

Forum Review

The Redox Regulation of PI 3-Kinase–Dependent Signaling

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ABSTRACT

Signal transduction via PI 3-kinases plays an important role in regulating the cellular processes of cell growth, survival, proliferation, and motility. The stimulated generation of reactive oxygen species is a necessary component of the signal transduction mechanisms by which many growth factors and cytokines activate this signaling pathway and elicit their cellular responses. Evidence now supports the oxidative inactivation of both tyrosine phosphatases acting upstream of PI 3-kinase, and of the lipid phosphatase PTEN as components of the normal stimulated regulation of PI 3-kinase signaling. However, the effects of chronic oxidative stress appear rather different, particularly a proposed role for nitrosylation of Akt and other targets leading to inhibition of PI 3-kinase signaling during diabetic insulin resistance in muscle. Recently, evidence has also begun to emerge, indicating that physiological redox signaling may display the same tight spatial and temporal specificity as seen with many other signal transduction systems in terms of targeting individual proteins for modification, and of enzymatic reversal mechanisms. This review will focus upon the details of these and other roles for reactive oxygen and nitrogen species in the regulation of PI 3-kinase signaling, both during acute stimulation and chronic oxidative stress, and the evidence for their significance. *Antioxid. Redox Signal.* 8, 1765–1774.

INTRODUCTION

THE COMPLEX BEHAVIOR of the cells of higher multicellular organisms is regulated by multilayered signal transduction pathways and networks that integrate information from several sources to control a cellular response. This review will focus upon the redox-dependent regulation of the PI 3-kinase signaling pathway, due to the significance of the pathway in regulating critical biological processes, such as cell growth, survival, proliferation, and motility, and also because of the role of redox modification in regulating the activity of the signaling pathway. Not only is there good evidence that the stimulated production of reactive oxygen species is required for the normal activation of PI 3-kinase–dependent signaling by many stimuli, but there are also suggestions that this signaling pathway, as the principal mediator of the cellular responses to insulin and insulin-like growth factors (IGF1), may play a special role in responding to the local redox environment and rates of metabolism at the level of the organism (31).

The PI 3-kinase signaling pathway

Interest has focused on PI 3-kinase signaling due to the activation of this pathway by many growth factors, hormones, cytokines, and extracellular matrix components, and the requirement for signaling via PI 3-kinase in the promotion by these stimuli of cellular responses such as cell growth, survival, proliferation, and motility (5, 30, 80). PI 3-kinase signaling is of particular interest in the field of cancer research, as at least half of all human tumors are believed to display elevated activity of this signaling pathway, many activators and positive components of the pathway are oncogenes, and the principal cellular inhibitor of the pathway, the lipid phosphatase, PTEN, is an important tumor suppressor (71, 81).

The phosphoinositide 3-kinase (or PI 3-kinase) signaling pathway as it will be considered in this review comprises the class I PI 3-kinase enzymes that catalyze the synthesis of the lipid second messenger phosphatidylinositol 3,4,5-trisphosphate (PtdIns(3,4,5)P₃), and also the downstream targets for

activation by this second messenger, the best characterized of which is probably the serine/threonine kinase Akt, also known as protein kinase B (PKB) (Fig. 1) (6, 40, 80). The broader PI3-kinase family comprises a rather diverse set of enzymes, including the Class II and III PI 3-kinase enzymes, but as these latter enzymes do not make $\text{PtdIns}(3,4,5)\text{P}_3$ or regulate the same signaling targets as the Class I enzymes (83), they will not be considered further here.

The pathway involves the stimulated synthesis of the second messenger $\text{PtdIns}(3,4,5)\text{P}_3$ at low concentrations from the relatively abundant membrane phospholipid phosphatidylinositol 4,5-bisphosphate [$\text{PtdIns}(4,5)\text{P}_2$]. $\text{PtdIns}(3,4,5)\text{P}_3$ can then regulate downstream signaling through the action of proteins that are able selectively to recognize and bind this lipid, most commonly through lipid binding protein domains of the pleckstrin homology class (PH domains), a subset of which bind specifically to $\text{PtdIns}(3,4,5)\text{P}_3$ (see Fig. 1) (80). These $\text{PtdIns}(3,4,5)\text{P}_3$ binding targets include the serine/threonine kinases Akt/PKB and PDK1, the tyrosine kinases of the Tec/Btk family, several guanine nucleotide exchange factors for the GTPases rac and cdc42 and several other proteins of uncertain function (30, 68, 82). $\text{PtdIns}(3,4,5)\text{P}_3$ is in turn metabolized by at least two classes of phosphatases. The tumor suppressor, PTEN, is a principal regulator of both basal and stimulated $\text{PtdIns}(3,4,5)\text{P}_3$ levels, as it dephosphorylates the 3 position of this lipid, converting it back to $\text{PtdIns}(4,5)\text{P}_2$ (44, 74). Contrastingly, another unrelated group of phosphatases, the 5-phosphatases, including SHIP, SHIP2, and SKIP, dephosphorylate the 5 position of $\text{PtdIns}(3,4,5)\text{P}_3$ to make significant amounts of $\text{PtdIns}(3,4)\text{P}_2$, which may not only remove the $\text{PtdIns}(3,4,5)\text{P}_3$ signal, but have interesting signaling properties of its own (15). Indeed, cellular treatment with hydrogen peroxide generally leads to a greater rise in the levels of $\text{PtdIns}(3,4)\text{P}_2$ than $\text{PtdIns}(3,4,5)\text{P}_3$, suggesting that this former lipid may play a significant role mediating cellular responses to generated ROS (79). Another route of synthesis of $\text{PtdIns}(3,4,5)\text{P}_3$ in response to oxidative stress via the action of a $\text{PI}(3,4)\text{P}_2$ 5-kinase has also been proposed, although the physiological significance of this route in higher organisms is currently unclear (23, 57).

EVIDENCE FOR THE REDOX REGULATION OF PI 3-KINASE-DEPENDENT SIGNALING

It has become clear over the last 10 years or so, that reactive oxygen species (ROS) are not simply toxic by-products of metabolism and are used not only in a specialized microbicidal role during phagocytosis, but also play crucial roles in many signal transduction networks (14, 63). This conclusion first arose from studies showing that numerous cellular signals, such as growth factors and cytokines, induced the cellular production of ROS, usually via a nonphagocytic NADPH oxidase complex, and then from later work showing that these ROS were required for efficient signal transduction (18, 62). The cellular stimuli for which ROS production is implicated as a necessary component of their signal transduction mechanism, include several stimuli known to activate the PI 3-kinase-Akt axis, such as PDGF, EGF, insulin, bFGF, TNF, angiotensin II, LPA, and LPS (4, 8, 22, 35, 43, 46, 54, 75).

Most of this experimental evidence for the accumulation of ROS in stimulated cells comes from the use of the ROS-responsive fluorescent dyes such as dichloro fluorescein diacetate and dihydrorhodamine (4, 46), although other methods such as electron paramagnetic resonance (EPR) spectroscopy (27) and chemical assays of released extracellular ROS (36) have also been used. The significance of a role for stimulated ROS production in specific signaling pathways has generally been supported by experiments affecting downstream signaling by intervention to control either the stimulus driven production of ROS, such as by using DPI, a small molecule inhibitor of the regulated NADPH oxidase activity that produces superoxide, or alternatively experimental intervention to change (usually enhance) the removal of ROS, for example, by overexpression of the hydrogen peroxide metabolizing enzyme catalase.

Specifically, a requirement for ROS production to activate Akt has been shown for angiotensin II, insulin, and EGF. In these experiments, overexpression of catalase causes a dramatic inhibition of the activation of Akt by insulin and angiotensin

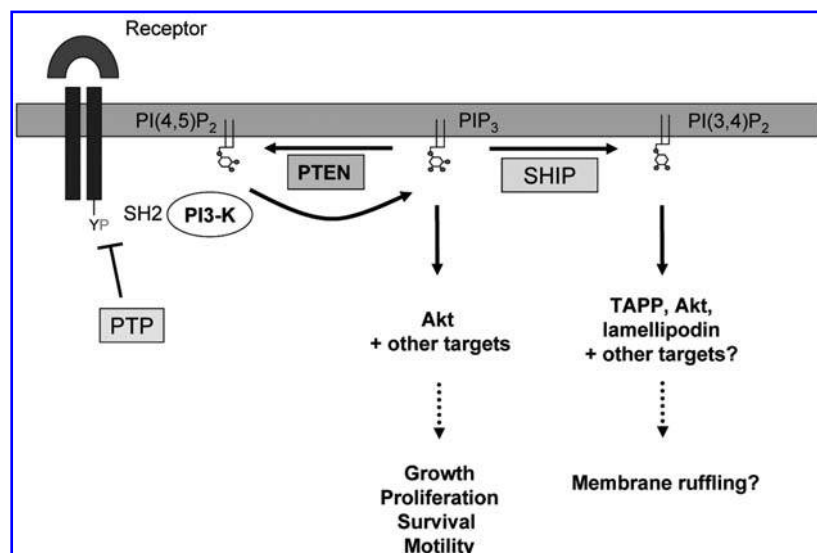


FIG. 1. A simplified model for PI 3-kinase signaling downstream of a tyrosine phosphorylated receptor. Receptor activation and phosphorylation lead to the recruitment and activation of PI 3-kinase enzymes. These phosphorylate the abundant phospholipid $\text{PtdIns}(4,5)\text{P}_2$ to generate $\text{PtdIns}(3,4,5)\text{P}_3$. This lipid signal in turn binds to its downstream target proteins. The activity of the pathway is opposed both by the action of tyrosine phosphatases that inhibit the activation of PI 3-kinase, and by the action of PTEN, a $\text{PtdIns}(3,4,5)\text{P}_3$ 3-phosphatase, that converts this signal back to $\text{PtdIns}(4,5)\text{P}_2$.

II (55, 78) and overexpression of peroxiredoxin II inhibits EGF-induced Akt phosphorylation (38). Similarly, insulin-stimulated Akt phosphorylation has also been shown to be blocked by DPI treatment (48). A recent study has expanded these points in some detail, showing that in fibroblasts overexpressing the NADPH oxidase component, Nox1, PDGF-stimulated PI 3-kinase activity was unaffected, but cellular PtdIns(3,4,5)P₃ levels in PDGF-stimulated cells were greatly increased relative to control cells without Nox1 expression (38). Similarly, overexpression of an inactive mutant of the hydrogen peroxide metabolizing enzyme peroxiredoxin II (PrxII) increased EGF-stimulated PtdIns(3,4,5)P₃ levels, whereas overexpression of wild-type PrxII led to a small decrease in both EGF-stimulated PtdIns(3,4,5)P₃ levels and Akt phosphorylation (38). Another strategy to address the role of ROS in Akt activation has been the use of two similar neuroblastoma cell lines that differ in their ability to generate ROS in response to stimuli. In these experiments, while both cell lines efficiently activated PI 3-kinase in response to insulin stimulation, only the cell line that accompanied insulin stimulation with stimulus-driven ROS generation also efficiently activated Akt (69).

It is worth noting that recent evidence has begun to emerge, supporting that as with many other signal transduction mechanisms, specificity exists within the targets for ROS, regulating the PI 3-kinase and other signaling pathways. For example, stimulation of primary endothelial cells with angiopoietin-1 (Ang-1) leads to the transient accumulation of ROS, as with many other ligands for receptor tyrosine kinases (RTK) and this ROS accumulation appears to play a role in controlling downstream responses to Ang-1 stimulation (25). However, although many downstream signaling responses, such as Ang-1-stimulated PAK1 and MAPK activation, and cell migration, were affected by several methods of experimental antioxidant intervention, Ang-1-stimulated Akt phosphorylation was unaffected by overexpression of catalase, superoxide dismutase, or treatment with peptides that block the activation of NADPH oxidase in these cells (25). Similarly, it has recently been shown that PrxII is specifically recruited to the activated PDGF-R and has a role in the attenuation of specific downstream signals including PLC γ activation (10). MEFs lacking the gene for PrxII display enhanced PDGF-stimulated receptor activation, PLC γ activation, proliferation, and migration, but appear unaffected in the phosphorylation of many tyrosine residues on the receptor, and the downstream activation of MAPK and Akt (10).

In addition to a role for low levels of endogenously generated ROS in the normal activation mechanisms of PI 3-kinase signaling by many stimuli, it is clear that chronic oxidative stress has an opposing effect, inhibiting the activation of PI 3-kinase signaling, particularly by insulin and IGF1. There is a strong correlation between chronic oxidative stress and insulin resistance, often seen in diabetic patients, and evidence showing that antioxidant treatment can greatly reduce this resistance, both in cultured cells and in mice and humans (17, 19, 47). However, this broad therapeutic strategy is somewhat inconsistent, and although some molecular mechanisms have been proposed, more research is clearly required to address the mechanisms of oxidative stress-induced insulin resistance and to validate antioxidant intervention as a therapeutic approach (19, 29, 67, 85). Currently, the best supported mecha-

nism appears to be obesity-associated nitrosylation of components of the insulin, PI 3-kinase Akt pathway, although this may be specific to skeletal muscle (7, 61, 85).

Nitric oxide (NO) is a free radical gas that has been appreciated for some years to act as an important biological signaling molecule. When produced by cells, it appears to mediate many of its effects through interaction with the heme group of soluble guanylyl cyclase. However, the regulated generation of nitric oxide has also been proposed to regulate several biological processes through the generation of other reactive nitrogen species (RNS) and the direct oxidation of cellular protein targets. It has become clear that NO plays an important role in muscular insulin resistance and the activation of PI3-kinase-Akt signaling by insulin. The most significant evidence for this is the finding that in mice, deletion of the gene for inducible nitric oxide synthase (iNOS) causes a dramatic protection from obesity-linked insulin resistance in muscle (61). Although the mechanism for this effect is uncertain, candidates have recently been proposed, including nitrosylation of Akt and other pathway components (see below) (7, 85).

It is important to note that in some ways the study of redox signaling is a field in its infancy. The very reversible nature of the modification of cellular components (in most cases described here, protein thiol groups) makes these redox state changes far more difficult to analyze experimentally than, for example, more stable (or stabilizable) posttranslational protein modifications, such as phosphorylation or acetylation. Many studies, by necessity, involve the treatment of cells with high doses of exogenous reactive oxygen and nitrogen species that cause nonspecific oxidation of many cellular components. Although it appears that physiological redox regulation of specific proteins may exhibit the same tightly controlled specificity seen with other signaling systems, sensitive experimental approaches to address these features are only just emerging (10, 24, 28, 56).

MECHANISMS OF REDOX REGULATION

It has been known for several years that cellular stimulation with hydrogen peroxide leads to the rapid activation of the protein kinase, Akt (33, 70), that appears to be reproducible in many cell types. Soon after, it was also shown that hydrogen peroxide stimulation leads to a rapid, though transient, rise in the levels of PtdIns(3,4,5)P₃, and a more sustained, and much larger accumulation of PtdIns(3,4)P₂ (79), both of which lipids can bind to the PH domain of Akt. Similarly, the rapid activation of cellular Akt by nitric oxide donors and peroxynitrite treatment has also been shown (32), although there seems to be slightly less consistency in these effects (85). Further studies described above have indicated that ROS play a role in the normal activation of PI 3-kinase signaling by many stimuli, and are beginning to give us some insight into the mechanisms by which these effects are mediated. These studies strongly suggest that targets for oxidation by ROS exist both above and below the level of PI 3-kinase enzymes. Specifically most of these studies implicate cysteine-dependent phosphatases of the protein tyrosine phosphatase family that act both on tyrosine phosphorylated receptors and

adaptors that oppose the activation of PI 3-kinase (21, 55), and the distantly related PtdIns(3,4,5)P₃ phosphatase PTEN, that directly metabolizes this lipid second messenger (43, 69) (Fig. 2).

There is a clear contrast between the regulation of the signal transduction pathways of higher organisms, and the mechanisms of regulation of simple, direct redox responsive systems, exemplified by the bacterial transcription factor OxyR, which is a direct target for oxidative modification, and regulates target genes participating in an antioxidant response. In contrast, it appears that higher signal transduction networks, such as the PI 3-kinase pathway, or stress activated protein kinase cascades, are often regulated at several points by redox dependent modifications, both through the tightly regulated localized generation of reactive oxygen and nitrogen species, and through cellular oxidative stress (1, 28, 76). It would appear that this reflects the need of such signal transduction networks to integrate information from multiple sources to determine a response.

Cysteine-dependent phosphatases: PTEN and PTPs

Research addressing mechanisms for the redox regulation of PI 3-kinase signaling has largely focused upon the family of cysteine-dependent phosphatases (CDPs), which includes the PI 3-phosphatase, PTEN, and the classical protein tyrosine phosphatases. Strong evidence now supports a physiological role for these molecules as targets of ROS in the normal regulation of PI 3-kinase signaling by many stimuli (45, 63, 64, 77).

The CDPs comprise a large diverse family of enzymes that share a conserved catalytic mechanism based upon a highly reactive cysteine residue in the context of a C(X)₃R motif. The human genome encodes around a hundred separate proteins that appear to be members of this phosphatase family, as well as several proteins lacking significant enzymatic activity, that have sequence identity to these active phosphatases (2, 3). These enzymes include firstly the classical protein tyrosine phosphatases (PTPs; 38 enzymes) that have activity specifically against phosphotyrosine, and the dual specificity

PTPs (61 enzymes) capable of dephosphorylating a wider range of substrates, including tyrosine, serine, or threonine residues and some phosphoinositide lipids. This latter group includes PTEN, the myotubularin phosphatases, and possibly the Sac and 4-phosphatase enzymes. In addition, the low molecular weight and cdc25 groups of phosphatases share the minimal catalytic motif and a rather similar three-dimensional structure, but display very different organizational topologies, and so would appear to have evolved independently (2).

It is the conserved catalytic mechanism of the CDPs that makes them good candidates as mediators of cellular redox signaling. The local environment around the active site of these enzymes lowers the pK_a of the catalytic cysteine, from around 8 for most cysteine residues, to around 5.5. This is believed to ensure that this cysteine exists as a thiolate anion at physiological pH, and to enhance its reactivity as a nucleophile during catalysis (64, 72) (Fig. 3A). However, these same properties that form the basis for the catalytic mechanism of the CDPs also make the active site cysteine reactive towards oxidizing agents such as reactive oxygen species. This enhanced sensitivity of the CDP active site cysteine relative to most cellular cysteine residues makes redox-dependent inactivation likely as a common mechanism of regulation of these phosphatases, and makes the family likely candidates as direct mediators of many cellular redox signaling pathways (13, 64, 77). Most significantly, a growing body of evidence supports both the role of oxidation in the regulation of these enzymes and their significance in mediating the effects of ROS and RNS on cellular signaling and function.

Several CDPs play important roles in regulating PI 3-kinase signaling, which split into two functional divisions (see Figs. 2 and 3B). The lipid PI 3-phosphatase PTEN metabolizes cellular PtdIns(3,4,5)P₃ and acts in direct opposition to PI 3-kinase, thus plays a principal cellular role inhibiting PI 3-kinase-dependent signaling. Additionally, since the Class 1A PI 3-kinase enzymes are defined by their activation through tyrosine kinase based signaling mechanisms, these activation mechanisms are opposed by protein tyrosine phosphatases,

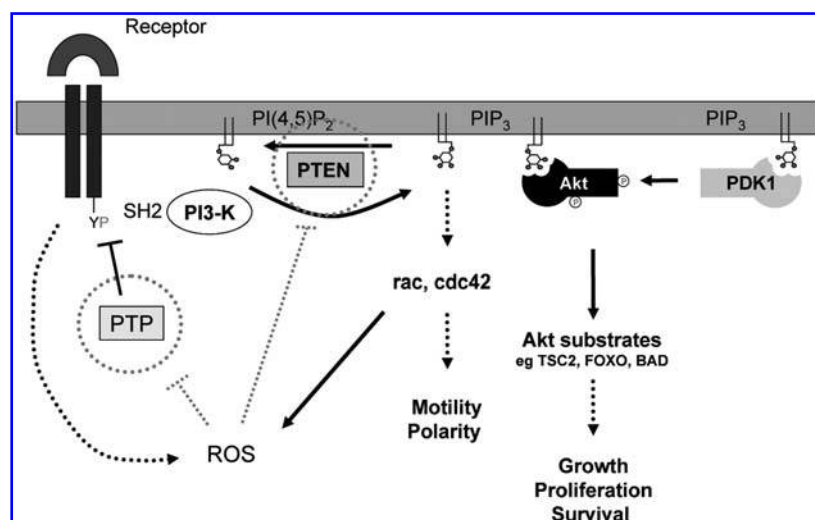


FIG. 2. Role of phosphatase oxidation in the activation of PI 3-kinase signaling. A simplified model for the activation of downstream signaling by PtdIns(3,4,5)P₃ is represented, highlighting the potential inhibitory roles of the oxidant sensitive protein tyrosine phosphatases (PTP) and PTEN. Evidence indicates that these phosphatases can be inactivated by reactive oxygen species (ROS) that are generated in response to receptor activation. The inhibition of PTPs and PTEN may be, at least in part, a temporary positive feedback process, as the receptor-stimulated rac-dependent generation of ROS is in some systems PI 3-kinase dependent, although PI 3-kinase-independent pathways to rac activation and ROS generation appear to exist downstream of some receptors.

FIG. 3. Cysteine-dependent phosphatase family catalysis and their oxidation relevant to PI 3-kinase signaling. (A) The proposed catalytic mechanism of the cysteine-dependent phosphatase family is shown, including the cysteine nucleophile and acidic residue, usually an aspartic acid, required for activity. (B) The cellular phosphatases relevant to PI 3-kinase signaling are shown that have been reported to become oxidized upon cellular stimulation, and the cell type in which these experiments were performed. These are detailed further in the text.

Cellular phosphatase oxidation		
Phosphatase	Stimulus	Cell type
PTP1B	EGF	A431
PTP1B	insulin	HepG2, 3T3L1, Rat1
SHP2	PDGF	Rat1
SHP2	T cell receptor	Jurkat
TCP45	insulin	Rat1
PTEN	LPS, PMA	RAW
PTEN	insulin	SK-N-SH, 293
PTEN	EGF	HeLa
PTEN	PDGF	NIH3T3

and several such phosphatases have been identified as targets in the redox regulation of PI 3-kinase signaling.

PTEN

PTEN is a principal regulator of cellular $\text{PtdIns}(3,4,5)\text{P}_3$ levels and inhibitor of PI 3-kinase signaling, and an important tumor suppressor (44, 74). It has been shown that PTEN is sensitive to rapid inactivation *in vitro* by hydrogen peroxide, and in this case can form a stable intramolecular disulfide bond between the active site cysteine (C124) and another proximal cysteine residue (C71), only about 5 Å apart in the PTEN crystal structure (42). PTEN has also been shown to be oxidized *in vitro* by *S*-nitrosothiols (87). Significantly, several studies have now shown that PTEN becomes oxidized in cells through endogenous generation of reactive oxygen species (and possibly reactive nitrogen species). This was first addressed in the murine macrophage cell line, RAW 264.7, in which the stimulated production of hydrogen peroxide and other ROS species by the phagocytic NADPH oxidase complex has been well studied. In these macrophages, stimulation with lipopolysaccharide and phorbol ester caused the oxidation of a fraction of the endogenous PTEN protein, as assessed using an alkylation protection assay and detected using a biotinylated alkylating agent, causing this apparent oxidized fraction to rise from 5% to 16% (43).

Most recently, and very significantly, the oxidation of PTEN has been demonstrated in cells stimulated with a range of peptide growth factors, in which the stimulated production of ROS is at greatly lower levels than found in macrophages. PTEN oxidation could be identified in neuroblastoma cells or HEK293 cells stimulated with insulin, in HeLa cells stimulated with EGF, and in fibroblasts stimulated with PDGF, using bandshift assays in addition to biotinylation and alkylation protection assay methods (38, 69). Despite the limited degree of PTEN oxidation in all of these studies, significant data support the functional significance of this PTEN oxidation. In PTEN null cells experimentally re-expressing PTEN from a virus, as with many other cell lines, acute stimulation with hydrogen peroxide caused a robust increase in cellular $\text{PtdIns}(3,4,5)\text{P}_3$ levels and downstream Akt/PKB activation. However, the original PTEN null cells neither accumulated $\text{PtdIns}(3,4,5)\text{P}_3$ nor activated Akt/PKB upon hydrogen peroxide stimulation (although turnover of the lipid is almost cer-

tainly increased), indicating the significance specifically of PTEN oxidation in the regulation of $\text{PtdIns}(3,4,5)\text{P}_3$ levels in these experiments (43). Similarly, in neuroblastoma cells in which insulin-stimulated PTEN oxidation could be detected, although the activation of PI 3-kinase was unaffected by insulin-stimulated ROS production, the activation of Akt/PKB was greatly reduced in cells not able to produce ROS upon insulin stimulation (69). These data indicate that insulin-stimulated ROS production appears not to affect the PI 3-kinase-dependent synthesis of $\text{PtdIns}(3,4,5)\text{P}_3$, but rather reduce the degradative capacity, strongly suggesting functionally significant PTEN inhibition.

PTEN oxidation has also been identified in cells overexpressing MnSOD, leading to downstream regulation of VEGF expression and angiogenesis (11). For the first time, this work implicates mitochondrial H_2O_2 in regulating PTEN, and also provides a novel mechanism by which ROS may regulate angiogenesis (11, 37, 51). Together, all these data support the hypothesis that PTEN is a direct target for oxidative inactivation by ROS produced in response to diverse cellular stimuli, and that this inactivation is significant in the regulation of downstream signaling responses.

Protein tyrosine phosphatases: PTP1B, SHP-2, and TC45

The PI 3-kinase signaling pathway as considered here relies upon the synthesis of $\text{PtdIns}(3,4,5)\text{P}_3$ from $\text{PtdIns}(4,5)\text{P}_2$ by the action of Class I PI 3-kinase enzymes (80). The class IB p110 γ enzyme is characterized by its activation by G-protein coupled receptor signaling through the interaction of G-protein $\beta\gamma$ subunits with the p101 or p84 PI 3-kinase regulatory subunits (73). On the other hand, Class IA PI 3-kinases (p110 α , β , and δ) are characterized by their recruitment and activation by tyrosine kinase signaling pathways via the SH2 domains of their corresponding regulatory subunits (p85 or p55) (80). This activation by tyrosine kinases is counteracted and suppressed in the unstimulated state by the action of PTP enzymes that, as described above, allows redox regulation through inhibition of these phosphatases (9, 84). Since these PTPs act on the signaling pathways stimulating the activation of PI 3-kinase, their actions are usually specific to particular stimuli, and as such, experimental approaches have tended to address the role of particular phosphatases in the regulation

by a particular ligand of several downstream signaling pathways including the PI 3-kinase/Akt axis.

Oxidation of PTPs and the regulation of PI 3-kinase activation by growth factors

Several studies have identified PTP1B and recently TC45 as targets for ROS-dependent oxidation during the activation of the PI 3-kinase pathway by insulin and other growth factors. PTP1B was the first CDP demonstrated to become oxidized by endogenously produced ROS, in A431 cells stimulated with EGF. This important study used radiolabeled iodoacetic acid to alkylate the active site cysteine of PTP1B, and showed that stimulation with EGF reduced the labeling by around 30% (41). Further studies have shown PTP1B oxidation in response to insulin, TC45 oxidation by insulin stimulation, SHP2 oxidation in response to PDGF stimulation or T-cell receptor engagement, and indeed inhibition of total PTP activity in response to insulin (39, 48, 49, 55, 56). These studies have used a number of different approaches in addition to loss of alkylating agent labeling, including loss of assayable activity after lysis and purification in anaerobic conditions and an apparent ROS-dependent loss of assayable activity despite the presence of reducing agents in the lysis buffer (which could be taken to indicate irreversible oxidation). One development in this technology was the use of an assay by Meng *et al.*, who lysed cells in buffers containing unlabeled iodoacetic acid to alkylate any reduced PTPs. These phosphatases could then be separated from the alkylating agent by gel electrophoresis and washing, before reducing and assaying in gel for the activity of phosphatases that had been protected from alkylation by the formation of a stable oxidized species (56). This, and subsequent adaptations to the method, have allowed the identification of phosphatase oxidation as a gain of assayable signal from a low background, rather than a less sensitive loss of total cellular activity.

DIRECT OXIDATION OF PATHWAY KINASES

PKB/Akt

Several studies have proposed that the PtdIns(3,4,5)P₃-dependent serine/threonine kinase Akt/Protein Kinase B is directly regulated through oxidation. The determination of the crystal structure of Akt revealed the unusual feature that the kinase domain of Akt contained an intermolecular disulphide bond between two cysteine residues (Cys297 and Cys311 of Akt2) at each end of the functionally critical activation loop (26). Further work on this aspect of the regulation of Akt has shown that the formation of this disulfide is induced in cultured cells during oxidative stress induced by 100 μ M hydrogen peroxide, but significantly that formation of this disulfide was inhibited by cellular overexpression of glutaredoxin (GRX) (58). An insight into how this disulfide regulates Akt function was also provided by this study, as although this oxidation did not appear to affect the kinase activity of purified Akt *in vitro*, oxidative stress induced not only the oxidation of

Akt, but its interaction with the protein phosphatase PP2A, believed to dephosphorylate and inactivate Akt. Akt oxidation, inactivation, and PP2A recruitment were all inhibited by glutaredoxin overexpression, suggesting that only the oxidized disulfided kinase is able to interact with PP2A, and that this interaction regulates the phosphorylation and activity of the kinase (58). Since these two cysteine residues in the Akt activation loop are conserved in several other kinases, it will be interesting to see whether this redox regulation of protein kinase activity by PP2A phosphatase recruitment is a widespread phenomenon.

In accordance with this model for a redox-regulated disulfide-dependent interaction of Akt with PP2A, this interaction has also been shown to be blocked by the thiol alkylating agent *N*-ethylmaleimide (86). However, these authors generally found that thiol alkylation blocked Akt activation, although the target(s) for this effect was not identified (86).

Most recently, Yasukawa *et al.* proposed that Cys244 is a site for regulatory nitrosylation and that this nitrosylation could be important in insulin resistance in diabetic and obese muscle. This study showed that incubation of cells with the nitric oxide donor, SNAP, caused Akt nitrosylation, inhibited its kinase activity, and blocked the phosphorylation of the Akt substrate Bad without affecting PI 3-kinase activity or the activating phosphorylation of PKB on Thr308 and Ser473. Further analysis identified Cys244 as a functionally significant site of nitrosylation, as mutation of Cys244 to serine blocked the nitrosylation and inactivation of PKB by SNAP (85). This study also revealed enhanced nitrosylation of Akt in the skeletal muscle of diabetic genetically obese mice that appeared to play a part in the insulin resistance of Akt in these mice (85). These results appear to be closely linked to work identifying nitrosylation of the insulin receptor, the insulin receptor substrate 1 (IRS1) and Akt in obese muscle, and may provide an important insight into the mechanisms by which chronic oxidative stress induced insulin resistance (7). This latter study also found that the obesity-associated nitrosylation of the insulin receptor, IRS1, and Akt were all reversed by antisense knockdown of iNOS expression (7). Together, these studies strongly suggest a role for reactive nitrogen species in obesity-associated insulin resistance in muscle.

It is worthy of note that both of these studies saw a reduction in Akt activity upon cellular treatment with the NO donors GSNO or SNAP, and no evidence for effects on Akt protein levels over periods up to 24 h (7, 85). Other studies have indicated that peroxynitrite treatment can activate Akt (32), and that ROS (not RNS) may be involved in the regulation of Akt protein stability, although the role of ROS in these studies may only be as an inducer of caspases and other apoptotic proteolytic programmes (50, 53).

PI 3-kinase p85 regulatory subunit

The p85 subunit of PI 3-kinase has recently been proposed as a direct target for tyrosine nitration. In a study addressing the oxidative mechanisms by which high glucose hyperglycemia induces the apoptosis of endothelial cells, the authors demonstrated that either high glucose incubation (25 mM) or peroxynitrite incubation (500 μ M) blocked the activation of the PI

3-kinase-Akt cell survival pathway (16). They also showed that these treatments caused the dissociation of the p85 and p110 subunits of PI 3-kinase, but not in cells treated with the peroxynitrite decomposition catalyst FeTPPS. Although the antibodies available for the detection of nitrotyrosine are rather poor, they also showed convincing direct data for the increased tyrosine nitration of p85 in response to either high glucose or peroxynitrite (16).

mTOR

The mammalian target of rapamycin (mTOR) kinase plays a central role in the regulation of cell growth through nutrient availability in eukaryotes. The relationship of mTOR with PI 3-kinase and Akt is complex, as mTOR is regulated at least in part through upstream PI 3-kinase and Akt signaling via the TSC proteins and Rheb, and mediates many of the effects of PI 3-kinase on cell growth, but also may play a role in the activation of Akt (52, 65). The regulation of mTOR has proved technically difficult to study, due to its large size, complexity, and the difficulty of assaying its activity *in vitro*. However, structural analysis of the C-terminal FATC domain revealed a disulfide bond between two conserved cysteine residues that appeared to regulate the flexibility of a loop within this domain, correlating with an apparent change in the stability of the whole protein (12). These authors proposed that this could be a mechanism by which cellular redox state can regulate the abundance and thus activity of mTOR (12).

CONCLUSION

It should be clear that we have begun to uncover mechanistic aspects explaining the roles of ROS and RNS in cell signaling. However, it remains the case that very few direct targets for redox modification have been identified that can be tied to individual biological effects, despite the strong evidence that such targets exist. Significantly, proteomic approaches to the identification of redox modified proteins are beginning to bear fruit (20, 60, 66).

An area of great general interest that seems almost certain to continue in the future, is the role of ROS and PI 3-kinase signaling in the regulation of the aging process. Several cellular studies have indicated that signaling via PI 3-kinase and Akt, through inhibition of FOXO transcription factors, suppress cellular antioxidant activity, particularly through inhibiting the expression of MnSOD (34) and catalase (59). It has been proposed that these effects may play an important role in the regulation of aging within the whole organism (31, 34), but although it seems clear that the insulin/IGF pathway through PI 3-kinase plays a role in regulating life span, molecular details of the aging process remain elusive.

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ABBREVIATIONS

CDP, cysteine-dependent phosphatase; EGF, epidermal growth factor; GSNO, *S*-nitrosoglutathione; IGF, insulin-like growth factor; iNOS, inducible nitric oxide synthase; PDGF, platelet derived growth factor; PI 3-kinase, phosphoinositide 3-kinase; PLC γ , phospholipase C gamma; PTP, protein tyrosine phosphatase; RNS, reactive nitrogen species; ROS, reactive oxygen species; SNAP, *S*-nitroso-*N*-acetylpenicillamine; SOD, superoxide dismutase.

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