

Review

Signalling by NO-induced protein S-nitrosylation and S-glutathionylation: Convergences and divergences

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Abstract

The role of nitric oxide in several signalling routes has been clearly established. In recent years increasing attention has been paid to its ability to produce covalent protein post-translational modifications in conjunction with other reactive oxygen and nitrogen species. Among these, the modification of cysteine residues has been shown to be of particular importance due to the functional relevance of many of them. In this review, we focus on the modification of the cysteine thiol by incorporation of a NO moiety (S-nitrosylation) or of a glutathione moiety (S-glutathionylation). Both modifications are produced by different reactions induced by nitric oxide-related species. We discuss the differences and similarities of both modifications, and their relationships, in regard to the biochemical mechanisms that produce them, including the enzymatic activities that may catalyze some of them and their subcellular compartmentalization. Even when biochemical knowledge is one step ahead of the demonstration of their pathophysiological relevance, we also describe the potential role of both modifications in several processes in which both post-translational modifications are involved.

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1. Nitric oxide and glutathione as conveyors of signals

As research on signal transduction has evolved, many pathways based on the successive involvement of defined proteins have been described. These are related one to another in a more or less clearly defined order that can be attributed to specific patterns of interaction among the components of the pathway. In many of these pathways, small molecules are involved as messengers, interacting with relatively specific receptors, and hence they can be included as defined elements of the pathway. Also, protein post-translational modifications such as phosphorylation are a

common mechanism for many pathways, but the specificity relies on the enzymes participating in the pathway.

Nitric oxide (NO), is considered a “classical” second messenger in signalling pathways, as it interacts by means of a thoroughly described reversible coordination bonding with its specific target, soluble guanylate cyclase (sGC). This interaction changes the conformation of sGC and activates it to produce cyclic GMP (cGMP), another small molecule that gives way to the activation of specific kinases. Indeed, other roles of NO rely on a similar kind of reversible coordination bonding that can change or modulate protein activities; one of the best characterized is the competition with O₂ for cytochrome c oxidase, leading to the inhibition of mitochondrial respiration.

Nitric oxide is a free radical, which makes it very unstable compared to many other chemical species (although it is relatively stable compared to other free radicals). This implies not only that it is rapidly decomposed but that, as it is able to

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react with other species, it produces a variety of radical and non radical compounds, collectively named “reactive nitrogen species” (RNS). RNS can modify lipids and DNA, as well as different protein residues, producing post-translational modifications that can alter protein functions. Among these post-translational modifications, S-nitrosylation (also called S-nitrosation; for a discussion of the terminology see [1,2]) has been thoroughly studied in the last decade. It is believed to be easily formed and destroyed in cellular environments, and it is involved in several cellular processes, thus being considered as a feasible signalling mechanism. When compared to other signalling mechanisms like phosphorylation, it presents unique features, the main one being the fact that its formation and degradation depend on chemical reactions without the aid of enzymatic catalysis. Thus, some concepts like specificity are based on different biochemical bases, and hence it has been proposed that it may represent a new paradigm in signal transduction [1].

Many features of S-nitrosylation, conceived as a signal transduction mechanism are shared by oxidative modifications induced by the so-called “reactive oxygen species” (ROS), and by RNS itself. The change of paradigm has been discussed for both sets of modifications [3], although each modification has special features. In this regard, S-nitrosylation shows some parallelism with sulfenic acid formation, as it is easily reversible [4]. Sulfinic and sulfonic acid formation are more stable modifications, that have been considered as irreversible in cell systems until the recent description of reversion enzymatic mechanisms for sulfinic acid [5,6]. Protein disulfide bond formation is a key redox modification that has been studied at length; it is largely dependent not only on the redox environment but also on protein structure. S-thiolation, the formation of a mixed disulfide between a protein thiol and a low molecular mass thiol, is also a reversible process. As glutathione is the most abundant intracellular low molecular mass thiol and a key regulator of the redox state, S-glutathionylation, the formation of a mixed disulfide with glutathione, can be considered as the most important thiolation, as it has been also shown to be the most abundant [7–9]. In this review, we will explore the similarities, differences and commonalities between S-nitrosylation and S-glutathionylation, as both modifications share many mechanistic and functional features that make them solid candidates as general mechanisms for signal transduction within the new paradigm described.

2. Biochemical mechanisms involved in the formation of the modifications

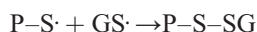
There are several chemical mechanisms that can lead to the formation of both S-nitrosylation and S-glutathionylation in protein cysteine thiols. A number of *in vitro* studies, using low molecular mass thiols or different proteins, provide detailed information, which may help to extend studies to the cell environment. However, the key issue in cellular systems is the need to understand not only the mechanisms, but its potential

occurrence in specific cellular compartments. We now describe some of these mechanisms and their relationship.

Formation of both modifications does not occur directly by addition of the species nitric oxide ($\cdot\text{NO}$) or glutathione (GSH) to the cysteine thiol (P-S-H), as a redox reaction is needed by losing one electron per sulphur atom (one in the case of nitrosylation and two in the case of glutathionylation), and every electron matters in chemistry. A direct reaction is only possible if a thyl radical is formed in the cysteine thiol ($\text{P-S}\cdot$) that would easily react with nitric oxide, a radical itself,



or with the thyl radical of glutathione,



Probably, this is restricted to certain special protein environments, as it has been described for calbindin in the presence of copper [10].

Oxidized species are the most important candidates for modifying a reduced thiol. N_2O_3 is the higher oxidation state (one-electron oxidation) for nitrogen oxides, formed by the reaction of NO with O_2 or with peroxynitrite, or from acidified nitrite, and has been considered the quintessential S-nitrosylating species [11,12].

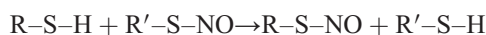


Oxidized glutathione (GSSG) would be the equivalent for glutathione,

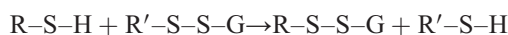


and an increase in GSSG levels has been postulated as the main mechanism for S-glutathionylation. This mechanism provided a link with the concept that the GSH/GSSG pair is the central parameter when considering the redox state of the cell, and explained the higher S-glutathionylation levels observed after oxidative bursts [13–17]. However, evidences have accumulated that argue against significant involvement of GSSG in many cell situations, based mainly on the fact that GSSG levels do not increase and the GSH/GSSG levels are maintained [7,18–20].

Another mechanism that can theoretically share some common features is the transfer of the modification between two different thiols. In the case of S-nitrosylation, it is transnitrosation



and is a fast reaction that is likely to occur quite easily in cells [21,22]. However, the disulfide exchange between glutathione and another thiol (including S-glutathionylation by GSSG), what could be called “transglutathionylation”,



is a slow reaction that is thermodynamically unfavoured based on typical redox potentials for cysteine residues [23]. This

Table 1
Reports since 1996 of proteins S-glutathionylated when treated with nitric oxide, GSNO or other RNS, either on purified proteins or in cells

Protein	Stimulus	References
p50	GSNO	[105]
Cathepsin K	GSNO	[107]
Aldose reductase	GSNO	[108,109]
Hemoglobin	GSNO	[105]
Creatine kinase	GSNO	[36,105]
Alcohol dehydrogenase	GSNO	[105]
Glycerol phosphate dehydrogenase	GSNO	[105]
Glutaredoxin	GSNO	[105]
Thioredoxin	GSNO	[105]
Carbonic anhydrase	GSNO	[35,105]
Glycogen phosphorylase b	GSNO	[35,105]
Glutathione reductase	GSNO	[110]
Ryanodine receptor	GSNO	[39,46,111]
Papain	GSNO	[38,112]
CFTR	GSNO	[113]
GAPDH	GSNO, decomposed GSNO	[38,105,114,115]
Cu,Zn-SOD	GSNO, decomposed GSNO	[105,115]
Actin	GSNO, cell treatments	[48]
c-Jun	GSNO, NO/GSH	[42,105]
Caspase-3	GSNO, SNAP+GSH	[102,104,105]
H-Ras	GSNO, ONOO ⁻	[35,37,89]
Microsomal GST 1	GSNO, ONOO ⁻ /GSH	[116]
Neurogranin/RC3	GSNO, decomposed GSNO	[117,118]
Neuromodulin/GAP-43	Decomposed GSNO	[118]
Calbindin	Decomposed GSNO	[115]
BSA	Decomposed GSNO	[115]
Ca ²⁺ -ATPase (SERCA)	ONOO ⁻	[83,85]
MMP-1,-8,-9	ONOO ⁻ /GSH	[119]
Tyrosine hydroxylase	ONOO ⁻ , NO ₂	[120]
PTEN	CysSNO*	[121]
Hsp70	SNAP in cells, eNOS activation	[48]
Vimentin	eNOS activation	[48]
Adenine nucleotide transporter	iNOS transgenesis	[48]
ATP synthase α -subunit	iNOS transgenesis	[48]

*S-nitrosocysteine (CysSNO) treatment of cells; S-glutathionylation not directly shown, although compatible with the results.

differences between the two modifications will gain importance in terms of stability or potential reversibility. Another case is constituted by proteins in which the different cysteines are selective for different modifications, and these affect protein function in distinct manners. An example of this is the ryanodine receptor channel (RyR1), where it was established that there were different reactive thiols with selectivity for S-nitrosylation [45] or S-glutathionylation [39,46], each leading to specific functional consequences.

The work of several laboratories has led to the conclusion that treatment with nitrosothiols induces protein S-glutathionylation in cells. In NIH-3T3 cells and rat hepatocytes, both S-glutathionylation and S-cysteinylation were detected when millimolar concentrations of S-nitrosocysteine were used, although the S-nitrosylation estimated was much higher [47]. More recently, a very appealing study describes several evidences for NO-induced protein S-glutathionylation by

nitrosothiol treatment of cells, eNOS activation in aortas and iNOS transgenic expression in mice hearts; indeed, they identify two or three glutathionylation targets in each system, thus providing additional evidence about the potential in vivo occurrence of the reaction [48].

3. Enzymatic mechanisms for the formation and breakdown of the modifications

Although S-nitrosylation and S-glutathionylation in cells can be explained by biochemical mechanisms, some enzymatic systems have been described that can accelerate some steps of their turnover. Regarding S-nitrosylation, and apart from the fact that certain protein targets have been described to be specifically assisted for their modification (reviewed in [49]), the main enzymatic process described so far is the GSNO reductase activity. It is exerted by the glutathione-dependent formaldehyde dehydrogenase (also called alcohol dehydrogenase class III) [50,51] and would presumably have a function of controlling the levels of intracellular GSNO and, indirectly, of protein S-nitrosothiols. This perspective adds even more lack of stability to the nitrosothiols formed in the cell, and it has been corroborated in several studies dealing with the nitrosothiol equilibrium.

Disulfide exchange is a slow chemical reaction that is accelerated in the intracellular environment by several enzyme families that mainly help to maintain the reduced state of intracellular thiols, both of proteins and of low molecular mass compounds like glutathione, by transferring the oxidizing equivalents to an acceptor cosubstrate. Thioredoxin (Trx) and glutaredoxin (reviewed in [17,52,53]) have been involved in the role of catalyzing breakage of protein mixed disulfides like S-glutathionylation. More recently sulfiredoxin, the enzyme that reverts protein sulfinic acid, has been added to this role [54]. A role in the formation could also be possible, as the reactions catalyzed by these enzymes are generally reversible, but then the cosubstrate should be predominantly in the oxidized form. This implies that GSSG would be the predominant form of the pair, in the case of glutaredoxin. In addition, glutathione S-transferase P has also been involved in S-glutathionylation formation [55].

4. Compartmentalization

Another important issue when considering the feasibility of both modifications in cells is subcellular compartmentalization. This is specially important due to the “multimolecular” and “submolecular” specificity derived from the chemical mechanisms described [1,3]. Furthermore, the short lifespan of some of the reactive species needs to be taken into consideration. This implies that the probability of the reaction between certain reactive species and certain proteins will be higher if the protein is in the same subcellular localization where the reactive species is produced.

In the case of S-nitrosylation, this has been studied mainly in terms of the NOS enzymes as they are the source for NO and

thus for other RNS. Since its molecular characterization [56] knowledge on the regulation of eNOS expression and activation has accumulated in a vast proportion. Undoubtedly the most important mode of regulation of eNOS in endothelial cells is related to post-translational modifications based on its dual acylation and interactions with a significant number of proteins which determine its topological fate. There are several examples of interactions of target proteins with NOS isoforms (see [57,58] for review), especially eNOS and nNOS, which are very tightly regulated in their subcellular localization, although iNOS subcellular localization has been also described to be regulated by acylation mechanisms [59]. A recent example of this target-NOS association is the interaction of the ryanodine receptor with eNOS [60]. In addition, eNOS has been shown to undergo S-nitrosylation both in the purified protein [61] and in a receptor-coupled mode in endothelial and COS-7 cells [62,63]. Functional consequences of this modification include the localized inhibition of eNOS activity by the NOS product itself, as S-nitrosylation was showed to disrupt the zinc tetrathiolate cluster and hence the active dimeric conformation of eNOS [61,62]. The same functional relevance of feedback inhibition by NOS products has been attributed to the S-nitrosylation of Hsp90, an activator of eNOS [32]. Of interest, studies in cells by Erwin et al. addressed the relevant issue of subcellular targeting, as loss of myristoylation lead to hypernitrosylation and to lack of regulation by VEGF and related changes in eNOS subcellular localization [63]. The link between acylation and other post-translational modifications of eNOS such as phosphorylation and S-nitrosylation is important due to the dynamic regulation of eNOS activity by its subcellular localization. Recent data by Iwakiri et al. show that S-nitrosylation is preferentially localized in the regions where transfected eNOS is localized, and can alter Golgi trafficking function by altering proteins that are sensitive to S-nitrosylation [64]. Of note, mitochondrial production of ROS could also be necessary for S-nitrosylation, as deduced from a subcellular localization study performed with a NONOate NO donor [65], while this was not the case when nitrosothiols were used [66] (methodological differences were also important in these two studies, see [67] for review).

The subcellular localization of glutathione has been debated at the same time as analytical advances have been developed and showed more clear differences in glutathione distribution. Early experiments detected an important presence of glutathione in the nucleus [68,69] while a more recent study has highlighted the presence of glutathione in perinuclear locations including mitochondria, showing also an uneven distribution in the cytosol [70]. Some efforts have been done to localize S-glutathionylated proteins, showing nuclear, perinuclear and discrete membrane localization [70]. Studies on other redox pairs like cysteine/cystine or thioredoxin have shown that they are also unevenly distributed and that each pair may have distinct equilibria depending on the localization (reviewed in [71]). Thus, further work will be needed to address this issue.

5. Potential role of S-glutathionylation in pathophysiological processes. Similarities and contrasts with S-nitrosylation

One of the major problems with non enzymatic-mediated post-translational modifications is establishing functional consequences in cells, tissues and organisms. To this end, and since our last review on this topic [34] significant efforts have been devoted to identify S-glutathionylation *in vivo*. Among these, the Cotgreave lab has put forward a technique to identify subcellular compartments of glutathione and mixed disulfides [70] as well as different proteomic approaches to identify S-glutathionylated proteins [72,73]. Inkeeping, several groups also applied redox proteomics to the identification of thiolated proteins [74,75] (see also [76–78] for review). However, although these approaches have facilitated the discovery of many proteins susceptible of becoming thiolated, the major leap forward leading to the establishment of causal relationships between S-glutathionylation (or S-nitrosylation) and human disease has yet to occur.

Currently, a significant number of clinical disorders or pathophysiological entities have been related to redox post-translational modifications. These comprise cardiovascular disease, diabetes (see non-comprehensive lists in [79,80]) and neural protein conformational disorders [81] among others. We will now comment some of the best characterized examples of proteins modified by S-glutathionylation in relationship to NO production and their pathophysiological correlates.

5.1. Sarcoplasmic/endoplasmic reticulum Ca^{2+} ATPase (SERCA)

In an effort to understand NO-mediated cGMP-independent vasodilatation, the laboratory of Richard Cohen identified that NO may stimulate calcium uptake into intracellular stores, thereby decreasing intracellular Ca^{2+} concentration and facilitating the uncoupling of the contractile machinery and vasorelaxation. SERCA is a key protein regulating the intracellular storage of Ca^{2+} , as it enhances refilling of Ca^{2+} sarcoplasmic and endoplasmic reticula. NO may regulate its function through both cGMP-dependent and independent mechanisms [82]. A key finding was the observation that this protein may result modified by several post-translational mechanisms in the presence of NO-related species [83,84]. Even more poignant was the discovery that peroxynitrite is able to activate SERCA by promoting S-thiolation in the context of arterial relaxation [85], an effect recapitulated by eNOS agonists. SERCA seems to have a specific target, Cys 674, whose modification results in the absence of NO-mediated increased activity. Furthermore this S-thiolation happens to occur *in vivo* and a decrease in its levels due to irreversible oxidation was found in atherosclerotic arteries. Overall, these data represent significant evidence suggesting the potential pathophysiological role of S-thiolated SERCA in vascular disease.

5.2. $p21^{Ras}$

Landmark work by Lander et al. showed that this oncogenic protein may become S-nitrosylated and that this may correlate with functional activation by converting it to its biologically active GTP-bound state [86]. Seminal work by the laboratory of Sharon Campbell has contributed to explain structure-functional relationships of Ras S-nitrosylation in Cys 118, and hence to gain mechanistic insight into the process of NO-mediated Ras guanine nucleotide dissociation in the presence of O₂ (see [87] for review). As it is the case with several other proteins, Ras may also become S-glutathionylated in the same cysteine and this was studied several years ago [35,37]. More recently, it has been suggested that this modification may mediate signalling by angiotensin II in vascular smooth muscle cells [88]. Peroxynitrite, albeit at moderately high concentrations, is able to thiolate Ras in endothelial cells, and this has been correlated with the activation of its downstream signaling effectors [89]. Of interest, the cysteine modification (not precisely determined) in myocytes is potentially reversible by thioredoxin [90]. In terms of pathophysiological findings, one of the most interesting observations situates ROS-induced S-thiolation of Ras as a mediator of cardiac myocyte hypertrophy in a strain-stimulated model [91].

5.3. Hemoglobin

Pioneering work by Stamler and cols. showed that hemoglobin (Hb) is a target for S-nitrosylation and that this modification may play a role in blood flow regulation [92]. This concept has evolved into many detailed studies of this interaction and roles for S-nitrosohemoglobin [93]. The binding of glutathione to the Cys-93 of Hb beta chain has been known for more than 20 years, and is associated with inhibition of Hb S polymerization, increased oxygen affinity and reduced alkaline Bohr effect [94,95]. This made it an interesting candidate to combat sickle cell anemia. However, neither the modification of Hb by glutathione nor by NO [96] have translated into effective treatments for sickle cell disease. In contrast, glutathionyl Hb has been widely documented in disease states such as uremia or diabetes (see [97] for review), and it is currently believed to be a consequence of the oxidative stress underlying these diseases. However, this may convert it in a very useful marker of oxidative stress in these conditions.

5.4. Caspase-3

More than a decade ago the antiapoptotic effect of NO was related to its potential inhibition of caspase-3 activation through cGMP-dependent and independent mechanisms [98]. In several elegant studies Mannick et al. documented that the Fas ligand was under the control of the NO pathway and that S-nitrosylation-denitrosylation of caspase-3 were mechanisms by which this ligand was controlling the general

process of apoptosis [99,100]. This same laboratory showed that S-nitrosylation of caspases could be linked to subcellular localization and that other caspases, such as caspase-9 could become S-nitrosylated [101]. Procaspase-3 undergoes S-nitrosylation in basal conditions in immune-response lineage cells on the catalytic cysteine, Cys163 [100]. Of interest, recent studies by Mitchell and Marletta described that the enzyme thioredoxin is involved in the process of S-nitrosylation of caspase-3 [102], and what is even more provocative, that S-nitrosylation of the critical cysteine residue within the catalytic site could be assisted by a nitrosopeptide that mimics the substrate configuration, thus providing an elegant example for a specific transnitrosation mechanism [103]. It should be noted that all these studies relied only on the indirect “biotin switch” technique.

S-glutathionylation of caspase-3 by GSNO or SNAP plus GSH has been described [102,104,105], and very recent observations claim that caspase-3 experiences S-glutathionylation on several thiol residues and that this process is intracellularly regulated by the thiol transferase glutaredoxin by a mechanism that was relevant for the regulation of endothelial cell death promoted by TNF- α [106]. Clearly, caspase-3 constitutes an important model to study both post-translational modifications at the cellular level, specially given its transcendence for the regulation of cell death, even when a definitive evidence establishing whole organism level implications still needs to be provided.

6. Conclusions and perspectives

It is clear that there is a chemical relationship among different cysteine post-translational modifications produced by both ROS and RNS and especially between S-nitrosylation and S-glutathionylation. This is supported by different experimental approaches that have shown a potential functional relevance in signal transduction, especially those arising from NO production. Also there is accumulating evidences of their (patho) physiological relevance in the cardiovascular system.

Much work is still needed to more precisely define the balance between the different modifications, the detailed mechanisms underlying the relationships, and their functional implications in physiological settings. Some years ago, we concluded that we were facing mainly an analytical problem [34]. Recent years have seen the development of a bunch of useful new methodologies, for example in proteomics or subcellular localization studies, that have moved the frontier of knowledge a bit further, but significant improvements in the analytical methodologies are still needed in order to gain deeper insight into the physiological relevance of these modifications.

Beyond this, one concept still holds: if several modifications are possible and are in certain ways homologous, they may be found when they are searched for. However, insight into the relative quantitative relevance of each modification is the crucial issue still to be chiselled out of the mist.

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