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Analysis of Short Tandem Repeats (STRs) in a Sample of Arab Minority in Russia

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Abstract

Autosomal short tandem repeats (STR) were examined in a sample of 196 unrelated individuals from the Arab minority residing in Voronezh, Russia. Whole blood samples were used to extract genomic DNA, and PCR amplifications were performed using COrDIS Plus with 19 autosomal STR loci. The allele frequencies of STR loci including D3S1358, TH01, D12S391, D1S1656, D10S1248, 22S1045, D2S441, D7S820, D13S317, FGA, TPOX, D18S51, D16S539, D8S1179, CSF1PO, D5S818, vWA, D21S11 and SE33 were calculated. Additionally, efficiency parameters for forensic purposes were determined, including matching probability (MP), power of discrimination (PD), polymorphism information content (PIC), power of exclusion (PE), typical paternity index (TPI), and expected paternity index. All loci showed high PD of ≥ 0.85 except for locus D3S1358. The PIC was found to be highest for the loci D18S51 and SE33 and lowest for D3S1358. The PE varied between 0.33 for TPOX and 0.80 for SE33. The combined matching probability (CMP) was estimated to be 7.32*10-22, and the combined discrimination power (CDP) was 0.999999. The combined exclusion probability (CEP) value for the 19 loci used in this study collectively was greater than 0.995884594. It was concluded that the COrDIS Plus loci can be used to establish a population database for the Arab minority in Russia, which can be utilized in forensic and paternity investigations.

Keywords: Short tandem repeat; Iraqi population; Allele frequencies statistical parameters.

تحليل التكرارات الترادفية القصيرة (STRs) في عينة من الأقلية العربية في روسيا

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الخلاصة

تم فحص التكرارات الجسدية الترادفية القصيرة (STR) في عينة من 196 فردًا من الأقلية العربية المقيمة في فورونيج في روسيا من غير المرتبطين وراثيا. تم استخدام عينات الدم لاستخلاص الحمض النووي وتم إجراء تفاعل تضاعف الحمض النووي المتسلسل باستخدام COrDIS Plus المتكون من 19 موضعًا من التكرارات الجسدية الترادفية القصيرة وحساب ترددات الأليلات لهذه المواضع والتي شملت كل من D3S1358 و TH01 و D12S391 و D1S1656 و D10S1248 و S104522 و D2S441 و D7S820 و D13S317 و FGA و TPOX و D18S51 و D16S539 و D8S1179 و CSF1PO و D5S818 و vWA و D21S11 و SE33. بالإضافة إلى ذلك، تم تحديد معلمات الكفاءة لأغراض الطب الشرعي، بما في ذلك احتمال المطابقة (MP)، وقوة التمييز (PD)، ومحتوى معلومات تعدد الأشكال (PIC)، وقوة الاستبعاد (PE)، ومؤشر الأبوة النموذجي (TPI) ومؤشر الأبوة المتوقع. أظهرت جميع المواضع PD عالية ≤ 0.85 باستثناء الموضع D3S1358. ووجد أن PIC كان الأعلى للمواضع D18S51 و SE33 والأدنى بالنسبة لـ D3S1358. تراوحت PE بين 0.33 لـ TPOX و 0.80 لـ SE33. كما تم تقدير احتمال المطابقة المجمع (CMP) عند 7.32 * 10−22 وكانت قوة التمييز المجمعة 0.999999 (CDP). كانت قيمة احتمال الاستبعاد المجمع (CEP) للمواضع الـ 19 المستخدمة في هذه الدراسة مجتمعة أكبر من 0.995884594. تم استنتاج ان من الممكن استخدام مؤشرات COrDIS Plus لإنشاء قاعدة بيانات سكانية للأقلية العربية في روسيا لاستخدامها في التحقيقات الشرعية وتحقيقات الأبوة.

1. Introduction

Voronezh is an industrial city in south east Russia, 550Km from Moscow. It is situated at the intersection of important transportation routes. According to the population census carried out at the end of 2021 by the Russian Federal State Statistics, the Arab population is estimated to be 16,329 people, representing a rather steady growth rate of 0.01% of the Russian population. Arab countries are not stated in this census [1], [2].

The majority of the eukaryotic genome is composed of repeated DNA sequences of different sizes and types, including long repeats, medium repeats, and short sequences referred to as satellites, minisatellites, and microsatellites, respectively [3-5]. Minisatellites are also identified as short tandem repeats (STRs), in which DNA repeat units are 2-6bp in length, they are repeated multiple times in tandem. The number of these repeated units at each STR locus varies significantly between individuals, making them highly polymorphic. Consequently, STR repeats provide an effective tool for purposes of human identification [5,6].

DNA profiling using STRs involves several key steps. First, DNA is extracted from biological samples, and specific STR loci are amplified using PCR; the small size of STR repeat units ensures that both alleles from a heterozygous individual are similar in size, facilitating straightforward amplification. Amplified PCR products are then analyzed by capillary electrophoresis for the detection and analysis of allele peaks. Determination of the genotype for each STR locus usually follows, and a unique combination of alleles across multiple STR loci forms a distinct genetic profile for each individual [5].

Autosomal STRs are found on non-sex chromosomes and are inherited from both parents, thus, the pattern of their inheritance follows the Mendelian principles. Their unique patterns create distinct DNA profiles with extremely low probabilities of random match. Thus, autosomal STR analysis remains a crucial technique for forensic application [7]

The STR markers can be lineage markers found on the Y chromosome and on mitochondrial DNA. These are passed paternally and maternally through generations without recombination (except when mutations occur). Lineage markers play a role in forensic cases where samples are degraded, such as in sexual assaults and identification of remains [5,8].
STR markers found on the X chromosome were also found to be useful in forensics and population genetic studies due to their specific structure and characteristics. Information gained from analysis of Y and X chromosomes, and mitochondrial DNA can be combined in forensic cases when DNA mixes are present [9].

Generally, the number of STR repeats varies significantly between individuals, thus decisive in forensic identification [5,6]. The COrDIS Plus short tandem repeat (STR) was used in this study, it incorporates the 13 CODIS loci (D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, CSF1PO, FGA, TH01, TPOX, and VWA) in addition to 5 other recommended by European national databases (D1S1656, D2S441, D10S11248, D12S391, and D22S1405) and the most powerful discriminatory STR locus, the SE33 [10].
In this study, our aim was to identify the most autosomal hypervariable STR loci in the Arab minority living in Voronezh, Russia, using the COrDIS Plus STR kit, and to assess the usage of these STR markers in forensic DNA typing. To the best of our knowledge, this is one of the rare studies conducted in an Arab minority in Russia. The highly hypervariable STR markers used in this study can be further implemented for forensic investigations, such as population studies, paternity testing, and identity testing, and ultimately in constructing a future reference database and ethnic group identification in other Arab minorities in Russia and different parts of the world.

2. Materials and Methods

Blood sample collection

Blood samples were collected from 196 unrelated, healthy Arab individuals residing in the city of Voronezh, Russia, for DNA extraction.

DNA extraction

For extracting DNA, the COrDIS Reagent kit (COrDIS, Russia) was used according to the manufacturer's instructions. Nanodrop was used to measure DNA quantity and purity (Thomson, Wilmington, DE) [11,12].

PCR amplification

A multiplex assay of 19 STR from the COrDIS Plus with amelogenin for gender determination was utilized, including the CODIS loci [13] and loci recommended by the European national databases [14] (D3S1358, D5S818, D7S820, 8S1179, D13S317, D16S539, D18S51, D21S11, CSF1PO, FGA, TH01, TPOX, and VWA, D1S1656, D2S441, D10S11248, D12S391, and D22S1405). The COrDIS Plus also included the locus SE33 (Table 1). PCR primers are designed to amplify fragments of less than 440 bp. PCR amplicons are less than 440bp in one amplification reaction and are labelled with green, blue, yellow, red, and orange dye, with the latter as a labelled sizing standard. A total of 1ng DNA template from each individual was used for amplification.

Table 1: COrDIS Plus loci information Amplification reactions were performed using a PCR machine (Veriti® PCR System from Applied Biosystems).

Locus	Gene Bank		Chromosome Localization
	Accession number	Allele	
D3S1358	NT_005997	18	3p21.31
TH01	D00269	9	11p15.5
D12S391	G08921	19.3	12p13.2
D1S1656	NC_000001.9	17	1q42
D10S1248	AL391869	13	10q26.3
D22S1045	AL022314	17	22q12.3
D2S441	AL079112	12	2p14
D7S820	AC004848	13	7q21.11
D13S317	AL353628	11	13q31.1
FGA	M64982	21	4q31.3
TPOX	M68651	11	2p25.3
D18S51	AP001534	18	18q21.33
D16S539	AC024591	11	16q24.1
D8S1179	AF216671	13	8q24.13
CSF1PO	X14720	12	5q33.1
D5S818	AC008512	11	5q23.2
VWA	M25858	18	12p13.31
D21S11	AP000433	29	21q21.1
SE33	V00481	26.2	6q14
Amelogenin X	M55418	X	Xp22.1-22.3
Amelogenin Y	M55419	Y	Yp11.2

Diluted amplicons (1:15) were analysed by electrophoresis using a 16-capillary ABI Prism® 3100 Genetic Analyzer.

Data collection

Gene Mapper v. 3.2 software (Applied Biosystems) was used to analyse data. Statistical analysis was performed, and allele frequencies, power of discrimination (PD), power of exclusion (PE), polymorphism information content (PIC), match probability (MP), and typical paternity index (TPI) were calculated for each locus.

3. Results

The information collected from the analysis of 19 autosomal STR loci was collected, and statistical analyses were performed to resolve alleles suitable for forensic and paternity analysis and investigations. It was found that 172 alleles had a frequency range of 0.003 - 0.5. The observed allele frequencies for the 19 STR loci in the Arab minority group in Russia are shown in Tables 2a and b.

Allele frequencies for each STR locus are presented in Table 2a and b, allele 15 of D3S1358 and 8 of TPOX showed the highest frequencies of 0.5, while, the lowest frequency of 0.003 was shown by the following alleles, D3S1358: 19,20, TH01:5, D2S441:26, 30.2, D7S820:14, TPOX: 7, D18S51: 21, 22, D8S1179: 9, 17, D5S818:8, D21S11: 27, 29.2 and SE33: 8, 24. Furthermore, the highest number of low-frequency alleles (19.2, 21.2, 22.2, 23.2, 29) was exhibited by this locus.

The highest allelic diversity was shown in loci: FGA, D21S11, and SE33 with 16 allelic variations, D2S441 and D18S51 with 14 and 13 allelic variations, respectively. Loci, D3S1358, TH01, D10S1248, D22S1045, TPOX, and CSF1PO exhibited the lowest allelic diversity with 6-7 alleles (Table 3). The highest observed heterozygosity (Ho) was shown by

loci D3S1358, FGA, and vWA of 89.29%, 87.76% and 84.2% respectively, while the Ho was shown by the TPOX locus of 63.27% (Table 4).

Forensic efficiency parameters, such as matching probability (MP), power of discrimination (PD), polymorphism information content (PIC), power of exclusion (PE), typical paternity index (TPI), and expected paternity index, were determined (Table 5). All loci showed high PD of ≥ 0.85 except locus D3S1358, which showed the lowest PD of 0.72. The PIC was found to be highest for the loci D18S51 and SE33 of 0.86 and lowest for D3S1358 of 0.59, and the PE varied between 0.33 for TPOX and 0.80 for SE33.

The combined matching probability (CMP) was estimated to be $7.32*10^{-22,}$ and the combined discrimination power (CDP) was 0.999999. The combined exclusion probability (CEP) value for the 19 loci used in this study, collectively, is greater than 0.995884594 (Table 6).

Table 2a. Allele Frequencies of ten autosomal STR Loci (D3S1358, TH01, D12S391, D1S1656, D10S1248, D22S1045, D2S441, D7S820, D13S317, FGA) in Arab minority in Russia.

Allele Repeat Units	Allele Frequency									
	D3S1358	TH01	D12S391	D1S1656	D10S1248	D22S1045	D2S441	D7S820	D13S317	FGA
5		0.003								
6		0.293				0.242				
7		0.186	0.023	0.010		0.202		0.015		
8		0.122	0.158	0.013		0.168		0.166	0.176	
9		0.237	0.133	0.018		0.260		0.107	0.089	
9.3		0.140				0.110				
10		0.018	0.247	0.253		0.018		0.286	0.056	
11			0.237	0.344				0.276	0.263	
12			0.186	0.288				0.133	0.332	
13			0.015	0.064				0.013	0.054	
14				0.010	0.077			0.005	0.032	
15	0.546				0.217					
16	0.143				0.250					
17	0.189				0.304					
18	0.117				0.140					0.0128
19	0.003				0.013					0.066
19.2										0.003
20	0.003									0.102
21										0.161
21.2										0.003
22										0.145
22.2										0.003
23										0.163
23.2										0.005
24										0.176
24.2										0.008
25										0.099
26							0.003			0.041
27							0.018			
28							0.102			0.010
29							0.222			0.003
29.2										
30							0.247			
30.2							0.003			
31							0.054			
31.2							0.143			

Table 2b. Allele frequencies of nine autosomal STR loci (TPOX, D18S51, D16S539, D8S1179, CSF1PO, D5S818, vWA, D21S11, and SE33) in the Arab minority in Russia.

Allele Repeat Units	Allele Frequency								
	TPOX	D18S51	D16S539	D8S1179	CSF1PO	D5S818	vWA	D21S11	SE33
5	0.003				0.013				
6						0.204	0.003	0.023	
7	0.003								
8	0.523		0.033	0.008		0.013			0.003
9	0.151		0.204	0.003	0.023	0.041			0.005
9.3					0.296				
10	0.094	0.018	0.110	0.071	0.276	0.115			0.038
11	0.179	0.015	0.276	0.064	0.265	0.311			0.046
12	0.051	0.133	0.217	0.099	0.380	0.293			0.069
13		0.176	0.138	0.319	0.046	0.212			0.194
14		0.191	0.023	0.173	0.010	0.015	0.069		0.125
15		0.115		0.202			0.092		0.212
16		0.107		0.059			0.253		0.082
17		0.097		0.003			0.296		0.089
18		0.087					0.204		0.031
19		0.041					0.077		0.046
19.2							0.015	0.179	
20		0.010					0.010		0.023
21		0.005							
21.2				0.138	0.319				
22		0.006							0.010
22.2									0.296
23									0.026
23.2						0.107			
24									0.003
24.2				0.005					
25								0.296	
26								0.008	
27								0.005	
28								0.156	
29								0.222	
29.2								0.005	
30								0.230	
30.2								0.028	
31								0.043	
31.2								0.089	

Table 3: Allelic Diversity of the forensic 19 autosomal STR loci in the Arab minority in Russia.

STR Locus	Total number of alleles observed	Types of alleles	Common allele/s	Rare allele/s
D3S1358**	6	15, 16, 17, 18, 19, 20	15	19,20
TH01**	6	5, 6, 7, 8, 9,9.3	6	5
D12S391	7	7, 8, 9, 10, 11, 12, 13	10	13
D1S1656	8	7, 8, 9, 10, 11, 12, 13, 14	11	7,14
D10S1248**	6	14, 15, 16, 17, 18, 19	17	19
D22S1045**	6	6, 7, 8, 9, 9.3, 10	9	10
D2S441*	14	26, 27, 28, 29, 30, 30.2, 31, 31.2, 32, 32.2, 33, 33.2, 34.2, 36	30	26, 30.2
D7S820	8	7, 8, 9, 10, 11, 12, 13, 14	10,11	14
D13S317	7	8, 9, 10, 11, 12, 13, 14	12	14
FGA*	16	18, 19, 19.2, 20, 21, 21.2, 22, 22.2, 23, 23.2, 24, 24.2, 25, 26, 28, 29	24	19.2,21.2, 22.2, 23.2, 29
TPOX**	6	7, 8, 9, 10, 11, 12	8	7
D18S51*	13	10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22	14	21, 22
D16S539	7	8, 9, 10, 11, 12, 13, 14	11	14
D8S1179	10	8, 9, 10, 11, 12, 13, 14, 15, 16, 17	13	9,17
CSF1PO**	6	9, 10, 11, 12, 13, 14	12	14
D5S818	7	8, 9, 10, 11, 12, 13, 14	11	8
vWA	7	14, 15, 16, 17, 18, 19, 20	17	20
D21S11*	16	26, 27, 28, 29, 29.2, 30, 30.2, 31, 31.2, 32, 32.2, 33, 33.2, 34, 34.2, 35	30	27,29.2
SE33*	16	8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24	15	8,24

Table 4. Numbers and percentages of high- and low-frequency alleles in the Arab minority in Russia (n = 196).

STR Locus	High frequency allele/s	No, of observations	Frequency	Low frequency allele/s	No, of observations	Frequency
D3S1358	15	214	0.546	19,20	1	0.003
TH01	6	115	0.293	5	1	0.003
D12S391	10	97	0.247	13	6	0.015
D1S1656	11	135	0.344	7,14	4	0.010
D10S1248	17	119	0.304	19	5	0.013
D22S1045	9	102	0.260	10	7	0.018
D2S441	30	97	0.247	26, 34.2, 36	1	0.003
D7S820	10,11	112,108	0.286, 0.276	14	2	0.005
D13S317	12	130	0.332	14	12	0.031
FGA	24	69	0.176	19.2,21.2, 22.2, 23.2, 29	1	0.003
TPOX	8	205	0.523	7	1	0.003
D18S51	14	75	0.191	21, 22	2	0.005
D16S539	11	108	0.276	14	9	0.023
D8S1179	13	125	0.319	9,17	1	0.003
CSF1PO	12	149	0.380	14	4	0.010
D5S818	11	122	0.311	8	5	0.013
vWA	17	116	0.296	20	4	0.010
D21S11	30	90	0.231	32, 33, 34, 34.2,35	1	0.003
SE33	15	83	0.212	8,24	1	0.003

Table 5: Observed and expected homozygosity and heterozygosity of the 19 autosomal STR in the Arab minority in Russia.

Locus	Matching Probability (MP)	Power of discrimination (PD)	Polymorphism Information Content (PIC)	Power of Exclusion (PE)	Typical Paternity Index (PI)	Paternity Index Expected
D3S1358	0.280	0.72	0.59	0.78	4.67	1.35
TH01	0.084	0.92	0.76	0.63	2.72	2.35
D12S391	0.068	0.93	0.78	0.44	1.69	2.55
D1S1656	0.122	0.88	0.68	0.48	1.88	1.85
D10S1248	0.089	0.91	0.74	0.49	1.92	2.19
D22S1045	0.073	0.93	0.76	0.49	1.92	2.40
D2S441	0.057	0.94	0.81	0.61	2.58	2.96
D7S820	0.079	0.92	0.75	0.56	2.27	2.33
D13S317	0.084	0.92	0.74	0.54	2.13	2.22
FGA	0.037	0.96	0.85	0.75	4.08	3.80
TPOX	0.155	0.85	0.62	0.33	1.36	1.47
D18S51	0.033	0.97	0.86	0.72	3.63	3.87
D16S539	0.068	0.93	0.77	0.50	1.96	2.53
D8S1179	0.062	0.94	0.78	0.54	2.13	2.56
CSF1PO	0.151	0.85	0.65	0.43	1.66	1.70
D5S818	0.100	0.90	0.72	0.49	1.92	2.05
vWA	0.080	0.92	0.76	0.52	2.04	2.35
D21S11	0.050	0.95	0.82	0.68	3.16	3.08
SE33	0.030	0.97	0.86	0.80	5.15	3.98
Combined Matching Probability (CMP)=			**7.321E-22**			
Combined Discrimination Power (CDP)=			**0.999999**			
Combined Exclusion Probability (CEP)=			**0.995884594**			

Table 6: Forensic efficiency parameters of 19 autosomal STR in the Arab minority in Russia.

Locus	Observed homozygosity %	Expected homozygosity %	Observed heterozygosity %	Expected heterozygosity %
D3S1358	10.71	36.62	89.29	63.38
TH01	18.37	21.00	81.63	79.00
D12S391	29.59	19.35	70.41	80.65
D1S1656	26.53	26.84	73.47	73.16
D10S1248	26.02	22.54	73.98	77.46
D22S1045	26.02	20.57	73.98	79.43
D2S441	19.39	16.64	80.61	83.36
D7S820	21.94	21.05	78.06	78.95
D13S317	23.47	22.10	76.53	77.90
FGA	12.24	12.69	87.76	87.31
TPOX	36.73	33.62	63.27	66.38
D18S51	13.78	12.47	86.22	87.53
D16S539	25.51	19.31	74.49	80.69
D8S1179	23.47	19.08	76.53	80.92
CSF1PO	30.10	28.99	69.90	71.01
D5S818	26.0	23.91	74.0	76.09
vWA	24.5	20.81	75.5	79.19
D21S11	15.8	15.79	84.2	84.21
SE33	9.7	12.09	90.3	87.91

4. Discussion:

One hundred ninety-six (n = 196) unrelated healthy individuals were selected for this study using COrDIS Plus with 19 STR markers. The data were collected, and the results were statistically analyzed for the applicability of these STR markers in forensic and paternity investigations among an Arab minority in Voronezh City, Russia. The allele frequency is the number of copies of an allele in a population divided by the total number of alleles in the same population [5,15]. The highest allele frequency of 0.5 was observed for alleles 15 and 8 at loci D3S1358 and TPOX, respectively (Table 2a, b). Locus TPOX is considered one of the least variable markers, showing variation in population studies [5]. Additionally, TPOX:8 was identified as one of the most prevalent alleles in Arab populations [16,17]. Similarly, in a previous study, allele 8 of TPOX exhibited the highest allele frequency in 456 unrelated individuals from Iraq living in Baghdad [18,19]. In this study, locus TOPX:8 showed one of the highest frequencies, thereby further validating the findings.

According to Butler, loci D21S11, D18S51, and FGA are some of the most polymorphic markers studied [5]. Data obtained in this study showed similar results, with some alleles from these loci exhibiting the lowest frequencies (Table 2a, b). This is also similar to data obtained from the mentioned loci with D18S51 and FGA showing the lowest frequency in 15 and 17 alleles, respectively, in 95 unrelated African-Jordanians [20,21].

Heterozygosity is a measure of genetic variability, i.e., diversity within and between populations. Expected heterozygosity can be evaluated from allele frequency, while observed heterozygosity can be estimated from individual genotypes; it depends on the genetic variability in the population and breeding level, which increases homozygosity [22,23]. In the studied Arab minority, all STR loci showed ≥ 70% heterozygosity except for locus TPOX, which showed 63.72%. The highest heterozygosity was shown by D3S1358 at 89.29%. These results, using the designated 19 STRs, reflect the high variation in the Arab population living in Russia used in this study.

The relative importance of each marker used in this study was determined through several measures, such as the PD, which is described as the probability of discrimination, i.e., it is defined as the probability that two individuals chosen at random will possess different genotypes for the tested marker. Since all of the analysed loci showed high PD (Table 5), they can be useful for identification purposes, with locus D3S1358 to a lesser degree, in the Arab minority living in Russia. On the other hand, the PE is strongly dependent on the level of heterozygosity, i.e., the power to exclude a non-related individual selected randomly in a specific population for paternity investigations. The marker SE33 exhibited the highest PE value of 0.80, while TPOX showed the lowest value of 0.33. An STR locus with PE > 0.50 is considered highly polymorphic [24-26]. Thus, most markers showed high polymorphism, including D3S1358, TH01, D2S441, D7S820, 13S317, FGA, D18S51, D16S539, D8S1179, vWA, D21S11, and SE33, while D12S391, D1S1656, D10S1248, D22S1045, CSF1PO, and D5S818 are considered moderately polymorphic. For this reason, these markers are useful in forensic cases and paternity testing. The PIC represents the probability that an offspring of a parent with a rare allele found on a specific locus will allow the deduction of the parental genotype at that locus [5]. Marker D18S51 and FGA exhibited the highest PIC values (Table 6). This finding is consistent with earlier research involving 1061 individuals from an Iraqi population [27,28]. Following this, a recent study conducted in 2025 by Jaber *et al.,* on 98 Arab individuals in Russia, using 23 STR markers, found that locus D18S51 similarly exhibited the highest power to distinguish between individuals. Correspondingly, SE33 showed a high PIC of 0.86% in the current study (Table 6), validating the PIC value of 0.87% reported in earlier studies [29,30].

The CMP and CDP values were 7.321E-22 and 0.999999, respectively, and the CEP for the 19 STR loci collectively considered is greater than 0.995884594. This is indicative of the adequacy of these STR markers for paternity and human identification analysis.
To the best of our knowledge, this is one of the very rare studies conducted on an Arab minority in Russia of this type. Our study investigated allelic frequencies and forensic efficiency statistical parameters for 19 autosomal STR loci in a population sample of the Arab minority in Russia. Findings from this study showed that most loci used in the COrDIS Plus were highly polymorphic; thus, these markers can be used for the construction of a forensic genetic database in the Arab minority population, a model that can be replicated for other Arab minorities in different parts of the world where genetic database information is lacking.

5. Conclusions

Data in this study demonstrated high genetic polymorphisms and discrimination power of STR markers used, suggesting that these loci can be efficiently used for forensic applications in other Arab minorities for purposes of forensic population diversity, paternity, and setting the stage for future establishment of reference population database construction of the Arab minority in Russia.

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Ethics approval

Ethical approval was obtained from the institutional Ethics Committee.

Consent for publication

All the authors have given written consent for the publication of this manuscript.

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Conflict of Interest

All authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] G. V. Golusov, "The Representation of Ethnic Muslims in Russia's Regional Legislative Assemblies," *Journal of Eurasian Studies*, vol. 3, no. 2, pp. 93-101, 2012.

[2] Federal State Statistics Service, "Национальный состав населения" *National Composition of the Population, vol. 5 of Results of the 2020 All-Russian Population Census*, Moscow: Federal State Statistics Service, 2022.

[3] S. B. Primrose, *Principles of Genome Analysis: A Guide to Mapping and Sequencing of DNA from Different Organisms*, 2nd ed. Malden, MA: Blackwell Science, 1998.

[4] M. Chambers and E. S. MacAvoy, "PCR and the Detection of Microbial Pathogens in Water," *Comparative Biochemistry and Physiology Part B: Biochemistry and Molecular Biology*, vol. 126, no. 4, pp. 455-476, 2000.

[5] J. M. Butler, *Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers*, 2nd ed. New York, NY: Elsevier Academic Press, 2005.

[6] J. M. Butler, *Advanced Topics in Forensic DNA Typing: Methodology*. New York, NY: Elsevier Academic Press, 2011.

[7] O. A. Mahmoud, M. A. Hameed, S. H. Muhi, F. B. Abd, S. M. Ibrahim, I. R. Hadi, D. A. Mohammed, and R. M. Attallah, "Advancements and Applications of STR Kits in Forensic DNA Profiling: A Comprehensive Review," *Baghdad Journal of Biochemistry and Applied Biological Sciences*, vol. 6, no. 1, pp. 1-17, 2025.

[8] J. Buckleton, M. Krawczak, and B. S. Weir, "The Interpretation of Lineage Markers in Forensic DNA Testing," *Forensic Science International: Genetics*, vol. 5, no. 2, pp. 78-83, 2011.

[9] I. Gomes, N. Pinto, S. Antão-Sousa, V. Gomes, L. Gusmão, and A. Amorim, "Twenty Years Later: A Comprehensive Review of the X Chromosome Use in Forensic Genetics," *Frontiers in Genetics*, vol. 11, pp. 926, 2020.

[10] X. Wu, J. L. Zheng, Y. Lou, X. H. Wei, B. J. Wang, and J. Yao, "Genetic polymorphisms of 20 autosomal STR loci in the Han population of Zhangzhou City, Southeastern China," *Legal Med. (Tokyo, Japan),* vol. 46, pp. 711-726, 2020.

[11] J. M. Abdullah, I. H. Hameed, and M. A. Kareem, "Detection of New Variant "Off-Ladder" at the D12S391, D19S433 and D1S1656 Loci and Tri-Allelic Pattern at the D16S539 Locus in a 21 Locus Autosomal Short Tandem Repeat Database of 400 Iraqi Individuals," *African Journal of Biotechnology*, vol. 14, no. 5, pp. 375-399, 2015.

[12] Z. M. Al-Jumaa, S. K. AL-Taee, M. T. Jaber, and A. M. Rahhawi, "Histopathological Alteration and Molecular Detection of Gills Rot Fungus in Carp Fish," *Journal of Applied Veterinary Sciences*, vol. 9, no. 4, pp. 54-59, 2024.

[13] R. R. Chaudhari and M. S. Dahiya, "Genetic Diversity of 15 Autosomal Short Tandem Repeats Loci Using the AmpFLSTR® Identifiler™ Kit in a Bhil Tribe Population from Gujarat State, India," *Indian Journal of Human Genetics*, vol. 20, no. 2, pp. 148, 2014.

[14] A. M. Foroughmand, M. H. Sanati, M. R. Noor-Davarani, M. R. Haerian-Ardakani, and A. R. Foroughmand, "Genetic Analysis of Two STR Loci (VWA and TPOX) in the Iranian Province of Khuzestan," *Iranian Journal of Basic Medical Sciences*, vol. 17, no. 8, pp. 583, 2014.

[15] B. Brinkmann, A. Carracedo, W. Bar, B. Budowle, A. J. Giusti, P. Gill, P. Lincoln, W. R. Mayr, B. Olaisen, and V. L. Pascali, "DNA Recommendations: Further Report of the DNA Commission of the ISFG Regarding the Use of Short Tandem Repeat System," *International Journal of Legal Medicine*, vol. 110, no. 3, pp. 175-176, 1997.

[16] M. A. Alenizi, W. Goodwin, S. Ismael, and S. Hadi, "STR Data for the AmpF STR Identifiler Loci in Kuwaiti Population," *Legal Medicine*, vol. 10, no. 6, pp. 321-325, 2008.

[17] Kh. Halah, A. S. Majeed, and M. Mohammed, "Allele Frequencies of 15 Autosomal STR Loci in Hilla City Population / Iraq," *Journal of Biotechnology Research Center*, vol. 40, no. 1, pp. 86-91, 2020.

[18] N. R. Al-Snan, S. Messaoudi, S. R Babu, and M. Bakhiet, "Population genetic data of the 21 autosomal STRs included in GlobalFiler kit of a population sample from the Kingdom of Bahrain," *PloS one*, vol. 14, no. 8, pp. 610-620, 2019.

[19] M. Ozeki and K. Tamaki, K. "Allele frequencies of 37 short tandem repeat loci in a Japanese population" *Legal medicine (Tokyo, Japan),* vol. 15, no. 6, pp. 342–346, 2013.

[20] Y. R. Salem, M. M. Hamad, A. Z. Elkarmi, and A. S. Jaran, "African Jordanian Population Genetics Database on Fifteen Short Tandem Repeat Genetic Loci," *Croatian Medical Journal*, vol. 46, no. 4, pp. 587-592, 2005.

[21] M. Whittle, N. L. Romano, and V. A. Negreiros, "Updated Brazilian genetic data, together with mutation rates, on 19 STR loci, including D10S1237" *Forensic science international*, vol. 139, no. 2, pp. 207–210, 2004.

[22] K. Ritland, "Estimators for pairwise relatedness and individual inbreeding coefficients," *Genetical Research*, vol. 67, no. 2, pp. 175-185, 1996.

[23] Y. Gao, Z. Zhang, Z. Wang, and S. Bian, "Genetic data of 15 STR forensic loci in eastern Chinese population" *Forensic science international*, vol. 154, no. 1, pp. 78–80, 2005.

[24] M. D. Shriver, L. Jin, E. Boerwinkle, R. Deka, R. E. Ferrell, and R. Chakraborty, "A Novel Measure of Genetic Distance for Highly Polymorphic Tandem Repeat Loci," *Molecular Biology and Evolution*, vol. 12, no. 5, pp. 914-920, 1995.

[25] M. M. T. Jaber, M. M. Al-Zubaidi, M. A. Sabbah, and A. A. Mhawesh, "STR Genotyping of Arabs Residence in Russia," *Russian Journal of Genetics*, vol. 61, no. 2, pp. 238-243, 2025.

[26] R. J. Jones, W. A. Tayyare, G. K. Tay, H. Alsafar, and W. H. Goodwin, "Population data for 21 autosomal short tandem repeat markers in the Arabic population of the United Arab Emirates," *Forensic Science International Genetic*, vol. 28, pp. 41–42, 2017.

[27] X. Xu, Z. Feng, and J. Yao, "Population data of 15 autosomal STR loci in Chinese Han population from Jilin Province, Northeast China" *Forensic science international. Genetics,* vol. 27, pp. 187–188, 2017.

[28] W. Hongdan, K. Bing, S. Ning, H. Miao, Z. Bo, G. Yuxin, Z. Bofeng, L. Shixiu, and Z. Zhaoshu, "Evaluation of the genetic parameters and mutation analysis of 22 STR loci in the central Chinese Han population" *International Journal of Legal Medicine*, vol. 131, pp. 103-105, 2017.

[29] X. Zou, Y. Li, P. Li, Q. Nie, T. Wang, Y. Hu, Y. Zhu, J. Li, and R. Tang "Genetic polymorphisms for 19 autosomal STR loci of Chongqing Han ethnicity and phylogenetic structure exploration among 28 Chinese populations," *International Journal of Legal Medicine*, vol. 131, pp. 1539–1542, 2017.

[30] M. M. J. Zeye, S. Y. Ouedraogo, P. Bado, A. A. Zoure, F. W. Djigma, X. Wu, and J. Simpore, "Forensic autosomal and gonosomal short tandem repeat marker reference database for populations in Burkina Faso," *Scientific reports,* vol. 14, no. 1, pp. 69-73, 2024.