Molecular screening of a group of male date palm varieties and confirmation of their genetic fingerprint

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Abstract:

The quality and type of pollen grains are of great importance for the production of date palm trees. Therefore, studying the genetic diversity at the molecular level among fifteen varieties of local male date palms growing in Mandali, Diyala, Iraq, is crucial. This study aimed to molecularly analyze and establish genetic fingerprints to standardize varieties and unify nomenclature. The study was conducted using ten ISSR primers and DNA sequencing technology. The results indicated that the ISSR primers yielded complementary sequences in the DNA of the studied date palm varieties, producing 80 bands, of which 55 were polymorphic. Most of the primers exhibited distinctive bands (either present or absent) for certain male varieties, which were identified as their genetic fingerprints. Notable variation was observed among the male varieties, which were clustered into different groups, reflecting differences in their genetic content Males within each group exhibited genetic similarity, suggesting a common origin. Based on these findings, four male varieties (2, 4, 6, and 11) were selected as representatives from different groups, and DNA sequencing was employed to determine their nucleotide sequences. The results revealed that these varieties are not registered in the NCBI database, and thus, they have been registered as the first entries from Iraq by the researchers.
Keywords: date palm males, genetic diversity, genetic fingerprinting, ISSR, DNA sequence

Introduction

Palm trees (*Phoenix dactylifera* L.) require specific practices due to their unique physiological structure, which distinguishes them from other trees. Female flowers are found on one tree and male flowers on another, necessitating the selection of high-quality pollen sources. This pollen can significantly influence certain fruit characteristics, such as shape, size, color, and ripening time, a phenomenon known as "Metaxenia."

One of the methods that contributes to increasing the quantity of dates produced in palm trees is the selection of male trees with high-quality pollen to complete the pollination process and increase the fruit set percentage. Among the most important characteristics of these male trees are the

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number of flower clusters, the quantity and viability of their pollen, and their compatibility with female trees in terms of the timing of their emergence and opening (12). Therefore, researchers have focused on studying the characteristics of some male varieties and selecting the best of them based on morphological characteristics. This is one of the easiest, least complicated, and oldest methods used, and it is still used to differentiate and demonstrate the genetic diversity of these varieties. This is what is called morphological indicators, which depend on the differences in the external appearance of the plant, such as the shape and arrangement of the leaves, the shape of the stem, the color of the flowers, the fruit peel, the texture, and the nature of vegetative growth (11) The use of phenotypic indicators for distinguishing date palm varieties has proven challenging for researchers, particularly in the absence of fruit, due to significant similarities influenced by environmental conditions and cultivation practices, especially among male varieties (8). Therefore, many methods have been developed to distinguish these varieties, including what is called molecular indicators, represented by molecular DNA markers (DNA markers technology), through the use of a number of techniques, the most important of which is the Inter-simple sequence repeats (ISSR) technology and DNA sequence technology, which is characterized by its high accuracy, speed of results, and uses in many fields, such as studying genetic diversity, fixing the genetic fingerprint, drawing genetic maps of date palm varieties, showing the genetic relationship between them, and solving the problem of the existence of more than one name for the same genetic makeup (9). A group of researchers conducted studies at the molecular level to study genetic diversity and fix the genetic fingerprint of the male date palm and concluded that it is possible to rely on these indicators reliably, including: (7), (10), (6), (3), (2), (4), (13), (5) (1).

Given the crucial role of pollen quality in date palm production, it is essential to conduct a molecular study of genetic diversity among fifteen local male date palm varieties growing in the Mandali district of Diyala Governorate, Iraq.

This study aimed to establish their genetic fingerprint and determine the similarity of their genetic origins in order to genetically filter them, ultimately leading to the identification of varieties and standardization of nomenclature.

Materials and Methods

The experiment was conducted to study the genetic diversity of date palm males growing in Mandali using molecular markers to determine their genetic fingerprint and molecularly screen them to determine their genetic origins. Fifteen male varieties were selected, including seed varieties and other local varieties widespread in the Mandali district, named after their growers: (seed plant 1, seed plant 2, Smeismi, yellow Smeismi, green, seed plant 3, seed plant 4, yellow, seed plant 5, lead, Ghannami, Ashrasi, Fahl, red, seed plant 6). These varieties are used as pollen varieties in the region. The trees were productive and as uniform as possible in age, height, and size, and free from pathogens and insects. The work was carried out in the biotechnology laboratories of Wahaj Al-Dana Company/Baghdad, and the DNA was extracted using an extraction kit produced by ZYMO RESEARCH, USA. Ten primers from the Inter-simple sequence repeats (ISSR) technology, shown in Table 1, were used, and the PCR products were

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electrophoresed to identify DNA fragments to differentiate between samples by the number and size of the resulting band on Agarose gel.

Table 1 shows the ISSR technology primers used in this study.

GC(%)	Tm (°C)	Sequence	Primer	NO.
47.2	**47.4**	**GAGAGAGAGAGAGAGAYT**	**UBC480**	1
47.1	**47**	**AGAGAGAGAGAGAGAGT**	**UBC807**	2
50	**50.6**	**AGAGAGAGAGAGAGAGCT**	**A35**	3
47.1	**45.7**	**CTCTCTCTCTCTCTCTT**	**813**	4
52.8	**48.5**	**GAGAGAGAGAGAGAGAYC**	**841**	5
47.1	**51.4**	**ACACACACACACACACT**	**825**	6
62.5	**56.8**	**GCGCGTGTGTGTGTGT**	**A34**	7
47.2	**53.1**	**TGTGTGTGTGTGTGTGRT**	**UBC858**	8
66.7	**62.2**	**GAGCAGCAGCAGCAGCAGC**	**UBC862**	9
52.9	**46.8**	**CTCTCTCTCTCTCTCTG**	**UBC815**	10

Statistical analysis for the outputs of genetic indicators:

The results of the multiplication process for the (ISSR) primers were taken based on the comparison of the presence or absence of cutoffs of parts DNA of Genetic structures different in every initiator and clear on the gel agarose, The presence of a piece of DNA is symbolized by the number (1) and its absence by the number (0). The primers duplication results data were fed into the computer within the NTSYS-pc (Numerical Taxonomy System) program. It was found:

1- The genetic distance between pure lines is determined by the following equation:
GD = 1-[2× (Nij/Ni + Ni)]
so an: Nij: represents the number of beams common to the j,i model: Ni : represents the number of packets in i-form ، Nj : represents the number of beams in j form

2- The percentage of polymorphism of the primers polymorphism or the proportion of divergent beams for each initiator was estimated based on the following equation:
Polymorphism = NP/Nt)×100)
Whereas :n.p= the number of divergent packets at the starter:Nt= the number of total packets of the initiator.

3- The percentage of discriminatory power for each initiator from the following equation:
Discriminatory power per initiator % = (number of differential packets of the initiator \ number of differential packets of all primers)× 100

4- The percentage of the efficiency of each initiator according to the following equation:
Initiator Efficiency% = (Total number of packets for the initiator / Number of packets for all initiators)× 100

The primers used for DNA sequence technology, the gene-specific primer rbcl: were used to stabilize the sequence of nitrogenous bases in the DNA of the four

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selected varieties in preparation for their registration in the NCBI.

Table 2 shows the primers used in this study along with their nucleotide sequences and the PCR test results.

Product size	GC (%)	Tm (°C)	Sequence	Primer
500-650 base pair	**42%**	**57.2**	**5′-ATGTCACCACAAACAGAGACTAAAGC-3′**	Forward
	47 %	**52**	**5′ - GTAAAATCAAGTCCACCACG -3′**	Reverse

Analysis of the Nitrogen Base Sequence of the Amplified Nucleic Acid (DNA)

1. The PCR-amplified products obtained using the forward and reverse primer (RBCL), which amplify the entire ribosomal internal transcribed spacer (RBCL) region important for plant identification, The DNA base pairs were submitted to Macrogen Company located in South Korea for sequencing.
2. The genetic tree and symmetry of the studied plants were analyzed, and the tree for the plants under study was determined using the Chromas program to identify the similarity and difference between the diagnosed plants and the plants registered globally. The genetic tree of the plants was determined by the nitrogen base sequence (Nucleotide sequence) of the amplified nucleic acid bands, utilizing the BLAST tool provided by National Center for Biotechnology Information (NCBI).

5- The sequenced apple cultivars were officially registered in the NCBI gene bank IN U.S.A as the first molecular entries from Iraq.

Results and Discussion

Genetic Fingerprinting and Variation via DNA Markers (ISSR Interactions):

The results of the ten ISSR primers used in this study yielded complementary sequences on the DNA of the fifteen studied stallions. These primers produced a total of 80 bands, averaging approximately 8 bands per primer. The number of bands ranged from 2 for ISSR 862 to 13 for ISSR A35. All primers exhibited distinct bands. The total number of different bands in the primers was (55) bands, representing (68.75%) of the total bands produced, with (5.5) bands per prefix, ranging between (2) bands in the primers ISSR 858 and ISSR 862 and (9) bands for the primers ISSR UBC 807, ISSR 813 and ISSR 815.

The following is a review of the primer results, shown in Table (3):

1- **ISSR UBC 480 Primer:** This primer provided a complement to its DNA in the studied stallions, whose DNA was amplified with this primer during PCR reactions. This primer showed (9) bands, with (5-8) bands. The number of different bands in this primer was (6), which is (66.66%). As for the efficiency of this primer, which represents the ratio of the total number of bands shown by this primer to the total number of bands

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in all primers, its efficiency became (11.25%). Meanwhile, its discriminatory power reached (10.91%), which represents the ratio of the number of different bands for this primer to the total number of different bands in all primers.

2- **ISSR UBC 807 Primer:** This primer contained (10) bands, with an average of (4-8) bands. The number of distinct bands in this primer was (9), representing (90%). The efficiency of this primer was (12.5%), and its discriminatory power was (16.36%). This primer showed a characteristic absent band for stallion 3 with a molecular size of (560) bp, and a characteristic manifest band for stallion 4 with a molecular size of (230) bp. These bands serve as markers or genetic fingerprints for these stallions.

3- **ISSR A35 Primer:** This primer produced (13) bands, with an average of (8-12) bands per day. Seven of these bands were of varying sizes, representing (53.84%) of the total number of bands. The primer's efficiency was (16.25%), while its discriminatory power was (12.72%). This primer also exhibited a unique absent band characteristic of stallion (1), with a molecular size of (400) bp, which serves as a genetic fingerprint for this stallion.

4- **ISSR 813 Primer:** This primer produced a total of (9) bands, ranging from (0-9) bands per day. The number of distinct bands in this primer was (9), representing (100%) of the total bands. Its efficiency was (11.25%) and its discriminatory power was (16.36%). Stallion (9) was distinguished by two visible bands with molecular sizes of (850) and (400) bp. These two bands serve as the genetic fingerprint for this stallion.

5- ISSR 841 Primer: The results showed that this primer contained (8) bands, ranging between (5-8) bands. The number of distinct bands was (3), representing (37.5%). Therefore, the efficiency of this primer was (10%), while its discriminatory power was (5.45%). Stallion (9) was distinguished by two absent bands with molecular sizes of (500) and (430) bp. These two bands serve as the genetic fingerprint for this stallion.

6- ISSR 825 Starter: This starter produced (9) main bands, with an average of (7) bands per stallion. The number of divergent bands was (4) bands, representing (44.44%). This starter recorded an efficiency of (11.25%) and a discriminatory power of (7.27%). Stallion (4) was distinguished by two bands, one absent and one present, with molecular sizes of (780) and (225) bp, respectively. These two bands serve as the genetic fingerprint of this stallion.

7- ISSR A34 Starter: This starter produced (6) bands, with an average of (2-6) bands. The number of divergent bands was (4), constituting (66.66%) of the total number of bands. The starter's efficiency was (7.5%), while its discriminatory power was (7.27%). This primer showed a characteristic absent band for stallion (1) with a molecular size of (200) bp, which serves as a genetic fingerprint for this stallion.

8- ISSR 858 Primer: This primer achieved a total of (5) bands, with an average of (3-5) bands. Two of these bands were heterozygous,

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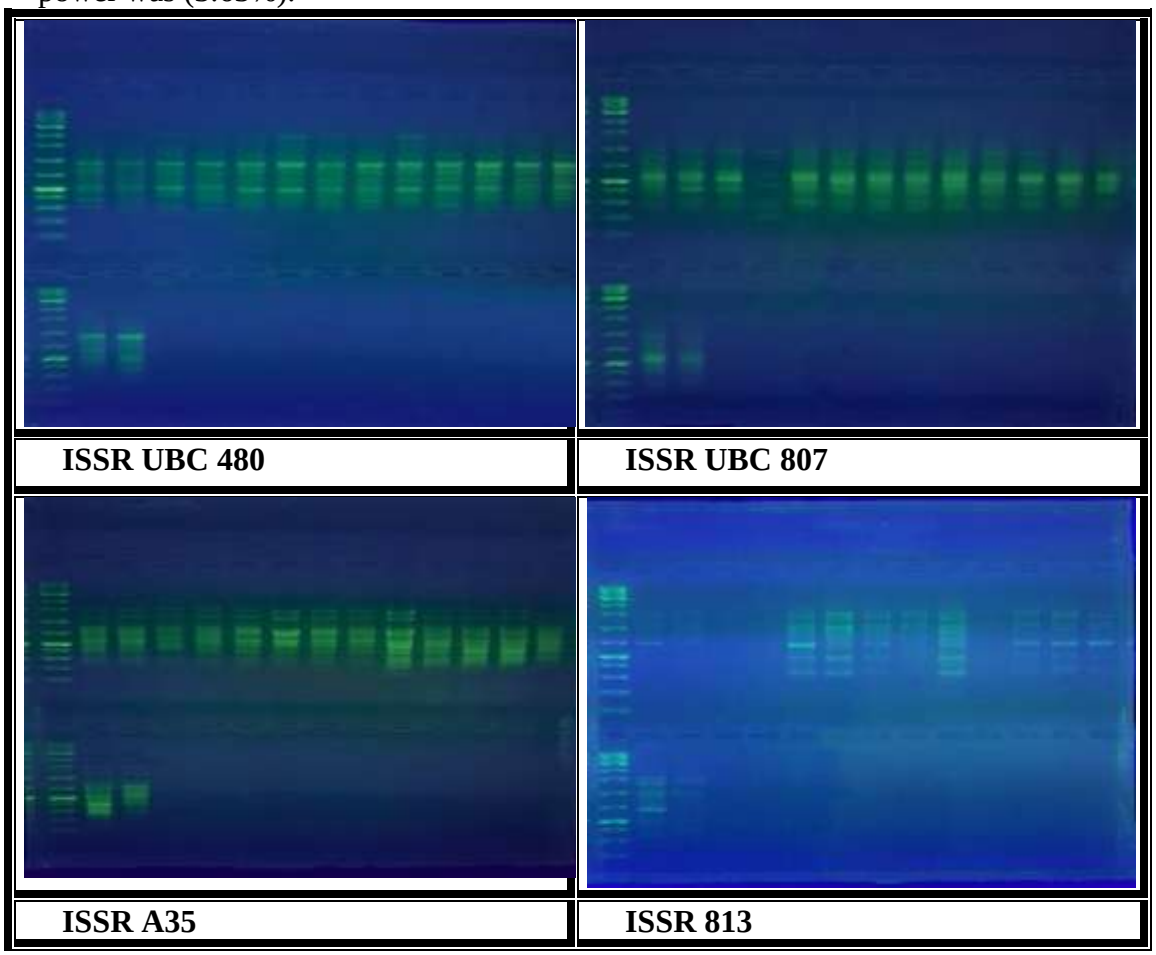
representing (40%) of the total bands. The efficiency of this primer was (6.25%), while its discriminatory power was (3.63%).

9- ISSR 862 Primer: This primer achieved (2) bands, with the number of bands ranging from (0-2). Two of these bands were heterozygous, representing (100%) of the total bands. The efficiency of this primer was (2.5%), while its discriminatory power was (3.63%).

10- ISSR 815 Primer: The number of bands for this starter reached (9) bands, all of which are different, with an average of (9-0) bands. The efficiency of this starter reached (11.25%) and its discriminatory ability reached (16.36%). Stallion (9) exhibited a unique band with a molecular size of (400) bp, serving as its genetic fingerprint, which is a genetic fingerprint for this stallion.



ISSR UBC 480 | **ISSR UBC 807**

ISSR A35 | **ISSR 813**

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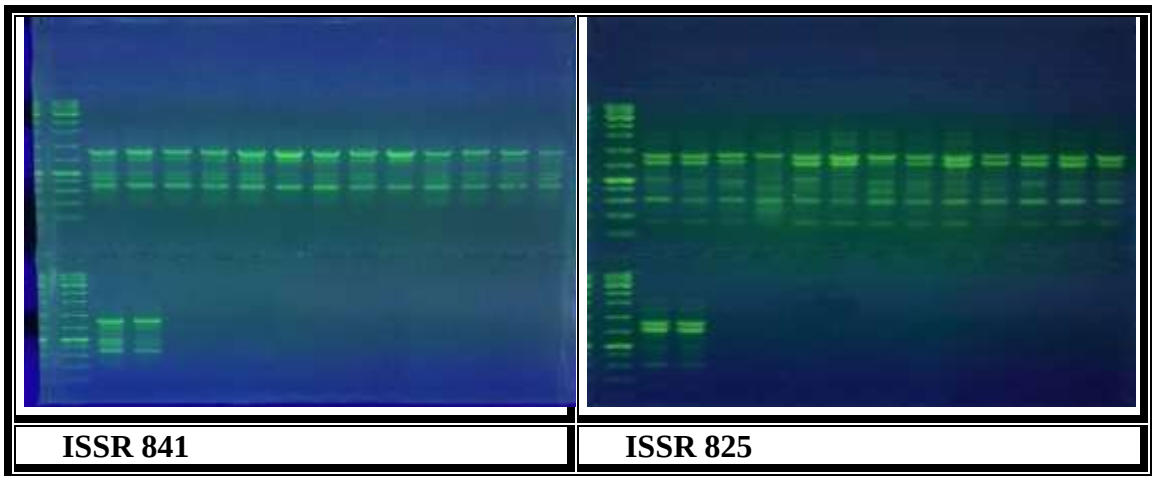

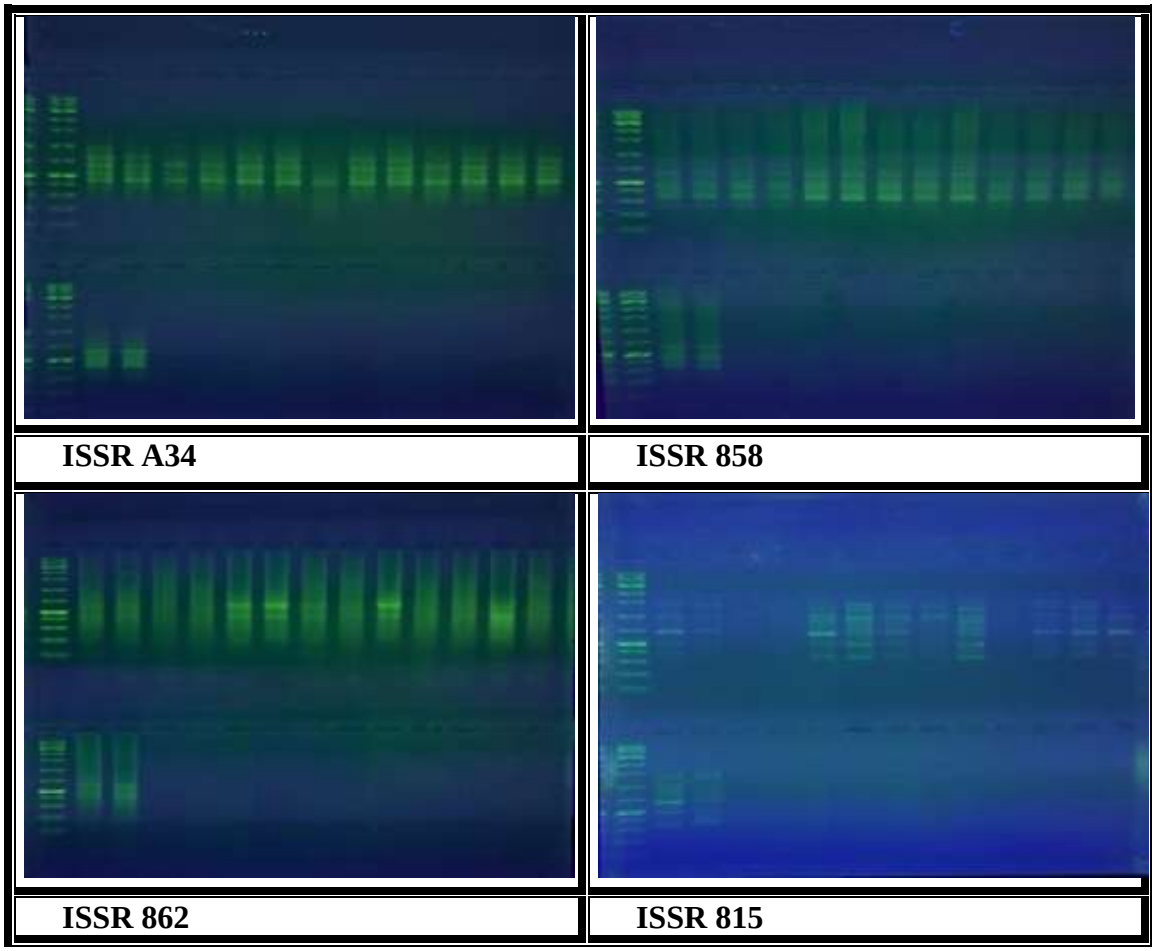

Figure 1: Products of the primers used on 1.5% agarose gels for pure strains .

To assess the genetic similarity between the stallions and determine the degree of convergence in their lineages and genetic material, the results obtained from ISSR primers were utilized. The presence of a band was assigned the symbol 1, and the

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absence of a band was assigned the symbol 0. The results are shown in Table 4. The table reveals that the highest genetic similarity was observed between stallions 11 and 12, reaching 0.939. This convergence may be attributed to their shared genetic material. The lowest genetic similarity was 0.5 between strains 3 and 9, likely due to their possessing different genetic material.

Based on the values obtained for the genetic similarity between the stallions and shown in Table (4), the genetic relationship that links them was found in the form of clusters, Figure (1), where the fifteen stallions were divided into two main groups: The first main group included the stallions (4, 8 and 3), and this group was divided into two subgroups. The first subgroup included the stallion (4), and the second subgroup included the two stallions (8 and 3).

Table 3 Shows the products of the primers from the packages. DNA and its efficiency and discrimination ability.

prefix symbol	Total number of resulting packages	Output packet rate	Number of different bands	Percentage of different packages %	Number of identical packages	Distinctive male date palm			Efficiency %	Discrimination ability %
						codeThe Distinctive male date palm	Molecular size of characteristic bandsbp	Type of distinction		
ISSR UBC 480	9	8-5	6	66.66	3	---	---	---	11.25	10.91
ISSR UBC 807	10	8-4	9	90	1	3 4	560 230	Absent phenomenon	12.5	16.36
ISSR A 35	13	12-8	7	53.84	6	1	400	Absent	16.25	12.72
ISSR 813	9	9-0	9	100	0	9 9	850 400	phenomenon phenomenon	11.25	16.36
ISSR 841	8	8-5	3	37.5	5	9 9	500 430	Absent Absent	10	5.45
ISSR	9	7	4	44.44	5	4 4	780 250	Absent pheno	11.25	7.27

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825								menon		
ISSR A34	6	6-2	4	66.66	2	1	200	pheno menon	7.5	7.27
ISSR 858	5	5-3	2	40	3	---	---	---	6.25	3.63
ISSR 862	2	2-0	2	100	0	---	---	---	2.5	3.63
ISSR 815	9	9-0	9	100	0	9	400	pheno menon	11.25	16.36
Total	80		55		25					

The second main group comprised the remaining stallions and was divided into subgroups. The first subgroup included stallion (9), the second subgroup included stallions (14 and 15), and the third subgroup included only stallion (13). The fourth subgroup was further divided into two subgroups: the first included stallions (5 and 6), and the second included stallions (12, 1, 7, 10, 2, and 11). These subgroups were then further divided into smaller clusters. This indicates a clear variation among the stallions at the molecular level, reflected in their genetic similarity values and their distribution into different groups. This reflects the differences in their genetic content and the efficiency of the ISSR used. The grouping of stallions in one group indicates their genetic similarity, and vice versa. These results are consistent with those of (7), (10), (6), , (3), (2), (4), (13), (5), and (1).

Based on the above results and some information the researcher has about some of the phenotypic characteristics and field performance of the studied stallions, four stallions were chosen: (4, 9, 6 and 11) as they fell into separate groups and represented a basic model of the groups.

Table 4 shows the genetic distance between the stallions under study.

15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	
														1	1
													1	0.813	2
												1	0.5	0.6	3

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												97	03	
										1	0.642	0.594	0.6	4
									1	0.618	0.551	0.768	0.824	5
								1	0.857	0.549	0.529	0.794	0.746	6
							1	0.853	0.853	0.559	0.609	0.815	0.791	7
						1	0.833	0.812	0.812	0.641	0.645	0.887	0.859	8
					1	0.72	0.757	0.836	0.787	0.562	0.5	0.68	0.707	9
					1	0.603	0.742	0.652	0.614	0.614	0.722	0.8	0.667	0.698	10
				1	0.746	0.77	0.877	0.836	0.789	0.814	0.597	0.6	0.859	0.833	11
			1	0.939	0.727	0.824	0.881	0.896	0.845	0.871	0.586	0.588	0.836	0.838	12
		1	0.848	0.844	0.763	0.712	0.785	0.773	0.729	0.729	0.578	0.607	0.794	0.825	13
	1	0.781	0.851	0.791	0.683	0.716	0.815	0.831	0.783	0.809	0.585	0.639	0.769	0.8	14
1	0.864	0.714	0.761	0.727	0.724	0.635	0.806	0.738	0.696	0.721	0.672	0.649	0.703	0.762	15

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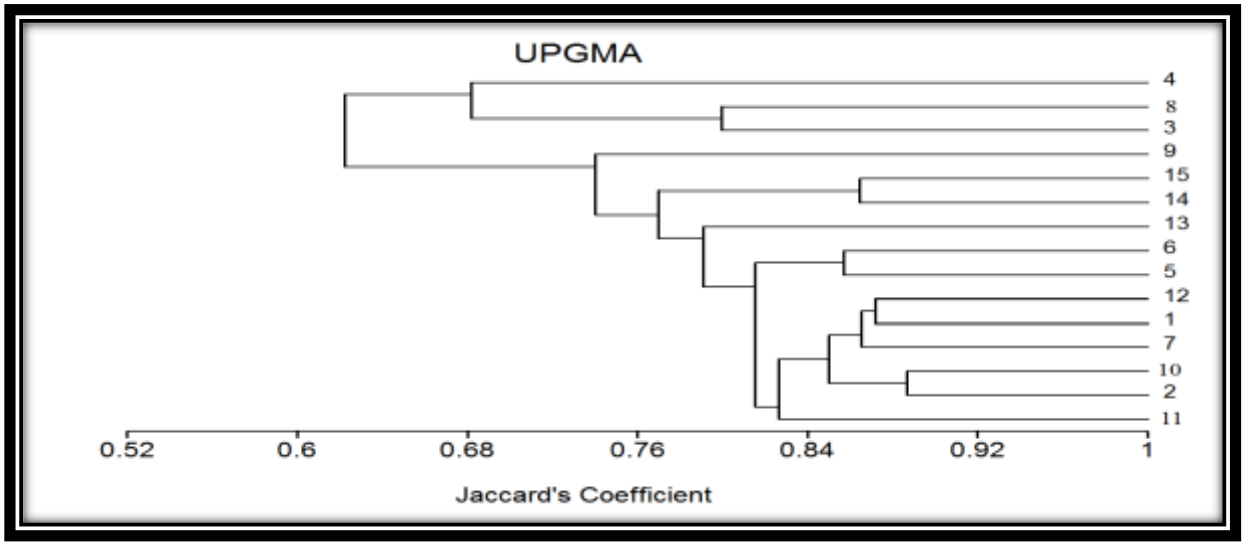

Figure 1. Cluster analysis plot (genetic tree) of the stallions under study according to ISSR-PCR indices

The nitrogenous base sequence of the four selected stallions was then determined using DNA sequencing technology in order to establish their genetic fingerprint at the nucleotide level of their DNA. Their data were also compared with the data recorded in the GenBank database of the National Center for Biotechnology Information (NCBI). It became clear that these stallions had not been registered at the level of Iraq, so they were registered as the first registration in Iraq and were given the codes and names as shown in Table 5:

Table 5: Codes and names proposed for stallions to be registered as first registrations in Iraq with the NCBI.

Sample number	Stallion code	NCBI registration name
1	**4**	**SAN1- Mandali**
2	**6**	**SAN2- Mandali**
3	**9**	**SAN3- Mandali**
4	**11**	**SAN4- Mandali**

Sample 1

Phoenix dactylifera voucher 2017 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast

Sequence ID: KX587668.1Length: 561Number of Matches: 1

Range 1: 8 to 561GenBankGraphicsNext MatchPrevious Match

Query 2 TGTTGGATTT-
AAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTACGA 60

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Sbjct 8
TGTTGGATTTAAAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTAC
GA 67

Query 61
AACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
GCC 120

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Sbjct 68
AACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
GCC 127

Query 121
TGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTG
TGTG 180

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Sbjct 128
TGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTG
TGTG 187

Query 181
GACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAAC
CGT 240

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Sbjct 188
GACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAAC
CGT 247

Query 241
TGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AGA 300

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Sbjct 248
TGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AGA 307

Query 301
AGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGCC
CT 360

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Sbjct 308
AGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGCC
CT 367

Query 361
ACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AGG 420

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Sbjct 368
ACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AGG 427

Query 421
CCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCTCT
ATT 480

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Sbjct 428
CCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCTCT
ATT 487

Query 481
GGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCGG
TTTA 540

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Sbjct 488
GGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCGG
TTTA 547

Query 541 TGAATGTCTACGCG 554

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Sbjct 548 TGAATGTCTACGCG 561

SAMPLE 2

Phoenix dactylifera voucher 2017 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast

Sequence ID: KX587668.1Length: 561Number of Matches: 1

Range 1: 7 to 561GenBankGraphicsNext MatchPrevious Match

Query 1 GTGTTGGATTT-
AAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTACG 59

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Sbjct 7
GTGTTGGATTTAAAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACT
ACG 66

Query 60
AAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTC
CGC 119

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Sbjct 67
AAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTC
CGC 126

Query 120
CTGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACT
GTGT 179

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Sbjct 127
CTGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACT
GTGT 186

Query 180
GGACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAA
CCG 239

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Sbjct 187
GGACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAA
CCG 246

Query 240
TTGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AG 299

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Sbjct 247
TTGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AG 306

Query 300
AAGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGC
CC 359

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Sbjct 307
AAGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGC
CC 366

Query 360
TACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AG 419

Sbjct 367
TACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AG 426

Query 420
GCCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCT
CTAT 479

Sbjct 427
GCCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCT
CTAT 486

Query 480
TGGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCG
GTTT 539

Sbjct 487
TGGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCG
GTTT 546

Query 540 ATGAATGTCTACGCG 554

Sbjct 547 ATGAATGTCTACGCG 561

SAMPLE 3

Phoenix dactylifera voucher 2017 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast

Sequence ID: KX587668.1Length: 561Number of Matches: 1

Range 1: 8 to 561GenBankGraphicsNext MatchPrevious Match

Query 2
TGTTGGATTTAAAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTAC
GA 61

Sbjct 8
TGTTGGATTTAAAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTAC
GA 67

ISSN 2072-3857

Query 62
AACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
GCC 121

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Sbjct 68
AACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
GCC 127

Query 122
TGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTG
TGTG 181

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Sbjct 128
TGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTG
TGTG 187

Query 182
GACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAAC
CGT 241

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Sbjct 188
GACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAAC
CGT 247

Query 242
TGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AGA 301

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Sbjct 248
TGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AGA 307

Query 302
AGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGCC
CT 361

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Sbjct 308
AGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGCC
CT 367

Query 362
ACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AGG 421

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Sbjct 368
ACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AGG 427

Query 422
CCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCTCT
ATT 481

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Sbjct 428
CCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCTCT
ATT 487

Query 482
GGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCGG
TTTA 541

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Sbjct 488
GGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCGG
TTTA 547

Query 542 TGAATGTCTACGCG 555

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Sbjct 548 TGAATGTCTACGCG 561

SAMPLE 4

Phoenix dactylifera voucher 2017 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast

Sequence ID: KX587668.1Length: 561Number of Matches: 1

Range 1: 8 to 561GenBankGraphicsNext MatchPrevious Match

Query 2 TGTTGGATTT-
AAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTACGA 60

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Sbjct 8
TGTTGGATTTAAAGCTGGTGTTAAAGATTACAAATTGACTTATTATACTCCTGACTAC
GA 67

Query 61
AACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
GCC 120

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ISSN 2072-3857

Sbjct 68
AACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCC
GCC 127

Query 121
TGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTG
TGTG 180

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Sbjct 128
TGAGGAAGCAGGGGCAGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTG
TGTG 187

Query 181
GACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAAC
CGT 240

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Sbjct 188
GACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATCGAAAC
CGT 247

Query 241
TGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AGA 300

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Sbjct 248
TGTAGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGA
AGA 307

Query 301
AGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGCC
CT 360

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Sbjct 308
AGGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTATTTGGTTTCAAAGCC
CT 367

Query 361
ACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AGG 420

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Sbjct 368
ACGAGCTCTACGTCTGGAGGATCTGCGAATTCCCACTTCTTATTCCAAAACTTTCCA
AGG 427

ISSN 2072-3857

Query 421
CCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCTCT
ATT 480

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Sbjct 428
CCCGCCTCATGGCATCCAAGTTGAAAGAGATAAGTTGAACAAGTATGGTCGGCCTCT
ATT 487

Query 481
GGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCGG
TTTA 540

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Sbjct 488
GGGATGTACTATTAAACCAAAATTGGGATTATCCGCAAAGAACTACGGTAGAGCGG
TTTA 547

Query 541 TGAATGTCTACGCG 554

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Sbjct 548 TGAATGTCTACGCG 561

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