Possible association between DNA repair gene variants and cannabis dependence in a Turkish cohort: a pilot study

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OBJECTIVE: Substance use disorder (SUD) has important effects on health and well-being. It is well known that genetic factors play a role in SUD. The purpose of this research was to investigate whether functional variants of DNA repair genes might be a risk factor for cannabis and/or synthetic cannabis dependence in a Turkish cohort.

METHODS: In total, 131 patients with cannabis and/or synthetic dependence and 70 healthy controls were included in this case-control study. XRCCI codon 399 (rs25487) and XRCC4 G1394 T (rs6869366) and XPD (rs13181) variants were determined by the polymerase chain reaction-restriction fragment length polymorphism assay (PCR-RFLP).

RESULTS: The XRCCI rs25487 GG genotype and G allele were significantly lower in patients compared to controls (p = 0.005; p = 0.002, respectively). XRCC4 rs6869366 TT genotype and T allele were more common in patients compared to controls (p = 0.001, p = 0.001, respectively). It was found that patients with XPD rs13181 Lys/Gln had a significantly higher risk of cannabis dependence than control did (p = 0.00). The subjects carried XPD rs13181 Gln/Gln genotype had a 2.2-fold increased risk for cannabis dependence (p = 0.010).

CONCLUSIONS: We demonstrated for the first time that DNA repair gene variants may alter individual vulnerability for SUD. This observation could be of further interest to researchers, as it could suggest new candidate genes, presumably crucial for the etiopathogenesis of the cannabis and/or synthetic cannabis dependence.

Introduction

Substance use disorder (SUD) present a worldwide danger to public health and have a severe social and economic effect on individuals and society. Among these substances, cannabis and marijuana are terms related to the plant Cannabis sativa and currently are the second most frequently smoked substance following tobacco [1]. This plant contains more than 400 chemical substances, and 60 of them account for its distinctive effect. D-9-tetrahydrocannabinol (THC) and cannabidiol (CBD) are two main ingredients of the C. sativa plant [2]. Nowadays, synthetic cannabinoids (SCs; e.g. Spice in Europe, K2 in the United States and Bonsai or Jamaica in Turkey) are among the most common substances of drug abuse in young adults in Turkey due to its euphoric and addictive effects.

Oxidative stress refers to an imbalance between the generation of free radicals and antioxidant defenses for repair. It has been proposed that oxidative stress plays a role in the pathogenesis of several distinct diseases, and may also be a part of the common pathogenic mechanism in numerous major mental disorders since the brain has relatively more vulnerability to oxidative damage [3]. Numerous studies have searched for the relation between oxidative stress and psychiatric diseases [4,5]; however, few have assessed the possible role of oxidative stress in SUDs. Oxidative stress can induce damage to DNA. Multiple, complementary DNA repair systems have evolved to protect the genome against the harmful effects of DNA lesions [6]. X-ray repair cross-complementing group 1 (XRCCI) is one of the essential genes in the base-excision repair pathway, encodes a protein that plays a role in the repair of DNA single-strand breaks [7]. XRCC4 is found on the chromosomal 5q14.2 and restores DNA double-strand breaks (DSBs) repair. Xeroderma pigmentosum group D (XPD, also referred as ERCC2) encodes a helicase that is a component of the transcription factor TFIIH. This factor is a key member of the nucleotide-excision repair pathway that accounts for influencing repairs to bulky adducts and UV-induced DNA damage [8]. DNA repair gene changes were shown to result in a decrease in DNA repair capacity. Therefore, we hypothesized that the XRCCI Arg399Gln
Genotyping was performed by the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method previously described [10]. Genotyping for each blood sample using the salting out procedure was performed in a final volume of 25 μL containing 65 mM tris-HCl (pH 8.9), 24 mM (NH4)2SO4, 3 mM MgCl₂, 0.05% Twin-20, 0.2 mM deoxynucleotide triphosphate solution, 0.3 μM solution of oligonucleotide primers [XRCC1 Arg399Gln (rs25487): F5′-AGT AGT CTG CTG GCT GTT C-3′, R5′-TCT CCC TGG TGT GAC AGT GAG AAA T-3′; XPD (rs13181): F5′-ATC CTG TCC CTA CTG GCC ATT C-3′, R5′-TGT GGA CGT GAC AGT GAG AAA T-3′; 20–100 ng DNA, and 2 U TaqDNA polymerase. PCR was performed using ABI-9600 with initial denaturation at 96°C for 3 min, then 32 cycles at 55°C for rs25487 and 58°C for rs13181 and then last cycle at 72°C for 8 min. Genotyping for XRCCI (rs25487), XRCRC4 (rs6869366), and XPD (rs13181) variants involved digestion of PCR products with MspI, HincII, and PstI restriction endonucleases, respectively, at 37°C for overnight incubation. All of the digestion products were visualized by electrophoresis on a 2% agarose gel. The experimental process was repeated twice for each sample.

Statistical analysis

Data were analysed using the Statistical Package for Social Sciences (SPSS) software version 15.0 for Windows (SPSS Inc., Chicago, IL). Mean and standard deviation were used for the presentation of continuous quantitative variables. Frequencies and percentages were used for categorical data. The XRCCI rs25487, XRCRC4 rs6869366, and XPD rs13181 overall genotype distribution were compared by the chi-square (χ²) test, and the specific genotype and allele distributions were compared by using Fisher’s exact test. The odds ratios (ORs) and 95% confidence intervals (CIs) were used to determine the relationships between the variants allelic and genotypic variants and their occurrence in the patients. The XRCCI rs25487, XRCRC4 rs6869366, and XPD rs13181 genotype distributions in both the patients and the healthy controls were analysed according to the Hardy–Weinberg equilibrium. p-Values smaller than 0.05 were considered significant.

Results

In this study, a total of 131 unrelated Turkish patients with cannabis and/or SC dependence and 70 individuals without any established disease diagnoses were evaluated for the XRCCI rs25487/XRCRC4 rs6869366/ XPD rs13181 variants. The distributions of the genotypes and alleles of the patients and healthy controls for XRCCI rs25487/XRCRC4 rs6869366/XPD rs13181 variants are presented in Tables 1–3.

XRCCI genotyping

For the XRCCI rs25487 variant, the frequencies of the GG, GA, and AA genotypes are 12.9%, 37.4%, and 49.7% in the patients and 30%, 34.3%, and 35.7%, respectively, among the controls; the differences were statistically significant. The XRCCI rs25487 GG genotype was significantly decreased in patients than in controls (12.9% versus 30%, p = 0.005, OR: 2.874, 95CI%: 1.396–5.915). XRCCI rs25487 G allele was...
lower in cannabis dependence patients compared to the control group, while XRRC1 rs25487 A allele was more common in the control group than the patients (\(p = 0.002\), OR: 1.923, 95CI%: 1.262–2.933).

**XRRC4 genotyping**

For the XRCC4 rs6869366 variant, the frequencies of the GG, GT, and TT genotypes are 1.5%, 19.1%, and 79.4% in the patients and 24.3%, 37.1%, and 38.6% among the controls, respectively; these differences were statistically significant. XRCC4 rs6869366 homozygous wild-type genotype (GG) and heterozygous genotype (GT) were significantly decreased in patients compared to the controls (\(p = 0.001\), OR: 19.111, 95CI%: 4.248–85.885; \(p = 0.007\), OR: 2.505, 95CI%: 1.306–4.808, respectively). Also, the frequency of the XRCC4 rs6869366T allele was found to be significantly higher in the control group compared to the patients (\(p = 0.001\), OR: 6.026, 95CI%: 3.615–10.044).

**XPD genotyping**

For the XPD rs13181 variant, the frequencies of the Lys/Lys, Lys/Gln, and Gln/Gln genotypes are 12.3%, 54.6%, and 33.1% in the patients and 12%, 37.1%, and 38.6%, among the controls, respectively; these differences were statistically significant. We found that the patients with XPD rs13181 Lys/Gln (\(p = 0.007\), OR: 0.434, 95CI%: 0.237–0.792) and XPD rs13181 Gln/Gln (\(p = 0.010\), OR: 2.268, 95CI%: 1.252–4.112) genotypes had a significantly higher risk of cannabis and/or SC dependence compared to the controls. No statistically significant association was determined between the allele frequencies of the patients and healthy control groups (\(p = 0.064\)).

**Discussion**

SUD is a multifactorial disorder; therefore, genetic interactions with factors including behavioral traits and environmental conditions could be involved in the development of addiction. Environmental factors such as peer pressure, parental monitoring, and the accessibility of a substance play a key role in the initial intention to drink, smoke, or take the substance. Family and twin studies have shown that genetic effects are associated with developing vulnerability to substance abuse [11]. Cannabis has been associated with numerous adverse effects in humans. In animal studies, Wolff et al. showed that THC breaks down complexes I, II, and III of the mitochondrial respiratory chain and mitochondrial coupling. It also enhances free radical
generation in the brain and increases mitochondrial free radical leakage [12]. It was reported that THC induces oxidative stress in several cell lines through the central cannabinoid receptor pathway [13]. Also, it was reported that THC caused important imbalances in oxidative status and increased the levels of oxidative stress-induced lipid peroxidation, protein carbonylation, and DNA damage [14]. Sarafian et al. found stress-induced lipid peroxidation, protein carbonylation, and DNA damage in oxidative status and increased the levels of oxidative stress in human endothelial cells [15]. Furthermore, it was reported that THC caused important imbalances in oxidative status and increased the levels of oxidative stress in several cell lines through the central cannabinoid receptor pathway [13]. Also, cannabis smoke stimulates the production of reactive oxygen species in human endothelial cells [15]. It has been reported that THC caused important imbalances in oxidative status and increased the levels of oxidative stress and oxidative DNA damage were also seen in autism spectrum disorder patients and in animal models relevant to this condition [18]. Besides, multiple evidence support the role of oxidative and nitrosative stress in the pathophysiology of major depression [19]. Therefore, we hypothesized whether DNA repair gene variants may be a risk factor for SUD. To the best of our knowledge, there is no report on the association between XRCC1 rs25487/XRCC4 rs6869366/XPD rs13181 gene variants and risk of SUD in a Turkish cohort. Our results show a significant association between these variants and risk of cannabis use disorder and/or SC dependence.

XRCC1 is a multi-domain protein which has a “scaffold” effect to attract other parts of the DNA base damage repair pathway. XRCC1 both interacts with other proteins in the repair process and coordinates with various repair proteins to increase the competence of DNA repair [20]. The significance of XRCC1 in providing genomics stability is implied by a higher frequency of spontaneous chromosome aberrations and deletions in XRCCI mutant cells and by embryonic lethality in XRCCI knockout mice [21]. Some previous studies have shown that XRCCI polymorphisms are linked with various autoimmune diseases, while other reports have reported no such relations [20]. The most common variant leads to the substitution of a glutamine for the normally occurring arginine at amino acid residue 399 [22]. Some studies have demonstrated that the XRCC1 rs25487 variant modifies XRCC1 protein function and decreases the ability of DNA damage removal following irradiation and exposure to genotoxic compounds more than threefold. The Gln allele of this variant was related to increased levels of DNA adducts and glycoprophin A variants, increased sister chromatid exchange frequencies, and enhanced sensitivity to ionizing radiation; however, two other studies reported no association between this polymorphism and increased DNA adduct levels [23]. It was reported that biallelic mutations in human XRCCI are associated with ocular motor apraxia, axonal neuropathy, and progressive cerebellar ataxia [24]. It has been reported that XRCCI rs25487 Gln/Gln and Arg/Gln genotypes were more common in patients with schizophrenia than healthy controls [25,26]. However, Celik et al. and Czarny et al. showed that XRCCI rs25487 variant had no significant association with obsessive-compulsive disorder (OCD) and recurrent depressive disorder [27,28]. In the present study, we found that XRCCI rs25487 variant GG genotype and G allele were lower frequency in patients with cannabis dependence (p < 0.05) (Table 1). XRCCI rs25487 G allele may be a protection from dependence.

XRCCI4 gene, an essential component of Non-Homologous End-Joining repair pathway, is reported to restore DNA DSBs. Despite numerous studies conducted on XRCCI4 variants and their association with psychiatric diseases, results remain uncertain. We also previously showed that XRCCI4 intron 3 VNTR variant DD genotype was associated with schizophrenia + nicotine dependence [29]. The G1394T variant is located in the promoter region of the XRCCI4 gene, and even the most subtle differences of the promoter region may regulate the biofunction of the gene product by down-regulating its expression. We found that XRCCI4 rs6869366 TT genotype and T allele were higher in patients compared to controls (Table 2). Our results suggest that XRCCI4 promoter −1394T allele might exert a modest positive effect on cannabis dependence risk when two copies of the allele are present. It also provides a valuable insight into the pathogenesis of cannabis and/or SC dependence. We thought this variant may have functional regulatory significance since the nucleotide change from G to T in the promoter region may be susceptible to cannabis and/or SC dependence risk. XRCCI4 rs6869366 G allele may be a protection from dependence.

The XPD gene maps to chromosome 19q13.3 and has 22 exons and 21 introns spanning approximately 2.3 kb. Since XPD is crucial in the biofunctions of multiple cells and XPD mutations have been studied in the pathogenesis of numerous genetic disorders, XPD genetic variants may hence be considered as a main genetic susceptibility factor [30]. Some variants in XPD gene exons have been described; Lys751Gln variant is one of the most common [31]. The XPD Lys751Gln variant is an adenosine (A) to cytosine (C) transition, which may
lead to modify from lysine to glutamine in exon 23 of the XPD gene. This variant may generate the most relevant alteration in XPD function and influence various protein interactions, decrease the activity of TFIIH complexes, affect DNA repair capacity and change the genetic susceptibility to diseases. People with XPD 751Gln/Gln have been shown to manifest suboptimal DNA repair capacity to remove UV photoproducts when compared to the XPD 751Lys/Lys and Lys/Gln genotypes [8]. Odemis et al. and Celik et al. found that XPD Lys751Gln variant Lys/Lys genotype frequency was increased in patients with schizophrenia and in OCD comparison to controls [26,27]. In the present study, we showed that Gln/Gln genotype was higher in subjects with cannabis and/or synthetic cannabis dependence than in healthy controls. The subjects carrying this genotype had a 2.2-fold increased risk for SUD. Because the XPD Lys751Gln variant Gln/Gln genotype reflects insufficient DNA repair, the result emphasizes the importance of DNA repair capacity in SUD.

The limitations of this research study should also be noted. First, we focused on only three variants involved in the DNA repair pathway, other regulatory variants in the DNA repair signalling pathway may also contribute to the pathogenesis of SUD. Second, owing to the relatively small sample size, the frequencies of some homozygous variants were low in groups and therefore reduced the statistical power. Finally, lack of assessment of expression levels of these proteins is also a limitation of this study.

In summary, we demonstrated for the first time a wider spectrum of DNA repair genes variants are important and independent genetic markers for SUD. Although the size of the investigated sample is small, these original results are promising and could lead to a new pharmacokinetic hypothesis for SUD. Ours results support the hypothesis that the XRCC1, XRCC4, and XPD gene variants are important and independent genetic markers for SUD. Further studies with a larger sample size investigating a wider spectrum of DNA repair genes variants are needed to support these results and better clarify its role in the genesis of SUD.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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