

Chapter 10

ALDH1L1 and ALDH1L2 Folate Regulatory Enzymes in Cancer



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Abstract Epidemiological studies implicate excess ethanol ingestion as a risk factor for several cancers and support the concept of a synergistic effect of chronic alcohol consumption and folate deficiency on carcinogenesis. Alcohol consumption affects folate-related genes and enzymes including two major folate-metabolizing enzymes, ALDH1L1 and ALDH1L2. ALDH1L1 (cytosolic 10-formyltetrahydrofolate dehydrogenase) is a regulatory enzyme in folate metabolism that controls the overall flux of one-carbon groups in folate-dependent biosynthetic pathways. It is strongly and ubiquitously down-regulated in malignant tumors via promoter methylation, and recent studies underscored this enzyme as a candidate tumor suppressor and potential marker of aggressive cancers. A related enzyme, ALDH1L2, is the mitochondrial homolog of ALDH1L1 encoded by a separate gene. In contrast to its cytosolic counterpart, ALDH1L2 is expressed in malignant tumors and cancer cell lines and was implicated in metastasis regulation. This review discusses the link between folate and cancer, modifying effects of alcohol consumption on folate-associated carcinogenesis, and putative roles of ALDH1L1 and ALDH1L2 in this process.

Keywords Folate · Cancer · Alcohol · ALDH1L1 · ALDH1L2 · Methylation · SNPs · Tumor suppressor

10.1 Introduction

Epidemiological studies implicate excess ethanol ingestion as a risk factor for several cancers and support the concept of a synergistic effect of chronic alcohol consumption and folate deficiency on carcinogenesis [1]. Alcohol consumption

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itself impairs folate metabolism through the enhanced coenzyme degradation or the inhibition of absorption, as well as through the influence on folate-related genes and enzymes [1, 2]. Among these targets, two major folate-metabolizing enzymes, ALDH1L1 and ALDH1L2, were considered. This review discusses the link between folate and cancer, modifying effects of alcohol consumption on folate-associated carcinogenesis, and putative role of ALDH1L1 and ALDH1L2 in this process.

10.2 Folate: Overview

Folate coenzymes are vital for cellular homeostasis due to their key role in transferring one-carbon groups in reactions of *de novo* nucleotide biosynthesis, metabolism of serine, glycine and histidine, and the regeneration of methionine from homocysteine [3]. The methionine biosynthesis is linked to the production of S-adenosylmethionine, a universal methyl donor in more than a hundred methylation reactions in the cell [4]. Folates also participate in the clearance of formate as CO₂ [5] and the formylation of methionyl-tRNA [3]; the latter process is essential for translation initiation in eukaryotic mitochondria [6]. Humans are unable to synthesize this coenzyme and must obtain it from the diet. Insufficient folate intake has dramatic consequences for the cell, including: deregulation of methylation processes [7]; altered protein expression [8]; and decreased DNA repair capability and accumulation of DNA damage leading to increased chromosomal aberrations and fragility [9, 10]. These mechanisms underlie reduced growth rate and impaired cell division caused by folate deficiency. Low folate status has been linked to increased risk for several types of cancer, neural tube defects, and cardiovascular diseases [7] though the association between folate and carcinogenesis, as well as cardiovascular diseases, is inconclusive at present. For the reason of the prevention of neural tube defects, in 1996 the FDA approved a mandatory fortification of several types of grain foods in the US with a synthetic form of the vitamin, folic acid. Though the overall importance of folate for human health was known for long time, the underlying molecular mechanisms are not fully understood and continue to emerge. This is exemplified by recent studies, which have underscored the significance of folate metabolism for ES cells [11], the contribution of folate-dependent carbon oxidation into the cellular energy balance [12, 13], and the role of folate enzymes in cancer progression and metastasis [14–19]. To further complicate the picture, a concept that parental folate intake or folate status can modify disease risk in offspring later in life has been recently proposed [20].

10.3 Interactions Between Alcohol Consumption and Dietary Folate: Implication for Cancer

The link between folate and cancer has been investigated for decades but this issue is complicated by the phenomenon that while in general folate intake protects against tumorigenesis, it also can promote the proliferation of existing neoplastic lesions [21]. This adverse effect is primarily associated with the increased demand of rapidly proliferating cancer cells for folate coenzymes to support enhanced nucleotide biosynthesis towards unlimited DNA replication. Thus, there is a dilemma that folate intake above basal requirements may increase the incidence of malignancies and cancer-related death, which has been increasingly recognized by the experts in folate field [22]. The tumorigenic response to dietary folate depends on numerous factors, including cancer subtypes, the timing or duration of vitamin administration, its dose and ingested form (synthetic folic acid vs. natural folate) [4, 21]. End-point effects of the vitamin could be further modified by other factors such as age, the status of vitamins B₆/B₁₂, and individual genotypic features including polymorphisms in folate enzymes [4, 20]. One of the factors known to affect folate metabolism is chronic alcohol consumption [1, 2].

Alcoholism is typically associated with folate deficiency due to reduced dietary folate intake [2]. Heavy alcohol consumption also decreases folate absorption, enhances urinary folate excretion and inhibits enzymes pivotal for one-carbon metabolism [1, 2]. While folate metabolism is involved in numerous key biochemical pathways (Fig. 10.1), the aberrant DNA methylation, due to the deficiency of methyl donors, was widely considered as a common downstream target of the folate-mediated effect of ethanol [23]. The negative effects of low intakes of nutrients, which provide dietary methyl groups, with high intakes of alcohol are additive in general [24]. In support of such association, it has been reported that the low methionine, low-folate diets and alcohol consumption increase the risk for colorectal cancer in men [25]. Therefore, to counteract the negative effects of alcohol consumption, the increased intake of nutrients providing dietary methyl groups is recommended [24].

In agreement with this notion, a protective effect of folate on alcohol-impaired processes has been demonstrated in experiments with cultured mouse embryos, where addition of the vitamin, in the form of folic acid, blocked ethanol-induced teratogenesis [26]. The microarray profiling further indicated that the effect of prenatal ethanol exposure on teratogenesis in mice, and associated mental retardation, were induced through alterations in the expression pattern of several micro RNAs in fetal brain. In line with this mechanism, increased folic acid prevented micro RNAs changes in response to ethanol. Though it is not clear whether a similar mechanism mediating the interaction between dietary folate and alcohol consumption could be activated in carcinogenesis, SNPs (single nucleotide polymorphisms) in the micro RNA bindings sites of thymidylate synthase were associated with gastric cancer risk and patient survival [27]. Perhaps the interaction between folate status and alcohol consumption in carcinogenesis involves multiple mechanisms and is likely cancer-type specific. Four main alcohol-associated cancers are liver, colon, breast

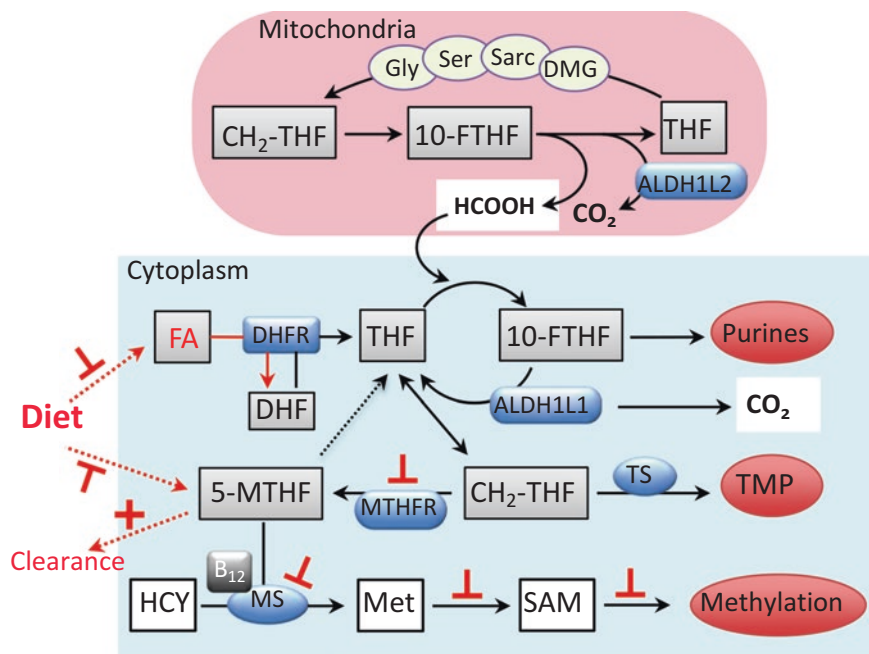


Fig. 10.1 Folate metabolism. Folate is taken up by the cell as folic acid (FA, supplements or fortified foods) or 5-methyl-THF (5-MTHF, natural diet). In the cell, FA is sequentially converted to dihydrofolate (DHF) and the active form of the coenzyme, tetrahydrofolate (THF) in reactions catalyzed by DHFR (dihydrofolate reductase). Acceptance of a one-carbon group (comes from serine, glycine, histidine or formate) converts THF to coenzymes directly participating in biosynthetic reactions (10-FTHF, 10-formyl-THF; CH₂-THF, 5,10-methylene-THF). HCY, homocysteine; SAM, S-adenosylmethionine; MS, methionine synthase; TS, thymidylate synthase; MTHFR, methylenetetrahydrofolate reductase. Reaction catalyzed by MS converts 5-MTHF to THF (dotted arrow). Overall, folate coenzymes provide one-carbon groups for three biosynthetic pathways: (i) methionine production; (ii) *de novo* purine generation; (iii) TMP synthesis. Mitochondrial folate metabolism provides one-carbon groups, derived from the degradation of serine, glycine, sarcosine (Sarc) or dimethylglycine (DMG), to the cytosolic folate pathways in the form of formate. Processes inhibited by ethanol are indicated by (⊥). Degradation of 5-methyl-THF is accelerated by ethanol (indicated by “+”)

and upper aerodigestive tract [23]. In agreement with such etiology, recent prospective cohort study indicated that the folate pathway is likely to be involved in alcohol-related colorectal cancer development [28]. Higher folate intake can also ameliorate the effect of alcohol consumption on the development of HCC (hepatocellular carcinoma) [29] and the risk of breast cancer [30]. A prospective study of alcohol consumption and the risk of colorectal cancer before and after folic acid fortification in the US showed that fortification may attenuate this risk [31]. Another case-control study indicated that folate-related enzyme polymorphisms modify the association between drinking habit and pancreatic cancer risk [32]. Studies of other cancer types did not provide a clear association between folate status, alcohol consumption and cancer risk [33, 34].

The effect of ethanol on folate metabolism could be direct, through the enhanced coenzyme degradation or the inhibition of absorption, as well as indirect, through the influence on folate-related genes and enzymes. The intracellular folate pool consists of several major forms of the coenzyme, which differ in the oxidation level of the bound one-carbon group and are interconvertible through multiple reactions catalyzed by more than a dozen enzymes (Fig. 10.1). Enzymes of folate metabolism bring one-carbon groups to the folate pool, oxidize/reduce the folate-bound groups, or utilize these groups in biosynthetic reactions. The role of folate enzymes in cancer is well established and some of them, including DHFR and thymidylate synthase, are canonical chemotherapeutic targets [35]. An additional association between folate enzymes and cancer is provided by epidemiologic studies, which linked SNPs in the *MTHFR* gene with the risk of several cancer types [23]. The combination of folate intake and SNPs in genes associated with methionine biosynthesis may contribute to breast [36] and gastric [37] cancer risk, indicating that folate intake-associated cancer risk can be further modified by gene-nutrient interactions. Towards this line, a cross-sectional analysis of 19 human studies indicated a role for folate enzymes and their SNPs in response to alcohol consumption [38]. The direct inhibitory effect of ethanol on the activities of MTHFR and MTR in an animal model was demonstrated as well [39]. As a likely cause of decreased liver SAM and reduced methylation capacity, this mechanism can contribute to carcinogenesis [23]. Of note, ethanol also decreases thymidylate synthase mRNA levels in regenerating liver after partial hepatectomy [40], the effect which could be translated into the impaired DNA synthesis and repair.

10.4 ALDH1L1 Role in Cancer

One of the most abundant folate enzymes is cytosolic 10-formyltetrahydrofolate dehydrogenase (FDH, ALDH1L1) [41]. Levels of this enzyme can reach about 1.2% of the total protein in rat liver cytosol [42, 43], suggesting an important role (proposed functions for the enzyme are summarized in Fig. 10.2). ALDH1L1 converts 10-formyl-THF to THF (tetrahydrofolate) and carbon dioxide in a NADP⁺-dependent reaction (Fig. 10.2). This reaction clears one-carbon groups (in the form of CO₂) from the cell thus limiting their flux toward folate-dependent biosynthetic reactions (Fig. 10.1) [44, 45]. It is also important for replenishing the pool of THF [46], which is the only folate coenzyme capable of accepting one-carbon groups and thus is central to folate metabolism [47]. In agreement with such function of ALDH1L1, genome-wide association studies revealed that SNPs in this gene are associated with serine to glycine ratio in serum [48] (THF is required for the reaction of the conversion of serine to glycine, Fig. 10.1). Furthermore, ALDH1L1 might regulate *de novo* purine biosynthesis [44, 49], formate degradation [5] and methylation status of the cell [45]. Another function originally proposed for this enzyme is to serve as the folate depot, though this hypothesis is primarily based on the phenomenon that the protein was purified in complex with THF [42].

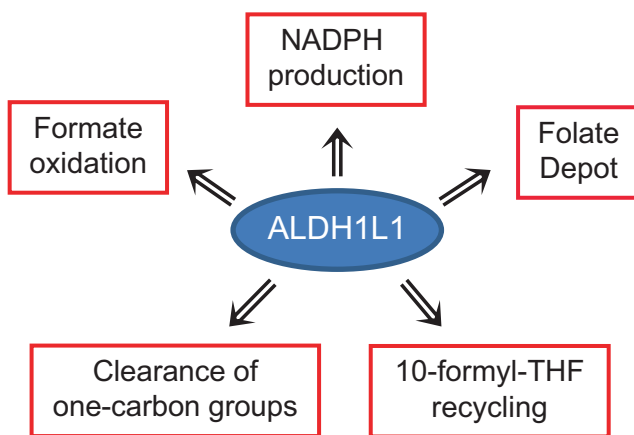


Fig. 10.2 Reaction catalyzed by ALDH1L1 and ALDH1L2 and proposed biological roles for the enzymes. *THF* tetrahydrofolate; *THF-CHO* 10-formyl-THF

ALDH1L1 is not ubiquitously expressed in human tissues: highest levels of its mRNA were detected in liver, kidney and pancreas while the levels in several tissues including placenta, spleen, thymus, small intestine, leukocytes, testis, and ovary were undetectable [44, 50]. Interestingly, ALDH1L1 is also differentially expressed in central nervous system during development: most quiescent cells in developing mouse brain are ALDH1L1 positive while proliferating cells do not express this protein [51]. Curiously, levels of this protein also significantly fluctuate (up to about seven-fold change) in the liver of golden-mantled ground squirrel depending on seasonal stages [52]. In further support of highly regulated expression of this protein, its levels were decreased in rat liver by clofibrate, a peroxisome proliferator [53] and increased in zebrafish embryos exposed to ethanol [54].

Perhaps most striking example of the ALDH1L1 regulation is its silencing in malignant tumors [44], which is achieved through methylation of the CpG island within the *ALDH1L1* promoter [55]. It contains 96 CpG pairs and covers the region between -525 and $+918$ bp of the *ALDH1L1* gene including the promoter, the entire exon 1, and a part of intron 1 immediately downstream of the exon. Bisulfite sequencing analysis revealed extensive methylation of the island (76%–95% of CpGs) in cancer cell lines. Analysis of the samples from patients with lung adenocarcinomas demonstrated methylation of the *ALDH1L1* CpG island in tumor samples and a total lack of methylation in respective normal tissues. The same phenomenon was observed in liver tissues: the CpG island was methylation free in DNA extracted from normal hepatocytes but was extensively methylated in a hepatocellular carcinoma. Levels of *ALDH1L1* mRNA and protein correlated with the methylation status of the island, with tumor samples demonstrating down-

regulation of expression or even complete silencing of the gene. The down-regulation of *ALDH1L1* mRNA in NSCLC (non-small cell lung cancer) [56], cervical cancer [57] and renal cell carcinoma [58] associated with the gene methylation was also demonstrated by microarray assays. The regulation of *ALDH1L1* through the promoter methylation could also be a common cellular response to the environmental conditions. Thus, it has been reported that the prolonged exposure to isoflavone through dietary supplementation significantly reduces *Aldh1l1* promoter methylation in rat mammary tissue [59]. In addition, the methylation of *ALDH1L1* could be responsible for the individual variation in the protein expression. For example, higher CpG methylation in the body of the *ALDH1L1* gene was significantly correlated with its lower transcript expression in normal breast tissue in women [60].

In agreement with the phenomenon that ALDH1L1 is down-regulated in proliferating tumors, re-expression of the protein in cancer cells produces drastic antiproliferative effects including cell cycle arrest and apoptosis [44, 49, 61–63]. These findings indicated that ALDH1L1 is a key regulator of proliferation and an implication has been made in the literature that this protein is a candidate tumor suppressor [44, 55, 57, 58, 64]. Furthermore, under-expression of this gene could be a marker of a more aggressive tumor phenotype. Thus, decreased expression of ALDH1L1 was associated with aggressive subtypes of sporadic pilocytic astrocytoma [64], poor prognosis in hepatocellular carcinoma [65], and low overall survival in neuroblastoma [66], while high expression of *ALDH1L1* mRNA correlates with better overall survival in breast cancer patients [67]. It should be mentioned that the association between decreased ALDH1L1 expression and malignant tumor progression could be cancer type-specific [68]. For example, though decreased expression of ALDH1L1 was demonstrated in NSCLC [55, 56], cervical cancer [57], renal cell carcinoma [58] and peripheral cholangiocarcinoma [69], the extent of its expression in other cancers is not clear. In line with the idea that ALDH1L1 prognostic role could be cancer type-specific, SNPs in the *ALDH1L1* gene were significantly associated with altered risk of breast cancer [70] and increased risk of hepatocellular carcinoma [71] and non-Hodgkin lymphoma [72–74] but no SNPs were associated with the risk of prostate cancer [75].

10.5 Role of Mitochondrial ALDH1L2 Enzyme in Cancer

Folate pathways are compartmentalized within the cell, mainly between cytoplasm and mitochondria [3, 76], though the compartmentalization was recently extended to the nucleus, where folate-dependent TMP biosynthesis takes place [77]. It has been suggested that the mitochondrial pathways mainly serve to provide one-carbon groups, in the form of formate, for incorporation into the cytosolic folate pool where they are utilized for biosynthetic purposes [3]. While some folate-dependent reactions are unique to cytoplasm or mitochondria, several of them take place in both compartments and are catalyzed by homologous enzymes, which are products of distinct genes [3, 78]. The oxidation of 10-formyl-THF to THF and CO₂ is one of

such reactions. Mitochondrial 10-fTHF dehydrogenase is encoded by the *ALDH1L2* gene, which originated via the duplication of the *ALDH1L1* gene and acquired a mitochondrial leader sequence [50]. Accordingly, two proteins share about 72% identity of the amino acid sequence and are close structurally and enzymatically [50, 79]. Their biological roles, however, could be quite different. While cytosolic ALDH1L1 is involved in the regulation of cellular proliferation, through the control of folate pools, ALDH1L2 is the key enzyme to provide reduced NADPH in mitochondria [12]. NADPH produced in this mitochondrial reaction is required for the reduction of oxidized glutathione, and the loss of ALDH1L2 shifts the ratio of GSH/GSSG. This in turn decreases the capacity of mitochondria to eliminate reactive oxygen species leading to oxidative stress [19].

The *ALDH1L2* gene was discovered relatively recently and its studies are limited so far. Of note, it can be up-regulated by certain drugs, though mechanism of this response were not studied. For example, *ALDH1L2* mRNA levels are strongly increased (up to 6.8-fold) in immortalized human B cells treated with ER stress inducers thapsigargin or tunicamycin [80]. *ALDH1L2* mRNA was also significantly up-regulated in human adrenocortical NCI-H295R cells treated with mitotane, an adrenolytic drug extensively used in combination with other cytotoxic drugs and as an adjuvant monotherapy in the treatment of adrenocortical carcinoma [81]. This effect, however, is hard to correlate with the pharmacological action of the drug. *ALDH1L2* mRNA was also up-regulated more than three-fold in mouse neonatal ovaries exposed to 3-methylcholanthrene, a potent ovotoxicant [82]. The question of whether the regulatory effects of these drugs on the *ALDH1L2* gene are associated with the cellular response to oxidative stress awaits further investigation. Curiously, the *ALDH1L2* gene expression was lost in CCL-131 Neuro-2a malignant neuroblastoma cells at acidic pH [83]. Likewise, levels of the ALDH1L2 protein were dramatically decreased in nonalcoholic steatohepatitis in rats fed fat-rich diet [84]. Another study has reported a different effect for ALDH1L2: the protein was elevated about two-fold in fibroblasts of the patient with short-chain acyl-CoA dehydrogenase deficiency [85]. Thus, it appears that levels of ALDH1L2 inversely correlate with fatty acid oxidation. It has been also suggested that both acidic pH and fatty acid oxidation deficiency induce metabolic reprogramming, driving the switch to OXPHOS and less glucose utilization in the former case and to biosynthetic processes in the latter case. In this regard, ALDH1L2 could be differentially regulated depending on the cellular demand for the energy production. Alternatively, the regulation could be driven by ROS levels as well as the ratio of reduced/oxidized glutathione but precise mechanisms controlling ALDH1L2 expression remain elusive.

Of note, ALDH1L2 has a different tissue-expression pattern than ALDH1L1 and in contrast to the cytosolic enzyme is highly expressed in cancer cell lines [50]. It has been recently reported that ALDH1L2 is up-regulated in human colorectal tumor tissues compared to normal tissues [86]. Furthermore, rates of recurrence-free survival and overall survival in patients with high expression of ALDH1L2 tend to be lower than in patients with low expression of the enzyme, the situation opposite to cytosolic ALDH1L1. Considering that ALDH1L2 is a mitochondrial protein, it should be pointed out that numerous recent studies specifically underscored the

role of mitochondrial folate pathways in cancer with the emphasis on folate-dependent metabolism of serine and glycine [14–16, 87–90]. In this regard, ALDH1L2 might be an important component providing THF for the serine to glycine conversion in mitochondria and for glycine degradation (Fig. 10.1).

Intriguingly, *ALDH1L2* was implicated as a metastasis-regulatory gene [18]. Thus, in a mouse melanoma metastasis model, a striking increase in the expression of this protein in liver, pancreas and lung metastases compared to subcutaneous tumors has been shown [18]. Of note, other folate enzymes tested in this study did not demonstrate such trend. In further support of the metastasis-promoting role of ALDH1L2, the silencing of the gene in melanoma by shRNA significantly reduced the frequency of circulating melanoma cells in blood and overall metastatic burden [18]. Interestingly, the reduced invasion of MDA-MB-435 cells after the treatment with anti-inflammatory agent indomethacin was associated with a significant elevation of *ALDH1L2* mRNA [91]. While the mechanism by which indomethacin leads to *ALDH1L2* gene up-regulation is not clear, it could be a compensatory cellular response to the increased ROS production caused by the drug. The cytosolic isoform, ALDH1L1, could be also associated with the metastatic potential of cancer cells [92]. In contrast to ALDH1L2, however, the cytosolic isoform inhibits cellular migration and invasion, the phenomenon rather associated with the decreased metastasis [93].

10.6 Effect of Ethanol on ALDH1L1/L2 Genes and Proteins

One of the folate-related effects of alcohol consumption could be the interaction of ethanol or its metabolites with folate enzymes [39]. Since the decrease of the ALDH1L1 expression could be associated with tumor promotion, metabolites inhibiting the activity of the enzyme or causing down-regulation of its expression would have pro-tumorigenic effect. Though studies of the effect of ethanol on ALDH1L1 are scarce, a role for the enzyme in mediation of the effect of alcohol intake on oral carcinogenesis has been proposed [94]. In another study, levels of ALDH1L1 were changed after liver transplant in recipients with alcoholic cirrhosis [95], implying the effect of chronic alcohol consumption on the enzyme. Interestingly, a recent study reported that alcohol consumption is associated with differentially methylated CpGs in the *ALDH1L1* gene in breast tissue of healthy women [60]. Furthermore, women carrying an allelic variant of the gene were more likely to have hypermethylated *ALDH1L1*, the phenomenon correlated with lower gene expression. These findings point toward a potential mechanism by which alcohol implements its folate-mediated tumorigenic effect in mammary tissue.

Chronic ethanol ingestion was reported to decrease hepatic ALDH1L1 dehydrogenase activity in rats [96]. The ethanol treatment also affected ALDH1L1 activities in brain and hepatic tissues of chicken embryos [97, 98]. It has been further demonstrated that the ALDH1L1 enzymatic activity is inhibited by acetaldehyde *in vitro* [99], which could be a mechanism of the ethanol effect on the enzyme and one of the mechanisms by which alcohol consumption changes folate status. It should be

noted that ALDH1L1 is capable, at least *in vitro*, to metabolize acetaldehyde to acetic acid [100], which would argue against such inhibitory effect. This reaction still could interfere with the folate-related catalysis of the enzyme thus affecting folate metabolism. ALDH1L1 has been also reported as a target for acetaminophen, which covalently modifies a key cysteine of the enzyme; this effect could contribute to the drug toxicity [101]. Since excessive alcohol consumption is a risk factor for acetaminophen-induced hepatotoxicity [102], ALDH1L1 could be a dual target towards liver damage. Whether this effect would contribute to carcinogenesis is not clear at present. Interestingly, ALDH1L1 can also counteract the effect of ethanol on folate metabolism by protecting THF from degradation [103]. The metabolism of acetaldehyde by xanthine oxidase generates superoxide radicals, which can cleave folates [104]. Of note, 5-methyl-THF, the most common form of natural folate, is highly susceptible to the degradation by superoxide [104]. In agreement with the mechanism of folate protection by ALDH1L1, up-regulation of the *ALDH1L1* gene prevented folate degradation and alleviated the oxidative stress induced by ethanol exposure in zebrafish embryos [54].

The role of ALDH1L2 in alcohol response and ethanol metabolism is even less clear due to the lack of corresponding studies. By analogy with the *ALDH1L1* gene, it can be hypothesized that ALDH1L2 is relevant to the interaction between ethanol and folate metabolism. Indeed, the implication that this gene is a part of alcohol dependence mechanism has been made in the literature [105]. Thus, in the study of genome-wide DNA methylation in discordant sib pairs with alcohol dependence, the deregulation of *ALDH1L2* gene through the promoter hypomethylation was associated with alcohol dependence [105].

10.7 Conclusion

ALDH1L1 and ALDH1L2 are key enzymes in the regulation of folate metabolism as well as downstream processes associated with folate-dependent biochemical reactions. While both enzymes catalyze the same reaction, their compartmentalization leads to the differential effect on overall cellular metabolism, regulating either reduced folate pools and purine biosynthesis (cytosolic ALDH1L1) or NADPH production and oxidative stress (mitochondrial ALDH1L2). Both enzymes were implicated in the proliferation of malignant tumors, though with opposite roles, tumor suppression in the case of the cytosolic enzyme and metastasis promotion in the case of the mitochondrial isoform. These enzymes were also implicated in the cellular response to alcohol consumption. Taking into account that both enzymes have essentially identical structural organization and enzymatic mechanism, it is likely that the direct effect of ethanol or its metabolites on ALDH1L1 and ALDH1L2 would be similar in both cases. However, considering differential regulation of the two isoforms, the overall effect of alcohol consumption on two enzymes would be more complex and not so direct. Clearly, more studies are needed to address the role of ALDH1L1 and ALDH1L2 in biology of malignant tumors and in potential mediation of the alcohol effect.

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