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Effect of SLC6A4 polymorphisms on serotonin in individuals with amphetamine use disorder in Basrah, Iraq

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ABSTRACT

Analysis of addictive behavior at the molecular level among drug addicts admitted to the drug addiction rehabilitation center in Basra, using some genes as molecular markers of addiction, during the period from October 2024 to October 2025. DNA was extracted from blood samples from two groups, and then amplified using polymerase chain reaction (PCR). The results showed that the highest rate of amphetamine addiction was among the 25-34 age group (59.17%), while the lowest rate was recorded in the 35-44 age group (54.97%). The results also indicated that the addiction rate to amphetamine (AMPH) reached 55.78%, the highest compared to other drugs, while addiction rates to other substances ranged between 4.7% and 24.26%.To use amphetamine addicts in molecular studies, a rapid urine test was performed on 80 individuals addicted to ten different drugs, including amphetamine. The current results show that 80% of participants were addicted to amphetamines, while addiction rates to other substances ranged between 0% and 7%. Based on polymerase chain reaction (PCR) analysis of the SLC6A4 gene polymorphism, two mutations were identified compared to the control group. These two mutations were homozygous (SS, 22.5%) and heterozygous (LS, 60%). In amphetamine addicts, the frequency of the S allele was higher (52.5%) than that of the L allele (47.5%). The current results show that amphetamine addicts carrying the LL genotype had the highest serotonin receptor concentration, at 152 ng/ml, while receptor concentrations were significantly lower in the SS genotype group, at 114 ng/ml. This study highlights the importance of molecular markers in understanding the mechanisms of addiction, as it revealed a clear link between SLC6A4 gene polymorphisms and high serotonin receptor concentration in amphetamine addicts, opening new horizons for accurate diagnosis and more effective personalized treatment.

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1. Introduction

Molecular Genetic Foundations of Substance Addiction and Associated Behaviours .

Substance addiction is a complex public health crisis with multifaceted consequences that permeate the social, biological, and psychological spheres of individuals' lives. Studies, such as those by[1] . Studies indicate that addiction is linked to decreased academic performance and productivity, disrupted relationships, and financial insecurity. It also impairs essential functions and negatively impacts physical and mental health. The effects vary depending on the type of substance used and the degree of dependence, ranging from non-addictive use to severe addiction, influenced by both biological and psychological factors. Psychological triggers stem from anxiety and are further exacerbated by[2] . epidemiological data for 2017 reveal that approximately (271) million people—equivalent to (5.5%)of the global adult population—used illicit drugs. Of these, (35.6) million suffered from substance use disorders. Cannabis remains the most prevalent substance, with (188) million people using it annually. Opioids follow, with (53) million people consuming them, a (56%) increase over previous estimates. Alarmingly, opioids are responsible for two-thirds of all deaths associated with substance use disorders[3]. Serotonin, a monoamine neurotransmitter, is essential in modulating a wide range of functions, including sleep, mood, food intake, vascular tone, pain, behavior, motor activity, and platelet activity[4]. Serotonin transporter (SERT) is an integral membrane protein expressed in neurons of the raphe nuclei of the brain. SERT is responsible for the rapid removal of the neurotransmitter serotonin from the synaptic cleft, terminating chemical signal transduction in serotonergic neurons [5] . SERT actively transports serotonin into neurons, reducing extracellular serotonin levels and regulating mood, sleep, appetite, and cognition[6].Serotonin transporter (SLC6A4) mutations, a 5-HTTLPR insertion/deletion variant (short "S" alleles and long "L" alleles), affect serotonin transporter expression. The S allele is associated with reduced transcriptional efficiency and increased susceptibility to stress-related depression [6] .SERT-N217S and SERT-A500T are rare inactivating mutations found in patients with treatment-resistant affective disorder. These mutations result in a partial loss of serotonin transporter function [7] .The (rs25531) (5-HTTLPR) SNP modifies the effect of the L allele, making it functionally similar to the S allele when present [8] .The SLC6A4 gene is located on chromosome 17q11.2, spans approximately 40 kilobases, and consists of (14) exons encoding a protein of (630) amino acids, with (12) domains. The promoter region of the SLC6A4 gene contains one of the most studied polymorphisms in psychiatric genetics, the serotonin transporter-associated polymorphism (5-HTTLPR) [9]. This region is characterized by an insertion/deletion of (44) base pairs, producing short (S) and long (L) alleles, which were originally described as containing (14) and (16) repeats, respectively [10] .Amphetamine, also known as dioxyephedrine (AMPH), is a psychostimulant and sympathomimetic drug that has devastating effects on the brain and body, causing severe neurological and physical consequences [11]. Its immediate effects include increased alertness, elevated heart rate, blood pressure, and body temperature, as well as loss of appetite [11] . Amphetamine stimulates the brain by affecting neurotransmitter systems such as dopamine, serotonin, and norepinephrine, leading to euphoria. However, it is a highly addictive substance [12].Therefore, the current study aimed to investigate addictive behaviour at the molecular level among drug users admitted to rehabilitation centres by using certain genes as molecular markers of addiction. Investigating the relationship between genetic variation (SNPs) in these molecular markers and the type of narcotic substance among drug users. Investigating the relationship between genetic variation (SNPs) in molecular markers and the type of behavioural, psychological and mental disorders among drug users.

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2.Materials and Methods

2.1. Sample Collection

Blood samples (from 80 individuals) were collected from the drug addiction treatment center at Al-Fayhaa Teaching Hospital in Basra. In addition to this, blood samples were also collected from volunteers (20 non-addicts). The ages of participants ranged from (14 > 45) years. Ten millilitres of urine samples were also collected from the addicts and analysed using a urine drug screening kit to confirm amphetamine use. The blood sample (5 ml) was divided into two tubes: (2) ml into an EDTA tube and (3) ml into a gel tube. Demographic data, including age, job, education, and others, were also collected. The ethical approval was authorized by the University of Basrah and Basrah Public Health Office.

2.2.Molecular Diagnosis

2.2.1.DNA Extraction

DNA was extracted from blood samples of (80) amphetamine addicts and (20) non-addicts using a custom extraction kit from the Taiwanese company Geneaid, according to the manufacturer's protocol. The concentration and purity of the DNA were measured using a nanodrop device in the central laboratory of the College of Education, Al-Qurnah, Department of Life Sciences. The DNA was then stored at -20°C until its use in subsequent steps.

2.2.2.polymerase chain reaction (PCR)

was used to study SLC6A4 polymorphisms in AMPH addicts. In the first round of PCR, the primer set (5' GAGGGACTGAGCTGGACAACCAC -3') was predesigned to target the specific region (528 base pairs) and (5' GGCGTTGCCGCTCTGAATGCC -3') was predesigned to target the specific region (484 base pairs) [13]. The reaction was performed in a total volume of 25 µL, consisting of Promega Go TaqIA® G2 Green Master Mix (12.5 µL), primers (1 µL each), nuclease-free water (4.5 µL), and gDNA (6 µL). PCR conditions were (94)°C for 2 minutes for 1 cycle, (94)°C and (60)°C for (30) seconds each, and (72)°C for 1 minute for (35) cycles, (72)°C for 5 minutes for 1 cycle. PCR products were analysed by electrophoresis on a 1% (w/v) agarose gel and visualized using a UV light detector.

2.2.3.Urine Test

Urine samples were collected by taking (10) ml from each addict and placing them in urine test tubes, then inserting the reagent into the tubes and waiting for the results for 3 minutes. These tests were conducted in the central laboratory of Al-Faihaa Teaching Hospital. The urine analysis reagent contains (10) types of narcotic substances, which are: - (AMPH) Amphetamine - THC) Tetrahydrocannabinol) – (MDMA) Methylenedioxymethamphetamine- (MOP) Morphine – (OPI) Opium - (TRA) Tramadol – (BAR) Phenobarbital - (BZO) Benzodiazepine- (TCA) Trichinella Antidepressants- ((BUP) Buprenorphine.

2.2.4.Serotonin concentrations

Serum serotonin concentrations in AMPH and non-addicts were determined using a human serotonin ELISA kit, The work was carried out in the central laboratory, Department of Life Sciences, College of Education, Al-Qurna. (Chemical Analysis Technology Laboratory) according to the manufacturer's instructions.

2.2.5.Statistical Analysis

Statistical analyses were performed using SPSS version 25. Data were analyzed using either the Chi-square test or one-way ANOVA. The differences were considered statistically significant when p was less than 0.01.

3.Results:
3.1.Demographic data
3.1.1.Detection of SLC6A4 Polymorphism

In this study, the polymorphism of the SLC6A4 gene, associated with the serotonin transporter, was analyzed in 80 individuals addicted to amphetamines and 20 non-addicted individuals using polymerase chain reaction (PCR), as shown in Figure 1. The results of the genetic analysis revealed two main types of mutations: SS and LS, in addition to the LL type. Comparing the mutation patterns between non-addicted individuals (Figure 1A) and addicted individuals (Figure 1B), homozygous SS mutations were observed in samples 12 and 13, while homozygous LL mutations were observed in samples 5, 8, and 9. Heterozygous LS mutations were the most common, observed in samples (1, 2, 3, 4, 6, 7, 10, 11, 14, and 15)

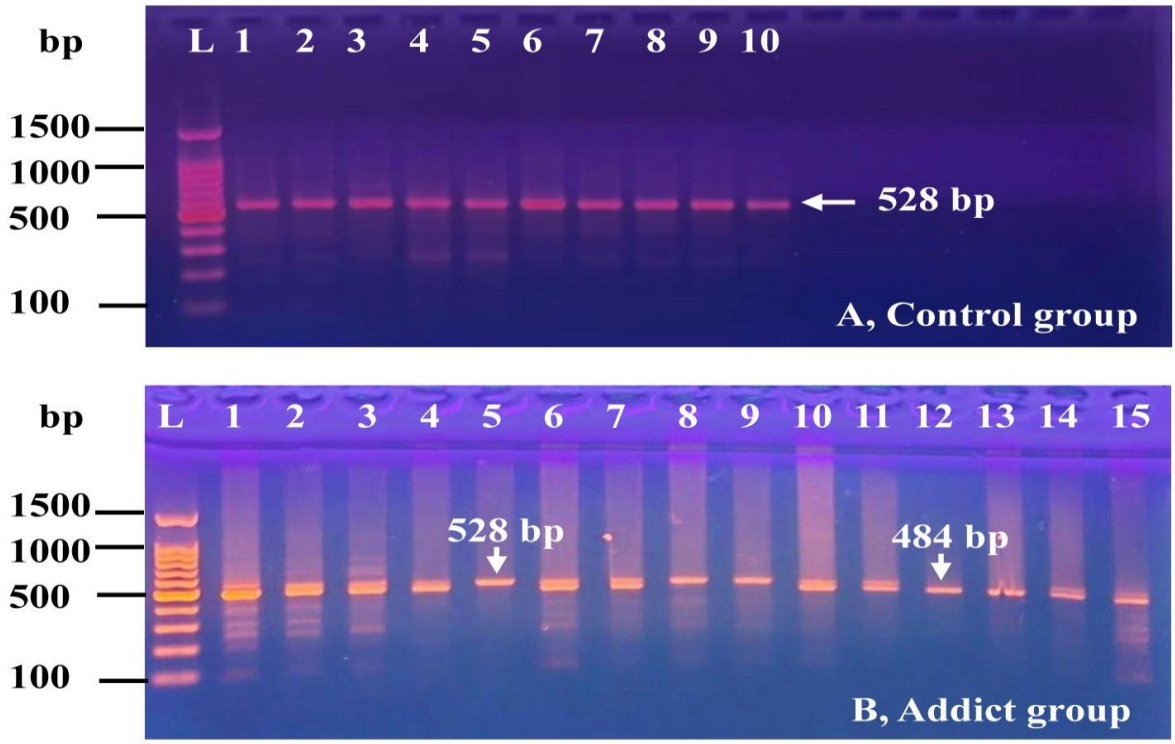

Fig.1. Polymorphism analysis of the SLC6A4 gene (5-HTTLPR region) using Electrophoresis on agarose gel with a concentration of 2%to compare genotypes between the two study groups. A represents the control samples, while B represents the addict samples.

The current results showed that the highest rate of amphetamine (AMPH) addiction was among the 25-34 age group at 59.17%, while the rate among other age groups ranged between 54.97% and 56.25%, with no statistically significant differences found when analyzing the results. As for trichloroacetic acid (TCA) addiction, the 14-24 age group recorded the highest rate at 7.5%, compared to rates ranging between 3.85% and 6.25% for other age groups, again without statistically significant differences. Regarding tetrahydrocannabinol (THC) addiction, the results showed that the highest rate was 11.36% in the 35-44 age group, while the rates ranged between 8.33% and 10.42% for other age groups, with no statistically significant differences. Regarding drug addiction, the highest rate (12.5%) was recorded in both the 14-24 and 45+ age groups, with statistically significant differences compared to other age groups. The results also indicated that the highest rate of opioid addiction (27.99%) was in the 35-44 age group, while rates ranged between 14.58% and 15.83% in other age groups. Accordingly, the statistical results showed statistically significant differences ($p<0.05$) when analyzed (Table 1). Drug use varies among age groups, with statistically significant differences only found in the overall rates of drug addiction and stimulant addiction.

Table 1. Prevalence of substance use disorder, classified by substance type and age group.

Age group	No.	AMPH %	TCA %	THC %	TRA %	ODS %	Chi-square
14 - 24	40	22(55)	3(7.5)	4(10)	5(12.5)	6(15)	99, *p*0.0001
25 - 34	120	71(59.17)	7(5.83)	10(8.33)	13(10.83)	19(15.83)	129,*p*0.0001
35 - 44	493	271(54.97)	19(3.85)	56(11.36)	9(1.83)	138(27.99)	111,*p*0.0001
45 ≥	48	27(56.25)	3(6.25)	5(10.42)	6(12.5)	7(14.58)	108,*p*0.0001
Total	701	391	32	75	33	170	
Chi-square	154.5	0.6305	0.8233	0.5368	10.37	7.956	
P value	0.0001	0.8894	0.8439	0.9107	0.0156	0.0469	

The current results show that the addiction rate to amphetamine reached %, registering the highest rate compared to other narcotic substances, with a statistically significant difference. In contrast, addiction rates to other substances ranged between 4.7% and 24.26% (Figure 1).

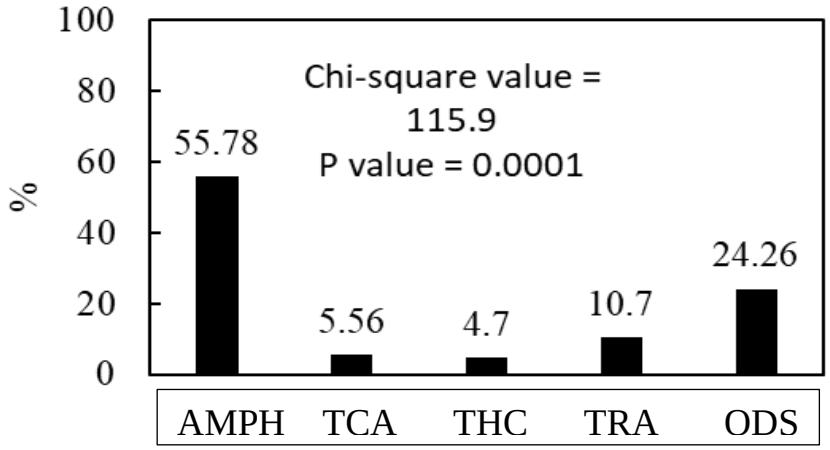

Fig. 2. Time distribution of substance use disorder cases over a year, classified by the type of substance used.

3.1.2. Urine testing of samples prior to their use in the molecular study

To use samples of AMPH addicts in the molecular study, rapid urine testing was performed on 80 samples of addicts for (10) narcotic substances, including AMPH. The results showed that the addiction rate to AMPH reached 80%, a significant difference compared to other narcotic substances. The addiction rate to other substances ranged between (0%) and (7%) (Figure 2).

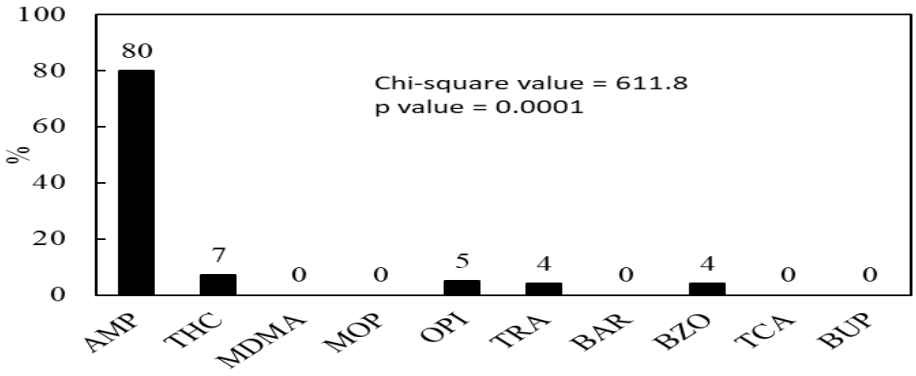

Fig. 3. The relative distribution of the types of drugs detected (based on the analysis of urine samples) in the study sample of 100 individuals with substance use disorder.

3.1.3. Mutations in the serotonin receptor gene

Table (2) shows the control and AMPH-addicted groups. The control group, with the wild-type (LL) genotype, recorded the highest percentage, reaching (100%), with a total of (20) samples, while the zygote-variant (LS) and mutant (SS) genotypes recorded no mutations, with each group recording (0%). As for the AMPH-addicted samples, the zygote-variant (LS) genotype recorded the highest percentage, reaching (60%), with a total of (48) samples out of (80), while the wild-type (LL) recorded the lowest percentage, reaching (17.5%), with a total of (14) samples out of (80). While the mutant genotype (SS) was recorded at (22.50%), which was (18) out of (80) samples. Therefore, the statistical results showed no significant differences (P<0.001) when the results were statistically analyzed (Table 2) between the samples of the control group and the samples of AMP addicts with regard to the SLC6A4 mutation.

Table 2. Frequency rate of the S allele pattern (of the 5-HTTLPR/rs25531 polymorphism) in the regulatory (promoter) region of the serotonin transporter gene (SLC6A4).

Sample	No.	Wild type		Mutant type				Total
		LL		LS		SS		
		No.	%	No.	%	No.	%	
Non addicts	20	20	100	0	0	0	0	100
Addicts	80	14	17.5	48	60	18	22.5	100
Total	100	34	34	48	48	18	18	100
Chi-square value = 20.28, p value = 0.0001								

Figure (4) illustrates the relative distribution of SLC6A4 gene genotypes. The highest percentage, 60%, was recorded for the heterozygous genotype (LS), indicating its prevalence among the studied sample. In contrast, the wild-type (LL) genotype was the lowest, at 18%, while the homozygous mutant genotype (SS) had an average percentage of 23%. Statistically comparing these percentages, the results showed highly significant differences between the various genotypes, with a significance value of (p<0.0001). This confirms that the distribution of these genotypes was not random and may reflect a potential association between SLC6A4 gene polymorphisms and the biological response associated with addiction

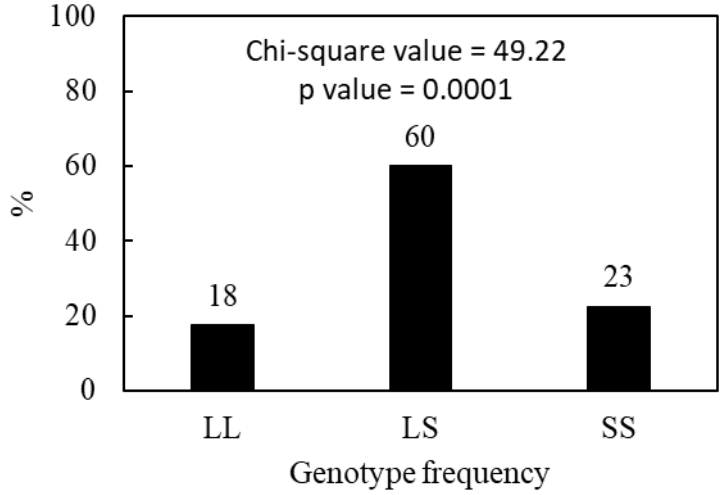

Fig. 4. The relative distribution of genotypes (LL, LS, SS) in the 5-HTTLPR polymorphism (SLC6A4 serotonin transporter gene promoter region) in a sample of amphetamine addiction patients.

The current results showed that the highest frequency of the (S) allele was (52.5%), while the lowest frequency of the (L) allele was (47.5%). Therefore, the statistical results showed significant differences ($p<0.0001$) when the results were analyzed statistically (Figure 5)

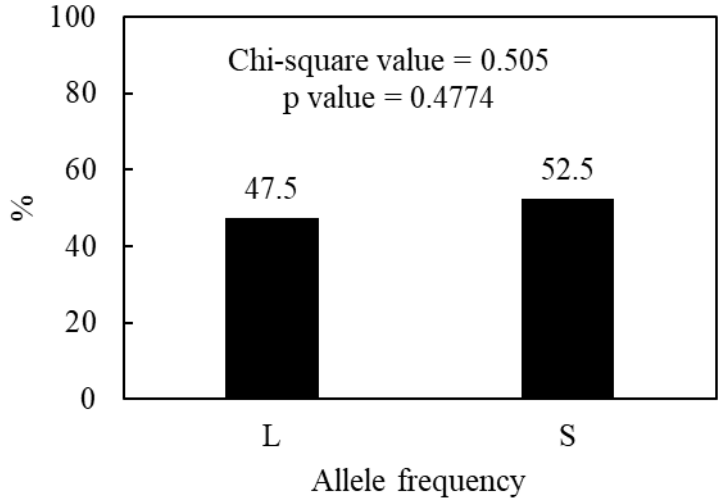

Fig. 5. The frequency ratio of the two alleles (L and S) in the 5-HTTLPR polymorphism (SLC6A4 gene) among individuals addicted to (AMPH).

3.1.4. The effect of single nucleotide polymorphisms on the serotonin transporter in AMPH addicts

A study of the effect of the SLC6A4 nucleotide polymorphism on the serotonin receptor in crystal meth (amphetamine - AMPH) addicts revealed clear differences in receptor concentrations between groups carrying different genotypes. The AMPH addicts with the LL genotype recorded the highest serotonin receptor concentration, averaging(152) ng/ml, while receptor concentrations were significantly lower in the SS genotype group, reaching (114) ng/ml, and in the LS genotype group, reaching (138) ng/ml. Statistical analysis of the results revealed significant differences between groups in serotonin receptor concentrations, indicating a potential effect of this polymorphism in the SLC6A4 gene on serotonin receptor regulation in amphetamine addicts . (Figure 6)

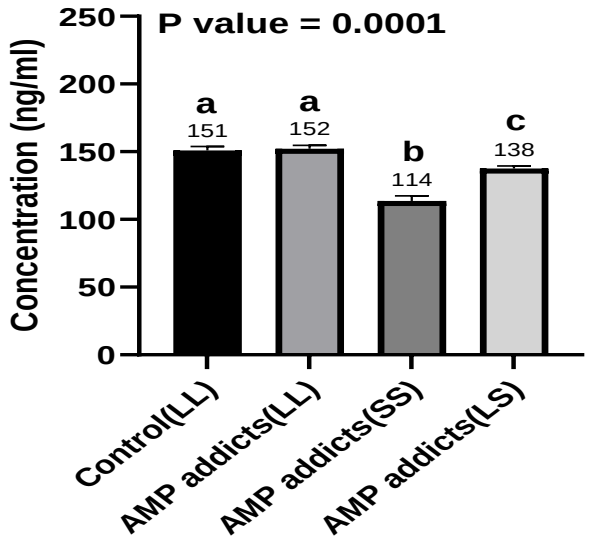

Fig. 6. The effect of single nucleotide polymorphisms (SNPs) in the regulatory (promoter) region of the serotonin transporter gene (SLC6A4) on gene expression or transporter function in individuals addicted to (AMPH).

4.Discussion

The serotonin receptor gene SLC6A4 was characterized using polymerase chain reaction (PCR) in amphetamine addicts (80 samples) and non-addicts (20 samples) (Figure 1 shows part of the results). The results of the current study showed two types of mutations (SS and LS), and the amphetamine addict (Figure B1) and non-addict (Figure A) models were compared to the amphetamine addict models. The mutation types were similar to dendritic mutations (SS for samples 12 and 13) and genotype mutations (LL for samples 5, 8, and 9), as well as heterozygous mutations (LS for samples 1, 2, 3, 4, 6, 7, 10, 11, 14, and 15) [14]. that the polymorphism of SLC6A4 is associated with the risk of addiction to methamphetamine and showed the pooled estimates(≈ OR 2.31) .

The study indicates that the 25-34 age group had the highest rate of amphetamine addiction (59.17%). This is attributed to interrelated factors including a sense of necessity, personal comfort, and improved performance, which may lead to enhanced functioning. Factors such as unemployment and a lack of awareness about the long-term health consequences also contribute to this demographic's increased susceptibility to addiction compared to other age groups [15]. The age group of (26–35) years was found to be the most addicted to amphetamines, accounting for (51.4%) of cases. This high proportion indicates that this age range represents a critical period in terms of social and psychological vulnerability for individuals. A previous study by [16]. confirmed that this age group (25–34 years) exhibits higher rates of amphetamine addiction compared to other age groups, reaching (27%). This is evident both in the number of hospital admissions due to amphetamine-related adverse effects and the upward trend of (6.35%) over the studied period. In contrast, the rates in other age groups (14–24) and (35–44) were (55%) and (54.97%), respectively, with no statistically significant differences observed. These findings suggest that age differences may not be the decisive factor in determining amphetamine abuse rates. Previous studies [17]. have also indicated similar conclusions. The level of amphetamine abuse did not show significant differences between age groups when receiving treatment at a rehabilitation center. Previous studies [18]. confirmed that the characteristics of psychological disorders and risks associated with amphetamine addiction were largely similar across age groups in rehabilitation centers, indicating that age groups do not influence their effects. The present study revealed that the highest rate of Tricyclic Antidepressant (TCA) use was among individuals aged (45) years and older, reaching (7.25%). This rate is higher than those observed in other age groups, which ranged from (3.85%) to (6.25%), with no statistically significant differences found upon analysis of the results. This elevated prevalence may be attributed to the association between advancing age and an increased incidence of mood disorders, anxiety, sleep disturbances, and chronic medical conditions. These factors may contribute to a higher frequency of TCA prescriptions by physicians for this demographic. This finding is consistent with previous studies [15]. which reported that (5.9%) of older adults living in nursing homes were using TCAs , The results of the current study revealed that the highest rate of THC users (11.36%) was observed in the (35–44)year age group. However, the rates among other age groups ranged between (8.33%) and (10.42%), with no statistically significant differences. This suggests that all age groups were exposed to the risk of THC addiction equally, a finding consistent with the report by [19], which also confirmed the absence of significant differences in THC addiction rates across age groups, with reported values (11.9%, 11.9%, 9.7%) being relatively similar to those found in this study. Regarding the prevalence of Tramadol addiction (TRA), the highest rate (12.5%) was recorded for both the (14-24 years) and (45 years and above) age groups. This was accompanied by statistically significant differences when the results were analysed compared to other age groups, ranging from (10%) for the (25-34 years) group to 1% for the (35-44 years) group. The (14-24-year-old) demographic is often driven by curiosity and peer influence, which may lead to the use of drugs like Tramadol due to its easy availability. Conversely, the(45) and above age group may use Tramadol for medical purposes to alleviate pain, which can increase the risk of addiction. This finding is consistent with the reports of [20].who noted the highest rates of Tramadol addiction among adolescents/young adults (14-24) and the elderly. Furthermore, the results of the current study indicated that the highest prevalence of ODS addiction reached (27.99%) for the (35-44 years) age group. In contrast, the rates for the other age groups ranged between (14.58%) and (15.83%). Consequently, statistical analysis revealed significant differences ($p<0.05$) with substantial statistical variance. This particular age group typically bears the greatest burden of responsibility and is exposed to significant financial, social, and professional pressures. This

aligns with the findings of [21]. who also reported the highest rate of ODS addiction in the (35-44) age group.

The results revealed that the addiction rate to Amphetamine (AMPH) reached (55 %), representing the highest proportion among illicit substances, with a statistically significant difference. In contrast, addiction rates for other substances ranged between (4.7% and 24.26%). This elevated rate is attributed to the ease of access to amphetamines. The annual report (2023, United Nations Office on Drugs and Crime) indicated that in (2021), an estimated (36) million people used amphetamines, (22) million used cocaine, and (20) million used "ecstasy"-type substances. The report further highlighted that the prevalence of amphetamine-type stimulant use is highest among men, with opioid users constituting (75%) of this demographic. It also emphasized that opioids are the category of substances that contribute most significantly to severe drug-related harm.

In the current study, when using samples of AMPH addicts for molecular analysis, rapid urine assays were performed on (80) samples of addicts across (10) drugs, including AMPH. The results showed that the addiction rate to AMPH reached 80%, a significant difference compared to other drugs. The addiction rate to other drugs ranged between 0% and (7%), due to the ease of access to the drug, whether online or in some social settings, as indicated by previous studies [22].

Table 2 presents the genotype distribution of the SLC6A4 polymorphism in the control group and the AMPH-addicted group. In the control group, the wild-type genotype (LL) was the most prevalent, observed in (100%) of the subjects (20 out of (20) samples). In contrast, neither the heterozygous genotype (LS) nor the mutant homozygous genotype (SS) was detected, with both occurring at(0%). Conversely, within the AMPH-addicted group (total n=80), the heterozygous genotype (LS) was the most frequent, accounting for (60%) (48 samples). The wild-type genotype (LL) showed the lowest prevalence at (17.5%) (14 samples), while the mutant genotype (SS) was present in (22.5%) of the samples (18 samples). Statistical analysis revealed a highly significant difference ($P<0.001$) in the SLC6A4 genotype distribution between the control and AMPH-addicted groups, as shown in Table 2. This finding is consistent with the report by [23],who noted a similarly high frequency (55%) of the CT heterozygous genotype in amphetamine addicts. This provides evidence that the T allele (whether in the heterozygous CT or mutant homozygous TT genotype) is strongly associated with susceptibility to amphetamine addiction.

The present study demonstrated that the SLC6A4 gene polymorphism (specifically, the 5-HTTLPR) affects serotonin transporter levels in crystal meth (methamphetamine) addicts, showing clear differences in concentration between groups carrying different genotypes . The control group with the LL genotype displayed a concentration of (151) ng/mL. In contrast, the group of methamphetamine addicts with the LL genotype recorded the highest serotonin transporter concentration at (152) ng/mL. Conversely, transporter concentrations were significantly lower in the group carrying the SS genotype, measuring (114) ng/mL, and in the group with the LS genotype, which measured (138) ng/mL . Statistical analysis of the results revealed significant differences between the groups in their mean serotonin transporter concentration levels. This indicates a potential influence of this SLC6A4 polymorphism on the regulation of the serotonin transporter in amphetamine addicts ،A marked reduction in serotonin transporter concentration has been observed in individuals with addiction who carry the SS genotype, reinforcing its well-established role as a genetic risk factor. The short (S) allele is associated with reduced transcriptional efficiency, leading to fewer serotonin transporters and less efficient serotonin reuptake. This creates a neurobiological profile characterized by increased anxiety and impulsivity. Consequently, these individuals may turn to stimulants, such as amphetamines, as a form of self-medication to alleviate these negative emotional states. A large-scale study [24] . supports this, showing that SS carriers had a (40%) higher likelihood of using stimulants to cope with stress (Odds Ratio [OR] = 1.98). Neuroimaging data also confirm a (20-30%) reduction in transporter density in key brain regions, such as the prefrontal cortex. [25] .

5. Conclusions

Addiction to Amphetamine is more prevalent than addiction to other substances, and it affects individuals across all age groups. A study investigating a genetic polymorphism in the SLC6A4 gene revealed three distinct genotypes among AMPH addicts. The most frequent genotype was LS (60%),

followed by SS (23%), and then LL (18%). Notably, the LS and SS genotypes were reported for the first time in this patient population, Furthermore, the results indicated that the frequency of the mutant L allele was below (50%). This suggests that the L allele influences the density of serotonin transporters. Analysis of the relationship between these genotypes and serotonin concentration showed that individuals with the LL genotype had the highest levels of serotonin. In contrast, the LS genotype did not appear to stimulate the receptor. The elevated serotonin levels associated with the LL genotype are likely to have a significant impact on the addictive behaviour of the individual.

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تأثير تعدد أشكال SLC6A4 على السيروتونين لدى الأفراد الذين يعانون من اضطراب تعاطي الأمفيتامين في البصرة، العراق

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معلومات البحث

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الكلمات المفتاحية

SLC6A4؛ السيروتونين؛ الأمفيتامين.

الملخص

تحليل السلوك الإدماني على المستوى الجزيئي بين المتعاطين الراقدين في مركز تأهيل مدمنين المخدرات في البصرة من خلال استعمال بعض الجينات كواسمات (كمؤشرات) جزيئية للإدمان.، خلال الفترة من أكتوبر 2024 إلى أكتوبر 2025. تم استخلاص الحمض النووي من عينات دم من مجموعتين، ثم تم تضخيمه باستخدام تفاعل البوليميراز المتسلسل (PCR). أظهرت النتائج أن أعلى معدل إدمان للأمفيتامين كان بين الفئة العمرية 25-34 عامًا (59.17%)، بينما سجلت الفئة العمرية 35-44 عامًا أدنى معدل (54.97%). اوضحت النتائج أن نسبة الإدمان على الأمفيتامين (AMPH) بلغت (55.78%)، مسجلةً أعلى نسبة مقارنةً بالمخدرات الأخرى ، بينما تراوحت نسب الإدمان على المواد الأخرى بين (4.7%) و(24.26%). لاستخدام مدمني الأمفيتامين في الدراسات الجزيئية، أُجريَ فحص سريع لعينات البول على 80 مدمنًا لعشرة أنواع من المخدرات، بما في ذلك الأمفيتامين. بينت النتائج أن نسبة إدمان الأمفيتامين بلغت 80%، بينما تراوحت نسبة الإدمان على المواد الأخرى بين 0 و7%. بناءً على تحليل تفاعل البوليميراز المتسلسل (PCR) لتعدد أشكال جين SLC6A4، تم تحديد طفرتين مقارنةً بمجموعة الضبط. كانت هاتان الطفرتان متماثلتين الزيجوت (SS، 22.5%) ومتباينتين الزيجوت (LS، 60%). لدى مدمني الأمفيتامين، كان تردد الأليل S أعلى (52.5%) من تردد الأليل(47.5%) L). اوضحت النتائج الحالية أن مدمني الأمفيتامين الذين يحملون النمط LL لديهم أعلى تركيز لمستقبلات السيروتونين، حيث بلغ 152 نانوغرام/مل، بينما كانت تركيزات المستقبلات أقل بشكل ملحوظ في مجموعة حاملي النمط SS، حيث بلغت 114 نانوغرام/مل. تُبرز هذه الدراسة أهمية المؤشرات الجزيئية في فهم آليات الإدمان، حيث كشفت عن ارتباط واضح بين تعدد أشكال جين SLC6A4 وارتفاع تركيز مستقبلات السيروتونين لدى مدمني الأمفيتامين، مما يفتح آفاقاً جديدة للتشخيص الدقيق ووعلاج شخصي أكثر فعالية.

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