Major genetic components underlying alcoholism in Korean population

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Alcohol metabolism is one of the biological determinants that could significantly be influenced by genetic polymorphisms in alcohol-metabolism genes. Alcohol dehydrogenase (ADH) converts alcohol to acetaldehyde, and aldehyde dehydrogenase (ALDH) converts acetaldehyde to acetate. The well-known genetic polymorphisms in ADH1B(His47Arg) and ALDH2(Glu487Lys) have dramatic effects on the rate of metabolizing alcohol and acetaldehyde, respectively. The protective allele of ADH1B (ADH1B/47His) encodes for a rapid ethanol-metabolizing enzyme, and the susceptible allele of the ALDH2 (ALDH2 487Lys) is strongly associated with decreased rate of metabolizing acetaldehyde. However, the combined genetic effects of both functional polymorphisms have not been clarified. The combined analysis of two polymorphisms among a Korean population (n = 1,032) revealed dramatic genetic effects on the risk of alcoholism. Individuals bearing susceptible alleles at both loci have 91 times greater risk for alcoholism [odds ratio (OR) = 91.43, P = 1.4 × 10^-32] and individuals bearing one susceptible and one protective allele at either loci have 11 times greater risk (OR = 11.40, P = 3.5 × 10^-15) compared with subjects who have both protective alleles. The attributable fraction of those genetic factors, calculated based on population controls, indicates that alcoholism in 86.5% of alcoholic patients can be attributed to the detrimental effect of ADH1B 47Arg and/or ALDH2 487Glu in Korean population.

INTRODUCTION

Alcohol metabolism occurs in two major steps: oxidation of alcohol to acetaldehyde by the alcohol dehydrogenases (ADHs) enzymes, especially by ADH1B, and further oxidation of acetaldehyde into acetate by aldehyde dehydrogenase enzymes (ALDHs), mainly by ALDH2. Encoding genes for these two representative alcohol-metabolizing enzymes display polymorphisms (ADH1B His47Arg and ALDH2 Glu487Lys) that show different alcohol/acetaldehyde oxidizing capability among individuals (1–4). The ADH1B/47His allele represents a much higher activity of ADH1B with ~40 times higher Vmax than the homozygotes for the ADH1B/47Arg form, which enables increased alcohol elimination from the blood after alcohol consumption (1,5). The ALDH2*487Lys allele encodes a catalytically inactive subunit (1,5), which causes alcohol-related adverse reactions including flushing, palpitation, nausea, headache, drowsiness, breathlessness and general discomfort (6). These adverse reactions in subjects with ALDH2*487Lys, as a result of excessive acetaldehyde accumulation, tend to reduce alcohol consumption, subsequently reducing the risk of alcoholism.

Many previous studies have reported genetic associations of ADH1B His47Arg and ALDH2 Glu487Lys with alcoholism, especially in Asian populations (7–12). However, the combined genetic effects of these two loci have not yet been clarified. In the current study, the combined genetic effects of ADH1B and ALDH2 genotypes were analyzed in a Korean population (n = 1032).

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RESULTS

In the Korean population, the ADH1B His47Arg polymorphism showed, as expected, a dramatic genetic association with the risk of alcoholism. Referent analysis of ADH1B His47Arg revealed that its genetic mode for the risk of alcoholism is apparently susceptible and recessive, when comparing the strength and magnitude of associations of heterozygotes and homozygotes for ADH1B*47Arg. Only 6.2% of normal controls had the ADH1B*47Arg/Arg genotype, compared with 34.1% in alcoholics [recessive mode; odds ratio (OR) = 7.80 95% confidential interval (CI), 5.18–11.75, P = 8.2 × 10−23]. In addition, the genotype distribution of ADH1B His47Arg showed severe deviation from Hardy–Weinberg equilibrium (HWE) (P = 3.17 × 10−28) in alcoholics, whereas no deviation was detected among normal controls. The deviation from HWE occurring only in alcoholics strongly suggests that a selection bias (or pressure) is also involved, which would be additional direct evidence of association of this polymorphism with the risk of alcoholism (Table 1).

The ALDH2Glu487Lys also showed apparent genetic effects on the risk of alcoholism [dominant mode; OR = 0.10 (95% CI, 0.06–0.15) and P = 3.6 × 10−21]. In contrast to ADH1B*47Arg, the genetic mode of ALDH2*487Lys clearly appeared to be protective and dominant in the referent analysis. Interestingly, subjects bearing ALDH2*487Lys/Lys appeared to have complete genetic protection against alcoholism (no homozygotes in alcoholics) (Table 1).

Next, in order to examine whether these two functional polymorphisms have any interaction effects on the risk of alcoholism, subgroup analysis according to genetic effects of each loci was performed. The results were that similar magnitudes of genetic effects with those of all subjects were shown for the two polymorphisms (Supplementary Materils, Table S1), suggesting clearly independent genetic effects on the risk of alcoholism.

To examine the combined genetic effect of ADH1B His47Arg and ALDH2 Glu487Lys, subjects were subdivided by genetic effects of both loci. Combined analysis revealed huge genetic effects on the risk of alcoholism, e.g. individuals bearing susceptible alleles at both loci were found to have 91 times greater risk for alcoholism (OR = 91.43, P = 1.4 × 10−32) and individuals bearing one susceptible and one protective allele at either loci had 11 times greater risk (OR = 11.40, P = 3.5 × 10−15) compared with subjects who have both protective alleles (Table 2). The results of this combined analysis are concordant with those of the separated analysis (independent effects; Supplementary Materils, Table S1) and clearly showed additive effects on the risk of alcoholism development.

The attributable fraction (AF) was calculated by OR (10.53) and frequency (subjects with one or two susceptible alleles for either loci; 75.2%) based on population controls (Table 2). AF indicates that alcoholism in 85.6% of alcoholic patients in the Korean population can be attributed to the detrimental effects of ADH1B*47Arg and/or ALDH2*487Glu.

DISCUSSION

Alcoholism [MIM# 103780] is a leading cause of morbidity and premature death. Several lines of evidence suggest a substantial genetic component to the risk for alcoholism. Alcoholism is believed to be a multifactorial and polygenic disorder involving complex gene-to-gene and gene-to-environment interactions. According to the National Council on Alcoholism and Drug Dependence (NCADD) and the American Society of Addiction Medicine (ASAM), ‘alcoholism is a primary, chronic disease with genetic, psychosocial and environmental factors influencing its development and manifestations. The disease is often progressive and fatal. It is characterized by continuous or periodic impaired control over drinking, preoccupation with the drug alcohol, use of alcohol despite adverse consequences and distortion in thinking, most notably denial’. In this study, by analyzing the well-known genetic polymorphisms in ADH1B(His47Arg) and ALDH2(Glu487Lys) in a large Korean sample (n = 1032), we were able to show that the combined effect of the two alleles has a huge impact on disease phenotype. The employment of the large sample gives the study a great statistical power, and the findings from this study might be, therefore, indisputable. In terms of combined analysis of two functional polymorphisms, <5% of people in the Korean population (disease and population controls) have susceptible/susceptible genotypes. In addition, although considerable allele frequency variation occurs even among East Asian populations, up to 25% of Asians have protective genotypes at both loci, whereas very
The patients used in this study (n = 549, all males; mean age = 46.1, range = 20–73), all of whom were

MATERIALS AND METHODS

Study subjects and genotyping of polymorphisms

The patients used in this study (n = 549, all males; mean age = 46.1, range = 20–73), all of whom were
alcohol-dependent according to the Diagnostic and Statistical Manual of Mental Disorders IV (DSM-IV) criteria (American Psychiatric Association, 1994), were recruited from Hangang Sacred Heart Hospital, Yong-In Mental Hospital, Hannam Hospital, Gumin Hospital, Hando Hospital (Hallym University groups) and another network of multicenter mental hospitals in Korea (Holy Family Hospital, Chamsarang Mental Hospital, Chunchon Mental Hospital; Catholic University groups). The patients had neither major medical nor co-morbid psychiatric illnesses other than alcohol-related disorders and/or nicotine dependence (43%). The controls were unrelated healthy male employees of Hangang Sacred Heart Hospital (n = 483, all male; mean age = 33.2 years, range = 20–77). Most of the participating employees were non-drinkers; only some were occasional light drinkers, as revealed by a drinking habit questionnaire. Subjects who had first-degree relatives with major psychiatric disorders, such as schizophrenia, mood disorders or substance-use disorders other than nicotine dependence, were excluded. Additional population controls (n = 384, all males) were used for AF calculation. The Institutional Review Board of each hospital approved the study, and informed consents were obtained.

The ADH1B His47Arg and ALDH2 Glu487Lys polymorphisms were genotyped using the TaqMan method (18), which has been described in our previous work (9,19).

Statistics

χ² tests were used to determine if the individual variants were in HWE. Logistic regression analyses, controlling for age as covariate, were used to calculate ORs and the P-values for case-control analysis. The AF was calculated by the formula AF = f(R – 1)/(1 + f(R – 1)), where f is the frequency of the risk factor in the population and R is the measure of the OR (20). In combined analysis (Table 2), several facts were considered when choosing a method of analysis, including (i) the two SNPs were not linked to each other, (ii) no significant interactions were detected between the SNPs, and (iii) both SNPs have obvious effects and their genetic modes are apparent [susceptible/recessive (ADH1B 47Arg) and protective/dominant (ALDH2 487Lys) in this study of a Korean population]. Based on these considerations, we have adopted one of the simplest methods of analysis, e.g. susceptible versus protective at two loci (four subgroups). The protective/protective subgroup was used as the referent for age as covariate, were used to calculate ORs and the P-values for case-control analysis. All statistical analyses were performed using SAS 9.1 (SAS Institute, Inc., Cary, NC, USA).

SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG Online.

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