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ALDH2 in Alcoholic Heart Diseases: Molecular Mechanism and Clinical Implications

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Abstract

Alcoholic cardiomyopathy is manifested as cardiac hypertrophy, disrupted contractile function and myofibrillary architecture. An ample amount of clinical and experimental evidence has depicted a pivotal role for alcohol metabolism especially the main alcohol metabolic product acetaldehyde, in the pathogenesis of this myopathic state. Findings from our group and others have revealed that the mitochondrial isoform of aldehyde dehydrogenase (ALDH2), which metabolizes acetaldehyde, governs the detoxification of acetaldehyde formed following alcohol consumption and the ultimate elimination of alcohol from the body. The ALDH2 enzymatic cascade may evolve as a unique detoxification mechanism for environmental alcohols and aldehydes to alleviate the undesired cardiac anomalies in ischemia-reperfusion and alcoholism. Polymorphic variants of the ALDH2 gene encode enzymes with altered pharmacokinetic properties and a significantly higher prevalence of cardiovascular diseases associated with alcoholism. The pathophysiological effects of ALDH2 polymorphism may be mediated by accumulation of acetaldehyde and other reactive aldehydes. Inheritance of the inactive ALDH2*2 gene product is associated with a decreased risk of alcoholism but an increased risk of alcoholic complications. This association is influenced by gene-environment interactions such as those associated with religion and national origin. The purpose of this review is to recapitulate the pathogenesis of alcoholic cardiomyopathy with a special focus on ALDH2 enzymatic metabolism. It will be important to dissect the links between ALDH2 polymorphism and prevalence of alcoholic cardiomyopathy, in order to determine the mechanisms underlying such associations. The therapeutic value of ALDH2 as both target and tool in the management of alcoholic tissue damage will be discussed.

Keywords

Alcohol; ALDH2; enzyme; metabolism; myocardial; transgenic mice

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1. Introduction - Alcohol and cardiac complications

Alcoholism remains the most widespread and devastating form of substance abuse in the United States and the rest of world. While light to moderate alcohol consumption may be associated with a reduced risk of cardiovascular diseases possibly through reduced coronary artery-related events (Djousse & Gaziano, 2008; Guo & Ren, 2010; Kloner & Rezkalla, 2007; O'Keefe et al., 2007; Skotzko et al., 2007; Xie et al., 2011), long-term alcohol abuse or binge drinking results in detrimental consequences to the heart, leading to mitochondrial defects, cell death, contractile dysfunction, heart rate variability, arrhythmias and cardiac remodeling (Guo & Ren, 2010; Lang et al., 2005; Laonigro et al., 2009; O'Keefe et al., 2007; Preedy et al., 2001; Richardson et al., 1998; Romanowicz et al., 2011; Spies et al., 2001). Heavy, chronic alcohol consumption (> 90 g of ethanol per day for > 5 years) (Laonigro et al., 2009; Piano, 2002) usually results in cardiac remodeling and contractile dysfunction characterized by dilated cardiomyopathy, also known as alcoholic cardiomyopathy, which represents an important source of the morbidity and mortality associated with alcoholism (Awtry & Philippides 2010; Iacovoni et al., 2010; Laonigro et al., 2009; Liang et al., 1999; Spies et al., 2001; Vary et al., 2008).

It is estimated that one out of every three alcohol-dependent individuals (alcoholics) displays alcoholic cardiomyopathy of varying severity (Iacovoni et al., 2010; Laonigro et al., 2009; Ren & Wold, 2008; Spies et al., 2001). This distinct form of congestive heart failure is responsible for 21-36% of all cases of non-ischemic dilated cardiomyopathy in Western society. Without complete abstinence, the 4 year mortality for alcoholic cardiomyopathy is close to 50% (Laonigro et al., 2009). Alcoholic cardiomyopathy, or alcoholic heart muscle disease, is often characterized by cardiac hypertrophy, disruption in myofibrillary architecture, reduced myocardial contractility (and resultant reductions in ejection fraction and stroke volume), myocardial fibrosis (Wang et al., 2005) as well as enhanced risk of arrhythmias, stroke and hypertension (Djousse et al., 2004; Higashiyama et al., 2011; Jones, 2005; Romanowicz et al., 2011; Schoppet & Maisch, 2001). Apart from the history of alcoholism these features are consistent with other dilated cardiomyopathies (Skotzko et al., 2009; Spies et al., 2001).

Clinical studies have shown that the pathology of alcoholic cardiomyopathy can be reversed by abstinence from alcohol (Piano, 2002; Skotzko et al., 2009). Nonetheless, this reversibility is apparently lost once the disease has progressed beyond some, as yet poorly defined point of severity (Jacob et al., 1991; Seiva et al., 2009). The diagnosis of alcoholic cardiomyopathy is made on the basis of deteriorating cardiac function, increased heart size and a history of alcohol abuse (Iacovoni et al., 2010; Laonigro et al., 2009). The occurrence of cardiomyopathy in chronic alcoholism has been well documented (Piano, 2002; Ren & Wold, 2008; Skotzko et al., 2009; Spies et al., 2001) although the precise cause of the myopathy is still poorly understood.

Individuals with alcoholic cardiomyopathy do not usually suffer from vitamin or nutritional deficiencies, suggesting the development of alcoholic cardiomyopathy is a result of alcohol intake rather than malnutrition (Laonigro et al., 2009). Electron microscopy examination of alcoholic hearts reveals a loss or disruption of myofibrils and dilated sarcoplasmic reticulum (SR) (Jaatinen et al., 1994). Mitochondria, which are considered the main target organelles for ethanol and its metabolite (Guo & Ren, 2010), display enlargement and disorganized cristae (Zhang et al., 2010). These morphological and functional cardiac defects will eventually result in heart failure. In addition, ample amounts of clinical and experimental findings have confirmed alcoholic damage in the heart originating from non-myogenic alterations such as tachycardia, arrhythmias, hypertriglyceridemia, hypertension and altered sympathetic tone (Bessembinders et al., 2011; George & Figueredo, 2010; Hering et al.,

2011; Ohira et al., 2009). Along the same line, alcohol misuse is also regarded as one of the excess burdens associated with certain sub-clinical vascular diseases (Hamer et al., 2010; Turcotte et al., 2002), which may affect cardiac function indirectly via undesirable hemodynamic regulation.

At present, a number of theories have been postulated for the onset and development of alcoholic cardiomyopathy including oxidative damage, deposition of triglycerides, altered fatty acid extraction, decreased myofilament Ca^{2+} sensitivity, impaired protein metabolism and mitochondrial anomalies (Awtry & Philippides, 2010; Djousse & Gaziano, 2008; Djousse et al., 2009; Iacovoni et al., 2010; Jing et al., 2011; Laonigro et al., 2009; Ren & Wold, 2008). Oxidative stress, apoptosis and mitochondrial damage have been observed in alcohol-induced myocardial dysfunction (Doser et al., 2009; Ge et al., 2011; Guo & Ren, 2010; McDonough, 2003). Altered intracellular Ca^{2+} homeostasis has been proposed to underscore the compromised mechanical function in alcoholic cardiomyopathy (Ren & Wold, 2008; Zhang et al., 2003).

Recent studies from our lab as well as others have revealed the participation of a number of intracellular Ca^{2+} cycling proteins, including sarco(endo)plasmic reticulum Ca^{2+} -ATPase (SERCA), Na⁺-Ca²⁺ exchanger and phospholamban in the impaired intracellular Ca^{2+} handling following alcohol consumption (Li et al., 2006; Oba et al., 2008; Zhang et al., 2003). The dynamic balance between protein synthesis and protein degradation is believed to play an essential role in the heart under normal and alcoholic conditions. Both actin and myosin content are decreased while the levels of β -myosin are elevated in the heart after prolonged alcohol consumption (Lang et al., 2005). More importantly, the loss of myofibrillar proteins occurs prior to the appearance of any detectable echocardiographic abnormalities in the heart (Lang et al., 2005; Vary & Summer, 2004), suggesting a critical role of protein synthesis in the pathogenesis of alcoholic cardiomyopathy.

Recent evidence from our laboratory also suggested that alcoholism may promote autophagy in an AMPK-dependent manner (Ge & Ren, 2011), although further evidence of alcoholismrelated changes in protein quality control machineries, such as ubiquitination and proteolysis, is still lacking in alcoholic hearts. Ethanol and its enzymatic metabolism also play a pivotal role through direct toxicity or indirect action of cell stress signaling activation. For example, the major ethanol metabolite acetaldehyde may contribute to cardiac dysfunction, hypertrophy and heart failure by either its direct toxicity or promoting elevated levels of catecholamines and reactive oxygen species (ROS) (Zhang et al., 2004, 2010). Other scenarios have also been speculated for alcoholic cardiomyopathy such as aldehydeprotein adduct formation (Niemela, 2001), acetaldehyde-derived DNA adduct formation (Yu et al., 2010), accumulation of fatty acid ethyl esters (Patel et al., 1997), or modifications of lipoprotein and apolipoprotein particles (Hannuksela et al., 2002).

Despite the ample clinical and experimental evidence endorsing most of these theories for the pathogenesis of alcoholic cardiomyopathy, none of these mechanisms may be considered as the ultimate culprit responsible for the development of alcoholic cardiomyopathy. It appears that the susceptibility to the detrimental effect of alcohol intake is a result of the complex interplay between genes and environmental factors (the latter including alcohol itself and other nutrients) (Crabb et al., 2004). As illustrated in Fig. 1, alcohol is metabolized mainly through a two-step enzymatic process involving alcohol dehydrogenase (ADH) and aldehyde dehydrogenase (ALDH), which break down ethanol into acetaldehyde and then acetate (Crabb et al., 2004; Manzo-Avalos & Saavedra-Molina, 2010). These two enzymes involved in alcohol metabolism are polymorphic and affect the elimination rate of ethanol or its metabolite acetaldehyde. As a result, genetic polymorphisms of ADH and ALDH2 alter the susceptibility to ethanol intake and the risk of alcoholism and alcoholic complications

(Pautassi et al., 2010). A highly active ADH or low (or mutant) ALDH protects against alcoholism but predisposes the organism to more severe alcoholic damage, an effect related to a pre-steady state burst in arterial acetaldehyde (Pautassi et al., 2010; Ren, 2007). The main ALDH isoform – the mitochondrial isozyme of ALDH or ALDH2 – and its cardiac effects along with its genetic variation are the subject of the present review.

2. ALDH2, metabolism of ethanol and acetaldehyde

2.1. Enzymology of alcohol metabolism

The effect of alcohol (ethanol) in various tissues depends on its blood concentration over time. After oral absorption, alcohol is readily absorbed by the gastrointestinal tract by passive diffusion through the stomach wall ($\sim 20\%$) or the small-intestinal wall ($\sim 80\%$). Elimination of alcohol is achieved mostly through metabolism (95-98%) with a small unchanged fraction being excreted through exhalation, sweating or urination (Manzo-Avalos & Saavedra-Molina, 2010). Ethanol distributed in the body fluid space is metabolized mainly through the hepatic oxidation catalyzed by the ADH, ALDH, cytochrome P450 2E1 (CYP2E1) and catalase enzymes, as depicted in Fig. 1 (Manzo-Avalos & Saavedra-Molina, 2010; Wu & Cederbaum, 2009; Wu et al., 2010). In particular, alcohol is metabolized into acetaldehyde (CH₃CHO) by ADH and CYP2E1 in cytoplasm and microsomes, respectively. Although CYP2E1 is pretty important in ethanol metabolism and toxicity, and is responsible for a number of ethanol-related drug interactions, it will not be emphasized in our present review. Due to the high capacity and the relatively high affinity ($K_m = 0.05-0.1 \text{ g/L}$) of ADH in hepatocytes, the enzyme gets saturated after only a few drinks, which decreases the rate at which ethanol is effectively metabolized. Once formed in the liver, acetaldehyde is oxidized by the mitochondrial isoform of ALDH (ALDH2) in an irreversible reaction to acetate. ALDH2 has a very low K_m value, which makes the elimination of toxic acetaldehyde soon after its formation highly efficient. The activated form of acetate, acetyl CoA, can be further metabolized into ketone bodies, fatty acids, amino acids and steroids in addition to oxidation in the Krebs cycle, leading to the formation of CO_2 and water as the end-products of ethanol oxidation (George & Figueredo, 2010; Manzo-Avalos & Saavedra-Molina, 2010).

Rates of ethanol metabolism by ADH and ALDH2 enzymes are, therefore, deemed critical in determining its toxicity because the intermediate product of this pathway acetaldehyde is highly toxic (ten times higher than ethanol). The maximal activities of ADH and ALDH are similar in the liver, making a comparable contribution for both enzymes in the overall control of the rate of alcohol oxidation (George & Figueredo, 2010; Manzo-Avalos & Saavedra-Molina, 2010). Both enzymes use the cofactor nicotinamide adenine dinucleotide (NAD⁺), which is reduced to NADH. As a result, the ratio NADH/NAD⁺ is significantly elevated following ethanol oxidation, resulting in an altered cellular redox state and adverse effects associated with alcohol consumption (Manzo-Avalos & Saavedra-Molina, 2010; McDonough, 2003).

In human subjects with ADH and ALDH2 variants, the rate of ethanol oxidation may be substantially influenced by enzyme kinetic properties such as the K_m , V_{max} and sensitivity to product inhibition of the variants (Crabb et al., 2004). Thus it is possible that components of alcohol metabolism and the concentrations of metabolic intermediates such as acetaldehyde may change despite an unaltered alcohol elimination rate under certain conditions.

2.2. ALDH2, alcohol metabolism and genetic polymorphisms

ALDH2 is one of 19 members of the ALDH gene family in humans that play a crucial role in the oxidation and detoxification of reactive aldehydes including the ethanol metabolite

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acetaldehyde in various organs and cells (Budas et al., 2009). Besides metabolism of acetaldehyde, ALDH2 also serves as a metabolic enzyme in the detoxification of other reactive aldehydes such as 4-hydroxy-2-nonenal (4-HNE) and conversion of nitroglycerin (from glyceryl trinitrate to 1,2-glyceryl dinitrate) (Budas et al., 2010; Chen et al., 2010; Ren, 2007; Zhang et al., 2004). Two major isoforms of ALDH, cytosolic and mitochondrial, are present and can be distinguished by electrophoretic mobilities, kinetic properties, and subcellular localizations.

The gene for mitochondrial ALDH, or ALDH2, in humans is found on chromosome 12. This gene encodes a mitochondrial isoform with a low K_m for acetaldehyde, and is localized in the mitochondrial matrix. All Caucasians studied are deemed homozygous for ALDH2 while approximately 50% of Asians are heterozygous and possess only one normal copy of the ALDH2 gene and one mutant copy encoding an inactive mitochondrial isozyme. Epidemiological studies have revealed a remarkably reduced risk of alcoholism due to alcohol intolerance, albeit with an increased risk of alcoholic complications, in Asians as compared with Caucasians; this is mainly associated with the greatly reduced activity of the mutant ALDH2 isozyme (Nishida et al., 2004; Peng & Yin, 2009). Similarly, incidence rates for alcoholic complication are greater in African-Americans and Native-Americans than in Caucasians, largely due to genetic polymorphisms in ADH and ALDH2, nutrition, and other factors (Chou et al., 1999; Russo et al., 2004). Although genetic variation in ALDH2 has been reported to affect alcohol metabolism in Europeans, it does not appear that such genetic variation in ALDH2 leads to the alteration in alcohol sensitivity, consumption, or risk of dependence in Europeans (Dickson et al., 2006). ALDH2 genetic polymorphisms have been shown to contribute to the effects of alcohol intake on liver (Takeshita et al., 2000) and bone formation (Shimizu et al., 2011). A meta-analysis of seven East Asian populations showed the association between ALDH2*2 allele and low HDL-C level (Hao et al., 2010). The ALDH2*2 allele encodes a protein with an amino acid change from glutamate to lysine (derived from the ALDH2*1 allele) and devoid of enzymatic activity. Allelic variation of ALDH genes, especially deficiency in ALDH2 due to such a point mutation in the active ALDH2*1 gene, alters blood acetaldehyde levels and decreases vulnerability for the development of alcoholism (Chen et al., 2009; Peng et al., 1999, 2002, 2007). Up to 50% of Asians carry mutant alleles of ALDH (ALDH2*2/1 and ALDH2*2/2) that resulted from a single point mutation of the active ALDH2*1 gene, producing a \sim 10 fold increase in blood acetaldehyde levels in the ALDH2-deficient individuals following alcohol intake compared with the ALDH2-intact populations (Nishimura et al., 2002; Peng & Yin, 2009; Yin & Peng, 2007).

Table 1 summarizes some of the most commonly seen biological and pathophysiological effects resulting from ALDH2 genetic variation. Interestingly, due to the acetaldehyde-associated feeling of discomfort, the gene of *ALDH2*2/2* may protect against the development of alcohol dependence and alcohol-related disease by discouraging alcohol consumption (Peng & Yin, 2009). In addition to the cardiac depressant response elicited by acetaldehyde as mentioned earlier, contribution of acetaldehyde to alcoholic cardiomyopathy was substantiated by the fact that the ALDH inhibitor, cyanamide, potentiates alcohol intake-induced rise of plasma cardiac troponin-T levels, a key index for myocardial cell death. It is believed that homozygosity for the *ALDH2*2* allele should help to inhibit the development of alcoholism. After a small dose of alcohol, cardiac and extracranial/intracranial arterial hemodynamic parameters as well as self-rated subjective sensations were strikingly responsive in homozygous *ALDH2*2* individuals as evidenced by pronounced cardiovascular hemodynamic effects as well as subjective perception of general discomfort for as long as 2 hr after alcohol ingestion.

3. Acetaldehyde and the heart

As mentioned above, acetaldehyde is formed when ethanol is oxidized primarily through cytosolic ADH (Fig. 1). It is a chemically reactive organic compound with a low molecular weight (44.05 Da) and boiling point (21°C). While liver is considered the primary site of oxidation, other organs (including the heart) participate in ethanol metabolism. Other than classic ethanol metabolism, acetaldehyde may be produced endogenously through the degradation of biological molecules such as that occurring during lipid peroxidation, in a manner similar to other reactive aldehydes including 4-HNE and malondialdehyde (Uchida, 2000; Wang et al., 2008). Acetaldehyde is about ten times more toxic than ethanol based on its LD₅₀ value. An ample amount of recent evidence from our lab and others has consolidated a pivotal role for acetaldehyde in the pathogenesis of alcoholic cardiomyopathy (Aberle et al., 2003; Aberle & Ren, 2003; Brown et al., 1999, 2001; Cai, 2008; Guo & Ren, 2010). Acetaldehyde may elicit a direct toxic effect on the heart or react with amino, hydroxyl, and sulfhydryl groups to interfere with or modify the structure and function of macromolecules such as proteins and enzymes.

Elevated circulating and cardiac acetaldehyde levels are seen in individuals consuming excessive amounts of alcohol (Espinet & Argiles, 1984; Hintz et al., 2003; Jankala et al., 2000; Nishimura et al., 2002; Watanabe et al., 1985). Moreover, blood acetaldehyde levels are found to be much higher in alcohol-dependent individuals after alcohol administration (Nuutinen et al., 1983; Oba et al., 2005). Impaired ALDH capacity such as in ALDH2 polymorphism may predominantly contribute to the elevated blood acetaldehyde levels (Nuutinen et al., 1983). Blood acetaldehyde levels were found to be $\sim 5 \mu$ M in normal subjects and 30 to 125 μ M in Asians with defective ALDH2 following heavy alcohol intake (Chen et al., 1999; Nishimura et al., 2002; Watanabe et al., 1985).

Elevation in blood acetaldehyde levels may not be directly and proportionally correlated with the rise in blood alcohol levels due to the apparent difference in ethanol metabolism in various populations. It is perceived that blood levels of acetaldehyde rather than ethanol play a more significant role in the pathogenesis of alcoholic cardiomyopathy (Zhang et al., 2004). Acetaldehyde may trigger cardiac hypertrophy or dilated cardiomyopathy associated with a significant increase in the hypertrophic marker skeletal actin and ANF (Li & Ren, 2008; Liang et al., 1999). Direct effects of acute (5 to 10 min) acetaldehyde exposure on cardiovascular function have been extensively studied (Aberle & Ren, 2003; Aistrup et al., 2006; Brown et al., 1999, 2001; Brown & Savage 1996; Ren et al., 1997; Savage et al., 1995). Acetaldehyde produces vasoconstriction and positive inotropic and chronotropic responses at concentrations of 3 mM or below. Higher concentrations of acetaldehyde (>3 mM) elicit cardiac depression, vasodilatation and hypotension (Brown & Carpentier, 1989, 1990). The acetaldehyde-induced negative inotropic response in the heart seems to be associated with decreased SR Ca²⁺ release (Ren et al., 1997; Savage et al., 1995) or inhibition of voltage-dependent Ca²⁺ channels (Morales et al., 1997). Our earlier studies revealed that acetaldehyde depresses cardiomyocyte contractile amplitude, maximal velocity of contraction/relaxation, and prolonged duration of relaxation and intracellular Ca²⁺ clearance (Aberle et al., 2004; Aberle & Ren, 2003; Ren et al., 1997). In addition to its apparent cardiac toxicity, acetaldehyde may also interfere with gene expression and protein synthesis in the heart (Siddig et al., 1993). Acetaldehyde may regulate the expression of apoptosis-related genes en route to development of alcoholic cardiomyopathy (Fernandez-Sola et al., 2006; Jankala et al., 2002). However, due to the impracticality of administering acetaldehyde to humans, it is difficult to assess the pathophysiological and epigenetic effects of acetaldehyde exposure in human subjects to determine its role in alcoholic cardiomyopathy. On the other hand, using metabolic inhibitors to alter acetaldehyde levels

has been proven to be rather nonspecific, ineffective, toxic and difficult to manage (Preedy et al., 2007; Ren, 2007; Ren & Wold, 2008).

To better assess the role of acetaldehyde in alcohol-induced tissue damage, cardiac-specific ADH overexpression transgenic mice were generated in our labs (Duan et al., 2002; Hintz et al., 2003; Liang et al., 1999). The mice with overexpression of ADH driven by the α -myosin heavy chain promoter displayed exacerbated alcoholic cardiomyopathy following alcohol consumption (Duan et al., 2002; Hintz et al., 2003; Liang et al., 1999). Moreover, ADH exacerbated alcohol exposure-induced mitochondrial dysfunction manifested as decreased mitochondrial membrane potential (MMP) and accumulation of mitochondrial O_2^{-} . Myocardium from ethanol-treated mice displayed enhanced apoptosis shown as elevated expression of Bax and Caspase-3 and decreased expression of Bcl-2, the effects of which with the exception of Caspase-3 were augmented by ADH. ADH accentuated ethanolinduced increase in the mitochondrial death domain components pro-caspase-9 and cytochrome c in the cytoplasm (Guo & Ren, 2010), suggesting that acetaldehyde toxicity possibly through mitochondrial damage is permissive to the development of alcoholic cardiomyopathy. Our study further revealed that the ADH transgene-accentuated cardiac contractile depression in response to ethanol exposure was more pronounced in females than males despite similar cardiac acetaldehyde levels between the two genders following alcohol challenge (Duan et al., 2003). These findings attribute a role of acetaldehyde in the genderrelated difference of alcoholic cardiomyopathy. In addition, ADH transgene itself does not affect morphological, mechanical and intracellular Ca²⁺ properties, suggesting that the transgene is not innately harmful. Moreover, the NADH/NAD+ ratio was similar in ADH and FVB wild-type mice chronically consuming alcohol (Liang et al., 1999), thus not favoring a key role of depletion of NAD⁺ as an adequate factor for enhanced cardiac damage in ADH transgenic mice after chronic alcohol intake.

Although the availability of ADH transgenic mice has greatly supported the acetaldehyde theory in the development of alcoholic cardiomyopathy, caution needs to be taken in data interpretation. Acetaldehyde often initiates cell and tissue injury at a level of 50 to 100 μ M or higher. However, the concentrations of acetaldehyde usually achieved in the body are in the low micromolar range following moderate ethanol intoxication (Tominaga, 2009; Tsukamoto et al., 1989). Certain tissues such as the brain exhibit an even lower level of acetaldehyde. Therefore, the jury is still out as to whether acetaldehyde is the main mediator of cytotoxic effects induced by ethanol. Other hypotheses postulated for alcoholic cardiomyopathy include oxidative damage, lipid peroxidation, altered membrane integrity as well as acetaldehyde-induced hemodynamic effects in the vasculature (Ren et al., 2002; Ren & Wold, 2008; Zhang et al., 2004). These pathological processes may work in concert with acetaldehyde to produce a synergistic effect on the function of protein and membrane phospholipids following alcohol intake (Cederbaum et al., 2009; Wu & Cederbaum, 2009; Wu et al., 2010). Given the absence of convincing human case study data on heart function following chronic alcohol intake, it is still premature to conclude that acetaldehyde is the ultimate cause of alcoholic cardiomyopathy.

4. ALDH2 and cardiac function in alcoholism

Public health guidelines usually recommend avoidance of excessive alcohol consumption in order to lessen the alcohol-associated health burden (Russo et al., 2004). In particular, alcoholism is an avoidable risk factor for cancer (Druesne-Pecollo et al., 2009). Functional variants in genes involved in alcohol metabolism lead to dramatic differences in exposure to carcinogenic acetaldehyde, suggesting a likely interaction of genetic susceptibility and alcoholism in cancer. Polymorphisms in alcohol metabolism alter folate metabolism and thus cancer risk. Not surprisingly, inactive or mutant forms of ALDH2 are considered an

independent risk factor for aerodigestive tract cancers including carcinomas of the pancreas, liver and esophagus due to the carcinogenicity of acetaldehyde (Druesne-Pecollo et al., 2009; Yang et al., 2010). Fig. 2 summarizes the spectrum of pathophysiological and behavioral effects of ALDH2 in multiple organ systems.

Substantial clinical and experimental evidence recently revealed a novel beneficial role of ALDH2 in the pathological process of cardiovascular diseases including ischemiareperfusion injury, arrhythmia and alcoholism (Budas et al., 2009; Chen et al., 2008, 2010; Doser et al., 2009; Koda et al., 2010; Ma et al., 2009, 2010; Ren et al., 2009). To better understand the role of ALDH2 in the onset and development of alcoholic cardiomyopathy, we made transgenic mice overexpressing low K_m ALDH2 using the chicken β-actin promoter to achieve non-specific overexpression of the enzyme (Doser et al., 2009). The cardiac-specific α -myosin heavy chain promoter was not chosen for ALDH2 overexpression because diffusion of acetaldehyde from peri-cardiac regions would easily offset the facilitated acetaldehyde removal from cardiac tissue. Reports from our lab have provided convincing evidence that ALDH2 is capable of attenuating both acute and chronic alcohol exposure-induced myocardial morphological and functional injury (Doser et al., 2009; Li & Ren, 2008; Ma et al., 2009). In the absence of alcohol intake, the ALDH2 transgene did not exhibit any effect on myocardial and cardiomyocyte function or any of the other biochemical markers tested. Chronic alcohol intake triggered cardiac geometric and contractile dysfunction including decreased left ventricular wall thickness and septal thickness, enlarged left ventricular systolic and diastolic diameters, reduced fractional shortening, cardiomyocyte peak shortening, maximal velocities of contraction and relaxation as well as prolonged relaxation duration associated with dysregulated intracellular Ca²⁺ release and SR Ca²⁺ uptake (Doser et al., 2009). Interestingly, myocardium and cardiomyocytes from ALDH2 transgenic mice displayed mitigated alcohol-induced mechanical anomalies. Oxidative stress, as indicated by lipid peroxidation and protein carbonyl formation, was significantly elevated in hearts and other tissues in wild-type FVB mice following chronic ethanol consumption, the effects of which were attenuated by the ALDH2 transgene. These findings are somewhat consistent with the previous findings of myopathic alteration following alcohol intake featured by compromised myocardial contractility (Iacovoni et al., 2010; Ma et al., 2009; Skotzko et al., 2009; Spies et al., 2001; Zhang et al., 2004). Several hypotheses have been put forward with regards to chronic alcohol intake-induced cardiac anomalies including lipid peroxidation (Hintz et al., 2003), oxidative damage (Ren & Wold, 2008), mitochondrial dysfunction (Ma et al., 2009), and altered membrane properties (Cederbaum et al., 2001). Although earlier findings from our lab demonstrated that overexpression of ALDH2 alleviates alcohol and acetaldehydeinduced cell injury caused by alcohol and acetaldehyde both in vivo and in vitro (Li et al., 2004, 2006; Ma et al., 2009), little is known about the precise mechanism of the protection due to ALDH2 transgene. Interestingly, seminal findings from Mochly-Rosen's laboratory have unveiled an emerging role of ALDH2 against myocardial ischemic injury courtesy of its dual dehydrogenase and reductase activities (Budas et al., 2009; Chen et al., 2008, 2010). The concept of ALDH2 as a new and promising therapeutic target in cardiovascular diseases received further consolidation from our recent work that revealed that overexpression of the ALDH2 transgene may alleviate ischemia/reperfusion injury, post-ischemic-reperfusion injury, and ischemic cardiac dysfunction. Consistent with this, the ischemia-reperfusion injury may be exacerbated by ALDH2 knockout (Ma et al., 2011). Nonetheless, the mechanism(s) of action behind protection by ALDH2 against ischemia-reperfusion injury may be diverse, involving bioactivation of nitroglycerin, preventing the degranulating effects of toxic aldehydes and lessening the production of free radicals, 4-HNE and ultimately mitochondrial dysfunction (Budas et al., 2009; Chen et al., 2010). ALDH2 is known for its role in the metabolism of the ethanol metabolite acetaldehyde. Besides acetaldehyde, ALDH2 serves as a critical metabolic enzyme in the detoxification of other

reactive aldehydes such as 4-HNE and conversion of nitroglycerin (from glyceryl trinitrate [GTN]) to 1,2-glyceryl dinitrate (1,2-GDN) (Budas et al., 2009; Chen et al., 2010).

Using a transgenic model with inactive ALDH2, ethanol and acetaldehyde concentrations in blood, brain, and liver were scrutinized between ALDH2-/- and ALDH2+/+ wild-type mice following alcohol gavages. Much higher blood acetaldehyde but not alcohol levels were found in ALDH2-/- mice compared with ALDH2+/+ mice 1 hr after alcohol challenge, consistent with the observation of elevated blood acetaldehyde levels (by ~10 fold) in patients with defective ALDH2 as compared to those in normal individuals (Nishimura et al., 2002). ALDH2 enzyme metabolized 94% of acetaldehyde produced from ethanol (Isse et al., 2005). These data indicate that ALDH2 is a major enzyme for acetaldehyde metabolism. To evaluate the role of facilitated acetaldehyde metabolism on tissue and cell injury caused by alcohol or acetaldehyde, we overexpressed ALDH2 driven by the non-specific chicken β actin promoter in human umbilical vein endothelial cells (HUVEC) and fetal human cardiac myocytes. Our results demonstrated that ALDH2 overexpression significantly attenuates ethanol and acetaldehyde-induced oxidative stress and apoptosis (Li et al., 2004, 2006), suggesting that facilitation of acetaldehyde breakdown lessens its cellular toxicity. These results support the notion that acetaldehyde may directly elicit cell injury because facilitation of its metabolism by ALDH2 alleviates cellular toxicity. These data from our group suggest that facilitated acetaldehyde breakdown with overexpression of ALDH2 may protect against alcohol-induced detrimental effects in the heart, liver and brain (Doser et al., 2009; Guo et al., 2009; Li et al., 2009; Ren et al., 2009), indicating the therapeutic potential of ALDH2 enzyme in alcoholic tissue damage. To the contrary, knockdown of ALDH2 accentuated the severity of alcoholic cardiomyopathy (Ma et al., 2010).

Results from our group showed that transgenic overexpression of ALDH2 effectively antagonizes myocardial hypertrophy and contractile defects elicited by alcohol intake through a mechanism that is associated, at least in part, with phosphorylation of ASK-1, GSK-3β, GATA4, and CREB (Doser et al., 2009). Moreover, alcohol treatment dampened phosphorylation of Akt and AMPK associated with up-regulated PP2A and PP2C, which was abrogated by ALDH2. ALDH2 significantly attenuated the decrease in Akt- and AMPK-stimulated phosphorylation of Foxo3 at Thr32 and Ser413, respectively, caused by ethanol. These results suggested that ALDH2 is cardioprotective against acute ethanol toxicity possibly through inhibition of protein phosphatases, leading to enhanced Akt and AMPK activation. Subsequently, inhibition of Foxo3 occurs followed by apoptosis and mitochondrial dysfunction (Ma et al., 2009). In contrast, ALDH2 deficiency led to a worsened cardiomyocyte function caused by ethanol, which may be due to upregulated expression of protein phosphatase, depressed Akt activation, and subsequently impaired mitochondrial function (Ma et al., 2010). ALDH2 also reversed the myocardial endoplasmic reticulum (ER) stress caused by ethanol. ALDH2 overexpression antagonizes the cardiac insulin insensitivity and contractile defect caused by chronic alcohol intake, possibly via improvement of insulin signaling at the levels of the insulin receptor, IRS, Akt, Foxo3a and JNK (Li et al., 2009).

5. Aldehyde accumulation, protein adduct formation and ALDH2 in alcoholic cardiac disease

Generation of protein-aldehyde adducts or acetaldehyde-derived DNA adducts as a result of excessive alcohol intake has been documented (Badger et al., 2003; Niemela 2001; Yu et al., 2010). Acetaldehyde can bind to reactive lysine residues, some aromatic amino acids, cysteine, or free α -amino groups (Niemela, 2001). The preferential targets of aldehyde or acetaldehyde adduct formation include erythrocyte membrane proteins, albumin, lipoproteins, hemoglobin, collagens, tubulin and cytochrome enzymes (Niemela, 1999,

2001; Yu et al., 2010). Although most aldehyde adducts are located in the liver (Jeong et al., 2000; Worrall et al., 2001), some may be found in the muscle, brain and blood cells. As a consequence of adduct formation, the physicochemical properties of proteins, nucleic acids and lipids may be compromised (Niemela, 1999). Chronic alcohol consumption contributes to formation of various DNA adducts. The acetaldehyde-DNA binding was demonstrated to overtly promote carcinogenesis in alcohol-dependent individuals (Niemela, 2001). Although formation of DNA adducts is deemed to be one of the early steps in carcinogenesis, whether these alcohol-related DNA adducts are true factors or initiators of cancer is still elusive. It was reported that acetaldehyde protein adducts and lipid peroxidation products may increase collagen mRNA levels and thus the levels of connective tissue proteins (Aroor & Shukla, 2004; Lieber, 1991). Moreover, the presence of specific protein adducts in alcoholdependent individuals has prompted the effort to identify new biological markers targeted for alcohol-induced diseases. Nonetheless, adduct assays often display insufficient sensitivities to be adopted in clinical practice at this time. Last but not least, the acetaldehyde-biogenic amine condensation products have been implicated to play an essential role in ethanol and acetaldehyde reinforcement (Melis et al., 2009; Talhout et al., 2007), although little is known about the effect of these acetaldehyde-biogenic amine condensation products on heart geometry or function. One of these condensation products, salsolinol, was shown to regulate cardiac contractile function and thus may mediate the myocardial responses elicited by acetaldehyde (Sokolova et al., 1990). Further study is warranted to elucidate the precise role of the acetaldehyde-biogenic amine condensation products in the alcohol and acetaldehyde-elicited myocardial structural and functional responses, and the effect of ALDH2 on such biogenic amine condensation products.

6. Autophagy and ALDH2 in alcoholic heart disease

Autophagy plays a pivotal role in the heart to maintain physiological cardiac function by engulfing damaged proteins or macromolecular structures (Gottlieb & Carreira, 2010; Gottlieb & Mentzer, 2010; Gurusamy & Das, 2009a, 2009b; Zhang & Ren, 2010). Despite the beneficial effects, an unfavorable role of autophagy has been documented in a number of human diseases such as cancer and cardiovascular and neurodegenerative diseases (Levine & Kroemer, 2008). Thus, autophagy has been considered as a double-edged sword for both disease pathogenesis and prevention (Gurusamy & Das, 2009b). Elevated autophagy promotes survival in response to mild stress, such as brief ischemia and a low grade of oxidative stress, by removing damaged organelles and by recycling of macromolecules to maintain cellular homeostasis (Levine & Kroemer, 2008; Ma et al., 2011; Zhang & Ren, 2010). On the other hand, prolonged ischemic injury may elicit excessive upregulation of autophagy, resulting in cell death due to excessive self-digestion of essential organelles and proteins (Ma et al., 2011; Sciarretta et al., 2010; Zhang & Ren, 2010). Manipulation of autophagy has been deemed as a potential therapeutic target for heart diseases (Levine & Kroemer, 2008). However, the role of autophagy in alcoholic cardiomyopathy remains unclear.

Recent study from our laboratory revealed that ALDH2 promotes cardiomyocyte survival during ischemia, whereas inhibition of autophagy improves cell survival during reperfusion (or reoxygenation), indicating a paradoxical role of autophagy in ischemia and ischemia/ reperfusion phases. This is consistent with the observation that inhibition and induction of autophagy mitigate, respectively, the ALDH2-offered protection against ischemia and ischemia/reperfusion (Ma et al., 2011). Our data further demonstrated that ischemia-induced AMPK activation is increased and decreased, by ALDH overexpression and knockout, respectively. Likewise, reperfusion-induced Akt phosphorylation is augmented and attenuated by ALDH2 overexpression and knockout, respectively. These data favor the notion that ALDH2 turns on AMPK to inhibit mTOR signaling and facilitate autophagy

during ischemia. However, AMPK is replaced by Akt during reperfusion. Akt activation turns on mTOR to suppress autophagy. Thus, mTOR serves as a converging point for ALDH2-mediated activation of Akt and AMPK signaling molecules in ischemia and ischemia-reperfusion (Ma et al., 2011). This dual regulatory paradox appears to underscore the homeostatic machinery for ALDH2-elicited cardioprotection against ischemia-reperfusion injury (Zhang & Ren, 2010).

Our data also revealed a role of ALDH2 as a metabolic enzyme in the detoxification of 4-HNE. 4-HNE along with malondialdehyde, are highly reactive aldehydes known to directly compromise cardiomyocyte contractile dysfunction (Aberle et al., 2004; Folden et al., 2003). Our data revealed that ALDH2 attenuates 4-HNE-induced cardiomyocyte contractile dysfunction, while cardiac 4-HNE accumulation is accentuated in the ALDH2 knockout mice in response to ischemia-reperfusion (Ma et al., 2011; Zhang & Ren, 2010). These findings further suggest a role for aldehyde detoxification in the protection by ALDH2 against ischemia-reperfusion injury. This protection may be mediated by lifting the inhibition of 4-HNE on LKB1/PTEN-mediated regulation of AMPK and Akt, respectively.

Somewhat similar to its beneficial properties in ischemia-reperfusion injury (Ma et al., 2011), ALDH2 overexpression was found to protect against cardiac geometric and contractile anomalies caused by alcohol likely through inhibition of autophagy (Ge & Ren, 2011). Very recent findings from our group revealed that the change in cardiac mechanical and autophagic responses caused by alcohol intake were associated with dampened activation of Akt/AMPK and their downstream signal mTOR. ALDH2 transgene appears to offer its protection in the heart by reversing alcohol-induced changes in AMPK, Akt and mTOR, en route to mitigating alcohol-induced autophagy induction and contractile dysfunction. Akt and AMPK are essential regulators of autophagy, survival, energy metabolism and contractile function in the heart (Arad et al., 2007; Clerk et al., 2003; Li & Ren, 2006). Our previous report indicated that cardiomyocyte contractile dysfunction caused by acute alcohol exposure is associated with a reduced Akt activity but an enhanced AMPK activation (Guo et al., 2010; Li & Ren, 2006). ALDH2 overexpression reconciled the dampened phosphorylation of Akt and AMPK along with facilitated autophagy in response to alcohol intake. Given that activation of AMPK promotes while activation of Akt suppresses autophagy (Ma et al., 2011), our data favor a pivotal role of Akt- rather than AMPK-dependent regulation of autophagy in chronic alcoholism and ALDH2 transgeneelicited myocardial responses. Our results revealed that inhibition in phosphorylation of Akt, mTOR and STAT3 caused by alcohol intake was restored by ALDH2 overexpression, favoring the notion that overexpression of ALDH2 rescues geometric and contractile anomalies caused by alcohol intake by inhibiting alcohol-induced autophagy through an Akt-mTOR-STAT3 dependent mechanism (Ge & Ren, 2011). However, given that acute alcohol challenge compromises cardiac contractile function in conjunction with facilitating the activation of AMPK, which should trigger autophagy induction (Guo et al., 2010), caution needs to be taken with regards to the role of autophagy in the regulation of cardiac function during various stages of alcoholism.

More recent findings from our group suggested that ALDH2 may execute its protective effect against alcoholic heart injury and autophagy by restoring Notch signaling (Ge & Ren, 2011). Inhibition of Notch1 with the γ -secretase inhibitor N-[N-(3,5-difluorophenacetyl)-1- alany1]-S-phenyglycine t-butyl ester (DAPT) exaggerated acute ethanol exposure-induced cardiomyocyte contractile dysfunction, apoptosis and autophagy. In our hands, ALDH2 ablated alcohol-induced suppression of phosphorylation of mTOR and STAT3. mTOR complex 1 (mTORC1) was shown to positively regulate Notch signaling through STAT3 in the regulation of cell differentiation (Ma et al., 2010). In addition, development of tumors as a result of hyperactive mTOR signaling is often associated with aberrant high STAT3/Notch

activity, while inhibition of Notch signaling extends survival (Ma et al., 2010). Although the role of Notch has not been elucidated in the regulation of autophagy and alcoholic complications, the fact that the Notch pathway acts as a positive regulator of the PI3K/Akt/mTOR pathway favors its likely important role in the regulation of autophagy and consequently cardiac function (Chan et al., 2007).

7. Summary and clinical perspectives

ALDH2 is capable of mitigating cardiac remodeling and myocardial dysfunction following chronic alcohol ingestion (Doser et al., 2009), possibly through facilitated acetaldehyde detoxification. Blood acetaldehyde levels are ~10-fold higher in humans with defective ALDH2 (e.g., Asians and African Americans) than normal individuals following alcohol ingestion. Allelic variation of ALDH genes, especially ALDH2, due to a point mutation in the active *ALDH2*1* gene, significantly alters vulnerability to alcoholism and alcoholic complications. Using genetically modified ALDH2 models, several studies have suggested a cardioprotective role of ALDH2 to counteract cardiac remodeling and myocardial dysfunction following alcohol intake. Therefore, ALDH2 may possess important therapeutic potential against alcoholic and other forms of myocardial damage. Because convincing human case studies on interaction between ALDH2 gene polymorphisms and heart function following chronic alcohol intake are lacking, caution must be taken when evaluating the role of ALDH2 and acetaldehyde detoxification in the pathogenesis and management of alcoholic cardiomyopathy.

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Abbreviations

1,2-GDN	1,2-glyceryl dinitrate				
4-HNE	4-hydroxy-2-nonenal				
ADH	Alcohol dehydrogenase				
ALDH	Aldehyde dehydrogenase				
CYP2E1	Cytochrome P450 2E1				
DAPT	N-[N-(3,5-difluorophenacetyl)-1-alany1]-S-phenyglycine t-butyl ester				
ER	Endoplasmic reticulum				
GTN	Glyceryl trinitrate				
HUVEC	Human umbilical vein endothelial cells				
MMP	Mitochondrial membrane potential				
\mathbf{NAD}^+	Nicotinamide adenine dinucleotide				
ROS	Reactive oxygen species				
SERCA	Sarco(endo)plasmic reticulum Ca ²⁺ -ATPase				
SR	Sarcoplasmic reticulum				

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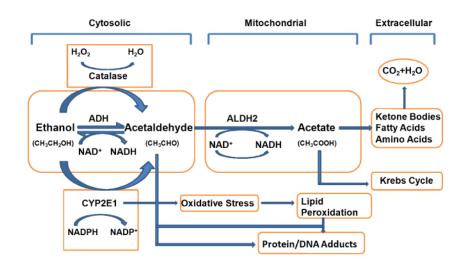


Fig. 1.

Ethanol metabolism pathway. Ethanol is metabolized into acetaldehyde through the cytosolic enzyme alcohol dehydrogenase (ADH), the microsomal enzyme cytochrome P450 2E1 (CYP2E1) and the peroxisomal enzyme catalase. The ADH enzyme reaction is the main ethanol metabolic pathway involving an intermediate carrier of electrons, namely nicotinamide adenine dinucleotide (NAD⁺), which is reduced by two electrons to form NADH. Acetaldehyde is metabolized mainly by aldehyde dehydrogenase 2 (ALDH2) in the mitochondria to acetate and NADH before being cleared into the systemic circulation.

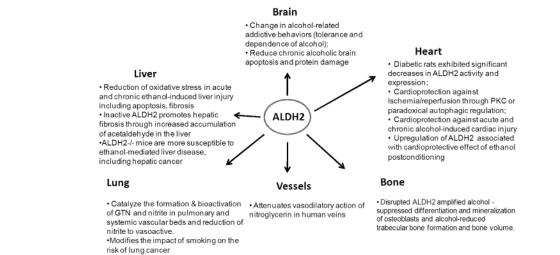


Fig. 2.

Involvement of ALDH2 enzyme in the regulation of multiple organ functions. GTN = glyceryl trinitrate; PKC = protein kinase C.

Table 1

Examples of ALDH2 polymorphisms and associated pathophysiological responses.

ALDH2 genotype	Glu487Lys	ALDH activity	Effect	Reference
ALDH2*2/2	Lys/Lys	Inactive	Less alcohol consumption, highest alcohol sensitivity, less periodontitis progression	(Nishida et al., 2010)
			Facial flushing, nausea, drowsiness, headache, positive patch testing after drinking	(Harada et al., 1981; Ishibashi et al., 2010)
			A risk conferring factor for alcohol dependence	(Vaswani et al., 2009)
			Decreased suicide behavior	(Hishimoto et al., 2010)
			Increased risk of myocardial infarction	(Jo et al., 2007)
			Increased morbidity of osteoporosis	(Yamaguchi et al., 2006)
			Increased risk of esophageal cancer	(Yang et al., 2010)
ALDH2*1/2	Glu/Lys	Inactive	Suicide behavior in male	(Hishimoto et al., 2010)
			Increased risk of squamous cell carcinoma of upper aerodigestive tract, head and neck cancer in moderate and heavy drinkers	(Yokoyama et al., 2010)
			Increased risk of myocardial infarction	(Jo et al., 2007)
			Increased risk of esophageal cancer among never/ rare, moderate and heavy drinkers, as well as among ex-drinkers.	(Yang et al., 2010)
ALDH2*1/1	Glu/Glu	Active	Higher alcohol consumption, lowest alcohol sensitivity	(Nishida et al., 2004)
			Decreased facial flushing, nausea, drowsiness, headache, positive patch testing after drinking	(Harada et al., 1981; Ishibashi et al., 2010)
			Increased suicide behavior	(Hishimoto et al., 2010)
			Increased colorectal cancer risk	(Gao et al., 2008)
			Decreased risk of myocardial infarction	(Jo et al., 2007)