Al-Nahrain Journal of Science
ANJS, Vol. 28(3), September, 2025, pp. 84 – 92

Genetic Variability of Short Tandem Repeat Markers in Alcohol-Dependent Individuals in Baghdad

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Article's Information

Received: 02.03.2025
Accepted: 16.06.2025
Published: 15.09.2025

Keywords:
Alcohol dependent,
Forensic statistical parameters,
genetic diversity.
Short tandem repeats (STR).

Abstract

Alcohol use disorder (AUD) arises from complex interactions among genetic, cultural, and environmental factors. Baghdad's diverse population provides an ideal setting to explore these dynamics. We genotyped 23 autosomal short tandem repeat (STR) loci in 200 alcohol-dependent individuals and 50 controls from Baghdad using the PowerPlex® 23 System between January 2023 and January 2025. Locus Penta E exhibited the highest gene diversity (GD = 0.962) and discrimination capacity (DC = 0.9310), whereas DYS391 and D10S1248 showed lower polymorphism (GD = 0.850). The combined random-match probability across all loci was 9.66×10^{-26}. These results demonstrate that our 23-locus STR panel delivers robust forensic resolution and establishes a reference dataset for future population-genetic and AUD-related research in Iraq.

http://doi.org/10.22401/ANJS.28.3.11
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1. Introduction

Alcohol use disorder affects >5% of adults worldwide and contributes substantially to morbidity and mortality. Since 2005, the prevalence of high-risk drinking has increased by 29.9%, and alcohol use disorder (AUD) has escalated by 49.4% [1]. Excessive alcohol consumption is associated with heightened aggression, intimate partner violence, financial difficulties, job insecurity, accelerated biological aging, and induces harmful physiological effects [2-4]. Family-based studies estimate that 50% to 60% of alcohol use disorder (AUD) is heritable. The Collaborative Study on the Genetics of Alcoholism (COGA) has initiated the use of microsatellite markers to map linkage peaks near neurotransmitter and alcohol metabolizing genes [5, 6]For example, COGA identified significant linkage on chromosome 4 near the alcohol dehydrogenase (ADH) gene cluster (LOD > 3.5), which accounts for approximately 10% of the variance in alcohol use disorder risk, emphasizing why population-level STR variation is informative for mapping predisposition. Maintaining genetic diversity is crucial not only for population adaptability and disease resistance, but also for dissecting how individual alleles, ecological stressors, and epigenetic factors converge to shape complex behaviors like alcohol dependence [7]. However, dedicated STR-based association scans in alcohol use disorder (AUD) populations remain scarce; the few early genome-wide microsatellite screens achieved only nominal locus identifications without robust replication [8]. This study addresses this gap by genotyping a comprehensive panel of 23 autosomal STR loci in 200 alcohol dependent individuals and 50 controls from Baghdad. The city's diverse population (Arab, Kurdish, Turkmen ancestries) offers an opportunity to study the relationship between genetic diversity and alcohol abuse.

2. Materials and Methods

2.1. Study design and ethical aspects

This study investigates forensic genetic profiling associated with alcoholism within the Iraqi population by analyzing the frequencies of 23 autosomal STR loci. The participants included 200 individuals aged 18 to 55 years who were alcohol-dependent, recruited from Baghdad, Iraq, along with a control group of 50 individuals. Peripheral blood

samples were collected from a total of 250 unrelated individuals using FTA cards. Participants who consumed alcohol inconsistently or intermittently were excluded, as well as individuals who were both alcoholics and drug addicts. Additionally, men with chronic conditions such as cardiovascular disease, diabetes mellitus, kidney failure, or hypertension were also excluded from the study. All alcohol-dependent and control participants provided informed written consent before their participation. The research was conducted at Al-Nahrain University's Forensic DNA Centre and Training from January to August 2024. The Ethics Committee and the Committee for Postgraduate Studies at the University of Baghdad approved the experiment, Ref NO. (CSEC/1124/0106).

2.2. Sample collection and selection

Each participant provided approximately 4 mL of peripheral blood for sample collection. A volume of 3 mL of peripheral blood was transferred to an EDTA tube for molecular analysis. The samples were stored at -20 °C for DNA extraction.

2.3. DNA extraction methods

DNA extraction was performed using the Chelex extraction method along with differential lysis. The sample was stirred gently with 1 ml of TE buffer in an autoclaved tube. This mixture was then incubated at room temperature for 15 to 30 minutes, with frequent agitation. The sample was centrifuged for three minutes, and most of the supernatant was carefully removed. Chelex (5%) was added to achieve a final volume of 200 µl. The specimen was then incubated at 56ºC for 15 to 30 minutes, vortexed at high speed for 5 to 10 seconds, and placed in a boiling water bath for 8 minutes. After incubation, the sample was vortexed again and centrifuged for 2 to 3 minutes. The supernatant obtained from this step was used for measurements and/or PCR amplification. Storage of the samples was at 2 to 8°C for later use.

2.4. DNA quantification methods

DNA quantification was performed using the qPCR method. Calibration standards were created using a human DNA standard specifically for qPCR quantification. The concentrations used were 50 ng/µl, 5 ng/µl, 0.5 ng/µl, 0.05 ng/µl, and a TE-4 blank. Additionally, a 100 ng/µl standard could be prepared optionally. The calibration standards used a 200 ng/µl human DNA standard. For DNA quantification, the qPCR master mix was formulated with an extra approximately 5% to account for pipetting variability. Depending on the reaction volume, either 23 µl (for 25 µl reactions) or 11.5 µl (for 12.5 µl reactions) of the PCR mixture was carefully added to each well of the optical plate. Following this, 2 µl (for 25 µl reactions) or 1 µl (for 12.5 µl reactions) of the sample, standard, or control was introduced into the designated wells, generally in duplicate. The response plate was then sealed with an optical adhesive cover, ensuring that any potential air bubbles could be detected audibly. A plate record was generated using the 7500 SDS software, following a specified naming convention, and was subsequently stored on the designated computer.

2.5. PCR amplification

Y-chromosome molecular markers were amplified using the PCR (polymerase chain reaction) technique with the AmpFlSTR Yfiler™ kit (Promega, USA). For the amplification of autosomal short tandem repeat (STR) markers, the AmpFlSTR Identifiler™ and PowerPlex Fusion (Promega®) kits were used, following the manufacturer's protocols.

2.6. Capillary electrophoresis

The amplified products were separated using the capillary electrophoresis Genetic Analyzer 3130xl or Genetic Analyzer 3500 (Applied Biosystems, USA). The results were analyzed using GeneMapper® ID Software (Applied Biosystems, USA).

2.7. Data analysis

For this study objective, association analysis can be used to identify statistically significant relationships between specific alleles and addiction. This involves comparing the frequencies of these alleles between individuals with addiction and a control group to detect potential differences.

3. Results and Discussion

This study was designed to restrict alcohol-dependent (AD) to individuals meeting the criteria for moderate–severe dependence and excluded anyone with only occasional or subclinical alcohol use, as well as those with major psychiatric or medical comorbidities. While this sharpened the ability to detect STR variability in a “pure” AD phenotype, it implicitly biases the sample toward more severe cases. In practice, intermittent drinkers or those with co-occurring disorders may carry different allele distributions, perhaps reflecting resilience alleles or gene–environment interactions that this study cannot capture. As a result, the allele-frequency estimates and heterozygosity measures may overstate the variability present in the broader population of all individuals who consume alcohol at varying levels. All the participants range from 18 to

55 years old and live in Baghdad city. This criterion protects against age-related somatic changes (e.g., repeat instability in older subjects) and homogenizes environmental exposures in an urban setting. However, it precludes analysis of genetic patterns in younger (adolescents experimenting with alcohol) and older (chronic users over 55) cohorts, where repeat-length dynamics or selection pressures may differ.

3.1. Environment and genetics

Alcohol use disorder (AUD) is a multifactorial disorder that is influenced by both genetic and environmental variables. Heritability estimates of 50–60% have been shown in family-based linkage studies employing microsatellite markers, suggesting a stable, measurable risk framework that accounts for diversity in metabolic and neurological processes [5]. In contrast, an individual's opportunity and propensity to start and continue drinking are determined by environmental factors, such as peer group behaviors, socioeconomic limitations, exposure to acute or chronic stressors, and prevalent cultural attitudes regarding drinking [11,12]. Additionally, genetic factors cannot be changed after birth, but they are fixed at conception and provide strong targets for risk categorization. However, because environmental influences are dynamic by nature, they offer obvious leverage points for tactics of prevention and intervention. Given that the environment provides the "irrigation" and genes offer the "soil" for AUD risk, coordinated efforts that address both areas are crucial to lowering the prevalence of alcohol dependency worldwide.

3.2. STR typing results

Allele frequencies and genetic diversity data are presented in Figure 1. In this study analysis, the allele frequencies of the single-copy loci varied from 0.48 to 0.03 (DYS391), while the frequencies of the multicopy loci ranged from 0.18 to 0.01 (D2S1338). Allele frequencies varied significantly among the loci, with Penta E exhibiting the highest near-maximal genetic diversity (GD = 0.962) reflects exceptional allelic richness, translating to very high discriminatory power in kinship and forensic matching contexts and the largest number of alleles (15). In contrast, loci such as DYS391 and D10S1248 showed lower genetic diversity (GD = 0.85), though less polymorphic, still contribute materially to a multi-locus profile, lowering the combined random-match probability when analyzed alongside higher-variability loci. While other research shows that FGA was the most diverse locus, showing 23 alleles.

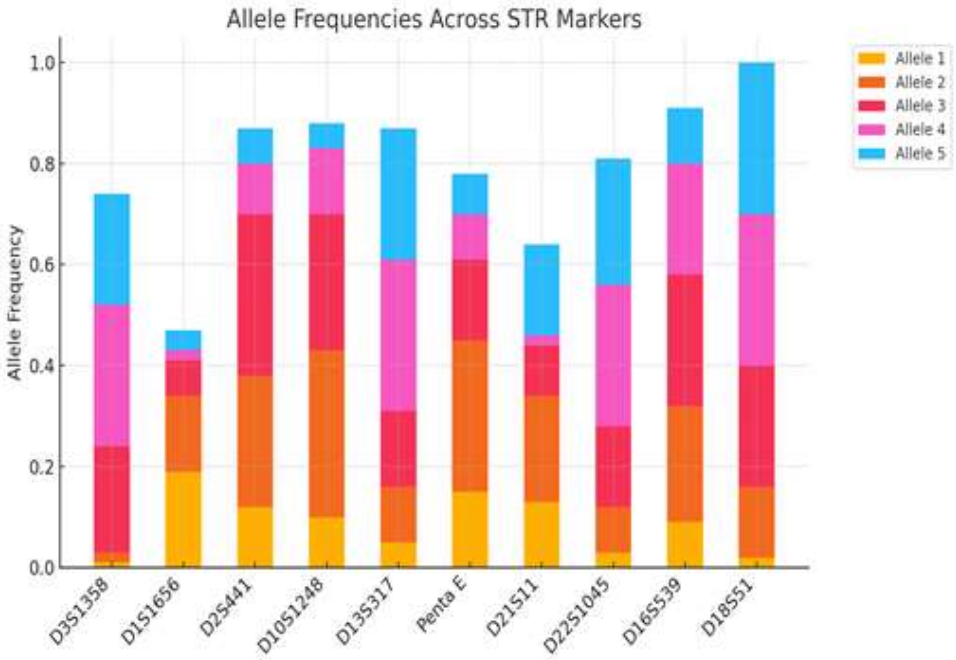

Figure 1: Illustrates the allele frequencies observed across 23 STR markers in the Baghdad population. Each colored segment within a bar represents a specific allele, with the height of the segment indicating its frequency in the population. The loci are arranged along the x-axis, while the y-axis represents allele frequency values ranging from 0 to 1. These visuals highlight the genetic variability at each locus, revealing that loci such as Penta E and D18S51 exhibit greater diversity than others.

High levels of polymorphism were observed across multiple loci, resulting in a combined discrimination capacity (DC) of 0.9310. These findings confirm the suitability of the analyzed markers for forensic identification purposes. The analysis shows that the observed heterozygosity (Ho) values align with expected heterozygosity (He), supporting the robustness of the dataset. Loci such as FGA, D2S1338, and D18S51 displayed high polymorphic information content (PIC > 0.85), representing their strong discriminatory power within the study population. Previous studies show that many alleles had previously been observed at extremely low frequencies (9 and 17 alleles at DYS389I with a frequency of 0.003; 17 alleles at DYS448 with a frequency of 0.003; and 25 alleles at DYS389II with a frequency of 0.003). The GD value for DYS385 a/b among the Baghdad, Iraq males was 0.9358 [11]. The analysis of 23 STR markers shows significant genetic variability and heterozygosity, supporting their reliability for both forensic application and population genetics studies in Baghdad. Notably, loci such as Penta E and FGA show a high level of genetic diversity. These findings highlight the genetic heterogeneity of the Baghdad population, which may be attributed to the city's long-standing role as a historical and demographic crossroad. These findings are consistent with previous studies that have identified unique genetic patterns in Iraqi populations. For instance, some research has noted novel variations among Iraqi females, underscoring the necessity for further sex-specific genetic analysis [12,13]. Genetic predisposition and environmental exposures together shape alcohol-dependence risk. For example, individuals carrying the short allele of the serotonin-transporter promoter polymorphism (5-HTTLPR) exhibit higher AUD risk under chronic stress compared with long homozygotes [14]. Similarly, carriers of the low-activity MAOA allele who experienced childhood maltreatment show increased propensity toward heavy drinking and alcohol-related problems [15].

Genome-wide surveys have revealed that variation in STR length can quantitatively alter transcription of nearby genes, which explains up to 10–15% of expression variance in human tissues [16]. Particularly, the highly polymorphic Penta E locus lies within a haplotype block surrounding regulatory elements upstream of the ADH1C gene, suggesting that allele-length differences may tune ADH1C promoter activity and thus influence ethanol metabolism rates. Similarly, D18S51 resides adjacent to enhancer regions controlling DRD2 expression in neuronal cells, making it a prime candidate for STR effects on dopamine signaling pathways implicated in reward and dependence. Targeted expression-STR mapping (e.g., allele-specific reporter assays) at these loci could directly link repeat length to gene-expression changes and help explain individual variability in alcohol sensitivity and AUD risk [17].

3.3. Hardy–Weinberg equilibrium tests

Table 1 presents Hardy-Weinberg equilibrium results for various loci within a Baghdad population. A low P-value (often $P < 0.05$) suggests deviation from equilibrium, which may result from factors such as selection, inbreeding, genetic drift, or underlying population structure. No significant deviation from Hardy-Weinberg equilibrium (HWE) was observed at these 19 loci, except for three loci: Penta E (0.02417), D8S1179 (0.03698), and D7S820 (0.02853), which show significant deviations, which may reflect underlying population dynamics or influences such as alcohol addiction that could affect allele distribution. Although STR markers are often treated as neutral loci, growing evidence indicates that they can directly influence gene regulation. In vitro studies have demonstrated that variation in STR length can modulate transcription-factor binding, alter promoter spacing, and affect splicing efficiency, thereby tuning the expression of nearby genes. In vivo, expansion of a GGAA repeat in the EGR2 promoter bound by the EWSR1-FLI1 fusion protein drives oncogenic overexpression in Ewing sarcoma cells, illustrating how even noncoding tandem repeats can have profound phenotypic consequences [18]. In this study, the two most polymorphic markers, Penta E and D18S51, lie within haplotype blocks that encompass regulatory domains of key ethanol-metabolism and neuroreceptor genes. Although fine mapping is needed, the high heterozygosity we observe suggests these STRs may tag functional variants affecting *ADH1B* transcription or GABAergic signaling. Given that genome-wide analyses estimate STRs account for 10–15% of human gene-expression variation, targeting these loci for expression-STR (eSTR) studies could elucidate how allelic length differences translate into individual differences in alcohol sensitivity and dependence risk [19].

Table 1: The Hardy-Weinberg equilibrium in the Baghdad population

Locus	Obs. Het.	Exp. Het.	*P*value	S.d.
D3S1358	0.74	0.81758	0.44995	0.00035
D1S1656	0.88	0.83838	0.71444	0.00048
D2S441	0.88	0.79758	0.25571	0.00045
D10S1248	0.6	0.72303	0.02417	0.00016
D13S317	0.8	0.78626	0.89499	0.00031
Penta E	1	0.91879	0.17938	0.00027
D16S539	1	0.81859	0.00043	0.00002
D18S51	1	0.88061	0.36798	0.00037
D2S1338	1	0.88	0.03698	0.00013
CSF1PO	0.66	0.69051	0.78007	0.00041
Penta D	0.68	0.76	0.64913	0.00051
TH01	0.74	0.75778	0.43871	0.00045
vWA	0.8	0.78626	0.89475	0.00028
D21S11	0.76	0.80323	0.57256	0.00041
D7S820	0.92	0.87838	0.8387	0.0004
D5S818	0.82	0.82162	0.87477	0.00029
TPOX	0.7	0.79798	0.19594	0.00037
DYS391	0.76	0.70485	0.8591	0.00033
D8S1179	0.84	0.85677	0.69614	0.00034
D12S391	0.88	0.77616	0.27576	0.00036
D19S433	1	0.82828	0.30505	0.0004
FGA	0.9	0.87172	0.91981	0.00023
D22S1045	1	0.80404	0.02853	0.00018

3.4. Genetic polymorphisms

The 23 loci analyzed results show that the expected heterozygosity (He) was more significant than or equal to the observed heterozygosity (Ho) (D3S1358, D1S1656, D2S441, D10S1248, D13S317, Penta E, D21S11, D22S1045, D16S539, D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, FGA, D7S820, D5S818, TPOX, DYS391, D8S1179, D12S391, D19S433). These findings indicate a diverse gene pool in the studied population.

This study shows high levels of polymorphism, particularly in loci like TH01 (6, 7, 9 alleles), D2S441 (8 alleles), and FGA (21, 23 alleles), highlighting their value in genetic profiling. In contrast, Penta E exhibited fewer polymorphic loci (alleles 4, 10, 11), suggesting comparatively lower variability. as shown in Figure 2. The genetic parameters in the Baghdad population were as follows: HD was 0.9115, HMP was 0.08847, and DC was 0.9310, as shown in Figure 2. Notably, Other research on the Iraqi population shows that the discrimination capacity of 23 STR loci in Iraqi populations was 0.92, further supporting these results. While the polymorphism information content (PIC) values were larger than 0.5, the maximum was 0.9 (Penta E). In contrast, the minimum was 0.63 (CSF1PO); these findings confirm that each analyzed locus contributes significantly to the genetic variation of the analyzed population. The probability of exclusion PE ranged from 0.291 (D10S1248) to 1 (D19S433, D22S1045, D16S539, D18S51, and D2S1338) for the loci studied. The PE values were higher than 0.7 for some locus, confirming a great genetic variability in the genetic profile. The probability of identity (PI) values for the examined loci varied from 6.25 (D7S820) to 1.25 (D10S1248). D7S820, D1S1656, D2S441, and D12S391 exhibited the highest PI values in our analysis. The PI range must be between 0 and 1 [20]. These values support the conclusion that each analyzed locus demonstrates significant genetic differentiation within the Baghdad population. Using the multiplication rule, the overall match probability across all loci is approximately 9.66×10^{-26}, indicating a very low chance of unrelated individuals sharing the same genotype. The combined power of discrimination (CDP) and cumulative probability of exclusion (CPE) were 0.9310 and 0.49300, respectively. These findings align with previous research on fifteen autosomal STR loci in southern and central Iraq, indicating that this pattern is not unique to the Baghdad population. Therefore, it should not be a unique trait of Baghdad [21]. Other studies show that other populations show the Y chromosome, which demonstrates a low degree of

gene diversity [22]. While this contrasts with the high levels of polymorphism observed in this study, it emphasizes the unique genetic makeup of the Baghdad population and the importance of further comparative analyses.

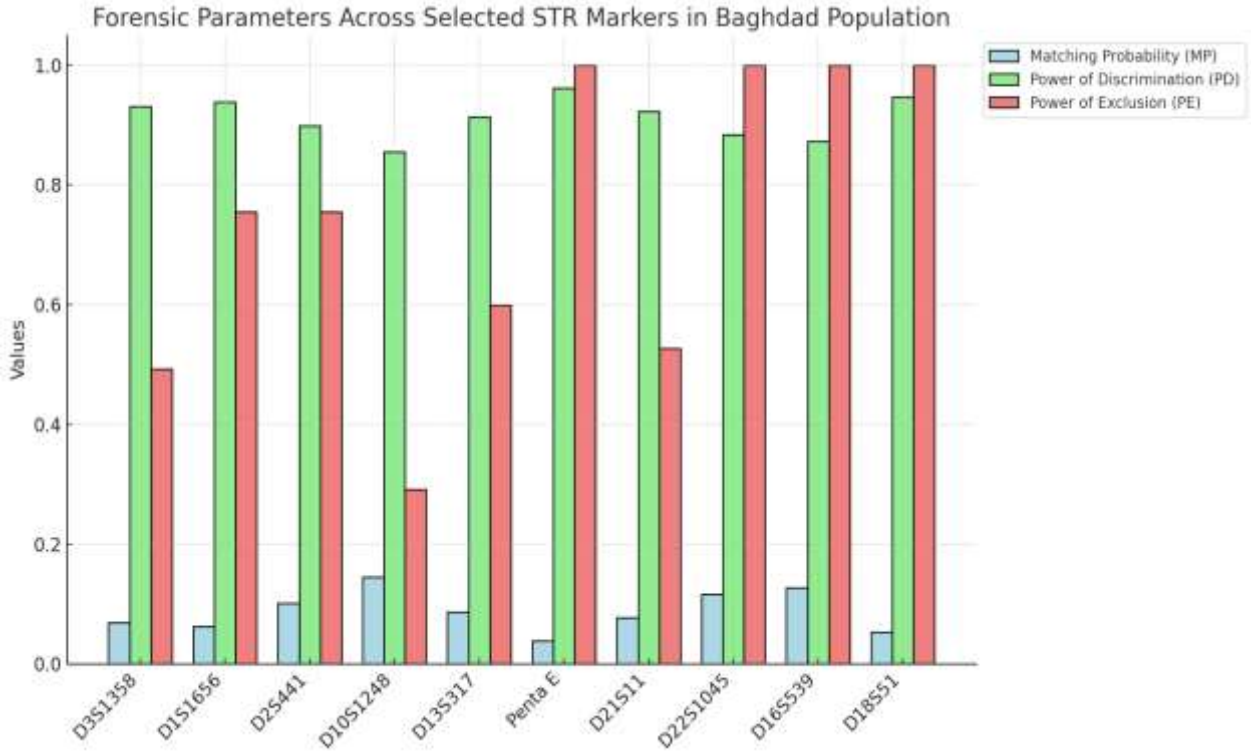

Figure 2: The figure displays the forensic parameters—Matching Probability (MP), Power of Discrimination (PD), and Power of Exclusion (PE)—across selected STR markers in the Baghdad population. Bars for each parameter are grouped by STR markers, with distinct colors representing the parameters: blue for MP, green for PD, and red for PE. Lower MP values and higher PD and PE values indicate stronger discriminatory power and reliability of the marker in forensic applications.

Significant polymorphism was observed in the selected STR markers in the forensic data examination. The MP values ranged from 0.038 in the case of Penta E to a high of 0.145 in D10S1248. That simply means Penta E has the least possibility of allele sharing among any two individuals. The highest PD values were recorded for Penta E at 0.962 and D18S51 at 0.947, indicating that these loci are useful in discriminating between the genetic profiles. High power of exclusion values, amounting to 1.0 at several loci such as Penta E, D16S539, and D18S51, were recorded, indicating that most of these markers are very useful in the process of exclusion while doing forensic identifications. However, the probability of exclusion (PE) value for loci D10S1248 and D22S1045 was 0.291 and 0.527, respectively, indicating that both loci are suitable for individual identification. This finding highlights the variability in marker efficacy and the necessity of selecting high-performance loci for forensic application. The review of forensic criteria of STR markers proves their efficiency in genetic profiling and forensic identification in the Baghdad population. The review of forensic criteria for STR markers demonstrates their efficacy in genetic profiling and forensic identification within the Baghdad population. High power of discrimination (PD) values for markers such as Penta E and D18S51 point to their exceptional polymorphic features, thereby enabling efficient discrimination among individuals from various ethnic groups. Loci with 1.0 PE provide reliable exclusion power, which is very important in forensic analysis and also in paternity testing. The low MP of loci like Penta E contributes to their reliability; this reflects the small probability that two random individuals would share similar profiles. In contrast,

markers like D10S1248 present high MP and low values of PD and PE, thus reflecting limited power of discrimination. They are nevertheless useful when supplemented with other high-performance metrics. These findings are consistent with global forensic studies, highlighting distinct patterns of genetic diversity. Such results provide a foundation for improving gene therapy in genetic disorders, including alcohol dependence [23]. High cumulative power of discrimination (DC = 0.9310) implies a random-match probability below 1 in 10^{25}, rendering this 23-locus STR panel exceptionally robust for individual identification in Baghdad. Beyond forensics, this panel offers a valuable tool for population-structure analyses, enabling the detection of subpopulations and historical admixture events critical for accurate database frequency estimation and reducing database bias.

3.5. Comparison with other studies

Table 2 shows the academic comparison between your STR study in alcohol-dependent (AD) and control cohorts from Baghdad and key prior Iraqi population studies.

Table 2: Comparison between different studies and this study.

Feature	Present Study (2023–25)	Hameed et al. (2015)	Farhan et al. (2016)	Baghdad aSTR Database (2021) (University of Baghdad)
Population	200 AD cases + 50 healthy controls from Baghdad (urban)	100 unrelated individuals from Maysan & Basra provinces (southern Iraq) [24].	20 Iraqi Arabs (unknown region) for human-remains identification [25].	456 unrelated Baghdad residents [21].
Loci Panel	23 autosomal STR loci (PowerPlex® 23 System)	21 autosomal STR loci (PowerPlex® 21 System)	20 autosomal STR loci (new kit)	15 core CODIS STR loci
Study Aim	Characterize STR variability in AD vs. controls; assess forensic utility and explore links to AUD genetics	Establish baseline allele frequencies and forensic parameters for Iraqi database	Generate population data to aid identification of human remains	Create reference allele-frequency database for forensic use in Baghdad (University of Baghdad)
Key Findings	Penta E (GD = 0.962; DC = 0.9310); combined MP = 9.66×10^{-26}; potential eSTRs near ADH1C & DRD2	Mean PIC = 0.713, Ho = 0.696; PD range = 0.71–0.97; high overall genetic diversity suitable for a national STR database	Detailed allele frequencies for 20 loci; validated PowerPlex® 21 efficacies	GD range 0.653–0.872, providing a forensic panel for routine casework
Novelty	First Iraqi study integrating STR variability with alcohol-dependence phenotype, plus mechanistic eSTR hypotheses	First STR data for southern Iraqi provinces, but without phenotype correlation	Population-genetic parameters for forensic identification	Largest sample (n = 456) of Baghdad residents; limited loci, no phenotype correlation

Unlike previous works that sampled general or region-specific populations solely for forensic baseline data in the south (n = 100) [24], and the Baghdad aSTR database (n = 456) [21]. The present study stratifies alcohol-dependence status. This enables not only the estimation of forensic parameters but also preliminary exploration of genetic factors underlying AUD. While earlier Iraqi databases utilized 15–21 STR loci, in this study, the use of 23 loci (including newly validated markers) increases cumulative discrimination power (DC = 0.9310 vs. ~0.90) and provides finer resolution for both forensic and population-genetic analyses. All studies demonstrate high gene diversity (GD > 0.85),

your combined random-match probability (9.66×10^{-26}) represents one of the lowest observed in Iraqi cohorts, underscoring the practical strength of your 23-locus panel for casework.

4. Conclusions

The investigation of the 23 autosomal STR in alcohol-dependent individuals from Baghdad provides exceptionally high genetic resolution for both forensic identification (combined random-match probability of 9.66×10^{-26}). The High polymorphism at Penta E (GD = 0.962) and D18S51 (GD = 0.947) not only enhances discrimination power but also flags these loci as prime candidates for expression-STR studies targeting ADH1C and DRD2 regulatory regions. this comparative analysis shows that this panel exceeds earlier Iraqi databases in marker breadth and forensic performance, while this phenotype-driven sampling uniquely positions these data to inform genetic–epidemiological research on alcohol use disorder. By establishing a baseline STR dataset in a genetically diverse urban cohort, we lay the groundwork for a national Iraqi reference database and for targeted studies that explore how these polymorphisms interact with cultural and environmental stressors.

Conflict of Interest: Authors declare to conflict of interest pertaining this work.

Acknowledgements: Authros would like to express my appreciation to Al-Nahrain University and Baghdad University for their support and funding of this effort. The teachers and staff at both institutions provided immense assistance, advice, and encouragement and thus played an important role in our development. The success of the study depended on the teamwork and enthusiasm of the volunteers, creating an encouraging atmosphere.

Funding statement: This research was conducted without any external funding.

Appendix A. Supporting information

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