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## Variants near CCK receptors are associated with electrophysiological responses to prepulse startle stimuli in a Mexican American cohort

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### Abstract

Neurophysiological measurements of the response to prepulse and startle stimuli have been suggested to represent an important endophenotype for both substance dependence and other select psychiatric disorders. We have previously shown, in young adult Mexican Americans (MA), that presentation of a short delay acoustic prepulse, prior to the startle stimuli can elicit a late negative component at about 400 msec (N4S), in the event-related potential (ERP), recorded from frontal cortical areas. In the present study we investigated whether genetic factors associated with this endophenotype could be identified. The study included 420 (age 18 – 30 years) MA men (n=170) and women (n=250). DNA was genotyped using an Affymetrix Axiom Exome1A chip. An association analysis revealed that the *CCKAR* and *CCKBR* (cholecystokinin A and B receptor) genes each had a nearby variant that showed suggestive significance with the amplitude of the N4S component to prepulse stimuli. The neurotransmitter cholecystokinin (*CCK*), along with its receptors, *CCKAR* and *CCKBR*, have been previously associated with psychiatric disorders, suggesting that variants near these genes may play a role in the prepulse/startle response in this cohort.

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#### CONFLICT OF INTEREST

NJS is a founder and stock holder in Cypher Genomics and paid consultant for the following companies: Human Longevity, Inc., MD Revolution, and Click Therapeutics.

All of the authors declare that they have no conflicts of interests.

#### ETHICAL STANDARDS

##### Ethical Approval

All procedures performed in studies involving human participants were in accordance with the ethical standards of the institution and/or national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards.

##### Informed Consent

Informed consent was obtained from all individual participants included in the study.

## Keywords

Mexican Americans; startle response; EEG; ERP; alcohol dependence

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The identification of neurophysiological endophenotypes associated with psychiatric disorders may help in determining the causal relationship between clinical phenomena associated with the disorder and basic molecular processes that are in large part determined by genetic factors. One psychophysiological measure that has been used as a potential endophenotype for a number of psychiatric disorders is the acoustic startle reflex (ASR) and prepulse inhibition of the startle (PPI). The startle reflex is a constellation of responses usually indexed by eye blink responses (Swerdlow et al., 1992), but also by electrophysiological recordings from cortical areas that may index cognitive responses to startle (Ehlers et al., 2011; Ford et al., 1999; Ford et al., 1994; Putnam & Roth, 1990). Prepulse inhibition of the startle (PPI) refers to the fact that if a weak stimulus is presented prior to the presentation of the startle stimuli (prepulse) the response to the startle is reduced in amplitude. It has been suggested that prepulse inhibition is an index of automatic sensorimotor gating (Geyer & Swerdlow, 2001). In prepulse facilitation (PPF), the response to the startle is enhanced by short or long delay prepulses. PPF has been suggested to reflect a combination of alerting, attention and/ or arousal (Filion et al., 1998; Hsieh et al., 2006; Ludewig et al., 2003).

The anatomical substrates of the neurobehavioral responses (ASR/PPI/PPF) to the presentation of the startle stimuli have been extensively investigated in clinical and preclinical studies (Braff, Geyer, Light, et al., 2001; Braff, Geyer, & Swerdlow, 2001; Kumari et al., 2005; Swerdlow et al., 1994). Startle responses involve a complex neural network extending from brainstem nuclei via the thalamus to higher order cortical areas that may regulate cognitive responses to startle (Campbell et al., 2007; Fendt et al., 2001; Kumari et al., 2005; Neuner et al., 2010; Schall et al., 1999). There is some evidence that the cognitive response to ASR/PPI may share a common underlying neurophysiology with some behavioral and clinical measures of cognition that require response inhibition (Filion et al., 1999). For instance, both performance on 3 the Wisconsin Card Sorting Task and PPI of startle have been suggested to reflect prefrontal cortical function and dysfunction (Filion et al., 1999; Swerdlow & Geyer, 1999). Impairments in frontal lobe function and associated behaviors, such as executive functioning, have been an important theoretical construct in the understanding a number of behavioral disorders, such as schizophrenia (Bagney et al., 2013; Chan et al., 2014; Eisenberg & Berman, 2010; Holmen et al., 2012; Owens et al., 2010), bipolar disorders (Erol et al., 2014; Kulkarni et al., 2010; Yen et al., 2009; Zimmerman et al., 2006) and substance use disorders (Fernandez-Serrano et al., 2010; Gierski et al., 2013; Loeber et al., 2009; Maurage et al., 2014; van der Plas et al., 2009; Zorko et al., 2004). If frontal cortical responses to the startle stimuli index some aspect of frontal lobe functioning involving higher cognition, then psychiatric disorders postulated to involve some aspects of frontal lobe dysfunction should also have startle deficits such as anxiety disorders (De Pascalis et al., 2013), schizophrenia (De Koning et al., 2014; Swerdlow et al., 2014), post-traumatic stress disorder (Grillon et al., 1996), and alcoholism (Ehlers et al., 2011; Marin et al., 2012).

The present investigation used a startle paradigm with short delay prepulse-plus-startle stimuli, that elicits a large frontal negative slow wave designated the N4S component (Ehlers et al., 2011). In the present study, we used this endophenotype in an association analysis using an Affymetrix Axiom Exome1A array, to explore potential genetic factors underlying the N4S component response to prepulse startle stimuli in a young adult Mexican American cohort that has been previously well characterized clinically (Criado & Ehlers, 2007; Criado et al., 2014; Ehlers et al., 2009, 2010; Ehlers et al., 2012; Ehlers & Phillips, 2007; Ehlers et al., 2011; Ehlers et al., 2014).

## MATERIALS AND METHODS

### Sample ascertainment

To investigate risk and protective factors for the prepulse inhibition and startle response in a select population of Mexican American young adults, we investigated a cohort of 420 (age 18 – 30) Mexican American men (n=170) and women (n=250). Participants were recruited using a commercial mailing list that provided the addresses of individuals with Hispanic surnames in 11 zip codes in San Diego County. The mailed invitation stated that potential participants must be of Mexican American heritage, between the ages of 18 and 30 years, residing in the United States legally, and able to read and write in English. Based on a phone interview, participants were excluded if they were pregnant, were nursing, or currently had a major medical or neurological disorder or head injury. All participants identified as having over 20% Hispanic heritage, with 92% reporting over 50% Hispanic heritage. The Semi-Structured Assessment for the Genetics of Alcoholism (SSAGA) (Bucholz et al., 1994), was used to make lifetime substance use and other psychiatric disorder diagnoses according to DSM-III-R and DSM-IV criteria. There have been several studies that have evaluated the concurrent diagnostic validity of the SSAGA across alcohol and drug dependencies, major depression, anxiety disorders, and antisocial personality disorder (Bucholz et al., 1994; Hesselbrock et al., 1999). These findings indicate that the SSAGA is a highly reliable and valid instrument for use in studies of psychiatric disorders, including substance dependence. The protocol for the study was approved by the Institutional Review Board (IRB) at The Scripps Research Institute, and written consent was obtained for all participants. Participants were asked to refrain from alcohol and drug usage for 24 hours prior to the testing.

### Startle ERP collection and analysis

Recordings were obtained from participants who were seated on a hospital bed in a sound-attenuated room. Acoustic startle stimuli were presented binaurally through headphones. The behavioral response to the startle (eye blink) is recorded using electrodes placed below and lateral to the eye as described (Braff, Geyer, & Swerdlow, 2001). The auditory stimuli consist of 45 trials. These trials include randomly presented startle stimuli (115 dB white noise burst for 40 msec n=30) and prepulse-startle stimuli (85 dB white noise burst for 20 msec-duration) immediately (<5 msec) followed by the startle (115 dB white noise burst for 40 msec n=15). Each individual startle and/or prepulse startle trial is separated by an interval of 15 seconds. Background white noise was presented for the entire session at a level of 60 dB. The behavioral variables assessed included: ASR magnitude on startle trials and prepulse trials as determined by quantification of the eye blink response as described below.

Seven channels of ERP data (FZ, CZ, PZ, F3, F4, F7, and F8, referenced to linked ear lobes with a forehead ground, international 10–20 system) were obtained using gold-plated electrodes with impedance held below 5 K $\Omega$ . Frontal electrodes were emphasized in the montage as previous data had suggested that ERP decrements in frontal areas distinguished subjects with a risk for alcohol dependence (Bauer, 1997). An electrode placed left lateral infraorbitally and reference to the left earlobe was used to monitor both horizontal and vertical eye movements. ERP signals were amplified (time constant 0.3 s, 35 Hz low pass) using a Nihon Kohden EEG machine and were transferred on-line to a PC. The combined gain of the EEG amplifiers and the analog-to-digital multiplexer amplifier was 50K.

The eye blink and ERP trials were simultaneously digitized at a rate of 256 Hz (bandwidth 0.5–35 Hz). Individual trials where the EEG or eye blink exceeded  $\pm 250$  microvolts (<5% of the trials) were eliminated before averaging. The N4S component of the ERP was quantified using a computerized peak detection routine that identifies baseline-to-peak amplitudes (in  $\mu$ V) within the specified latency window (350–500 msec). The eye blink amplitude was also assessed using this routine. The latency window for the eye blink was 50–120 msec. The baseline was determined by averaging the 150 ms of pre-stimulus activity obtained for each trial. The routine is user-driven and each peak detection must be verified by the user. All peaks were quantified by one investigator, and verified by a second investigator, both of whom were blind to participants' characteristics.

The N4S component of the ERP was also evaluated to determine if it was altered as a function of alcohol dependence, antisocial personality disorder/conduct disorder (ASPD/CD), affective/anxiety disorders (ANYAXAF), and any other drug dependence (AnyDrugDep). In this analysis, regionally averaged N4S component responses to startle and prepulse/startle were compared between those participants with and without the psychiatric disorders using ANCOVA (co-varying for gender).

### Sample preparation and genotyping

For all subjects, DNA was extracted from blood samples, followed by genotyping using an Affymetrix Exome1A chip. The DNA samples were prepared and the exome chip genotyping was performed on the Affymetrix Axiom Exome 1A Array according to the Affymetrix Axiom 2.0 Assay Manual Workflow documentation. The Affymetrix Exome 1A chip contains 247,222 markers. Variant quality from the exome chip genotyping was initially assessed according to Affymetrix best practices (Affymetrix, 2011). Plink version 1.07 (Purcell et al., 2007) was used to calculate Hardy-Weinberg (HWE) p-values on the set of unrelated samples, followed by the removal of 653 variants with an HWE  $p < 10^{-10}$ .

### Association analysis

PLINK was used to test for genome-wide association for the N4S component of the event-related potential (ERP) in response to acoustic startle stimuli following the presentation of a prepulse. PLINK was run with linear regression model parameters and with one million permutations. Gender and age were included as covariates. To determine the effect of extreme outliers in the phenotypic values, custom R code was written to generate winsorized phenotype values at 5% and 95% cutoffs, which were then used as the phenotype values in

PLINK. Manhattan plots were generated using Manhattan R library (Stephen Turner, <http://gettinggeneticsdone.blogspot.com/2011/04/annotated-manhattan-plots-and-qq-plots.html>). Annotations of the variants were obtained from the Affymetrix Exome 1A chip description file. Multiple test correction p-value thresholds were calculated for the Affymetrix Exome1A chip using the Genetic Type 1 Error Calculator (GEC) software (Li et al., 2012). The UCSC Genome Browser (Kent et al., 2002) was also utilized to visualize the genomic region containing the significant SNPs.

In order to determine if the SNPs that were significantly associated with the pre-pulse response phenotype were shared with the alcohol dependence trait, we used the multivariate version of the PLINK software (Ferreira & Purcell, 2009) with covariates age and gender.

### LD analysis

In order to check for linkage disequilibrium across the *CCKAR* and *CCKBR* gene regions, PLINK was utilized to extract a subset of variants for analysis based on the physical position of these genes on chromosomes 4 and 11, respectively. In particular, a region of chromosome 4 from genomic location 25,450,000–28,000,000 and chromosome 11 from genomic location 6,100,000–6,500,000, were extracted from the data set. Haploview (Barrett et al., 2005) was used to calculate the LD statistics and visualize the haplotype block structure of the gene regions.

## RESULTS

### Demographics of the Mexican American population

The demographics for the full sample of individuals (N=420) that were included in the association analysis are shown in Table 1. The subjects were a mean age of 23.6 (range 18 – 30) years at the time of interview, with 40% of the sample being male and 60% of the sample being female. Participants had a mean of 13.3 years of education (SD=1.8), and a mean income of \$30,000-\$49,000. Using self-reported ancestry based on grandparent origin, 92% of the participants reported at least 50% Hispanic heritage. The mean BMI was 27 (SD=7, range 17 – 64). Approximately 29% (N=123) of the participants were diagnosed with alcohol dependence according to DSM-III-R guidelines, indicating that these subjects had symptoms from 3 or more symptom groups, out of 9 possible symptom groups. Eleven percent (N=45) of the participants were diagnosed with conduct disorder or antisocial personality disorder/conduct disorder. Thirty-one percent (N=132) of the participants has a lifetime diagnosis of affective and/or anxiety disorder. Twenty-seven percent (N=115) of the participants had a diagnosis of another drug disorder (nicotine, cannabis, hallucinogens, stimulants, sedatives, opioids).

The mean N4S amplitude was evaluated using ANCOVA (co-varying with gender) as a function of alcohol dependence, ASPD/CD, any affective and/or anxiety disorder, and any other drug dependency. Participants with a lifetime diagnosis of alcohol dependence had significantly increased amplitude N4S responses to prepulse/startle stimuli as compared to participants with no alcohol dependence diagnoses ( $F=6.535$ ;  $p=0.011$ ). There were no

significant associations between the N4S amplitude to prepulse stimuli phenotypic trait and ASPD/CD, ANYAXAF, or AnyDrugDep diagnoses.

### Association analysis

Figure 1 contains the Manhattan plot for the amplitude of the N4S response to prepulse stimuli phenotypic trait tested in the association analysis across the entire genome, using covariates age and gender, and applying a minor allele cutoff of 0.01. Although there were 5 total variants which exhibited p-values  $\leq E-05$  after association, as shown in Table 2, there were only two variants (rs2171755 and rs58905541) that showed suggestive significance and possessed plausible gene functions for this phenotype. One protective variant (rs2171755; NC\_000004.12:g.26502338T>C) is located 12kb upstream from the *CCKAR* gene in a MIRb class SINE repetitive element, and is common in our sample, with an allele frequency of 0.36. The rs58905541 variant is a risk variant (NC\_000011.10:g.6296157C>T) located 24kb downstream from the *CCKBR* gene in a DNaseI hypersensitivity cluster, with an allele frequency of 0.018. The variant retained its significance through permutation and winsorization and the exclusion of covariates age and gender. The association values for these two variants, along with the allele and genotype frequencies, are shown in Table 3. The minor allele frequencies of these variants in the 1000 Genomes project was obtained from the dbSNP website (<http://www.ncbi.nlm.nih.gov/SNP/>).

From the multivariate association analysis of the N4S response to prepulse stimuli phenotypic trait and alcohol dependence diagnosis phenotype, we found that the inclusion of the alcohol dependence phenotype did not significantly alter the association of the SNPs with the prepulse phenotype. That is, the p-values were significant whether we used univariate PLINK (rs2171755 p-value=1.79E-05; rs58905541 p-value=1.11E-06), or multivariate PLINK (rs2171755 p-value=9.36E-05; rs58905541 p-value=5.77E-06). Additionally, the weights determined by multivariate PLINK demonstrated that the prepulse phenotype had a strong correlation to the SNPs (rs2171755 weight for prepulse = 0.995; rs58905541 weight for prepulse = 0.999), while the alcohol dependence phenotype had a very weak correlation (rs2171755 weight for alcohol dependence = 0.026; rs58905541 weight for alcohol dependence = 0.109). These results suggest that the prepulse phenotype is driving the significance of the association for these two SNPs.

### Multiple test correction

Multiple test correction p-value thresholds were calculated for the Affymetrix Axiom Exome1A chip using the Genetic Type 1 Error Calculator (GEC) software (Li et al., 2012), and the thresholds generated were thereby used to determine that the variants could be characterized to possess suggestive significance. In particular, for the Affymetrix Axiom Exome1A chip at a minor allele frequency of 0.01 or greater, the threshold for a suggestive p-value was calculated as 2.53E-05, significant p-value as 1.27E-06, and highly significant p-value as 2.53E-08.

### LD analysis

The linkage disequilibrium (LD) was calculated across the *CCKAR* and *CCKBR* gene regions. The average  $D'$  value across the SNP pairs in the *CCKAR* region was 0.77 in this

data set. No other SNPs on the Affymetrix chip were found to be in high LD with the variant near the *CCKAR* gene. The average  $D'$  value across the SNP pairs in the *CCKBR* region was 0.85 in this data set. While no SNP was found to be in complete LD with rs58905541, the SNP with highest LD was rs1462983 ( $D'=0.837$ ,  $r^2=0.023$ ,  $LOD=2.19$ ,  $CI=0.37-0.95$ ). This SNP was located in OR56B4 (olfactory receptor, family 56, subfamily B, member 4) and possessed a positive beta value, suggesting it is a risk factor. However, rs1462932 was not significantly associated with the prepulse inhibition response phenotype in our sample when using PLINK for the analysis.

## DISCUSSION

The present study confirmed previous observations in this population of an increase in prepulse facilitation of the N4S ERP component to the acoustic prepulse stimuli (Ehlers et al., 2011). In the present study, we used this endophenotype in an association analysis using an Affymetrix Axiom Exome1A array, to explore potential genetic factors underlying the N4S component response to prepulse startle stimuli in this young adult Mexican American cohort. The results of the present study suggest that variants located near *CCKAR* and *CCKBR* (cholecystokinin A and B receptor) genes are suggestive to be associated with the N4S ERP response to prepulse startle stimuli in this Mexican American cohort. The rs2171755 variant (NC\_000004.12:g.26502338T>C) is located 12kb upstream from the *CCKAR* gene in a MIRb class SINE repetitive element. Interestingly, a variant in a MIRb class SINE repetitive element has been reported to be associated with human cognition (Gosso et al., 2007). The rs58905541 variant (NC\_000011.10:g.6296157C>T) is located 24kb downstream from the *CCKBR* gene in a DNaseI hypersensitivity cluster. Variants in regulatory regions of the genome, such as DNase I hypersensitive sites, have been found to be associated with a number of diseases (Consortium, 2012; Maurano et al., 2012). Additionally, both SNPs show phylogenetic conservation in the UCSC Genome Browser alignment tracks in Figure 2. Since it has been reported that phenotype-associated variants occur more frequently in evolutionarily constrained regions of the genome (Parker et al., 2009), it suggests that these SNPs are likely to be real and functional. Therefore, it is feasible that the non-coding variants found in this present study could potentially play a role in the N4S ERP response to prepulse stimuli.

The neurotransmitter cholecystokinin (*CCK*) is widely present in the human body and in the central nervous system, where it modulates the dopaminergic system (Crawley & Corwin, 1994). Because of its potential modulation of the dopaminergic system and associated reward pathways, *CCK* has been investigated in a number of studies as a candidate gene for substance dependence and other behavioral disorders. *CCK*, along with its two receptors, *CCKAR* and *CCKBR*, have been previously associated with anxiety and panic disorders (Maron et al., 2008; Wilson et al., 2012), schizophrenia (Christoforou et al., 2007; Sanjuan et al., 2004), nicotine dependence (Takimoto et al., 2005), and alcohol dependence (Miyasaka et al., 2004; Okubo & Harada, 2001; Okubo et al., 2002). Although one study reported no association between *CCK* and *CCKBR* with alcohol dependence (Vanakoski et al., 2001), the study was performed using a Finnish population and did not examine the same significant SNPs that were determined in our study. Besides possible neurological influences of *CCK* on alcohol addiction, it has also been found that *CCK* through activation



of CCKA receptors protects the gastric mucosa against ethanol-induced gastric damage in rats (Konturek et al., 1995). In the context of alcoholism, variation in CCK activity in the gut could allow for the ingestion of greater or lesser amounts of alcohol, which in turn could influence liability towards alcoholism.

Further evidence of the role of CCK in the regulation of startle responses is supported by studies where the administration of CCK-related peptides has been found to influence the startle response in rats and humans. In particular, infusion of CCK has been found to enhance the acoustic startle response in rats (Feifel et al., 2001; Feifel & Swerdlow, 1997; Fendt et al., 1995), and some CCK antagonists attenuate startle responses (Feifel et al., 1999; Josselyn et al., 1995). In human subjects, CCK infusion has also been demonstrated to increase eye-blink startle as well as produce a mild increase in anxiety and heart rate as well as increases in plasma concentrations of ACTH, cortisol, prolactin and growth hormone (Shlik et al., 1999). Since CCK peptides have been demonstrated to enhance anxiety, several studies have investigated the role of the CCK system in anxiety and panic disorders, using CCK-related peptide administration as a challenge method (Koszycki et al., 2012; Maron et al., 2008). These CCK challenge studies were able to explore genetic factors in panic disorders by performing candidate gene analyses to find alleles that may be associated with greater sensitivity to the CCK peptides. One study found an association of the tryptophan hydroxylase gene isomer 2 (*TPH2*) with subjects experiencing panic attacks after CCK infusion (Maron et al., 2008). Another study found an association to the *CCKBR* gene in subjects with greater pre-challenge anxiety (Koszycki et al., 2012). Additional studies have utilized CCK-peptide infusion to determine its effects on EEG and ERP measures in healthy human subjects (Knott et al., 2002; Knott et al., 2003). CCK-4 infusion was found to delay the latencies of N100 and P200 components of the ERP that was elicited during an auditory oddball task (Knott et al., 2002). During EEG recording of resting subjects, CCK-4 infusion was also found to increase asymmetry and reduce coherence of the slow-wave activity at mid-temporal recording sites (Knott et al., 2003). Taken together, these studies suggest a plausible role for CCK variants in the regulation of brain activity and behavior.

Impairments in frontal lobe function and associated behaviors such as executive functioning have been suggested to underlie anxiety disorders (Castaneda et al., 2008) as well as a number of other behavioral disorders such as schizophrenia (Bagney et al., 2013; Chan et al., 2014; Eisenberg & Berman, 2010; Holmen et al., 2012; Owens et al., 2010), bipolar disorders (Erol et al., 2014; Kulkarni et al., 2010; Yen et al., 2009; Zimmerman et al., 2006) and substance use disorders (Fernandez-Serrano et al., 2010; Gierski et al., 2013; Loeber et al., 2009; Maurage et al., 2014; van der Plas et al., 2009; Zorko et al., 2004). Interestingly, schizophrenia and bipolar disorders also demonstrate significant clinical comorbidity with substance use disorders (Regier et al., 1990) and may also share genetic susceptibility factors (Schizophrenia Working Group of the Psychiatric Genomics, 2014; Schuckit et al., 2003). There is also some data to suggest that they may share common endophenotypes such as deficits in some aspects of responses to startle (Kohl et al., 2013), although this hypothesis requires further testing and confirmation.

In summary, in the present study, associations between the N4S ERP response to acoustic prepulse startle stimuli, were determined using association analyses. Our results suggest that

variants located in regulatory non-coding regions near the cholecystokinin A and B receptors may play a role in the prepulse/startle response. However, the results of this study should be interpreted in the context of several limitations. First, the findings may not generalize to the general American population of mixed heritage or all Mexican Americans, or all Hispanic young adult Americans. Over half of the participants in the present were women and thus findings may not generalize to previous studies that have focused on samples of entirely male participants. Second, the study was limited to young adults between the ages of 18 and 30 years, and the sample size may limit the interpretation of the results. Despite these limitations, this report represents an important step in an ongoing investigation to determine risk and protective factors associated with development of substance use disorders in this select Mexican American population.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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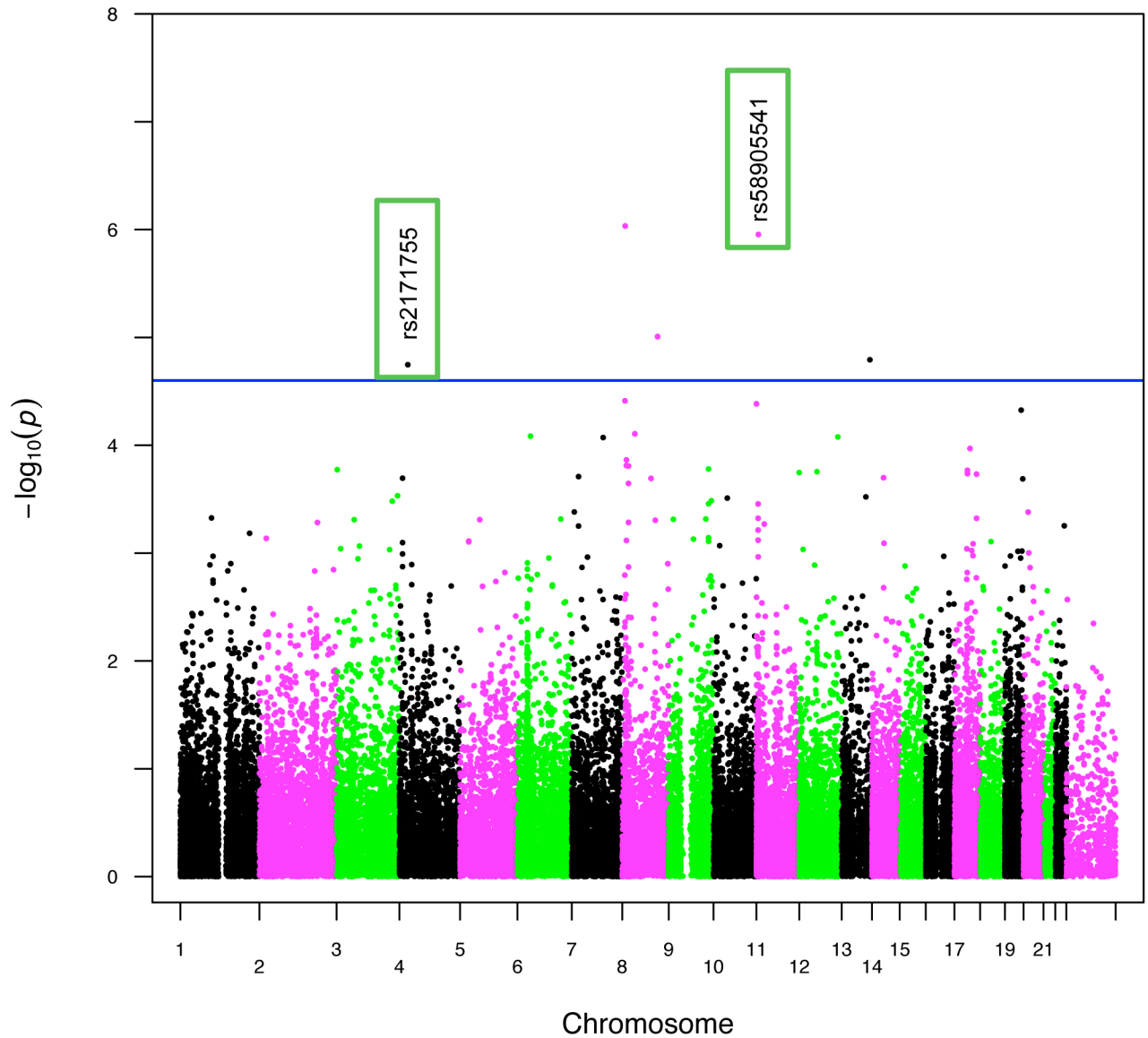
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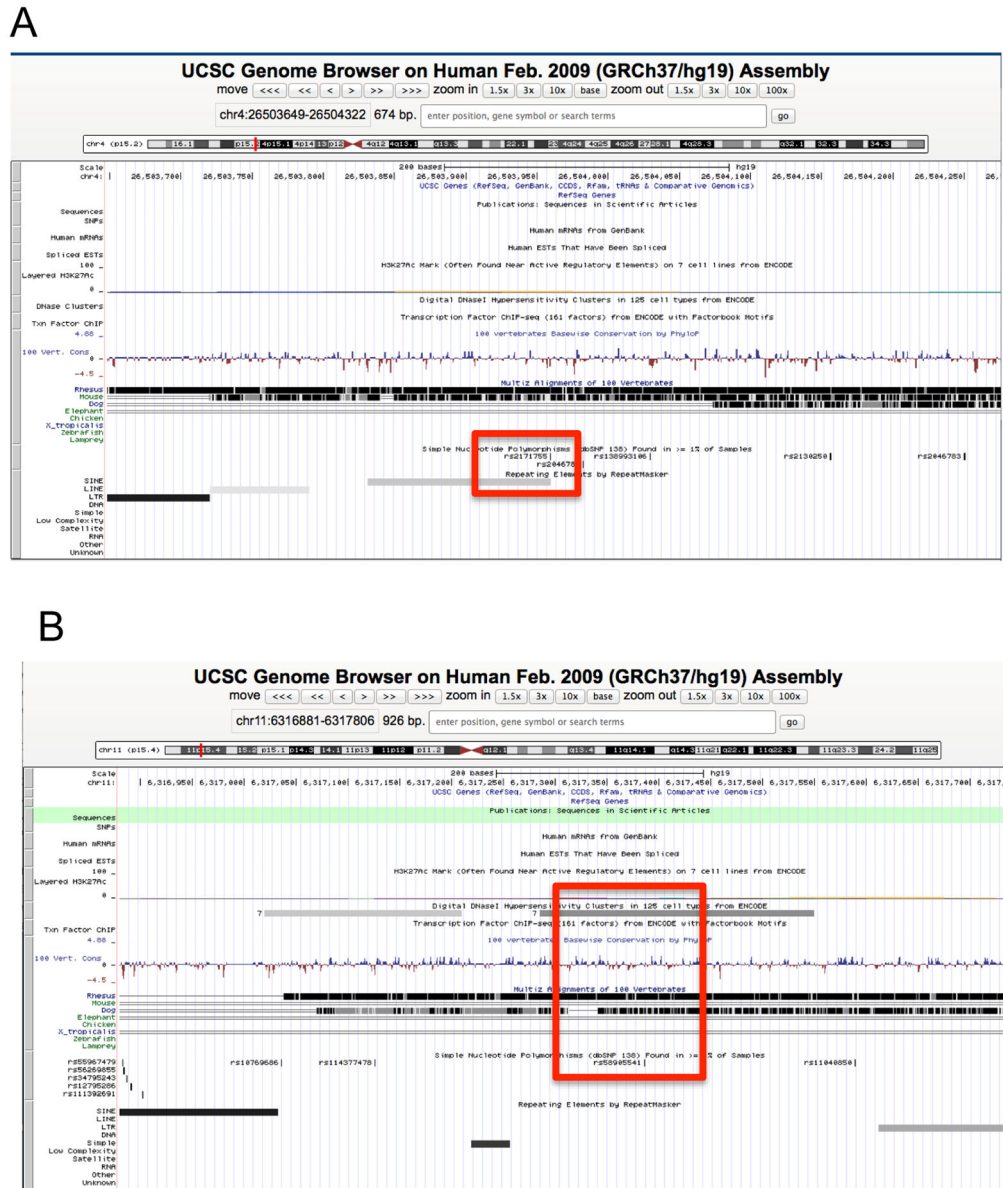
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**Figure 1. Manhattan plot for prepulse phenotype**

Manhattan plot across all chromosomes, using covariates age and gender. Minor allele frequency cutoff of 0.01 applied to the plot. Suggestive significance line calculated from GEC software. Green rectangles in plot highlight SNPs rs2171755 and rs58905541.





**Figure 2. UCSC Genome Browser view of the SNP locations**  
 This figure shows the genomic location of the SNPs rs2171755 and rs58905541.

**Table 1**

Demographics for Mexican American study participants

	Male	Female	Total
<b>Participants</b>	170 (40%)	250 (60%)	420
<b>Age: mean(sd), [range]</b>	23.7 (3.9), [18–30]	23.5 (3.8), [18–30]	23.6 (3.8), [18–30]
<b>Self-reported MA heritage &gt;= 50%</b>	90.60%	92.60%	91.60%
<b>BMI: mean(sd), [range]</b>	27.6 (6.0) [17.3–52.3]	27.2 (7.4) [16.9–64.4]	27.3 (6.9) [16.9–64.4]
<b>Education in years: mean(sd), [range]</b>	13.2 (1.7), [9–17]	13.4 (1.8), [7–18]	13.3 (1.8), [7–18]
<b>Income: mean(sd), [range]</b>	4.8 (2.1), [1–9]	4.2 (2.1), [0–9]	4.4 (2.2) [0–9]
<b>Alcohol Dependence, # of subject affected</b>	63 [63/170 = 37%]	60 [60/250 = 24%]	123 [123/420 = 29.3%]
<b>Pre-pulse inhibition: mean(sd), [range]</b>	13.07 (8.38), [0.01–50.63]	15.48 (9.18), [0.01–60.12]	14.51 (8.93), [0.01–60.12]
<b>Startle: mean(sd), [range]</b>	12.28 (6.70), [0.01–36.28]	15.12 (8.00), [0.01–47.09]	13.97 (7.62), [0.01–47.09]

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**Table 2**

Significant variants for prepulse phenotype

Chr	Position	dbSNP RS ID	Association p-value	MAF	Location of nearest gene	Description of nearest gene
4	26503960	rs2171755	1.79E-05	0.3607	12kb upstream, CCKAR	cholecystokinin A receptor
8	9649769	rs7830613	9.25E-07	0.4485	9kb downstream, TNKS	tankyrase, TRFI-interacting ankyrin-related ADP-ribose polymerase
8	111264112	rs1403843	9.83E-06	0.4613	83kb downstream, CSMD3	CUB and Sushi multiple domains 3
11	6317387	rs58905541	1.11E-06	0.0176	24kb downstream, CCKBR	cholecystokinin B receptor
13	108518444	rs1771137	1.61E-05	0.1518	FAM155A	family with sequence similarity 155 member A

**Table 3**

Allele frequencies, genotype frequencies, and association analysis results

dbSNP RS ID	rs2171755	rs58905541
Minor Allele	C	T
1000GENOMES AF (ALL)	0.455	0.129
1000GENOMES AF (AMR)	0.403	0.044
<b>Present Study Sample</b>		
Overall MAF	0.361	0.018
Genotype counts	59/185/176	0/15/405
Frequency	0.1405/0.4405/0.419	0/0.03571/0.9643
HWE p-value	0.3463	1
<b>Association analysis with no covars</b>		
Beta +/- StdError	-2.512 +/- 0.6165	11.56 +/- 2.283
T-stat	-4.0750	5.0650
P-value	5.517E-05	6.15E-07
<b>Association following winsorization</b>		
Beta +/- StdError	-1.947 +/- 0.5209	8.738 +/- 1.934
T-stat	-3.7380	4.518
P-value	2.116E-04	8.14E-06
<b>Permutation testing</b>		
Number of permutations performed	901,000	1,000,000
Empirical adaptive P-value	4.44E-05	1.30E-05
<b>Association analysis with covars</b>		
(Unscaled Beta, P-value)		
Additive	-2.658, 1.789E-05	11.24, 1.114E-06
Sex	2.675, 2.155E-03	2.167, 1.207E-02
Age	-0.07525, 0.5007	-0.06604, 0.5519
(Scaled Beta, P-value)		
Additive	-0.2068, 1.789E-05	0.2337, 1.114E-06
Sex	0.1471, 2.155E-03	0.1192, 1.207E-02
Age	-0.03204, 0.5007	-0.02812, 0.5519

The minor allele frequencies from the 1000 Genomes project, 1000GENOMES AF (ALL=total subjects and AMR=Admixed American subjects) were obtained from the 1000Genomes website (<http://www.1000genomes.org/>).

Abbreviations: MAF=minor allele frequency; HWE=Hardy-Weinberg equilibrium.