METABOLISM OF SULFUR-CONTAINING AMINO ACIDS

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INTRODUCTION

It has long been recognized that L-methionine (Met) is metabolized by transmethylation and transsulfuration, but recent studies have provided more information about the regulation of flux through these pathways and about the fate of the transferred methyl group and sulfur atom. The role of the polyamine pathway and the possible role of a transamination pathway in Met metabolism were demonstrated more recently. L-Cysteine (Cys) metabolism has received relatively little attention, but the interpretation of several recent studies in light of the older literature provides some new insights. The intent of this review is to provide an overview of current knowledge about pathways of sulfur-containing amino acid metabolism in mammalian tissues and the physiological regulation

of flux through these pathways. Most of the research on sulfur-containing amino acid metabolism has focused on the liver and, hence, so does this review. However, the relative roles of the liver and other tissues in the metabolism of Met and Cys in vivo have not been well established, so extrahepatic tissues may also play a significant role in Met and Cys metabolism.

METHIONINE METABOLISM

The Formation and Utilization of S-Adenosylmethionine

The first step in Met metabolism is the formation of the high-energy sulfonium compound, S-adenosyl-L-methionine (AdoMet). AdoMet is both the methyl donor for transmethylation reactions and the precursor of decarboxylated AdoMet [dAdoMet; S-adenosyl(5')-3-methylthiopropylamine], which is the aminopropyl donor for the synthesis of polyamines. Met adenosyltransferase (EC 2.5.1.6) catalyzes the formation of AdoMet by transfer of the adenosyl moiety of ATP to the sulfur atom of Met. Multiple isozymes of Met adenosyltransferase exist in mammalian tissues (112, 113, 116, 134, 138, 139, 206, 209, 216). Three isozymes (I, II, and III) have been identified in rat liver (206). Met adenosyltransferase-I (α) shows Michaelis-Menten kinetics with a $K_{\rm m}$ for Met of 41 μM, is slightly inhibited by AdoMet, and comprised about 15% of the total Met adenosyltransferase activity in rat liver preparations when activity was assayed at 25 μ M Met. Met adenosyltransferase-II (γ), which also appears to be the isozyme found in normal rat kidney, has a Met concentration required for half-maximal velocity $[S_{0.5} (Met)]$ of 8 μ M, is strongly inhibited by AdoMet, and comprised about 5% of the total activity in rat liver. The predominant isozyme in rat liver, Met adenosyltransferase-III (β), has a $S_{0.5}$ (Met) of 215 µM and demonstrates positive cooperative modulation by AdoMet at physiological metabolite concentrations (50–150 µM Met, 50–200 µM AdoMet). Thus, the velocity of AdoMet synthesis in extraheptic tissues would be expected to be nearly maximal, relatively unaffected by an increase in Met concentration, and sensitive to feedback/product inhibition by AdoMet. In contrast, the velocity of AdoMet synthesis by the high- $K_{\rm m}$ hepatic isozyme should increase in response to elevated Met and AdoMet levels, permitting rapid clearance of excess Met by the liver.

The Met adenosyltransferase isozyme pattern is altered in fetal and neoplastic liver and in liver of patients with hereditary tyrosinemia, with a marked reduction in levels of the high- $K_{\rm m}$ isozyme, MAT-III (112, 113, 116, 139, 216). Gaull et al (71) and Finkelstein et al (62) studied children with low levels of hepatic Met adenosyltransferase activity (8–18% of control values for adults) concomitant with the presence of normal amounts of enzyme in erythrocytes, cultured fibroblasts, and lymphoid cell lines. Despite persistent hypermethioninemia, these patients were free of adverse symptoms. Although he-

patic Met adenosyltransferase activity in one child was 8% of the control level when activity was assayed at 1 mM Met, it was 39% of control levels when the assays were performed with 6–12 μ M Met. It seems probable that these children lacked active Met adenosyltransferase-III, but had normal levels of the low- $K_{\rm m}$ isozymes.

AdoMet serves as the methyl donor for essentially all known biological methylation reactions with the notable exception of those involved in methylation of L-homocysteine (Hcy). The co-product of transmethylation, S-adenosyl-L-homocysteine (AdoHcy), is hydrolyzed to yield Hcy, which can be remethylated to Met or condensed with serine to form cystathionine. Formation of cystathionine commits the Met molecule to catabolism by the transsulfuration pathway. These transmethylation reactions and the transsulfuration pathway are depicted in Figure 1.

A second fate of AdoMet involves its decarboxylation to form dAdoMet, which is the donor of aminopropyl groups for synthesis of spermidine and

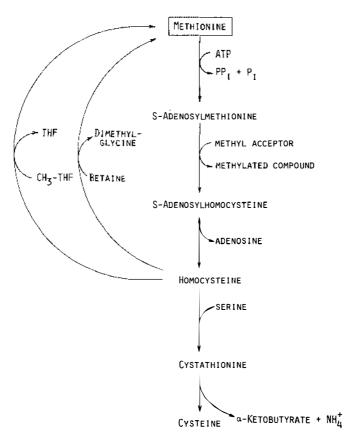


Figure 1 The transmethylation-transsulfuration pathway.

spermine. Polyamine synthesis also results in the formation of 5'-methylthioadenosine (MTA) from dAdoMet. The sulfur and methyl group of MTA may be reincorporated into Met by the MTA salvage pathway, whereas the aminopropyl group does not appear to be recycled. The reactions involved in polyamine synthesis and MTA salvage are summarized in Figure 2.

Few estimates have been made of the relative flux of AdoMet through these two pathways. Recycling of Hcy and of MTA to Met can lead to underestimation of the magnitude of AdoMet flux through either transmethylation reactions or the polyamine pathway. Giulidori et al (72) measured the ¹⁴CO₂ produced by intact rats given intravenous S-adenosyl-[1-14C]Met or S-adenosyl-[3,4-¹⁴C]Met. They suggested that 30% of the irreversibly catabolized AdoMet was used for the aminopropylation pathway following decarboxylation. About 70% of the AdoMet apparently was catabolized by the transsulfuration pathway following transmethylation, as there was no evidence for nonenzymatic decomposition of AdoMet. These estimates are probably maximal for decarboxylation-aminopropylation and minimal for transmethylation because the authors made no corrections for Hcy recycling or for incomplete or differential recovery of the carbon atoms as CO₂. The recovery of the 1-carbon should have been substantially greater than that of the 3- and 4-carbons because of direct decarboxylation of AdoMet or of α -ketobutyrate compared to metabolism of the 3- and 4-carbons via the tricarboxylic acid cycle.

Iizasa & Carson (89) estimated the relative rates of polyamine synthesis and transmethylation from AdoMet in malignant human and murine cell lines deficient in MTA phosphorylase. These cells did not detectably cleave MTA

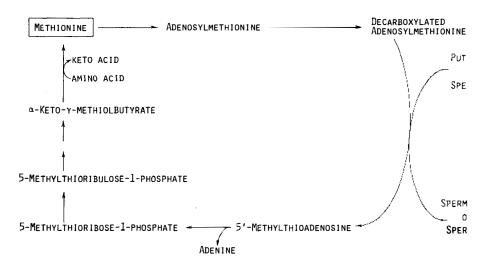


Figure 2 The polyamine pathway.

and did not appreciably metabolize Hcy. Both MTA and Hcy were excreted into the growth medium. During exponential growth of lymphoblasts, the MTA excretion rate was 80–130 and the Hcy excretion rate was 210–290 pmol·h⁻¹·10⁶ cells⁻¹; thus, MTA excretion represented about 30% of the AdoMet consumption in these rapidly growing cells. Both the rates of MTA and Hcy production would be expected to be substantially lower in non- or slowly dividing cells.

The Transmethylation and Transsulfuration Pathway

METHYLATION REACTIONS The methyl group of AdoMet is transferred to a nitrogen, oxygen, or sulfur atom of a wide range of compounds in reactions catalyzed by numerous methyltransferases. The major use of labile methyl groups appears to be for the formation of creatine from guanidinoacetate. Mudd & Poole (132) reported urinary excretions of creatinine that were approximately 15–16 mmol·day⁻¹ in men and 10 mmol·day⁻¹ in women, whereas other methylated compounds excreted in urine, including creatine, only accounted for 1.6–2.6 meq of labile methyl groups·day⁻¹.

Loss of labile methyl groups via oxidation of the carbon to C-1 intermediates at oxidation levels of formaldehyde, formate, or CO₂ appears to occur primarily via formation and degradation of sarcosine, as shown in Figure 3 (129, 225a, 229). Based on sarcosine excretion by a female sarcosinuric patient, Mudd et al (129) estimated that about 1.5–3.0 mmol of labile methyl groups were oxidized via the sarcosine pathway each day when the subject was on a relatively normal dietary intake; total daily utilization of Met methyl groups in transmethylation reactions was estimated to be 13-14 meq. Intake of labile methyl groups (Met or choline) beyond the apparent requirement of approximately 14 meq per day resulted in nearly equimolar increases in sarcosine production beyond those accounted for by choline degradation; this sarcosine was presumably synthe sized via the glycine methyltransferase reaction. De novo synthesis of methyl groups via the tetrahydrofolate (THF) system appeared to be minimal when labile methyl intake was sufficient or excessive. The labile methyl group intake beyond which additional methyl groups were used for sarcosine production was in agreement with the sum of methyl group utilization for various methylation reactions under basal conditions; this agreement suggests that Mudd and coworkers have accounted for most, if not all, of the major routes of Met methyl group utilization (129, 132). It seems clear that the major daily requirement for labile methyl groups is for creatine formation and that the major mechanism for removal of excess methyl groups is via sarcosine production and degradation.

Data from studies with intact rats are also consistent with metabolism of excess Met methyl carbon via the combined action of Met adenosyltransferase (probably isozyme-III), glycine methyltransferase (EC 2.1.1.20), and sarco-

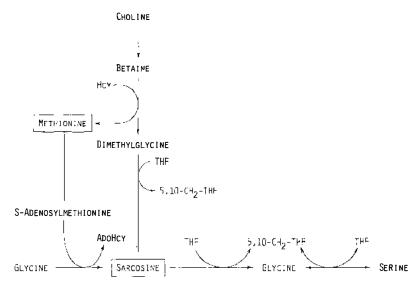


Figure 3 Pathway for methyl group oxidation.

sine dehydrogenase (EC 1.5.99.1). In intact rats given intraperitoneal injections of [Me- 14 C]Met, up to 40% of the label incorporated into hepatic proteins was recovered in serine and a smaller amount was found in Cys (2, 3). The labeling of serine presumably occurred via conversion of sarcosine to glycine and $N^{5,10}$ methylene-tetrahydrofolate (methylene-THF) (225a, 229)] in the reaction catalyzed by sarcosine dehydrogenase, followed by conversion of glycine and methylene-THF to serine in the reversible reaction catalyzed by serine hydroxymethyltransferase (EC 2.1.2.1). A small amount of label was presumably incorporated into Cys by utilization of the labeled serine in the transsulfuration pathway. As would be expected if production of sarcosine is dependent upon the availability of excess labile methyl groups, both the conversion of the Met methyl carbon to CO_2 and the incorporation of the methyl carbon into serine were decreased when the rats were fed choline-devoid or Met-deficient diets (2).

Recently, Wagner (225b) reported that glycine methyltransferase is allosterically inhibited by the polyglutamate form of N^5 -methyltetrahydrofolate (methyl-THF), which accumulates in the cell during Met deficiency. Thus, regulation of glycine methyltransferase may play a role in conservation of labile methyl groups when Met intake is inadequate.

Oxidation of excess labile methyl groups via sarcosine production and degradation appears to be dependent upon the methylation of glycine rather than upon phosphatidylcholine turnover, both of which generate sarcosine from the methyl group of AdoMet. Case et al (26) showed that phosphatidylcholine turnover did not account for a significant amount of Met methyl group oxidation

in the intact rat. Additionally, phosphatidylcholine biosynthesis by methylation of phosphatidylethanolamine or by incorporation of pre-formed choline appears to be regulated to maintain a relatively constant level of phosphatidylcholine in tissues (29, 159). As expected, increased incorporation of label from [Me-¹⁴C]Met into tissue phosphatidylcholine was observed in rats fed choline-devoid diets, whereas decreased incorporation was observed in rats fed Metdeficient diets (2, 3). This is in marked contrast to the similar effects that changes in either Met or choline intake had on the conversion of the methyl carbon of Met to serine, sarcosine, or CO₂.

METABOLISM OF S-ADENOSYLHOMOCYSTEINE AdoHcy is hydrolyzed to adenosine (Ado) and Hcy by AdoHcy hydrolase (EC 3.3.1.1). This reaction is apparently the sole means of intracellular removal of AdoHcy in mammalian tissues (44, 46). The reaction is reversible with the equilibrium far in the direction of synthesis ($K_{eq} = 1 \mu M$), but hydrolysis occurs in vivo when Ado is removed by Ado deaminase (EC 3.5.4.4) or Ado kinase (EC 2.7.1.20) and when Hcy is removed by cystathionine β-synthase (EC 4.2.1.22), betaine-Hcy methyltransferase (EC 2.1.1.5), or Met synthase (tetrahydropteroylglutamate methyltransferase, EC 2.1.1.13). AdoHcy hydrolase contains tightly bound NAD⁺, which participates in the catalytic process (69). The $S_{0.5}$ of the rat or mouse liver enzyme for AdoHcy has been reported to range from 0.75 to 20 μM when measured with low concentrations of enzyme (41, 69, 95, 219) and to be 120 μM at cellular concentrations of enzyme (219); tissue concentrations of AdoHcy range from <0.8 to 56 nmol·g⁻¹ (43, 61, 83, 221, 226).

Hydrolysis of AdoHcy is inhibited by the presence of either product, Hcy or Ado, and inhibition is accompanied by the accumulation of AdoHcy and AdoMet (84, 168). Purine nucleoside toxicity (observed in children with Ado deaminase deficiency or purine nucleoside phosphorylase deficiency and in patients treated with 9-β-D-arabinofuranosyladenine) as well as the growth inhibitory properties of MTA may be mediated partially through inhibition of AdoHcy hydrolase (16, 21, 53, 68, 94, 106, 160). Inhibition of AdoHcy hydrolase may lead to decreased intracellular Met synthesis from Hcy and altered folate metabolism due to the methyl trap effect (16, 21), inhibition of intracellular transmethylation reactions (22, 106), and inhibition of Ado kinase (68).

The cellular concentration of AdoHcy itself or the ratio of AdoMet to AdoHcy may serve as a feedback regulator of biological methylation reactions. Most methyltransferases that utilize AdoMet as the methyl donor are inhibited by AdoHcy, and the inhibitory constants vary over a wide range (K_i for AdoHcy = 1-35 μ M; K_m for AdoMet = 1-570 μ M) (22, 23, 83, 84, 98). Whether or not regulation of methyltransferase reactions by AdoHcy occurs under physiological conditions is questionable, because the ratio of the concen-

tration of AdoHcy to that of AdoMet is relatively low compared to that required for inhibition of methyltransferases, and the activity of AdoHcy hydrolase is higher than that of Met adenosyltransferase in most tissues (43, 45, 61, 83, 226). However, when AdoHcy levels in perfused rat liver or in intact rats or mice were increased as a result of inhibition of AdoHcy hydrolase by Ado, Hcy, or 9-β-D-arabinofuranosyladenine, a parallel increase in AdoMet levels was generally seen; the increased levels of AdoMet were probably the result of decreased utilization of AdoMet by methyltransferases that were inhibited by AdoHcy (46, 78, 84). However, when high amounts of both Ado and Hcy were added, a further increase in the concentration of AdoHcy without a parallel increase in the concentration of AdoMet was observed; this increase was presumably due to synthesis of AdoHcy by reversal of the hydrolase reaction (84).

Data from studies with rat hepatocytes and from in vitro experiments with nearly cellular levels of enzyme (10 μ M) and of substrates (2 μ M Ado, 50 μ M AdoHcy) suggest that a substantial portion of cellular AdoHcy hydrolase exists as a stable complex with Ado (219, 220). This enzyme does not appear to participate in the metabolic hydrolysis of AdoHcy but functions instead as an Ado-binding protein in intact cells. The Ado sequestered by the enzyme was not available for synthesis of AdoHcy in the presence of Hcy or for deamination by Ado deaminase (219).

REMETHYLATION OF HOMOCYSTEINE TO SYNTHESIZE METHIONINE The transmethylation-transsulfuration pathway has a branch point at the level of Hcy, as shown in Figure 1. Hcy may be remethylated to Met in the reaction catalyzed by Met synthase or in that catalyzed by betaine-Hcy methyltransferase. It may also be used for resynthesis of AdoHcy by reversal of the hydrolysis catalyzed by AdoHcy hydrolase, as discussed above, or irreversibly converted to cystathionine via the reaction catalyzed by cystathionine β-synthase. This branch point is an important regulatory locus (64, 129, 132).

Met synthase is widely distributed in mammalian tissues (59, 97, 230). It is responsible for the de novo synthesis of Met methyl groups from one-carbon units in the THF coenzyme system. It utilizes methyl-THF as the methyl donor and methylcobalamin as a tightly bound coenzyme. A catalytic amount of AdoMet is required, which apparently is involved in generating the active form of the B_{12} -coenzyme or in stimulating methyltransferase activity (19, 20, 123, 124). The $K_{\rm m}$ of rat liver Met synthase for Hcy is 60 μ M (55).

Met synthase is clearly important in Hcy metabolism. This is evidenced by the elevated levels of homocyst(e) ine and normal or low concentrations of Met that are found in plasma of human patients with inborn errors of metabolism affecting the availability of methyl-THF or active B₁₂-coenzyme and, hence, the activity of Met synthase (77, 85, 131, 169, 177). The inactivation of Met

synthase by exposure of intact animals to nitrous oxide decreased tissue concentrations of Met and AdoMet and impaired essential methylation reactions (119, 120, 223).

In Met deficiency and in vitamin B_{12} deficiency (which presumably mimics a Met deficiency at the cellular level) methyl-THF accumulates in the cell at the expense of other forms of folate (170, 174, 225b). This decreased use of methyl-THF is caused by a lack of active Met synthase (vitamin B₁₂ deficiency) or by a lack of Hcy, the methyl group acceptor (Met deficiency). Addition of Met, by increasing the availability of Hcy or by increasing the concentration of AdoMet, results in demethylation of methyl-THF. AdoMet inhibits the conversion of methylene-THF to methyl-THF by methylene-THF reductase (EC 1.1.99.15), a reaction that is essentially irreversible under physiological conditions (36, 109, 225). Inhibition of the reductase occurred at concentrations of AdoMet that were somewhat greater than the normal range for tissue concentrations, and this inhibition was reversed by the presence of AdoHcy (15, 109). Activation of Met synthase by AdoMet is unlikely to play a role in the demethylation of methyl-THF, because Met synthase was fully stimulated at normal tissue concentrations of AdoMet and was unaffected by addition of AdoHcy (15).

Demethylation of methyl-THF causes a redistribution of THF derivatives to other coenzyme forms and allows flux of one-carbon units to other reactions; it also increases the hepatic concentration of total folate and causes a large increase in the hepatic levels of pteroylpolyglutamates (30, 42, 105). Methyl-THF is a poor substrate for rat liver pteroylpolyglutamate synthetase. Thus, methyl-THF taken up from the plasma must be converted to THF via the methyltransferase reaction before it can be converted to a pteroylpolyglutamate, the form of folate that is preferentially retained by tissue (30, 118, 225, 225b). A direct stimulatory effect of Met on the transport of folates in mammalian cells has also been suggested (91).

Unlike Met synthase, which is widely distributed in mammalian tissues, betaine-Hcy methyltransferase is generally found in high concentrations only in mammalian liver (59). Activity has been found in kidney and pancreas of some species (131, 230); substantial levels of activity have been reported for both liver and kidney of human infants and children (131). The enzyme is specific for Hcy, but certain analogs of betaine can also serve as the methyl donor (5, 182). The reported $K_{\rm m}$ values of the human liver enzyme for Hcy and betaine are 120 and 100 μ M, respectively, whereas those for the rat liver enzyme are 15–21 and 49–56 μ M, respectively (57, 182).

Betaine-Hcy methyltransferase is inhibited in vitro by the presence of dimethylglycine and possibly by Met, both products of the reaction, and by preincubation with AdoMet (57, 65, 182). Substantial inhibition of the rat liver enzyme by $50 \mu M$ Met has been reported (57), but the human liver enzyme was

unaffected by Met (182). A protective effect of AdoHcy on the inactivation of betaine-Hcy methyltransferase by AdoMet has been demonstrated (64, 65); higher levels of AdoHcy that are clearly unphysiological appear to inhibit (competitively with Hcy) the methyltransferase (60).

Hepatic betaine-Hcy methyltransferase activity was increased in rats fed diets that contained no Met and also in those fed diets with high levels of protein or Met (58, 59). Supplemental betaine or choline also induces the enzyme (66, 74). Thus, the enzyme appears to respond to the increased need for labile methyl group transfer or conservation of Hcy when Met intake is low, to the need to metabolize Hcy when Met intake is high, and also to the need to dispose of betaine when betaine or choline intake is high.

The availability of betaine appears to influence conservation or recycling of the Hcy moiety of Met. This suggests that, at least when dietary Met is limited or when Hcy removal by other reactions is blocked, both betaine-Hcy methyltransferase and Met synthase are essential for adequate methylation of Hcy to Met. Addition of betaine to liver slices increased the recycling of the Hcy moiety of Met (8, 230). Betaine supplementation of the diet of fruit bats that had been treated with nitrous oxide (which severely inhibits Met synthase) resulted in reduced weight loss and delayed onset of neurological impairment (224). Furthermore, betaine therapy has been effective in decreasing the Hcy concentration and increasing the Met and Cys concentrations in plasma of patients with homocystinuria (186, 228).

CATABOLISM OF HOMOCYSTEINE—THE TRANSSULFURATION PATH-Cystathionine synthase catalyzes the replacement of the β -OH group of L-serine with Hcy to form cystathionine. Cystathionine synthase contains tightly bound pyridoxal 5'-phosphate and also possesses serine sulfhydrase activity (102, 103). The translational product of the synthase gene appears to be a polypeptide of 63,000 kd, which is initially assembled into a tetramer. This product is subject to limited post-translational proteolysis, which reduces the M_r of the original subunit to 48,000 and is associated with a change from a tetrameric to a dimeric structure, a 30-fold decrease in the K_m for Hcy, and a 60-fold increase in specific activity (103, 104, 183, 184). This active form of the enzyme has a $K_{\rm m}$ of 0.6–0.8 mM for Hcy and 0.1-0.4 mM for serine (103, 184). Proteolytic activation may be tissue specific; it has been observed in human and rat liver but not in human fibroblast extracts (103, 183, 184). Cystathionine synthase is also activated by AdoMet (63, 64), but the effects of proteolytic cleavage and activation by AdoMet are not additive (102). Activation by AdoMet does not appear to be related to the presence of a soluble effector and presumably involves some modification of the enzyme structure (63). Cystathionine synthase may also be activated in vitro by high levels of AdoHcy (60).

The AdoMet concentration may be an important physiological regulator of cystathionine synthase activity. Supplementation of a low Met diet with cyst(e) ine instead of Met results in less hepatic cystathionine synthase activity, which may occur as a result of less activation of the enzyme by AdoMet in vivo (67). The ability of Cys to replace a portion of the dietary Met may be due to this effect on cystathionine synthase activity, but a primary effect of Cys on utilization of Met for protein synthesis could also explain the reduced flux of Met to Cys (196). Patients with a genetic deficiency of Met adenosyltransferase activity have a concomitant decrease in cystathionine synthase activity, which is possibly due to the absence of activation by AdoMet. Although the hypothesis has not been tested, it is tempting to speculate that some of the beneficial effect of betaine therapy in patients with homocystinuria may be related to the resulting increase in Met and, hence, AdoMet levels, which could stimulate cystathionine synthase activity and increase the irreversible flux of Hcy through the transsulfuration pathway.

Finkelstein & Martin (64) studied the metabolism of Hcy using incubation systems reconstituted to contain enzymes (from tissue extracts) and reactants at concentrations that approximated those present in vivo. Systems were modeled on the liver of rats fed chow, 3.5% casein, or 55% casein. They measured flux of Hcy through the reactions catalyzed by Met synthase, betaine-Hcy methyltransferase, and cystathionine synthase by adding either 5-[Me-14C]methyl-THF, [Me-14C]betaine, or L-[3-14C]serine to otherwise identical tubes and measuring the labeled product, Met or cystathionine. When the system was modeled on the liver of chow-fed rats, the activities of Met synthase, betaine-Hcy methyltransferase, and cystathionine synthase accounted for 27, 27, and 46%, respectively, of the Hcy consumed. Inhibition of Met synthase or betaine-Hcy methyltransferase shifted relative flux through the three pathways in a manner suggesting that Met synthase had the highest affinity for Hcy and that cystathionine synthase had the least. This suggestion is consistent with the reported $K_{\rm m}$ values for these two enzymes (55). The finding that 54% of the Hcy consumed was converted to Met is also consistent with estimates of the extent of remethylation of Hcy to Met in human subjects (129, 132), in the perfused rat liver (55) and in the intact rat (189), all of which were about 50%. Changes in flux through the three pathways in the systems modeled on the livers of rats fed 3.5% casein or 55% casein could be largely explained by changes in enzyme, substrate, and effector concentrations.

Cystathionase (cystathionine γ -lyase, EC 4.4.1.1) catalyzes the γ -cleavage of cystathionine to form Cys and α -ketobutyrate, the final step of the transsulfuration pathway. This pyridoxal 5'-phosphate-dependent enzyme also catalyzes the deamination of homoserine and the desulfhydration of cyst(e)ine (142, 237). The K_m for cystathionine of cystathionase purified from liver of

several species has been reported to be in the range of 0.3 to 3.5 mM (14, 222, 237).

The importance of the transsulfuration pathway in Met metabolism is suggested by a number of observations. The ability of Cys to replace a substantial portion of dietary Met on a nearly equimolar basis (187, 200) and the incorporation of Met or Hcy sulfur into Cys and, thence, into cysteinyl residues of protein and glutathione (9, 202, 211, 212) suggest that transsulfuration is a major pathway for metabolism of Met sulfur. Reduced levels of cystathionine synthase or cystathionase activity in humans with inborn errors of metabolism or in animals fed vitamin B₆-deficient diets result in elevated levels of homocyst(e)ine and cystathionine in plasma and urine (55, 130, 176, 185, 203). Inhibition of cystathionase with an irreversible inhibitor, propargylglycine, markedly reduced ³⁵SO₄ excretion in rats given [³⁵S]Met or L-[³⁵S]cystathionine (but not in rats given [35S]cysteine) and equally depressed the metabolism of L-[carboxy-n-propyl-1-14C]cystathionine and [1-14C]Met to 14CO₂ (47, 193, 195). Treatment of hepatocytes or intact rats with propargylglycine also resulted in the excretion or accumulation of labeled cystathionine formed from labeled Met (9, 193). The accumulation of homocyst(e) ine and cystathionine as well as the reduction in oxidation of Met to SO_4^{-2} and CO_2 when flux through the transsulfuration pathway is reduced clearly demonstrates the importance of this pathway in normal Met metabolism.

The Polyamine Pathway

FORMATION AND UTILIZATION OF DECARBOXYLATED S-ADENO-The polyamine pathway is important for the synthesis of the polyamines, spermidine and spermine, and possibly for the synthesis of methylthio compounds. The importance of these compounds in cellular physiology is not yet well understood, but the present evidence suggests that they are essential for normal growth (208). As shown in Figure 2, polyamines are synthesized in mammalian cells from ornithine and AdoMet by the actions of ornithine decarboxylase and AdoMet decarboxylase, which provide putrescine and dAdoMet, and of spermidine synthase and spermine synthase, which catalyze the transfer of the aminopropyl group from dAdoMet to putrescine to form spermidine and to spermidine to form spermine (149, 166, 208). The MTA formed from dAdoMet during polyamine synthesis is salvaged by conversion of the methylthioribose moiety into Met and of adenine into adenine nucleotides (7, 96, 166). Polyamine degradation leads to formation of a number of derivatives, but there is no evidence for any reutilization of the aminopropyl group of polyamines (150, 172).

The activated aminopropyl group needed for polyamine synthesis is generated by decarboxylation of AdoMet in a reaction catalyzed by AdoMet decarboxylase (EC 4.1.1.50); this reaction commits the Met molecule to the

polyamine pathway. AdoMet decarboxylase contains a covalently linked pyruvoyl group, which is essential for enzymatic activity, and does not contain pyridoxal 5'-phosphate (39, 143, 145). The activity of AdoMet decarboxylase is regulated by changes in the concentration of putrescine, an activator of the enzyme. AdoMet decarboxylase is activated over a physiological range of putrescine concentrations (0–50 μ M), probably by a decrease in the apparent K_m of the enzyme for AdoMet (157, 158, 163). Increased ornithine decarboxylase activity can indirectly increase the supply of dAdoMet by increasing the cellular concentration of putrescine, which, in turn, activates AdoMet decarboxylase (145, 149). This mechanism may ensure that a parallel supply of dAdoMet and putrescine is available and, therefore, that putrescine is efficiently converted to spermidine.

AdoMet decarboxylase activity is also regulated in mammalian tissues by changes in the amount of enzyme protein. The enzyme turns over rapidly with a $t_{1/2}$ of less than 2 h in most tissues (173). The amount of enzyme protein is increased in response to spermidine depletion and to a variety of physiological and nutritional treatments (86, 92, 122, 128, 144, 145, 148, 151, 152, 154, 178, 213). Some studies indicate that high levels of dAdoMet can inhibit AdoMet decarboxylase and limit its accumulation (144, 236), but physiological levels of dAdoMet are probably not high enough to have an effect.

It is likely that the supply of dAdoMet limits the rate of spermidine and spermine synthesis. Concentrations of dAdoMet in rat tissues have been reported to be 0.9–2.5 nmol per gram wet weight compared to AdoMet concentrations of 23–67 nmol per g wet wt (81, 147). The rapid utilization of dAdoMet (so that it does not accumulate in the cell) may be related to the coordinated regulation of putrescine and dAdoMet production (149), to the presence of spermidine synthase and spermine synthase activities at levels that are in substantial excess of that of AdoMet decarboxylase (161), and to the high affinities of the aminopropyltransferases for dAdoMet ($K_m = 0.6$ and 1.1 μ M for spermine synthase and spermidine synthase, respectively) (140, 164).

Polyamine synthesis appears to be the major, if not the only, route for the further metabolism of dAdoMet. Decarboxylated AdoMet accumulated to levels that were many-fold the control levels in cells cultured in vitro and in ventral prostate of intact rats when its utilization was blocked by inhibition of ornithine decarboxylase or of spermidine synthase (35, 121, 144, 151, 152). In incubations of soluble protein from rat liver with putrescine (as substrate for spermidine synthase) and adenine (to inhibit MTA degradation by MTA phosphorylase), inhibition of AdoMet decarboxylase by methylglyoxal bis-(guanylhydrazone) (MGBG) blocked formation of labeled MTA from S-[8-14C]adenosyl-L-methionine and of labeled spermidine from S-adenosyl-L-[2-14C]methionine; the decreased production of MTA and spermidine was accompanied by a nearly equimolar decrease in disappearance of AdoMet (44). A

similar dose-dependent effect of MGBG on MTA synthesis was observed in studies with human lymphoblastoid cell lines (96).

SALVAGE OF METHYLTHIORIBOSE FOR RESYNTHESIS OF METHIONINE indicated in Figure 2, the MTA formed from dAdoMet during polyamine synthesis is metabolized by MTA phosphorylase to adenine and 5methylthioribose-1-phosphate (54, 70, 96). The primary fate of 5methylthioribose-1-phosphate in cell-free homogenates of ratliver is the formation of Met (6, 7). Carbons from the ribose portion, the carbon and hydrogens of the methyl group, and the sulfur of MTA are all incorporated into Met. Thus, the pathway by which MTA is converted to Met involves modifications in the ribose portion of the molecule to form the α-aminobutyrate portion of Met rather than a transfer of the methylthio group to an acceptor molecule (7). The steps involved in the conversion of 5-methylthioribose-1-phosphate to Met have been partially elucidated (6, 214, 215). 5-Methylthioribose-1-phosphate undergoes isomerization to 5-methylthioribulose-1-phosphate (215), which is then converted to α -keto-y-methiolbutyrate, the keto acid precursor of Met. The intermediates and reactions involved in this conversion have not been fully characterized; the pathway appears to include formation of a phosphate ester, removal of the phosphate to form an intermediate at the oxidation state of ribose, and subsequent stoichiometric consumption of O₂ and production of formate (215). The final step in the pathway for Met synthesis is the transamination of the keto acid, which may be catalyzed by glutamine aminotransferase **(6)**.

This pathway for MTA metabolism is physiologically important for the removal of MTA as well as for the conservation of the adenine and methylthioribose moieties of AdoMet. MTA is a strong inhibitor of the aminopropyltransferases involved in polyamine production (80, 146), of AdoHcy hydrolase (53, 160), and of adenosine kinase (68). Inhibition is not seen in vivo because a low concentration of MTA (1–2 nmol·g⁻¹ in most rat tissues) is normally maintained in mammalian tissues due to the action of MTA phosphorylase (147, 171).

The Transamination Pathway of Methionine Metabolism

Benevenga and coworkers (11, 24, 191) proposed that Met is metabolized by an alternate pathway that involves transamination as the initial step. Met is transaminated to α -keto- γ -methiolbutyrate (perhaps by cytosolic glutamine aminotransferase) in the presence of α -keto- γ -methiolbutyrate, pyruvate, the keto acids of the branched-chain amino acids, or phenylpyruvate (12, 114, 115, 127, 191). Apparently, the keto acid of Met is transported into the mitochondria on the pyruvate carrier (115) where it is decarboxylated (perhaps by the

branched-chain keto acid dehydrogenase complex) to give 3-methylthiopropionyl-CoA (40, 115, 191). 3-Methylthiopropionate (3-methylthiopropionyl-CoA) may be further metabolized to methanethiol, hydrogen sulfide, sulfate, carbon dioxide, and possibly formaldehyde and formate, but the details of these conversions have not been elucidated (12, 25, 31, 192).

The role of a pathway of Met metabolism that is independent of the formation of AdoMet is not well established in the intact cell or animal, but deserves further consideration. Metabolic studies with isolated rat hepatocytes support a role of the transamination pathway of Met metabolism (115), and continuous infusion tracer dilution studies in intact sheep support the existence of some alternate pathway of Met metabolism (12). Additional support for the transamination pathway comes from studies indicating that metabolites produced by the transamination pathway may be related to the marked toxicity of Met in the rat (190).

Evidence for an alternate pathway of Met metabolism must be considered in light of the many data indicating that only the transmethylation-transsulfuration pathway is quantitatively important in the oxidation of the sulfur atom and methyl group of Met. Many of the observations of increased oxidation of the methyl group of Met in rats fed diets with excess Met can be explained, at least partially, by increased flux of Met through the Met adenosyltransferase, glycine methyltransferase, and sarcosine dehydrogenase system (10, 25, 126, 136). Experiments with labeled AdoMet and labeled Met suggest that the sulfur atom and methyl and carboxyl carbons of these two compounds are similarly metabolized in the intact rat, which is consistent with the conversion of Met to AdoMet prior to its oxidation (72). "Abnormal" metabolites of Met that would be formed by the transamination pathway have not been observed in man and animals under conditions where "normal" metabolism is partially blocked and where plasma Met is elevated; in fact, intermediates of the transsulfuration pathway have been found in increased amounts under these conditions (56, 130, 155, 186).

CYSTEINE (AND METHIONINE SULFUR) METABOLISM

The Cysteinesulfinate Pathway: Taurine Production

Cys, whether from an exogenous source or formed from serine and the sulfur of Met by the transsulfuration pathway (or possibly by direct sulfhydration of serine), is metabolized by the animal to yield either taurine (2-aminoethanesulfonate) and CO_2 or sulfate, urea, and CO_2 (108, 111). Several pathways of Cys metabolism have been demonstrated, but the physiological roles of these are not well understood.

The cysteinesulfinate pathway of Cys metabolism is depicted in Figure 4.

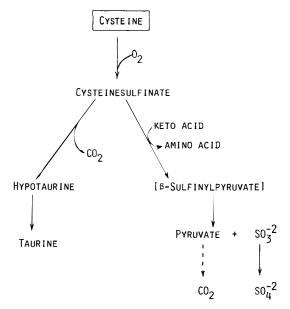


Figure 4 The cysteinesulfinate pathway.

The oxidation of Cys to cysteinesulfinate is catalyzed by Cys dioxygenase (EC 1.13.11.20), an iron-containing enzyme that seems to be specific for Cys, with an apparent $K_{\rm m}$ of 0.45 mM (232). Cysteinesulfinate may then be decarboxylated to hypotaurine (2-aminoethanesulfinate) by action of cysteinesulfinate decarboxylase (EC 4.1.1.29), a pyridoxal 5'-phosphate-dependent enzyme that has an apparent $K_{\rm m}$ for cysteinesulfinate of 0.045-0.17 mM and that can also use cysteic acid (cysteinesulfonate) as a substrate (75, 135). Brain glutamate decarboxylase (EC 4.1.1.15) can also catalyze the decarboxylation of cysteinesulfinate (135). Alternatively, cysteinesulfinate may undergo transamination or oxidative deamination to form the putative intermediate, β -sulfinylpyruvate, which spontaneously decomposes to yield pyruvate and sulfite (180).

About 70–90% of the cysteinesulfinate oxidized by rat hepatocytes or by intact rats or mice was converted to hypotaurine plus taurine (37, 38, 73, 199); this indicates that, under normal conditions, the rat or mouse metabolizes cysteinesulfinate primarily to taurine rather than to pyruvate and sulfite. Apparent flux of cysteinesulfinate through the transamination pathway in the intact mouse was increased when cysteinesulfinate decarboxylase was inhibited by β -methylene-DL-aspartate (73); this conversion of cysteinesulfinate to pyruvate and sulfite was presumably catalyzed by aspartate aminotransferase, which has a $K_{\rm m}$ for cysteinesulfinate of 3–25 mM (162, 231).

In mammals, hypotaurine is apparently oxidized to taurine via a poorly

characterized enzymatic reaction that appears to require NAD⁺, Cu^{+2} , and O_2 (101, 137). The apparent K_m of the enzyme for hypotaurine is 0.20 mM (101, 137). The rates of hypotaurine oxidation catalyzed by rat or mouse tissues in vitro are too low to account for the rates observed in vivo (137, 153). Hypotaurine does not usually accumulate in mammalian tissues (82), but substantial levels have been found in rat liver after partial hepatectomy (204). Hypotaurine may also undergo transamination to sulfinylacetaldehyde, which presumably decomposes to sulfite and acetaldehyde, but this reaction appears to make a very minor contribution to hypotaurine metabolism in mammalian tissues (50, 51, 73).

The cysteinesulfinate pathway seems to be the major route of taurine formation in mammals. This conclusion is supported by the detection of labeled cysteinesulfinate and taurine in tissues of animals given labeled Cys (141), by the presence of the enzymes involved in the conversion of Cys to cysteinesulfinate and hypotaurine in most mammalian tissues (38, 233), and by the general association, both within and among species, of hepatic cysteinesulfinate decarboxylase activity with the capacity of the animal to synthesize taurine (38, 76, 234).

Hepatic Cys dioxygenase activity was elevated in rats fed diets with excess Met, Cys or protein (34, 99, 194, 199). These increases in Cys dioxygenase activity appeared to parallel an increase in the hepatic Cys concentration to 0.2–0.3 μ mol per gram wet weight (control level, 0.1 μ mol·g⁻¹) and to precede an increase in hepatic taurine concentration to 6–8 μ mol per gram wet tissue (control level, 3–4 μ mol·g⁻¹) (99).

In contrast to the increase in Cys dioxygenase activity, cysteinesulfinate decarboxylase activity in rat liver decreased to approximately 50% of control levels in rats fed excess protein or excess Cys (34, 117, 199). As expected, decreased cysteinesulfinate decarboxylase activity was associated with decreased oxidation of cysteinesulfinate in hepatocytes isolated from rats that had been fed a high-Cys diet (197). However, these hepatocytes oxidized Cys to CO₂ and to taurine as rapidly or more rapidly than did cells from control animals. Thus, the low cysteinesulfinate decarboxylase activity did not appear to be rate-limiting for Cys oxidation in hepatocytes from rats fed excess Cys.

Studies in animals have yielded conflicting results. Estimates of the oxidation of Cys or cysteinesulfinate to CO₂ in intact rats fed a high-Cys diet were the same as for control rats (199), whereas excess dietary Met or Cys generally led to an increase in the urinary excretion of Cys sulfur as taurine (34, 194). Rats fed excess protein had markedly reduced levels of hepatic cysteinesulfinate decarboxylase activity but elevated levels of urinary taurine (13). These observations seem to suggest that, in animals fed excess protein or sulfurcontaining amino acids, either Cys is oxidized primarily by cysteinesulfinate-

independent pathways or increased Cys dioxygenase activity compensates for the decrease in cysteinesulfinate decarboxylase activity.

Taurine is used in conjugation reactions (i.e. bile acids) but does not otherwise appear to be further metabolized by mammalian tissues (52). Taurine that is not reabsorbed by the kidney is excreted as such in the urine (205); renal clearance of taurine in the rat appears to adapt to alterations in the sulfur amino acid and taurine content of the diet (28). Taurine is also secreted as taurine-conjugated bile acids and then degraded to sulfate by intestinal microorganisms (79, 201, 205). The sulfate formed in the intestine is largely reabsorbed and excreted in the urine with little sulfur being excreted in the feces (79, 107, 188). Most [35S]taurine administered orally or intravenously to rats was excreted as [35S]taurine rather than as [35S]sulfate (79).

Other possible pathways of taurine production from cysteine sulfur in mammalian tissues have been identified. One involves the reaction of 3'phosphoadenosine-5'-phosphosulfate and serine to form cysteic acid, which may be decarboxylated to form taurine; this pathway appears to make a very minor, if any, contribution to taurine production in mammals (87, 125). Cysteinesulfinate may be oxidized nonenzymatically to cysteic acid, which may be decarboxylated by cysteinesulfinate decarboxylase to yield taurine; the rate of conversion of cysteinesulfinate to cysteic acid appears to be too slow for this route of taurine production to be significant (199, 210). Another pathway involves the production of cysteamine (2-mercaptoethylamine) followed by formation of hypotaurine via action of cysteamine dioxygenase (48, 88). Cysteamine production from Cys appears to be a branch of the coenzyme A synthetic pathway, with cysteamine being produced from pantetheine by action of pantetheinase; other possible routes of taurine production via cysteamine have also been proposed (27, 165). Further investigation of this potential route of taurine synthesis is needed.

The quantitative significance of taurine production in Cys metabolism in animals varies substantially among species. Indirect estimates based on the evolution of ¹⁴CO₂ by animals following intraperitoneal injections of [1-¹⁴C]-or [3-¹⁴C]-labeled cyst(e)ine indicate that about 70–80% of Cys is converted to taurine in the intact male rat (199, 233, 234), whereas only about 20% of the Cys that is oxidized is converted to taurine in the kitten (38). However, the rat, like other animals, excretes much more Cys sulfur as sulfate than as taurine (34, 108); this suggests that the estimate of 70–80% for Cys conversion to taurine in the rat may be high. Recent studies of Cys metabolism in hepatocytes suggest that only about 25% of Cys oxidation in rat liver involves production of hypotaurine and taurine (37).

Desulfuration Pathways of Cysteine Metabolism

Production of pyruvate and inorganic sulfur from Cys may occur by several pathways that do not involve conversion of Cys to cysteinesulfinate (195). In

contrast to the production of pyruvate and SO_3^{-2} (which is readily oxidized to sulfate by sulfite oxidase) from cysteinesulfinate, these desulfuration pathways all involve the release of Cys sulfur in a reduced oxidation state. Data from studies with rat liver mitochondria (227), the perfused rat liver (179), and hepatocytes (37, 197) suggest that a substantial amount of Cys may be metabolized by cysteinesulfinate-independent pathway(s). Wainer (227) demonstrated production of ³⁵SO₄ by rat liver mitochondria incubated with [³⁵S]Cys at a rate that was not substantially decreased by addition of cysteinesulfinate. In experiments with livers from 72-hour starved rats, Simpson & Freedland (179) found that perfusion with 10 mM cysteinesulfinate in addition to 10 mM [U-14C]Cys decreased the recovery of radioactivity in glucose by only 30%. The pattern for accumulation of nitrogenous products was markedly different when cells were incubated with 25 mM Cys than when they were incubated with 25 mM cysteinesulfinate. Increased production of urea and ammonia accounted for the nitrogen from ~80\% of the oxidized Cys, whereas hypotaurine plus taurine accounted for 80-90% of the oxidized cysteinesulfinate (M. H. Stipanuk, unpublished observations). In other studies with rat hepatocytes, 25 mM cysteinesulfinate reduced recovery of the 1-carbon of Cys in CO₂ by 30-40% when the Cys concentration in the incubation medium was 0.2-1.0 mM, but by only 10% when the Cys concentration was 25 mM (M. H. Stipanuk, unpublished observations). Thus, high Cys concentrations may favor Cys catabolism by desulfuration pathways.

Pyruvate and reduced inorganic sulfur can be produced by the cleavage of cystine to pyruvate, ammonia, and thiocysteine, which is catalyzed by cystathionase, followed by further enzymatic or nonenzymatic reaction of thiocysteine with the enzyme or another thiol to reform a disulfide accompanied by release of sulfide (195, 235). The apparent $K_{\rm m}$ of rat liver cystathionase for L-cystine has been estimated to be about 0.03-0.07 mM compared with 0.8-3.5 mM for L-cystathionine and 15-20 mM for L-homoserine (222, 235, 237). Thus, cystine should compete favorably with other substrates for the enzyme. Pyruvate and sulfane sulfur can also be formed by transamination of Cys with α -ketoglutarate (or pyruvate) to form β -mercaptopyruvate, which may undergo desulfuration (or transsulfuration) catalyzed by \(\beta\)-mercaptopyruvate sulfurtransferase (4, 90, 218). The K_m of purified Cys:α-ketoglutarate aminotransferase for Cys is about 22 mM, whereas its $K_{\rm m}$ for aspartate is about 0.06–0.5 mM (4, 217). Thus, it is unlikely that Cys is a good substrate for transamination in vivo. Sulfide may also be formed from the substitution of the thiol group of Cys with a variety of thiol compounds to form the corresponding thioether in a reaction catalyzed by cystathionine synthase (18, 110, 156). However, cystathionine synthase apparently has a much higher K_m for Cys (36 mM) than for L-serine (2–8 mM) or Hcy (0.1–9 mM) (17, 103, 133).

All three of these pathways appeared to play a role in the production of acid-labile sulfide from Cys by liver and kidney homogenate systems designed

to approach physiological values for substrate concentrations and pH (195, 198), but the role of these pathways in the intact animal has not been assessed. Because of the existence of multiple pathways, blocking one pathway may have little effect on the overall ability of the animal to metabolize Cys. Patients with a genetic lack of β -mercaptopyruvate sulfurtransferase excrete low levels of the mixed disulfide of β -mercaptolactate and Cys, which suggests that at least a small amount of Cys is metabolized by transamination in vivo (32, 33). These patients excrete normal levels of urinary sulfate. Inhibition of cystathionase by propargylglycine had no effect on sulfate production from Cys (195), but metabolites potentially produced via action of cystathionase on Cys have been observed in urine of rats (49). Patients who have low levels of cystathionine synthase appear to convert Met and Cys to sulfate normally (155).

If sulfur were released from Cys as sulfane sulfur, the sulfide presumably would be oxidized to sulfate prior to its excretion. Inorganic sulfur metabolism has received little attention in recent years, but the elegant experiments of Koj et al (100), published in 1967, support a central role of thiosulfate in the oxidation of sulfide by animal tissues. Based on studies with $(^{35}S \cdot SO_3)^{-2}$ and $(S \cdot ^{35}SO_3)^{-2}$, they proposed that thiosulfate is an intermediate in the formation of sulfate from sulfane sulfur. Their work clearly suggests that sulfide must be incorporated into thiosulfate (and that the outer S must become the inner S in SSO_3^{-2}) prior to its oxidation to sulfate and, also, that SO_3^{-2} formed from SSO_3^{-2} is not reincorporated into SSO_3^{-2} to any extent:

$$2HS^{-} + 2O_2 \rightarrow (SSO_3)^{-2} + H_2O$$
 1.

$$(SSO_3)^{-2} + 2GSH \rightarrow HS^- + HSO_3^- + GSSG$$
 2.

$$SO_3^{-2} + \frac{1}{2}O_2 \rightarrow SO_4^{-2}$$
 3.

The results obtained by Szczepkowski et al (207) in tracer experiments with intact rats suggest that thiosulfate is a normal intermediate in the production of sulfate from Cys in the animal. When a large excess of unlabeled thiosulfate was injected at the same time as [35S]cystine, the excretion of radioactive sulfur as urinary thiosulfate was about 20-fold that of control rats who did not receive thiosulfate, and the excretion of radioactive sulfur as urinary sulfate was markedly reduced. The appearance of increased urinary levels of thiosulfate as well as of sulfite in individuals with sulfite oxidase deficiency due to inborn errors of metabolism (93, 175) or dietary molybdenum deficiency (1) also supports a central role of thiosulfate in sulfur metabolism. Because mammalian tissues do not have an enzymatic system for reducing sulfite or sulfate to sulfide, incorporation of 35S from [35S]Cys into thiosulfate also indicates that sulfur is released from Cys as sulfane sulfur.

Sulfane sulfur appears to be incorporated into some pool of reduced sulfur that has a relatively long half-life in the intact animal. In contrast to the rapid

excretion of label from injected $(S^{.35}SO_3)^{-2}$ or $^{35}SO_4^{-2}$, labeled sulfur from injected $(^{35}S\cdot SO_3)^{-2}$ or from metabolized $[^{35}S]$ Met or $[^{35}S]$ Cys is slowly excreted in the urine (34, 107, 181, 193, 194). Schneider & Westley (167) demonstrated the existence of a slowly metabolized pool of sulfur that was formed from the outer but not the inner sulfur of thiosulfate. They suggested, based on studies in intact rats, that elemental sulfur associated with protein and polythionate sulfur $(^{-}O_3SS_nSO_3^{-})$ are likely possibilities for the form of this retained intermediate that is subsequently slowly metabolized to provide reduced sulfur. Thus, it is conceivable that Cys is metabolized by pathways that involve release of sulfide followed by incorporation of the sulfur into some pool of reduced sulfur that has a relatively long half-life prior to its oxidation to sulfate.

SUMMARY AND CONCLUSIONS

Met metabolism occurs primarily by activation of Met to AdoMet and further metabolism of AdoMet by either the transmethylation-transsulfuration pathway or the polyamine biosynthetic pathway. The catabolism of the methyl group and sulfur atom of Met ultimately appears to be dependent upon the transmethylation-transsulfuration pathway because the MTA formed as the co-product of polyamine synthesis is efficiently recycled to Met. On the other hand, the fate of the four-carbon chain of Met appears to depend upon the initial fate of the Met molecule. During transsulfuration, the carbon chain is released as α -ketobutyrate, which is further metabolized to CO_2 . In the polyamine pathway, the carboxyl carbon of Met is lost in the formation of dAdoMet, whereas the other three carbons are ultimately excreted as polyamine derivatives and degradation products.

The role of the transamination pathway of Met metabolism is not firmly established. Cys (which may be formed from the sulfur of Met and the carbons of serine via the transsulfuration pathway) appears to be converted to taurine and CO₂ primarily by the cysteinesulfinate pathway, and to sulfate and pyruvate primarily by desulfuration pathways in which a reduced form of sulfur with a relatively long biological half-life appears to be an intermediate. With the exception of the nitrogen of Met that is incorporated into polyamines, the nitrogen of Met or Cys is incorporated into urea after it is released as ammonium [in the reactions catalyzed by cystathionase with either cystathionine (from Met) or cystine (from Cys) as substrate] or it is transferred to a keto acid (in Cys or Met transamination).

Many areas of sulfur-containing amino acid metabolism need further study. The magnitude of AdoMet flux through the polyamine pathway in the intact animal as well as details about the reactions involved in this pathway remain to be determined. Both the pathways and the possible physiological role of alternate (AdoMet-independent) Met metabolism, including the transamination

pathway, must be elucidated. Despite the growing interest in taurine, investigation of Cys metabolism has been a relatively inactive area during the past two decades. Apparent discrepancies in the reported data on Cys metabolism need to be resolved. Future work should consider the role of extrahepatic tissues in amino acid metabolism as well as species differences in the relative roles of various pathways in the metabolism of Met and Cys.

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