

RESEARCH HIGHLIGHT

Protein S-sulfhydration as a major sources of H₂S bioactivity

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The physiological and biomedical importance of hydrogen sulfide (H₂S) has been extensively studied in our body. H₂S can be endogenously produced in a variety of cells and tissues by cystathionine γ -lyase, cystathionine β -synthase, and/or 3-mercaptopyruvate sulfurtransferase, and is involved in the regulation of vascular function, cell growth, insulin secretion, neurotransmission, myocardial contractility, inflammation, and nociception, etc. H₂S post-translationally modifies proteins by yielding a hydropersulfide moiety (-SSH) in specific cysteine residue(s), termed as S-sulfhydration. It is becoming increasingly recognized that S-sulfhydration is a major source of H₂S bioactivity. In this research highlight, we discuss our latest published findings which demonstrate the S-sulfhydration regulation of proteins by H₂S and their importance in aging and cancer protection.

Keywords: H₂S; Cysteine; S-sulfhydration; Post-translational modification

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In 2002, Wang first created and defined the word “gasotransmitter”, and described the criteria for being a gasotransmitter^[1]. Hydrogen sulfide (H₂S), joining with nitric oxide (NO) and carbon monoxide, is an important member in the gas transmitter family^[1, 2]. Not only from the environment and industry activity, H₂S can also be endogenously produced in our body by specific enzymes, including cystathionine γ -lyase, cystathionine β -synthase, and/or 3-mercaptopyruvate sulfurtransferase, which are expressed or can be induced in most of cell types^[3-5]. H₂S can freely penetrate into the cell membrane independent of any cognate membrane receptors or other transportation machineries^[1]. Accumulated evidence demonstrated that H₂S is almost involved in all life functions, including cell growth, glucose metabolism, insulin secretion,

neurotransmission, myocardial contractility, inflammation, energy generation, and redox balance, etc^[2]. Despite a wealth of recent publications suggesting the important physiological roles for H₂S, its molecular mechanisms of action remain poorly defined. It is proposed that the major signaling mechanism of H₂S is through the S-sulfhydration of reactive cysteine residues on target proteins by yielding a hydropersulfide moiety (-SSH), with the potential to confer functional changes, which is analogous to S-nitrosylation of proteins by NO^[5].

Multiple cellular functions are controlled through the post-translational modification of proteins, including phosphorylation, glycosylation, ubiquitination, methylation, and S-nitrosylation, etc. Post-translational

Table 1. S-sulfhydrated proteins and their functional changes

S-sulfhydrated proteins/electrophiles	Tissue/cell types	Outcome	Targeted cysteine residues	Detection methods	Reference
GAPDH	Liver/HEK-293	NADH generation	150	BSA/TSA/MS	5,7
Actin	Liver	Actin polymerization	N/A	BSA	5
β -tubulin	Liver	N/A	N/A	BSA	5
Kir6.1	Aorta/HEK-293	Opening of K_{ATP} channel/vasorelaxation	43	BSA	3
NF- κ B/p65	Liver/HEK293 /Macrophage	Anti-apoptosis	38	BSA/MS	8,9
PTP1B	Hela/HEK-293	Restoration of ER homeostasis	215	BSA/MS	10
8-nitro-cGMP	Fibroblasts	Inhibition of cardiac cell senescence and oxidative stress	N/A	BSA	11
Keap1	Fibroblasts	Nrf2 activation and inhibition of oxidative stress	151	BSA	12,13
Parkin	Brain/SH-SY5Y cells	Higher parkin E3 ligase activity/neuroprotective action	95	BSA/MS	14
Platelet proteins	Platelet	Anti-thrombogenesis	N/A	BSA	15
Androgen receptor	Prostate cancer cells	Androgen receptor dimerization	611/614	BSA	16
MEK1	Endothelial cells/fibroblasts	PARP-1 activation/DNA damage repair	341	BSA	17
eNOS	Endothelial cells	NO generation and endothelial cell growth	443	BSA	18
P66Shc	Cortex/SH-SY5Y cells	Anti-oxidant	59	BSA	19
Ca ²⁺ TRP channels	Bone marrow mesenchymal stem cells	Ca ²⁺ influx and osteogenic differentiation	N/A	BSA	4
Membrane proteins	Heart	Cardioprotection	N/A	BSA	20

Note: BSA, biotin switch assay; TSA, tag-switch assay; MS, mass spectrometry

modifications are key mechanisms to increase proteomic diversity and serve to sense and transduce cellular signals in a precisely coordinated manner [6]. The amino acid cysteine in protein is quite reactive, and oxidative modification of cysteine residues is an important mechanism that regulates protein structure and ultimately functions, including S-nitrosylation, S-glutathionylation, and S-sulfenylation, etc [6]. Since the first paper describing H₂S S-sulfhydration of protein in 2009 [5], there have been a dozen of proteins observed to be modified by H₂S through S-sulfhydration, as demonstrated by modified biotin switch assay and/or liquid chromatography-tandem mass spectrometry (LC-MS/MS) (Table 1) [3-5]. It is predicted that, by change in electrostatic environment, hydrophobicity, contiguity and orientation of aromatic side chains, and proximity of target thiols to transition metals or redox centres, S-sulfhydration can alter protein conformation and the final function and activity of target proteins [16, 21].

It is well known that H₂S at physiological relevant concentrations suppresses oxidative stress and protects from cell death. The relative low concentration and the small molecular weight of H₂S make it hard to directly scavenge reactive oxygen species. Our recent paper discovered that H₂S S-sulfhydrates Keap1, which subsequently stimulates Nrf2 nuclear translocation and induces anti-oxidant gene transcription and glutathione production. Deficiency of H₂S enhanced oxidative stress and promoted cellular aging [12]. Nrf2 is a master

transcription factor that regulates the expressions of a group of antioxidant genes. Nrf2 activation can be attributed to the dissociation from Keap1 through posttranslational modulation of crucial cysteine residues in Keap1 protein. In normal condition, Keap1 is basically S-sulfhydrated, and exogenously applied H₂S increases but removal of endogenous H₂S reduces Keap1 S-sulfhydration. The cysteine residues 151 in Keap1 BTB domain is required for H₂S-mediated S-sulfhydration. H₂S interacted with cysteine residues 151 leading Keap1 conformational change, which trigger Nrf2 release from Keap1 following its nuclear translocation and anti-oxidant gene transcription. H₂S-induced activation of Nrf2 is not caused by increased Nrf2 protein expression, Nrf2 phosphorylation, or Nrf2 S-sulfhydration.

More recently, we made another discovery that H₂S effectively inhibits androgen receptor (AR) transactivation by S-sulfhydrating both cysteine 611 and 614 located in the DNA binding domain (DBD) of AR [16]. AR signaling is essential for the normal development and functions of prostate as well as the initiation and progression of prostate cancer. AR is a nuclear receptor, which is often activated as DBDs bind as dimers to two hexameric sequences orientated as direct or inverted repeats. The interaction of H₂S and AR through both cysteine 611 and 614 may destroy zinc-sulfur cluster and cause a structural change in AR-DBD, triggering abnormal AR dimerization and DNA binding ability. It is still unclear how H₂S S-sulfhydration of cysteine-611/614 alters AR zinc-finger structure and

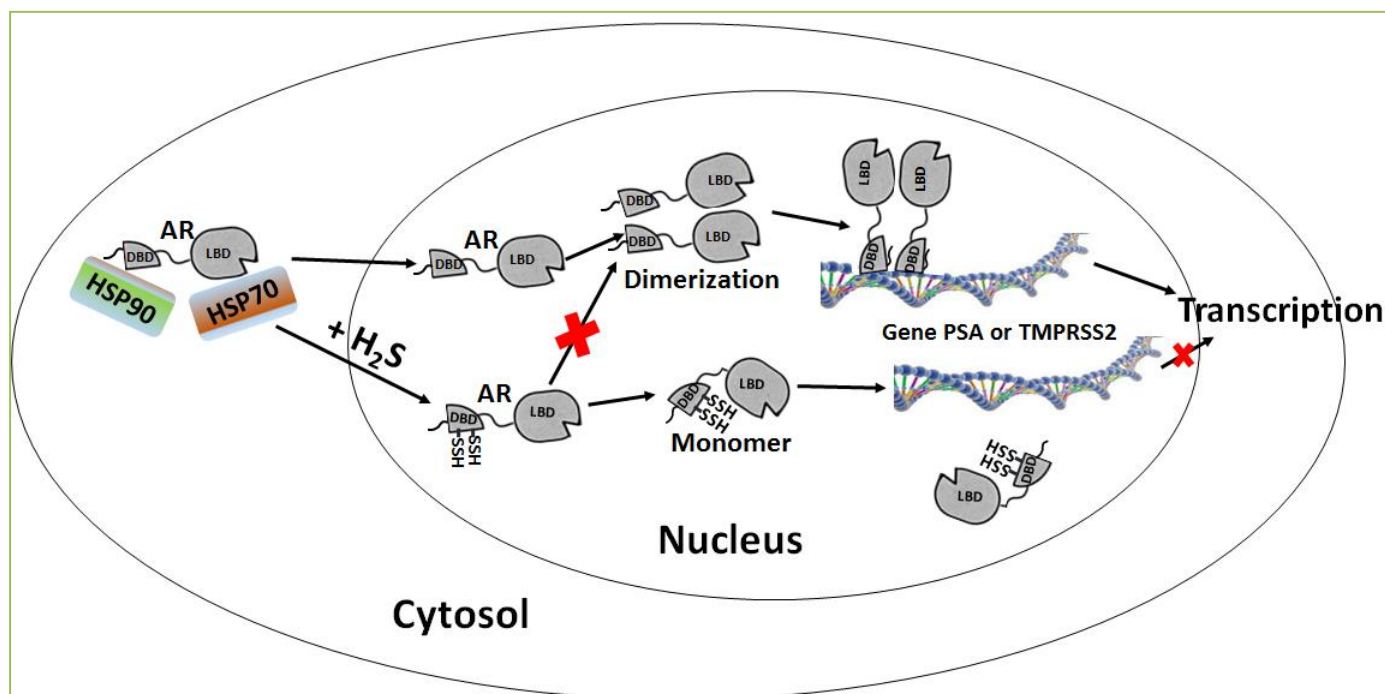


Figure 1. S-sulfhydration regulation of androgen receptor (AR) by H₂S. H₂S represses AR transactivation by S-sulfhydrating cysteine residues 611/614 located in the DNA binding domain (DBD). AR S-sulfhydration leads to reduced AR dimerization following lower AR binding with the promoters of prostate-specific antigen (PSA) and TMPRSS2, two AR-targeted genes, while AR S-sulfhydration does not affect heat shock protein (HSP) 70 and 90 interaction with AR and AR nuclear translocation.

dimerization. H₂S suppressing AR downstream gene expression were not due to the alteration of AR interaction with heat shock proteins and AR nuclear localization (Figure 1). We further observed that glucocorticoid receptor and estrogen receptor α , another two hormone receptors containing highly identical DBD as AR, are not S-sulfhydrated by H₂S, indicating the specificity of cysteine S-sulfhydration by H₂S in target proteins. Maintenance of sufficient level of H₂S could effectively inhibit ant androgen-resistant growth of prostate cancer cells. Based on these discoveries, H₂S can not only serve as a valuable prognosis indicator but also an effective therapeutic target for treatment of both early state of prostate cancer and castration-resistant prostate cancer.

In summary, our studies reveal that protein S-sulfhydration serves an important role in a wide range of H₂S-mediated signaling pathways, including protein activity, localization, stability, and interaction, and stress response. Compared with the large number of S-nitrosylated proteins which have been identified, the observed S-sulfhydrated proteins and the specificity of target cysteine are incompletely understood. Protein de-sulfhydration/trans-sulfhydration, the removal or transfer of SH group from cysteine thiol side in proteins, is very important but never reported so far. It is also not clear whether S-sulfhydration or de-sulfhydration/trans-sulfhydration is spontaneous and unregulated, or catalyzed

by enzymes and other cellular constituents [21]. Similar to S-nitrosylation, the formation or removal of an individual S-sulfhydration can depend on many factors including the reactivity of the individual cysteine residues, its surrounding environment, and the composition of the local redox-environment, etc. Advances in the detection of S-sulfhydration will facilitate research directed at the identification of S-sulfhydrated proteins in both health and diseases. There is a long way to fully understand the stories of S-sulfhydration and de-sulfhydration/trans-sulfhydration, but I believe we do have a bright future.

Conflict of interests

The authors declare no conflict of interests.

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