Entrega de l'Abstract

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Títol de la recerca: **Association between the candidate gene for schizophrenia p250GAP and schizotypy: Study in healthy population**
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Abstract (màxim 500 paraules):

INTRODUCTION

The dimensional view of schizophrenia (SZ) suggests that schizotypal traits, which are present in the general population, are genetically related to schizophrenia (Kendler et al. 1993). A number of studies have shown that schizotypy may reflect a spectrum of variation describing a predisposition to psychosis. Studies of schizotypy may thus facilitate the dissection of genetic components of schizophrenia.

Hypofunction of the glutamate N-Methyl-d-Aspartate (NMDA) receptor is strongly implicated in the pathophysiology of SZ (du Bois and Huang, 2007). The p250GAP is a brain-enriched NMDA receptor-interacting RhoGAP. This gene is involved in spine morphology, which has been shown to be altered in the post-mortem brains of patients with schizophrenia (Zavitsanou et al. 2002).

In a previous study, Ohi and colleagues (2012) have suggested that a genetic variation in the p250GAP gene might increase susceptibility not only for schizophrenia but also for schizotypal traits in a Japanese population.

The aim of our study was to examine whether the variability in the p250GAP was associated with schizotypy scores and dimensions in a sample of healthy Catalan individuals using well established questionnaires.

PARTICIPANTS AND METHODS:

The sample included 547 undergraduate enrolled in Psychology courses at the Universitat Autònoma de Barcelona (UAB)(456 women, 91 men) with a mean age of 20.6 years (SD=4.1).

All the individuals completed self-reported questionnaires assessing schizotypy. These questionnaires included the four Wisconsin Schizotypy Scales (WSS) (Magical Ideation, Perceptual Aberration, Physical Anhedonia and Revised Social Anhedonia). Exploratory and confirmatory factor analyses of the four WSS scales reliably produced two factors, positive and negative schizotypy, that account for 80% of the variance.

DNA was obtained for all the participants and 4 SNPS along p250GAP gene were genotyped using

Taqman 5'exonuclease assay (rs2298599, rs546239, rs3740829, rs3796668).

RESULTS.

In our preliminary analysis we have studied the association between the negative and positive factors from the WSS and genotypes of the 4 analyzed SNPs. No significant associations were found (negative schizotypy factor. P>0.05 and positive schizotypy: P>0.05, for all the SNPs); neither when we studied the association in the sample of males and females independently.

DISCUSSION.

These findings do not seem to support a recent work associating the variability of p250GAP and schizotypy. However, we still have a number of missings in the genotypes of some individuals and we need to reconstruct haplotypes for the individuals with PHASE program. A haplotype-based test of association with the positive and negative schizotypy factors will allow the evaluation of these negative results in the context of this candidate gene across the continuum of psychosis and genetic differences between the Japanese and the Catalan population.

Authorship:

I have contributed to the extraction of DNA and preparation of the plates for the genotyping assays. I have genotyped all the proposed markers and have conducted the statistical analyses of the present work.

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