold. As such, tumor angiogenic cells would be more dependent on the antioxidant system and more vulnerable to further oxidative stress induced by exogenous ROS-generating agents or compounds that inhibit the antioxidant system. A further increase of ROS stress in these cancer cells using exogenous ROS-modulating agents is likely to cause elevation of ROS above the threshold level, leading to cell death. This might constitute a biochemical basis to design therapeutic strategies to selectively kill tumor angiogenic cells using ROS-mediated mechanisms [259].

In human retinopathies, abnormal angiogenesis is a hallmark and a cause of this pathology. Here, high oxygen tension induces ROS production that cannot be scavenged by antioxidants. As a result, superoxide anion and hydrogen peroxide levels have shown to be substantially elevated in animal models of diabetic retinopathy or retinopathy of prematurity. Even normal retinas seem to be particularly sensitive to oxidative stress, due to a high consumption of oxygen, high levels of oxidation substrates and exposure to light. Interestingly, it has been demonstrated that ischemic retinopathy is substantially diminished in ATM-deficient mice in which excessive ROS are inhibited [260]. ATM deficiency also lowered tumor angiogenesis and enhanced the antiangiogenic action of VEGF blockade. These data suggest that pathological neoangiogenesis requires DNA damage response (DDR)-mediated oxidative defense and that agents that promote excessive ROS generation may have beneficial effects in the treatment of neovascular disease [261].

Another aspect related to oxidative stress and retinopathies is the production of oxidized lipids. One of the main consequences of ROS production is peroxidation of lipids which results in their functional modification. Peroxidation affects cellular membrane lipids, in particular polyunsaturated fatty acid (PUFA). These oxidation reactions can generate secondary compounds that are even more destructive than ROS themselves. DHA, one of the easily oxidizable PUFAs, represents 60 % of the PUFAs in the retina and the product of its oxidation serves as a biomarker for oxidative stress-induced injury in age-related macular degeneration [65].

Altogether, these findings make very urgent to improve the technologies and model to study ROS signaling in vivo with the idea to design new therapeutic strategies aiming at ROS signaling modulation in different pathological contexts.

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