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Sulfur as a Signaling Nutrient Through Hydrogen Sulfide

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Abstract

Hydrogen sulfide (H_2S) has emerged as an important signaling molecule with beneficial effects on various cellular processes affecting, for example, cardiovascular and neurological functions. The physiological importance of H_2S is motivating efforts to develop strategies for modulating its levels. However, advancement in the field of H_2S -based therapeutics is hampered by fundamental gaps in our knowledge of how H_2S is regulated, its mechanism of action, and its molecular targets. This review provides an overview of sulfur metabolism; describes recent progress that has shed light on the mechanism of H_2S as a signaling molecule; and examines nutritional regulation of sulfur metabolism, which pertains to health and disease.

Keywords

hydrogen sulfide; signaling; sulfur metabolism; nutrition; sulfide oxidation

INTRODUCTION

Sulfur was likely among the first nutrients used by ancient forms of life on Earth—along with other inorganic substrates such as H_2 , CO, and N_2 —for the production of energy and as building blocks of life. Sulfur-utilizing organisms can be divided into two groups: sulfur reducing and sulfur oxidizing (143, 188, 202). Sulfate-reducing microorganisms are anaerobic and include bacteria and archaea that obtain energy by coupling the oxidation of organic compounds or molecular hydrogen to the reduction of sulfate in a process known as sulfate respiration (24, 188). Other inorganic sulfur compounds can also serve as electron acceptors, including sulfite, thiosulfate, and elemental sulfur, producing hydrogen sulfide (H₂S) (24, 188). Sulfate-reducing bacteria are believed to be among the oldest microorganisms and can be traced back 3.5 billion years (24). Sulfur-oxidizing microorganisms include both aerobic and anaerobic organisms (91, 143, 188) and oxidize H₂S to elemental sulfur or further, to other oxidized sulfur compounds (e.g., sulfate) to generate reducing power.

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Many invertebrate organisms thrive in sulfur-rich ecosystems and rely on sulfurmetabolizing endosymbionts to grow as well as to avoid the toxic effects of H_2S (13, 64, 65, 92). A well-studied example of such an invertebrate is the giant tube worm *Riftia pachyptila*, which lives in deep-sea hydrothermal vents that are sulfide rich (264). The ability to oxidize sulfide and its coupling to energy production is conserved in higher eukaryotes, and sulfide serves as an energy source for mammalian cells, providing reducing equivalents for the electron transport chain (271).

Mammals assimilate sulfur primarily from the diet in the form of the sulfur-containing amino acids methionine and cysteine, which are precursors for the synthesis of various sulfur-containing metabolites essential for cellular homeostasis. On the one hand, H_2S was long considered to be an environmental toxin produced by geochemical activity and by anaerobic organisms, including intestinal bacteria. The ability of animal tissues to degrade H_2S was viewed as a defense mechanism against intestinal or environmental exposure to H_2S . On the other hand, the therapeutic effects of sulfur springs have been known for several hundred years (52, 176, 195, 239). Curiously, although the ability of mammalian tissues to produce H_2S was known for a while, the possible physiological significance of this phenomenon did not get much attention until recently, with the discovery of the varied physiological effects of H_2S in systems including the cardiovascular, intestinal, and central nervous system (198, 210, 299).

METABOLISM OF SULFUR-CONTAINING AMINO ACIDS

Sulfur Metabolism

In addition to their utilization as building blocks for protein synthesis, the sulfur-containing amino acids methionine and cysteine are precursors for the synthesis of important sulfur metabolites such as H₂S and glutathione (GSH), the main cellular redox buffer (Figure 1). Methionine also provides cells with methyl groups that are used in various methylation reactions. The first step in methionine metabolism is its reaction with adenosine triphosphate (ATP), catalyzed by methionine adenosyltransferase, to produce S-adenosylmethionine (AdoMet), a universal methyl donor in transmethylation reactions. The transfer of the methyl group from AdoMet by a variety of methylases yields S-adenosylhomocysteine (AdoHcy), which is rapidly hydrolyzed to adenosine and homocysteine via the action of AdoHcy hydrolase. Homocysteine occupies a critical junction point in the sulfur network. It can be methylated to regenerate methionine or it can be used to synthesize cysteine and H_2S in the transsulfuration pathway. Remethylation of homocysteine by methionine synthase (MS), through transfer of a methyl group from 5-methyl tetrahydrofolate, completes the methionine cycle. In liver and in kidney, a second enzyme, betaine homocysteine methyltransferase (BHMT), also remethylates homocysteine to methionine using betaine as the methyl donor. Neither MS nor BHMT supports de novo methionine synthesis. Instead, their role is to recycle methionine consumed by AdoMet-dependent methylation reactions via the methionine cycle. Furthermore, AdoMet is utilized for polyamine synthesis, which generates methylthioadenosine as a byproduct. Methionine can also be recovered from methylthioadenosine via a salvage pathway. Therefore, under conditions of methionine conservation, activation of methionine recycling and salvage pathways provides a

mechanism for synthesizing AdoMet and polyamine without net methionine consumption. In normal cells, ~1% of the total AdoMet is diverted into polyamine synthesis, and this number can increase up to 100-fold in transformed cells (208, 243, 248, 275).

A second metabolic fate of homocysteine is its usage in the transsulfuration pathway that results in the irreversible exit of sulfur from the methionine cycle and into the synthesis of cysteine, H₂S, and other metabolites. The transsulfuration pathway comprises two enzymatic steps. In the first step, homocysteine is condensed with serine to form cystathionine in a reaction catalyzed by cystathionine β-synthase (CBS) followed by cleavage of cystathionine to α -ketobutyrate, ammonia, and cysteine in a reaction catalyzed by γ -cystathionase (CSE). In mammalian tissues, the transsulfuration pathway is irreversible. Hence, cysteine cannot be converted back to methionine, a capacity that is only present in lower organisms and renders methionine an essential amino acid for mammals. The transsulfuration pathway is present in the majority of tissues, including liver, kidney, pancreas, small intestine, and immune cells (macrophages, T cells, dendritic cells) (74, 87, 88). Although the presence of CSE in brain is debated (74, 119, 128), conversion of [³⁵S]-methionine into [³⁵S]-cysteine was observed in cultured human and murine neurons and astrocytes and in mouse brain slices (296), which provides evidence for an intact transsulfuration pathway in this organ. In contrast, the transsulfuration pathway does not appear to be intact in spleen, testes, heart, and skeletal muscle (74, 119).

Cysteine can be directed to several metabolic fates in addition to H_2S , and it is used for the synthesis of various other sulfur-containing metabolites, including GSH, coenzyme A (CoA), and taurine (Figure 1). Cysteine is a limiting substrate for fueling the synthesis of sulfur metabolites present at high intracellular concentrations, for example, GSH [up to 10 mM (164)] and taurine [ranging from 10 to 50 mM (114)]. The transsulfuration pathway is a significant source of cysteine in mammals, and its inhibition results in an ~50% decrease in GSH levels in cultured cells (26, 88, 183, 296) and in tissues (44, 59, 282). GSH is synthesized from cysteine in two ATP-dependent steps (164). In the first step, γ glutamylcysteine is produced from glutamate and cysteine, catalyzed by γ -glutamatecysteine ligase (GCL), which constitutes the rate-limiting step in GSH synthesis. In the second step, GSH is produced from γ -glutamylcysteine and glycine in a reaction catalyzed by GSH synthetase. The activity of GCL is subject to feedback inhibition by GSH that provides its redox sensitivity (228, 246) and is regulated by cysteine availability (169). Excess cysteine is committed to the oxidative degradation pathway by cysteine dioxygenase (CDO), which oxidizes cysteine to cysteinesulfinic acid, which in turn can be catabolized to pyruvate and sulfate via transamination or decarboxylated by cysteinesulfinate decarboxylase to produce hypotaurine. The latter is converted to taurine by a putative hypotaurine dehydrogenase (267). Hypotaurine can also be produced by oxidation of cysteamine, the end product of CoA degradation, in a reaction catalyzed by cysteamine dioxygenase (63).

Dietary Requirements

While the diet is the only source of methionine in mammals, cysteine can be produced from methionine via the transsulfuration pathway. The daily requirement of sulfur amino acids for

humans is $\sim 13-15$ mg/Kg (81, 152), with up to 89% of this is obtained as cystine, the oxidized disulfide form of cysteine (117, 151, 232). It is estimated that after digestion of food proteins, up to 20% of the methionine can be metabolized in gastrointestinal tissues (229). Excess dietary methionine has adverse physiological effects, although the mechanisms of its toxicity are not clear (19, 30, 81, 283, 304). In addition to being synthesized in the cysteine oxidation pathway, taurine is an abundant nonprotein amino acid that is obtained from the diet. Taurine is included in some energy drinks, although its usefulness in these drinks is questionable (48). In cats, which cannot synthesize taurine, it is an essential nutrient (325). The highest taurine concentrations are found in liver, muscle, and retina (114). The physiological role of taurine is not well understood, and functions ranging from an osmolyte (114, 181, 284), a neuromodulator (9, 113), an immunomodulator (245), and an antioxidant for detoxification of hypochlorous acid in immune cells (114) have been considered. Taurine deficiency leads to several abnormalities including blindness in some animals, decreased capacity for physical exercise, and heart dysfunction (113, 269, 303, 325). Recently, roles for taurine in intracellular pH buffering and stabilization of mitochondrial function have been proposed (100). Most other sulfur metabolites, such as AdoMet, exist at low concentrations in biological materials, and dietary input is not considered to be a significant source of sulfur. AdoMet is sold as the nutraceutical "SAMe" and is used in the treatment of alcoholic liver disease (25, 220) and for neurological problems (191, 205, 236) such as depressive disorders and Alzheimer's disease. The pharmacological activity of SAMe is likely to be associated with its role as a universal methyl donor rather than with its sulfur content.

Transport of Sulfur Metabolites

The cellular concentration and turnover of sulfur metabolites are impacted by transport systems that connect pools across cell membranes. Plasma methionine levels in mouse, rat, and human are in the range of 20–100 μ M (78, 97, 122, 165, 290, 293). Cysteine and GSH are present as a mixture of their reduced and oxidized forms, with total levels being ~100–200 μ M for cysteine and ~10–25 μ M for GSH (165, 227, 290, 293). In fact, the cysteine/ cystine and GSH/oxidized glutathione levels represent redox nodes that buffer the extracellular redox potential, which is dynamically maintained by intracellular redox metabolism (182, 316). Fundamental cellular properties such as progression through the cell cycle and cell-cell interactions in the immune and neuroimmune systems are correlated with changes in the extracellular redox potential (182, 316). The concentration of taurine is ~50–90 μ M in human and ~200–400 μ M in rodent plasma (78, 165, 179, 293). Plasma concentrations of other sulfur metabolites such as homocysteine, AdoMet, and cystathionine are in the low micromolar range or they are present in trace quantities (11, 57, 97). Circulation provides a route for the exchange of sulfur compounds between different tissues.

In mammalian cells, cysteine is transported by multiple transport systems including the ubiquitous sodium-dependent systems A and ASC and sodium-independent systems L and *asc* (203, 257, 298). These transport systems can provide rapid uptake or efflux of cysteine depending on cellular demand. For cystine, the major transport system is x_{C^-} , which provides sodium-independent uptake of cystine in exchange for glutamate (203, 298). Despite its significance in cell metabolism, methionine transport across mammalian cell

membranes is poorly studied. In hepatocytes, methionine transport is fast, reversible, and Na⁺-independent and provides equilibration of methionine between the cytoplasm and extracellular compartment (136, 147, 244). The system L transporter, LAT3, is primarily responsible for methionine transport in hepatocytes (16, 147). There are major gaps in our knowledge with regard to methionine transport in other cells. Upregulation of amino acid transporters in response to amino acid deprivation is well known (46). For instance, the cystine-glutamate exchanger is upregulated in human hepatocarcinoma cells deprived of cysteine/cystine (157, 252). Taurine is actively transported into cells by a specific Na⁺- dependent transporter, TAUT (98). Genetic disruption of the *taut* gene results in dramatically decreased tissue taurine levels (303).

Due to the unusual γ -peptide bond between glutamate and cysteine, GSH is not destroyed by intracellular peptidases. GSH turnover is provided by its transport to the extracellular compartment and its degradation by the successive action of γ -glutamyl transpeptidase and a dipeptidase associated with the exterior surface of the cell membrane. The products of GSH hydrolysis are the component amino acids glutamate (as 5-oxoproline), cysteine, and glycine (164). The trans-membrane GSH cycle is thus a source of cysteine for the extracellular compartment, which is available to other cells and also helps maintain the cysteine/cystine redox poise. Reduced and oxidized GSH as well as GSH conjugates are pumped out by multi-drug-resistance transporters, contribute to GSH turnover, and detoxify xenobiotics (17, 20, 35). Additionally, some members of the family of organic anion transporters are involved in GSH export (17, 20). Although the transport of GSH into cells has been reported in yeast (17), analogous transporters appear to be absent in most mammalian cells with the exception of the small intestine epithelial cells (115), immortalized mouse brain endothelial cells (133), renal basolateral membranes (153, 154), and a rat kidney cell line, NRK-52E (155).

Transmembrane transporters for homocysteine, if they exist, are not known. Hepatocytes can transport homocysteine from cells to the extracellular medium (261). Similarly, little is known about the transport of AdoMet across the plasma membrane, although its transport efficiency is expected to be low because the ratio of AdoMet in tissues to plasma is ~1000:1 (11, 57, 146). AdoMet import into cells is also inefficient, as indicated by transport studies using extracellular AdoMet (243).

The permeability coefficient estimated for H_2S in human erythrocyte membrane is >0.01 cm s⁻¹, which is rapid enough to establish equilibration across the membrane in a fraction of a second (123), suggesting that H_2S transport across cells might occur via diffusion. In contrast, the sulfide anion would require facilitated transport, and it is proposed that the anion exchanger AE1 in human erythrocyte membranes serves this function (123).

Regulation of Sulfur Metabolism by Diet

Metabolism of diet-derived nutrients occurs primarily in the liver, which plays a central role in regulating circulating levels of sulfur metabolites in blood (166). Excess dietary intake of methionine or cysteine/cystine has toxic side effects (19) and if sustained can reduce growth and promote brain lesions and retinal degeneration (19, 211, 270). In an average diet, ~50% of methionine taken up by hepatocytes is regenerated by the action of MS and BHMT,

constituting the methionine conservation mode in metabolism (146). The remaining $\sim 50\%$ of methionine is metabolized via the transsulfuration pathway, which constitutes the only metabolic sink for methionine in mammals. Excess dietary intake of methionine activates its disposal via a sharp (~10-fold) increase in the rate of its consumption and conversion to cysteine in the hepatic transsulfuration pathway (Figure 2a) (75, 146, 185, 222). Interestingly, stable blood methionine levels are maintained despite fluctuations in dietary intake, including prolonged starvation (4, 5, 165). The mechanism of this stabilization is not clear and probably includes a shift toward its increased conservation via the methionine cycle and enhanced methionine supply from protein degradation. Switching between the methionine conservation and methionine disposal mode is provided by AdoMet-dependent allosteric regulation (Figure 2a). Under conditions of methyl group sufficiency, CBS is activated by AdoMet to increase diversion of homocysteine to the transsulfuration pathway. In parallel, AdoMet inhibits the remethylation of homocysteine to methionine by MS indirectly by inhibiting methylenetetrahydrofolate reductase (MTHFR), which provides the methyl group donor 5-methyl tetrahydrofolate, required by MS. At high concentrations, AdoMet also activates methionine adenosyltransferase III to further increase the conversion of methionine to AdoMet. Therefore, AdoMet has multiple targets for regulation and functions as an allosteric regulator, allowing for a sharp metabolic transition from the methionine conservation mode at low-to-normal methionine supply to the methionine disposal mode when the methionine supply is in excess (146). In the methionine conservation mode, the rate at which methionine is used for AdoMet synthesis is controlled by methionine adenosyltransferase I to support cellular methyl transfer reactions (Figure 2b). The expression of enzymes involved in the methionine disposal mode increases under prolonged increase in dietary methionine supply (75, 234). Under these conditions, cysteineand homocysteine-dependent H₂S synthesis is predicted to increase by substrate-level activation. However, mechanistic insights into how cysteine is directed to H₂S synthesis in the normal or low metabolic mode are lacking.

Excess dietary cysteine is actively catabolized via desulfuration or oxidative degradation by CDO (267), which is highly expressed in liver (231, 267). CDO expression increases dramatically in response to increased dietary intake of protein or sulfur-containing amino acids (60–62, 268). Deletion of the CDO gene in mice leads to a significant increase in serum and tissue cysteine levels (231) and is associated with increased postnatal mortality, growth abnormality, and connective tissue problems (288). Overexpression of CDO in HepG2 cells reduces intracellular cysteine levels (62). Turnover of the intracellular GSH pool, which serves as a cysteine reservoir as well as an antioxidant, can be adjusted to respond to cellular cysteine needs (164).

The transsulfuration pathway is also activated under oxidative stress conditions (88, 183, 296) and downregulated by antioxidants (294), and the resulting changes in cysteine production are mirrored in GSH synthesis (88, 183, 296). Redox regulation of methionine metabolism is most likely provided by the redox sensitivity of MS (41), methionine adenosyltransferase (MAT), and CBS (238, 274).

Cysteine represents a highly regulated second junction in sulfur metabolism that can be directed into alternate pathways. Cysteine is consumed in the synthesis of GSH and CoA.

Although the quantitative significance of the flux of cysteine into CoA synthesis has not been assessed, it is believed to be small in comparison to GSH, which consumes cysteine at a rate that is comparable to its consumption by protein synthesis (222, 265, 291). However, a twofold increase in plasma cysteine levels in CDO-knockout mice results in only a negligible increase in GSH levels (231). The cellular concentration of cysteine is kept low by the action of CDO, which is upregulated at the transcriptional and posttranscriptional levels when dietary cysteine input is high. In contrast, under conditions of cysteine scarcity, CDO is ubiquitinated and targeted for proteasomal degradation (267). Tissue expression levels of CDO coincide with expression levels of the downstream enzyme cysteinesulfinate decarboxylase (267).

In rat hepatocytes, cysteine is cleared oxidatively via CDO (\sim 63%) and by transamination/ desulfuration (\sim 37%), leading to H₂S production (267) (Figure 1). Approximately 66% of cysteinesulfinic acid produced in the CDO reaction is converted to hypotaurine and taurine, and \sim 34% is catabolized to pyruvate and sulfate (267). When the dietary intake of cysteine or methionine increases, cysteine catabolism via the CDO-dependent pathway increases significantly, whereas the amount metabolized via the desulfuration branch is more or less unchanged (18, 267).

In normal rat hepatocyte suspensions, the average rates of production of taurine plus hypotaurine, sulfate, and GSH are 33, 46, and 110 pmol min⁻¹ mg⁻¹ protein, respectively (18). Assuming that ~10% of cell mass is protein, we estimate that these rates are 198, 276, and 660 µmol h⁻¹ Kg⁻¹ cells. From these numbers and the partitioning of cysteine metabolic fluxes presented above, we estimate that the rate of H₂S production is ~180 µmol h⁻¹ Kg⁻¹ cells, i.e., ~27% the rate of GSH synthesis. This value is within the same order of magnitude reported for the average rate of H₂S production (484 µmol h⁻¹ Kg⁻¹) in mouse liver (292). The interesting insight that emerges from this semiquantitative metabolic flux analysis is that the rate of hepatic H₂S production is comparable to the rates of taurine and GSH syntheses and must be taken into account during consideration of total metabolic sulfur balance or turnover. A cellular rationale for maintaining low cysteine levels is to avoid increased H₂S production that can in turn affect varied physiological processes.

H₂S METABOLISM

Enzymology of H₂S Production

 H_2S is produced from the sulfur-containing metabolites cysteine and homocysteine by the enzymes of the transsulfuration pathway, CBS and CSE (43, 254), and from 3mercaptopyruvate catalyzed by mercaptopyruvate sulfurtransferase (MST) and thioredoxin (170, 250) (Figure 1). CBS catalyzes the first irreversible step in the transsulfuration pathway, condensing homocysteine and serine to form cystathionine, which is cleaved by the second enzyme, CSE, to give cysteine. In addition to these canonical reactions, CBS and CSE exhibit substrate promiscuity and catalyze various H_2S -generating reactions from cysteine and homocysteine (43, 254) (Table 1). H_2S production by CBS and CSE results in the formation of two novel sulfur metabolites, lanthionine and homolanthionine (43, 254). Homolanthionine is reportedly elevated in urine of homocystinuric individuals (212), making it a potentially useful marker for homocysteine-dependent H_2S production.

The MST/thioredoxin system generates H₂S from 3-mercaptopyruvate (250) produced by transamination of cysteine that is catalyzed by cysteine (or aspartate) aminotransferase (286) (Figure 1). An alternative pathway for 3-mercaptopyruvate production involves oxidative deamination of D-cysteine catalyzed by D-amino acid oxidase, an activity that is localized in peroxisomes (111, 249). Mercaptopyruvate is desulfurated by MST to generate pyruvate and an active site per-sulfide, which transfers the sulfane sulfur to an acceptor and releases H₂S in the presence of reductants (170, 251). Kinetic analyses indicate that thioredoxin is an efficient acceptor of the MST-bound persulfide and can generate H₂S in the presence of thioredoxin reductase and nicotinamide adenine dinucleotide phosphate (NADPH) (171, 315). Although CBS, CSE, and MST are efficient at catalyzing H₂S generation under maximal velocity conditions, their relative contributions to endogenous H₂S generation vary with the tissue and are determined by the concentrations of the respective substrate and the expression levels of the enzymes (128).

The transsulfuration pathway plays a central role in sulfur metabolism (Figure 1). Commitment of homocysteine to the transsulfuration pathway serves at least two important functions: (*a*) to reduce levels of methionine under conditions of excess and to reduce levels of the toxic metabolite homocysteine and (*b*) to synthesize cysteine, an important precursor of other metabolites and the limiting substrate for GSH synthesis. Cysteine is a reactive amino acid, and its cellular concentration is maintained in the 80–100 μ M range in most tissues (290) except in kidney, where its concentration is ~1 mM (266).

Unlike the other gas-signaling molecules CO and NO, whose synthesis is known to be highly regulated, H₂S appears to be primarily generated by housekeeping enzymes, and little is understood about how it is regulated. Additionally, based on kinetic considerations, the enzymes involved in H₂S biogenesis appear to be better poised to utilize substrates in the canonical, i.e., non-H2S-generating, reactions. For example, serine, with an ~7- to 8-fold higher cellular concentration and ~4-fold lower K_M value as compared to cysteine, would be the preferred substrate for CBS under physiological conditions. Similarly, the relative intracellular concentrations of aspartate [0.7 mM in liver and 4 mM in brain (293)] versus cysteine [80-100 µM (290)], together with their K_M values for cysteine/aspartate aminotransferase [1.6 mM and 22 mM for aspartate and cysteine, respectively (7)], suggest that aspartate would be used preferentially by cysteine/aspartate aminotransferase. These considerations raise the obvious question as to how these enzymes are diverted away from catalyzing the canonical reactions and toward H₂S generation. CBS and CSE are cytoplasmic enzymes, although their nuclear localization has been seen under certain conditions (6, 129). MST is localized both in the cytoplasm and in the mitochondrion, suggesting a specific role for this enzyme in mitochondrial H₂S-based energy production. In agreement with this, mitochondrial cysteine concentration is high, $\sim 0.7-1$ mM, which would favor cysteine transamination by cysteine/aspartate aminotransferase (285). The regulation of H₂S biogenesis is an area that clearly deserves further attention.

Enzymology of H₂S Oxidation

The rapid metabolic removal of H_2S involves its oxidation to thiosulfate and sulfate, which was established by early metabolic labeling studies (55). The main H_2S oxidation product

excreted in urine is sulfate (27), whereas thiosulfate is the major end product of the colonic epithelium, which is exposed to high concentrations of sulfide produced by intestinal bacteria (85). H₂S is oxidized via a mitochondrial pathway linked to ATP production (103, 217), making H₂S the first known inorganic substrate for the electron transfer chain in mammals (94). Bacterial H₂S oxidation pathways are relatively well characterized (reviewed in 184). In mammals, four enzymes—sulfide quinone oxidoreductase (SQR), persulfide dioxygenase or ethylmalonic encephalopathy 1 (ETHE1), a sulfurtransferase or rhodanese, and sulfite oxidase—convert H₂S to persulfide, sulfite, thiosulfate, and sulfate, respectively (103) (Figure 3). In the first step, H_2S is oxidized by SQR, a flavoprotein localized in the inner mitochondrial membrane, forming a protein-bound persulfide. Two electrons from the oxidation of H₂S are transferred via flavin adenine dinucleotide to ubiquinone and then to the electron transport chain (42). The SQR-bound persulfide is transferred to an acceptor such as GSH or sulfite, resulting in the generation of GSH persulfide (103) or thiosulfate (120), respectively. Although the physiological acceptor for the SQR reaction is not known, GSH persulfide serves as substrate in the next step catalyzed by ETHE1 (103, 279). Furthermore, increased GSH synthesis by administration of the cysteine precursor Nacetylcysteine improves H₂S clearance in patients with ethylmalonic encephalopathy caused by mutations in the *ethel* gene (289), implicating GSH as the persulfide carrier in the sulfide oxidation pathway. ETHE1 contains a nonheme mononuclear iron and oxidizes the persulfide to sulfite (127).

Recently, an alternative mechanism has been proposed based on the observation that sulfite, the product of the ETHE1 reaction, is an efficient acceptor of the SQR-borne persulfide and is converted to thiosulfate (120). If thiosulfate is formed during the SQR reaction, an additional sulfurtransferase such as rhodanese would have to be invoked to transfer the sulfane sulfur from thiosulfate to GSH to feed into the ETHE1 reaction (Figure 3). The experimental evidence for this step is lacking, and clearly, further studies are required for a better understanding of the organization of the H_2S oxidation pathway. Sulfite is efficiently converted to thiosulfate by rhodanese in a reaction in which GSH persulfide functions as the sulfane sulfur donor (103). Thiosulfate can be converted to sulfate by the actions of thiosulfate reductase (40) and sulfite oxidase (49).

Recent studies using sensitive methods to measure tissue H_2S and kinetic studies on the rates of H_2S formation and clearance have allowed assessment of steady-state H_2S levels, which are in the 10–30 nM range in many tissues (84, 292, 309). Endogenous H_2S biogenesis in liver drains a significant pool of sulfur that is ~27% of the flux into GSH synthesis. However, in contrast to GSH that is maintained at 1–10 mM steady-state concentrations, steady-state H_2S levels are ~10⁵-fold lower. These data provide compelling evidence for a high flux of sulfur through the sulfide oxidation pathway to account for its low tissue concentrations (292), and indeed, experimental evidence supports a high capacity for H_2S oxidation by tissues (23, 55).

Regulation of Tissue H₂S Levels and Turnover

Despite the increasing number of reports in recent years on the physiological effects of H_2S , the field suffers from a paucity of reliable methods to determine tissue H_2S concentrations.

The values reported for normal H₂S concentrations vary over several orders of magnitude, with values in the hundreds of micromolar range representing the upper limit (196, 197). Accurate determination of tissue H₂S concentrations is mired in technical difficulties and experimental artifacts. Sulfide can easily leach out from iron-sulfur clusters that are abundant, resulting in gross overestimations of the free sulfide pool (84, 160, 196, 258). Exposure of rats to 800 ppm H₂S in air (~36 μ M) leads to 100% mortality within minutes (229). Assuming equilibration between air and blood H₂S levels provides an estimated upper limit of ~36 μ M for lethal H₂S blood concentration. Recent studies using sensitive methods such as sulfur chemiluminescence detection coupled to gas chromatography report tissue H₂S concentrations in the low nanomolar range (84, 197, 292, 309).

Tissue rates of H_2S production at physiologically relevant substrate concentrations range from 30–500 µmol h⁻¹ Kg⁻¹ tissue (292). Thus, intracellular H₂S concentrations could reach lethal levels in <60 minutes unless efficient routes for H₂S degradation existed. Indeed, the experimental data on H₂S clearance rates by murine liver, kidney, and brain demonstrate that these tissues maintain low steady-state H₂S levels in the nanomolar range by efficiently oxidizing H₂S (292), findings that are in agreement with other reports of low H₂S levels in vivo (84, 160, 196, 258).

The intestinal mucosa is exposed to high concentrations of H_2S produced by the degradation of sulfur-containing organic compounds and by dissimilatory sulfate reduction by the resident microflora. It is estimated that the total intestinal H₂S production can reach up to 12 mmol per day, which is equivalent to 6.6 μ mol h⁻¹ Kg⁻¹ body weight for a 75-Kg person (85). Hence intestinal H_2S production could result in lethal concentrations in ~5 hours. This toxicity problem is averted by efficient H₂S oxidation in situ by the host, i.e., in the cecal and right colonic mucosa, which exhibit sulfide oxidation activity that are ~4- and 20-fold higher than in liver and muscle, respectively (85). It is unclear how much of the intestinal H₂S reaches the blood and other organs. Intestinal H₂S can influence total body H₂S levels under pathological conditions such as ethylmalonic encephalopathy (198). Indeed, it was shown in a recent study on the *ethel*^{-/-} mouse model for ethylmalonic encephalopathy that treatment with metronidazole, an antibiotic effective against anaerobic bacteria, causes an increase in the median survival time from 27 to 49 days (289). These data are consistent with a significant contribution of intestinal H₂S to systemic H₂S levels. Interestingly, a similar shift in median survival time (from 27 to 54.5 days) was observed when the mice received the GSH precursor N-acetylcysteine. Treatment with a combination of metronidazole and N-acetylcysteine had an additive effect and increased median survival time to 71.5 days. Additionally, combination therapy with metronidazole and Nacetylcysteine caused a marked clinical improvement in five children with ethylmalonic encephalopathy (289).

Based on the preceding discussion, it is clear that the levels of H_2S can be modulated by its production and/or its oxidation. Low steady-state concentrations of H_2S combined with a high rate of its turnover implies that the H_2S level can spike transiently, allowing for passage of a signal. Although the H_2S -producing enzymes in the transsulfuration pathway, particularly CBS, are highly regulated (226), their pertinence to H_2S production is not

known. Much less is known about the reaction mechanisms and regulation of enzymes involved in H₂S oxidation (103, 120, 127).

One level at which H₂S generation could be regulated is by substrate and cofactor availability. Critical enzymes in the sulfur network are dependent on cofactors obtained from the diet, including vitamins B_6 , B_{12} , and folic acid in addition to zinc (Figure 1). Hence, dietary input of cysteine and homocysteine and the precursor methionine in addition to zinc and the B vitamins can modulate H₂S production. In addition, oxidative stress modulates the transsulfuration pathway and is relevant to diseases such as diabetes (66, 241, 281, 300). Elevated homocysteine, as found in homocystinuric patients, can increase CSEdependent endogenous H₂S production (43, 254). AdoMet, an allosteric activator of CBS, enhances CBS activity ~2-fold in both the canonical and H₂S-producing reactions (314). Testosterone (219, 295), glucocorticoids (223), epidermal growth factor, transforming growth factor- α , cyclic adenosine monophosphate (cAMP), dexamethasone (69), and insulin (223) also modulate CBS activity. Nitric oxide (NO) reportedly stimulates H₂S production in rat fetal membranes and in aorta (209, 328) and increases CSE mRNA expression in aortic smooth muscle cells (328). Since MST-dependent H₂S biogenesis requires coupling to a reductant (e.g., the NADPH/thioredoxin reductase/thioredoxin) system (315), H₂S production by MST is expected to be sensitive to the intracellular redox status. Inhibition of 3-mercaptopyruvate production by cysteine/aspartate aminotransferase by aspartate that competes with cysteine (7), or by the reaction products glutamate or oxaloacetate, can decrease H₂S production by MST.

Several pharmacological inhibitors of CBS and CSE are quite widely used to modulate H_2S production and include propargylglycine, β -cyanoalanine, aminoethoxyvinylglycine, aminooxyacetic acid, hydroxylamine, and trifluoroalanine (3, 15, 299, 307). With the exception of propargylglycine, which is a mechanism-based inhibitor of CSE, the remaining compounds are relatively nonspecific and target other pyridoxal 5'-phosphate (PLP) enzymes (15). Propargylglycine is widely used in cell culture (26, 88, 183, 296) and in vivo (44, 59, 282) experiments. However, at high concentrations, propargylglycine also inhibits alanine aminotransferase ($K_i = 3.9 \text{ mM}$) (38) and the cysteine/aspartate aminotransferase (at 100 mM propargylglycine) (273). Thus, in principle, the effect of propargylglycine in cell culture could result from inhibition of H_2S production by MST in addition to CSE.

β-cyanoalanine is used to target CSE and is a reversible inhibitor (180, 214, 328). However, it also inhibits aspartate decarboxylase and alanine aminotransferase (12, 51). Aminoethoxyvinyl-glycine, widely used to inhibit PLP-dependent ethylene synthesis in plants (323), also inhibits purified human CSE (262) and the transsulfuration pathway in cultured human astrocytes (296). Aminooxyacetic acid, an inhibitor of aminotransferases (225), is used to target CBS in vitro (2, 56, 107) and in vivo (235) but also inhibits CSE (15). Hence, aminooxyacetic acid is likely to inhibit all three routes for H₂S synthesis in cells. Despite this nonspecificity, aminooxyacetic acid inhibited H₂S production significantly less than did propargylglycine in smooth muscle cells (107), which might be due to a combination of factors such as poorer availability and a weaker inhibition constant. Although hydroxylamine is used as a specific CBS inhibitor (2), it is also widely used as a reagent for releasing the cofactor from PLP-dependent enzymes in general. Trifluoroalanine

is an irreversible inhibitor of PLP-dependent enzymes, which catalyze β - or γ -elimination reactions including CBS and CSE (253, 254, 262). Although it is ~4-fold more selective for CBS than for CSE (15), it has off-target activities as well.

H₂S AS A SIGNALING MOLECULE

Protein Persulfidation

A growing number of reports suggest a role for protein persulfidation (or S-sulfhydration) in H₂S-based signaling (186). Persulfidation can occur by the direct nucleophilic attack of the sulfide anion on an oxidized cysteine (e.g., a sulfenic acid, S-nitrosyl, or disulfide) by a transfer of an existing persulfide or by the nucleophilic attack of a cysteine thiolate on oxidized forms of H_2S [e.g., hydrogen disulfide (H_2S_2) or polysulfides] (95, 126) (Figure 4). The unstable chemical nature of persulfides and the absence of known mechanisms for achieving target specificity raise obvious questions regarding the prevalence and physiological relevance of this modification in H₂S-based signaling. However, the functional consequences of persulfidation on the activities of some enzymes have been recognized for over four decades (34, 101, 167). Although protein sulfhydration has been reported to be as prevalent as phosphorylation, with 10–25% of liver proteins being persulfidated, these data need to be treated with caution because they were obtained using a modified biotin switch assay (186), which lacks the specificity to distinguish between persulfides and thiols (204). The development of persulfide-specific reagents combined with direct demonstration of the persulfide modification in proteins is needed to assess the prevalence and validate the existence of this protein modification.

Persulfidation of some proteins has been demonstrated by mass spectrometric analysis, including glyceraldehyde-3-phosphate dehydrogenase (GAPDH), in which persulfidation increases activity (186), and the p65 subunit of nuclear factor- κ B (NF- κ B), which increases its antiapoptotic function in response to tumor necrosis factor- α (TNF α) treatment by increasing DNA binding and the transcriptional activity of NF- κ B (247). *S*-nitrosylation of the same cysteine residues in GAPDH (247) and the p65 subunit of NF- κ B (135) have opposing functional consequences. Persulfidation of the active site cysteine in protein tyrosine phosphatase (PTP)-1B inhibits its activity, resulting in the accumulation of phosphorylated PERK (protein kinase RNA-like endoplasmic reticulum kinase) and an enhanced cellular response to endoplasmic reticulum (ER) stress (149). Persulfidation of ATP-sensitive potassium channels results in channel opening and hyperpolarization of endothelial smooth muscle cells, leading to vasodilation (187, 328).

Interaction of H₂S with S-Nitrosothiol

The interaction between NO and H_2S signaling pathways is increasingly invoked as a potential mechanism for the action of H_2S . NO and H_2S exhibit some synergistic physiological effects that indicate cross talk between the two signaling systems (50, 71, 107, 162, 218, 280). Hints about a potential molecular mechanism for the interaction between the H_2S and NO signaling pathways came with the identification of thionitrous acid [*S*-nitrosothiol (HSNO)] generated by the reaction of H_2S and NO donor compounds (Figure 5*a*) (308). H_2S treatment blunts the effect of NO donor compounds and inhibits the NO-

dependent increase in cyclic guanosine 3',5'-monophosphate (cGMP) levels, indicating adduct formation between H₂S and NO (308). Formation of HSNO by the reaction of H₂S with *S*-nitrosothiols, e.g., *S*-nitrosoglutathione (GSNO), has been demonstrated (73). HSNO freely diffuses through membranes, facilitates transnitrosation, and, in principle, can generate NO+, NO–, and HNO, potentially eliciting diverse specificities and physiological functions (73). The formation of HNO in vivo has been demonstrated using a nitroxyl-sensitive fluorescence probe (73). Despite its known cardioprotective role (76, 83, 134, 168, 206), the physiological relevance of HNO as a signaling molecule has been debated. Formation of HNO by a direct displacement of GSNO by GSH has been proposed (Figure 5) (255, 311). In these studies, formation of hydroxylamine and nitrous oxide in the reaction mixture indicated HNO formation because nitrous oxide can be generated by decomposition of the HNO dimerization product, hyponitrous acid (14, 260, 311).

The properties of HSNO investigated by high-level ab initio calculations indicate that the SNO group exists in mixed electronic states, with a predominant RS^-/NO^+ resonance structure accounting for its overall reactivity (276, 277). Recent studies indicate that the electronic structure of *S*-nitrosothiol (RSNO) could be modulated by its specific interactions with residues in proteins (272). A nucleophilic attack on the sulfur atom in the ion pair by a thiolate would yield HNO. In analogy with this, a nucleophilic attack by the sulfide anion on the sulfur atom in the RS^+/NO^- resonance form could produce HNO and a persulfide, representing a mechanism for persulfide formation. In the case of HSNO and H₂S as reactants, the products would be HNO and HSSH. It has been proposed that the pharmacological effects of sodium nitroprusside [Na₂Fe(CN)₅(NO)], used intravenously as a potent vasodilator, is mediated in part by HNO (72, 321). HNO can also function as a nitrosylating agent (82), and modulation of voltage-dependent K⁺ channels in the vascular system in rats has been reported (116). The effect of Angeli's salt, an HNO donor, on myocyte contractility mimics the effects of sodium nitroprusside plus H₂S treatment (321).

Electrophile Sulfhydration

Sulfhydration of various electrophiles, including 8-nitro-cGMP nitro derivatives and keto derivatives of unsaturated fatty acids and cyclopentenone prostaglandin, has been demonstrated recently (193) (Figure 5b) and provides an additional molecular mechanism for H₂S signaling. Electrophiles function as signaling molecules and primarily react with cysteine residues to initiate signaling (77, 237, 259, 287). Protein modification by electrophiles such as S-guanylation by nitro-cGMP and electrophilic lipid-protein interactions (242, 259) mediates various redox-dependent signaling pathways (237) such as cGMP-dependent NO signaling (36). Denitration and sulfhydration of nitrated cGMP by H₂S block inducible nitric oxide synthase (iNOS)-dependent guanylation of H-Ras, a modification that activates H-Ras to signal cell senescence in response to stress (240, 312). Protein S-guanylation levels were increased by CBS knockdown in various human cell lines in culture (193). Increased 8-SH-cGMP levels and loss of H-Ras activation were proposed to be responsible in part for the protective role of H₂S in myocardial infarction-associated heart failure (193). The functional consequences for sulfhydration of compounds such as cyclopentenone prostaglandin (15d-PGJ2), which mediates electrophilic lipid-protein interactions by specifically modifying cysteine residues (259) and suppresses angiogenesis

(45, 80), are not known. The interaction between the H_2S and NO signaling pathways might be more common and also more complex than previously thought, and H_2S could modulate NO-based signaling either by mediating transnitrosylation between target molecules or by competing with NO for the same reactive cysteines.

Interaction of H₂S with Metal Centers

Another mechanism for H_2S -dependent signaling can be realized through its interaction with metal centers in the active sites of proteins. Depending on the stereoelectronic characteristics of the center, H₂S can reduce or coordinate to the metal (Figure 6). In hemeproteins, high H₂S concentrations promote heme reduction in polar active sites, whereas heme H₂S complexes are stabilized in nonpolar active sites (215). Because sulfide has a stronger nucleophilic character compared to water, it can displace water that generally fills empty coordination sites at metal centers in proteins. H₂S binds to both heme a_3 and Cu_B in the binuclear center (104) and reversibly inhibits cytochrome c oxidase, leading to a decrease in the metabolic rates and inducing a state of suspended animation in animals (32). The inhibition constant for sulfide is $0.2 \,\mu\text{M}$ for purified cytochrome c oxidase (213) and ~20 µM for intact cells (159). In isolated mitochondria, the maximal rates of respiration and ATP production were achieved in the presence of 10 µM H₂S, but the rates decreased with increasing sulfide concentration owing to inhibition of cytochrome c oxidase (322). Decreased ROS generation is another consequence of cytochrome c oxidase inhibition by H₂S and is believed to account for the protective effects of H₂S donors in ischemiareperfusion-associated cardiac injury. Invertebrates living in sulfide-rich habitats use different forms of hemoglobin to transport sulfide to symbiotic bacteria to protect themselves from H₂S toxicity (297). It is not known whether coordination or reduction of metal centers by H₂S is involved in H₂S metabolism and signaling. Reduction of methemoglobin by H_2S can potentially lead to oxidative clearance of H_2S (28). Under aerobic conditions, H₂S can react with methemoglobin to form sulfhemoglobin, which represents an alternative sink for H₂S (192).

PHYSIOLOGICAL EFFECTS OF H₂S

The Effects of H₂S in the Central Nervous System

A physiological effect of H_2S unrelated to its toxicity was first reported in the central nervoussystem (CNS) where it was found to activate *N*-methyl-D-aspartate (NMDA) receptor-mediated responses and to facilitate induction of hippocampal long-term potentiation in the 10- to 130-µM concentration range (2). At higher concentrations (320 and 640 µM), sodium hydrosulfide (NaHS) inhibited synaptic transmission. In fact, reversible effects of H_2S on neuronal transmembrane potentials and currents were observed in toxicological studies with H_2S concentrations ranging from 30 to 400 µM (145). Expression of the GABA_B receptor subunits 1 and 2 is upregulated by H_2S , whereas expression of the GABA_B receptor subunit 2 but not 1 is inhibited by hydroxylamine, a nonspecific inhibitor of H_2S biogenesis (99). H_2S can affect levels of epinephrine, norepinephrine, and serotonin in brain (150, 233, 256, 302).

H₂S increases intracellular Ca²⁺ in neurons, astrocytes, and microglia by increasing Ca²⁺ influx into the cytoplasm from extracellular and intracellular compartments (86, 158, 190, 320), which can affect the interaction between these cells. Activation of voltage-dependent Ca^{2+} channels or transient receptor potential channels by H₂S is believed to be the underlying mechanism for intracellular Ca²⁺ increase (137, 138). H₂S can act as a neuroprotectant in the CNS by increasing production of GSH and by suppressing oxidative stress in mitochondria (140, 141). An H₂S-induced increase in GSH production is achieved through multiple mechanisms, including increased cystine and cysteine transport and activation of GCL without a concomitant change in the enzyme levels (140, 141). Although antioxidant activity via direct interaction between H2S and reactive oxygen species has been invoked (137, 138), this seems unlikely to be a quantitatively significant mechanism owing to the low concentrations of H₂S in comparison with other antioxidants (e.g., GSH). Intraperitoneal treatment of pregnant rats with NaHS protects the fetal brain from damage caused by ischemia reperfusion, and this correlated with enhanced GSH levels (140). Cysteine supplementation promotes proliferation and differentiation of neuronal stem cells to neurons and astroglia, an effect that was attenuated by knockdown of CBS expression using siRNA (301). The neuroprotectant effects of H₂S could also be due to its antiinflammatory and antiapoptosis activities (109) and the stabilization of membrane potentials (110, 139).

H₂S Effects in the Cardiovascular System

The first report of the effects of H₂S on the cardiovascular system indicated that it induced smooth muscle relaxation in the portal vein and the thoracic aorta (at 0.03–1.0 mM concentration) and enhanced vasorelaxation by NO (107). The relaxation mechanism is associated with opening of ATP-sensitive K⁺ channels in an ATP-independent manner (328). H₂S-induced vasorelaxation is partially attenuated by removal of the endothelium, by inhibition of NO synthase, or by blockade of Ca²⁺-dependent K⁺ channels, suggesting that H₂S might stimulate endothelial cells to release one or more factors to facilitate smooth muscle relaxation (327). However, H₂S pretreatment is also reported to induce vasoconstriction by scavenging endothelial NO (10) and inhibiting the vasorelaxant effect of the NO donor sodium nitroprusside (327). Furthermore, at NaHS concentrations ranging from 5 to 100 µM, a reversal of its vasodilatory effects caused by phenylephrine precontracted rat thoracic aorta rings was observed in a mechanism that is likely to involve cAMP and AMP cyclase (163). In fact, H₂S-induced vasoconstriction and vasodilation in addition to multiphasic behavior have been observed in multiple vessels from different organisms (199). It is likely that the response of blood vessels to H_2S depends on multiple factors including vessel type, species, observation time, and H₂S concentration. Another variable that influences the effects of H₂S on the smooth muscle of blood vessels is O₂, with low and high concentrations inducing vasorelaxation and contraction, respectively (144).

Mice in which the *CSE* gene is disrupted exhibit hypertension in comparison with wild-type animals (319), although in a separate study, CSE-knockout mice were reported to be normotensive (118). The relaxation effect of H_2S on smooth muscle cells has also been observed in guinea pig ileum (107) and in the human corpus cavernosum strips, where effects were in the 0.1 to 10 mM range (56). H_2S can inhibit proliferation and cause

apoptosis of vascular smooth muscle cells (317, 318) and stimulate proliferation of vascular endothelial cells (39, 207). In these studies, the most significant effects were observed at H_2S concentrations ranging from 10 to 500 μ M.

 H_2S exerts a cardioprotective effect, and injecting 2.8 µmol Kg⁻¹ day⁻¹ or 14.0 µmol Kg⁻¹ day⁻¹ NaHS into rats treated with isoproterenol, which induces infarct-like myocardial necrosis, improved hemodynamic parameters, decreased subendocardial necrosis, and reduced animal mortality (89). In an isolated rat heart model for ischemia reperfusion, the addition of 1 µM NaHS to the perfusion buffer significantly reduced myocardial damage, whereas 0.1 µM and, surprisingly, 10 µM NaHS had no effect (125). Pretreatment with ATP-sensitive potassium channel blockers glibenclamide and sodium 5-hydroxydecanoate abrogated the protective effect of 1 µM NaHS. In another study using isolated rat heart and cultured myocytes, protection against ischemia reperfusion injury was also observed, albeit at significantly higher NaHS concentrations (10–100 µM) (31). In an in vivo mouse model for ischemia reperfusion injury, similar protective effects were seen using 0.1 to 6.4 µmol Kg⁻¹ H₂S, and maximal protection was obtained with an H₂S dose of 0.64 µmol Kg⁻¹ (67). Significant protection against ischemia reperfusion injury was also achieved by cardiac-specific overexpression of CSE (67).

Endoplasmic Reticulum Stress

The ER provides a specialized compartment for folding of proteins targeted for the cell surface or for secretion. These proteins are rich in disulfide bonds critical for stability and function and for redox-dependent signaling. The ER lumen provides an oxidizing environment required for the formation of disulfide bonds and harbors stringent quality control mechanisms for ensuring fidelity. Various conditions, such as infection, inflammation, increased synthesis of secreted proteins in response to pathological conditions, or conditions that jeopardize protein folding, lead to compromised ER function and induction of the ER stress response. Misfolded proteins in the ER lumen activate autophosphorylation of ER-resident kinases including PERK. The latter in turn phosphorylates and inhibits eukaryotic initiator factor 2α (eIF2 α), resulting in the inhibition of general protein synthesis to provide a window for the reestablishment of cellular homeostasis. Sulfhydration of an active site cysteine in PTP1B, a phosphatase that dephosphorylates PERK, results in inactivation leading to accumulation of phosphorylated PERK and enhanced cellular response to ER stress (149). Sulfhydration of PTP1B in response to ER stress is dependent on CSE activity (149). In agreement with these results, ER stress results in ATF4 (activating transcription factor 4)-dependent increase in CSE expression. Mouse embryonic fibroblast cells lacking the CSE gene are susceptible to ER stress-induced cell death (58). These results suggest regulatory and protective roles for H_2S during ER stress. ER stress accompanies many diseases such as diabetes (108), and it is chronically activated in all major cell types involved in atherosclerotic lesions (108, 189), which suggests that an enhanced ER stress response induced by H_2S could be partly responsible for the beneficial effects of H₂S.

Roles of H₂S in Aging

Because of its multiple physiological effects, H_2S can influence aging and age-related diseases such as cardiovascular diseases, neurodegenerative diseases, diabetes, and cancer (326). The nematode *Caenorhabditis elegans*, when grown in the presence of 50 ppm H_2S , exhibits increased thermo-tolerance and a 70% increase in life span (172). H_2S -induced life span increase in *C. elegans* is associated with increased expression of several age-related, stress-response, and antioxidant genes and protects animals against paraquat toxicity (221). Deletion of the *sir-2.1* gene encoding an NAD-dependent deacetylase abolished H_2S effects on thermotolerance and life span (172). H_2S also increases life span of the short-lived *mev-1 C. elegans* mutant (221). Mutations in *mev-1* encoding a homolog of the succinate dehydrogenase complex subunit C lead to hypersensitivity of animals to oxygen and paraquat and cause premature aging. Similarly, an increased mortality rate due to deficiency of *mpst-1* (encoding an MST ortholog) is reversed by exposing worms to H_2S , which indicates the importance of MST in H_2S production in this organism (221).

In mice, exposure to low levels of H_2S induces a suspended animation–like state by reversible inhibition of cytochrome c oxidase accompanied by a lowering of the metabolic rate and body temperature (32). Additional evidence indicates the importance of sulfur metabolism to aging. For instance, a low-methionine diet increases life span in rats (201) and in mice (173) and improves metabolic parameters (173). In agreement with these results, in hepatocytes from the long-lived Snell dwarf mice, methionine transport is several-fold lower, producing a functional methionine deficiency (293). In contrast, humans chronically exposed to H_2S in industrial settings (for an average of 12.0 ± 8.5 years) apparently exhibit signs of accelerated aging, detected by a statistically significant increase in serum levels of p53 and interleukin 8 (1).

H₂S-RELATED DEFICIENCIES IN SULFUR METABOLISM AND DISEASE

Enzymes poised at the sulfur metabolic junctions determine the partitioning of intermediates between alternative pathways and are strictly regulated. Deficiencies of these junction enzymes have pleiotropic consequences that affect major organ systems, including the cardiovascular and neuronal systems. High plasma homocysteine is an independent risk factor for cardiovascular diseases (224) and can result from deficiencies in CBS, MS, and other enzymes involved directly or indirectly in supporting sulfur metabolism at the homocysteine junction. Mutations in CBS are the most common cause of homocystinuria, and more than 150 mutations have been identified (148). Mutations in the CBS gene affect the ocular, cardiovascular, skeletal, and central nervous systems (47, 174, 224). Genetic deficiencies as well as low dietary levels of B12 and B6, the cofactors for MS and CBS, respectively, can result in increased homocysteine levels. Other factors that lead to homocystinuria include a functional deficiency in MS caused by mutations in its gene or in the auxiliary protein methionine synthase reductase required for its reactivation, or a deficiency of its B₁₂ cofactor or folate substrate (96, 156, 305, 306, 310). The B₁₂ cofactor is targeted to MS via a complex mechanism, and defects in the trafficking proteins also lead to homocystinuria (21, 22, 90). Patients with MS deficiency present with a range of clinical abnormalities, including megaloblastic anemia and various neurological complications, such

as developmental problems, mental retardation, seizures, cerebral atrophy, and ataxia (263, 305). A low B_{12} level during pregnancy is correlated with neural tube defects (142, 174). MTHFR catalyzes the formation of 5-methyltetrahydrofolate, the methyl group donor in the reaction catalyzed by MS (Figure 1). MTHFR deficiency affects cellular folate metabolism, and a common polymorphism, C677T, which results in an alanine-to-valine substitution, leads to a thermolabile enzyme that is correlated with increased plasma homocysteine levels (79, 132). The prevalence of this polymorphism varies in different populations and ethnic backgrounds and is 5–15% in the United States and Europe (68, 132). During the catalytic cycle of MS, the B_{12} cofactor is occasionally oxidized and must be reduced to restore enzyme activity. MS reductase, a flavoprotein, provides the electron for the reductive activation of MS, and several mutations associated with homocystinuria have been described in its gene (156, 200, 310). A common MS reductase polymorphism with an ~51% prevalence in the US population is the I22M variant (310), which is correlated with coronary artery disease (37) and Down syndrome (105) and activates MS with lower efficiency (200).

Although plasma H_2S levels have not been measured in patients with deficient CBS and MS activities, kinetic studies predict that CSE-dependent H_2S production would be elevated in homocystinuric patients (43). In fact, homolanthionine, a by-product of the CSE-catalyzed condensation of two moles of homocysteine to generate H_2S , was detected in the urine of homocystinuric but not normal individuals, which indicates that H_2S formation is indeed elevated (212). Elevated homocysteine owing to defects in the remethylation pathway is expected to shift its utilization to the transsulfuration pathway and consequently to result in elevated H_2S synthesis (43).

In mouse models, deletion of CSE results in diminished plasma H₂S levels (319). Perturbations in sulfur metabolism have been reported in diabetic patients (102, 106, 112, 230) as well as in animal models of diabetes. The activities of CBS and CSE as well as homocysteine level (121) and H₂S production (324) are increased in the liver and kidney of streptozotocin-induced diabetic rats, a model for type 1 diabetes. CSE expression and H₂S production are also higher in pancreatic β -cells in Zucker diabetic fatty rats, a model for type 2 diabetes, compared to Zucker diabetic lean rats (313). However, plasma H_2S levels are low in nonobese diabetic mice (33). Patients with coronary artery occlusion or multivessel lesions showed significantly lower plasma H₂S concentrations (124). Brain H₂S levels in patients with Alzheimer's disease are reported to be severely decreased (70). In patients with Down syndrome, serum homocysteine, methionine, AdoMet, and AdoHcy levels are significantly decreased whereas DNA methylation is increased (216), consistent with the presence of an extra copy of CBS on chromosome 21. Interestingly, urine thiosulfate is twofold higher in patients with Down syndrome compared to controls (29), indicating increased H₂S metabolism (131). Neuronal damage resulting from elevated H₂S production has been proposed to contribute to mental retardation in these patients (130).

In macrophages, CSE expression is reportedly increased in response to LPS and cytokines, with a concomitant increase in H_2S production (194). Increased plasma H_2S concentration also accompanies LPS-induced inflammation in mice (161). Patients with septic shock also display increased plasma H_2S (93). LPS treatment has been reported to increase serum sulfite levels in rats (178). Higher serum sulfite levels have also been reported in patients

with pneumonia, and neutrophils obtained from these patients produced higher amounts of sulfite in vitro compared to cells obtained after recovery (177), indicating increased synthesis of H_2S during the acute phase of the disease. Mutations in MST lead to mercaptopyruvate cysteine disulfiduria, an inborn error of metabolism characterized by mental retardation and elevated urinary excretion of mercaptopyruvate cysteine disulfide (53, 54).

More than 20 mutations have been described in patients with ethylmalonic encephalopathy due to deficiencies in ETHE1 (175, 278). Ethylmalonic encephalopathy is an autosomal recessive disorder characterized by severe pathophysiological abnormalities affecting the brain, gastrointestinal tract, and peripheral vessels; it leads to death in the first decade of life (175). Patients with ethylmalonic encephalopathy show unusual vascular features, acrocyanosis, bleeding abnormality due to microscopic hematuria and hemoperitoneum, hemorrhage, and dilated tortuous retinal vessels. Neuropathological features of the disease are necrotic lesions in the basal ganglia and in the brain stem (8). Biochemically, these patients exhibit increased plasma levels of H_2S , thiosulfate, and ethylmalonic acid; C4 and C5 acylcarnitines; elevated urinary excretion of ethylmalonic acid; and lactic acidemia. Cytochrome c oxidase activity is lower in skeletal muscles, presumably owing to inhibition by elevated H_2S levels (279).

CONCLUSIONS AND FUTURE DIRECTIONS

Recent years have witnessed exciting progress in elucidating the beneficial physiological effects of H₂S and in discovering potential mechanisms of its signaling action, such as via HSNO. However, the understanding of H₂S biology is hampered by significant gaps in our knowledge of the regulation of endogenous steady-state tissue H_2S levels, the rapid modulation of H_2S for inducing signaling, and the molecular targets of H_2S . Development of reliable methods for the detection and quantitation of H_2S and its targets of action is urgently needed to clarify controversies on its physiological effects. Because of the volatility and high turnover rates of H_2S in tissues, methods to quantify H_2S as well as techniques for H₂S sample preparation are crucial for obtaining reliable data. Although various probes to visualize endogenous H₂S levels have been developed, the majority lack the required stringency in specificity for H_2S , a fast response time, and the ratiometric output needed for quantitative analyses in cell-based assays (197). The intimate connection between dietary inputs into sulfur metabolism, particularly B vitamins and the amino acids methionine and cysteine, emphasizes the potentially important role of nutrition in modulating sulfur homeostasis and H₂S-based signaling. Studies assessing the interaction between nutrition and H₂S-based signaling represent another important gap in knowledge that warrants filling.

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Glossary

H_2S	hydrogen sulfide
GSH	glutathione
AdoMet	S-adenosylmethionine
AdoHcy	S-adenosylhomocysteine
MS	methionine synthase
BHMT	betaine homocysteine methyltransferase
CBS	cystathionine β -synthase
CSE	γ-cystathionase
СоА	coenzyme A
GCL	γ-glutamate-cysteine ligase
CDO	cysteine dioxygenase
MTHFR	methylenetetrahydro-folate reductase
MST	mercaptopyruvate sulfurtransferase
SQR	sulfide quinone oxidoreductase
ETHE1	persulfide dioxygenase or ethylmalonic encephalopathy 1
GAPDH	glyceraldehyde-3-phosphate dehydrogenase
ER	endoplasmic reticulum

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Figure 1.

Simplified scheme of sulfur metabolism with an emphasis on the H₂S-generating reactions. In addition to the amino acids methionine and cysteine, the other significant dietary inputs into the pathway are the vitamins B₂ (flavin), B₆ (pyridoxal phosphate), and B₁₂ and zinc. Abbreviations: AdoHcy, *S*-adenosylhomocysteine; AdoMet, *S*-adenosylmethionine; BHMT, betaine homocysteine methyltransferase; CAT, cysteine/aspartate aminotransferase; CBS, cystathionine β -synthase; CDO, cysteine dioxygenase; CoA, coenzyme A; CSE, γ -cystathionase; DMG, dimethylglycine; GCS, γ -glutamylcysteine synthetase; GS, glutathione synthetase; GSH, glutathione; H₂S, hydrogen sulfide; MAT, methionine adenosyltransferase; MST/Trx, mercaptopyruvate sulfurtransferase/thioredoxin; MTHFR, methylenetetrahydrofolate reductase; THF, tetrahydrofolate; Trx, thioredoxin; Zn, zinc.



Figure 2.

Switching of methionine metabolism between the disposal (*a*) and conservation (*b*) modes is regulated by AdoMet. The thick arrows qualitatively depict increased metabolic flux. The dashed lines indicate activation (*red*) and inhibition (*blue*) by AdoMet to control flux in response to low and high methionine supply. Abbreviations: AHC, AdoHcy hydrolase; GNMT, glycine *N*-methyltransferase; MAT-I/III, liver-specific methionine adenosyltransferase isoforms I and III; MT, methyltransferase.

SO,2-

50₄²⁻



Figure 3.

The mitochondrial sulfide oxidation pathway. Sulfide quinone oxidoreductase (SQR) constitutes the first enzyme in this pathway and oxidizes H_2S , generating a protein-bound persulfide. Two routes for the transfer of the persulfide to sulfite (*path 1*) or to an alternative acceptor (Ac in *path 2*) are shown. In path 1, the thiosulfate formed in the SQR-catalyzed reaction has to be converted to glutathione disulfide (GSSH) for further oxidation by ethylmalonic encephalopathy 1 (ETHE1). In path 2, if glutathione (GSH) is the acceptor, then the resulting GSSH product can directly serve as the substrate for ETHE1. However, if some other molecule serves as the proximal persulfide acceptor from SQR, then a sulfurtransferase (ST) such as rhodanese (Rhd) would likely be necessary to transfer the persulfide group to GSH for further oxidation. CSA and SO denote cysteine sulfinic acid and sulfite oxidase, respectively.



Figure 4.

Molecular mechanisms for protein persulfidation. Persulfidation of targets can occur via several mechanisms, including (1) a nucleophilic attack of sulfide on a disulfide, (2) cysteine sulfenic acid, or (3) cysteine-S-nitrosothiol; (4) a reaction between a protein thiolate and H_2S_2 or polysulfide; or (5) a transsulfuration reaction in which the sulfane sulfur from an existing persulfide is transferred to a different acceptor. Abbreviations: HNO, nitroxyl; HSSH, hydrogen disulfide; SNO, S-nitrosocysteine; SOH, sulfenic acid; SSH, persulfide.



Figure 5.

Potential molecular mechanisms for H₂S signaling via *S*-nitrosothiol (HSNO) or sulfhydration of electrophiles. (*a*) Formation of HSNO results in cross talk between the NO and H₂S signaling pathways. HSNO can mediate transnitrosylation directly or can react further with another mole of H₂S, generating HNO. (*b*) Sulfhydration of electrophiles 8-nitro-cGMP and 15-deoxy- 12,14-prostaglandin (15d-PGJ2) by H₂S forms the corresponding thio adducts. Abbreviations: HNO, nitroxyl; HSSH, hydrogen disulfide; SNO, *S*-nitrosocysteine.



Figure 6.

Reaction of H_2S with heme. The product of the interaction between H_2S and ferric heme is dictated by the properties of the heme pocket. Although H_2S coordinates to the ferric heme ion without additional redox chemistry in polar (high-dielectric-constant) sites, reduction to the ferrous heme is favored in nonpolar (low-dielectric-constant) sites.

Table 1

$H_2S\mbox{-generating}$ reactions catalyzed by CBS and CSE

Enzyme	Substrates	Products
CBS ¹	Cysteine	Serine + H ₂ S
	Cysteine + homocysteine	Cystathionine + H_2S
	Cysteine + cysteine	Lanthionine + H ₂ S
CSE ²	Cysteine	$Pyruvate + H_2S + NH_3$
	Cysteine + cysteine	Lanthionine + H_2S
	Homocysteine	$\alpha\text{-Ketobutyrate} + H_2S + NH_3$
	Homocysteine + homocysteine	Homolanthionine $+$ H ₂ S
	Homocysteine + cysteine	Cystathionine + H_2S

¹Taken from (254);

 2 taken from (43). Abbreviations: CBS, cystathionine β -synthase; CSE, γ -cystathionase; H₂S, hydrogen sulfide; NH₃, ammonia.