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# Evaluation of Forensic Efficiency Parameters of 19 Autosomal STR Markers in a Population Sample of Arabs Residing in Voronezh, Russia

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**Abstract**

The accuracy of DNA profile identification is significantly enhanced by increasing the number of STR markers that are examined. Forensic markers' usefulness depends on the population, necessitating regional studies. This study aims to provide a better understanding of the effectiveness of autosomal STR loci as a forensic tool by comparing the genetic factors found in Arabs living in Voronezh, Russia, to published datasets from other Arab groups. Blood samples were collected from 98 unrelated Arab volunteers. Using a 3130XL Genetic Analyzer, DNA typing was conducted for 19 polymorphic STR loci and the Amelogenin locus with the use of the GOrDIS Plus kit. The analysis revealed a high degree of polymorphism, with the number of alleles per locus ranging from 6 to 36. The highest allele frequency observed was 0.5816 at the TPOX locus. The observed heterozygosity (Ho) and expected heterozygosity (He) values were generally consistent, indicating that the population is largely in Hardy–Weinberg equilibrium (HWE). The forensic parameters demonstrated high discriminatory power: the Power of Discrimination (PD) ranged from 0.813 to 0.962, the Polymorphism Information Content (PIC) from 0.58 to 0.86, and the Power of Exclusion (PE) from 0.388 to 0.689. High Ho was observed at FGA and D21S11 loci (87.76% and 87.8%, respectively), while TPOX showed the lowest Ho (63.27%).In conclusion, the Analysis of Molecular Variance (AMOVA) and pairwise FST analysis indicated that Arabs residing in Voronezh, Russia, show strong genetic similarities with Arab populations in Europe and Arab countries. These findings underscore the robustness of the selected STR markers for forensic applications within this population and contribute valuable data to the global forensic genetic database.

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## 1. Introduction

In the forensic sciences, identifying one human from the other relies upon the variation in their genetic backgrounds. DNA profiling using short tandem repeat, or STR, markers remains the first lining workhorse for this. And is not about to fade away [1,2]. Short tandem repeats are non-coding DNA regions that cumulatively account for around 3% of the human genome and occur every 10,000 nucleotides [3,4]. The human genome has thousands of STR markers, but only a handful are used in forensic DNA and human identity testing. The chance of two people having a different DNA profile is increased by looking at a select group of loci [5,6].

But, the increase in the examined loci will add to it. Researchers are identifying new STR markers all the time, and their powers of discrimination and overall forensic efficiency vary according to different ethnic groups or populations. [7,8,9]. Several parameters were established as a quality control for the STR database such as forensic parameters [matching probability (MP), power of discrimination (PD), polymorphism information content (PIC), power of exclusion (PE)] and paternity parameters such as paternity index (PI) [10,11]. Previous studies have not addressed STR genotyping of the Arab population in Russia. The aim of present study is to Evaluate of forensic efficiency parameters of 19autosomal STR markers in a population sample of Arabs residing in Voronezh Russia and to compare with sample of Arabs residing in different countries [12,13].

## 2. Materials and Methods

### 2.1. Ethical Considerations

The study was conducted in compliance with the Declaration of Helsinki and received approval from the Forensic DNA Research and Training Center, Al-Nahrain University (DN 628: 13th Sep 2023). All participants provided written informed consent..

### 2.2. Sample collection and DNA extraction

Blood samples were collected from ninety eight unrelated Arabs volunteers residing in Voronezh, Russia. It is important to highlight that this study did not routinely gather precise demographic information, such as specific geographical origin within Arab countries, age distribution, and socioeconomic background, which limits the representativeness of the population. DNA extraction was accomplished using the GOrDIS EXTRACT Reagent (GOrDIS, Russia) according to manufacturer's instructions.

### 2.3. Polymerase chain reaction and DNA typing:

Amplification of 19 polymorphic STR markers: D3S1358, TH01, D12S391, D1S1656,D10S1248, D22S1045, D2S441, D7S820, D13S317, FGA, TPOX, D18S51, D16S539, D8S1179, CSF1PO, D5S818, VWA, D21S11, SE33 and human amelogenin locus were performed by using GOrDIS Plus kit (GOrDIS, Russia). The parameter of PCR was done according to manufacturer's instructions [14,15]. The STR genotyping was conducted using 3130XL Genetic Analyzer 16-capillary array system (Applied Bio systems, Foster City, CA, USA) according to the manufacturer's protocols. The system used POP-7™ Polymer and Data Collection Software along with Gene Mapper® V3.2 software (Applied Biosystems, Foster City, CA, USA). Allele sizing was achieved by comparing each sample's alleles with allelic ladders for the corresponding loci. Quality control was maintained by including positive and negative controls in every PCR run, and all procedures adhered to the guidelines recommended by the International Society for Forensic Genetics (ISFG).

### 2.4. Population Structure Analysis:

We used Arlequin software version 3.5.2.2 to do Analysis of Molecular Variance (AMOVA) and pairwise FST calculations to look at genetic differentiation and population structure [15]. These studies were performed to assess the genetic connections between our research groups and previously documented Arab communities.

## 3. Results and Discussion

In the present study, the number of alleles per locus was ranged from 6 for TH01 and D22S1045 to 36 for D2S441 markers. The total number of alleles observed was 153 and the highest frequency was 0.5816 in allele 8 for TPOX locus, while lowest frequency was 0.005 that seen in some of alleles for different loci (Table 1-2). Forensic parameter presented in (Table-3), high heterozygosity at loci indicates greater allelic diversity, which enhances the discriminatory power and reduces the probability of a random sample matching another sample by chance. The FGA locus showed higher observed heterozygosity (Ho) of 87.76%, while TPOX showed a lower observed heterozygosity (Ho) of 63.27%.The observed heterozygosity (Ho) and expected heterozygosity (He) values were generally consistent, indicating that the population is largely in Hardy-Weinberg equilibrium. Random matching probability was ranged from 0.038- 0.187. Power of discrimination reflects the probability of correctly distinguishing between two individuals, The FGA locus had the highest value of 0.962, while the TPOX locus had the least value of 0.813. Typically, two parameters are utilized to measure the degree of polymorphism at a locus; heterozygosity and Polymorphism Information Content or PIC. The PIC's Average Value was 75% while Minimum is 58% and Maximum is 86%. The informative values back up heterozygosity values that indicate a great deal of genetic polymorphism. The exclusion power for all STR markers was high, ranging from 0.388-0.689. The paternity index is an important part of paternity testing because it shows how likely it is

that the alleged father may pass on the obligatory allele compared to a random male. The PI values in this study demonstrate that different genetic loci can provide varying quantities of information, ranging from 0.196 for D12S391 to 4.08 for FGA and D21S11. Loci like FGA and D21S11 with high PI values make paternity testing more accurate and reliable, hence they are important for forensic genetic analysis.

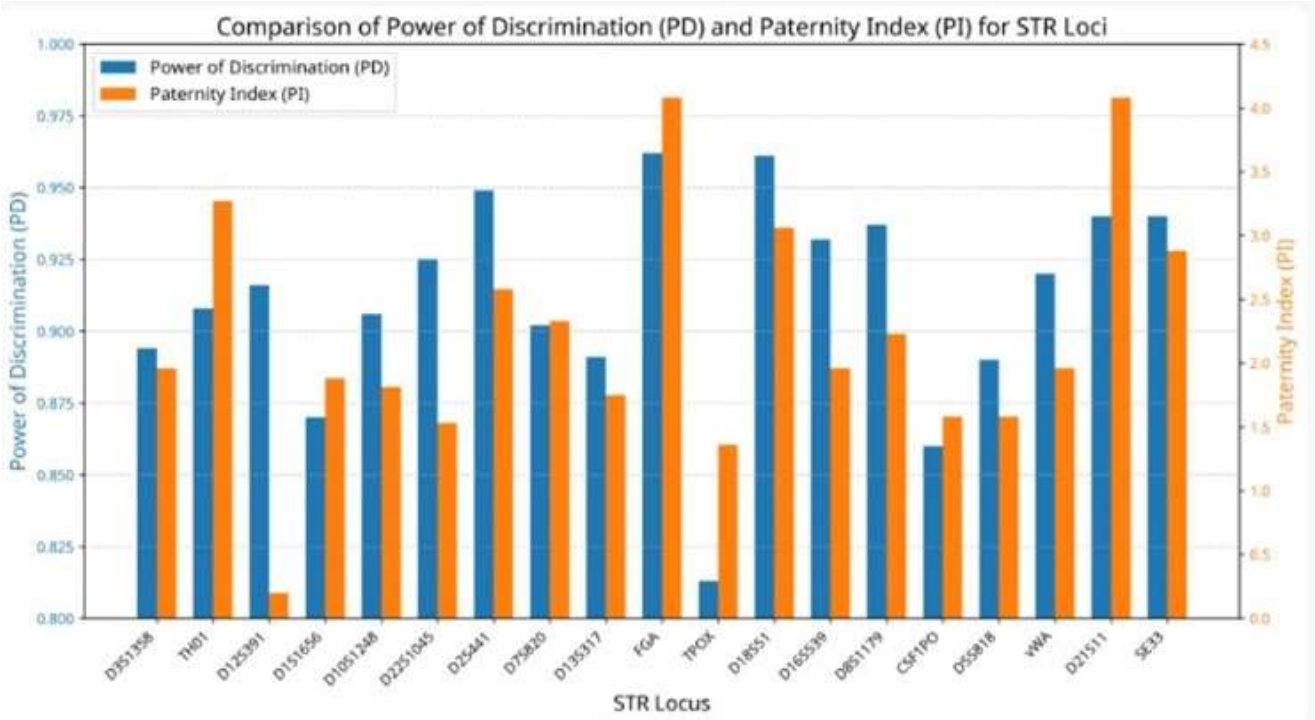



Figure 1: Comparison of Power of Discrimination (PD) and Paternity Index (PI) for 19 Autosomal STR Loci.

### 3.1. Population Structure Analysis Results

The AMOVA analysis showed that differences across populations made up 2.3% of the overall genetic diversity, while differences between individuals within populations made up 97.7%. The pairwise FST values between our Voronezh Arab population and other Arab populations varied from 0.0012 to 0.0045, signifying negligible genetic difference (Table 4). Understanding Locus-Specific Diversity: The notable high observed heterozygosity (Ho) and discriminatory power at the FGA and D21S11 loci (PD > 0.94, PI = 4.08) are significant. FGA is very polymorphic because it has a tetra nucleotide repeat structure and is located in a section of the genome that changes a lot. This makes it one of the most useful markers in forensic genetics. On the other hand, the TPOX locus has less diversity (PD = 0.813, PI = 1.36), which means it is less polymorphic. This reduced variability is common for TPOX in many populations around the world. This is generally because the repeat area is more limited, which makes it less useful as a stand-alone marker. This polymorphism that is particular to this locus is very important for choosing the best STR markers for forensic databases.

Table 1: Allele frequencies for (D3S1358- FGA) genetic loci in Arabs residing in Voronezh Russia (n=98)

| Allele | D3S1358 | TH01 | D12S391 | D1S1656 | D10S1248 | D22S1045 | D2S441 | D7S820 | D13S317 | FGA |
|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 0.000 | 0.296 | 0.000 | 0.000 | 0.000 | 0.265 | 0.000 | 0.000 | 0.000 | 0.000 |
| 7 | 0.000 | 0.209 | 0.005 | 0.005 | 0.000 | 0.184 | 0.000 | 0.000 | 0.000 | 0.000 |
| 8 | 0.000 | 0.122 | 0.194 | 0.010 | 0.000 | 0.133 | 0.000 | 0.179 | 0.133 | 0.000 |
| 9 | 0.000 | 0.199 | 0.107 | 0.026 | 0.000 | 0.265 | 0.000 | 0.102 | 0.071 | 0.000 |
| 9.3 | 0.000 | 0.168 | 0.000 | 0.000 | 0.000 | 0.138 | 0.000 | 0.000 | 0.000 | 0.000 |
| 10 | 0.000 | 0.005 | 0.316 | 0.250 | 0.000 | 0.015 | 0.000 | 0.291 | 0.041 | 0.000 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 11 | 0.000 | 0.001 | 0.209 | 0.362 | 0.000 | 0.000 | 0.000 | 0.291 | 0.306 | 0.000 |
| 12 | 0.000 | 0.000 | 0.153 | 0.286 | 0.000 | 0.000 | 0.000 | 0.117 | 0.367 | 0.000 |
| 13 | 0.010 | 0.000 | 0.000 | 0.056 | 0.000 | 0.000 | 0.000 | 0.010 | 0.056 | 0.000 |
| 14 | 0.036 | 0.000 | 0.016 | 0.005 | 0.092 | 0.000 | 0.000 | 0.102 | 0.026 | 0.000 |
| 15 | 0.240 | 0.000 | 0.000 | 0.000 | 0.240 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| 16 | 0.311 | 0.000 | 0.000 | 0.000 | 0.311 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| 17 | 0.255 | 0.000 | 0.000 | 0.000 | 0.245 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| 18 | 0.148 | 0.000 | 0.000 | 0.000 | 0.107 | 0.000 | 0.000 | 0.000 | 0.000 | 0.015 |
| 19 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.000 | 0.000 | 0.000 | 0.000 | 0.077 |
| 19.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 |
| 20 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.097 |
| 21 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.158 |
| 21.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 |
| 22 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.143 |
| 23 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.128 |
| 23.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 |
| 24 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.173 |
| 24.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.010 |
| 25 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.128 |
| 26 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.046 |
| 27 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.015 | 0.000 | 0.000 | 0.005 |
| 28 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.153 | 0.000 | 0.000 | 0.005 |
| 29 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.219 | 0.000 | 0.000 | 0.000 |
| 29.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| 30 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.184 | 0.000 | 0.000 | 0.000 |
| 30.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.000 | 0.000 | 0.000 |
| 31 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.046 | 0.000 | 0.000 | 0.000 |
| 31.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.133 | 0.000 | 0.000 | 0.000 |
| 32.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.153 | 0.000 | 0.000 | 0.000 |
| 33.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.087 | 0.000 | 0.000 | 0.000 |
| 36 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.000 | 0.000 | 0.000 |

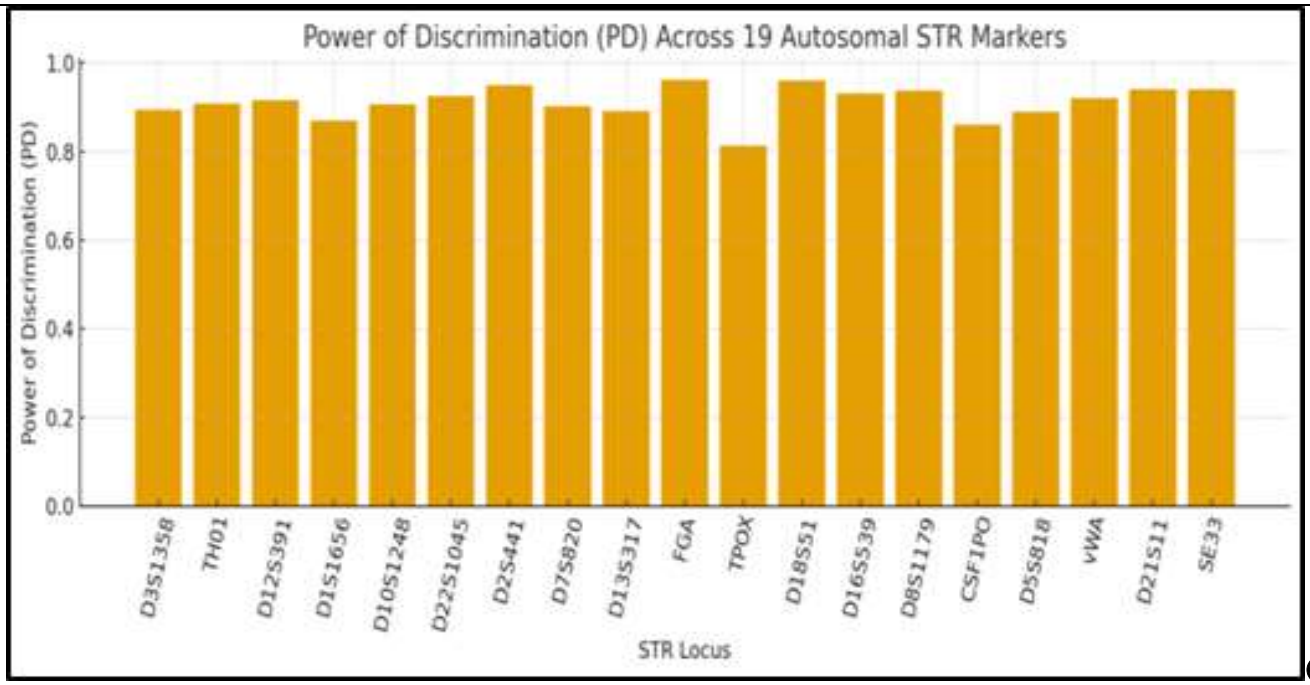
Table 2: Allele frequencies for (TPOX - SE33) genetic loci in Arabs residing in Voronezh Russia (n=98)

| Allele | TPOX | D18S51 | D16S539 | D8S1179 | CSF1PO | D5S818 | vWA | D21S11 | SE33 |
|---|---|---|---|---|---|---|---|---|---|
| 8 | 0.5816 | 0.000 | 0.026 | 0.015 | -0.000 | 0.015 | 0.000 | 0.000 | 0.005 |
| 9 | 0.102 | 0.000 | 0.204 | 0.005 | 0.026 | 0.031 | 0.000 | 0.000 | 0.010 |
| 10 | 0.1122 | 0.010 | 0.143 | 0.107 | 0.265 | 0.097 | 0.000 | 0.000 | 0.071 |
| 11 | 0.1531 | 0.015 | 0.255 | 0.066 | 0.286 | 0.327 | 0.000 | 0.000 | 0.087 |
| 12 | 0.051 | 0.143 | 0.194 | 0.056 | 0.367 | 0.311 | 0.000 | 0.000 | 0.097 |
| 13 | 0.000 | 0.168 | 0.153 | 0.301 | 0.046 | 0.209 | 0.000 | 0.000 | 0.296 |
| 14 | 0.000 | 0.214 | 0.026 | 0.194 | 0.010 | 0.010 | 0.061 | 0.000 | 0.143 |
| 15 | 0.000 | 0.138 | 0.000 | 0.209 | 0.000 | 0.000 | 0.082 | 0.000 | 0.214 |
| 16 | 0.000 | 0.092 | 0.000 | 0.041 | 0.000 | 0.000 | 0.276 | 0.000 | 0.066 |
| 17 | 0.000 | 0.092 | 0.000 | 0.005 | 0.000 | 0.000 | 0.296 | 0.000 | 0.010 |
| 18 | 0.000 | 0.066 | 0.000 | 0.000 | 0.000 | 0.000 | 0.204 | 0.000 | 0.000 |
| 19 | 0.000 | 0.041 | 0.000 | 0.000 | 0.000 | 0.000 | 0.071 | 0.000 | 0.000 |
| 20 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.010 | 0.000 | 0.000 |
| 21 | 0.000 | 0.010 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| 22 | 0.000 | 0.010 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| 26 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.010 | 0.000 |
| 27 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.010 | 0.000 |
| 28 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.148 | 0.000 |

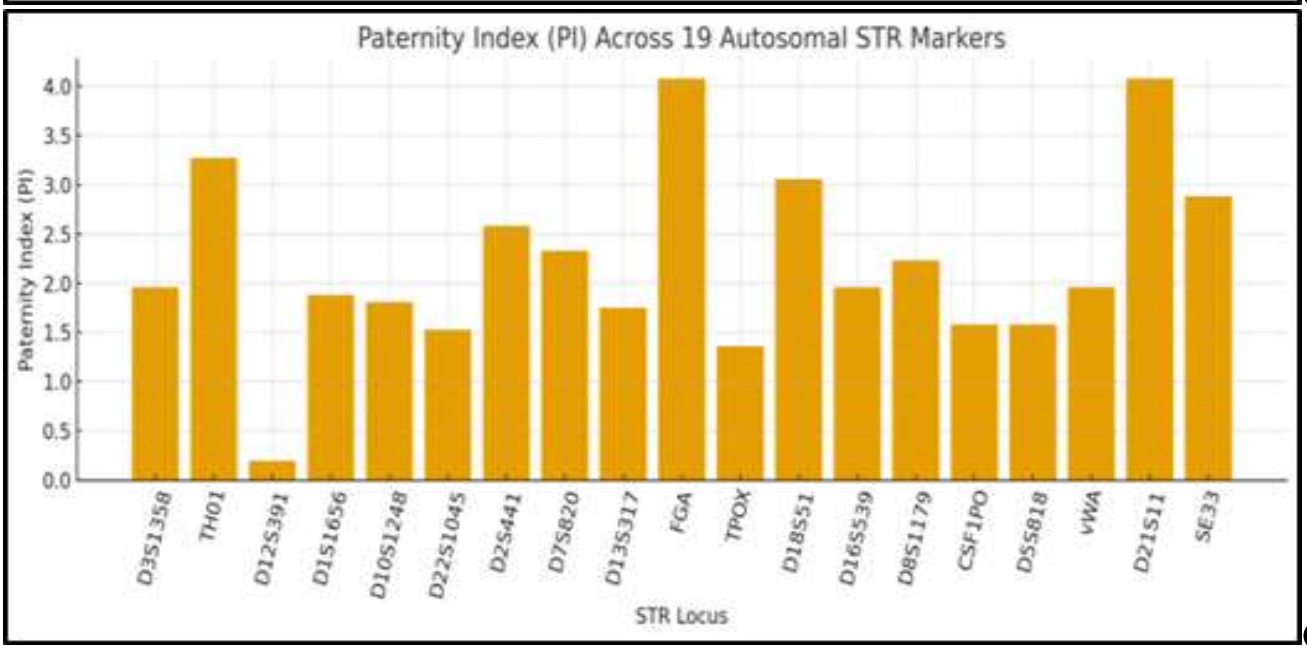
| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 29 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.255 | 0.000 |
| 29.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.010 | 0.000 |
| 30 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.214 | 0.000 |
| 30.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.000 |
| 31 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.056 | 0.000 |
| 31.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.082 | 0.000 |
| 32.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.158 | 0.000 |
| 33 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.000 |
| 33.2 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.046 | 0.000 |

Table 3: statistical parameters of forensic importance for 19 autosomal STR loci in 98 unrelated Arabs residing in Voronezh Russia Genetic loci Forensic Efficiency parameters (D3S1358- Observed Expected Matching Power of Polymorphism Power of Paternity SE33) Heterozygosit Heterozygosit Probability Discrimination Information Exclusion Index y (Ho) y (He) (MP) (PD) Content (PIC) (PE) (PI)

| Genetic loci (D3S1358 - SE33) | forensic efficiency parameters | | | | | | |
|---|---|---|---|---|---|---|---|
| | Observed Heterozygosity (Ho) | Expected Heterozygosity (He) | Matching Probability (MP) | Power of Discrimination (PD) | Polymorphism Information Content (PIC) | Power of Exclusion (PE) | Paternity Index (PI) |
| D3S1358 | 73.49% | 76.51% | 0.101% | 0.894% | 0.72% | 0.501% | 1.96% |
| TH01 | 84.69% | 79.38% | 0.092% | 0.908% | 0.750% | 0.689% | 3.270% |
| D12S391 | 74.49% | 79.15% | 0.084% | 0.916% | 0.750% | 0.501% | 0.196% |
| D1S1656 | 73.47% | 72.81% | 0.130% | 0.870% | 0.670% | 0.484% | 1.880% |
| D10S1248 | 72.45% | 77.36% | 0.094% | 0.906% | 0.730% | 0.467% | 1.810% |
| D22S1045 | 67.35% | 79.68% | 0.075% | 0.925% | 0.760% | 0.388% | 1.53% |
| D2S441 | 80.61% | 85.25% | 0.051% | 0.949% | 0.82% | 0.61% | 2.58% |
| D7S820 | 78.57% | 78.26% | 0.098% | 0.902% | 0.740% | 0.57% | 2.33% |
| D13S317 | 71.43% | 75.08% | 0.109% | 0.891% | 0.700% | 0.45% | 1.75% |
| FGA | 87.76% | 88.31% | 0.038% | 0.962% | 0.860% | 0.75% | 4.08% |
| TPOX | 63.27% | 61.90% | 0.187% | 0.813% | 0.580% | 0.33% | 1.36% |
| D18S51 | 83.67% | 87.18% | 0.039% | 0.961% | 0.850% | 0.61% | 3.06% |
| D16S539 | 74.49% | 81.89% | 0.068% | 0.932% | 0.780% | 0.50% | 1.96% |
| D8S1179 | 77.55% | 81.54% | 0.063% | 0.937% | 0.780% | 0.55% | 2.23% |
| CSF1PO | 68.37% | 71.75% | 0.14% | 0.86% | 0.66% | 0.40% | 1.58% |
| D5S818 | 68.4% | 74.97% | 0.11% | 0.89% | 0.70% | 0.40% | 1.58% |
| vWA | 74.5% | 78.73% | 0.08% | 0.92% | 0.75% | 0.50% | 1.96% |
| D21S11 | 87.8% | 83.84% | 0.07% | 0.94% | 0.81% | 0.75% | 4.08% |
| SE33 | 82.7% | 82.79% | 0.06% | 0.94% | 0.80% | 0.65% | 2.88% |


Power of Discrimination (PD) Across 19 Autosomal STR Markers
Power of Discrimination (PD)
1.0
0.8
0.6
0.4
0.2
0.0
D3S1358
TH01
D12S391
D1S1656
D10S1248
D22S1045
D2S441
D7S820
D13S317
FGA
TPOX
D18S51
D16S539
D8S1179
CSF1PO
D5S818
VWA
D21S11
SE33
STR Locus

(a)


Paternity Index (PI) Across 19 Autosomal STR Markers
Paternity Index (PI)
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
D3S1358
TH01
D12S391
D1S1656
D10S1248
D22S1045
D2S441
D7S820
D13S317
FGA
TPOX
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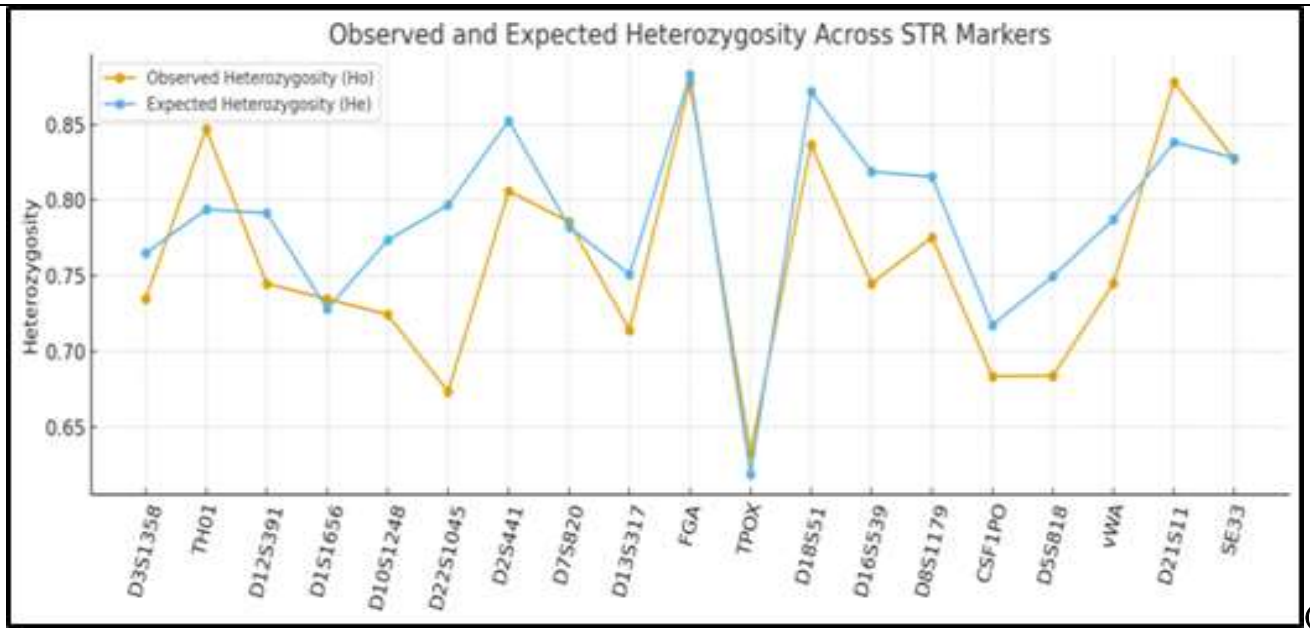
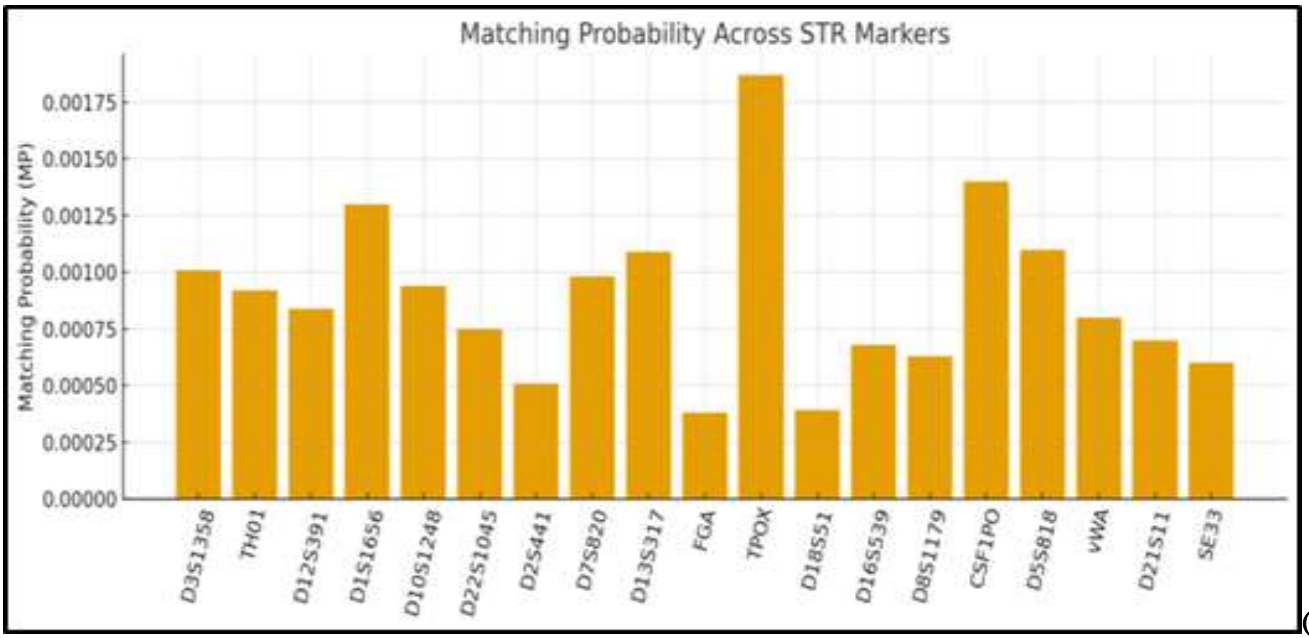
CSF1PO
D5S818
VWA
D21S11
SE33
STR Locus

(b)


Observed and Expected Heterozygosity Across STR Markers
Observed Heterozygosity (Ho)
Expected Heterozygosity (He)
Heterozygosity
0.85
0.80
0.75
0.70
0.65
D3S1358
TH01
D12S391
D1S1656
D10S1248
D22S1045
D2S441
D7S820
D13S317
FGA
TPOX
D18S51
D16S539
D8S1179
CSF1PO
D5S818
VWA
D21S11
SE33

(c)


Matching Probability Across STR Markers
Matching Probability (MP)
0.00175
0.00150
0.00125
0.00100
0.00075
0.00050
0.00025
0.00000
D3S1358
TH01
D12S391
D1S1656
D10S1248
D22S1045
D2S441
D7S820
D13S317
FGA
TPOX
D18S51
D16S539
D8S1179
CSF1PO
D5S818
VWA
D21S11
SE33

(d)

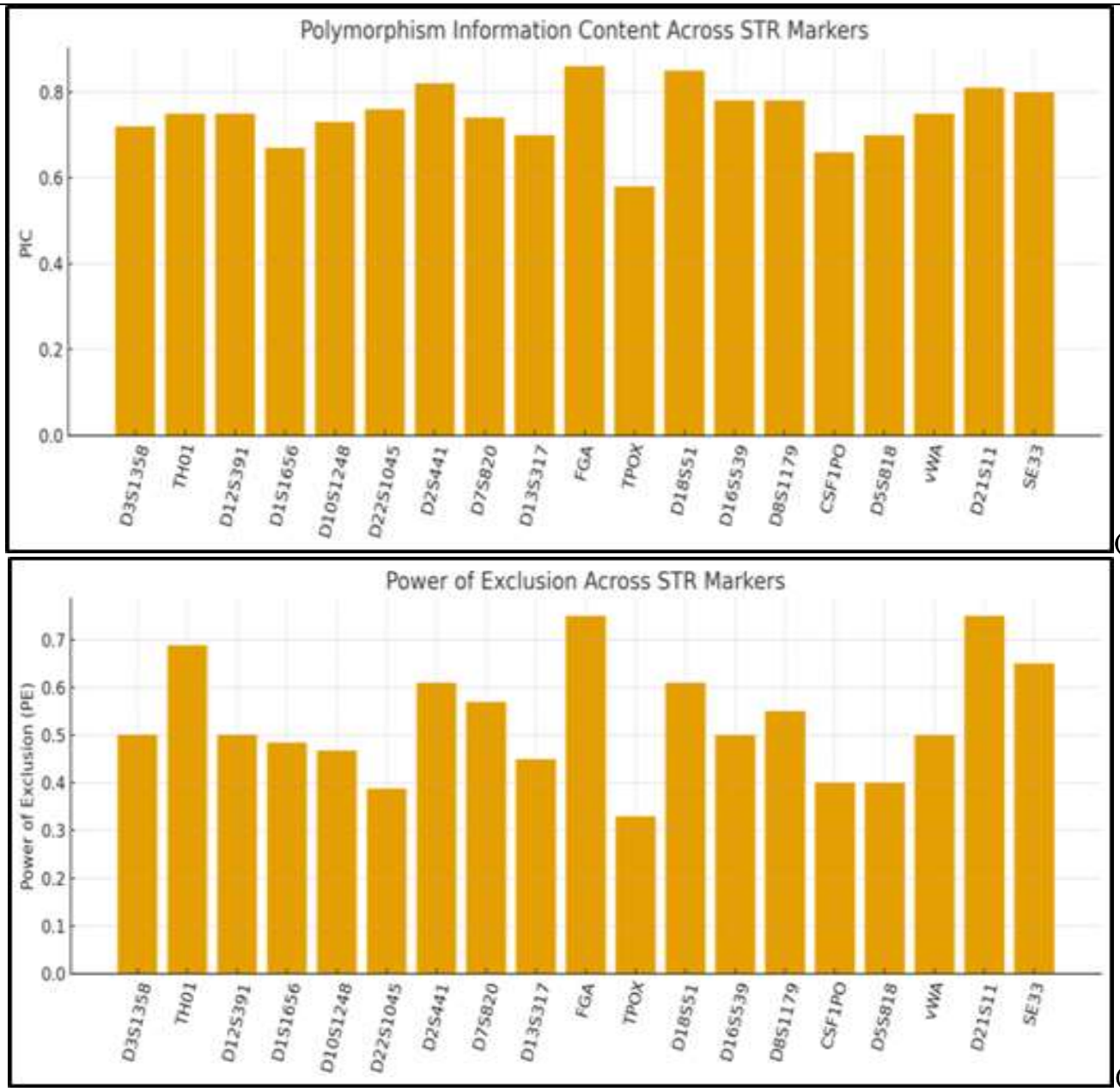



Figure 2: (a): Power of Discrimination (PD) (b):Paternity Index (PI), (c):Observed vs Expected Heterozygosity (Ho & He), (d):Matching Probability (MP), (e):Polymorphism Information Content (PIC), (f):Power of Exclusion (PE) for 19 Autosomal STR Loci.

Table 4: Comparison of key forensic parameters for selected STR loci between Arabs residing in Voronezh, Russia and other Arab

| STR Locus | Population | Ho (%) | PD | PIC | PI | Reference |
|---|---|---|---|---|---|---|
| FGA | Voronezh, Russia | 87.76 | 0.962 | 0.860 | 4.08 | Present study |
| | Tunisia | 89.1 | 0.961 | 0.853 | 4.02 | [19] |
| | Jordan | 89.9 | - | - | - | [16] |
| | Egypt | 86.7 | - | - | - | [17] |
| | Saudi Arabia | 88.2 | 0.958 | 0.851 | 3.95 | [13] |
| | European Arabs* | 88.3±0.4 | 0.961±0.002 | 0.855±0.003 | 4.12±0.07 | [10,11,12] |
| TPOX | Voronezh, Russia | 63.27 | 0.813 | 0.580 | 1.36 | Present study |
| | Tunisia | 65.2 | 0.821 | 0.592 | 1.42 | [19] |
| | Jordan | 67.5 | - | - | - | [16] |
| | Egypt | 60.3 | - | - | - | [17] |
| | Saudi Arabia | 62.8 | 0.815 | 0.585 | 1.38 | [13] |
| | European Arabs* | 65.3±1.2 | 0.821±0.004 | 0.592±0.008 | 1.44±0.04 | [10,11,12 |
| D21S11 | Voronezh, Russia | 87.8 | 0.940 | 0.810 | 4.08 | Present study |
| | Tunisia | 88.5 | 0.942 | 0.815 | 4.12 | [19] |
| | Jordan | 89.2 | - | - | - | [16] |
| | Egypt | 86.9 | - | - | - | [17] |
| | Saudi Arabia | 87.6 | 0.941 | 0.812 | 4.05 | [13] |
| | European Arabs* | 88.4±0.9 | 0.943±0.003 | 0.816±0.005 | 4.12±0.08 | [10,11,12] |

*European Arabs: Data from Arab groups in France, Spain, and the UK were combined. HO stands for observed heterozygosity, PD is for power of discrimination, and PIC stands for polymorphism information content. PI: Paternity Index.

Statistical Analysis Summary: The ANOVA results showed that there were no significant differences between Voronezh Arabs and other Arab groups for any of the loci that were looked at ($p > 0.05$ for all comparisons). FST scores ranged from 0.0012 to 0.0045, which means that there wasn't much genetic variation between the groups. All populations clustered together with little branching, which revealed that all Arab tribes share the same genetic makeup, no matter where they live. Previous studies in Arab populations residing in France, Spain and the UK revealed high allelic diversity, with number of alleles per locus generally ranging between 7 and 35. High diversity observed at FGA and D21S11 loci, furthermore, TPOX locus in previous European studied showed high frequency of specific alleles, often around allele 8 and this locus consistently showed lower heterozygosity in both previous and present studies, suggesting it is less polymorphic in Arab populations. Also, PI values in European Arabs show similar trends, with FGA and D21S11 consistently having the highest PI values, often above 4.0, making them particularly valuable in paternity cases. Lower PI values are also observed at loci like D12S391, consistent with the Voronezh study. [16,17,18]. In similar manner, A study conducted on an Arab population in Saudi Arabia reported a comparable range, with the number of alleles per locus ranging from 5 (TPOX) to 28 (FGA). A study from Kuwait also found out the number of alleles per locus ranged from 5 to 33. Thus, these studies show a similar trend of high allelic diversity in different Arab populations with high diversity in FGA and related markers [19,20,21]. Findings obtained in the current study are close to those obtained from research conducted

in Arab regions as per observed heterozygosity. In 2017, Zayed et al. conducted a study in Jordan, where they found that FGA also had high heterozygosity (89.9%), whereas TPOX had lower heterozygosity (67.5%). In a study on Egyptian people the FGA locus had observed heterozygosity of 86.7%, while TPOX had lower 60.3% [22-24]. The data presented above indicates the FGA locus is highly polymorphic as it displays a high degree of heterozygosity in Arab population from the ArabWorld and Outside Arabian Peninsula. The values of Power of Discrimination (PD), Polymorphism Information Content (PIC) and Paternity Index (PI), for FGA locus are similar to that reported in; Arab Countries; A research was done in Tunisia which revealed that PD, PIC and PI for FGA locus was (0.961, 0.853 and 4.02 respectively) [25,26,27]. TPOX locus shows lower values but it shows less polymorphic across several Arab populations as shown by its lower PIC and PI values. Also, in the case of the Voronezh study, random matching probability values ranged between 0.038 and 0.187 with the lowest probability of FGA locus at 0.038 indicating discriminatory power. The AE locus has the least direct match probability and LE is the most informative locus as the most likely LR comes from a scenario with fetal-maternal combination [28-30].

### 3.2. Forensic Applications

The genetic diversity criteria derived from this study has considerable ramifications for forensic applications. Loci like FGA and D21S11 have a lot of discriminating power, which makes them particularly valuable for identifying people in forensic situations involving Arab communities. These data could be incorporated into national forensic databases to improve the accuracy of statistical studies in paternity testing and criminal investigations. The genetic profile of Arabs residing in Russia is crucial in comprehending DNA evidence in instances involving individuals from diverse tribes or nations.

### 3.3. Limitations

There are a few things that this study should know are wrong with it. We can't properly judge how representative our findings are among different Arab subpopulations because we don't have enough comprehensive demographic data for our sample group. In the future, studies should try to include more detailed demographic data to better understand genetic architecture in Arab communities and make forensic genetic databases more useful.

## 4. Conclusion

In conclusion, the study successfully evaluated the forensic efficiency requirements of 20 autosomal STR markers within the Arab population in Voronezh, Russia. The results show that there is a lot of variation in alleles, especially at the FGA and D21S11 loci. This shows that these markers are reliable for forensic use in this group. The low FST values indicate a substantial genetic linkage between this Arab group and other global populations. These results provide substantial data for integration into national and international forensic databases, enhancing the accuracy of identification verification and paternity assessment for Arab individuals in Russia and neighboring regions.

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## References

[1] Shehab, M. J.; Namaa, D. H. S.; AL-Zubaidi, M. M.; "Assessment of Short tandem Repeat profiling that obtained from Some Biological Sources as Forensic Tool." Int. J. Med. Toxicol. Leg. Med. 25(4): 90-96, 2022.

[2] Jaber, M. M.; Al-Zubaidi, M. M.; Sabbah, M. A.; Mhawesh, A. A.; "STR Genotyping of Arabs Residence in Russia." Russ. J. Genet. 61(2): 238-243, 2025.

[3] Butler, J.; "Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers." 2nd Edn., Elsevier, Burlington, (660), 2005.

[4] Butler, J. M.; "Genetics and genomics of core STR loci used in human identity testing." J. Forensic Sci. 51: 253-265, 2006.

[5] Weir, B. S.; "The rarity of dna profiles." Ann. Appl. Stat. 1(2): 358–370, 2007.

[6] AL-Eitan, L. N.; Darwish, N. N.; Hakooz, N. M.; Dajani, R. B.; "Assessing the forensic efficiency of the GlobalFiler STR loci among the genetically isolated Chechen subpopulation in Jordan." Gene. 720: 144078, 2019.

[7] Zeye, M. M. J.; Ouedraogo, S. Y.; Bado, P.; Zoure, A. A.; Djigma, F. W.; Wu, X.; Simpore, J.;

"Forensic autosomal and gonosomal short tandem repeat marker reference database for populations in Burkina Faso." Sci. Rep. 14(1): 7369, 2024.

[8] Foroughmand, A. M.; Sanati, M. H.; Noor-Davarani, M. R.; Haerian-Ardakani, M. R.; Foroughmand, A. R.; "Genetic Analysis of Two STR Loci (VWA and TPOX) in the Iranian Province of Khuzestan." Iran. J. Basic Med. Sci. 17(8): 583, 2014.

[9] El-Sibai, M.; Platt, D. E.; Haber, M.; Xue, Y.; Youhanna, S. C.; Wells, R. S.; Izaabel, H.; et al.; "Genetic structure of the Levant reveals an ancient fertility cult." BMC Genet. 10(1): 15-22, 2009.

[10] Martínez-Cadenas, C.; Zhou, N; Wang, M; Zhao, X; Mijiti, A; Dang, W; Gailike, B; et al.; "Genetic diversity and structure in the Arabian Peninsula and surrounding regions." PLoS ONE. 5(10): e13454, 2010.

[11] Jobling, M. A.; Hellani, A.; González, A. M.; Larruga, J. M.; "Arab Y-chromosome diversity and its relationship with STR markers: A study in the UK." Forensic Sci. Int. Genet. 6(4): e105-e112, 2012.

[12] Alenizi, M.; Salih, A.; Alenizi, H.; Al Jabber, J.; Ziab, J.; Al Harbi, E.; Isameal, S.; et al.; "Genetic analysis of 15 autosomal STR loci in the Saudi Arabian population." Forensic Sci. Int. Genet. 35: 75-80, 2018.

[13] Wu, X.; Zheng, J. L.; Lou, Y.; Wei, X. H.; Wang, B. J.; Yao, J.; "Genetic polymorphisms of 20 autosomal STR loci in the Han population of Zhangzhou City, Southeastern China." Leg. Med. 46(2): 101-126, 2020.

[14] Al-dabbagh, S.Y.A.; Rasheed, B.Y.; Al-Jumaa, Z.M. Molecular Diagnosis of *Mycoplasma gallisepticum* in Turkey in Mosul City. Vet. Pract. 22: 1-3, 2021.

[15] Al-Jumaa, Z.; AL-Taee, S.; Jaber, M.; Rahhawi, A.; "Histopathological Alteration and Molecular Detection of Gills Rot Fungus in Carp Fish." J. Appl. Vet. Sci. 9(4): 54-59, 2024.

[16] Excoffier, L.; Lischer, H. E.; "Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows." Mol. Ecol. Resour. 10(3): 564-567, 2010.

[17] Novokmet, N.; Marjanović, D.; Skaro, V.; Projić, P.; Lauc, G.; Grahovac, B.; Mohar, B.; et al.; "Forensic efficiency parameters for the 15 STR loci in the population of the island of Cres (Croatia) " Coll. antrop. 33(4): 1319–1322, 2009.

[18] Ossmani, H. E.; Talbi, J.; Bouchrif, B.; Chafik, A.; "Allele frequencies of 15 autosomal STR loci in the southern Morocco population with phylogenetic structure among worldwide populations" Leg. Med. (Tokyo, Japan), 11(3): 155–158, 2009.

[19] Jones, R. J.; Tayyare, W. A.; Tay, G. K.; Alsafar, H.; Goodwin, W. H.; "Population data for 21 autosomal short tandem repeat markers in the Arabic population of the United Arab Emirates." Forensic Sci. Int. Gene. 28: e41–e42, 2017.

[20] Wang, H.d.; Shen, C.; Liu, W.; Chun, S.; Wen, L.; Yu, Z.; Guard, Y.; Jiang, Y.; Hai, Q.; et al; "Allelic frequency distributions of 21 non-combined DNA index system STR loci in a Russian ethnic minority group from Inner Mongolia, China" J. Zhej. Univ. Sci., 14: 533–540, 2013.

[21] Helmy, M.; Alessia, V.D.; Rafael, B.; "Forensic efficiency parameters of 15 autosomal STR loci in an Egyptian population sample." J. Forensic Sci. 61(1): 222-227, 2016.

[22] Flores, S.; Sun, J.; King, J.; Eisenberg, A.; Budowle, B.; "Allele frequencies for 15 autosomal STR loci and haplotype data for 17 Y-STR loci in a population from Belize." Int. J. Leg. Med. 129(6): 1217–1218, 2015.

[23] El Andari, A.; Othman, H.; Taroni, F.; Mansour, I.; "Population genetic data for 23 STR markers from Lebanon." Forensic Sci. Int. Genet. 7(4): e108–e113, 2013.

[24] Al-Snan, N. R.; Messaoudi, S.; R Babu, S.; Bakhiet, M.; "Population genetic data of the 21 autosomal STRs included in GlobalFiler kit of a population sample from the Kingdom of Bahrain." PLoS One. 14(8): e0220620, 2019.

[25] Hongdan, W.; Bing, K.; Ning, S.; Miao, H.; Bo, Z.; Yuxin, G.; Bofeng, Z.; et al.; "Evaluation of the genetic parameters and mutation analysis of 22 STR loci in the central Chinese Han population." Int. J. Leg. Med. 131(1): 103–105, 2017.

[26] Mahmood, H. K.; Salman, N. F.; Salih, K. M.; Mahdi, F.; "Frequency of Y-chromosome STRs using PowerPlex® Y23 System in Iraqi population." Egypt. J. Forensic Sci. 10(11), 2020.

[27] Chaudhari, R. R.; Dahiya, M. S.; "Genetic diversity of 15 autosomal short tandem repeats loci using the AmpFLSTR(®) Identifiler™ kit in a Bhil Tribe Population from Gujarat state,

India." Indian J. Hum. Genet. 20(2): 148–152, 2014.
[28] Zou, X.; Li, Y.; Li, Q.; Nie, T.; Wang, Y.; Hu, Y.; Zhu, J.; et al.; "Genetic polymorphisms for 19 autosomal STR loci of Chongqing Han ethnicity and phylogenetic structure exploration among 28 Chinese populations." Int. J. Leg. Med. 131: 1539–1542, 2017.
[29] Xu, X.; Feng, Z.; Yao, J.; "Population data of 15 autosomal STR loci in Chinese Han population from Jilin Province, Northeast China." Forensic Sci. Int. Genet. 27: 187–188, 2017.
[30] Ozeki, M.; Tamaki, K.; "Allele frequencies of 37 short tandem repeat loci in a Japanese population." Leg. Med. 15(6): 342–346, 2013.