META-ANALYSIS OF THE EFFECTS OF ALCOHOL DEHYDROGENASE GENOTYPE ON ALCOHOL DEPENDENCE AND ALCOHOLIC LIVER DISEASE

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Abstract — The purpose of this paper is to assemble and evaluate existing data on the effect of genetic variation in ADH2 and ADH3 on the risk of alcohol dependence, and on the risk of alcoholic liver disease. Calculations of odds ratios and their confidence limits, and tests for heterogeneity of the results from the available studies, have been performed. It is clear that possession of the ADH2-2 allele increases the risk of alcohol dependence, but it increases the risk of alcoholic liver disease among alcoholics. ADH3 variation also has significant effects on alcohol dependence, which may be due to linkage to ADH2; the ADH3 effect differs significantly between Asian and European subjects. Therefore ADH genotype has substantial effects on risk of alcohol dependence and alcoholic liver disease, but more work is needed on the generalizability of these findings to non-Asian populations, and on possible mechanisms.

INTRODUCTION

The possible relationship between alcohol dehydrogenase (ADH) genotype and the risk of alcohol dependence or alcohol-related disease has been a subject for investigation ever since the polymorphic variants of ADH2 and ADH3 were recognized. Recently, reliable polymerase chain reaction (PCR)-based methods for ADH genotyping have facilitated studies with substantial numbers of subjects. Although the results of these studies indicate a significant role for ADH variation in determining the genetic risk for alcoholism, experience with the proposed association between alcoholism and the Taq polymorphism in the dopamine D2 receptor locus suggests a need for caution (see, for example, Gelernter et al., 1993). Association studies are susceptible to effects from linkage disequilibrium and population stratification, and like any other kind of epidemiological study the results may not agree across different authors’ reports. Therefore it is desirable to compare all available data, to check whether the results are homogeneous and similar across different populations, and to arrive at the best estimate of the relative risk associated with different alleles of the gene(s) in question.

Over the past 5 years, a number of papers on ADH genotype and alcoholism risk have appeared. Most of them report results from Chinese or Japanese subjects, who are more suitable than Europeans for ADH2 studies, but less suitable for ADH3 studies, because of the different gene frequencies between these population groups. A smaller number of studies have examined association between ADH type and the risk of progression to alcoholic liver disease. Because this information leads to hypotheses about mechanisms, and potentially to the establishment of variation in alcohol metabolism and in metabolite concentrations as a major determinant of alcohol-related disease, it is important to establish the soundness and consistency of these results.

METHODS

Data

A search for all papers containing the terms ('alcohol dehydrogenase' or 'ADH') and ('type' or 'genotype') and ('dependence' or 'alcoholism'), and referring to studies on human subjects, was conducted on the Medline files between 1990 and September 1996. Other papers were added where known. This yielded 17 papers with relevant information. Five (Chao et al., 1994b; Nakamura
et al., 1994, 1996; Higuchi et al., 1995, 1996) were excluded, because they reported data which appeared to be repeated in other papers (already included in this analysis) by the same authors. After initial analysis of the results, which showed ADH2 effects on both dependence and liver disease, but in different directions, two further papers (Ricciardi et al., 1983; Couzigou et al., 1990) were excluded because the groups compared were control (non-alcoholic) subjects and alcohol-dependent subjects with liver disease.

Data were extracted from the remaining ten papers (Thomasson et al., 1991; Gilder et al., 1993; Higuchi, 1994; Chao et al., 1994a; Thomasson et al., 1994; Maezawa et al., 1995; Muramatsu et al., 1995; Nakamura et al., 1995; Yamauchi et al., 1995; Tanaka et al., 1996) on ADH2 and ADH3 genotype frequencies in the groups classified by the authors as: (1) controls; (2) alcohol dependence without diagnosed liver disease; (3) alcohol dependence and also alcoholic liver disease.

The allele and genotype frequencies were calculated. All subjects had ADH2-1 or ADH2-2 alleles only; no subjects were reported as having ADH2-3, which is believed to be present only in people of African descent. All data were converted, where necessary, to the actual number of subjects or chromosomes rather than the percentage in each group.

Eight papers contained data on ADH2 genotype in groups classified as either control or alcohol-dependent. Five contained data on ADH3 genotype in control and dependent groups. Three of the papers contained data on ADH2 frequencies in alcohol-dependent subjects free of known alcoholic liver disease and also on subjects with both dependence and alcoholic liver disease, and only one contained data on ADH3 types in these two groups.

Four of the papers contained Tables or data which allowed the effects of ADH2 genotype on alcohol dependence to be contrasted across aldehyde dehydrogenase (ALDH2) groups. Two contained sufficient information to allow this to be done for ADH3 and ALDH2.

Statistical methods

Tests for homogeneity of odds ratio (OR) across studies, calculation of the OR for each study and the associated 95% confidence intervals (CI), and (where there was no evidence of heterogeneity across studies) the OR and 95% CI for the combined data, were performed using StatXact-Turbo (Cytel Software Corporation, Cambridge, MA, USA).

Procedure

Firstly, ORs were calculated from the ADH2 and ADH3 allele frequencies in each group (control, dependence only, or dependence with alcoholic liver disease). This gives an estimate of the allele effect on the assumption of additive effects; that is, the difference between the 11 and 12 genotypes is the same as that between the 12 and 22 genotypes. This gives greater statistical power because of greater numbers, but will not distinguish between additive and dominant genetic effects.

Subsequently the ORs were compared across genotype to test whether heterozygotes were intermediate in risk between the homozygote groups. This was done by calculating ORs for 11 vs 12, 12 vs 22 and 11 vs 22 groups, using the number of subjects with each genotype.

Comparison of ADH2 and ADH3 effects between the ALDH2-11 and ALDH2-12 groups was achieved by extracting and summing the numbers of control and alcoholic subjects, by ALDH2 and either ADH2 or ADH3 genotypes. The resulting summary tables were tested for homogeneity of odds ratios, in order to determine whether ALDH2 type modifies the effects of ADH types.

RESULTS

Risk of alcohol dependence by ADH2

The effects of ADH2-1 vs ADH2-2 type on the odds ratio for dependence are shown in Fig. 1. The positive values indicate a greater risk of alcohol dependence associated with ADH2-1 than with ADH2-2.

There was an apparent difference between the results of Gilder et al. (1993), on European subjects, and the rest, on Asian subjects. However, the test for homogeneity (across all eight reports) showed that the ORs were not significantly different (Breslow–Day statistic 6.733, \( P = 0.457 \)). The estimated common OR was 2.78, 95% CI = 2.42–3.21, \( P < 0.0001 \). Therefore
Fig. 1. *ADH2* and alcohol dependence, from allele frequencies.
The odds ratios (shown by the horizontal columns) and their 95% confidence intervals (shown by the error bars) were calculated for each paper individually, and for all of them.

Fig. 2. *ADH3* and alcohol dependence, from allele frequencies.
The odds ratios (shown by the horizontal columns) and their 95% confidence intervals (shown by the error bars) were calculated for each paper individually.
each ADH2-1 allele seems to be associated with an almost threefold increase in dependence risk, compared to an ADH2-2 allele.

Risk of alcohol dependence by ADH3

Results for the effect of ADH3 type on dependence are shown in Fig. 2. For ADH3 variation, studies on European subjects made it easier to test the hypothesis of association, because the ADH3-1 and ADH3-2 gene frequencies are approximately equal. Nevertheless, the study using European subjects (Gilder et al., 1993) showed negative results, whereas most of the studies on Asians showed a significant effect of ADH3 genotype. The test for heterogeneity (taking all five reports) was highly significant: Breslow-Day statistic 24.1, \( P = 0.0001 \). By including only the Asian groups, no heterogeneity of results across studies was found: Breslow-Day statistic 6.085, \( P = 0.108 \). For the four Asian studies, the common OR was 0.38, 95% CI 0.29–0.51, \( P < 0.0001 \).

Risk of alcoholic liver disease by ADH2

Figure 3 shows the combined data for ADH2 and alcoholic liver disease. Note that the comparison is with alcoholics without known liver disease, rather than with non-alcoholic controls, because only subjects with alcohol dependence are at risk of alcoholic liver disease. Although there are only three reports available, the results are compatible with each other (test for homogeneity of odds ratios, \( P = 0.355 \)) and the estimate of the common odds ratio is 0.565, 95% CI 0.385–0.825, \( P = 0.0024 \).

Risk of alcoholic liver disease by ADH3

For ADH3, there is only one relevant report (Chao et al., 1994a); the OR is 1.01, 95% CI 0.46–2.31. It seems that ADH3 type has little or no effect on alcoholic liver disease, but an effect up to a twofold difference in risk would still be compatible with the data so far.

Relative effect of one or two copies of ADH2-2 or ADH3-2

Figure 4 summarizes the relative risk for subjects with 11 genotype compared to either 12 or 22 genotypes. The figure shows firstly the effect of ADH2 genotype on alcohol dependence risk, secondly the effect of ADH3 genotype on alcohol dependence risk (Asian subjects only), and thirdly the effects of ADH2 genotype on alcoholic liver disease.

Comparisons were also made between 12 heterozygotes and 22 homozygotes. For alcohol dependence, ADH2-12 heterozygotes were at significantly greater risk than ADH2-22 homozygotes (common OR 1.60, 95% CI 1.30–1.98, \( P < 0.0001 \)), but ADH3-12 heterozygotes and ADH3-22 homozygotes had essentially the same risk (common OR 1.00, 95% CI 0.27–3.16). For alcoholic liver disease, the risk was less in the ADH2-12 heterozygotes than in the ADH2-22 homozygotes (common OR 0.73) but not significantly so (95% CI 0.40–1.33).

Does ALDH2 type modify the ADH2 or ADH3 effects?

The calculated odds ratios for ADH2*1 vs ADH2*2 alleles were 2.74 (95% CI 2.25–3.34) for the ALDH2*11 subjects and 3.88 (95% CI 2.69–5.58) for the ALDH2*12 subjects. These odds ratios were not significantly different (\( P = 0.106 \)). Similarly, the effects of ADH3 on dependence, and of ADH2 on liver disease, did not differ significantly between the ALDH2*11 and ALDH2*12 groups (homogeneity \( P = 0.643 \) and 1.000, respectively).

DISCUSSION

ADH2 type and alcohol dependence

ADH type undoubtedly has an effect on alcohol dependence in Asians, as shown by aggregation of the data from multiple independent studies. The ADH2-1 allele is associated with a greater risk. Several reports have shown that this is not conditional upon ALDH2 status (Higuchi, 1994; Maezawa et al., 1995; Nakamura et al., 1995), and this is confirmed by the analysis of ADH2 odds ratios by ALDH2 type, shown above.

There may also be an effect of ADH2 in Europeans, but the small number of ADH2-2 alleles encountered in European subjects (whether control or alcoholic) makes this uncertain. At least 90% of most European populations are ADH2-11, with <10% heterozygotes and a very small proportion of ADH2-2 homozygotes. If we postulate that the frequency of the ADH2-11
Fig. 3. ADH2 and alcohol liver disease, from allele frequencies.
The odds ratios (shown by the horizontal columns) and their 95% confidence intervals (shown by the error bars) were calculated for each paper individually, and for all of them.

Fig. 4. Calculated odds ratios for homozygotes and heterozygotes for ADH2 and ADH3.
Comparisons were made of the 12 heterozygotes (open columns) and the 22 homozygotes (shaded columns) against the 11 homozygotes. Error bars show the 95% confidence intervals. (Note the logarithmic scale.)
genotype is 90% in controls and 95% in alcoholics, it would require 863 controls and 863 alcoholics to have a 90% chance of detecting a difference at the $P < 0.01$ level (see Table A3 in Fleiss, 1981). However, the failure to show an ADH effect on dependence in European studies is not due to the absence of the inactive forms of ALDH among this population.

Examination of the results for each ADH2 genotype showed that the heterozygotes were intermediate in risk between the two homozygous groups. The OR estimates suggest that the ADH2-12 heterozygotes are rather closer to the ADH2-22 group than to the ADH2-11 group, but in both comparisons the difference was highly significant.

ADH3 type and alcohol dependence

In Asians, ADH3-1 is associated with lower risk. However, comparison across genotypes shows that the difference is essentially between ADH3-11 subjects, on the one hand, and homozygotes or heterozygotes with an ADH3-2 gene, on the other. Comparison of the ADH3-12 and ADH3-22 groups shows no significant difference. The case of ADH3 in Europeans is different; there is significant heterogeneity of the ORs for ADH3, which is removed when only the reports from Asia are considered. This suggests that the ADH3 effect may be due to the known association of ADH3-2 with ADH2-1 in Asians, but further data are needed from other populations.

Alcoholic liver disease

ADH2 type has a significant effect on the probability of liver disease in alcohol-dependent subjects, and this appears to increase across genotype in the order 11 < 12 < 22. This is the opposite order to the dependence risk, and these opposing effects mean that studies which compare only control (non-dependent) subjects against alcoholics with cirrhosis may give falsely negative results. For this reason, two such studies were omitted from the analysis of published results.

GENERAL CONCLUSIONS AND COMMENTS

The effect of variation at the ADH2 or ADH3 loci is substantial. Calculation of the relative risks between ADH2-11, ADH3-22 subjects, on the one hand, and ADH2-22, ADH3-11 subjects on the other, implies an ~20-fold difference in the probability of alcohol dependence among Asian subjects. To put this in some perspective, data from a nationally representative population sample in the USA (Light et al., 1996) showed that having a second- or third-degree relative; a first-degree relative; and both first- and second- or third-degree relatives with alcohol dependence was associated with 50%, twofold, and fourfold increases in DSM-III-R alcohol dependence risk, respectively. In the same study, being female rather than male decreased risk by ~50%. Apart from ADH deficiency, ADH type is the most potent known influence on alcoholism.

From the information available so far, we cannot be sure whether these ADH effects are general, or restricted to Asian subjects. Indeed, we cannot exclude variation at another, closely linked, locus as the true cause. The ADH2 polymorphism is widespread (Goede et al., 1992) and further information on ADH type and alcohol use in non-Asian subjects is likely to appear soon.

There is also a need for information relevant to the mechanisms of the ADH effect. The assumption that these effects on dependence risk or risk of alcoholic liver disease are mediated by differences in ethanol metabolism, and possibly by consequential differences in acetaldehyde concentration, is not strongly supported by experimental evidence from the limited number of studies in vivo (Yamamoto et al., 1993; Whitfield, 1994). Further consideration will need to be given to possible mechanisms of these ADH effects.

REFERENCES


ADH GENOTYPE, ALCOHOL DEPENDENCE AND ALCOHOLIC LIVER DISEASE


