

TITLE:

The interaction between the ZNF804A gene and cannabis use on the risk of T psychosis in a non-clinical sample

RUNNING TITLE: ZNF804A and cannabis use interaction on schizotypy

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## ABSTRACT

**Objective.** The ZNF804A gene and cannabis use are risk factors for psychosis, both of which have also been associated with schizotypic traits. This study aimed to test whether ZNF804A (rs1344706) modulates the relation between cannabis use and schizotypy levels in a general population sample.

**Method.** The sample consisted of 389 Spanish non-clinical subjects (43% males, mean age=21.1(2.19)). Schizotypy was evaluated with the three factors of the Schizotypal Personality Questionnaire-Brief (SPQ-B): Cognitive-Perceptual (CP), Interpersonal (I) and Disorganized (D). Subjects were classified as cannabis users or non-users. Multiple linear regressions were conducted to test the effect of genetic and environment factors and their interaction on SPQ-B scores. Sex and anxiety scores (evaluated with SCL) were included as covariates.

**Results.** The analyses showed a significant linear relationship between the ZNF804A and SPQ-I: homozygotes AA showed higher scores ( $p=0.001$ ). An interaction between cannabis use and rs1344706 on SPQ-CP was observed: among individuals AA, cannabis users presented higher scores than non-users, while among individuals CC, cannabis users presented lower scores compared to non-users ( $p=0.005$ ).

**Conclusion.** These results add evidence on that the ZNF804A modulates schizotypy and suggest that schizotypy levels are influenced by an interaction between the exposure to cannabis and the ZNF804A genotype.

**Keywords:** ZNF804A, cannabis, psychosis, schizotypy, gene-environment interaction

### Significant outcomes:

- Our study supports the notion that the gene ZNF804A has an effect on a psychosis vulnerability marker such as schizotypy in healthy individuals.
- The association between cannabis use and schizotypy is modulated by the ZNF804A gene.

### Limitations:

- Cross-sectional design and self-referred measures of schizotypy and cannabis use may constitute an inherent source of bias.
- Non-existent previous studies testing ZNF804Axcannabis interaction, the sample size and the non-availability of a replication sample make necessary further studies to confirm the results.

## **1. Introduction**

Psychotic disorders, including schizophrenia (SZ), are among the most severe and impairing conditions, with lifetime prevalence around 3% (1). Psychotic disorders are multifactorial disorders determined by genetic, environmental risk factors and the interaction between these factors (2,3).

As regards to genetic factors, twin and family studies have estimated that the heritability of SZ is between 64% and 81% (4,5). Moreover, genome-wide association studies (GWAS) have reported a substantial polygenic component that contributes to the risk for these disorders (6,7). These studies have allowed identifying several new candidate genes for SZ and one of the most relevant is the *ZNF804A* gene. Subsequently, this association has been further explored and replicated, which has enhanced the understanding of its involvement in SZ (7–11).

*ZNF804A* (2q32.1) is expressed throughout the foetal and adult human brain, especially in the medial temporal lobe and brain cortices (12,13). Despite the exact functions of *ZNF804A* still remains unclear, proteins with zinc finger domains are known to play a variety of roles, including binding to DNA, transcriptional regulation, gene expression and DNA–protein interactions (11,14,15). In this regard, molecular and bioinformatic studies suggest that *ZNF804A* likely has pivotal roles in cell physiology by its involvement in neurodevelopment regulation (8), synaptic plasticity (16) and also with brain structure and function (12,17). More specifically, *ZNF804A* has been reported to be involved in early neurite outgrowth and in regulating spine maintenance and the ability of neurons to respond to activity-dependent stimuli (16).

As a putative transcription factor, *ZNF804A* has a large number of potential targets both in the developing foetus and the adult brain, including genes that are involved in neuronal migration, neurite outgrowth and synaptic transmission (18). Interestingly,

some of the genes regulated by *ZNF804A*, such as the Dopamine Receptor D2 (*DRD2*) or Catechol-O-Methyltransferase (*COMT*), are directly involved in dopaminergic transmission and have been associated with schizophrenia (19). Therefore, current evidence suggests that dysregulation of *ZNF804A* could contribute to the altered neuronal and synaptic structures that are associated with psychotic and other neurodevelopmental disorders (20).

Within *ZNF804A* gene, the rs1344706 single-nucleotide polymorphism (SNP) has been repeatedly associated with psychosis (6,9,10,21) and the A variant has been identified with an increased risk for these disorders. In addition, two independent studies have shown that the risk allele of rs1344706 is associated with reduced expression of *ZNF804A* RNA, both in brain tissue of foetus and in individuals with schizophrenia, bipolar disorder or major depression disorder(12,13).

Two studies have also associated the rs1344706 with a vulnerability marker for psychosis, such as schizotypy (22,23). Schizotypy is a set of personality traits encompassing behaviours, cognitions and emotions that resemble the signs and symptoms of psychotic disorders in the general population. Schizotypy encompasses perceptual impairments and unusual views or ideas, a loss of normal emotional, physical and social functions and odd behaviour and speech, among other traits(24). Due to the clinical resemblance between schizotypy and psychotic symptoms it has been suggested that overlapping aetiological factors might underlie the two phenotypes (25). Therefore the study of the genetic underpinnings of vulnerability traits in non-clinical samples constitutes a useful framework within which to investigate aetiological factors of psychotic disorders (26).

One of the environmental risk factors most strongly implicated with the emergence of psychotic symptoms and disorders is the use of cannabis (27,28). Cannabis can induce psychotic symptoms through the activation of the endocannabinoid system, which is an

endogenous system that modulates dopamine neurotransmission (29). Interestingly, cannabis use has also been associated with schizotypy, being the positive and the disorganized dimensions of schizotypy the most strongly related (30–33). However, only a relatively small proportion of cannabis users develop psychotic symptoms, which means that other factors might explain the interaction between cannabis and psychosis risk (34). In this context, epidemiological studies have found that the risk for psychosis associated with cannabis use is increased in individuals with genetic vulnerability to psychosis (positive family history) (35). Similarly, familial correlation of schizotypal scores varies depending on the exposure to cannabis, which confirms the importance of gene-cannabis interaction in the expression of psychosis vulnerability markers (36,37).

As regard to gene-cannabis interaction, some studies have shown the interaction between dopaminergic neurotransmission related genes (*COMT* and *AKT1*) and cannabis use on psychosis risk (35). Taking into consideration these previous studies, and the regulatory roles of *ZNF804A* both neurodevelopmental processes and gene expression, it is therefore of interest to study the interaction between *ZNF804A* and cannabis use in order to increase the knowledge of the underlying mechanism by which cannabis increases the risk for psychosis. Despite that both *ZNF804A* gene and cannabis use have been independently described as genetic and environmental risk factors not only for psychosis but also for a psychotic vulnerability marker such as schizotypy, there are no studies assessing the GxE between *ZNF804A* gene and the cannabis use in psychosis.

Therefore, this study aimed to investigate the impact of cannabis use on schizotypal personality traits conditional to the genetic variability at *ZNF804A* gene in a general population sample. We hypothesized that the SNP rs1344706 within the *ZNF804A* gene would modulate the relationship between a well known environmental risk factor for psychotic disorders such as cannabis and the schizotypy levels in adult healthy subjects.

## **2. Method**

### **2.1. Sample**

The sample consisted of 389 subjects from the Spanish general population who were recruited in 2004-05 at the campus of the Jaume I University in Castelló (Spain).

Exclusion criteria were the presence of any major medical illness affecting brain function, neurological conditions, and personal history of head injury or psychiatric medical treatment. These areas were screened by trained psychologists by using a short interview designed for this study that included selected items of psychiatric diagnosis structured scales such as Structured Clinical Interview for DSM-IV (SCID-I) (38) and Familiar Interview for Genetic Studies (FIGS) (39). Specific questions about psychiatric assistance, psychotropic medication, hospital admissions and suicide attempts were asked to the participants.

Ethical approval was obtained from local research ethics committees. All participants provided written consent after being informed about the study procedures and implications. All procedures were carried out according to the Declaration of Helsinki.

### **2.2. Measures**

The schizotypal personality was measured with Schizotypal Personality Questionnaire-Brief (SPQ-B) (40). The SPQ-B consists of 22-items self-report scale and comprises three identifiable factors (cognitive-perceptual (CP), interpersonal (I) and disorganized (D)). The CP and the I factors included 8 items each one and the D factor 6 items, and the final score of each factor was calculated as the sum of all the items of each factor. These factors include the evaluation of the presence of odd ideas, paranoia, lack of close personal relationship, suspiciousness and odd behaviour and speech. The participants

were screened for their anxious symptomatology by means of the 23-item scale of the revised version of the Symptom Check List, SCL-90-R (41). Clinical information was available for 100% of individuals.

Life-time cannabis use was assessed with one question regarding the frequency of consumption “never”, “sometimes”, “monthly”, “weekly” or “daily”. This variable was then dichotomized in: cannabis use (daily, weekly, and monthly) or non-cannabis use (sometimes or never). This information was available for 98.9% of individuals.

Similarly, participants were asked about the use of other illicit drugs (i.e. amphetamine-type stimulants, cocaine, heroin and other opioids, or ecstasy) and were classified as other drugs users (daily, weekly, and monthly) or other drugs non-users (occasionally or never).

### **2.3. Molecular analyses**

Genomic DNA from each individual was extracted from buccal mucosa samples by means of a cotton swab using the BuccalAmp DNA (Epicentre® Biotechnologies, Madison, WI). The SNP (rs1344706) atZNF804A gene was determined using Applied Biosystems TaqMan 5' exonuclease assays. Polymerase chain reaction plates were read on ABI PISM 7900HT instrument with SDS 2.4 software (Applied Biosystems). The genotyping call rate for the SNP was 100%.

## **2.4. Statistical analyses**

All data were processed using PASW statistics (SPSS Inc., Chicago Illinois, USA) and Stata v. 14 (StataCorp, 2013).

The Student's t test and ANOVA test were used to compare the means of continuous variables between two or more groups, respectively. Chi-squared test were performed to analyze the distribution of qualitative variables between groups.

Multiple linear regressions were conducted to test the effect of genetic and environment factors and their interaction on SPQ-B scores. First, the main effect of the independent variables (rs1344706 and cannabis use) was tested in the same model on each SPQ dimension (SPQ-CP, SPQ-I, SPQ-D). Second, the interaction between rs1344706 and cannabis use on each SPQ-dimension was analyzed. Sex, SCL anxiety scores and the use of other drugs were included as covariates.

The presence of Hardy-Weinberg equilibrium was examined using the chi-squared test with PLINK v1.07 (42).

Considering that three models were tested (effect of cannabis and genotype on the three SPQ dimensions), significant p-value threshold was established at 0.017 (0.05/3).

### **3. Results**

#### **3.1 Sample description**

Participants (n=389) were university students (43% males) with a mean age at interview of 21.11 years (sd=2.19). The SPQ-Band SCL-anxiety mean scores (sd) were as follows: SPQ-CP 1.57(1.49), SPQ-I 2.76(2.12), SPQ-D 1.15(1.23) and SCL-A 4.20(4.99).

The 29% of individuals were classified as cannabis users and 12% of individuals were classified as other drugs users.

The genotypic frequencies were in Hardy-Weinberg equilibrium and allelic frequencies were similar to those described for European population in 1000 Genomes Project (MAF=38%). The genotypic frequencies were as follows: 31.2% AA, 47.0% AC and 21.8% CC.

There were no statistically significant differences between cannabis users and non-users on age, genotype, SCL scores and the SPQ-CP and SPQ-I. However, there were significant differences on sex (60% of the cannabis non-users were females ( $\chi^2=5.8$  p=0.016)) and SPQ-D (cannabis users had higher SPQ-D scores than non-users (t=-2.38 p=0.017 R<sup>2</sup>=0.21)).

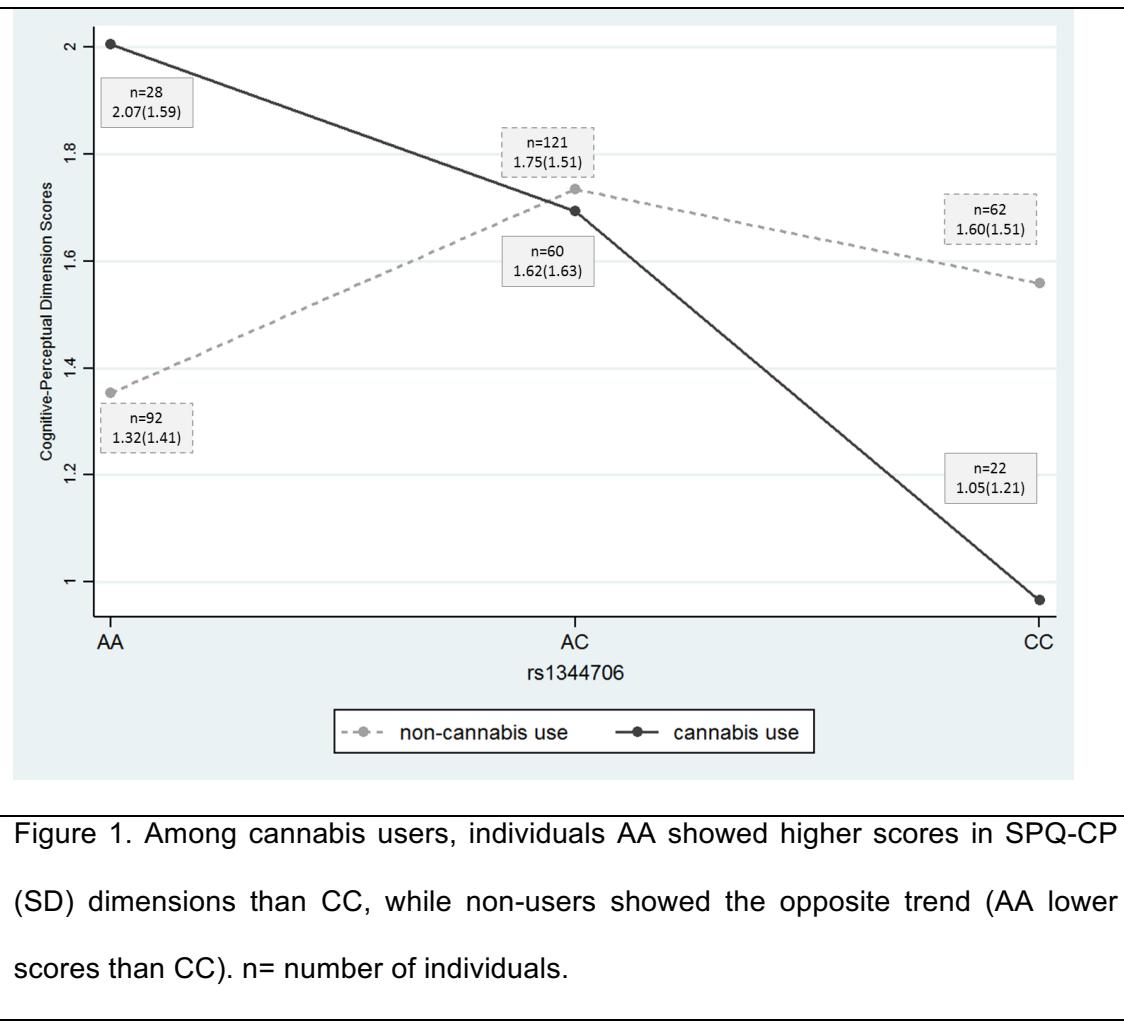
#### **3.2 Effects of cannabis use and ZNF804A genotype on SPQ-B**

Regarding the Interpersonal schizotypy factor, a significant linear relationship between the genotype and the schizotypal scores was observed: homozygotes AA showed higher Interpersonal schizotypal scores ( $\beta=-0.16$  SE=0.14 p=0.001 R<sup>2</sup>=0.13). The mean (sd) SPQ-I scores for each genotype were as follow: AA (3.19 (0.19)), AC (2.65 (0.15)) and CC (2.36 (0.22)). No effect of cannabis use nor the interaction between genotype x cannabis was detected on SPQ-I.

In reference to the Cognitive-Perceptual factor, no effect of the main factors (genotype and cannabis) was observed. However, the interaction analysis showed the interplay between cannabis use and rs1344706 on SPQ-CP ( $\beta=0.21$  SE=0.44 p=0.005 R<sup>2</sup>=0.19): depending on the *ZNF804A* genotype the exposure to cannabis is associated differently to Cognitive Perceptual schizotypal scores (Figure 1). Heterozygous individuals showed similar SPQ-CP scores regardless of their cannabis use, while in the two homozygous groups (AA or CC) the cannabis use showed contrary effects. Among individuals AA, cannabis users presented higher scores than non-users, while among CC cannabis users presented lower scores compared to non-users.

In order to better detail the interaction analysis, we tested the effect of the genotype on SPQ-CP score separately in the group of cannabis users and non-users. Linear regression analyses showed that there is a significant effect of the genotype on SPQ-CP only in the group of cannabis users ( $\beta=-0.20$  SE=0.20 p=0.025 R<sup>2</sup>=0.04). Then, within cannabis users group, AA homozygotes have the highest SPQ-CP ratings while within cannabis non-users there are no significant differences among genotypic groups.

Finally, no significant effect of the genotype, cannabis use or the interaction was observed on SPQ-D.



#### **4. Discussion**

This study adds evidence on that *ZNF804A* gene may exert certain effect on psychosis proneness, measured as schizotypal traits in healthy subjects. In addition, our findings suggest, for the first time, that genetic variability at the *ZNF804A* gene may modulate the relationship between the cannabis use and psychotic proneness.

On the one hand, we have observed an association between the rs1344706 with SPQ-I. Particularly, we found that homozygotes AA showed higher Interpersonal schizotypal scores. This result is in line with different studies reporting the association of this variant with schizophrenia risk (e.g., 6,10), and it is also consistent with two previous studies that found this variant associated with schizotypy in general population sample (22,23). In regard to the two prior non-clinical population based studies, Yasuda et al. (2011) reported that A carriers showed higher disorganization dimension, but they did not describe differences in the other schizotypal factors. In the second study, although the direction of association was opposed to what expected, Stefanis et al. (2013) reported an association between paranoid and disorganized dimensions and rs1344706. Differences in the results among our study and the two previous studies might be explained by different sample characteristics, such as differences in sample size, ethnic origin or age and sex distributions. For instance, Yasuda's study consisted of 176 Japanese individuals with a mean age of 36.8 ( $sd=11.5$ ) years. In Stefanis' study, although the subject's mean age (21 years,  $sd=1.9$ ) was similar to our study, 100% of the subjects were men undergoing military service. Despite these differences, our results add onto the body of evidence that the *ZNF804A* gene might be involved in the pathogenesis of schizophrenia.

On the other hand, we have not observed an effect of cannabis use *per se* and either of the genotype on schizotypy ratings. However, the GxE interaction analyses have shown that the cannabis use seems to act as a modifier of the association between the

rs1344706 genotype and Cognitive Perceptual schizotypal scores. Among cannabis users, individuals AA showed higher scores in SPQ-CP dimensions than CC, while non-users showed the opposite trend. As observed when the effect of the genotype on SPQ-CP score was tested separately in the group of cannabis users and non-users, the rs1344706 genotype is linearly related with SPQ-CP scores only in the group of cannabis users.

For the interpretation of this GxE interplay, it is essential to understand the biological function of *ZNF804A* gene and the effect of a polymorphic variant in it. As mentioned, *ZNF804A* is presumably involved in the development and function of neural and synaptic structures (43), that regulates the expression of other genes, some of which have been directly or indirectly previously associated with schizophrenia (19,44).

To this respect, it was first considered whether the risk allele affects the expression of *ZNF804A* or even other genes. Two studies converge in showing that the SNP rs1344706 has a cis-acting effect on *ZNF804A* expression in the human foetal brain (12,13), a critical period in neurodevelopment. Specifically, these studies showed reduced expression associated with the risk allele; however, allelic direction still remains controversial due to contradictory results from other studies (45,46). Nonetheless, it can be hypothesized that the dysregulation of *ZNF804A* expression could have an effect on important neurodevelopmental processes that ultimately might increase the risk to develop psychosis in adolescence. However, since rs1344706 maps to an intronic region, the mechanisms causing these expression changes remains poorly understood. In this sense, a recent study suggested that the *MYT1L* and *GATA2* genes, which are involved in oligodendrocyte and neuronal differentiation and have been previously associated with schizophrenia, are strong candidates for regulating *ZNF804A* expression via rs1344706 (47). However, further effort is needed in determining the proteins that interact with the rs1344706 motif in order to elucidate the mechanism by which this SNP affects the *ZNF804A* expression.

Some limitations of this study must be acknowledged. First, the cross-sectional design is not the optimal to test causal associations and the retrospective measures may constitute an inherent source of bias. However, the genetic and environmental variables were selected based on previous findings and the analyses had a directional hypothesis also defined according to evidence (48,49). Second, participants were self-referred for the study, which may have introduced a selection bias into our sample. Despite these limitations, we would like to outline the design of this study as an intrinsic strength, because the assessment of the association between cannabis use and schizotypy aims to overcome the presence of multiple confounding factors inherent to psychosis; such as medication or the heterogeneous symptomatology of the disorder.

Further analyses in independent samples are required to replicate the present results and also to improve the knowledge of the etiological mechanism underlying the risk for psychosis, both in general population and in clinical samples.

In conclusion, our study supports the notion that the gene ZNF804A has an effect on a psychosis vulnerability marker such as schizotypy in healthy individuals from the population, and shows for the first time that this effect can be modulated by cannabis use.

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