Symposium on ‘Alcohol: nutrient and gene interactions’

Overview of the role of alcohol dehydrogenase and aldehyde dehydrogenase and their variants in the genesis of alcohol-related pathology

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Alcohol dehydrogenase (ADH) and mitochondrial aldehyde dehydrogenase (ALDH2) are responsible for metabolizing the bulk of ethanol consumed as part of the diet and their activities contribute to the rate of ethanol elimination from the blood. They are expressed at highest levels in liver, but at lower levels in many tissues. This pathway probably evolved as a detoxification mechanism for environmental alcohols. However, with the consumption of large amounts of ethanol, the oxidation of ethanol can become a major energy source and, particularly in the liver, interferes with the metabolism of other nutrients. Polymorphic variants of the genes for these enzymes encode enzymes with altered kinetic properties. The pathophysiological effects of these variants may be mediated by accumulation of acetaldehyde; high-activity ADH variants are predicted to increase the rate of acetaldehyde generation, while the low-activity ALDH2 variant is associated with an inability to metabolize this compound. The effects of acetaldehyde may be expressed either in the cells generating it, or by delivery of acetaldehyde to various tissues by the bloodstream or even saliva. Inheritance of the high-activity ADH b2, encoded by the ADH2*2 gene, and the inactive ALDH2*2 gene product have been conclusively associated with reduced risk of alcoholism. This association is influenced by gene–environment interactions, such as religion and national origin. The variants have also been studied for association with alcoholic liver disease, cancer, fetal alcohol syndrome, CVD, gout, asthma and clearance of xenobiotics. The strongest correlations found to date have been those between the ALDH2*2 allele and cancers of the oro-pharynx and oesophagus. It will be important to replicate other interesting associations between these variants and other cancers and heart disease, and to determine the biochemical mechanisms underlying the associations.

Alcohol dehydrogenase: Aldehyde dehydrogenase: Liver: Cancer

Alcohol is used by a large number of individuals and its metabolism parallels that of other nutrients. While the use of small amounts of alcohol has a beneficial effect for cardiovascular health, consumption of large amounts has well-known effects on the liver, heart, pancreas and the nervous system, and less well-recognized influences on other disease, especially cancers. The susceptibility of individuals to the ill effects of alcohol consumption appears to be a result of complex interactions between genes and the environment (the latter including both the alcohol itself and other nutrients). The enzymes involved in alcohol metabolism are polymorphic and it is their contribution to differential risk of alcoholism and some of its complications that is most understood. These enzymes and the effects of their genetic variation are the subject of the present review.

Abbreviations: ADH, alcohol dehydrogenase; ALDH, aldehyde dehydrogenase; AUC, areas under the blood alcohol concentration curves; C/EPB, CCAAT-enhancer-binding proteins; FPM, first-pass metabolism; Vmax, maximum velocity.

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Gastrointestinal absorption and first-pass metabolism

First-pass metabolism (FPM) is the difference between the amount of a drug administered orally and the amount reaching the systemic circulation and, conceptually, is a result of metabolism of the drug by the gut or liver during the absorption phase. FPM is important because it reduces the amount of a drug reaching target organs and may also predispose gut tissues to injury from alcohol metabolism. The gastrointestinal tract, similar to the liver, contains cytochrome P450s and alcohol dehydrogenases (ADH). Ingested ethanol is absorbed slowly from the stomach, during which process it may be subject to oxidation. Ethanol leaving the stomach is very rapidly absorbed from the upper small intestine. Ethanol absorbed across the gut mucosa is carried to the liver by the portal vein, where a small proportion is metabolized before leaving that organ. To determine the magnitude of FPM, ethanol is administered orally or intravenously and the concentration of ethanol in the blood (blood alcohol concentration) is measured over time. The areas under the blood alcohol concentration curves (AUC) are calculated for each route of administration and the FPM is the difference in AUC between the two routes (Julkunen et al. 1985; Caballeria et al. 1987).

Lieber’s group pioneered studies on FPM, establishing that FPM is easiest to detect with low doses of ethanol (0.3 g/kg, equivalent to approximately 20 g ethanol or two social drinks) when gastric emptying is slowed by the presence of food (Julkunen et al. 1985). Larger doses of ethanol or conditions under which gastric emptying is rapid make the difference between the AUC too small to measure accurately. While the phenomenon of FPM is well established, the organ in which it occurs is not. Some reports favour the stomach as a major site (Lim et al. 1993). The gastric mucosa contains several ADH (γ-ADH, χ-ADH and σ-ADH, see p. 51) that could be involved in the metabolism of ethanol. Under circumstances in which gastric ADH activity is decreased, e.g. in women (Frezza et al. 1990; Seitz et al. 1993), individuals with atrophic gastritis, alcoholics (DiPadova et al. 1987) and individuals taking certain medications (Roine et al. 1990; Caballeria et al. 1991), the magnitude of FPM is reduced. σ-ADH, a major gastric ADH isozyme, is absent in the stomach biopsies of about 30% of Asians, and those lacking this enzyme had lower FPM of ethanol (Dohmen et al. 1996), suggesting that σ-ADH is important in gastric oxidation of ethanol. The relationship between FPM and the rate of gastric emptying suggests that prolonged contact of the ingested alcohol solution with the stomach favours absorption of the alcohol transgastrically, where it would be subject to oxidation in the stomach mucosal cells. Rapid gastric emptying would have the opposite effect. Oral administration of alcohol resulted in a substantially higher blood alcohol level and AUC in the fasted as compared with the fed state (DiPadova et al. 1987). All these findings are consistent with an important role for the stomach mucosa in FPM of ethanol.

However, other interpretations of these data have been published. The assertion that gastric ADH (Yin et al. 1997) or FPM (Ammon et al. 1996) is reduced in women is contested. Some investigators have found no correlation between gastric ADH activity and FPM (Brown et al. 1995). Importantly, the total ADH activity in the stomach, calculated based on the mass of the mucosa and its ADH activity, does not account for the amount of ethanol metabolized, as indicated by the observed differences between the AUC of oral and intravenous alcohol (Yin et al. 1997). Furthermore, the human and rat σ-ADH have markedly different kinetic properties. The $K_m$ for ethanol for the human enzyme is 40 mM, whereas that for the rat enzyme is eighty times greater, yet FPM for the two species is similar in magnitude. These arguments suggest that FPM also occurs in the liver. Hepatic FPM is dependent on the rate at which ethanol is absorbed, since at low rates of absorption, leading to low portal venous ethanol concentrations, ethanol could be extracted by the relatively-low-$K_m$ hepatic ADH isozymes. At higher rates of absorption and higher portal ethanol concentrations, these enzymes will be saturated. Experimentally, the systemic AUC of ethanol concentration is very sensitive to the rate of portal venous administration of ethanol (Smith et al. 1992; Levitt & Levitt, 1994). This alternative explanation can also account for the lack of FPM seen with high doses of ethanol or rapid gastric emptying.

To clarify this issue, Ammon et al. (1996) gave ethanol intravenously and $^3$H-labelled ethanol by mouth or into the duodenum. This method reduced the intra-subject variability by permitting an estimate of both gastric and hepatic FPM simultaneously. They found that FPM was about 8–9% of the oral dose and estimated that the gastric contribution to FPM was about 6% of the oral dose. It seems safe to conclude that the FPM of oral ethanol is usually a small percentage (perhaps $\leq 10$) of the total body ethanol elimination, and when gastric emptying is rapid or the ethanol dose consumed is high it is quantitatively even less important. Gender differences in FPM are probably not major (Ammon et al. 1996). The overall importance of FPM might lie in the potential for gastric FPM to protect the liver and other organs from low doses of ethanol, and for certain drugs to block FPM (Roine et al. 1990; Caballeria et al. 1991), resulting in intoxication from smaller-than-expected doses of ethanol. Furthermore, this process is an obvious point of intersection of diet and timing of meals with ethanol consumption.

Overview of hepatic ethanol metabolism and its regulation

After absorption and passage through the liver, ethanol is distributed in the body water space and is largely metabolized in the liver to acetaldehyde by ADH in the cytosol and the cytochrome P450IE1 in microsomes. Although cytochrome P450IE1 is important in ethanol toxicity and in mediating several drug–ethanol interactions, it will not be further considered in the present discussion. Acetaldehyde is converted by aldehyde dehydrogenases (ALDH) (especially the mitochondrial ALDH2 isozyme) to acetate, which is released from the liver and metabolized by the heart and muscle (Lumeng & Davis, 1970). The rate of ethanol metabolism by ADH and ALDH2 may be critical in determining its toxicity because the intermediates of this
pathway are themselves potentially toxic. The maximal activities of ADH and ALDH in the liver are similar, so that each enzyme contributes to the overall control of the rate of alcohol oxidation.

Modelling of alcohol oxidation in rat liver indicated that ADH activity was controlled in part by the total activity of the enzyme as well as product inhibition by NADH and acetaldehyde (Crabb et al. 1983). Liver NADH levels are elevated during alcohol oxidation because the first enzyme in the malate–aspartate shuttle, malate dehydrogenase, has a high $K_m$ for NADH (Crow et al. 1982, 1983). Thus, in a steady-state ADH is operating below its maximum velocity ($V_{\text{max}}$). Flux through the pathway is also sensitive to the total activity of ADH. Reduction in total ADH activity (as occurs in fasting) reduced the ability of the liver to oxidize ethanol in rats, but increases in activity did not increase the metabolic rate proportionally (Crabb et al. 1983). This outcome is presumed to be a result of the inability to increase acetaldehyde oxidation and, therefore, an increase in steady-state acetaldehyde concentration may limit the rate of ethanol metabolism. In human subjects with ADH and ALDH2 variants with markedly different kinetic properties the rate of ethanol oxidation should be influenced by the $K_m$, $V_{\text{max}}$ and sensitivity to product inhibition of the variants. This relationship raises the possibility that under certain conditions pathways of alcohol metabolism and the concentrations of metabolic intermediates change but the alcohol elimination rate does not.

The rate of ethanol clearance from the blood in the pseudo-linear segment of the elimination curve varies by two- to threefold between individuals (Kopun & Propping, 1977; Martin et al. 1985). The test–retest reliability in the oral ethanol challenge method of determining the alcohol elimination rate is open to criticism, but substantial between-individual variation was recently confirmed using the oral ethanol challenge method of determining the alcohol elimination rate (i.e. a steeper blood ethanol disappearance curve) sometimes observed at high blood ethanol concentrations. Class III ADH (β ADH, for pyrazole-sensitive isozyme) was first found in human liver; it has a higher $K_m$ for ethanol and is less sensitive to inhibition by pyrazole derivatives. Class I enzymes are very abundant in the liver and are therefore believed to play a major role in hepatic alcohol metabolism. Class II ADH (π ADH, for pyrazole-insensitive isozyme) is mainly expressed in the stomach and oesophagus (Ehrig et al. 1990). As it has a high $K_m$ it may contribute to increased rates of alcohol elimination (i.e. a steeper blood ethanol disappearance curve) sometimes observed at high blood ethanol concentrations. Class III ADH (γ ADH) is expressed in all tissues studied, is virtually inactive with ethanol but is capable of metabolizing longer-chain alcohols and ω-hydroxy-fatty acids (Pares & Vallee, 1981). This enzyme also exhibits glutathione-dependent formaldehyde dehydrogenase activity (Koivusalo et al. 1989). Recent additions to this family of enzymes are class IV and (tentatively) classes V and VI. The class IV enzyme has been purified from the stomach and oesophagus.

### Enzymology of alcohol metabolism

**Alcohol dehydrogenases**

The enzymes responsible for the bulk of alcohol oxidation are the ADH. All are dimeric Zn-containing enzymes with a subunit molecular weight of 40 kDa. These enzymes are classified based on enzymic properties and the extent of sequence similarities. Only enzyme subunits belonging to the same class can heterodimerize. The heterodimers have genetic properties described by the active sites acting independently. Classes I, II and possibly IV are predicted to participate in ethanol oxidation in vivo. The properties of the enzymes in each of these classes are summarized in Table 1 (Bosron & Li, 1986, 1987). Class I contains α, β and γ isozymes. These enzymes have a low $K_m$ for ethanol and are highly sensitive to inhibition by pyrazole derivatives. Class I enzymes are very abundant in the liver and are therefore believed to play a major role in hepatic alcohol metabolism. Class II ADH (β ADH, for pyrazole-sensitive isozyme) is mainly expressed in the stomach and oesophagus (Ehrig et al. 1990). As it has a high $K_m$ it may contribute to increased rates of alcohol elimination (i.e. a steeper blood ethanol disappearance curve) sometimes observed at high blood ethanol concentrations. Class III ADH (γ ADH) is expressed in all tissues studied, is virtually inactive with ethanol but is capable of metabolizing longer-chain alcohols and ω-hydroxy-fatty acids (Pares & Vallee, 1981). This enzyme also exhibits glutathione-dependent formaldehyde dehydrogenase activity (Koivusalo et al. 1989).

Recent additions to this family of enzymes are class IV and (tentatively) classes V and VI. The class IV enzyme has been purified from the stomach and oesophagus.

### Table 1. Properties of alcohol dehydrogenases (ADH) in man

<table>
<thead>
<tr>
<th>Gene locus</th>
<th>New nomenclature</th>
<th>Subunit type</th>
<th>$K_m$ (ethanol)†</th>
<th>$V_{\text{max}}$†</th>
<th>Tissue distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class I</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ADH1</td>
<td>ADH1A</td>
<td>α</td>
<td>4</td>
<td>54</td>
<td>Liver</td>
</tr>
<tr>
<td>ADH2</td>
<td>ADH1B</td>
<td>β</td>
<td>0.05–34.0†</td>
<td>–</td>
<td>Liver, lung</td>
</tr>
<tr>
<td>ADH3</td>
<td>ADH1C</td>
<td>γ</td>
<td>0.6–1.0†</td>
<td>–</td>
<td>Liver, stomach</td>
</tr>
<tr>
<td>Class II</td>
<td>ADH4</td>
<td>π</td>
<td>34</td>
<td>40</td>
<td>Liver, cornea</td>
</tr>
<tr>
<td>Class III</td>
<td>ADH5</td>
<td>ζ</td>
<td>1000</td>
<td>–</td>
<td>Most tissues</td>
</tr>
<tr>
<td>Class IV*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ADH7</td>
<td>ADH4</td>
<td>σ, μ</td>
<td>20</td>
<td>1510</td>
<td>Stomach, oesophagus, other mucosas</td>
</tr>
<tr>
<td>Class V*</td>
<td>ADH6</td>
<td>ADH5</td>
<td>–</td>
<td>30</td>
<td>?</td>
</tr>
<tr>
<td>Class VI*</td>
<td>ADH8</td>
<td>ADH6</td>
<td>–</td>
<td>–</td>
<td>Not detected in man, found in deer mouse and rat liver</td>
</tr>
</tbody>
</table>

$V_{\text{max}}$, maximum velocity.
† Kinetic constants vary with the isozyme, see Table 2.

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*Gene locus New nomenclature Subunit type $K_m$ (ethanol)† $V_{\text{max}}$† Tissue distribution

*Tissue distribution

*Kinetic constants vary with the isozyme, see Table 2.

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Designated either μ-ADH (for the mucosal isozyme; Yin et al. 1990) or σ-ADH (for the stomach isozyme; Moreno & Pares, 1991), it is structurally distinct from classes I, II and III (Stone et al. 1993; Farres et al. 1994a; Pares et al. 1994; Satre et al. 1994). Its high Km for ethanol may be an adaptation for the high concentration of ethanol in the gastric mucosa after ethanol consumption. The fact that this enzyme has such a high Km for ethanol suggests that other alcohols may be its physiological substrates. σ-ADH has the highest Vmax of any of the known ADH and is very active with retinol as substrate (Stone et al. 1993). Its expression in a variety of epithelia (oesophagus, stomach, vagina, naso-pharynx and cornea) and the importance of retinol in the integrity of these tissues suggest that σ-ADH has a role in retinol conversion to retinal. It is the first ADH expressed in the embryonic mouse and its sites of expression correlate with the production of retinoic acid (Ang et al. 1996a,b). Class V ADH, encoded by the ADH6 gene, is expressed at the mRNA level in the liver and in the stomach, but the enzyme itself has not been purified. In vitro expressed enzyme had an isoelectric point of about 8.6, a high Km for ethanol (about 30 mM) and moderate sensitivity to pyrazole inhibition (Cheng & Yoshida, 1991; Yasunami et al. 1991). An additional class of ADH (tentatively designated class VI) was reported in the liver of deer mice (Peromyscus maniculatus; Zheng et al. 1993) and rats (Hoog & Brandt, 1995) and class VII ADH was cloned from chicken (Kedischvili et al. 1997); to date the human homologues have not been found. There is a new nomenclature for ADH, shown in Table 1, but the remainder of the present review will use the older system.

The class I enzymes and their mRNA are quite abundant in liver. The genes are approximately 15kb in size with nine exons (Duester et al. 1986). The ADH promoters contain binding sites for general transcription factors (e.g. TATAA-binding factors, upstream stimulatory factor (Potter et al. 1991a), CCAAT box-binding transcription factor, or nuclear factor 1, which appears to function as a negative factor (Edenberg et al. 1993), and Sp1-like factors (Brown et al. 1992)) as well as tissue-specific factors (e.g. hepatocyte nuclear factor 1, D-box-binding protein and CCAAT-enhancer-binding proteins (C/EBP, C/EBPα and β; Stewart et al. 1990, 1991; Potter et al. 1991b)). Exceptions are the ADH5 and ADH7 promoters, which lack TATAA boxes. The ADH5 promoter is G + C rich, a characteristic of housekeeping genes.

ADH are expressed in a variety of extrahepatic tissues, albeit at lower levels than in the liver. High levels of class I ADH mRNA were found in the kidney, stomach, duodenum, colon and uterus of rats (Estonius et al. 1993), with lower levels in many organs, including the lung, small intestine and hepatic Ito cells (Yamauchi et al. 1988). Very low levels were found in the brain, thymus, muscle or heart (Estonius et al. 1993). Class I ADH has also been found in blood vessels (Allali-Hassani et al. 1997), a finding relevant to the alcohol-induced flush reaction. Surveys of ADH expression patterns in human tissue have been published (Engeland & Maret, 1993; Estonius et al. 1996). The expression of ADH in gut mucosa and breast is relevant to studies on the effect of alcohol on cancers of these organs. The oral mucosa expresses σ and χ ADH (Dong et al. 1996). Class II ADH was detected in liver and duodenum (Estonius et al. 1993). σ ADH is expressed in stomach and oesophageal mucosa at high levels. The colon expresses γ ADH in the mucosa and β ADH in the muscle layer (Yin et al. 1994). Breast tissue expresses relatively high levels of class I ADH (Triano et al. 2003), but the isozyme involved is not known. Enzyme extracted from breast was apparently saturated at 10 mM ethanol, which would be consistent with either β or γ ADH. Human placenta expresses χ ADH only (Pares & Vallee, 1981).

The expression of ADH is regulated to a certain extent in the liver. Binding sites for thyroid hormone, retinoic acid (Duester et al. 1991; Harding & Duester, 1992) and glucocorticoid receptors (Winter et al. 1990) have been identified in the upstream regions of class I ADH genes. In vitro promoter studies suggest that the genes are regulated (retinoic acid and glucocorticoids activating transcription and thyroid hormone antagonizing the effect of retinoic acid; Harding & Duester, 1992), but smaller effects are seen in vivo. This disparity may be the result of effects of the hormones on protein synthesis and turnover as well as on transcription (Quali & Crabb, 1992; Dipple et al. 1993). Growth hormone increased ADH activity in intact animals and cultured hepatocytes (Mezey & Potter, 1979; Mezey et al. 1986b; Potter et al. 1989, 1993), while androgens (Mezey et al. 1986a) and thyroid hormones (Mezey & Potter, 1981; Dipple et al. 1993) decreased it. Liver ADH activity is also decreased substantially by fasting (Bosron et al. 1984) and protein restriction (Lumeng et al. 1979).

The effect of ethanol on ADH expression is complex. Studies in rodents have shown that ethanol can increase ADH activity in male rats by reducing testosterone levels (Rachamin et al. 1980). The doses of ethanol delivered to rats or mice via the use of liquid diets does not have significant effects on liver ADH. However, higher doses achieved by intragastric delivery of ethanol induced liver ADH activity and resulted in cyclic changes in blood alcohol despite continuous infusion. This effect was shown to result from induction of the transcription factor C/EBPβ and suppression of C/EBPγ and a truncated inhibitory form of C/EBPβ termed LIP (He et al. 2002). In addition, chronic intragastric infusion of ethanol increases portal vein endotoxin and sensitizes the liver to endotoxin actions (Enomoto et al. 2000). Mezey’s group (Potter et al. 2003) reported that endotoxin can induce ADH mRNA, protein and activity. This effect was correlated with increased binding of upstream stimulatory factor to the ADH promoter. In man less is known. The amount of ADH in the liver is not influenced by chronic drinking; the activity is normal in heavy drinkers without liver disease and there is a progressive reduction in ADH activity as liver injury progresses (Panes et al. 1989). Although there are controversial data about women having higher alcohol elimination rates, orchiectomy increased alcohol elimination rates in human subjects (Mezey et al. 1988).

Of the seven human ADH gene loci, two are polymorphic, and the frequency of the different alleles depends on ethnic background. Both polymorphic alleles involve class I ADH genes; three alleles exist for ADH3 and three for ADH2 (Burnell & Bosron, 1989). The kinetic properties
ADH3 polymorphism did not affect alcohol elimination rate of ethanol metabolism (Thomasson et al. 1995). To date, different ADH2*2 genotypes have been correlated, at most, with only a small proportion of the between-individual differences in alcohol elimination rates (Mizoi et al. 1994). The ADH2*3 polymorphism has been shown to be associated with a 10% increase in the rate of ethanol metabolism (Thomasson et al. 1995). The ADH3 polymorphism did not affect alcohol elimination (Couzigou et al. 1991).

Table 2. Properties of polymorphic forms of human alcohol dehydrogenase (ADH)*

<table>
<thead>
<tr>
<th>Gene locus</th>
<th>Subunit type</th>
<th>Km (ethanol)‡</th>
<th>Vmax‡</th>
<th>Population§</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADH2<em>1 (ADH1B</em>1)</td>
<td>β1</td>
<td>0.05</td>
<td>9</td>
<td>Caucasians, African-Americans</td>
</tr>
<tr>
<td>ADH2<em>2 (ADH1B</em>2)</td>
<td>β2</td>
<td>0.9</td>
<td>400</td>
<td>Asians</td>
</tr>
<tr>
<td>ADH2<em>3 (ADH1B</em>3)</td>
<td>β3</td>
<td>34</td>
<td>300</td>
<td>African-Americans</td>
</tr>
<tr>
<td>ADH3<em>1 (ADH1C</em>1)</td>
<td>γ1</td>
<td>1-0</td>
<td>87</td>
<td>All groups</td>
</tr>
<tr>
<td>ADH3<em>2 (ADH1C</em>2)</td>
<td>γ2</td>
<td>0-63</td>
<td>36</td>
<td>Caucasians</td>
</tr>
<tr>
<td>ADH3<em>3 (ADH1C</em>3)†</td>
<td>γ3</td>
<td></td>
<td></td>
<td>Native Americans</td>
</tr>
</tbody>
</table>

Vmax, maximum velocity.
*The kinetic constants are noted for the homodimers of the subunits listed (Bosron & Li, 1986, 1987; Ehrig et al. 1990). Heterodimers behave as if the active sites were independent.
†The third ADH3 allele was recently discovered and the enzymic characteristics are unknown (Osier et al. 2002).
‡Km values are expressed in mM and the Vmax values are given in terms of turnover numbers (min⁻¹), as in Table 1.
§Populations that have high allele frequencies for these variants. The alleles are not limited to those populations.

and population distributions of these allelic enzymes are shown in Table 2. The isozymes encoded by the three ADH2 alleles, which differ at a single amino acid residue, vary markedly in Km for ethanol and Vmax. β1 is most common in Caucasians, has a low Vmax and a very low Km for ethanol. β2, originally designated ‘atypical’ ADH (von Warburg et al. 1964), is found in Asians and Ashkenazi Jews in Israel and the USA (Neumark et al. 1998). It has a substantially higher Vmax and somewhat higher Km compared with β1. The β3 isozyme was first detected in liver extracts from African-Americans (Bosron et al. 1980) because of its lower pH optimum than the other ADH isozymes. It has also been found in Southwest Native Americans. It has a high Km for ethanol and high Vmax. Smaller differences in enzymic properties are observed between the products of the ADH3 alleles. The γ1 isozyme has about twice the Vmax of the γ2 isozyme, while their Kms for ethanol are similar. γ1 ADH is found at a high frequency in Asians and African-Americans; Caucasians have about equal frequency of γ1 and γ2 ADH alleles (Burnell & Bosron, 1989). The recently described ADH3*3 allele has not been enzymically characterized (Osier et al. 1999). Edenberg’s laboratory (Edenberg et al. 1999) recently reported polymorphisms in the promoter of the ADH7 gene, encoding π ADH, which affect promoter activity in vitro. The other ADH loci have not been found to be polymorphic to date.

It could be predicted that individuals expressing the variants of ADH2, in particular, would have different alcohol elimination rates; specifically, those with ADH2*2 and ADH2*3 would be predicted to metabolize ethanol more rapidly. This difference has been difficult to demonstrate, in part because a given isozyme constitutes a small proportion of the total alcohol-oxidizing capacity of the liver and because alcohol elimination rates are rather variable, even among individuals of the same ADH genotypes, or even twins (Kopun & Propping, 1977; Martin et al. 1985). To date, different ADH2*2 genotypes have been correlated, at most, with only a small proportion of the between-individual differences in alcohol elimination rates (Mizoi et al. 1994). The ADH2*3 polymorphism has been shown to be associated with a 10% increase in the rate of ethanol metabolism (Thomasson et al. 1995). The ADH3 polymorphism did not affect alcohol elimination (Couzigou et al. 1991).

Table 3. Properties of human aldehyde dehydrogenases (ALDH)

<table>
<thead>
<tr>
<th>Gene locus</th>
<th>Structure‡</th>
<th>Km (Ach)</th>
<th>Tissue distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class 1 ALDH1</td>
<td>α4</td>
<td>30 µM</td>
<td>Many tissues, liver &gt; kidney</td>
</tr>
<tr>
<td>Class 2 ALDH2</td>
<td>α4</td>
<td>1 µM</td>
<td>Low levels in many tissues</td>
</tr>
<tr>
<td>ALDH5*</td>
<td>?</td>
<td>?</td>
<td>Low levels in most tissues, placenta</td>
</tr>
<tr>
<td>Class 3 ALDH3</td>
<td>α2</td>
<td>11 µM</td>
<td>Stomach, liver, cornea</td>
</tr>
<tr>
<td>Other enzymes†</td>
<td>ALDH4</td>
<td></td>
<td>Glutamate γ-semialdehyde dehydrogenase</td>
</tr>
<tr>
<td>ALDH6</td>
<td></td>
<td></td>
<td>Retinal dehydrogenase</td>
</tr>
<tr>
<td>ALDH7,8</td>
<td></td>
<td></td>
<td>Related to ALDH3</td>
</tr>
<tr>
<td>ALDH9</td>
<td></td>
<td></td>
<td>ALDHE3</td>
</tr>
<tr>
<td>ALDH10</td>
<td></td>
<td></td>
<td>Fatty aldehyde dehydrogenase</td>
</tr>
</tbody>
</table>

Ach, acetaldehyde.
*ALDH5 is tentatively assigned to class 2 because of sequence similarities to ALDH2 and the presence of a potential mitochondrial leader sequence.
†It is not likely that ALDH6-10 play any role in metabolism of acetaldehyde.
‡The structure of the enzymes is indicated by α2 for dimers and α4 for tetramers.

Aldehyde dehydrogenases

Acetaldehyde is further metabolized by NAD⁺-dependent ALDH (Table 3). These enzymes have broad substrate specificity for aliphatic and aromatic aldehydes, which are irreversibly oxidized to their corresponding carboxylic acids. The ALDH are expressed in a wider range of tissues than the ADH isozymes. The nomenclature for ALDH has been revised; they have been tentatively classified as class 1 (low Km, cytosolic), class 2 (low Km mitochondrial) and class 3 (high-Km ALDH, such as those expressed in tumours, stomach and cornea) based on kinetic properties and sequence similarities.

The most important enzymes for acetaldehyde oxidation are cytosolic ALDH1 and mitochondrial ALDH2 (Greenfield & Pietruszko, 1977). Both are tetrameric enzymes composed of 54 kDa subunits. ALDH1 has a low Km for
acetaldehyde (about 30 μM) and is exquisitely sensitive to disulfiram (Antabuse; Alpharma AS, Oslo, Norway) in vitro (Greenfield & Pietruszko, 1977; Dickinson et al. 1981). ALDH2 has a submicromolar $K_m$ for acetaldehyde and is less sensitive to disulfiram in vitro. These enzymes have high inhibition constants for NADH and, thus, are not inhibited by the high NADH:NAD$^+$ that is established in cytosol and mitochondria during the oxidation of ethanol. The enzymes are distributed more or less evenly across the liver acinus. ALDH1 and ALDH2 mRNA are expressed in a variety of human tissues in addition to the liver (Stewart et al. 1996b); ALDH2 mRNA is particularly abundant in the kidney, muscle and heart. Low levels of ALDH1 and ALDH2 mRNA are found in the placenta, brain and pancreas, which may be relevant to the genesis of fetal alcohol syndrome, alcoholic neurotoxicity and chronic alcoholic pancreatitis. In man the oral mucosa expresses ALDH3, the oesophagus expresses ALDH1 and ALDH3, the stomach expresses ALDH1, 2 and 3, while the colon expresses predominantly ALDH1, and the lung expresses ALDH2 (Yin et al. 1993, 1994, 1997). The breast is reported to express ALDH1 and ALDH3 (Steerama & Sladek, 1997) and the placenta expresses low levels of ALDH5 mRNA (Stewart et al. 1996b).

The control of expression of these enzymes has been studied. The $ALDH1$ gene was cloned (Hsu et al. 1989) and the promoter was studied in transfection and DNA-binding assays. 5‘ Flanking DNA (2-6 kb) permitted expression of reporter constructs in hepatoma cells; a minimal promoter was shown to bind nuclear factor Y/CCAAT-binding protein 1 and octamer factors (Yanagawa et al. 1995). The $ALDH2$ gene has been more intensively studied. It has no TATAA box (Hsu et al. 1988); similar to ALDH1, it has a binding site for the ubiquitous CCAAT-box-binding protein nuclear factor Y/CCAAT-binding protein 1 near the transcription start site (Stewart et al. 1996a). Pinaire et al. (1999) described a site designated FP330-3‘ that is bound and activated by hepatocyte nuclear factor-4 and retinoid X receptor, while apoA regulatory protein-1, chicken ovalbumin upstream promoter–transcription factor and PPAR-δ oppose this activation. These authors concluded that it is likely that the FP330-3‘ site integrates the effects of several transcription factors in different tissues and this process may explain why ALDH2 is highly expressed in liver and kidneys.

Additional ALDH enzymes are known, but their role in alcohol metabolism is unknown. Pietruszk’o’s laboratory (Kurys et al. 1989, 1993) purified and cloned an enzyme designated ALDH3E. This enzyme has properties similar to ALDH1; it is expressed in the cytosol and has a $K_m$ for aliphatic aldehydes of about 30–50 μM (Kurys et al. 1989), but is only 40% similar to ALDH1 or ALDH2 at the amino acid level (Kurys et al. 1993). This enzyme has a low $K_m$ for aminoaaldehydes such as 4-aminobutyraldehyde and hence may metabolize compounds derived from polyamines such as spermine and betaine aldehyde (Chern & Pietruszko, 1995). Its gene (designated $ALDH9$) was recently cloned (Lin et al. 1996). $ALDH3$ (originally known as ALDH$^+$; Hsu & Chang, 1991) is unique among the $ALDH$ genes in that it lacks introns. The enzyme has 70% sequence similarity to ALDH2 and is predicted to may be a mitochondrial leader sequence. If so, ALDH5 may be classified as the second class 2 ALDH. The $ALDH5$ gene is also polymorphic at two different residues: valine or alanine at position 69; leucine or arginine at position 120 (Hsu & Chang, 1991; Sherman et al. 1994). It is not known at present whether these substitutions alter the enzymic properties of ALDH5. The highest levels of ALDH5 mRNA are expressed in the liver, kidney and skeletal muscle (Stewart et al. 1996b).

ALDH3 and ALDH4 are abundant in liver extracts, have considerably higher $K_m$ for aliphatic aldehydes than the class 1 and 2 enzymes and higher affinity for aromatic aldehyde substrates. The class 3 ALDH3 family includes the cytosolic, tetrachlorodibenzoparadioxin (dioxin)-inducible ALDH, the hepatoma-associated ALDH and the corneal and stomach ALDH3 (Lindahl, 1992; Algar et al. 1993). The stomach form might participate in the oxidation of acetaldehyde generated during gastric metabolism of ethanol. ALDH4 appears to be glutamic γ-semialdehyde dehydrogenase. ALDH6 is a retinal dehydrogenase. ALDH7 and ALDH8 have been cloned (Hsa et al. 1995), but enzymological characteristics for these enzymes are not yet known. They are related to ALDH3. ALDH9 represents the gene for ALDHE3, and ALDH10 encodes the fatty ALDH that is deficient in Sjogren-Larsson syndrome.

Similar to the class I ADH, the $ALDH2$ gene is polymorphic and the variants demonstrate the vital role of ALDH2 in ethanol oxidation. Alcohol consumption causes facial flushing in a large proportion of Japanese, Chinese and Koreans (Wolff, 1972, 1973). The reaction has even been seen in Asian infants given alcohol, suggesting a genetic basis. Family studies suggested that the flush reaction is inherited as a dominant trait (Schwitters et al. 1982). The flushing reaction correlates with the accumulation of acetaldehyde (Zeiner et al. 1979; Goedde et al. 1983; Enomoto et al. 1991a). In non-flushers drinking alcohol elicits a small increase in acetaldehyde levels (to 5–10 μM); in flushers the levels are variable, but may exceed 100 μM (Enomoto et al. 1991a). The similarity between the Asian flush reaction and the disulfiram flush reaction (Asmussen et al. 1948) suggests that ALDH deficiency might be the explanation. A large percentage (about 40%) of Japanese have been found to lack ALDH2 activity in hair root and liver samples (Harada et al. 1981, 1982) and most of these individuals flushed when they drank alcohol. Thus, ALDH2 appears to play a crucial role in maintaining low levels of acetaldehyde during alcohol oxidation.

The mutation responsible for the deficiency is a G→A substitution that results in replacement of glutamate with lysine at position 487 in ALDH2 (Hempel et al. 1984; Yoshida et al. 1984). The normal allele is termed $ALDH2^+1$ and the mutant allele is designated $ALDH2^*2$. $ALDH2^*2$ homozygotes have essentially no ALDH2 activity, while heterozygotes have markedly reduced but still detectable activity; hence, ALDH2 deficiency is a dominant negative trait (Crabb et al. 1989). Consistent with enzyme activity measurements, homozygotes experience far higher acetaldehyde levels after they drink alcohol than do heterozygotes (Enomoto et al. 1991a).
Measurement of ALDH2 activity in the livers of controls and individuals with ALDH2 deficiency suggested that about 40% of total liver ALDH activity is ALDH2 and 60% comprises other forms (ALDH1, ALDH3; SJ Yin, personal communication). The ALDH2*2 allele encodes an enzyme with a much increased $K_{m}$ for NAD+$\text{^2}$ and a reduced $V_{\text{max}}$ when compared with the wild-type enzyme (Farres et al. 1994b). Thus, it is predicted to be virtually inactive under conditions occurring in liver mitochondria. The two ALDH2 alleles have been expressed in tissue culture cells (Xiao et al. 1995). Transduction of ALDH2*2 resulted in expression of a low-$K_{m}$ ALDH with the expected isoelectric point. The ALDH2*2 allele directed expression of an inactive protein. Transduction of ALDH2*2 into ALDH2*1 expressing cells reduced the low $K_{m}$ activity substantially. The extent of reduction in activity suggested that only tetramers containing either three or four wild-type subunits are active. Moreover, the ALDH2*2 polypeptides were less stable in the transduced cell lines, further reducing the level, and thus activity, of heterotetramers (Xiao et al. 1996) and contributing to the dominance of the ALDH2*2 allele. The x-ray crystal structure of ALDH2 shows that amino acid 487 is situated in a region of the protein involved in subunit-subunit interactions (Steinmetz et al. 1997). Introduction of a positive charge by substitution of a lysine for glutamate disrupts essential ionic bonds and is predicted to inactivate the adjacent subunits and explain the dominance of the mutation.

Studies of the effect of ALDH2 deficiency on alcohol metabolism rates are limited by the adverse effects of the flush reaction. Preliminary studies failed to show a difference in alcohol elimination rates between flushers and non-flushers (Mizoi et al. 1979; Inoue et al. 1984), but a subsequent study detected reduced rates of elimination in individuals with ALDH2 deficiency when controlled for ADH genotype (Mizoi et al. 1994). This finding would be consistent with product inhibition of ADH by elevated intrahepatic acetaldehyde levels.

A polymorphism in the ALDH2 promoter was simultaneously reported by Harada et al. (1999) and Chou et al. (1999). This A/G variant occurs at approximately 360 bp upstream from the start site and is adjacent to a site bound by transcription factors belonging to the steroid receptor family. The A allele is less active than the G allele in reporter gene transfection assays. Harada et al. (1999) showed that the A allele was also less common in a group of alcoholics with active ALDH2. These variants were found in all ethnic groups examined. It will be very interesting to see if the observations on the association of the A allele with protection from alcoholism can be extended to Caucasians and Africans.

**Correlation between genetic variants and risk of alcoholism and organ-specific injury**

The genetic predisposition to alcoholism has been amply demonstrated by a number of classical genetic studies, such as twin, adoption and high-risk familial clustering studies. Despite use of unbiased approaches such as genome-wide screening, the strongest genetic associations identified to date are those related to the ADH and ALDH2 genes. Specifically, individuals having the genes encoding high-activity ADH (B2 ADH encoded by ADH2*2) or the dominant negative allele for ALDH2 (ALDH2*2) are at reduced risk of alcoholism, while those with ALDH2*2 are at much higher risk of oro-pharyngeal cancer. Associations with other disorders are less strong at present. Most work has concentrated on an imbalance between the rate of acetaldehyde production and disposal as the likely explanation for associations between ADH and ALDH2 polymorphisms and various pathologies. This thinking is strongly influenced by the phenomenon of the alcohol flush reaction. However, additional mechanisms by which the inheritance of different isozymes alters risk for disease need to be considered in order to interpret the association studies. These mechanisms include: interference by ethanol in the metabolism of retinol or other metabolites by ADH or ALDH2 and effects of ethanol on redox state and the metabolism of compounds such as steroid hormones. In addition, oxidative stress induced by ethanol and effects of acetaldehyde on signalling pathways in various tissues may also prove to be important.

**Alcohol dehydrogenase**

**Effects on risk of alcoholism.** Despite the small effect of ADH genotype on alcohol elimination rate, ADH genotypes, particularly the presence of an ADH2*2 allele, are related to differences in alcohol-drinking behaviour. Among Chinese living in Taiwan the ADH2*2 allele was found to be substantially more common in the non-alcoholic group than in the alcoholics (Thomasson et al. 1991). Similar findings have been reported in the Atayal natives of Taiwan (Thomasson et al. 1994), the Maori of New Zealand (Chambers et al. 2002), in Spanish patients (Borrás et al. 2000) and among Jews living in the USA or in Israel (Neumark et al. 1998). There was no apparent effect of ADH2 alleles on the quantity and frequency of drinking in Japanese men (Takeshita et al. 1994), although the number of individuals with the genotypes expected to predispose to the highest consumption (individuals homozygous for both ALDH2*1 and ADH2*1) is small because of the allele frequencies in this population. A more recent study indicated that ADH2*1 was more common in heavy drinkers than in moderate drinkers (Tanaka et al. 1997). Moreover, the ADH3*1 allele was also more prevalent in the non-alcoholics than in the alcoholics (Shen et al. 1997) in Asians, but there is no apparent effect of the ADH3 locus on alcohol consumption or alcoholism rates in Caucasians (Gilder et al. 1993). The mechanism for this protective effect is uncertain. Since the ADH2*2 allele encodes the highly-active B2 ADH isozyme, it has been postulated that faster conversion of alcohol to acetaldehyde could be ‘protective’ against heavy drinking and alcoholism. However, alcohol elimination rates and peak blood acetaldehyde levels were not influenced by the ADH2*2 genotype (Mizoi et al. 1994).

Fewer studies on the relationship between the ADH2*3 allele and risk of alcoholism or drinking behaviour have been carried out. The presence of ADH2*3 was associated with a negative family history of alcoholism.
(Ehlers et al. 2003) and with greater alcohol expectations (Ehlers et al. 2003). However, the ADH2*3 allele was not found at a different frequency in alcoholics and controls in a study of >200 African-Americans (Taylor et al. 2003). On the other hand, the presence of ADH2*3 was associated with a lower ‘maximum number of drinks’ among Mission Indians in California, USA (Wall et al. 2003). Additional work is needed to find out whether this allele modifies more characteristics associated with the subtle aspects of alcohol consumption.

**Effect on risk of liver disease.** The evidence for genetic risk factors for alcoholic liver disease is less strong than that for alcoholism. The largest study, the US Veterans Administration Twin Panel Study, showed a higher concordance for cirrhosis in monozygotic twins than in dizygotic twins, indicating a genetic component to the risk (Hrubec & Omenn, 1981). Re-analysis of the database supported this conclusion, but found that most, but not all, of the genetic liability for cirrhosis was the result of shared risk for alcoholism (Reed et al. 1996). No specific candidate genes that confer risk or protection against alcoholic liver disease have been firmly established, but there are hints that the ADH polymorphisms may play some role.

The effect of ADH variants on the risk of alcoholic liver disease could be complex (Lumeng & Crabb, 1994). High-activity ADH variants decrease alcoholism risk, but if individuals with these isozymes persist in drinking, hepatic injury might result from high intrahepatic concentrations of acetaldehyde. One study has demonstrated increased risk of alcoholic liver diseases among ADH2*2 hetero- or homozygotes (Yamauchi et al. 1995), and pooling two other studies with this study (Chao et al. 1994; Tanaka et al. 1996), provided evidence of a substantial increase in risk of cirrhosis in the subjects with ADH2*2.

**ADH3** is polymorphic in Caucasians. Two studies of the prevalence of ADH3*1 and ADH3*2, in patients from the UK (Day et al. 1991) and from France (Poupon et al. 1992), have suggested that ADH3*1, encoding the more active enzyme, may be more common in those with alcoholic liver diseases. When the data from the two studies were pooled, the prevalence of ADH3*1 was 0.65 in alcoholics with cirrhosis and 0.55 in controls (Day et al. 1993) and the difference approached significance. However, a lower ADH3*1 allele frequency was reported in individuals with cirrhosis in another study (Sherman et al. 1994). Thus, the effect of this polymorphism is uncertain.

An additional ADH genetic variant, which occurs within an intron, is a Pvu II restriction fragment length polymorphism in the ADH2 gene. It is not known whether the variant alters the expression of the gene or is linked to another susceptibility locus. The B allele was found at a considerably higher frequency in alcoholics and seemed to be more common in patients with cirrhosis rather than alcoholic hepatitis (Sherman et al. 1993).

**Contributions of alcohol dehydrogenase to other disorders.** Although the majority of ethanol is eliminated by hepatic oxidation, ADH is expressed in many tissues (Saleem et al. 1984; Engeland & Maret, 1993; Estonius et al. 1996), and there is the opportunity, therefore, for alcohol either to be metabolized to potentially-injurious acetaldehyde or to interfere with the metabolism of compounds normally oxidized by this enzyme. Retinoic acid, generated from retinol oxidation, plays an important role in the regulation of embryonic development, spermatogenesis and epithelial differentiation by serving as a ligand for members of the nuclear receptor family. Based on careful kinetic studies of all human ADH family members, ethanol at concentrations found in heavy drinkers can effectively block the oxidation of retinol to retinoic acid. Accordingly, Yin et al. (1999) further suggested that inhibition of retinol oxidation by ethanol might contribute to testicular atrophy, oligosperma, psoriasis and the increased incidence of oral, oesophageal and colo-rectal cancers in chronic alcoholics. Indeed, an association between ADH2*1 and testicular atrophy in alcohol abusers has been reported (Yamauchi et al. 2001). Several studies have attempted to link ADH genotype with risk of fetal alcohol syndrome. One study found a protective effect of ADH2*3 (McCarver et al. 1997), while another found it to be a risk factor (Stoler et al. 2002). Another study reported that ADH2*2 is protective against fetal alcohol syndrome (Viljoen et al. 2001).

A small study indicated that ADH2*2 may be more prevalent in individuals with alcoholic pancreatitis than in alcoholics who do not have this complication (Matsushita et al. 1996). There may also be an association between the homozygous ADH3*1 genotype and risk of oral cancer (Coutelle et al. 1997; Harty et al. 1997); however, this gene is not reported to be active in the oral mucosa (Dong et al. 1996). Epidemiological evidence points to an increased risk of rectal cancer in heavy drinkers. Seitz et al. (1996) have found ADH activity in the rectum that is similar in magnitude to that found in the stomach. Recently, it was reported that alcohol consumption increases the risk of adenomatous colon polyps to a greater extent in individuals homozygous for ADH3*1 than in other genotypes (Tiemersma et al. 2003).

There has been much interest in the potential interaction between alcohol, ADH genotype and risk of breast cancer. Epidemiological studies suggest an increase in breast cancer among women who drink more than one or two standard drinks per d. ADH is highly expressed in the mammary epithelium, which lacks low- Km ALDH; hence, there may be local metabolism of ethanol in the breast tissue (Triano et al. 2003). One study reported an increased risk of breast cancer among premenopausal, but not postmenopausal, women who were ADH3*1 homozygotes (Freudenheim et al. 1999), while another study found no such association (Hines et al. 2000). The most recent study found an interaction between the ADH2*2 allele in Caucasian women and alcohol consumption among patients with breast cancer (Sturmer et al. 2002). The ADH2*2 allele was more common in the women with breast cancer. Among the women with breast cancer those with ADH2*2 were less likely to drink more than once per week than those with ADH2*1.

**Aldehyde dehydrogenase 2**

**Effects on risk of alcoholism.** Japanese studies demonstrated that ALDH2 deficiency reduced the quantity and
frequency of alcohol consumption by men and the risk of alcoholism (Higuchi et al. 1992). This effect was confirmed in other Asian populations by the observation that individuals who were alcoholic (Goedde et al. 1983; Harada et al. 1983, 1985) or who had alcoholic liver disease (Shibuya & Yoshida, 1989) rarely had ALDH2 deficiency or an ALDH2*2 allele. In Japan about 41% of controls were ALDH2 deficient, while only 2–5% of alcoholics were ALDH2 deficient (Harada et al. 1983). In Taiwanese males the frequency of the ALDH2*2 allele was 30% in a non-alcoholic control group and 6% in alcoholics (Thomasson et al. 1991). Similar results were reported by other research groups. The protective effect of being heterozygous for ALDH2*2 appears to be decreasing over time in Japan (Higuchi et al. 1994), i.e. the frequency of ALDH2*2 heterozygotes among alcoholics is increasing, presumably because of environmental and cultural changes. However, ALDH2*2 homozygotes are nearly absolutely protected against alcoholism, presumably because of the severity of their flushing (Higuchi et al. 1994; Chao, 1995). This phenomenon has been observed in other countries (China and Pacific islands; Agarwal et al. 1981; Goedde et al. 1983, 1989; Goedde & Agarwal, 1987) with a somewhat different prevalence of the ALDH2*2 allele, as well as in Asians living in Canada, suggesting that the flush reaction is protective against alcoholism for biochemical rather than cultural reasons (Tu & Israel, 1995).

Effect on risk of liver disease. ALDH2 deficiency may be a two-edged sword for the reasons mentioned earlier for ADH2*2, since individuals with mild flushing who can tolerate heavy drinking may suffer from the hepatic effects of elevated acetaldehyde concentrations. There has been one small study suggesting that ALDH2*2 heterozygotes who drink heavily develop alcoholic hepatitis at a lower cumulative alcohol consumption than those with active ALDH2 (Enomoto et al. 1991b). When the results of several studies were combined the prevalence of ALDH2*2 was substantially higher in the alcoholic patients with cirrhosis than in those without cirrhosis (Chao et al. 1994; Yamauchi et al. 1995; Tanaka et al. 1996). With the apparent increase in the number of alcoholics heterozygous for ALDH2*2 in Japan, ALDH2 deficiency may become an important risk factor in that population.

Effects on other health risks. ALDH2 deficiency is associated with alcohol-induced asthma, thought to result from the effect of increased circulating or locally-generated acetaldehyde on the airways (Takada et al. 1994). Several groups have reported that ALDH2 deficiency is associated with increased risk of oesophageal and oropharyngeal cancer (Yokoyama et al. 1996a,b,c). The activity of ADH is considerably higher than that of ALDH in the oesophagus, which would predispose this tissue to injury during ethanol oxidation (Yin et al. 1993, 1997). It is also possible that the phenomenon reflects increased exposure of the oropharynx and oesophagus to acetaldehyde in the saliva (Vakevainen et al. 2000, 2001). The amount of acetaldehyde in saliva is increased in ALDH2*2 heterozygotes given alcohol, and this amount falls when alcohol oxidation is inhibited by 4-methylpyrazole, suggesting that the acetaldehyde is generated in the salivary glands. An additional observation is the association between ALDH2 deficiency and a mitochondrial DNA mutation and diabetes in Japanese subjects. It was hypothesized that ALDH2 deficiency predisposed the patients to mutagenic effects of acetaldehyde on mitochondrial DNA (Suzuki et al. 1996). No effect of ALDH2 deficiency on the risk of stomach cancer or hepatoma has been reported.

Summary

Many lines of evidence indicate that the genetic variation in ADH and ALDH2 contribute to the risk of alcoholism and the susceptibility to certain alcohol-induced pathologies. Most of the evidence has come from association studies, which of course do not prove a causative relationship. The next challenge is to confirm the findings and to understand the biochemical mechanisms responsible for the risk and susceptibility, which will point toward a better understanding overall of the disease processes.

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