

# Nuclear Folate Metabolism

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## Keywords

thymidylate, folate, replitase, neural tube defects, DNA synthesis

## Abstract

Despite unequivocal evidence that folate deficiency increases risk for human pathologies, and that folic acid intake among women of childbearing age markedly decreases risk for birth defects, definitive evidence for a causal biochemical pathway linking folate to disease and birth defect etiology remains elusive. The de novo and salvage pathways for thymidylate synthesis translocate to the nucleus of mammalian cells during S- and G2/M-phases of the cell cycle and associate with the DNA replication and repair machinery, which limits uracil misincorporation into DNA and genome instability. There is increasing evidence that impairments in nuclear de novo thymidylate synthesis occur in many pathologies resulting from impairments in one-carbon metabolism. Understanding the roles and regulation of nuclear de novo thymidylate synthesis and its relationship to genome stability will increase our understanding of the fundamental mechanisms underlying folate- and vitamin B<sub>12</sub>-associated pathologies.



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### Folate:

a water-soluble B vitamin (vitamin B<sub>9</sub>) that carries and chemically activates one-carbon units for biosynthetic reactions

### Neural tube defect (NTD):

a common congenital abnormality that results from failure of neural tube closure during neurogenesis that affects 0.5 to 60 in 10,000 births worldwide

### dTMP:

deoxythymidine monophosphate or thymidylate

### AdoMet:

S-adenosylmethionine

## INTRODUCTION

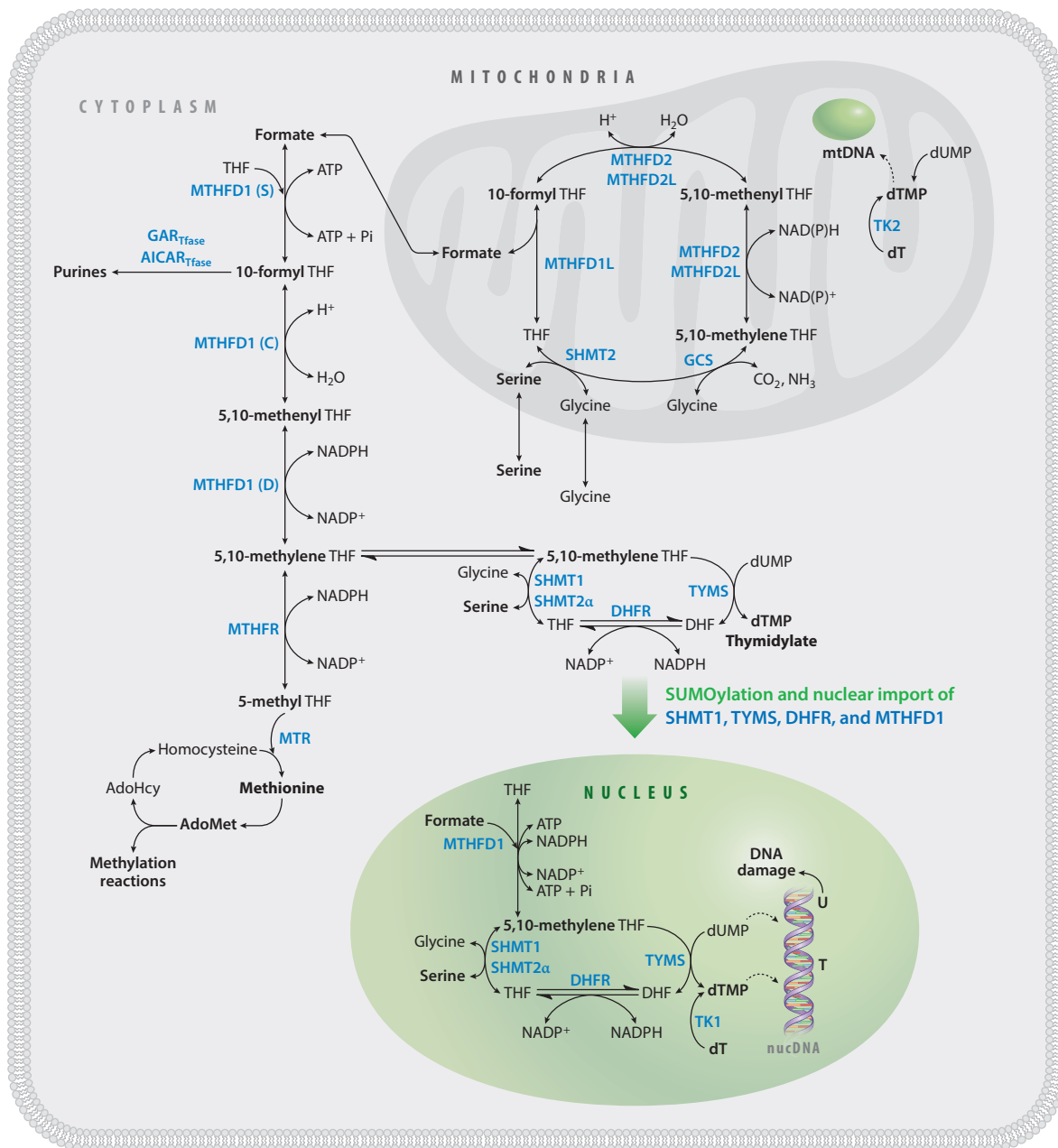
Shortly following the discovery of folate, a water-soluble B vitamin, in the early 1940s as an essential nutrient required for cell proliferation (57), research rapidly led to the development of anticancer, antimicrobial, and anti-inflammatory folate antagonists, including methotrexate and pemetrexed, that are important and widely used pharmaceuticals in oncology and rheumatology. Meanwhile, advances in human nutrition research established the role of folate in health, as folate deficiency was demonstrated to increase risk for a variety of human pathologies, including certain cancers, anemia, neurodegeneration, and birth defects. Evidence that folic acid administration could markedly reduce a woman's risk of having a neural tube defect (NTD)-affected pregnancy led to public health initiatives, including food fortification, to increase blood folate levels in women of reproductive age and thereby decrease rates of birth defects, most notably NTDs such as spina bifida and anencephaly (145).

Despite unequivocal evidence that folate deficiency increases risk for human pathologies, and that folic acid intake among women of child-bearing age markedly decreases risk for NTDs, definitive evidence for a causal biochemical pathway linking folate to disease and birth defect etiology remains elusive. Many molecular mechanisms underlying the linkage between folate metabolism and pathology have been proposed. Folate functions as an enzyme cofactor that chemically activates and carries single carbons for the synthesis of purines and thymidylate (dTMP) and for the remethylation of homocysteine to methionine (**Figure 1**) (44). Methionine is an essential amino acid required for protein synthesis as well as for cellular methylation reactions through its conversion to S-adenosylmethionine (AdoMet), a cofactor required for more than 100 methylation reactions (44). As such, folate cofactors are essential for DNA and RNA synthesis, chromatin



methylation, phospholipid biosynthesis, genome stability, cell proliferation, and the synthesis and catabolism of numerous metabolites. These anabolic pathways function as a highly interconnected network known as folate-mediated one-carbon metabolism (FOCM), and folate deficiency and other factors that perturb the function of folate simultaneously influence all pathways within the network (**Figure 2**) (122). Therefore, identifying the causal pathways and molecular mechanisms for individual folate-associated pathologies has proven to be challenging (122).

**FOCM:**  
folate-mediated  
one-carbon  
metabolism



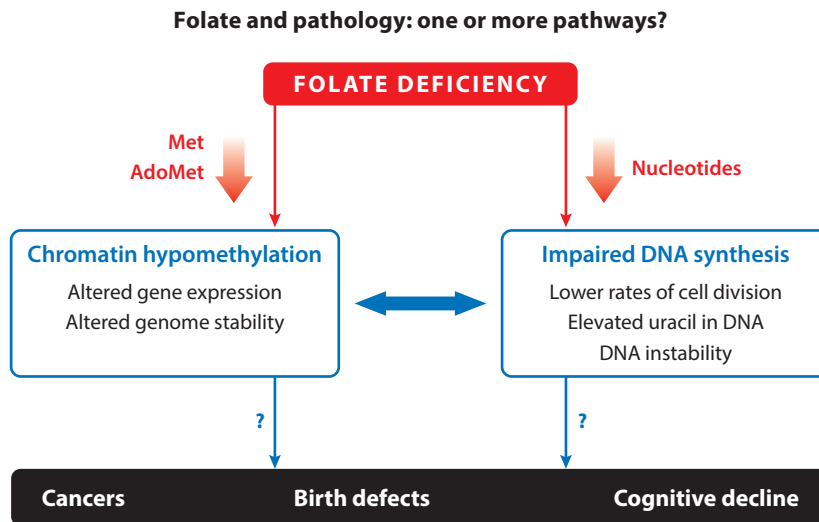
(Caption appears on following page)



**Figure 1** (Figure appears on preceding page)

FOCM is compartmentalized within the cell. FOCM compartmentalization enables efficient metabolic flux of THF-activated one-carbon units to biosynthetic reactions and cycling of THF. One-carbon metabolism in the cytosol includes the remethylation of homocysteine to methionine and the de novo synthesis of purines and thymidylate. Nuclear de novo dTMP biosynthesis requires TYMS, DHFR, MTHFD1, SHMT1, and SHMT2 $\alpha$ . These enzymes are SUMOylated and imported into the nucleus at the onset of S-phase. The *Shmt2* gene is expressed as two transcripts: SHMT2, for mitochondrial one-carbon metabolism, and SHMT2 $\alpha$ , which functions in the cytosol and nucleus. Formate and serine are the primary one-carbon sources for cytosolic and nuclear FOCM. The hydroxymethyl group of serine enters the pool of activated one-carbon units through the SHMT-catalyzed reaction in the cytosol and mitochondria. In mitochondria, serine and glycine are converted to formate, which traverses to the cytosol and nucleus, where it is condensed with THF by MTHFD1. MTHFD1 is a trifunctional enzyme possessing formylTHF synthetase (S), methenylTHF cyclohydrolase (C), and methyleneTHF dehydrogenase (D) activities. 5,10-MethyleneTHF is synthesized by SHMT or MTHFD1 and used for de novo dTMP synthesis. Thymidylate is also produced through the salvage of dT nucleoside by the action of TK1 in the cytosol and nucleus and of TK2 in mitochondria. Abbreviations: AdoHcy, S-adenosylhomocysteine; AdoMet, S-adenosylmethionine; AICAR<sub>Tfase</sub>, aminoimidazolecarboxamide ribonucleotide transformylase; DHFR, dihydrofolate reductase; dT, deoxythymidine; dTMP, deoxythymidine monophosphate; dUMP, deoxyuridine monophosphate; FOCM, folate-mediated one-carbon metabolism; GAR<sub>Tfase</sub>, glycylamide ribonucleotide tranformylase; MTHFD1, methylenetetrahydrofolate dehydrogenase 1; MTHFR, methylenetetrahydrofolate reductase; MTR, methionine synthase; mtDNA, mitochondrial DNA; SHMT, serine hydroxymethyltransferase; SUMO, small ubiquitin-like modifier; THF, tetrahydrofolate; TK, thymidine kinase; TYMS, thymidylate synthase.

FOCM is compartmentalized in the cell in the mitochondria, the cytosol, and the nucleus (Figure 1). The function of FOCM in mitochondria is to generate one-carbon units in the form of formate for one-carbon metabolism in the cytosol and to generate dTMP and N-formylmethionine tRNA for mitochondrial DNA and protein synthesis, respectively. The role of cellular compartmentation in the functioning of the network has been reviewed recently (137). This review focuses



**Figure 2**

Folate and pathology. Impaired folate-mediated one-carbon metabolism is associated with biomarkers including decreased Met and AdoMet, which leads to chromatin hypomethylation, as well as decreased nucleotide synthesis, which leads to decreased cell division and increased uracil misincorporation into DNA. Impaired folate-mediated one-carbon metabolism is also associated with pathologies including cancer, neurodegenerative disease, and neural tube defects. All of these pathologies are complex traits, making it difficult to understand causal mechanisms that link impaired folate-mediated one-carbon metabolism to pathology. Abbreviations: AdoMet, S-adenosylmethionine; Met, methionine.



on recent advances in our understanding of nuclear de novo dTMP synthesis and nuclear FOCM, and their emerging roles in the etiology of folate-associated pathologies.

## NUCLEAR FOLATE METABOLISM AND THE DISCOVERY OF THE REPLITASE

dTMP biosynthesis occurs in cells through both a nucleotide salvage pathway and a folate-dependent de novo synthesis pathway (**Figure 1**). The salvage pathway involves a single enzyme, thymidine kinase 1 (TK1), that phosphorylates thymidine to dTMP. The de novo synthesis of dTMP includes the enzymes serine hydroxymethyltransferase 1 and 2 $\alpha$  (SHMT1 and SHMT2 $\alpha$ , encoded by separate genes) and methylenetetrahydrofolate dehydrogenase 1 (MTHFD1), which catalyze the conversion of tetrahydrofolate (THF) to 5,10-methyleneTHF using serine and formate as formaldehyde donors, respectively. Thymidylate synthase (TYMS) requires 5,10-methyleneTHF to reductively methylate deoxyuridine monophosphate (dUMP) to dTMP, generating dihydrofolate (DHF). In this reaction, the folate cofactor serves not only as a formaldehyde donor, but also as a source of reducing equivalents. To complete the cycle, DHF is reduced to THF by the nicotinamide adenine dinucleotide phosphate (NADPH)-requiring enzyme dihydrofolate reductase (DHFR).

Early studies in 1965 demonstrated the presence of folate-dependent enzymes including SHMT and TYMS in nuclear fractions of rat liver (21), where the authors postulated, “It seems that the enzymatic synthesis of dTMP from deoxyuridyate is effected, in part at least, in the cell nucleus” (21, p. 36C). Previous to these findings, dTMP synthesis was assumed to occur exclusively in the cytosol, as for cytosine and purine nucleotide biosynthesis. Nucleotides synthesized in the cytosol can be shuttled to both the nucleus and the mitochondria in support of DNA synthesis for DNA replication and repair.

Another study found SHMT and enzymes that catabolize homocysteine in rat brain nuclei. Methionine synthase (MTR), which uses 5-methylTHF to convert homocysteine to methionine, was not identified in nuclei in this study (107). Mouse liver exposed to exogenous  $^{14}\text{C}$ -labeled folic acid contained labeled folate within nuclei 30 min following infusion, and nuclear levels of the label remained stable for up to 120 min. In contrast, mitochondrial  $^{14}\text{C}$ -folate levels continued to increase after 30 min in this study (114). In subsequent studies, 24-h perfusion of rat liver with labeled folic acid resulted in 32% of the labeled folate localizing to nuclei and 25% to mitochondria (160). Interestingly, almost all nuclear and mitochondrial folates presented as folate polyglutamates (126), indicating that they were able to function as metabolic cofactors. This is because folate enters cells as the monoglutamate form of the vitamin, but after entry into the cell it is converted to a polyglutamate form containing three to nine glutamate residues lined though unusual  $\gamma$ -glutamyl peptide bonds. The folate polyglutamate peptide aids in cellular retention of the vitamin and increases the affinity of folate for folate-dependent enzymes by as much as 1,000-fold (136, 144). The mechanism for folate transport into mitochondria is well established (84), whereas mechanisms for folate accretion in nuclei are unknown. During folate deficiency in mice, folate levels in the cytosol deplete markedly, whereas nuclear folate levels are resistant to depletion (40).

The first evidence that FOCM functioned in the nucleus was reported in 1980 in a landmark paper by Prem Veer Reddy & Pardee (106). This study identified six enzyme activities from S-phase nuclei from the Chinese hamster embryo fibroblast cell line CHEF/18 that cosedimented in sucrose density gradients (106). The multienzyme complex was termed the replitase and was present in S-phase nuclei but absent from nuclei in G<sub>1</sub>-phase. The replitase was found to contain the activities of DNA polymerase, TK1, DHFR, TYMS, nucleoside 5'-phosphate kinase, and ribonucleotide reductase (RNR) (96, 106, 158) (**Table 1**). Later, other proteins including c-myc

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**TK1:** thymidine kinase 1

**SHMT:** serine hydroxymethyltransferase

**MTHFD1:** methylenetetrahydrofolate dehydrogenase 1

**THF:** tetrahydrofolate

**TYMS:** thymidylate synthase

**DHFR:** dihydrofolate reductase

**MTR:** methionine synthase

**Replitase:** a multienzyme complex containing enzymes responsible for deoxyribonucleotide synthesis and DNA synthesis including, DNA polymerase, TK1, DHFR, TYMS, nucleoside 5'-phosphate kinase, and RNR

**RNR:** ribonucleotide reductase

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**Table 1** Components of the replitase identified in 1980

Component	Reference(s)
DNA polymerase	96, 106
Thymidine kinase	96, 106
Dihydrofolate reductase	96, 106
Nucleoside 5'-phosphate kinase	96
dTMP synthase	106, 158
Ribonucleotide reductase	96
Topoisomerase	96
DNA methyltransferase	96, 115
c-Myc	133
Calmodulin-binding protein	135
Calmodulin	135

Abbreviation: dTMP, deoxythymidine monophosphate.

(133), calmodulin, and calmodulin-binding protein (135) were identified as components of the replitase. Subsequent studies indicated that TYMS was active in live cells during S-phase only when it was present in the nucleus and only when it was associated with the replitase, even though the enzyme was present in the cytosol during all stages of the cell cycle (105). The observation that the replitase was present in S-phase cells was replicated in proliferating T cells by another research group (115). The replitase was purified as 20–30-nm spheres from isolated calf thymus nuclei in S-phase but again absent in nuclei from G<sub>1</sub>-phase cells. Curiously, both the *de novo* and the salvage pathway enzymes were present in the replitase.

The Pardee group provided evidence that the dTMP synthesis components of the replitase functioned as a coordinated unit that generated and channeled deoxyribonucleotides to DNA polymerase during DNA synthesis in living permeabilized cells. The replitase restricted the incorporation of exogenous deoxynucleotide triphosphates into DNA (106). Incorporation of exogenous deoxynucleotide triphosphates that entered permeabilized cells into DNA occurred only when RNR was inhibited with hydroxyurea.

The concept that the enzymes of the replitase functioned as a single unit, and that inhibition of a single enzyme within the replitase impaired all catalytic functions of the replitase, was controversial. Inhibition of DNA polymerase, RNR, or topoisomerase impaired TYMS activity in CHEF/18 cells (143), and inhibition of DNA repair in human foreskin fibroblasts resulted in decreased DNA synthesis activity as well as TYMS activity. The magnitude of the inhibition was the same for both enzymes (18). These findings led to the hypothesis that the replitase synthesizes and channels deoxythymidine triphosphate (dTTP) directly to DNA polymerase in CHEF/18 cells (19, 106). Chiba et al. (29) used a different approach to test this hypothesis in L1210 cells. Their study showed that inhibition of RNR by hydroxyurea, or of DNA polymerase by aphidicolin, impaired DNA synthesis up to 100% but with corresponding decreases in TYMS activity of only 65% and 60%, respectively. The authors concluded that TYMS activity was not completely dependent on or linked to RNR or DNA polymerase activity as previous studies suggested but nonetheless was sensitive to inhibition of enzymes within the replitase. The authors attributed the inhibition of TYMS to imbalances in deoxynucleotide triphosphate pools resulting from reductions in RNR or DNA polymerase activity. Rode et al. (112) also observed that reductions in TYMS activity were linked to reductions in DNA polymerase or RNR activity in mouse L1210 cells and human CCRF-CM and SKL7 tumor cells to varying degrees. Importantly,



they also observed that impairments in TYMS activity were temporally delayed relative to RNR and DNA polymerase activity, supporting the hypothesis that decreased TYMS activity resulted from alterations in nucleotide pools rather than from allosteric interactions within the replisome multienzyme complex (112). This hypothesis that nucleotide imbalances impaired TYMS activity in whole cells was tested by examining the ability of nucleotide imbalances to inhibit replisome activity in CHEF/18 cells (102). This study not only replicated the finding that both RNR and DNA polymerase inhibitors impaired TYMS activity in cells, but also demonstrated that these inhibitors inhibited the dTMP salvage pathway, which is catalyzed by TK1. Furthermore, these changes in TYMS and TK1 enzyme activities occurred without alterations in nucleotide pools. This finding supported a mechanism of cross-inhibition in which an inhibitor of one enzyme in the replisome complex impaired the activity of other enzymes in the complex. This study was performed in cells that were almost completely synchronized in S-phase. Although this is a strength of the study, it did not allow for quantification of the temporal delay in TYMS or TK1 inhibition following inhibition of RNR or DNA polymerase activity.

Investigation into the role of the replisome in nuclear folate-dependent de novo dTMP biosynthesis lost momentum in the 1980s, potentially because studies of *Saccharomyces cerevisiae* demonstrated that TYMS localized to the nuclear periphery but not to the nucleus during S-phase (104). This finding indicated that nuclear localization of TYMS was not required for DNA synthesis in all eukaryotes. Rather, studies focused on understanding the functioning of the folate-dependent pathways in the cytosol, including de novo dTMP biosynthesis and the interaction of TYMS with other folate-dependent pathways. Empirical and mathematical modeling studies from Schirch and colleagues (118, 131, 132) and other research groups (136) revealed that the intracellular concentration of folate-utilizing enzymes was 2- to 10-fold higher than the intracellular concentration of folate, necessitating a competition among folate-utilizing enzymes for a limited pool of folate coenzyme cofactors (54). This competition is particularly pronounced for 5,10-methyleneTHF, which exists at a branch point in one-carbon metabolism. TYMS can utilize 5,10-methyleneTHF for dTMP synthesis or methylenetetrahydrofolate reductase (MTHFR) can irreversibly convert it to 5-methylTHF (**Figure 1**). Isotope tracer studies indicated that 5,10-methyleneTHF is directed toward de novo dTMP synthesis at the expense of homocysteine remethylation under folate-deficient conditions (50, 97) or as a result of increased SHMT1 expression (54). Initially, this observation was explained as a kinetic competition for 5,10-methyleneTHF cofactors between the enzymes MTHFR and TYMS and did not account for compartmentation of de novo dTMP biosynthesis in the nucleus. The roles of the salvage and de novo dTMP synthesis pathways in the nucleus remained unexplained.

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#### **MTHFR:**

methylenetetrahydrofolate reductase

#### **SUMO:**

small ubiquitin-like modifier

#### **SUMOylation:**

covalent modification of enzymes with the SUMO protein, which regulates nuclear import of enzymes, multienzyme complex formation, and protein turnover

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## **SMALL UBIQUITIN-LIKE MODIFIER-DEPENDENT LOCALIZATION OF THE DE NOVO SYNTHESIS PATHWAY IN MAMMALIAN CELLS**

Investigation into the role of nuclear dTMP biosynthesis was renewed following an exploratory study that sought to identify SHMT1-interacting proteins. Studies using a yeast two-hybrid system identified UBC9, an E3 small ubiquitin-like modifier (SUMO) ligase, as an SHMT1-interacting protein. Covalent posttranslational SUMO modification (SUMOylation) targets proteins for nuclear translocation, influences enzyme activity, and can be essential for enabling or enhancing protein-protein interactions through noncovalent interactions with SUMO-interacting motifs (53). The interaction between SHMT1 and UBC9 indicated that SHMT1, as well as other members of the de novo dTMP synthesis pathway, may be subject to SUMO modification leading to nuclear translocation. SHMT1, TYMS, and DHFR, as well as MTHFD1, contained consensus sites for SUMO modification, and the recombinant proteins were substrates for UBC9-mediated



SUMOylation in vitro (8, 62, 152). Similarly, large-scale screens for SUMOylated proteins in human cells identified the enzymes of the de novo dTMP biosynthesis, and these data were comprehensively compiled and recently reviewed (53). However, large-scale proteomics screens have not identified SUMOylation of the dTMP salvage enzymes TK1 or thymidylate kinase, which converts dTMP to deoxythymidine diphosphate, in human cells (53), although they were identified as components of the nuclear replitase. This difference indicates that there could be more than one mechanism to translocate the enzymes of the replitase into the nucleus.

Tandem affinity purification of SHMT1-binding partners from S-phase and UV-treated HeLa cells indicated that SHMT1 physically interacted with the enzymes of the de novo dTMP synthesis complex, as well as with numerous enzymes required for DNA replication and repair, including nuclear lamin proteins (7). Not surprisingly, many but not all proteins identified in 1980 as part of the replitase were directly or indirectly physically associated with SHMT1 (**Table 1**) (7, 106). Of interest, SHMT1-interacting proteins included proliferating cell nuclear antigen (which acts as a sliding clamp during nuclear DNA replication), UBC9, and lamin proteins (7). SHMT1 was confirmed to bind lamin A/C and B1 directly and tightly (7). UBC9 was also identified as an SHMT1-interacting protein. UBC9 is responsible for covalent modification of target proteins with the SUMO protein; target proteins are modified on conserved lysine residues with the consensus motif [IVL]KXE, where X can be any amino acid and the amino acids in brackets can be either isoleucine, valine, or leucine (53, 152). SUMOylation of SHMT1 is essential for its nuclear import and may be required for formation of the replitase multienzyme complex in the nucleus (7, 8, 152).

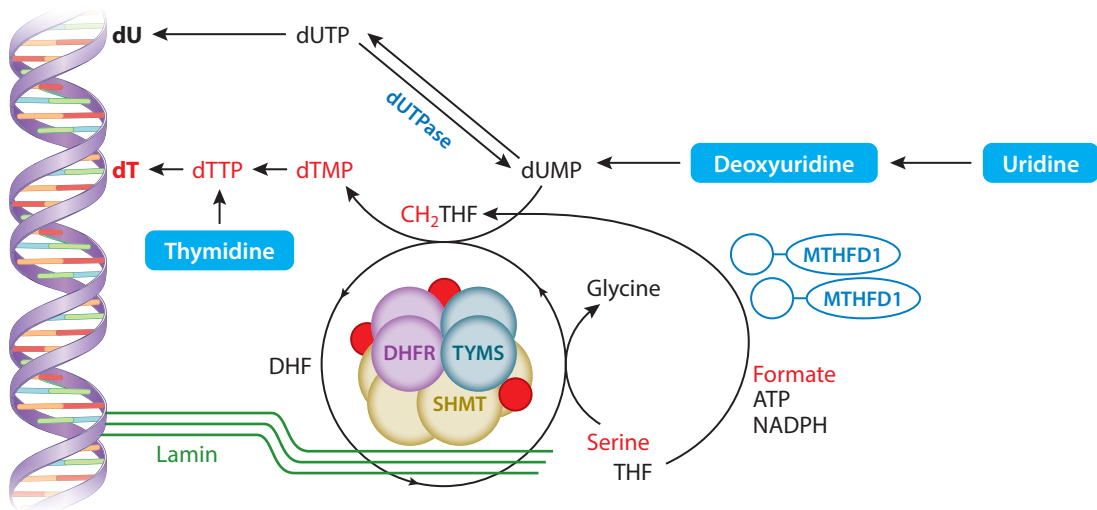
### **EVIDENCE FOR A LOCALIZATION OF THE DE NOVO dTMP BIOSYNTHESIS COMPLEX TO THE NUCLEAR LAMINA AND SITES OF DNA SYNTHESIS**

SHMT (and likely SHMT2 $\alpha$ ), TYMS, DHFR, and MTHFD1 undergo SUMO-dependent translocation to the nucleus at the G<sub>1</sub>/S boundary in MCF-7 and HeLa cells and remain in the nucleus during S- and G<sub>2</sub>/M-phases when they have an intact SUMOylation site (152). MTHFD1, TYMS, and DHFR fluorescent fusion proteins colocalized with SHMT and nuclear lamin proteins during S- and G<sub>2</sub>/M-phases in HeLa cells (7). The de novo dTMP synthesis complex was enriched at origins of replication of an extrachromosomal plasmid, indicating de novo dTMP biosynthesis occurs at the replication fork (**Figure 3**) (7).

Importantly, expression of SHMT1 or SHMT2 $\alpha$ , the nuclear isozyme of mitochondrial SHMT2 that provides functional redundancy with SHMT1 (6), is essential to tether the de novo dTMP synthesis enzymes TYMS and DHFR to DNA and the DNA replication machinery (7). Formation of the multienzyme complex responsible for nuclear de novo dTMP biosynthesis is also essential to prevent accumulation of uracil in DNA, as has been demonstrated in mice (73). Furthermore, expression of a catalytically inactive SHMT1 mutant also increases rates of de novo dTMP biosynthesis in cultured cells (97), emphasizing the importance of SHMT1 expression, localization, and function as a scaffold protein in dTMP synthesis independent of its catalytic activity. This finding is consistent with observations showing that formate, through MTHFD1 activity, provides most folate-activated one-carbon units for de novo dTMP synthesis (as opposed to serine through catalytic activity of SHMT) (54).

Knockout mouse models of de novo dTMP synthesis enzymes have helped further elucidate that SHMT serves as an essential scaffolding protein at sites of DNA synthesis, whereas MTHFD1 supplies the one-carbon units from formate for dTMP synthesis (7) (**Figure 1**). *Mthfd1* is an essential gene in mice (77), whereas *Shmt1* is not (75) likely owing to functional redundancy with SHMT2 $\alpha$  (6). The primary phenotypes resulting from loss of SHMT1 activity in mice are a





**Figure 3**

The de novo thymidylate synthesis pathway as a nuclear multienzyme complex at sites of DNA replication. SHMT, TYMS, and DHFR are SUMOylated covalently attached to the SUMO protein (red circles) at S-phase after which they translocate to the nucleus and form a multienzyme complex. This multienzyme complex is anchored to nuclear lamin proteins and DNA by SHMT (SHMT1 and/or SHMT2 $\alpha$  isozymes). Both serine (through catalytic activity of SHMT1 and/or SHMT2 $\alpha$ ) and formate (through catalytic activity of MTHFD1) serve as one-carbon sources for the generation of CH<sub>2</sub>THF. TYMS catalyzes conversion of dUMP to dTMP, which is converted to dTTP and incorporated into DNA as dT (the T base in DNA). Alternatively, dUMP can be converted to dUTP, which is then incorporated into DNA as deoxyuridine (known as uracil misincorporation). The dUTPase enzyme converts dUTP to dUMP, which both limits dUTP accumulation and provides dUMP substrate for TYMS. Abbreviations: ATP, adenosine triphosphate; DHF, dihydrofolate; DHFR, dihydrofolate reductase; dT, deoxythymidine; dTMP, deoxythymidine monophosphate; dTTP, deoxythymidine triphosphate; dUMP, deoxyuridine monophosphate; dUTP, deoxyuridine triphosphate; MTHFD1, methylenetetrahydrofolate dehydrogenase 1; NADPH, nicotinamide adenine dinucleotide phosphate; SHMT1, cytoplasmic serine hydroxymethyltransferase 1; SUMO, small ubiquitin-like modifier; THF, tetrahydrofolate; TYMS, thymidylate synthase.

fourfold increase in uracil levels in liver and colon DNA and the development of folic acid-responsive NTDs (12, 75). Loss of *Shmt1* expression has minimal impact on homocysteine remethylation (12, 75). Similarly, uracil in nuclear DNA is also elevated in a mouse model of increased SHMT1 expression; in this mouse model, overexpression of SHMT1 impaired its localization to the nucleus (73). In contrast, mice lacking one copy of *Mthfd1* and consuming a folate-deficient diet were protected from uracil accumulation in colon DNA and did not develop NTDs (13, 78). As described below, both observations are likely explained by the preferential translocation and enrichment of MTHFD1 protein to liver nuclei in *Mthfd1*<sup>gt/+</sup> mice consuming a folate-deficient diet (40).

The MTHFD1 protein is partitioned between the nucleus and the cytosol to support nuclear de novo dTMP synthesis and homocysteine remethylation, respectively. The partitioning of MTHFD1 between these two compartments appears to be regulated robustly. Human *MTHFD1* single-nucleotide polymorphisms are associated with adverse pregnancy outcomes such as NTDs and congenital heart defects (20, 100, 101). Identification of a proband with severe MTHFD1 deficiency by exome capture sequencing has further advanced our understanding of the role of MTHFD1 in nuclear one-carbon metabolism and de novo dTMP synthesis (41, 64, 148). The proband presented with classical signs of impaired vitamin B<sub>12</sub> metabolism (e.g., elevated plasma homocysteine, decreased plasma methionine, and megaloblastic anemia) as well as severe combined immunodeficiency (SCID) (64, 148). The proband inherited deleterious mutations in both

**SCID:**  
severe combined  
immunodeficiency



*MTHFD1* alleles, resulting in an early stop codon in the cyclohydrolase/dehydrogenase domain and an R173C mutation in the NADP<sup>+</sup> binding site in the other allele. Levels of full-length *MTHFD1* protein were reduced by 50% in patient fibroblasts, which exhibited decreased methionine and de novo dTMP synthesis, whereas de novo purine synthesis was unaffected. However, the *MTHFD1*-catalyzed incorporation of formate into methionine in protein was reduced by 90% in patient fibroblasts, whereas formate incorporation into dTMP was reduced by only 50% (41). Subsequent studies indicated that *MTHFD1* was preferentially partitioned into the nucleus of patient fibroblasts compared with control fibroblasts, thereby protecting nuclear de novo dTMP synthesis at the expense of methionine synthesis in the cytoplasm. Interestingly, the mitochondrial *MTHFD2* protein colocalized with newly synthesized DNA in the nuclei of U251, HeLa, and HCT116 cells (125). *MTHFD2* overexpression also increased HCT116 cell proliferation, even when *MTHFD2* lacking functional dehydrogenase activity was overexpressed (125). This observation suggests that the function of *MTHFD2* within the nucleus is distinct from its catalytic activity.

In summary, *SHMT1* partitioning between the cytoplasm and nucleus impacts dTMP synthesis but has little impact on homocysteine remethylation capacity (73). This is not the case for *MTHFD1* partitioning. Impaired *MTHFD1* activity reduces rates of homocysteine remethylation and de novo dTMP synthesis (16), resulting in uracil incorporation and accumulation in DNA (41). *MTHFD1* protein is preferentially enriched in the nucleus during folate deficiency (40), without changes in *MTHFD1* expression. Loss of *MTHFD1* activity also results in increased *MTHFD1* protein partitioning into the nucleus of human fibroblasts (41), such that nuclear enrichment of *MTHFD1* supports nuclear de novo dTMP synthesis at the expense of supplying one-carbon units for homocysteine remethylation in the cytosol (40, 41). Nuclear localization of *MTHFD1* also accounts for the observation that even when *SHMT1* is expressed, formate remains the major source of one-carbon units required for nuclear de novo dTMP synthesis (40, 54). More recent studies have demonstrated that 5-formylTHF (a potent, slowly binding inhibitor of *SHMT1*) is enriched in the nucleus, indicating that *SHMT1* activity is inhibited mostly within the nuclear compartment (99) (**Figure 1**).

## **PRESENCE OF OTHER FOLATE-RELATED PATHWAYS IN THE NUCLEUS**

To date, there is no strong evidence that either folate-dependent de novo purine biosynthesis or homocysteine remethylation occurs outside the cytosol. Enzymes required for de novo purine biosynthesis form a multienzyme complex in mammalian cells cultured under purine-deficient conditions, but these enzymes and the complex localize exclusively to the cytosol (3, 39). Likewise, homocysteine remethylation to methionine also appears to be a cytosolic process, as the enzymes that compose this cycle that converts homocysteine to methionine, including *MTHFR*, *MTR*, and methionine synthase reductase, are cytosolic (**Figure 1**) (47, 85, 107). Methionine is a precursor of AdoMet, the methyl group donor required for methylation of both DNA and histones within the nucleus.

In contrast to methionine synthesis, AdoMet synthesis occurs in both cytosolic and nuclear compartments. Methionine adenosyltransferase (*MAT*) isozymes, which synthesize AdoMet from methionine and adenosine triphosphate, localize to the nuclear compartment in rat liver in response to acute liver injury (36) and in Chinese hamster ovary cells (111). In Chinese hamster ovary cells, *MAT1* overexpression also selectively increases H3K27 trimethylation, suggesting a coupling between AdoMet synthesis and histone methylation (60, 111). In the process of serving as a methyl donor, AdoMet is converted to *S*-adenosylhomocysteine (AdoHcy), which is then recycled to homocysteine by the enzyme *S*-adenosylhomocysteine hydrolase (*SAHH*) (**Figure 1**) (83).



AdoHcy binds more tightly to many AdoMet-requiring enzymes than AdoMet does, therefore acting as an inhibitor of the methyltransferase enzymes (28). SAHH also translocates to the nucleus (36), presumably to limit nuclear AdoHcy levels and prevent methyltransferase inhibition (60).

Glycine *N*-methyltransferase (GNMT) localizes to the nucleus. It is a cytosolic protein that primarily regulates the cellular methylation potential (also known as the AdoMet-to-AdoHcy ratio) by catalyzing the conversion of AdoMet and glycine to *N*-methylglycine (sarcosine) and AdoHcy. GNMT expression is highest in human liver, kidney, and pancreas, but GNMT is also expressed in heart, brain, lung, testes, and ovary (35). In rat liver, it composes as much as 3% of total cytosolic liver protein (159) and is present in rat liver nuclei (68, 159). Its primary function is to limit AdoMet accumulation by catabolizing AdoMet, thereby suppressing and regulating intracellular AdoMet levels and, by extension, the AdoMet-to-AdoHcy ratio and the cellular methylation potential (35, 72). GNMT is also a tight, 5-methylTHF-binding protein, and 5-methylTHF binding inhibits GNMT catalytic activity. GNMT is found in nuclei of normal and transformed human cells (35, 68). In cancer cells, nuclear localization of GNMT induces apoptosis independent of GNMT catalytic activity (35), indicating that its 5-methylTHF-binding activity may play an important physiological role. Interestingly, partitioning of GNMT to the nucleus increases during folate deficiency in HepG2 cells. Furthermore, GNMT overexpression limits uracil accumulation in DNA (147). The metabolic role of GNMT in the nucleus is not clear, and GNMT has not been identified as a component of the replitase. But mice lacking GNMT expression exhibit elevated uracil in DNA, indicating impaired de novo dTMP synthesis, and the levels of uracil in DNA in this model are not responsive to dietary folate (147). 5-MethylTHF is a major folate form in the nucleus during vitamin B<sub>12</sub> deficiency (99). Accumulation of 5-methylTHF impairs de novo dTMP biosynthesis through a methyl trap (an accumulation of 5-methylTHF at the expense of other folate cofactors), resulting in inhibition of de novo dTMP biosynthesis (124). This suggests that GNMT may play a critical role in sequestering nuclear 5-methylTHF, which is an inhibitor of SHMT1, but further experiments are required to elucidate the role of GNMT in nuclear de novo dTMP synthesis.

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**GNMT:** glycine  
*N*-methyltransferase

**Uracil  
misincorporation:**  
incorporation of  
deoxyuridylate into  
DNA during DNA  
replication opposite an  
A base on the template  
strand

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## URACIL IN DNA AS A BIOMARKER OF IMPAIRED NUCLEAR FOLATE-MEDIATED ONE-CARBON METABOLISM

Serum and tissue biomarkers of impaired FOCM include depressed AdoMet levels and elevated homocysteine and AdoHcy levels (32, 54), leading to hypomethylated DNA and protein (including histones), which affects gene expression and DNA stability (45, 46, 59, 61). Impaired FOCM also depresses de novo dTMP synthesis (16), resulting in uracil misincorporation and accumulation in nuclear DNA (**Figure 4**). The relationship between B-vitamin nutrition and DNA uracil content is not fully understood. Uracil has been suggested to be a biomarker of folate (16) and vitamin B<sub>12</sub> status (63), but not all studies agree. Uracil accumulated in DNA of proliferating cells threefold higher than in quiescent cells, indicating that misincorporation during replication is the major source of DNA uracil (4). Uracil levels in white blood cells did not correlate with folate status in females 20–23 years old but did correlate inversely with vitamin B<sub>12</sub> status in folate-replete individuals (63). In a study of 86 human subjects with a previous colorectal adenoma, high levels of folic acid (5 mg/day) and vitamin B<sub>12</sub> (1.25 mg/day) supplementation increased levels of uracil DNA by 5.37 fmol/μg DNA in the rectal mucosa (141). Levels of uracil accumulation in DNA differ by tissue in mice (95). Homozygous deletion of the uracil excision repair enzyme uracil-DNA *N*-glycosylase (UNG) elevates nuclear DNA uracil levels by approximately twofold in liver and kidney but over sixfold in testes and spleen during folate deficiency (95). *Ung* encodes both nuclear and mitochondrial UNG isozymes, and folate-deficient *Ung*<sup>−/−</sup> mice, but not folate-deficient wild-type mice, exhibit increased mitochondrial DNA content in brain (67). However,







the nucleus and mitochondria that are interconnected through the shuttling of serine, glycine, and formate; (e) feedback and feedforward interactions with other metabolic pathways that are connected to FOCM through upstream and downstream interactions; (f) dependence of the pathways on other B-vitamin cofactors including vitamin B<sub>6</sub>, vitamin B<sub>12</sub>, riboflavin, and niacin; and (g) penetrant genetic variants (44, 122). Because folate-dependent pathways generate purine and thymidine nucleotides for DNA synthesis, and AdoMet for methylation of both DNA and chromatin, the functioning of this metabolic network influences the expression and stability of the genome. Therefore, the genome is a reservoir of biomarkers that report on the functioning of folate metabolism (**Figure 2**). The illustrative examples below provide evidence for the role of nuclear de novo dTMP biosynthesis in the etiology of folate-responsive pathologies.

## CANCER AND CHEMOTHERAPY

Almost immediately following the discovery of folate as an essential metabolic cofactor for DNA synthesis, folate analogs, otherwise referred to as antifolates, were developed to inhibit dTMP and purine nucleotide biosynthesis and have proved to be effective antimicrobial and antineoplastic agents that are still widely used (142). More recently, human epidemiological, genetic, and biochemical studies and animal studies have conclusively demonstrated that impairments in FOCM, resulting from dietary deficiencies or genetic manipulations, contribute to the initiation or progression of epithelial and potentially other cancers, especially colon cancer (80, 81). Maintenance of adequate folate status is essential for cancer prevention (82, 146), but elevated cellular folate concentrations have been proposed to promote carcinogenesis or tumor growth; however, the evidence base is limited. Meta-analyses have not supported increased cancer risk associated with dietary folic acid (43).

Pharmaceuticals targeting folate-dependent de novo dTMP synthesis enzymes include aminopterin, methotrexate, and nucleoside analogs (49). Methotrexate binds to DHFR, inhibiting its activity (1). DHFR binds its own messenger RNA, which prevents translation such that DHFR represses its own production (1, 9, 24). Resistance to methotrexate can develop when methotrexate prevents DHFR from binding to its own messenger RNA, interfering with the repressed translation (15). The 19-bp deletion polymorphism in intron-1 of DHFR affects DHFR transcription and translation. This polymorphism increases risk for several folate-associated pathologies, but risk seems to vary among populations (for a review, see Reference 1). DHFR activity is important both for de novo dTMP synthesis and for the conversion of dietary folic acid to THF, which is believed to occur in the cytosol. The effect of methotrexate on nuclear de novo dTMP synthesis has not been explored.

5-Fluorouracil (5-FU) inhibits TYMS, which leads to impaired dTMP production and cell death. More specifically, the 5-FU metabolite, 5-fluorodeoxyuridine monophosphate (FdUMP), forms a stable ternary complex with TYMS and 5,10-methyleneTHF, leading to formation of a covalent bond between FdUMP and TYMS. This covalent bond inactivates TYMS (116, 128), leading to dUMP accumulation and dTTP depletion. 5-FU is widely used in the treatment of breast, colorectal, epithelial, esophageal, and pancreatic cancers (71). Antifolates such as pemetrexed and raltitrexed also inhibit TYMS and are currently used to treat lung and colorectal cancers (49). Antifolate-induced impairments in dTMP biosynthesis increase genomic uracil incorporation and levels (73, 79) and increase DNA repair rates (119, 120), resulting in futile cycles of uracil misincorporation and base excision. These futile cycles ultimately lead to accumulation of DNA strand breaks and cell death owing to inadequate dTTP. FdUMP can also be converted to 5-fluorodeoxyuridine triphosphate (FdUTP) by thymidylate kinase, which converts FdUMP to 5-fluorodeoxyuridine diphosphate (FdUDP), and by nucleoside diphosphate kinase, which then



converts FdUDP to FdUTP. FdUTP incorporation into DNA also contributes to 5-FU-mediated toxicity. In mammalian cells, 5-FU treatment can lead to higher levels of 5-FdU incorporation into DNA than of uracil incorporation into DNA. Conversely, in yeast cells exposed to 5-FU, uracil levels in DNA exceed those of 5-FdUTP (123). Yeast synthesize dTMP exclusively in the cytosol, raising the possibility that nuclear localization of TYMS may be a key modifier of the mechanism of action of 5-FU. In fact, evidence is emerging that nuclear compartmentation of the de novo dTMP synthesis pathway alters 5-FU efficacy in mammalian cells. Increased nuclear TYMS levels are associated with poorer response to 5-FU and with decreased survival in colorectal carcinoma (154). The common *SHMT1* variant, *SHMT1* C1420T (rs 1979277), results in an amino acid substitution (Leu474Phe) located near the site where SHMT1 interacts with the SUMO ligase enzymes (152). The *SHMT1* C1420T polymorphism impairs SHMT1 SUMOylation and nuclear localization (5) and may decrease nuclear de novo dTMP synthesis capacity. Interestingly, the *SHMT1* C1420T polymorphism is associated with better response and longer progression-free survival in colorectal cancer patients treated with a 5-FU combination therapy (5-FU, leucovorin, irinotecan) (22). Taken together, these studies suggest that nuclear localization of the de novo dTMP biosynthesis pathway may be a critical modifier of toxicity induced by 5-FU and other antifolates. This raises the possibility that accounting for nuclear localization of the de novo dTMP synthesis pathway and modifiers thereof may be useful in improving antifolate efficacy (31).

## NEURAL TUBE DEFECTS

NTDs are a class of birth defects that result from failure of the neural folds to close during neurulation. Even the least severe NTDs can result in lifelong disability. Several genetic and environmental factors increase risk for NTDs, but the strongest among these is blood folate levels (140). Clinical observations in the 1960s indicated that reduced maternal folate status was associated with an elevated risk for NTDs (55, 56, 127). Accordingly, further studies indicated elevated maternal homocysteine as a risk factor for NTDs (86, 129). Folic acid supplementation decreased NTD occurrence (34) and recurrence (93) rates by as much as 70% in randomized controlled trials and population-wide fortification initiatives (27, 87, 117). The metabolic mechanisms linking folic acid supplementation or FOCM to NTD pathogenesis are an active area of investigation, and most women with an NTD-affected pregnancy do not exhibit overt folate deficiency (66, 88, 90). In addition to inadequate dietary folate intake, genetic variations that affect cellular folate accumulation including folate absorption, transport, metabolic processing, intracellular retention, and catabolism may also impair folate status (74). Genetic variations that affect the activity, stability, or intracellular trafficking of folate-dependent metabolic enzymes, as well as deficiencies of other required nutrients for adequate FOCM functioning (such as vitamin B<sub>12</sub> and choline), also affect folate status. In fact, case-control studies demonstrate an association between low maternal vitamin B<sub>12</sub> status and NTD risk (38, 48, 51, 52, 66, 91, 109, 134, 151, 162), but causal relationships remain to be elucidated.

It is hypothesized that increased folic acid intake may decrease NTD incidence by compensating for genetically linked impairments in folate utilization or secondary nutrient deficiencies (14). The *MTHFR* C677T polymorphism, which varies widely among human populations, has been associated with NTD risk in some but not all epidemiologic studies (155–157, 161). This polymorphism causes a single amino acid substitution, which decreases the stability of the MTHFR protein, effectively decreasing MTHFR activity and 5-methylTHF levels, leading to elevated homocysteine. However, because the *MTHFR* C677T polymorphism effectively alters the distribution of folate-activated one-carbon forms to less chemically stable forms (e.g., 10-formylTHF levels rise at the expense of 5-methylTHF levels), the polymorphism also results in lower folate



status. Recent studies have shown that the association of the *MTHFR* C677T polymorphism with NTD risk is due to its effect on lowering folate levels in red blood cells (33, 139). In support of this conclusion, mouse models with decreased *Mthfr* expression exhibit elevated homocysteine but do not develop NTDs (70). Similarly, polymorphisms in genes that regulate homocysteine catabolism through the transsulfuration pathway are sometimes associated with high levels of plasma homocysteine but are not commonly associated with increased NTD risk (70).

Formate has been linked to folic acid-resistant NTDs. Mitochondrial FOCM produces formate from serine or glycine, and formate is the primary source of one-carbon units for all cytoplasmic FOCM reactions, including de novo dTMP synthesis, de novo purine synthesis, and homocysteine remethylation (54, 137). Mouse models with disrupted mitochondrial FOCM, including *Mthfd1L* (17) and glycine cleavage system knockout models, develop NTDs that are rescued with formate supplementation. NTDs in these models are not responsive to folic acid (92, 94, 98). De novo purine biosynthesis has not been associated with NTD risk either in human single-nucleotide polymorphism association studies or in mouse models, but in general, data are lacking for mouse models of impaired de novo purine synthesis. In summary, there is little evidence that homocysteine remethylation to methionine or de novo purine biosynthesis is directly involved in NTD pathogenesis and that the supply of formate for FOCM is critical for the prevention of NTDs.

To date, *Shmt1*<sup>+/-</sup> and *Shmt1*<sup>-/-</sup> mouse models represent the only models of reduced folate-dependent enzyme activity that develop folic acid-responsive NTDs (11, 12). The *Shmt1*<sup>+/-</sup> and *Shmt1*<sup>-/-</sup> mouse models reflect human NTD pathogenesis in that NTDs are low penetrance and folic acid responsive. The lack of lethality in *Shmt1*<sup>-/-</sup> mice and the incomplete penetrance of the NTDs in this model may be due in part to functional redundancy provided by SHMT2 $\alpha$  (6). The primary phenotype of the *Shmt1*<sup>+/-</sup> and *Shmt1*<sup>-/-</sup> mice is elevated uracil in genomic DNA: These mice do not exhibit elevated homocysteine (75). SHMT1 nuclear localization is required to prevent uracil misincorporation in mouse liver and colon (75, 76, 79), and in a mouse model in which SHMT1 expression is restricted mostly to the cytosol, uracil levels in DNA are also elevated (73). Taken together, these data suggest that inadequate SHMT1 nuclear localization or inadequate de novo dTMP nuclear complex formation causes folic acid-responsive NTDs in mice. These data also suggest that associations of elevated homocysteine with NTDs reflect NTD-associated impairments in folate status, but that elevated homocysteine is not on the causal pathway of NTD pathogenesis. The *SHMT1* C1420T variant is associated with increased risk for NTDs in humans (110). Further studies are required to determine whether depressed rates of de novo dTMP synthesis or uracil accumulation in the nuclear genome is causally related to NTD incidence.

## FOLATE-MEDIATED ONE-CARBON METABOLISM IN HEMATOPOIESIS

Megaloblastic anemia can result from drug-induced impairments in de novo dTMP synthesis (121). Folate or vitamin B<sub>12</sub> deficiency also leads to megaloblastic anemia owing to inadequate nucleotide synthesis, resulting in impaired DNA replication and cell division in red blood cell precursors. In addition to overt folate deficiency, inborn errors of metabolism (IEMs) involved in folate absorption or metabolism are also associated with megaloblastic anemia. Hereditary folate malabsorption results from an IEM in the proton-coupled folate transporter (PCFT) and presents with whole-body folate deficiency and the onset of macrocytic anemia, among other complications early in life (163). PCFT expression is highest at the apical brush border membrane of the small intestine, and PCFT transport activity is optimal in the low-pH environment of the duodenum and jejunum (164). Patients with a DHFR IEM also frequently present with megaloblastic anemia, and other complications, such as peripheral neuropathy (10, 25), also arise. As indicated above,



multiple mechanisms ensure nuclear de novo dTMP synthesis is protected during folate deficiency and other impairments in FOCM. Hence, severe nutritional, genetic, and other insults (e.g., chemotherapeutic agents) to FOCM are required to compromise nuclear de novo dTMP synthesis, leading to megaloblastic anemia.

Megaloblastic anemia is a diagnostic indicator of vitamin B<sub>12</sub> deficiency resulting from an accumulation of folate cofactors such as 5-methylTHF due to lack of MTR activity. MTR catalyzes remethylation of homocysteine to methionine by using 5-methylTHF as a cofactor (**Figure 1**). The inhibition of MTR and subsequent accumulation of 5-methylTHF, at the expense of other folate cofactors, is known as the methyl trap. The methyl trap is believed to cause megaloblastic anemia owing to impairments in dTMP synthesis, leading to uracil accumulation in DNA because the cells are starved for THF (124). The MTR-catalyzed conversion of homocysteine to methionine occurs exclusively in the cytosol, but the accumulation of 5-methylTHF cofactors during vitamin B<sub>12</sub> deficiency occurs in both the cytosol and the nucleus (99). Hence, the nuclear compartment is sensitive to the methyl trap, implicating impairment of nuclear de novo dTMP synthesis as a cause of megaloblastic anemia.

Interestingly, an IEM in dUTPase, the enzyme that degrades dUTP and thereby limits its accumulation and incorporation into DNA (**Figure 4**), causes megaloblastic anemia. This observation further highlights the importance of nuclear de novo dTMP biosynthesis complex formation, which is essential to limit uracil in DNA (73), in the pathophysiology of megaloblastic anemia. Because dUTPase is a source of dUMP, the precursor of dTMP, this IEM may impair de novo dTMP synthesis. Alternatively, this may also suggest that uracil in DNA, as opposed to impaired de novo dTMP synthesis in isolation, may be causal in the development of megaloblastic anemia.

SCID results from inadequate T and B cell function, as well as from mitochondrial disorders, and is associated with several metabolic defects including IEMs in nucleotide, carbohydrate, amino acid, and lipid metabolism (69). Adenosine deaminase (ADA) deficiency is a common IEM that causes SCID. ADA is required for purine catabolism, and ADA deficiency results in accumulation of deoxyadenosine. Deoxyadenosine accumulation inhibits RNR, which results in inadequate synthesis of deoxyribonucleotides for DNA replication, leading to impaired DNA synthesis (138). Human mutations in *MTHFD1* are associated with SCID (23), highlighting the importance of nuclear de novo dTMP synthesis, in addition to impaired purine synthesis (as in ADA deficiency), for lymphocyte proliferation and effective immune response. Furthermore, the lack of association between IEMs that elevate homocysteine (cystathionine  $\beta$ -synthase or MTHFR deficiency) and SCID suggests that the presentation of SCID in *MTHFD1* deficiency is likely caused by impaired nuclear de novo dTMP synthesis. *MTHFD1*-deficient patient fibroblasts exhibited increased levels of phosphorylated histone H2AX ( $\gamma$ H2AX), which is a marker of DNA strand breaks that result from uracil excision repair pathways. Interestingly, fibroblasts from patients with SCID resulting from ADA deficiency did not exhibit either impaired de novo dTMP synthesis or increased nuclear  $\gamma$ H2AX levels (41, 42). This finding suggests that *MTHFD1* and ADA deficiencies cause SCID by distinct mechanisms.

## NEURODEGENERATIVE DISEASES

Folate or vitamin B<sub>12</sub> deficiency in the absence of low dietary intake of these vitamins can be attributable to malabsorption due to inflammatory bowel disease and bariatric surgery, alcoholism, autoimmune disorders, or other conditions that impair cellular import. Pernicious anemia, an autoimmune condition that targets parietal cells, results in vitamin B<sub>12</sub> deficiency, leading to myelin degeneration in the spinal cord and subsequently to a condition known as subacute combined degeneration, which consists of both myelin degeneration in the spinal cord and peripheral



neuropathy (degeneration of the peripheral nerves, which are external to the spinal cord). The clinical signs of these conditions include impaired balance and coordination, muscle weakness, and sensory abnormalities. Nerve cells connecting the central nervous system to voluntary muscles must communicate across long ranges using electrical impulses. Myelin establishes efficiency in this communication by preventing leakage of electrical charges, thereby increasing the speed of conduction. Case studies have shown that intramuscular injection of vitamin B<sub>12</sub> resolves the anemia and peripheral neuropathy, indicating that correcting this disease-induced nutritional deficiency results in clinical improvement.

The mechanisms underlying vitamin B<sub>12</sub>-related neurodegeneration remain unestablished. Vitamin B<sub>12</sub> may support myelin synthesis within the cell by providing methyl groups for phosphatidylcholine synthesis in the Schwann cell membranes that compose the myelin sheath (37). Vitamin B<sub>12</sub> is also required for synthesis of neurotransmitters (37). Studies of pigs exposed to nitrous oxide, which oxidizes the vitamin B<sub>12</sub> cofactor and thereby inactivates MTR, suggested that methionine supplementation rescued demyelination in some but not all nitrous oxide-treated animals (149), implying that additional mechanisms may be involved in pathogenesis of vitamin B<sub>12</sub> deficiency-induced subacute combined degeneration and peripheral neuropathy.

Peripheral neuropathy is a complex disease whose risk is associated with interacting environmental, pathophysiological, and genetic factors. Genetic causes of peripheral neuropathy include both highly penetrant genetic mutations associated with IEMs and more common genetic polymorphisms that interact with environmental and disease factors that contribute to risk. Chemotherapeutic agents, some of which act as antifolate compounds that impair de novo dTMP and DNA synthesis and decrease genome stability, can cause peripheral neuropathy (26, 113, 150). Similarly, environmental toxins such as arsenic have been associated with development of peripheral neuropathy in humans (108). Arsenic impairs de novo dTMP synthesis by causing excessive SUMOylation and degradation of MTHFD1 and SHMT1, leading to decreased genome stability (62). Hence, folate-associated neurological disorders may result from impairments in nuclear de novo dTMP synthesis, leading to DNA damage and loss of Schwann cells.

## SUMMARY

In mammals there is increasing evidence that de novo dTMP synthesis must occur in the nucleus to provide sufficient dTTP for DNA replication (89). It is unclear why nuclear compartmentation of the de novo dTMP synthesis pathway is unique to mammals as lower eukaryotes conduct all deoxyribonucleotide metabolism in the cytosol. The provision of dTTP directly at sites of DNA synthesis may allow cells to limit uracil incorporation into DNA, genome instability, and subsequent cell death. SHMT1 is the most critical enzyme for efficient nuclear de novo dTMP synthesis because it is the scaffold protein that connects this pathway to the nuclear lamina; hence, changes in SHMT1 expression directly impact de novo dTMP synthesis capacity. However, it is the partitioning of MTHFD1 between the cytosol and the nucleus that appears to mediate the balance between the provision of one-carbon units between de novo dTMP synthesis and homocysteine remethylation. The mechanisms whereby changes in MTHFD1 activity and cellular folate levels regulate partitioning of MTHFD1 between these two compartments remain to be elucidated. Understanding the roles and regulation of nuclear de novo dTMP synthesis will likely increase our understanding of numerous folate- and vitamin B<sub>12</sub>-associated pathologies.

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