TNFα-dependent hepatic steatosis and liver degeneration caused by mutation of zebrafish s-adenosylhomocysteine hydrolase

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Hepatic steatosis and liver degeneration are prominent features of the zebrafish ducttrip (dtp) mutant phenotype. Positional cloning identified a causative mutation in the gene encoding S-adenosylhomocysteine hydrolase (Ahcy). Reduced Ahcy activity in dtp mutants led to elevated levels of S-adenosylhomocysteine (SAH) and, to a lesser degree, of its metabolic precursor S-adenosylmethionine (SAM). Elevated SAH in dtp larvae was associated with mitochondrial defects and increased expression of tnfa and pparγ, an ortholog of the mammalian lipogenic gene. Antisense knockdown of tnfa rescued hepatic steatosis and liver degeneration in dtp larvae, whereas the overexpression of tnfa and the hepatic phenotype were unchanged in dtp larvae reared under germ-free conditions. These data identify an essential role for tnfa in the mutant phenotype and suggest a direct link between SAH-induced methylation defects and TNF expression in human liver disorders associated with elevated TNFα. Although heterozygous dtp larvae had no discernible phenotype, hepatic steatosis was present in heterozygous adult dtp fish and in wild-type adult fish treated with an Ahcy inhibitor. These data argue that AHCY polymorphisms and AHCY inhibitors, which have shown promise in treating autoimmunity and other disorders, may be a risk factor for steatosis, particularly in patients with diabetes, obesity and liver disorders such as hepatitis C infection. Supporting this idea, hepatic injury and steatosis have been noted in patients with recently discovered AHCY mutations.

KEY WORDS: Lipid metabolism, Liver disease, Methionine metabolism, Methylation, TNF alpha, Zebrafish

INTRODUCTION

Hepatic steatosis, the accumulation of lipid within hepatocytes, is a critical step in the pathogenesis of human diseases such as alcoholic liver disease, non-alcoholic fatty liver disease associated with the metabolic syndrome, chronic hepatitis C infection and other disorders. In more severe forms of these conditions, the liver becomes inflamed and fatty liver progresses to non-alcoholic steatohepatitis (NASH). Understanding the factors affecting this progression is vital because steatohepatitis is a risk factor for cirrhosis, liver failure and hepatocellular carcinoma.

Several pathogenic mechanisms appear to contribute to the development of hepatic steatosis and steatohepatitis, and it has been proposed that multiple ‘hits’ are required for disease progression. Hepatocytes accumulate lipid when its synthesis, uptake, secretion and/or utilization are altered (Browning and Horton, 2004; Fromenty et al., 2004). Although the events that initiate most steatotic disorders are now beginning to be more clearly defined, it has been recognized for many years that methionine metabolism, which is altered in patients with alcoholic liver disease and other chronic liver disorders associated with steatosis, may play a contributory role (Diehl, 2005; Duong et al., 2006; Esfandiari et al., 2005; Innis and Hasman, 2006; Kharbanda, 2007; Lu et al., 2002; Mato et al., 2008; Wortham et al., 2008; Zhu et al., 2003).

Mitochondrial dysfunction, endoplasmic reticulum stress, sensitization to cytokine-induced liver injury and reduced methyltransferase activities have all been implicated in mediating the effects of methionine metabolism defects in the mammalian liver.

The recessive lethal zebrafish mutant ducttrip (dtp) was recovered in a screen for exocrine pancreas mutants (Yee et al., 2005). Initial phenotypic analysis showed normal differentiation of early dtp exocrine progenitors, whereas their proliferation, terminal differentiation and survival were disrupted at later stages (Yee et al., 2005). Subsequent experiments, described in this report, reveal hepatic steatosis, mitochondrial dysfunction and liver degeneration in all dtp larvae, as well as a milder phenotype in adult heterozygous dtp carriers. Positional cloning identified a causative mutation in the gene encoding S-adenosylhomocysteine hydrolase (Ahcy), the enzyme that hydrolyzes S-adenosylhomocysteine (SAH) to homocysteine and adenosine, a pathway that has been linked to mitochondrial dysfunction (Song et al., 2007) and hepatic steatosis. These findings argue that a heritable reduction in Ahcy activity may be a predisposing genetic risk factor for hepatic steatosis. Consistent with such a role for AHCY in humans, steatosis and liver injury were reported in hypermethioninemic patients recently shown to carry homozygous AHCY mutations (Baric et al., 2005; Baric et al., 2004; Buist et al., 2006).

MATERIALS AND METHODS

Fish lines

Procedures for mutagenesis and screening for dtp are reported elsewhere (Yee et al., 2005). Heterozygous adult males were used for all studies of dtp carriers; fish were identified by genotyping (details available upon request). Wild-type TLF strain fish were used for all morpholino injections and drug treatments.

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Genetic mapping and positional cloning of the dtp locus
To generate larvae for mapping, dtp carriers were mated with wild-type WIK zebrafish, and their progeny were subsequently mated to screen for mutant dtp hybrids. Standard Z-markers were used to perform coarse mapping of dtp to chromosome 6. Available in silico sequences were used to derive closer dinucleotide repeat markers. Primer sequences for acby, chmp4a and eif2s2 were obtained from in silico sequences (www.sanger.ac.uk) and individual exons were sequenced. The marker within acby reflects the actual mutation, which takes advantage of the T-to-C mutation that removes an NlaIII (CATG) site in exon 8. This polymorphism is the zero recombinant polymorphism. For the wild-type mRNA, a full-length EST was obtained (www.openbiosystems.com) and engineered into pcS2+ (+); mRNA was then synthesized using mMessage mMACHINE (Ambion). For the mutant mRNA, the mutation was introduced using site-directed mutagenesis and the mRNA was synthesized identically to that of the wild type.

Mass spectroscopy
Whole larvae were snap-frozen in a dry-ice bath prior to mass spectroscopy for SAM, SAH and AHCY. For SAM and SAH, a mixture of internal standards (250 ng/ml each of [3H]-SAM and [35S]-SAH) was added to the tube containing larvae. Larvae were resuspended in acetic acid, sonicated and protein isolated by methanol precipitation. An aliquot of the supernatant was analyzed by mass spectrometer (TSQ 7000, Thermo Finnigan), with chromatography on a YMC ODS S-3 column (Waters, Milford, MA, USA) on a linear gradient of water and acetonitrile at 4°C. The ratio of peak area for the analyte to its stable isotope internal standard was used to calculate the concentrations of SAM and SAH. Data for each time point and condition represent means of at least three pairs of larvae measured separately, with s.e.m. indicated.

Tissue preparation and staining
Adult male genotypic heterozygotes, drug-treated fish or control were prepared as indicated elsewhere in the text. Livers were removed immediately following sacrifice, fixed in paraformaldehyde, and then processed. Portions of the livers were also saved for RNA isolation or mitochondrial preparation for GSH determination. Larvae and livers were stained using Hematoxylin and Eosin in accordance with standard methodology. Staining with Oil Red O was performed by first washing sections in 60% triethyl phosphate, then staining in 1% Oil Red O in triethyl phosphate, followed by rinsing and counterstaining in Celestin Blue (www.ebsciences.com/histology/gma_oilredo.htm).

In situ hybridization and Ahcy immunostaining
In situ hybridizations were performed on staged embryos and larvae as described (Matthews et al., 2004). Genotyped embryos were used for the TNFα rescue experiments. An anti-human AHCY antibody (Abcam) was used for immunohistochemistry following standard procedures.

Adult 3-deaza-adenosine treatment, mitochondrial preparation and GSH determination
Adult TLF siblings were treated with 2.5 mg/ml 3-deaza-adenosine in system water for the times indicated. Mitochondria were isolated from whole larvae or adult livers using the Mitochondrial Isolation Kit (Sigma). Glutathione concentrations were determined spectrophotometrically using the Glutathione Assay Kit (Sigma).

Morpholino and mRNA injections
Morpholinos (Gene-Tools) were (5’ to 3’): ACY-5’, CATGTGAGCCTT-GTCTGTCTGGTA; ACY-IE5, CTCAAGGTGTTTTAAAAACACA-CAC; TNFα-5’, AGGTCACAATGTTCGTAATTCTGA; TNFα-IE4, TTAGTTCCAGGTTGTATCTACAG. Morpholinos to acby and tnfa were injected into the yolk at 2 dpf, as described previously (Stenkamp and Frey, 2003). Injection of the acby AUG morpolino or splice donor (exon 5) morpholino also had similar effects. Knockdown was confirmed using the antibody directed against Acby or TNFα described above.

Injections of mRNA (10 pg) were performed at the 1-cell stage, as described previously (Matthews et al., 2005). mRNA of wild-type or mutant acby was synthesized using standard methods. Injection of azacytidine (azaC) was performed at 2, 3 and 4 dpf by injecting 1 mg/ml azaC (in water) into the yolk in volumes comparable to the morpholino injections.

Western blots and methylosytino staining
Protein and genomic DNA extractions were performed on midsections of 5-dpf larvae using standard protocols. Western blotting was performed using a standard protocol; antibodies were obtained from Abcam.

For the immuno-slot blot, genomic DNA was denatured and applied on a slot filtration apparatus (Bio-Rad), and hybridized following the Bio-Rad protocol. Methylosytino staining was performed using an anti-methylosytino antibody (GeneTex, Abcam) and the remainder of the protocol was identical to a standard western blotting protocol, except for the use of Tris-buffered saline. Genomic DNA was counterstained with Methylene Blue. Quantification was performed using ImageJ or Adobe Photoshop, which produced identical results.

Quantitative PCR
Real-time quantitative PCR was performed on 4-dpf midsections, as described (Matthews et al., 2004). Primer pairs used for amplification were as published (Lorent et al., 2004; Matthews et al., 2004) or as follows (5’ to 3’): tnfa-F3, GAGCCCTGATCTGAAAACCTTG; tnfa-B3, CAG-TCTGTCTTCCTCTCAGTAAATTG; srebp1-F1, GGAAAGAAGCTGACTC-GAAGATGGCC; srebp1-B1, TGAGCTCACAGAAACACACCG; pparg-F1, TGAAAAATGCCCCCTGCTGATG; pparg-B1, GGAAAAAAC-CCTGAGATGCTCNG; gpx-1e1, GCTGTCAGCTGAGACTTT; gpx-1r1, CTTGGCTGATGTGAGACCTT; eif2s2-F1, CTGAAGTTAAAGATGCACCGCCATG; eif2s2-B1, ATTTAAAGTAGGCGCCCATG. Data points represent the mean of at least three sets of 4-5 pooled midsections, with s.e.m. indicated. Statistical significance was determined using Student’s t-test.

RESULTS
Hepatic steatosis in dtp mutants
The recessive lethal dtp mutation was identified in a chemical mutagenesis screen for zebrafish pancreas mutants (Yee et al., 2005). Homozygous dtp larvae, which survive to 9-10 days post-fertilization (dpf), have minimal exocrine tissue but show normal endocrine development (Yee et al., 2005). Subsequent work identified severe liver defects in all homozygous dtp larvae beginning at 3 dpf. Histological analyses showed a small, necrotic-appearing liver in 5-dpf mutants, although initial changes in hepatocyte appearance were manifest at 3 dpf (Fig. 1A-J). Ultrastructural examination of 5-dpf dtp hepatocytes revealed condensation of mitochondrial cristae, with widening and rarefication of the matrix between the inner mitochondrial membrane and the cristae, and an accumulation of lipid globules (Fig. 1M-P). Oil Red O staining of dtp liveis confirmed the presence of neutral lipid in the cytoplasm of 5-dpf mutant hepatocytes (Fig. 1K,L). TUNEL and Acridine Orange stainings of 4-dpf and 5-dpf larvae were negative (not shown), suggesting non-apoptotic cell death in the mutant liver. These data show that the dtp mutation causes progressive liver and exocrine pancreas degradation during the developmental period when cells in both tissues are normally rapidly proliferating. Furthermore, the dtp mutation is associated with hepatic steatosis and mitochondrial defects.

Positional cloning of the dtp locus identifies mutation of a conserved residue in the 8-adenosylhomocysteine hydrolase gene
A positional cloning strategy was used to identify the targeted gene responsible for the dtp phenotype. High-resolution meiotic mapping of the dtp locus defined a 200 kb region on zebrafish chromosome
that delimited three candidate genes (Fig. 2A), one of which, \textit{ahcy}, was favored because of its established role in methionine metabolism and steatosis. Sequencing of cDNAs derived from \textit{dtp} larvae did not identify mutations in the coding regions of the chromatin-modifying protein 4B (\textit{chmp4b}) or eukaryotic translation initiation factor 2B \(\beta\) subunit (\textit{eif2s2}) genes (data not shown). By contrast, a C-to-T transition was present in exon 8 of \textit{ahcy} cDNA recovered from homozygous \textit{dtp} larvae, but not their wild-type siblings (not shown). This missense mutation was predicted to substitute threonine for a methionine residue that is conserved in eukaryotic and prokaryotic Ahcy proteins (Fig. 2B). The methionine residue targeted by the \textit{dtp} mutation resides in the NAD-binding domain (Hu et al., 1999; Hu et al., 2001; Tanaka et al., 2004; Turner et al., 1998), a region of the Ahcy protein that is crucial for enzyme activation (Li et al., 2007). For this reason, we predicted that Ahcy activity was reduced in \textit{dtp} mutants.

Ahcy catalyzes the breakdown of SAH to adenosine and homocysteine and thus plays an important role in methionine metabolism (Fig. 2C). SAH is derived from S-adenosylmethionine (SAM), a methionine metabolite that is considered to be the principal methyl donor used by methyltransferases that modify DNA, RNA, lipids and proteins (Chiang et al., 1996). SAH is a potent inhibitor of methyltransferases (Chiang, 1998; Chiang et al., 1996). Given its important role in methionine metabolism, \textit{ahcy} is predicted to be an essential gene in zebrafish, as suggested by studies in mammals (Miller et al., 1994). As with many zebrafish mutants, survival during early development is most likely explained by maternally supplied \textit{ahcy} mRNA and Ahcy protein, which were both identifiable in zebrafish embryos at 3 hours post-fertilization (hpf) (Fig. 2D,H). Examination of older embryos revealed widespread \textit{ahcy} expression through 24 hpf but not in the wild type (K). (M-P) Electron micrographs of the enlarged nuclei (compare N with M, arrowheads), mitochondrial defects (compare P with O, m) and lipid droplets (P, arrows) in 5-dpf \textit{dtp} hepatocytes. c, canaliculus; eso, esophagus; liv, liver.

**Methionine metabolism is disrupted in \textit{dtp} larvae**

Since reduced Ahcy activity is predicted to increase SAH levels and secondarily inhibit a large number of methylation reactions, we hypothesized that the \textit{dtp} liver phenotype might arise from impaired methylation. To explore this hypothesis, we first measured total SAM and SAH levels in \textit{dtp} embryos and larvae and their wild-type siblings using mass spectrometry. In wild-type embryos and larvae, SAH levels were relatively stable between 2 and 5 dpf, while SAM levels increased modestly (Fig. 3A, blue lines). By contrast, levels of SAH and SAM were increased in \textit{dtp} mutants during these stages.
were rescued by injection of mRNA encoding wild-type, but not $dtp$ SAM levels and the reduced SAM:SAH ratio in 2-dpf methyltransferases (Chiang et al., 1996). The elevated SAH and utilization associated with SAH-mediated inhibition of previously, and is thought to be secondary to reduced SAM. Elevated SAM associated with Ahcy inhibition has been reported (Fig. 3A,B, red lines), while the SAM:SAH ratio was reduced. ahcy expression is evident through 24 hpf. Expression at 48 hpf and 72 hpf is restricted to the liver (yellow arrow), intestine (green arrow) and pancreas (blue arrow). (H) Immunostaining at sphere stage, showing ubiquitous immunoreactive Ahcy protein.

(Fig. 3A,B, red lines), while the SAM:SAH ratio was reduced. Elevated SAM associated with Ahcy inhibition has been reported previously, and is thought to be secondary to reduced SAM utilization associated with SAH-mediated inhibition of methyltransferases (Chiang et al., 1996). The elevated SAH and SAM levels and the reduced SAM:SAH ratio in 2-dpf $dtp$ mutants were rescued by injection of mRNA encoding wild-type, but not $dtp$, Ahcy protein, confirming that the mutant Ahcy is either inactive or has greatly reduced activity (Fig. 3C,D). Microinjected $ahcy$ mRNA did not rescue the methionine metabolism defect, hepatic steatosis or hepatic degeneration of 5-dpf $dtp$ larvae when injected into 1-cell stage embryos or the yolk at 2 dpf (data not shown), most likely because of the short half-life of the mRNA.

To directly examine the effects of the $dtp$ mutation on methylation, we assayed global DNA methylation and global lysine methylation in tissue from mutant larvae enriched for liver. Both DNA and lysine methylation, as measured by anti-methylcytosine and anti-methyl-lysine immunoblots, were decreased in $dtp$, a finding consistent with a global inhibition of methylation caused by elevated SAH or decreased SAM:SAH (Fig. 3E,F). The effect of elevated SAH on lipid methylation was determined by measuring the ratio of phosphatidylethanolamine (PE) to its methylation product phosphatidylethanolamine (PC) in $dtp$ mutants. Although elevated SAH is predicted to inhibit the activity of phosphatidylethanolamine methyltransferase (Pemt), the hepatic enzyme responsible for the metabolic conversion of PE to PC, the ratio of these two metabolites was normal (see Fig. 5S2 in the supplementary material), most likely because of the utilization of yolk-derived PC, or the synthesis of PC from yolk-derived choline via the Kennedy pathway [cytidine 5-diphospho (CDP)-choline pathway] (McMaster and Bell, 1997), rather than a lack of Pemt inhibition. This finding is important because a reduced PC:PE ratio causes severe steatohepatitis in mice (Zhu et al., 2003), and therefore it might be expected to be reduced in $dtp$ mutants.

**The expression of lipogenic genes, of genes responsive to oxidative stress and of $tnfa$ is increased in $dtp$ larvae**

Microarray analyses have been used to identify gene expression patterns altered in patients and rodent models with hepatic steatosis (Chung et al., 2005; Deaciuc et al., 2004; Esfandiar et al., 2005; Younossi et al., 2005). These studies have reported changes in the expression of genes involved in lipid metabolism, inflammation and fibrosis, and in genes encoding cytokines and proteins activated in response to oxidative stress. We compared the expression of some of these genes in $dtp$ mutants and their wild-type siblings using real-time quantitative PCR. As in the other steatosis models, we found elevated expression of the lipogenic genes pparg and srebp1, the reactive oxygen species (ROS)-responsive gene gpx and the cytokine $tnfa$ (NM 212859.2) in $dtp$ larvae, although the elevation of srebp1 only approached statistical significance (Fig. 4A-C). Interestingly, pparg also functions as an anti-inflammatory gene, but its role in hepatic steatosis is likely to be related to its lipogenic functions. Expression of a second zebrafish $tnf\beta$ gene, $tnf\beta$ (NM 1024447.1) was unchanged between wild type and $dtp$ (data not shown). Western analysis confirmed a 3-fold elevation of Tnfa protein levels in $dtp$ larvae (Fig. 4D) and whole-mount RNA in situ hybridization experiments showed increased $tnfa$ expression in the liver, intestine and swim bladder of most $dtp$ larvae examined (Fig. 4E,F).

**Tnfa mediates hepatic steatosis and degeneration in $dtp$ larvae**

To assess the effect of elevated Tnfa in $dtp$ mutants, we assayed the effect of $tnfa$ knockdown induced by antisense morpholinos. Injection of a $tnfa$ morpholino into the yolk of 2-dpf $dtp$ larvae decreased Tnfa protein expression (Fig. 4E), demonstrating the effectiveness of morpholino-mediated knockdown at later embryonic stages, as previously reported (Stenkamp and Frey,
2003). The livers of the morpholino-injected dtp larvae were significantly larger than those of sibling dtp mutants injected with vehicle control (Fig. 4H,I), and the histological appearance of the hepatocytes more closely resembled wild-type hepatocytes, thus confirming rescue of the hepatic phenotype [Fig. 4J,K; rescue was present in 13 of 17 genotyped dtp–/– larvae analyzed by transferrin a (tfa) in situ or tissue staining]. Ultrastructural analysis showed reduced steatosis in the hepatocytes of morpholino-injected dtp larvae and an improvement in the appearance of the mitochondria (Fig. 4L). Injection of tfa morpholino into wild-type larvae had no effect on liver size, histology or ultrastructure (data not shown). These data confirm a central role for Tnfα in the dtp phenotype.

**tnfa expression, hepatic steatosis and degeneration persist in gnotobiotic dtp larvae**

TNF expression is activated in hepatic macrophages (Kupffer cells) and circulating mononuclear cells in patients with alcoholic liver disease and non-alcoholic steatohepatitis (Hoek and Pastorino, 2002; Tomita et al., 2006). The gut microbiota is believed to activate TNF transcription start site did not identify any CpG islands (Sanger elements. Together, these data argue against the idea that elevated tnfa expression in azaC-treated larvae would be expected to impact liver histology or ultrastructure (data not shown).

Having excluded a role for the gut microbiota in tnfa activation, we sought to determine whether reduced DNA methylation at tnfa regulatory elements could account for increased Tnfα levels in dtp mutants. We treated zebrafish larvae with 5-azacytidine (azaC), a nucleoside analog that reversibly inhibits DNA methyltransferases (Jones and Taylor, 1980). AzaC treatment inhibits methylation of hemimethylated cytidine residues in the DNA of replicating cells. Surprisingly, azaC injection into the yolk of 2- to 4-dpf zebrafish had little effect on larval morphology, even though DNA methylation levels were halved (see Fig. S4 in the supplementary material). In addition to their normal gross liver morphology, histological analysis of the azaC-injected larvae revealed no evidence of hepatic steatosis or of liver degeneration, nor was there any ultrastructural evidence of mitochondrial defects (Fig. S4 in the supplementary material). Furthermore, quantitative RT-PCR showed no increase in tnfa expression in azaC-treated larvae (see Fig. S4 in the supplementary material). Finally, analysis of tnfa regulatory elements within 4 kb upstream to 1 kb downstream of the transcription start site did not identify any CpG islands (Sanger Centre zebrafish genome sequence version 7.0; data not shown). Together, these data argue against the idea that elevated tnfa levels in dtp larva arise from reduced DNA methylation at tnfa regulatory elements.

**Steatosis and reduced mitochondrial antioxidants in adult zebrafish treated with the Ahcy inhibitor 3-deaza-adenosine**

Mitochondrial glutathione (mGSH) acts as a scavenger of ROS, and depletion of mGSH is associated with several models of hepatic steatosis and steatohepatitis (Garcia-Ruiz and Fernandez-Checa, 2006). mGSH depletion also sensitizes hepatocytes to injury and cell death caused by TNFα (Mari et al., 2006). Given that the ultrastructural analyses suggest mitochondrial dysfunction in dtp hepatocytes, we attempted to measure mGSH levels in liver mitochondria derived from dtp larvae. Reduced liver size limited the recovery of sufficient mitochondria to perform this assay. A
sufficient number of liver mitochondria were however recovered from adult zebrafish treated with the Ahcy inhibitor 3-deaza-adenosine (deazaA) (Guranowski et al., 1981). DeazaA treatment for 7 days increased liver 
\textit{tnfa} expression and caused hepatic steatosis (Fig. 5). Although these fish had only mild hepatocyte mitochondrial ultrastructural defects (data not shown), a modest yet highly significant reduction of mGSH was evident (Fig. 5D).

Despite causing steatosis and mitochondrial dysfunction, deazaA treatment had only a modest effect on methionine metabolism, as liver SAH levels were unchanged and SAM levels were elevated in these fish (Fig. 6A). Homocysteine levels, however, were reduced following 7 days of deazaA treatment, supporting reduced Ahcy function (5.62±1.89 ng/mg liver in untreated fish versus 2.89±1.08 in treated fish; \(P=0.03\)). The levels of SAM and SAH in the livers of heterozygous adult male \textit{dtp} fish were similar to those in the deazaA-treated livers (Fig. 6B). These metabolic defects were interesting because although mild steatosis was present in deazaA-treated adult fish, pronounced hepatic steatosis was evident in all of the adult male heterozygous \textit{dtp} fish we examined (Fig. 6C-F) (\(n=11\)). \textit{tnfa} expression was modestly increased in the liver of adult heterozygous \textit{dtp} fish (Fig. 6G), similar to that in the adult fish treated with deazaA. Furthermore, adult \textit{dtp} heterozygotes demonstrated elevated expression of \textit{pparg} (Fig. 6H) and of the ROS-sensitive gene \textit{trx} (Fig. 6I), similar to that in homoygous larvae and consistent with other models of hepatic steatosis (Chung et al., 2005; Deaciuc et al., 2004; Esfandiari et al., 2005; Younossi et al., 2005). In contrast to heterozygous adults, hepatic steatosis was not detected in 5-dpf heterozygous \textit{dtp} larvae (not shown).

**DISCUSSION**

**Causative loss-of-function mutation of \textit{ahcy} in zebrafish \textit{dtp} mutants**

In this report we describe the hepatic phenotype associated with a loss-of-function mutation of the gene encoding zebrafish S-adenosylhomocysteine hydrolase (Ahcy), a methionine metabolism enzyme that is highly conserved in prokaryotes and eukaryotes. These data complement previously published studies showing the...
effect of this mutation on the proliferation and survival of exocrine pancreas progenitor cells in zebrafish dtp mutant larvae (Yee et al., 2005). Multiple lines of evidence described in this report support the identification of ahcy as the dtp gene. These include tight genetic linkage, mutation of a highly conserved methionine residue in a functional domain of the Ahcy protein, altered levels of methionine metabolites that were not rescued by ahcy<sup>dtp</sup> mRNA injections (indicating reduced function of the dtp Ahcy protein), and partial phenocopy of dtp by ahcy knockdown and Ahcy inhibition. In addition to these findings, no mutations were identified in the coding regions of other genes in the critical interval surrounding the dtp locus.

**Comparable methionine metabolism defects in dtp larvae and chronic liver disease patients**

Methionine metabolism is disrupted in patients with alcoholic liver disease and other chronic liver conditions, and there is strong experimental evidence linking such defects to the development of steatosis that can progress to cirrhosis, liver failure and liver cancer (Kharbanda, 2007). SAM depletion and/or a reduced SAM:SAH ratio are important consequences of altered methionine metabolism, as evidenced by the ability of SAM or its metabolic precursor, betaine, to delay disease progression in animal liver disease models and in patients with alcoholic liver disease (Lu et al., 2001; Villanueva and Halsted, 2004). SAM depletion in chronic liver conditions arises from nutritional deficiencies coupled with reduced activity of the methionine metabolism enzyme methionine synthase (MAT1A) and reduced BHMT gene expression (Kharbanda, 2007; Lu et al., 2002). This reduces SAM synthesis, elevates cellular SAH (because hydrolysis of SAH by Ahcy is reversible), and reduces the SAM:SAH ratio. By contrast, SAM and SAH are both elevated in dtp, but the SAM:SAH ratio is reduced because the rise in SAM is proportionately less than that in SAH. Increased SAH in dtp is a direct effect of reduced Ahcy activity, whereas SAM levels increase in dtp because of SAH-mediated inhibition of methyltransferases.

**Association of methionine metabolism defects, mitochondrial dysfunction and changes in methylation potential in dtp mutants**

Regardless of the cause, methionine metabolism defects induce a complex set of cellular responses that disrupt hepatocyte lipid metabolism and, in some instances, activate apoptotic or non-apoptotic cell death pathways. Mitochondrial dysfunction is one of the more commonly reported defects. Cytosolic SAM is imported into mitochondria by a specific transporter that is inhibited by high levels of cytosolic SAH (Agrimi et al., 2004; Horne et al., 1997; Song et al., 2007). Reduced mitochondrial SAM caused by elevated SAH is predicted to disrupt mitochondrial function through a variety of mechanisms arising from altered methylation potential [discussed by Song et al. (Song et al., 2007)]. Although the transporter that imports GSH into mitochondria has not been identified, it is known that reduced SAM:SAH alters mitochondrial membrane fluidity (Colell et al., 1997), thereby disrupting the import of GSH, an important antioxidant. Reduced mGSH leads to the oxidation of mitochondrial proteins, lipid and DNA by ROS that are normally quenched by GSH. These oxidative modifications cause mitochondrial dysfunction, which in turn increases ROS production and causes further mitochondrial damage. Ultimately, this decreases hepatocyte lipid utilization, which contributes to steatosis.

Although we did not directly assess the effect of elevated SAH on mitochondrial SAM transport, several lines of evidence show that mitochondrial dysfunction is important to the development of liver steatosis and degeneration in dtp mutants. First, all homozygous dtp larvae had pronounced liver mitochondrial ultrastructural defects. Second, mGSH levels were reduced in the liver of deazaA-treated adult fish that had steatosis. Third, mitochondrial ultrastructure improved in dtp larvae rescued by tnfa knockout. The latter finding is noteworthy because TNFα inhibition improves mitochondrial function in mammalian steatosis models (Garcia-Ruiz et al., 2006).
Fig. 7. Mechanistic model of hepatic steatosis and liver degeneration caused by Ahcy deficiency. Mutation of ahcy disrupts Ahcy activity, increasing cellular SAH. This alters mitochondrial function and reduces cellular methylation potential, thereby altering the expression of lipogenic genes such as tnfα and pparg, possibly through an epigenetic mechanism involving alteration of the histone methylation code. This leads to enhanced lipid synthesis, reduced lipid utilization and, possibly, enhanced lipid uptake, as well as to the sensitization of hepatocytes to TNFα-induced cell death. Additional, as yet unidentified effects of altered SAH or altered methylation potential might also play a mechanistic role in the dtp phenotype.

In addition to causing mitochondrial dysfunction, methionine metabolism defects are predicted to alter total cellular methylation potential, as a reduced SAM:SAH ratio and/or elevated SAH inhibit a wide range of cytosolic and nuclear methyltransferases (Chiang et al., 1996). Up to 75% of all mammalian transmethylation reactions occur in the liver (Xue and Snoswell, 1986), and elevated liver SAH has been shown to inhibit the methylation of histones, DNA and lipids in a dose-dependent fashion (Duerre and Briske-Anderson, 1981). Mat1, Pemt and Gnmf knockout mice all develop steatosis, as do human patients with GNMT deficiency (Li et al., 2006; Lu et al., 2001; Luka et al., 2006; Martinez-Chantar et al., 2008; Zhu et al., 2003). Elevated SAH also causes steatosis and liver degeneration in murine adenosine kinase deficiency (Xue and Snoswell, 1986; Bode and Bode, 2005; Mathurin et al., 2000; Wigg et al., 2001). ahcy is strongly expressed in the intestine of zebrafish larvae, and for this reason we initially thought that altered permeability of the intestinal epithelium to the gut microbiota might activate tnfα expression in dtp mutants. However, tnfα expression was unchanged in gnotobiotic dtp larvae, indicating that there was a different cause for the enhanced expression.

Because of the known effects of Ahcy inhibition on methylation, we speculated that an epigenetic mechanism, such as reduced DNA methylation at the tnfα or another gene locus, could activate tnfα expression in dtp, such as occurs during hematopoietic stem cell differentiation (Sullivan et al., 2007). However, our analysis of the putative tnfα promoter region in the zebrafish genome database did not identify any CpG islands, and reduced DNA methylation caused by azAC did not activate tnfα expression in zebrafish larvae. Thus, we considered changes in DNA methylation an unlikely cause of enhanced tnfα expression.

Global methylated lysine was also reduced in dtp, raising the possibility that changes in histone methylation might epigenetically activate tnfα expression. Supporting this idea, reduced levels of the inhibitory marker dimethyl-H3K9 correlate with increased Tnfα expression in endotoxin-stimulated human mononuclear cells (El Gazzar et al., 2007). A reduction in the number of inhibitory trimethyl-H3K27 marks also correlates with activation of gene expression during development, differentiation and response to immune stimuli (Agger et al., 2007; Cloos et al., 2008; Jepsen et al., 2007). In contrast to these studies suggesting that tnfα expression can be activated by the removal of inhibitory methyl marks, Ara and colleagues recently reported that lipopolysaccharide-induced activation of Tnfα expression in mouse macrophages is associated with increased levels of an activating methyl mark, trimethyl-H3K4, and that this was inhibited by SAH (Ara et al., 2008). We speculate that these conflicting data are likely to be attributable to stimulus- and cell type-dependent changes in methylation potential, and that Ahcy inhibition in dtp alters the balance between methylation and demethylation of histone H3 lysine residues associated with the tnfα promoter, or tnfα regulatory loci, in liver mononuclear immune cells (Kupffer cells), or possibly even hepatocytes, as suggested by the tnfα expression pattern in dtp larvae. Consistent with this model, pharmacological inhibition of Ahcy causes cell type-specific changes in gene expression in cancer cells and T-cell subsets (Lawson et al., 2007; Tan et al., 2007). A related epigenetic mechanism of gene regulation has also been reported in mouse ES cells (Pasini et al., 2008).

In summary, extensive evidence from human liver disease patients, animal liver disease models and in vitro systems indicates a causative role for altered methionine metabolism in steatosis, steatohepatitis and liver degeneration. Our analyses of dtp mutants, adult heterozygous dtp fish and adult fish treated with the Ahcy inhibitor deazaA extend these observations to zebrafish. As summarized in Fig. 7, our data suggest that tnfα overexpression and mitochondrial dysfunction are
the principal causes of the dtp liver phenotype. This model of TNFα-mediated steatosis is novel as there are no previous reports of altered methylation potential activating tnfα gene expression. However, as pointed out in Fig. 7, we cannot exclude the possibility that other factors contribute to the dtp phenotype.

**Relationship of the zebrafish and human Ahcy deficiency phenotypes**

Clinical manifestations of human Ahcy deficiency have been reported in only three patients (Baric et al., 2005; Baric et al., 2004; Buist et al., 2006). Motor and neurological defects were the prominent presenting symptoms in two siblings that are compound heterozygotes for two hypomorphic AHCY alleles. The first-identified patient also demonstrated biochemical hepatitis and mitochondrial abnormalities on liver biopsy at the age of 12 months (Baric et al., 2004), whereas the second patient had no demonstrable liver abnormalities, presumably because of an earlier diagnosis at age 3 months (Baric et al., 2005). A third, 26-year-old patient had comparable motor and neurological symptoms, in addition to hepatic steatosis and mitochondrial abnormalities evident on liver electron micrographs (Buist et al., 2006). It is intriguing that within this group of three AHCY-deficient patients, there appears to be a progression of mild to moderate liver disease with age, similar to our findings with the dtp heterozygotes. By contrast, pronounced hepatic steatosis and degeneration in homozygous dtp larvae most likely result from the combined effect of more severe Ahcy deficiency coupled with the rapid rate of hepatic metabolism of yolk-derived lipid nutrients in zebrafish larvae.

**Steatosis in dtp heterozygotes suggest that AHcy polymorphisms might be heritable risk factors for steatosis in liver disease patients**

Although heterozygous dtp larvae are indistinguishable from homozygous wild-type siblings and develop normally with no apparent reduction in fecundity or lifespan, as adults these fish develop pronounced hepatic steatosis. Surprisingly, liver SAH levels were not significantly elevated and SAM levels were elevated ~2-fold, raising the SAM:SAH ratio in these fish. Comparable SAM and SAH levels were noted in deazaA-treated adult fish that also developed steatosis. These findings were unexpected, as reduced Ahcy activity is expected to increase SAH levels and decrease the SAM:SAH ratio. We speculate that these biochemical findings result from either variable sensitivity of hepatic methyltransferases to SAH or increasing metabolism of homocysteine via betaine homocysteine methyltransferase (Bhmt) (see Fig. S5 in the supplementary material).

Regardless of the mechanism that accounts for the observed SAM and SAH levels in dtp heterozygous and deazaA-treated adult fish, hepatic steatosis in these fish raises the question of whether human AHCY polymorphisms that have only mild effects on methionine metabolism might be a risk factor for the development of steatosis associated with obesity, alcohol consumption and other conditions, such as chronic hepatitis C infection or drug-induced steatosis. Polymorphisms in the methionine metabolism gene MTHFR and hyperhomocysteinemia have been reported to promote steatosis and fibrosis in chronic hepatitis C patients (Adinolfi et al., 2005), and human AHCY polymorphisms that alter protein thermostability have already been described (Fumic et al., 2007). Given the potentially beneficial effects of AHCY inhibitors in treating cancer and autoimmune diseases (Hermes et al., 2008; Lawson et al., 2007; Tan et al., 2007), the population of patients that may benefit from AHCY genotyping could increase significantly in the near future. Molecular analysis of other zebrafish mutations that cause hepatic steatosis (Sadler et al., 2005) might identify additional heritable risk factors.

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**Supplementary material**

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/136/5/865/DC1

**References**


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**Steatosis in zebrafish ahcy mutants**

**RESEARCH ARTICLE**

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**DEVELOPMENT**