

## Forum Editorial

# Peroxidase: A Term of Many Meanings

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### Abstract

Peroxidase research has been instrumental in defining the principles of chemical catalysis. By now, enzymes termed peroxidases represent a heterogeneous group of distinct enzyme families that operate by different catalytic principles and fulfill diverse biological functions, detoxifying  $\text{H}_2\text{O}_2$  being just one of many aspects.  $\text{H}_2\text{O}_2$ -dependent synthesis of secondary metabolites is the domain of heme peroxidases and related enzymes operating by transition metal catalysis, that often is mediated by free radical formation. Instead, the coenzyme-free glutathione peroxidases and peroxiredoxins only catalyze two-electron transitions and, thus, can reliably remove hydroperoxides without causing radical-mediated collateral damage. However, their ability to use hydroperoxides for the formation of specific disulfide bonds with and within particular proteins broadens their spectrum of biological activities to differentiation phenomena, redox regulation of metabolic processes, redox sensing, and signalling. The present Forum Editorial tries to guide the reader through the 190 years of equally bewildering and fascinating research on peroxidases up to the topical frontiers of the field that are addressed in this issue. *Antioxid. Redox Signal.* 10, 1485–1490.

### Emerging Catalytic Principles

THE HISTORY OF PEROXIDASES starts in the early 19<sup>th</sup> century when the interpretation of biological phenomena was still dominated by the theory of vitalism. In 1818, the French baron Louis Jacques Thénard discovered “eau oxygénée” ( $\text{H}_2\text{O}_2$ ) (75) and also observed that this novel compound is easily broken down by biological tissue. In contrast to the general thinking in those times, Thénard did *not* attribute the accelerated decomposition of  $\text{H}_2\text{O}_2$  by biological material to a mysterious “vital force,” but to the presence of a particular “substance,” thus anticipating the concept of catalysis, which was later developed by Jöns Jacob Berzelius (3). The miraculous catalytic power was finally attributed to an “enzyme” that appeared to be ubiquitous in nature and, as a kind of prototype of a natural catalytic entity, was called “catalase” by Loew in 1900 (45) (now EC 1.11.1.6). A decomposition of  $\text{H}_2\text{O}_2$ , associated with the formation of colored compounds from polyphenols, was also detected in plants and animals already in the 19<sup>th</sup> century by Schönbein (69) and named “peroxidases” (now EC 1.11.1.7) by Linossier (44). During the first half of the last century, catalases and peroxidases were isolated, and their catalytic mechanism

was recognized to be similar: In both cases, the “hematin” prosthetic group was shown to be oxidized to yield “compound I” by the strong oxidant  $\text{H}_2\text{O}_2$  ( $E_0$  for its reduction to water = 1.776 V) and then reduced again by  $\text{H}_2\text{O}_2$  itself ( $E_0$  for its oxidation to dioxygen = –0.682 V) in catalase, which thus catalyzes a dismutation of  $\text{H}_2\text{O}_2$ , or by an other reductant in the other peroxidases (36, 76). Due to the typical redox-sensitive spectral characteristics of their prosthetic group, the heme peroxidases soon became the favorite playground of spectroscopists, and fertilized many fields of biochemistry such as enzyme kinetics, the stopped-flow analysis of fast reactions (7, 68), and the biology of respiration and oxidative phosphorylation (9).

Up until the 1970s, it almost remained a dogma that peroxidases (EC 1.11.1.-) are heme proteins (8, 54). This fascination by heme catalysis hampered the appreciation of unrelated proteins sharing reaction specificity with the heme peroxidases. When Gordon C. Mills described a novel peroxidase that apparently was devoid of any colored prosthetic group (51), his discovery was accepted with great scepticism. In fact, the enzyme was declared not to exist at a meeting of the Federation of the American Societies of Experimental Biology in the early 1960s (Gerald Cohen, Mount Sinai School

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of Medicine, New York, 2001, personal communication). Mills' glutathione peroxidase (now known as GPx-1; EC 1.11.1.9) had to wait for 16 years until it resurrected as the first selenoprotein to be discovered by Flohé (24) and Rotruck (66) in 1973 and, thus, marks the beginning of the still evolving field of selenium biochemistry (27, 43). In retrospect, selenium catalysis could explain the extraordinary rate constants for the reaction of glutathione peroxidases with hydroperoxides (46, 65) that had been shown to be equivalent to, or even higher than, those of heme peroxidases (26). GPx-type proteins have meanwhile grown up to a large and diversified family. Many of them turned out not to be specific for glutathione but react with protein thiols (*i.e.*, thioredoxin-type proteins), which renders their historic name obsolete (47). Their remaining characteristic feature is a redox-active (seleno)cysteine residue that is integrated into the protein chain and, in the 3-D structure (18), forms the center of a catalytic triad (Sec, Gln Trp) (18) or, more precisely, of a tetrad (Sec, Gln, Asn, Trp) (78). In most of the family members, the selenocysteine is actually replaced by cysteine, which usually results in lower specific activity. But rate constants near those observed with heme or selenoproteins may also be seen with some of the Cys homologues of GPxs (47), revealing that even a simple cysteine residue, if appropriately activated by its protein environment, can account for efficient peroxidatic activity. A prerequisite of the reactivity of C<sub>P</sub> is a low pK<sub>a</sub> of its thiol or selenol, respectively, since only the thiolate or selenolate forms, as strong nucleophiles, can readily attack the hydroperoxide to produce a sulfenic or selenenic acid derivative. However, the rate constants calculated for thiolates of several low molecular weight thiols are comparatively low, falling within the range of 18–26 M<sup>-1</sup> sec<sup>-1</sup> (84). Therefore, additional effects such as proton shuttling and polarization of the peroxide bond have to be considered to account for the enzymatic rate constants in the range of 10<sup>5</sup>–10<sup>7</sup> (78) or >10<sup>8</sup> M<sup>-1</sup> s<sup>-1</sup> in the case of the seleno-enzymes (26). Similarly, low rate constants have been calculated for the oxidative inactivation of catalytic cysteine in tyrosine phosphatases (14), suggesting that unlikely only a low pK<sub>a</sub> can account for the oxidation of a crucial thiol under physiological conditions.

Sulphur catalysis is also the hallmark of the most recently evolving peroxidase family, the peroxiredoxins (EC 1.11.1.15). Here the cysteine sulphur is activated by coordination with a threonine (or serine) residue and the positive charge of a nearby arginine (23). What now has become known under the term "peroxiredoxin" (Prx) was originally discovered by electron microscopy as the 10-membered ring-shaped macromolecule "torin" of erythrocytes far ahead of its functional characterization (30). More commonly, the discovery of peroxiredoxins is ascribed to Earl Stadtman and Sue Goo Rhee who described a "thiol-specific antioxidant protein" of yeast (37) that later turned out to be a thioredoxin peroxidase (64). Since, the peroxiredoxin family has grown up in the databases to more than 500 entries that comprise at least five distinct molecular clades (41). The common denominator is the above-mentioned catalytic triad in which the "peroxidatic cysteine" (C<sub>P</sub>) is oxidized by a hydroperoxide to a sulfenic acid (61). Thus far, the mechanism is analogous to that of the glutathione peroxidases. As in glutathione peroxidases, also the regeneration of the ground-state enzyme is usually achieved by thiols but depends on

the subfamilies. In a so-called "typical 2-cysteine peroxiredoxin" the proximal reductant of the sulfenic acid is a cysteine residue (C<sub>R</sub> for "resolving cysteine") of a second subunit within the oligomeric protein; in "atypical 2-cysteine peroxiredoxins," the C<sub>R</sub> is a cysteine of the same subunit. In both cases, the primarily formed inter- or intra-subunit disulfide bond is then typically reduced by "redoxins," that is, proteins with a thioredoxin fold and containing a Cys–X–X–Cys (or Cys–X–X–Sec) motif such as the flavin-based disulfide reductases of bacteria (59), the wide-spread thioredoxins (25), or the tryparedoxins of kinetoplasts (4, 55). In the 1-cysteine peroxiredoxins, the sulfenic acid form has to be directly reduced by substrate itself. For most of the 1-cysteine peroxiredoxins, the physiological reductant is still unknown; it may be glutathione (62) or ascorbate (53). Despite operating with sulphur catalysis, the rate constants for the oxidative and reductive part of peroxiredoxin catalysis may be impressive, the *k'*<sub>+1</sub> and *k'*<sub>+2</sub> values ranging from 2 × 10<sup>3</sup> to 4 × 10<sup>7</sup> M<sup>-1</sup>s<sup>-1</sup> and 4 × 10<sup>4</sup> to 1 × 10<sup>7</sup> M<sup>-1</sup>s<sup>-1</sup>, respectively (79).

Starting from the 1950s, peroxidases using NADH (EC 1.11.1.1) or NADPH (EC 1.11.1.2) as reductant have been repeatedly described and characterized as flavoproteins (11, 52). To our best knowledge, however, direct involvement of a flavin cofactor in hydroperoxide reduction has never been demonstrated. Instead, the hydroperoxide acceptor appears to be a reactive cysteine again (60). Moreover, the metabolic links of GPx-type and Prx-type peroxidases to Cys–X–X–Cys and other cysteine-containing proteins, to GSH, other low molecular weight thiols and finally to NAD(P)H now provide a molecular basis for the majority of NAD(P)H-dependent peroxidase activities that were believed to represent enzymatic entities. Prominent examples are the alkylhydroperoxide reductases of enterobacteria (Ahp) being a two-component system of a disulfide reductase (AhpF) and a peroxiredoxin (AhpC) (6, 74), related thioredoxin-dependent Prxs of *Escherichia coli* (5), *Mycobacterium tuberculosis* (35), *Plasmodium* sp. (15), and others (16), and the "trypanothione peroxidase" activity of kinetoplasts that reflects a complex redox cascade comprising the NADPH-dependent trypanothione reductase, tryparedoxin, and tryparedoxin peroxidase (55), homologous mitochondrial isozymes, and an equally NADPH/trypanothione/tryparedoxin-dependent GPx-type peroxidase (4, 42). In all these examples, the flavin is not directly involved in the peroxidatic function but belongs to the disulfide reductase of the system.

In short, nature does not rely on a single catalytic principle to reduce hydroperoxides. The catalysis of peroxidases may depend on iron (or manganese) porphyrin prosthetic groups, the highly reactive heteroatom selenium, an activated sulphur or, as not yet mentioned, exotic metal cofactors such as vanadate (81, 82).

### Antioxidant, Pro-Oxidant, and Synthetic Roles of Peroxidases

The diversity of catalytic mechanisms of peroxidases is reflected in diverse, in part opposite, roles. The obvious reflex to consider peroxidases as antioxidant enzymes, because they eliminate H<sub>2</sub>O<sub>2</sub>, other hydroperoxides, or peroxynitrite, misleads in most cases.

It has for long been recognized that mammalian heme-

containing haloperoxidases (EC 1.11.1.8 and 1.11.1.10) are by no means "antioxidants." Clearly, myeloperoxidase, eosinophil peroxidase (39), salivary peroxidase (40), and lactoperoxidase (29) use  $\text{H}_2\text{O}_2$  to generate more aggressive oxidants to fight intruding micro-organisms (38), and the bactericidal cocktail produced by these enzymes also accounts for oxidative tissue damage in infectious and inflammatory diseases (13). In fact, heme peroxidases in general, with the notable exception of catalases, rather tend to promote than to inhibit oxidative damage, because the reduction of the oxidized enzymes ("compound I") is often achieved by one-electron transitions, which implies formation of free radicals from the reducing substrates that may lead to chain reactions. In prokaryotes, heme proteins often display both catalase and peroxidase activity (86). Accordingly, these enzymes are pivotal to the elimination of  $\text{H}_2\text{O}_2$ , but may simultaneously promote oxidations, as is, for example, evident from the oxidative activation of isoniazid to the real bactericidal agent by KatG in *Mycobacterium tuberculosis* (72).

The oxidative potential of heme peroxidases, however, may also be used for specific syntheses. One of the best documented examples is the synthesis of thyroid hormones by iodide peroxidase (70, 71). The ability to halogenate organic compounds is, however, not restricted to heme peroxidases but is equally achieved by the vanadium enzymes (81). Another example of specific synthesis is the formation of prostaglandin H from arachidonate by the heme peroxidase component within the cyclo-oxygenase complex (56). Heme peroxidases of plants are also implicated in the synthesis of secondary metabolites (2), but it remains a challenge to work out the specific functions of the individual plant enzymes which *in toto* are presumed to have more functions than a Swiss army knife (57).

In contrast, peroxidases operating by selenium or sulphur catalysis tend to only catalyze two-electron transitions and, thus, allow a safer forecast of their metabolic role. They were, and still are, widely assumed to lower hydroperoxide levels, thereby counteracting oxidative stress without any complications due to unspecific by-products. In essence, this expectation could be corroborated. Free radical intermediates of GPx- or Prx-type peroxidases have never been detected and ample evidence accumulated reveals that, at least for GPx-1 in mammals (22), the Prx-dominated trypanothione system of kinetoplasts (4) and bacterial AhpC and thioredoxin peroxidases (16) are indeed important antioxidant devices. Nevertheless, the seemingly semantic question remains whether these enzymes are primarily used to reduce hydroperoxides or, as, for instance, iodide peroxidase, use hydroperoxides for purposes that are unrelated to antioxidant defence. GPx-4 (EC 1.11.1.12) may be quoted as striking example for the latter option: During mammalian spermiogenesis, GPx-4 behaves like a "moonlighting protein" in transforming itself, at the expense of hydroperoxides, from an active peroxidase into a constituent of the mitochondrial sheath (80), a process that is indispensable for appropriate sperm function (21). Mechanistically, the oxidized selenocysteine specifically selenylates a cysteine residue of GPx-4 itself, whereby its peroxidase activity is abrogated and GPx polymers are synthesized (49). A "pro-oxidant" role is also observed with the nuclear form of GPx-4: It promotes chromatin condensation by catalyzing protein disulfide formation (12). Similarly, the products of

peroxiredoxin catalysis (*i.e.*, oxidized redoxins), may have a greater physiological impact than a small decline of the concomitant hydroperoxide tone (see below). Furthermore, peroxiredoxins tend to thiolate other proteins *via* their oxidized  $\text{C}_\text{P}$  (33), a phenomenon that is gaining increasing attention in the context of redox regulation.

### Thiol-Dependent Peroxidases In Redox Regulation

The concept of protein phosphorylation/dephosphorylation (20) has long overshadowed the relevant redox processes in metabolic regulation. In the meantime, redox sensitivity of many phosphorylation cascades has been firmly established (19), and it thus has become evident that both regulatory principles are interrelated and complementary (10). Moreover, the upstream effectors such as insulin, other hormones, cytokines, and growth factors themselves proved to induce the formation of  $\cdot\text{O}_2^-$ ,  $\text{H}_2\text{O}_2$ , or lipid hydroperoxides, which modulate their signaling cascades (1, 17, 28, 48, 50).

Interestingly, probably the first enzyme reported to be redox regulated was a phosphatase. Starting in 1965, Pontremoli and Horrecker reported on the activation of fructose diphosphatase and, in consequence, gluconeogenesis by physiological disulfides such as cystamine and oxidized CoA (58), and later hydroperoxide exposure was shown to induce gluconeogenesis in perfused rat liver (73). Also protein phosphatase activity proved to be modulated by redox events (31). Typically, these phosphatases are inhibited by  $\text{H}_2\text{O}_2$  and, thus, protein kinase-mediated signaling is often enhanced under oxidizing conditions. This mode of oxidant-dependent modulation of protein phosphorylation has now become a generally accepted regulatory principle (63). Other modes of redox regulation of signaling cascades that primarily depend on phosphorylation are, for example, the inhibitory binding of reduced, but not oxidized thioredoxin to the apoptosis signal regulating kinase-1 (ASK1) (67), facilitating DNA binding of NF $\kappa$ B by reduced thioredoxin (32), and the oxidation of pivotal cysteines in Keap1 that results in nuclear translocation and activation of the transcription factor Nrf2 (34).

The molecular analysis of redox phenomena with regulatory impact still appears to be rudimentary. The ideas that redox regulation is just a consequence of the cellular "redox potential," "peroxide tone," "thiol/disulfide status," or "free radical generation" are unsatisfactory, since they do not meet two basic requirements of meaningful regulatory circuits: i) specificity of messengers, and ii) separate switches to control activation and termination. Clearly, aggressive radicals such as  $\text{OH}\cdot$  or  $\text{RO}\cdot$  that attack a large variety of biomolecular targets can be disregarded as specific effectors of regulatory processes. Related concern may also be valid for  $\text{H}_2\text{O}_2$ , peroxynitrite or lipid peroxidation products, but these less promiscuously reacting oxidants may be rendered more specific by peroxidases acting as peroxide sensors which, as oxidized forms, selectively interact with target proteins. Alternatively, the target protein itself might sense the oxidant by means of an exceptionally reactive thiol, as is proposed for some phosphatases. For regulatory and chemical reasons, such activation process can hardly be reversed by a direct backward reaction. A sulfenic acid, once formed by the reaction of a hydroperoxide with a protein target, is not re-

versed by lowering the peroxide tone, and a sulfinic acid requires enzymatic repair (85). Mixed disulfides between target proteins and GSH or other proteins are not readily reversed either when the thiol/disulfide status returns to normal, but are regenerated with the aid of glutaredoxin, thioredoxin, or others. A few examples of how thiol-dependent peroxidases contribute to redox regulation have been reported in recent years. Vivancos and coworkers (83) describe a yeast peroxiredoxin acting as  $H_2O_2$  sensor in the activation of the transcription factor Pap1 which regulates anti-oxidant gene transcription in response to  $H_2O_2$ . Interestingly, the Pap1 activation occurs only at low  $H_2O_2$  concentrations, which implies that a protective mechanism is triggered before the peroxide can cause unspecific damage. At high peroxide exposure, the peroxiredoxin is inactivated due to oxidation to a sulfinic acid and instead triggers the mitogen-activated protein kinase Sty1 pathway, the latter event being specifically reversed by the sulfiredoxin Srx1 (83). A second example involves a GPx-type protein, Orp1, as  $H_2O_2$  sensor. When the C<sub>P</sub> of Orp1 is oxidized to the sulfinic acid form, it becomes disulfide-linked to the transcription factor Yap1 which thereby is activated; the shut-off part of the regulatory circuit (*i. e.*, regeneration of reduced Orp1 and Yap1 from the hetero-dimer), is then catalyzed by thioredoxin (77). In both cases, in analogy to the GPx4 polymerization mentioned above, the peroxidases themselves act as protein-thiylating agents, which might turn out to be regulatory principle that is by far more important than lowering the peroxide level.

### Why a Forum Issue Now?

It may seem impossible to squeeze a diversified field such as the peroxidases into a small ARS issue. The attempt may also appear superfluous in view of the realm of published reviews. However, the area is at present developing so quickly that most of these compilations are already out-dated at the time of publication. More importantly, many aspects of the area have not yet reached the awareness of most researchers that were interested in "oxidative stress" and related problems. The focus has long been on oxidant-derived pathology, the long known benefits of the oxidative burst in the defence against infections has hardly become a priority issue of the various clubs dedicated to free radicals research, and the emerging interest in redox regulation still suffers from limited understanding of underlying mechanisms.

As it commonly happens in biochemistry, also in the peroxidase field mechanistic analyses in micro-organisms and small experimental animals are paving the way to medical application, although it is hard to forecast what of the emerging knowledge will turn out to be valuable. The intention of the guest editors, therefore, was to present some topical state-of-the-art reviews and stimulating papers in order to broaden the vision towards the following aspects: (a) the fundamental differences of peroxidase families and the diversity within the peroxidase families; (b) the evolutionary diversifications of antioxidant enzyme systems, particularly in pathogens, and their possible therapeutic implications; (c) unsuspected peroxidase functions that might help to unravel signalling specificity, complexity of redox regulation, and metabolic adaptation; and (d) molecular mechanisms of per-

oxidases which, beyond their stand-alone interest, may disclose general features of peroxide susceptibility of biomolecules.

We accompany this Forum issue with the hope of convincing the reader that one of the oldest subjects of biochemical sciences ever was, and still is, good for surprises and, in view of its theoretical and practical implications, deserves continuing attention.

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