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Association of GABA_A receptor α_2 subunit gene (GABRA2) with alcohol dependence-related aggressive behavior

Dubravka Svob Strac^a, Gordana Nedic Erjavec^a, Matea Nikolac Perković^a, Korona Nenadic Sviglin^b, Fran Borovecki^c, Nela Pivac^a

^aDivision of Molecular Medicine, Rudjer Boskovic Institute, Zagreb, Croatia

^bCenter for Alcoholism and other Addictions, Psychiatric Hospital Vrapce, Zagreb, Croatia

^cDepartment for Functional Genomics, Center for Translational and Clinical Research, School of Medicine, University of Zagreb, University Hospital Center Zagreb, Zagreb, Croatia

Correspondence to:

Nela Pivac, Ph.D., Senior Scientist

Dubravka Svob Strac, PhD, Research Associate

Division of Molecular Medicine

Rudjer Boskovic Institute

Bijenicka cesta 54, 10 000 Zagreb, Croatia

Phone: + 385 1 457 1207, + 385 1 457 1365; Fax: + 385 1 456 1010

E-mail: npivac@irb.hr, dsvob@irb.hr

Abstract

Alcohol dependence is a common chronic disorder precipitated by the complex interaction between biological, genetic and environmental risk factors. Recent studies have demonstrated that polymorphisms of the gene encoding the GABA_A receptor α_2 subunit (GABRA2) are associated with alcohol dependence in different populations of European ancestry. As aggression often occurs in the context of alcohol dependence, the aim of this study was to examine the allelic and haplotypic association of GABRA2 gene with alcohol dependence and related aggressive behavior in subjects of Eastern European (Croatian) origin.

Genotyping of the 3 single nucleotide polymorphisms (SNPs) across the GABRA2 gene (rs567926, rs279858 and rs9291283) was performed in patients with alcohol dependence (N = 654) and healthy control subjects (N = 574). Alcohol-dependent participants were additionally subdivided according to the presence/absence of aggressive behavior and type of alcohol dependence according to the Cloninger's classification.

The association of rs279858 with alcohol dependence yielded nominal significance level. Haplotype analysis revealed a high degree of linkage disequilibrium (LD) for rs567926 and rs279858, but not for rs9291283 polymorphism in the GABRA2 gene. In patients with alcohol dependence, the A-C (rs567926 and rs279858) haplotype carriers were more likely to demonstrate aggressive behavior. The same haplotype (present only in 1.6% of all subjects) was significantly more often present in patients with a combination of early onset alcohol abuse and aggression, corresponding to the Cloninger's type II alcoholism subgroup. These findings support the involvement of GABRA2 gene in alcohol dependence-related aggressive behavior.

Keywords: aggression, alcohol dependence, Cloninger's classification, GABRA2, haplotype, polymorphism

1. Introduction

Alcohol dependence is a highly prevalent chronic disorder associated with a wide range of physical, mental, social, functional, legal and economic consequences. This complex disease, precipitated by the interaction between biological, genetic and environmental risk factors, is heterogeneous in its etiology and phenotype characteristics, such as the age of onset, drinking behavior, as well as comorbid disorders (Köhnke, 2008). The findings that alcoholism shows no classic pattern of inheritance, and that alcohol affects various targets in the brain, suggest that genetic vulnerability to alcoholism is likely to be due to multiple contributing genes encoding proteins in many neurotransmitter systems and signal transduction pathways (Enoch, 2008). GABA_A receptors, the major inhibitory neurotransmitter receptors in the brain (Korpi et al., 2002), are implicated in the acute and chronic effects of alcohol, including sedation, anxiolysis, lack of motor coordination, ethanol preference, tolerance, dependence and withdrawal (Kumar et al., 2009).

Genomewide linkage studies suggest that several GABA_A receptor gene clusters might influence the susceptibility for alcohol dependence, including the cluster of GABA_A receptor subunit genes (α_2 , α_4 , β_1 , γ_1) located on chromosome 4p13-12 (Reich et al., 1998). Different studies demonstrated that various polymorphisms in the genes encoding GABA_A receptor subunits are associated with alcoholism in different populations of European ancestry (Covault et al., 2004; Enoch et al., 2006; Lappalainen et al., 2005; Li et al., 2014; Sander et al., 1999; Soyka et al., 2008). However, recent findings suggest that the association of alcohol dependence with markers and haplotypes in the middle and 3' region of the GABRA2 gene might also be due to the linkage disequilibrium (LD) with risk-related variants in the adjacent GABRG1 gene (Covault et al., 2008; Drgon et al., 2006).

Alcohol consumption has been often linked to violence and aggression (Beck and Heinz, 2013), while aggression-related personality traits have been suggested to mediate

individual responses to alcohol (Bjork et al., 2004). Alcohol-related aggression also occurs frequently in the context of chronic alcohol consumption and dependence (Beck and Heinz, 2013) and various studies estimate that up to 50% of alcohol-dependent men display violent behavior (Giancola et al., 2009). Research conducted on the involvement of GABRA2 gene in alcohol use and impulse control behavior, suggested its role in hyperexcitability, impulsivity, aggression or externalizing spectrum disorder (Dick et al., 2006, 2009; Heitzeg et al., 2014; Simons et al., 2013; Villafuerte et al., 2013, 2014). These findings are in line with the results of many studies demonstrating the involvement of GABAergic system in aggressive behavior (Takahashi and Miczek, 2014).

The aim of the present study was to determine the allelic and haplotypic association of the GABRA2 gene with alcohol dependence and alcohol dependence-related aggressive behavior in Caucasian subjects of East European (Croatian) origin. Therefore, three single nucleotide polymorphisms (SNPs) located in the 5' and central region of the GABRA2 gene and in the intergenic region between GABRA2 and GABRG1 genes were analyzed: rs567926 (3' flanking region), rs279858 (exon 5) and rs9291283 (intron 3).

All these SNPs have been previously reported to be associated (individually and in haplotype block with other SNPs) with alcohol dependence (Covault et al., 2004; 2008; Edenberg et al., 2004; Fehr et al., 2006; Ittiwut et al., 2008; Lappalainen et al., 2005; Soyka et al., 2008). The distribution of the GABRA2 gene variants in alcohol-dependent patients and healthy subjects, corrected for gender, age and nicotine dependence was determined. In order to elucidate possible behavioral effects of GABRA2 variations, the group of participants with alcohol dependence was additionally subdivided according to the presence/absence of aggressive behavior and type of alcohol dependence according to the Cloninger's classification.

2. Materials and methods

2.1. Subjects

A total of 1228 unrelated Caucasian subjects of East European (Croatian) origin, including 574 healthy control subjects and 654 medication-free patients with alcohol dependence, were enrolled in the study. All subjects were recruited during the period between 2005 and 2009 from the Centre of Alcoholism and Other Addictions, Psychiatric Hospital Vrapce and University Hospital Centre Zagreb, Croatia.

The diagnosis of alcohol dependence was done using the Structured Clinical Interview (SCID), based on the DSM-IV criteria (American Psychiatric Association, 1994). The interview and the blood sampling were conducted after hospital admission prior to starting treatment. In addition to the SCID and a psychiatric interview, aggressive behavior was assessed using the Brown–Goodwin Assessment of Lifetime Aggression (Brown–Goodwin Scale; Brown et al., 1979). The questionnaire adapted from Brown–Goodwin Scale consisted of seven behavioral categories (Buydens-Branchey et al., 1989), translated into Croatian: problems with discipline in the armed forces; problems with discipline at work; assaults on other persons; property damage; incarceration for assaultive behavior; incarceration for other crimes; crimes that did not result in incarceration. These categories were evaluated with a 0–4 scale. The total maximum score was 28, and according to Buydens-Branchey et al. (1989), a cut-off score of 8 was designated for the presence of aggressive behavior (Buydens-Branchey et al., 1989). The alcohol-dependent patients with a combination of early onset of alcohol abuse (occurring before 25 years of age) and presence of aggressive behavior corresponded to type II alcoholism subgroup, while the patients with the late onset of alcohol abuse (occurring after 25 years of age) and without aggression corresponded to type I alcoholism subgroup, according to the Cloninger’s classification (Cloninger et al., 1988).

Healthy control subjects completed questionnaires regarding their medical history, drinking and smoking habits. Inclusion criteria were no current medication therapy, no

previous or current psychiatric disorders, no drug or alcohol abuse, no suicide attempts, no family history of psychiatric disorders (determined according to participants' self-report about the mental health status of their parents, grandparents, siblings and children), unrelated to other study participants, and belonging to the native ethnic group with at least three generations living in the region.

All participants were Caucasians of the East European origin from the same geographic area (i.e., from the Zagreb County, Croatia). The relative genetic homogeneity of the enrolled subjects was confirmed by the principal component analysis (PCA) performed with program PAST, Version 3.06 (Hammer et al., 2001). All participants agreed to give a blood sample, to participate in the study, and gave their written informed consent. The study was approved by the local Ethics committees and was carried out in accordance with the Helsinki declaration (1975).

Demographic and clinical sample characteristics of the control and alcohol-dependent individuals are listed in Table 1. The group of subjects with alcohol dependence was significantly older than the control group ($t = 14.78$, $df = 1226$, $p < 0.0001$; Student's t -test). Following ANOVA ($F(3,1224) = 75.58$; $p < 0.001$), Tukey test revealed that both alcohol-dependent males ($p < 0.001$) and females ($p < 0.001$) were significantly older than healthy men and women. Although both healthy and alcohol-dependent participants were predominantly male (89.02% and 81.19% respectively), the group of alcoholics included more females than control group ($\chi^2 = 14.59$, $df = 1$, $p = 0.0001$). Patients with alcohol dependence smoked more frequently ($\chi^2 = 99.96$, $df = 1$, $p < 0.0001$) than healthy participants.

2.2. Genotyping

Blood samples (8 ml) from alcohol-dependent patients and control subjects were drawn in a plastic syringe with 2 ml acid citrate dextrose anticoagulant. Genomic DNA was

isolated from peripheral blood leukocytes according to standard procedures by a salting out method. Three SNPs located in the 5' and central region of the GABRA2 gene and in the intergenic region between GABRA2 and GABRG1 genes on chromosome 4 were analyzed. Namely, rs567926 (3' flanking region), rs279858 (exon 5) and rs9291283 (intron 3) were genotyped using TaqmanTM probe-primer combinations (Cat. No. C_7537087_10, C_2073557_1_ and C_8262290_10), available from the Applied Biosystems Assay-on-DemandTM human SNP genotyping collection (Applied Biosystems, Foster City, CA, USA). Taqman-based allele-specific polymerase chain reactions and post-PCR fluorescence plate reads were performed according to the procedure described by Applied Biosystems, using an ABI Prism 7000 Sequencing Detection System apparatus. Briefly, 20 ng of genomic DNA was PCR amplified in 96-well plates using a 10 µl reaction volume for 40 cycles at 92°C for 15 s followed by 60°C for 60 s. Allele nucleotide designation of the analyzed SNPs refers to the chromosome plus strand sequence.

2.3. Data analysis

Statistical analyses were performed with GraphPad Prism version 4.00 (GraphPad Software, San Diego, CA, USA) and MedCalc version 12.0 (MedCalc Software, Mariakerke, Belgium). Age (expressed in years as mean \pm SD) was analyzed by Student's *t*-test, or with one-way analysis of variance (ANOVA) followed by Tukey's test. Possible deviations from Hardy-Weinberg equilibrium (HWE) were tested using goodness of fit χ^2 test. Genotype and allele frequencies (presented as numbers and percents) were evaluated by a χ^2 test of independence. Logistic regression analysis was used to derive corrected measures for association of individual SNPs with alcohol dependence in which age, sex and smoking were used as covariates, while the most frequent genotype was taken as the reference group. Odds ratios (ORs) and 95% confidence intervals (CIs) were reported as a measure of the effect size.

Haploview version 4.2 software (Barrett et al., 2005) was used to produce linkage disequilibrium (LD) matrices with D' set to 0.80 and to compute haplotype block structure. Best-estimate haplotype pairs for each subject were generated using PHASE version 2.0.2 software, which incorporates a Bayesian statistical method for reconstructing estimated haplotypes from population data (Stephens and Donnelly, 2003). Estimated haplotype frequencies were compared between different groups using a series of 2 x 2 contingency tables for each haplotype compared to the sum of all other haplotypes.

G*Power 3 Software (Faul et al., 2007) was used for conducting power analyses, i.e. to determine a priori sample size and to post hoc compute the achieved power. For the analysis of the genotype frequency of the 3 studied SNPs with a χ^2 -test (with $\alpha = 0.0166$; power $(1 - \beta) = 0.800$; and with a small effect size ($\omega = 0.15$; $df = 5$), total sample size was 727 and actual total sample size was 1228. Post-hoc computed achieved power $(1 - \beta)$ was 0.998. In a haplotype analysis of the 2 SNPs with a χ^2 -test (with $\alpha = 0.025$; power $(1 - \beta) = 0.800$; a small effect size ($\omega = 0.15$; $df = 1$), total sample size was 423, and actual total sample size was 654. Post-hoc computed achieved power $(1 - \beta)$ was 0.949.

3. Results

Genotype distributions in healthy as well as in alcohol-dependent subjects for rs567926 (controls: $\chi^2 = 0.273$, $p = 0.601$; AD subjects: $\chi^2 = 0.294$, $p = 0.587$), rs279858 (controls: $\chi^2 = 0.846$, $p = 0.358$; AD subjects: $\chi^2 = 0.040$, $p = 0.842$) and rs9291283 (controls: $\chi^2 = 0.139$, $p = 0.709$; AD subjects: $\chi^2 = 1.196$, $p = 0.274$) polymorphisms were in Hardy–Weinberg equilibrium (HWE). No significant differences in the frequency of the genotypes or alleles for all three investigated SNPs between alcohol-dependent and control individuals were detected using χ^2 -test (Table 2). However, logistic regression analysis with age, gender and nicotine dependence as covariates revealed nominal significance for rs279858 polymorphism (that disappeared after correction for multiple testing (i.e. $p = 0.0166$)),

suggesting that individuals carrying the T allele might have lower risk of alcohol-dependence (OD = 0.68, 95% CI = 0.47 to 0.98, $p = 0.0386$), when compared to carriers of CC homozygous genotype.

The genotype and allele distribution, for any specific SNP tested, was not significantly different between aggressive and non-aggressive alcohol-dependent patients, as well as between patients with a combination of early onset of alcohol abuse and aggressive behavior (Cloninger's type II alcoholism subgroup) and patients with the late onset of alcohol abuse without aggression (Cloninger's type I alcoholism subgroup) (Table 2).

To further examine the association of GABRA2 gene with alcohol dependence and related aggressive behavior, a haplotype analysis was performed. A high degree of linkage disequilibrium (LD) was revealed for rs567926 and rs279858, located in the central and 3' region, respectively, but not for rs9291283 located in the 5' region of the GABRA2 gene (Fig. 1). Similar patterns of LD were observed for the control group and the group with alcohol dependence when examined separately (data available on request).

The computation of the best-estimated haplotypes of rs567926 and rs279858 using PHASE, identified four most common 2-marker haplotypes (Table 3). There were no significant differences in the frequency of haplotypes between healthy and alcohol-dependent individuals. However, following a correction for multiple testing, alcohol-dependent A-C haplotype carriers were significantly more likely to demonstrate aggressive behavior ($\chi^2 = 5.774$, $df = 1$, $p = 0.0163$). The same haplotype was significantly ($\chi^2 = 6.296$, $df = 1$, $p = 0.0121$) more frequently present in patients with type II of alcohol dependence according to the Cloninger's classification, characterized with the early onset of alcohol abuse and aggressive behavior.

4. Discussion

The main findings of our study are nominal association (un-corrected for multiple testing) of rs279858 polymorphism with alcohol dependence, as well as significant higher frequency (following correction for multiple testing) of the A-C (rs567926 and rs279858) haplotype in alcohol-dependent individuals with aggressive behavior and with Cloninger's type II of alcohol dependence.

The rs279858 polymorphism is synonymous coding variant (Lys132Lys) in exon 5, which has previously been reported to be associated (individually and in haplotype block with other SNPs) with alcohol dependence (Covault et al., 2004; Edenberg et al., 2004; Fehr et al., 2006; Lappalainen et al., 2005) and subjective effects of alcohol (Haughey et al., 2008). Furthermore, rs279858 was one of the markers at the GABRA2 locus with nominal significant association with alcohol dependence in GWAS (Bierut et al., 2010) and in recent meta-analysis (Zintzaras, 2012). In the study using convergence of GWA and candidate gene studies for alcoholism, among candidate loci available for analysis, only rs279858 in GABRA2 ($p = 0.0052$, OR = 1.16) demonstrated an association with alcoholism (Olfson & Bierut, 2012). However, some studies have not confirmed these findings (Drgon et al., 2006; Enoch et al., 2006; Soyka et al., 2008).

Our results suggesting that individuals carrying the T allele might have lower risk of alcohol dependence, when compared to carriers of CC homozygous genotype, are in line with studies reporting that C allele was more frequent in the group of subjects addicted to alcohol (Covault et al., 2004; Fehr et al., 2006; Lappalainen et al., 2005), and was associated with a higher daily probability of drinking and heavy drinking in patients with alcohol dependence (Bauer et al., 2007). Moreover, some studies indicated that carriers of the C allele experience greater stimulatory and euphoric effects of alcohol (Arias et al., 2014).

Furthermore, we observed a high degree of linkage disequilibrium (LD) for rs279858 and rs567926 located in the central GABRA2 region and intragenic region between GABRA2 and GABRG1 genes, respectively, indicating that these two SNPs are good surrogates for each other, likely to be transmitted together, and therefore likely to capture similar genetic variance. Our findings of a haplotype block within GABRA2, which extends from the central area of the gene to the 3' end, and probable existence of another haplotype block in the 5' area of the gene, are consistent with the data of previous studies (Enoch, 2008). These results also suggest that the 3' GABRA2 haplotype block might extend to the 5' promoter region of GABRG1 gene, supporting previous reports about alcoholism risk variants located in the gene encoding the γ_1 subtype of GABA_A receptors (Covault et al., 2008).

In contrast to the studies that reported that less frequent of the two common yin-yang GABRA2 haplotypes accounts for increased risk of alcohol dependence (Covault et al., 2004; Edenberg et al., 2004; Fehr et al., 2006; Lappalainen et al., 2005), our study demonstrated no significant differences in the frequency of the two-marker (rs567926 and rs279858) haplotypes between alcohol-dependent subjects and controls.

The lack of association of this risk haplotype with alcohol dependence in our study might be explained by the differences in the origin of participants, as the role of genetic and environmental risk factors may be different in Croatian compared to other reported populations. Specifically, common environmental risk factors, such as level of exposure to alcohol and average alcohol consumption, may differ between various countries, potentially reflecting either a reduced or increased significance of genetic risk factors for alcohol dependence. In line with this hypothesis, population differences in association studies between the GABRA2 gene and alcoholism have also been observed (Covault et al., 2008; Enoch et al., 2006). In addition to ethnic differences, our results could be explained by the

sample size, selection of subjects, or the population stratification, but not with sexual dimorphism, since we conducted logistic regression correction for gender.

The GABRA2 gene variants have been associated with alcohol drinking behavior (Bauer et al., 2007), alcoholism-related β -EEG endophenotype (Edenberg et al., 2004), level of response to alcohol (Schuckit et al., 2004), subjective effects of alcohol (Haughey et al., 2008), co-occurring psychiatric disorders (Dick et al., 2006; Enoch et al., 2006), severity of alcohol withdrawal (Soyka et al., 2008), and potential treatment outcome (Bauer et al., 2007; Soyka et al., 2008). In addition, reported association of GABRA2 variants with impulsiveness (Villafuerte et al., 2013, 2014), childhood conduct disorder (Dick et al., 2006), and externalizing behavior (Dick et al., 2009) in alcohol-dependent subjects strongly suggests the role of GABRA2 gene in a general predisposition toward behavioral disinhibition processes and lack of impulse control.

Impulsivity has been identified as an important determinant of alcohol use and alcohol-related problems (Lejuez et al., 2010). High levels of impulsiveness (Lejuez et al., 2010), low stress tolerance (Daughters et al., 2008) and lack of control under distress (Villafuerte et al., 2013) can reinforce the moody and temper tantrum behavior and the inclination to behave aggressively when under the influence of alcohol (Beck and Heinz, 2013). Externalizing behaviors such as aggression and rule breaking (e.g., defiance, theft, and vandalism) seems to be influenced by both genetic and environmental factors (Simons et al., 2012).

It has been demonstrated that individuals with specific GABRA2 genetic variants displayed more aggression and hostility toward their romantic partners when they had been subjected to harsh parenting (Simons et al., 2013). On the other hand, to the best of our knowledge, this is the first report to show the haplotypic association of the GABRA2 gene with aggressive behavior in alcohol-dependent patients, as well as with Cloninger's type II alcoholism, characterized by early onset of alcohol abuse and aggression. However, as A-C

haplotype is rare (present only in 1.6% of all subjects enrolled in the study), its contribution to the overall phenotype of aggressive behavior in alcohol-dependent population or Cloninger's type II alcoholism is probably limited. It is now generally accepted that genetic risk for complex disorders, such as alcoholism and aggression, is likely to be due to numerous genetic variants, each of small effect, as well as to interaction of various genetic and environmental factors (Enoch, 2013).

Cloninger's classification (Cloninger et al., 1988) is one of the various methods of subtyping which have been proposed in order to overcome the biological, sociological and psychopathological heterogeneity of alcohol dependence and to more precisely define specific subtypes (endophenotypes) of alcoholism (Leggio et al., 2009). This classification distinguishes type I alcoholism with a relatively late onset, neurotic symptoms and minimal criminality, from the type II alcoholism with a relatively early onset (in the early 20s), elevated levels of antisocial behavior and delinquency which often begins during adolescence. Type I alcoholism, found in both female and male offspring of alcohol-dependent biological parents, is often cited as only moderate heritable (less than 40%), and influenced by postnatal environmental effects. In contrast, type II or "male-limited" alcoholism is suggested to be strongly heritable (estimated heritability of 90%), transmitted primarily from father to son, and showing moderate environmental influence (Cloninger et al., 1988). Early onset of alcoholism often reflects greater severity, including a higher risk for recurrence, as well as comorbid antisocial personality disorder (ASPD) and conduct disorder (Dick et al., 2006), which are seen significantly more often in Cloninger's type II than in type I alcohol-dependent patients. The GABRA2 genotype has been associated with drug dependence and antisocial behavior, which have been related to poor outcome (Dick et al., 2006).

In contrast to Cloninger's classification, Lesch's typology (Lesch et al., 1990) which distinguishes four types of alcohol-dependent subjects, depending on the family history of

alcoholism, patients' drinking patterns, previous personal psychopathology, origin of substance craving and hypothetical neurobiological background, is based mostly on environmental criteria. Hence, perhaps it is not surprising that no genetic background of this classification has been found thus far, including no association of GABRG1 and GABRA2 genes with Lesch's typology reported by Grzywacz et al. (2012).

Our results support a growing body of evidence linking GABA_A receptors with the development of alcohol tolerance, dependence and withdrawal symptoms (Korpi et al., 2002; 2009; Kumar et al., 2004; 2009; Staley et al., 2005; Enoch, 2008). Furthermore, the involvement of GABA_A receptors in aggressive behavior seems to be well established, although the effects may vary depending on the receptor subtype, its localization, and the type of aggressive behavior studied, possibly resulting in the individual differences in the propensity for escalated aggression induced by alcohol (Takahashi and Miczek, 2014).

GABA system exerts inhibitory effects on dopaminergic function in the nucleus accumbens (NAcc) (Steffensen et al., 1998), which increased activation has been associated with behavioral traits such as impulsiveness (Forbes et al., 2009), sensation seeking (Bjork et al., 2008), and externalizing behaviors (Yau et al., 2012). GABRA2 gene variation has been associated with individual differences in NAcc activation of adolescents during incentive anticipation, related to dopamine-specific motivated behaviors (Heitzeg et al., 2014). Moreover, aggression has been attributed to imbalance between glutamatergic excitation and GABAergic inhibition in limbic areas (Miczek et al., 2007), while modulation of GABAergic system by 5-HT in corticolimbic neurons is suggested as particularly relevant mechanism underlying specific forms of escalated aggressive behavior such as alcohol-heightened aggression (de Almeida et al., 2005).

Although the $\alpha_1\beta_2\gamma_2$ GABA_A receptor, the most abundant and widespread subtype in the adult brain, originates from the chromosome 5 gene cluster, the GABA_A receptor genes on

chromosome 4 are highly expressed in the mesolimbic dopamine reward pathway including hippocampus and dopaminergic neurons in the substantia nigra and ventral tegmental area (Okada et al., 2004). The α_2 subunit, which has been identified as the primary α GABA_A receptor subunit in these limbic regions (McKernan & Whiting, 1996), has been implicated in the development of addictions and is stimulated by stress (Enoch, 2008). The α_2 subunit plays a major role in the anxiolytic action of benzodiazepines and barbiturates (Löw et al., 2000) and in the hypnotic effects of combined exposure to ethanol and benzodiazepines (Täuber et al., 2003).

The observed haplotypic association of GABRA2 and alcohol dependence-related aggressive behavior might be due to the linkage disequilibrium of markers in GABRA2 and GABRG1 genes which has been reported in various populations of European ancestry (Covault et al., 2008; Drgon et al., 2006). Results from diverse cultural or ethnic groups might be useful in order to further characterize the genetic variations of GABA_A receptors associated with the alcohol dependence and related aggressive behavior, and to define the alcohol-related functional changes in GABRA2 and GABRG1 genes. Namely, no functional polymorphisms in these genes have yet been identified (Tian et al., 2005); however the results elucidating the functional significance of alternative splicing isoforms have been accumulating. Namely, Haughey et al. (2008) demonstrated that rs279858 variant resulted in changes of the GABRA2 mRNA levels in post-mortem prefrontal cortical tissue. Although numerous alternative splicing isoforms (Tian et al., 2005), as well as distant gene enhancers and suppressors on chromosome 4 (Enoch et al., 2008) may be potentially implicated in function, additional research is required to identify functional loci in this gene cluster.

The limitation of the study is that it analyzes only 3 SNPs in GABRA2 gene. However, given the evidence that genetic effects are likely to be small, the candidate gene approach has an advantage over GWAS due to the relative lack of multiple comparisons and

much lower threshold for significance (Holliday et al., 2013). In order to maximize the sample size and power to detect robust association, many GWAS include subjects of different ethnic origin or race, although a substantial number of variants across the genome differ in frequency between various populations (Rosenberg et al., 2010; Gelernter et al., 2014). In addition, subjects enrolled in GWAS are often drawn from large consortia with distinct ascertainment design (Bierut et al., 2010; Gelernter et al., 2014), resulting in potential genetic heterogeneity and decreased likelihood that GWAS would identify association to genes contributing specifically to particular phenotypes. The discovered loci reaching genome-wide significance have weak additive predictive power for specific phenotypes, which limits their clinical relevance for some traits (Ward & Kellis, 2012).

Moreover, another limitation of our study is that enrolled control subjects were younger than patients with alcohol-dependence. Therefore, we cannot exclude the possibility that these healthy subjects may develop alcohol dependence when getting older. This might explain the lack of detecting a significant genotype and/or haplotype association of the investigated SNPs with alcoholism. However, the only significant findings in this study were obtained in the alcohol-dependent group of patients subdivided according to aggressive behavior and Cloninger's type of alcoholism.

On the other hand, the advantages of our study lie in the large number of enrolled ethnically homogenous subjects (1228 Caucasian Croatian subjects from Zagreb County), confirmed by the principal component analysis, carefully determined specific alcohol-related phenotypes, correction for multiple testing, and a priori determined sample size and post hoc achieved power. For smaller numbers of variants, it is also possible to consider the joint effects of markers via haplotype association tests (Holliday et al., 2013), which was also performed in our study for rs567926 and rs279858.

In conclusion, besides supporting a moderate GABRA2 involvement in alcohol dependence, to the best of our knowledge, this is the first study to show a significant haplotypic association of this gene with aggression in alcohol-dependent subjects. In line with these findings, our results also suggest a possible role of GABRA2 gene in a more severe form of alcoholism, characterized by the early onset of alcohol abuse and presence of aggressive behavior. Our findings are consistent with studies showing that the GABAergic system is a potential target for promising novel therapeutics in the treatment of alcohol dependence, such as baclofen, gabapentin, topiramate and neuroactive steroids (Enoch, 2008; Korpi et al., 2002; Leggio et al., 2008). However, further studies should investigate whether GABRA2 genetic variants are associated with an increased risk of aggression in the general population.

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References

1. American Psychiatric Association. Diagnostic and statistical manual of mental disorders 4th ed. 1994; Washington, DC: American Psychiatric Press.
2. Arias AJ, Covault J, Feinn R, Pond T, Yang BZ, Ge W et al. A GABRA2 variant is associated with increased stimulation and 'high' following alcohol administration. *Alcohol Alcohol* 2014; 49: 1-9.
3. Barrett JC, Fry B, Maller J, Daly MJ. Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics* 2005; 21: 263-5.

4. Bauer LO, Covault J, Harel O, Das S, Gelernter J, Anton R et al. Variation in GABRA2 predicts drinking behavior in project MATCH subjects. *Alcohol Clin Exp Res* 2007; 31: 1780-7.
5. Beck A, Heinz A. Alcohol-related aggression-social and neurobiological factors. *Dtsch Arztebl Int* 2013; 110: 711-5.
6. Bierut LJ, Agrawal A, Bucholz KK, Doheny KF, Laurie C, Pugh E, et al.; Gene, Environment Association Studies Consortium. A genome-wide association study of alcohol dependence. *Proc Natl Acad Sci USA* 2010; 107: 5082-7.
7. Bjork JM, Hommer DW, Grant SJ, Danube C. Impulsivity in abstinent alcohol-dependent patients: relation to control subjects and type 1-/type 2-like traits. *Alcohol* 2004; 34: 133-50.
8. Bjork JM, Knutson B, Hommer DW. Incentive-elicited striatal activation in adolescent children of alcoholics. *Addiction* 2008; 103: 1308-19.
9. Brown GL, Goodwin FK, Ballenger JC, Goyer PF, Major LF. Aggression in humans correlates with cerebrospinal fluid amine metabolites. *Psychiatry Res* 1979; 1: 131-9.
10. Buydens-Branchey L, Branchey MH, Noumair D. Age of alcoholism onset. I. Relationship to psychopathology. *Arch Gen Psychiatry* 1989; 46: 225-30.
11. Cloninger CR, Sigvardsson S, Gilligan SB, von Knorring AL, Reich T, Bohman M. Genetic heterogeneity and the classification of alcoholism. *Adv Alcohol Subst Abuse* 1988; 7: 3-16.
12. Covault J, Gelernter J, Hesselbrock V, Nellissery M, Kranzler HR. Allelic and haplotypic association of GABRA2 with alcohol dependence. *Am J Med Genet B Neuropsychiatr Genet* 2004; 129B: 104-9.

13. Covault J, Gelernter J, Jensen K, Anton R, Kranzler HR. Markers in the 5'-region of GABRG1 associate to alcohol dependence and are in linkage disequilibrium with markers in the adjacent GABRA2 gene. *Neuropsychopharmacology* 2008; 33: 837-48.
14. Daughters SB, Sargeant MN, Bornovalova MA, Gratz KL, Lejuez CW. The relationship between distress tolerance and antisocial personality disorder among male inner-city treatment seeking substance users. *J Pers Disord* 2008; 22: 509–24.
15. de Almeida RM, Ferrari PF, Parmigiani S, Miczek KA. Escalated aggressive behavior: dopamine, serotonin and GABA. *Eur J Pharmacol* 2005; 526: 51-64.
16. Dick DM, Bierut L, Hinrichs A, Fox L, Bucholz KK, Kramer J et al. The role of GABRA2 in risk for conduct disorder and alcohol and drug dependence across developmental stages. *Behav Genet* 2006; 36: 577-90.
17. Dick DM, Latendresse SJ, Lansford JE, Budde JP, Goate A, Dodge KA et al. Role of GABRA2 in trajectories of externalizing behavior across development and evidence of moderation by parental monitoring. *Arch Gen Psychiatry* 2009; 66: 649-57.
18. Drgon T, D'Addario C, Uhl GR. Linkage disequilibrium, haplotype and association studies of a chromosome 4 GABA receptor gene cluster: candidate gene variants for addictions. *Am J Med Genet B Neuropsychiatr Genet* 2006; 141 B: 854-60.
19. Edenberg HJ, Dick DM, Xuei X, Tian H, Almasy L, Bauer LO et al. Variations in GABRA2, encoding the alpha 2 subunit of the GABA(A) receptor, are associated with alcohol dependence and with brain oscillations. *Am J Hum Genet* 2004; 74: 705-14.
20. Enoch MA. The role of GABA(A) receptors in the development of alcoholism. *Pharmacol Biochem Behav* 2008; 90: 95-104.
21. Enoch MA. Genetic influences on the development of alcoholism. *Curr Psychiatry Rep.* 2013; 15: 412.

22. Enoch MA, Schwartz L, Albaugh B, Virkkunen M, Goldman D. Dimensional anxiety mediates linkage of GABRA2 haplotypes with alcoholism. *Am J Med Genet B Neuropsychiatr Genet* 2006; 141 B: 599-607.
23. Faul F, Erdfelder E, Lang AG, Buchner A. G*Power 3: a flexible statistical power analysis program for the social, behavioral, and biomedical sciences. *Behav Res Methods* 2007; 39: 175-91.
24. Fehr C, Sander T, Tadic A, Lenzen KP, Anghelescu I, Klawe C et al. Confirmation of association of the GABRA2 gene with alcohol dependence by subtype-specific analysis. *Psychiatr Genet* 2006; 16: 9–17.
25. Forbes EE, Brown SM, Kimak M, Ferrell RE, Manuck SB, Hariri AR. Genetic variation in components of dopamine neurotransmission impacts ventral striatal reactivity associated with impulsivity. *Mol Psychiatry* 2009; 14: 60-70.
26. Gelernter J, Kranzler HR, Sherva R, Almasy L, Koesterer R, Smith AH et al. Genome-wide association study of alcohol dependence: significant findings in African- and European-Americans including novel risk loci. *Mol Psychiatry* 2014; 19: 41-9.
27. Giancola PR, Levinson CA, Corman MD, Godlaski AJ, Morris DH, Phillips JP et al. Men and women, alcohol and aggression. *Exp Clin Psychopharmacol* 2009; 17: 154-64.
28. Grzywacz A, Małecka I, Korostyński M, Przewłocki R, Bieńkowski P, Samochowiec J. GABA-A receptor genes do not play a role in genetics of Lesch's typology in Caucasian subjects. *Arch Med Sci* 2012; 8: 357-61.
29. Haughey HM, Ray LA, Finan P, Villanueva R, Niculescu M, Hutchison KE. Human gamma-aminobutyric acid A receptor alpha2 gene moderates the acute effects of alcohol and brain mRNA expression. *Genes Brain Behav* 2008; 7: 447-54.

30. Heitzeg MM, Villafuerte S, Weiland BJ, Enoch MA, Burmeister M, Zubieta JK et al. Effect of GABRA2 genotype on development of incentive-motivation circuitry in a sample enriched for alcoholism risk. *Neuropsychopharmacology* 2014; 39: 3077-86.
31. Holliday EG, Oldmeadow CJ, Maguire JM, Attia J. Candidate Gene Association Studies in Stroke; P. In *Stroke Genetics*, Sharma, J.F. Meschia (eds.), Springer-Verlag, London, 2013.
32. Ittiwut C, Listman J, Mutirangura A, Malison R, Covault J, Kranzler HR et al. Interpopulation linkage disequilibrium patterns of GABRA2 and GABRG1 genes at the GABA cluster locus on human chromosome 4. *Genomics*. 2008; 91: 61-9.
33. Köhnke MD. Approach to the genetics of alcoholism: a review based on pathophysiology. *Biochem Pharmacol* 2008; 75: 160-77.
34. Korpi ER, Gründer G, Lüddens H. Drug interactions at GABA(A) receptors. *Prog Neurobiol* 2002; 67: 113-59.
35. Kumar S, Fleming RL, Morrow AL. Ethanol regulation of gamma-aminobutyric acid A receptors: genomic and nongenomic mechanisms. *Pharmacol Ther* 2004; 101: 211-26.
36. Kumar S, Porcu P, Werner DF, Matthews DB, Diaz-Granados JL, Helfand RS et al. The role of GABA(A) receptors in the acute and chronic effects of ethanol: a decade of progress. *Psychopharmacology (Berl)* 2009; 205: 529-64.
37. Lappalainen J, Krupitsky E, Remizov M, Pchelina S, Taraskina A, Zvartau E et al. Association between alcoholism and gamma-amino butyric acid alpha2 receptor subtype in a Russian population. *Alcohol Clin Exp Res* 2005; 29: 493-8.
38. Leggio L, Kenna GA, Fenton M, Bonenfant E, Swift RM. Typologies of Alcohol Dependence. From Jellinek to Genetics and beyond. *Neuropsychol Rev* 2009; 19: 115-29.

39. Leggio L, Kenna GA, Swift RM. New developments for the pharmacological treatment of alcohol withdrawal syndrome. A focus on non-benzodiazepine GABAergic medications. *Prog Neuropsychopharmacol Biol Psychiatry* 2008; 32: 1106-17.
40. Lejuez CW, Magidson JF, Mitchell SH, Sinha R, Stevens MC, de Wit H. Behavioral and biological indicators of impulsivity in the development of alcohol use, problems, and disorders. *Alcohol Clin Exp Res* 2010; 34: 1334–45.
41. Lesch OM, Kefer J, Lentner S, Mader R, Marx B, Musalek M et al. Diagnosis of chronic alcoholism--classificatory problems. *Psychopathology* 1990; 23: 88-96.
42. Li D, Sulovari A, Cheng C, Zhao H, Kranzler HR, Gelernter J. Association of gamma-aminobutyric acid A receptor $\alpha 2$ gene (GABRA2) with alcohol use disorder. *Neuropsychopharmacology* 2014; 39: 907-18.
43. Löw K, Crestani F, Keist R, Benke D, Brünig I, Benson JA et al. Molecular and neuronal substrate for the selective attenuation of anxiety. *Science* 2000; 290: 131-4.
44. McKernan RM, Whiting PJ. Which GABA_A-receptor subtypes really occur in the brain? *Trends Neurosci* 1996; 19: 139-43.
45. Miczek KA, de Almeida RM, Kravitz EA, Rissman EF, de Boer SF, Raine A. Neurobiology of escalated aggression and violence. *J Neurosci* 2007; 27: 11803-6.
46. Miczek KA, Fish EW, De Bold JF, De Almeida RM. Social and neural determinants of aggressive behavior: pharmacotherapeutic targets at serotonin, dopamine and gamma-aminobutyric acid systems. *Psychopharmacology (Berl)* 2002; 163: 434-58.
47. Okada H, Matsushita N, Kobayashi K, Kobayashi K. Identification of GABA_A receptor subunit variants in midbrain dopaminergic neurons. *J Neurochem* 2004; 89: 7-14.

48. Olfson E, Bierut LJ. Convergence of genome-wide association and candidate gene studies for alcoholism. *Alcohol Clin Exp Res* 2012; 36: 2086-94.
49. Reich T, Edenberg HJ, Goate A, Williams JT, Rice JP, Van Eerdewegh P et al. Genome-wide search for genes affecting the risk for alcohol dependence. *Am J Med Genet* 1998; 81: 207-15.
50. Rosenberg NA, Huang L, Jewett EM, Szpiech ZA, Jankovic I, Boehnke M. Genome-wide association studies in diverse populations. *Nat Rev Genet* 2010; 11: 356-66.
51. Sander T, Ball D, Murray R, Patel J, Samochowicz J, Winterer G, et al. Association analysis of sequence variants of GABA(A) alpha6, beta2, and gamma2 gene cluster and alcohol dependence. *Alcohol Clin Exp Res* 1999; 23: 427-31.
52. Schuckit MA, Smith TL, Kalmijn J. The search for genes contributing to the low level of response to alcohol: patterns of findings across studies. *Alcohol Clin Exp Res* 2004; 28: 1449-58.
53. Simons RL, Lei MK, Stewart EA, Brody GH, Beach SR, Philibert RA et al. Social adversity, genetic variations, street code, and aggression: a genetically informed model of violent behavior. *Youth Violence Juv Justice* 2012; 10: 3-24.
54. Simons RL, Simons LG, Lei MK, Beach SR, Brody GH, Gibbons FX et al. Genetic Moderation of the Impact of Parenting on Hostility toward Romantic Partners. *J Marriage Fam* 2013; 75: 325-41.
55. Soyka M, Preuss UW, Hesselbrock V, Zill P, Koller G, Bondy B. GABA-A2 receptor subunit gene (GABRA2) polymorphisms and risk for alcohol dependence. *J Psychiatr Res* 2008; 42: 184-91.
56. Staley JK, Gottschalk C, Petrakis IL, Gueorguieva R, O'Malley S, Baldwin R et al. Cortical gamma-aminobutyric acid type A-benzodiazepine receptors in recovery from

- alcohol dependence: relationship to features of alcohol dependence and cigarette smoking. *Arch Gen Psychiatry* 2005; 62: 877-88.
57. Steffensen SC, Svingos AL, Pickel VM, Henriksen SJ. Electrophysiological characterization of GABAergic neurons in the ventral tegmental area. *J Neurosci* 1998; 18: 8003-15.
58. Stephens M, Donnelly P. A comparison of bayesian methods for haplotype reconstruction from population genotype data. *Am J Hum Genet* 2003; 73: 1162-9.
59. Takahashi A, Miczek KA. Neurogenetics of aggressive behavior: studies in rodents. *Curr Top Behav Neurosci* 2014; 17: 3-44.
60. Täuber M, Calame-Droz E, Prut L, Rudolph U, Crestani F. alpha2-gamma-Aminobutyric acid (GABA)_A receptors are the molecular substrates mediating precipitation of narcosis but not of sedation by the combined use of diazepam and alcohol in vivo. *Eur J Neurosci* 2003; 18: 2599-2604.
61. Tian H, Chen HJ, Cross TH, Edenberg HJ. Alternative splicing and promoter use in the human GABRA2 gene. *Brain Res Mol Brain Res* 2005; 137: 174-83.
62. Villafuerte S, Strumba V, Stoltenberg SF, Zucker RA, Burmeister M. Impulsiveness mediates the association between GABRA2 SNPs and lifetime alcohol problems. *Genes Brain Behav* 2013; 12: 525-31.
63. Villafuerte S, Trucco EM, Heitzeg MM, Burmeister M, Zucker RA. Genetic variation in GABRA2 moderates peer influence on externalizing behavior in adolescents. *Brain Behav* 2014; 4: 833-40.
64. Ward LD, Kellis M. Interpreting noncoding genetic variation in complex traits and human disease. *Nat Biotechnol* 2012; 30: 1095-106.
65. Yau WY, Zubieta JK, Weiland BJ, Samudra PG, Zucker RA, Heitzeg MM. Nucleus accumbens response to incentive stimuli anticipation in children of alcoholics:

relationships with precursive behavioral risk and lifetime alcohol use. *J Neurosci* 2012; 32: 2544-51.

66. Zintzaras E. Gamma-aminobutyric acid A receptor, α -2 (GABRA2) variants as individual markers for alcoholism: a meta-analysis. *Psychiatr Genet* 2012; 22: 189-96.

Tables

Table 1. The demographic and clinical characteristics of the samples

Subjects	Male	Female	Total
Healthy controls: n (%)	511(89.02%)	63(10.98%)	574(100%)
Age: mean \pm SD	40.01 \pm 12.22	42.63 \pm 12.62	40.30 \pm 12.28
Smokers: n(%)	161	21	182 (31.71%)
Non-smokers: n(%)	350	42	392 (68.29%)
Patients with alcoholism: n(%)	531(81.19%)	123(18.81%)*	654(100%)
Age: mean \pm SD	49.30 \pm 9.77	51.67 \pm 11.38	49.75 \pm 10.12*
Smokers: n(%)	327	67	394(60.25%)*
Non-smokers: n(%)	204	56	260(39.75%)
Patients with aggressive behavior: n(%)	156	14	170(25.99%)
Patients without aggressive behavior: n(%)	375	109	484(74.01%)
Cloninger's type I patients: n(%)	450	119	569(87.00%)
Cloninger's type II patients: n(%)	81	4	85(13.00%)

*** $p < 0.0001$ vs. control**

Table 2. Genotype and allele counts and frequencies of GABRA2 SNPs in control and alcohol-dependent subjects as well as in alcohol-dependent patients subdivided according to presence/absence of aggressive behavior and type of alcohol dependence according to Cloninger's classification

GABRA2 SNP	Genotype count (frequency)				Allele count (frequency)		
rs567926	AA	AG	GG	df = 2	A	G	df = 1
Healthy controls	196(34.15%)	284(49.48%)	94(16.38%)	$\chi^2=0.128$	676(58.85%)	472(41.15%)	$\chi^2=0.125$
Alcohol-dependent patients	218(33.33%)	325(49.69%)	111(16.97%)	$p=0.938$	761(57.00%)	574(43.00%)	$p=0.724$
Aggression	57(33.53%)	89(53.35%)	24(14.12%)	$\chi^2=1.432$	203(59.71%)	137(40.29%)	$\chi^2=0.439$
No aggression	161(33.26%)	236(48.76%)	87(17.97%)	$p=0.489$	558(57.65%)	410(42.35%)	$p=0.507$
Cloninger's type I	188(33.04%)	281(49.38%)	100(16.78%)	$\chi^2=1.132$	657(57.73%)	481(42.27%)	$\chi^2=0.721$
Cloninger's type II	30(35.29%)	44(51.76%)	11(12.94%)	$p=0.568$	104(61.18%)	66(38.82%)	$p=0.396$
rs279858	CC	TC	TT	df = 2	C	T	df = 1
Healthy controls	75(13.07%)	279(48.61%)	220(38.33%)	$\chi^2=1.789$	429(37.37%)	719(62.63%)	$\chi^2=1.118$
Alcohol-dependent patients	103(15.75%)	310(47.40%)	241(36.85%)	$p=0.409$	516(39.45%)	792(60.55%)	$p=0.290$
Aggression	24(14.12%)	88(51.76%)	58(34.12%)	$\chi^2=1.777$	136(40.00%)	204(60.00%)	$\chi^2=0.058$
No aggression	79(16.32%)	222(45.87%)	183(37.81%)	$p=0.411$	380(39.26%)	588(60.74%)	$p=0.809$
Cloninger's type I	93(16.34%)	268(47.60%)	208(36.55%)	$\chi^2=1.171$	454(39.89%)	684(60.11%)	$\chi^2=0.726$
Cloninger's type II	10(11.76%)	42(49.41%)	33(38.82%)	$p=0.557$	62(36.47%)	108(63.53%)	$p=0.394$
rs9291283	AA	AG	GG	df = 2	A	G	df = 1
Healthy controls	29(5.05%)	207(36.06%)	338(58.88%)	$\chi^2=2.319$	265(23.08%)	883(76.92%)	$\chi^2=1.292$
Alcohol-dependent patients	34(5.20%)	209(31.96%)	411(62.84%)	$p=0.314$	277(21.18%)	1031(78.82%)	$p=0.256$
Aggression	7(4.12%)	52(30.59%)	111(65.29%)	$\chi^2=0.871$	66(19.41%)	274(80.59%)	$\chi^2=0.858$
No aggression	27(5.58%)	157(32.44%)	300(61.98%)	$p=0.647$	211(21.80%)	757(78.20%)	$p=0.354$
Cloninger's type I	30(5.27%)	185(32.51%)	354(62.21%)	$\chi^2=0.745$	245(21.53%)	893(78.47%)	$\chi^2=0.649$
Cloninger's type II	4(4.70%)	24(28.23%)	57(67.06%)	$p=0.689$	32(18.82%)	138(81.18%)	$p=0.421$

Table 3. Counts and frequencies of four most common GABRA2 gene 2-SNP (rs567926 and rs279858) haplotypes in control and alcohol-dependent subjects, aggressive and non-aggressive alcohol-dependent patients and patients with type I and II alcohol dependence according to Cloninger's classification

Haplotype	Control Count (Frequency)	Alcoholics Count (Frequency)	χ^2 ; <i>p</i> value, df = 1
A-C	13(1.20%)	23(1.83%)	1.659; 0.198
A-T	662(57.60%)	742(56.66%)	0.291; 0.639
G-C	414(36.00%)	492(37.54%)	0.632; 0.426
G-T	59(5.20%)	51(3.97%)	2.198; 0.138
Haplotype	Aggressive alcoholics Count (Frequency)	Non-aggressive alcoholics Count (Frequency)	χ^2 ; <i>p</i> value, df = 1
A-C	11(3.37%)	12(1.305%)	5.774; 0.016*
A-T	193(56.63%)	547(56.56%)	0.002; 0.964
G-C	125(36.63%)	366(37.83%)	0.135; 0.713
G-T	11(3.37%)	41(4.305%)	0.700; 0.413
Haplotype	Cloninger's type I alcoholics Count (Frequency)	Cloninger's type II alcoholics Count (Frequency)	χ^2 ; <i>p</i> value, df = 1
A-C	16(1.46%)	7(4.49%)	6.296; 0.012*
A-T	644(56.53%)	98(57.28%)	0.067; 0.795
G-C	437(38.34%)	55(31.98%)	2.305; 0.129
G-T	41(3.66%)	10(6.25%)	2.051; 0.152

Figure Legends

Figure 1. LD plot for 3 GABRA2 SNPs in the entire Croatian sample. Pairwise SNP (D') values (x 100) of linkage and haplotype block are identified using the four-gamete rule. Darkened block indicate SNP pair without evidence of extensive recombination.

