Mesopotamia Journal of Agriculture

https://magrj.mosuljournals.com

PRODUCTION PERFORMANCE AND GENETIC SIMILARITIES IN UKRAINIAN AND LOCAL BROWN QUAIL

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Article information
Article history:
Received: 01/11/2023
Accepted: 17/12/2023
Published: 31/12/2023

Keywords:
Ukrainian and local quail hybrid, productive performance, genetic similarity and distance.

DOI:
http://10.33899/mja.2023.144335.1290

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ABSTRACT

Two lines of brown-colored Ukrainian (U) and local (L) quails, as well as cross (U×L) and reciprocal cross (L×U), were produced in the Agricultural Research Department's fields between March 1, 2023, and June 1, 2023. The purpose of the study was to determine the productive and genetic performance of these genetic groups. Over a period of eight weeks, the various birds' performances were evaluated using the: CEW g, HDP% and FCR (g feed/g egg mass). Moreover, estimates were also made of the genetic distance and similarity between the male and female of the groups. Therefore, the results were showed a significant increase ($P < 0.05$) in the Ukrainian quails and reciprocal cross (L×U) in the CEW (589.37 and 560.25) g and HDP (74.86 and 72.77) %, and a significant improvement ($P < 0.05$) in FCR (4.38 and 3.93) g feed/g egg mass) compared to the local quails and crossbreeding (U×L) quails. The genetic similarity between males and females of crossbreeding (U×L) is highest (0.8537), while that of local males and females of reciprocal cross (L ×U) is lowest (0.5244). while the genetic distance results supported the foregoing, with the local males and females of reciprocal crossbreeding (L ×U) having the highest genetic distance (0.6455) cM and the males and females of crossbreeding (U×L) having the least genetic distance (0.1582) cM.

INTRODUCTION

According to El-Masri *et al*. (2012) and Razuki *et al*. (2017), hybrid is one of the key techniques in genetic improvement programs that aims to improve the production, collect as many of the preferred genes as possible in the resulting hybrids, thereby increasing the proportion of genetic diversity, obtaining hybrid vigor, and improving genetic traits. Quail is one of the greatest experimental animals in genetics due to its significant traits, which include the production of eggs and meat, rapid growth, short generation times, and disease resistance (Momoh *et al*., 2014; Al-Tikriti, 2018; AL-Hamed, 2020 and Alkado *et al.*, 2022).

With the aid of contemporary technologies like RAPD-PCR technology, it is now possible to close the generational gap, encourage genetic selection for traits like feed efficiency, meat quality, egg production, improve the efficacy of preventing poultry diseases, and create genetically modified vaccines. The use of DNA markers

by poultry breeders has considerably profited from polymerase chain reaction technology (Salah, 2014; and Abdulrazaq, 2022).

Genetic primers, which are condensed nucleotide sequences intended to bind with particular DNA sequences, form the foundation of this method (Tanabe *et al*., 2019 and Taha *et al.*, 2021). Because they may detect variations in DNA sequences among organisms, random primers are associated with genetic similarities. This is so because they have a wide range of DNA binding sites, which causes the PCR reaction to amplify these DNA regions.

Genetic similarity, according to Willis and Wallace (2023), is the degree of genetic resemblance between two or more qualities. In general, the genetic similarity of male and female local brown and white quail was (0.00–1.00). (Eissa *et al*., 2014), Additionally, Istiak *et al*. (2018) found that the genetic similarity between white, Dhakaya, Rosetta, and yellow-brown quail was found to be between (23.43 to 55.15) % using seventeen primers and RAPD-PCR technology. Shimma and Tadano (2019) used 45 primers with RAPD-PCR technology to estimate the genetic differentiation between 12 commercial strains of Japanese white quail (Farm 1-A, Farm 1-B, Farm 1-C, Farm 2, Farm 3, Farm 4, Farm 5-A, Farm 5-B, Farm 6, Farm 7, Farm 8, and Farm 9) to be between (0.0028 and 0.0254).

In the current study, the genetic similarity and distance, as well as some productive traits, of two lines of Ukrainian and local (white and brown) feathered quail and their crossbreeds were studied.

MATERIALS AND METHODS

Ethical approve

The ethical and animal welfare committee of the College of Veterinary Medicine, University of Mosul, approved the study and sample collection, which took place between March 1 and June 1, 2023, under the number UM.VET.2023.027.

Place of experiments

The Livestock Division of the Nineveh Research Department conducted a study in the poultry fields between March 1 and June 1, 2023, to ascertain the genetic similarity and its relationship to the productivity of Ukrainian (U) and local (L) brown quail, as well as their hybrids (UL and LU). The chicks were raised and dispersed according to the pure line, cross and reciprocal cross breeding in 4 rooms, each measuring (2 1.2) m. The chicks were fed a diet had 22% crude protein and 2903 metabolic calories. growth diet until they were four weeks old, at which point a production diet comprising 18% crude protein and 2908 metabolic calories was gradually introduced. The following attributes were estimated:

1. Hen day production (HDP%) = (No. of egg product/No. of female) ×100.
2. Cumulative egg weight (CEW) = eggs weight through 8 weeks.
3. Feed Conversion Ratio (FCR) = egg mass/feed consumption (Al-Tammee, 2019**)**.

Blood collection

For each genetic group (Ukrainian and local brown quail, their cross, and reciprocal cross after slaughter), 5 ml of blood was individually taken from two

females and two males. the blood samples were frozen and kept at a temperature of (-20) °C.

DNA Extraction

DNA was isolated from quail blood using DNA Extraction Kit No. M-7822 (Promega, Canada), as directed by the manufacturer. Until the next test, the extracted DNA samples were stored at -20 °C.

Polymerase chain reaction (PCR)

Random amplified polymorphic DNA-PCR (RAPD-PCR) was used for the molecular characterization of quail using different primers Table (1). The primers were obtained from (IDT, USA). Briefly, the PCR reaction was prepared in 25 µl final volume containing 11 µl of PCR Free water 1 µl of the primer, and 3 µl of extracted DNA and 10 µl of Master Mix (GeNet Bio, Korea). The PCR reaction was performed by 40 Thermocycler (MultiGene Mini, USA), the program consists of initial denaturation step at 98°C for 1 min then followed by 34 cycles with 96°C for 30 sec for DNA denaturation, 35°C for 30 sec for primer annealing and 72°C for 59 sec for primer extension. Final extension was at 72°C for 6 min. The amplified products were separated using electrophoresis in 1 % agarose gel (Promega, USA), and 5 µl of each PCR product was loaded into the well of agarose gel. The electrophoresis was carried out using 1X TBE buffer (GeNetBio, Korea) at 100 V for 1 hour using power supply (BioRad, USA). A 10000 bp DNA ladder, 4 µl (Promega, USA) was used as standard molecular weight marker (Mikić, *et al.,* 2023).

Table (1): The sequence of primers and the bonding temperature used

No.	Primers	Sequence 5´➔ 3´	Temp.	Ref.
1	OPA-11	CAATCGCCGT	32	Salah, 2014
2	OPC-08	TGGACCGGTG	39	
3	OPA-13	CAGCACCCAC	34	
4	OPA-10	GTGATCGCAG	32	Eissa *et al*., 2014
5	OPA-18	AGGTGACCGT	36	
6	OPB-02	TGATCCCTGG	32	
7	OPB-10	CTGCTGGGAC	36	
8	OPE-06	AGATGCAGCC	36	
9	OPE-19	ACGGCGTATG	36	
10	OPL-07	AGGCGGGAAC	39	Istiak *et al*., 2018

Molecular genetic analysis

To determine how many polymorphic and monomorphic bands are there. Bands were graded visually based on their presence (1 point) or absence (0 points). According to Ezzulddin *et al.,* (2020), the following equation was used to determine genetic similarity (GS): GS = 2Na + Nb. Were Nab stands for the bands that entered between groups a and b. The total number of scrod bands for the same groups was Na+ Nb, genetic distance was calculated as GD = -In(S). Using the (NTSYS and MS Excel 2019) software, the dendrogram tree was created based on genetic similarity. Based on the following formula, the polymorphism of every primer was determined:- Since NP stands for polymorphic forms of random primer, and Nt is the total number

of primer domain samples. polymorphism = (Np / Nt) × 100 (Abdulrazaq, *et al*., 2020).

Statistical Analysis

The data are analyzed using Complete Randomized Design (CRD), and the significance of the differences between the genetic groups is determined using Du ncan's multi-range test (Al-Rawi and Khalaf Allah 1981). The statistical model was as follows: $Yij=\mu+Gi+eij$, where Yij represents the observed value for the j^{th} individual's i^{th} genotype, μ represents the overall mean, Gi represents the genotype effect (i=Ukrainian and Local), and eij represents a random error term

RESULTS AND DISCUSSION

Quail type effects on productive traits

The cumulative egg weight of the Ukrainian quail (589.37 g) was significantly higher ($P \leq 0.05$) than that of the local quail (137.73 g), as shown in Table (2). Additionally, there was a significant difference ($P < 0.05$) between the cross hybrids UM×LF (166.49 g) and reciprocal cross hybrids LM×UF (560.25 g) in the CEW. These findings could be explained by the positive genetic correlation between the weight of eggs and the weight at sexual maturity, and the live body weight (Al-Salhie and Al-Sudani, 2013 and Al-Takriti and Al-Nadawi, 2017). These results matched agree with (AL-Neemy, 2017; Al-Takriti and Al-Nadawi, 2017; Al-Kafajy *et al*., 2018; Ibrahim *et al*., 2022).

Table (2): Effect of the type of quail, cross and reciprocal cross on egg weight, HDP% and FCR

	CEW (g)	HDP (%)	FCRMass (g feed / g egg mass)
U	589.37+58.29 a	74.86+7.67 a	4.39+0.75 c
L	137.73+19.11 b	41.84+5.50 b	6.61+0.73 a
U×L	166.49+14.44 b	39.44+3.42 b	5.30+0.69 b
L×U	560.25+56.29 a	72.77+9.62 a	3.93+0.74 c

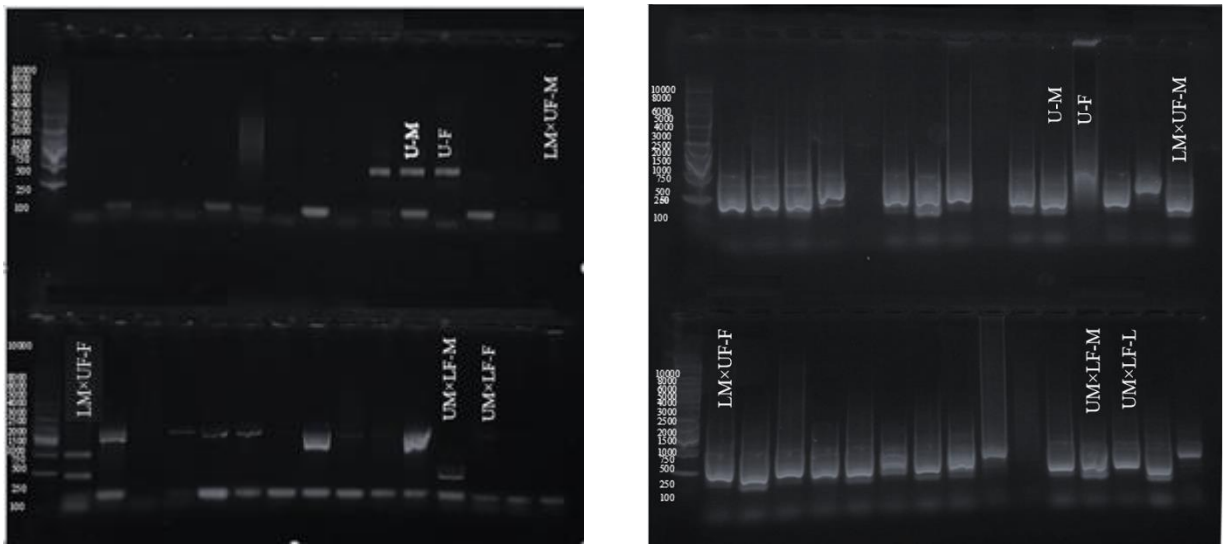
Different letters within the same column denote the presence of significant differences between groups when ($P < 0.05$). U=Ukrainian quail, L=Local quail, M=male, F=Female, CEW= cumulative egg weight, HDP%=Hen Day production percentage, FCRMass= Feed conversion ratio (g food / g egg mass).

Similar to this, the HDP% considerably increased ($P < 0.05$) for both the Ukrainian quail and the reciprocal cross hybrid (74.86 and 72.77%) in comparison to the rates for the local quail and the cross hybrid (41.84 and 39.44%). These outcomes complemented those of (AL-Neemy, 2017 and Hussen, and Saleh, 2019). The FCR (g feed/g egg mass) of Ukrainian quail and reciprocal hybrid quail (4.39 and 3.93) was found to be significantly improved (P 0.05) than that of local quail and cross hybrid quail (6.61 and 5.30), respectively. These findings were in agreement with (AL-Neemy, 2017; Hussen, and Saleh, 2019 who mentioned how the FCR was impacted by the relation between FC and egg mass.

RAPD-PCR marker identification

A total of 139 RAPD DNA bands were amplified using the 10 chosen primers Figures (1-6) and Table (3), from males and females of the pure lines of Ukrainian

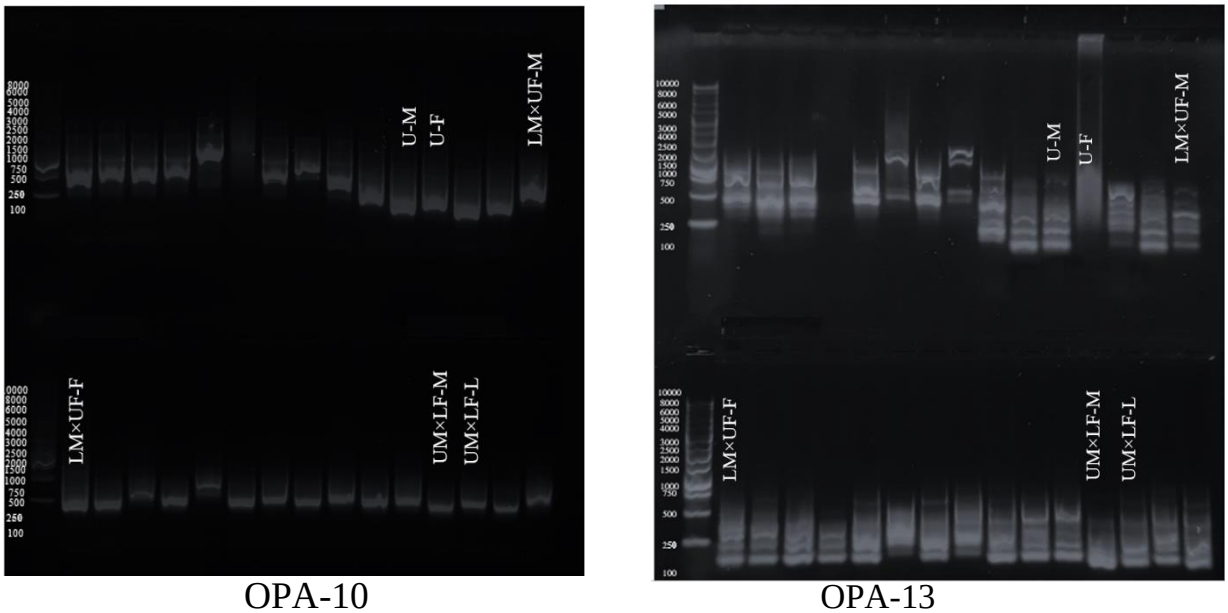
quail, brown local quail, their crosses, and reciprocal cross. The number of unique and polymorphic bands amplified by the electrophoresis for each of the ten randomly chosen primers varied, as shown in the Table (4) below:



OPA-11 OPL-07

Figure (1): Gel agarose for (OPA-11 and OPL-07) primers

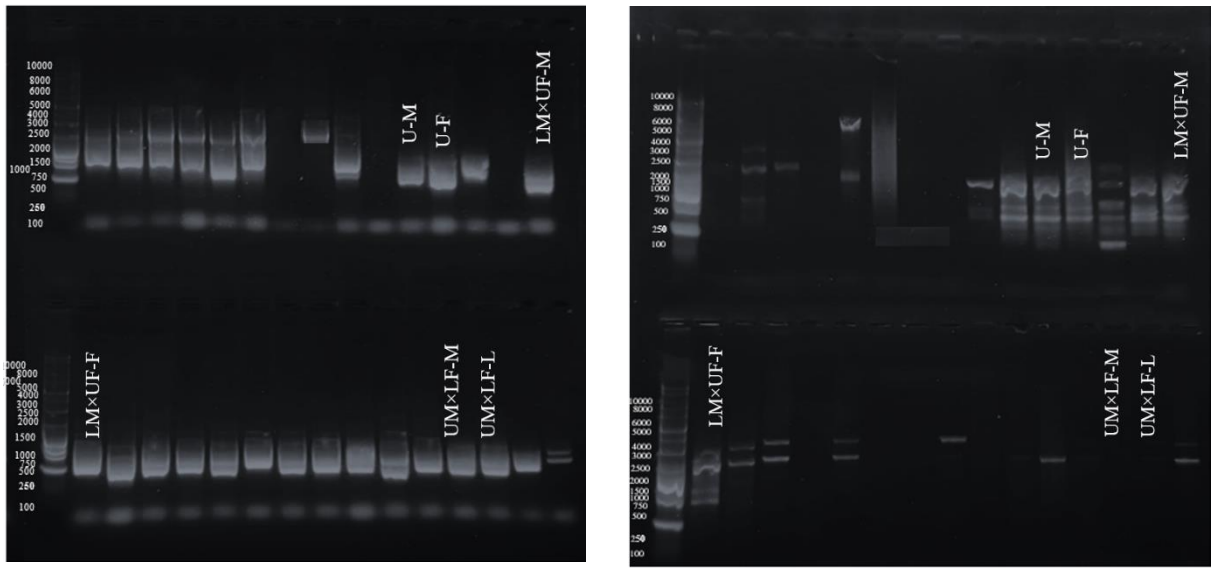
U-M=Ukrainian Male, U-F=Ukrainian female, LM×UF-M=male of reciprocal cross (local male and Ukrainian female), LM×UF-F= female of reciprocal cross (local male and Ukrainian female), UM×LF-M=male of cross (Ukrainian male and local female), UM×LF-F= female of cross ((Ukrainian male and local female).



OPA-10 OPA-13

Figure (2): Gel agarose for (OPA-13 and OPA-10) primers

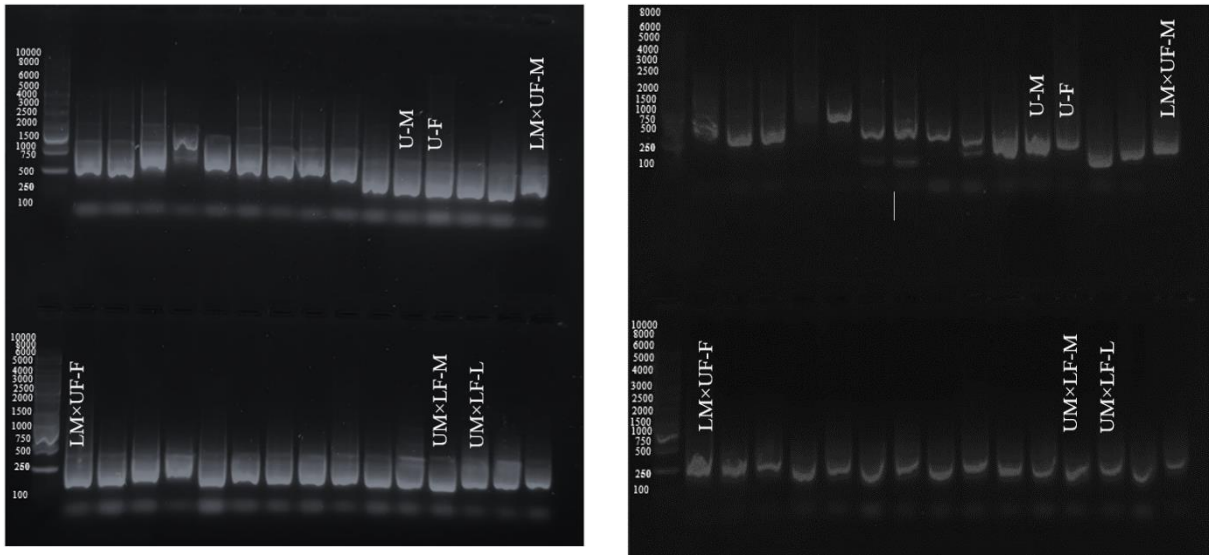
U-M=Ukrainian Male, U-F=Ukrainian female, LM×UF-M=male of reciprocal cross (local male and Ukrainian female), LM×UF-F= female of reciprocal cross (local male and Ukrainian female), UM×LF-M=male of cross (Ukrainian male and local female), UM×LF-F= female of cross ((Ukrainian male and local female).



OPA-18 OPB-02

Figure (3): Gel agarose for (OPA-18 and OPB-02) primers

U-M=Ukrainian Male, U-F=Ukrainian female, LM×UF-M=male of reciprocal cross (local male and Ukrainian female), LM×UF-F= female of reciprocal cross (local male and Ukrainian female), UM×LF-M=male of cross (Ukrainian male and local female), UM×LF-F= female of cross ((Ukrainian male and local female).



OPB-10 OPE-06

Figure (4): Gel agarose for (OPB-10 and OPE-06) primers

where is, U-M=Ukrainian Male, U-F=Ukrainian female, LM×UF-M=male of reciprocal cross (local male and Ukrainian female), LM×UF-F= female of reciprocal cross (local male and Ukrainian female), UM×LF-M=male of cross (Ukrainian male and local female), UM×LF-F= female of cross ((Ukrainian male and local female).

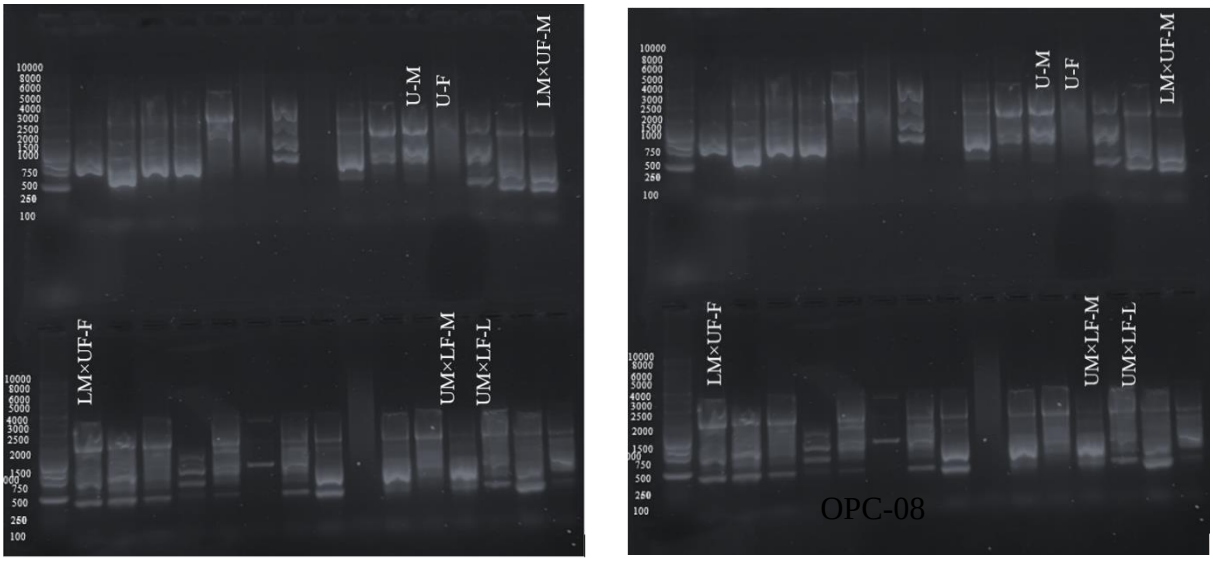


Figure (5): Gel agarose for (OPE-19 and OPC-08) primers
U-M=Ukrainian Male, U-F=Ukrainian female, LM×UF-M=male of reciprocal cross (local male and Ukrainian female), LM×UF-F= female of reciprocal cross (local male and Ukrainian female), UM×LF-M=male of cross (Ukrainian male and local female), UM×LF-F= female of cross ((Ukrainian male and local female).

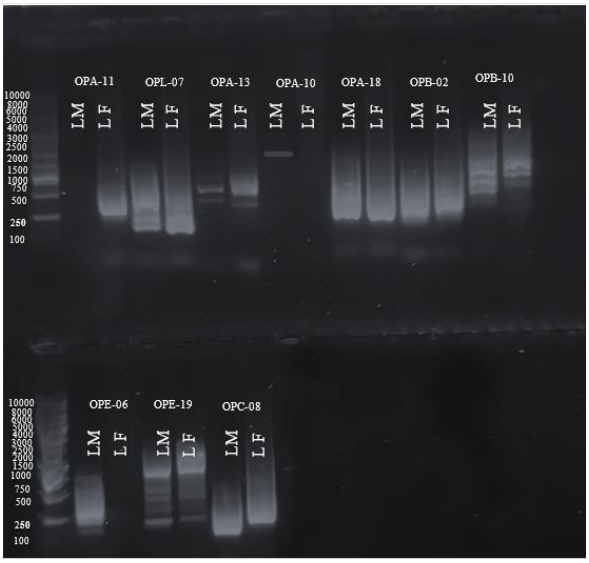


Figure (6): Gel agarose for 10 primers. where is, L-M=local Male, U-F=local female

The primer (OPC-08) amplified the highest number of amplified bands (22) and the highest discriminatory power (15.83%), whereas primer (OPA-11 and OPL-07) amplified the fewest bands (10) and the lowest discriminatory power (7.53%) for each of them. The distribution of the bands amplified between unique bands, with a total of 46 bands, and polymorphic bands, with a total estimated to be (139) bands, as shown in Table (4), these results are similar to findings of (Abdulrazaq, *et al*., 2020 and AL-Neemy *et al.*, 2021). The findings of the current study did not reveal any bands of monomorphic bands.

Table (3): Bands of RAPD-PCR for Ukrainian and local brown (males and females) of quail.

Primer	Bands	U-M	U-F	L×U-M	L×U-F	U×L-M	U×L-F	L-M	L-F	Primer	Bands	U-M	U-F	L×U-M	L×U-F	U×L-M	U×L-F	L-M	L-F
OPA-11	700	0	0	0	1	0	0	0	1	OPB-10	**1500**	0	0	0	0	0	0	1	0
	500	1	1	0	0	0	0	0	1		**1100**	0	0	0	0	0	0	1	0
	400	0	0	0	1	0	0	0	1		**750**	0	0	0	0	0	0	1	0
	380	0	0	0	0	0	0	1	0		**600**	1	1	1	0	0	0	0	0
	250	0	0	0	0	0	0	0	1		**500**	0	0	0	1	1	1	0	0
	240	0	0	0	0	1	0	0	0		**250**	0	0	1	0	0	0	0	0
OPL-07	700	0	0	0	0	0	0	0	1		**225**	1	0	0	0	0	0	0	0
	600	0	0	0	1	0	0	0	1		**215**	1	1	0	0	0	0	0	0
	490	0	0	0	1	0	0	0	0		**200**	0	0	0	1	0	1	0	0
	400	0	0	0	0	1	1	0	1		**125**	0	0	0	0	1	0	0	0
	240	0	0	0	0	1	0	1	0	OPE-06	1000	0	0	0	0	0	0	1	0
	150	0	0	0	0	0	0	0	0		300	0	0	0	1	0	0	0	0
OPA-13	2000	0	0	0	0	0	0	0	1		260	0	0	0	0	1	1	0	0
	1000	0	0	0	1	0	0	0	0		250	1	0	1	0	0	0	1	0
	750	0	1	0	0	0	0	0	0		100	0	0	0	0	0	0	1	0
	510	0	0	0	0	1	1	1	0	OPE-19	**510**	0	0	0	0	0	0	1	0
	500	0	0	0	0	1	0	0	0		**250**	0	0	0	0	0	0	0	1
	490	0	0	0	0	1	1	0	0		**150**	1	0	0	0	0	0	0	0
	350	0	0	0	0	0	0	1	0		**1600**	1	0	0	0	0	0	0	0
	300	0	0	0	1	1	0	0	0		**1400**	0	1	0	0	0	0	0	0
	110	1	0	0	0	0	0	0	0		**1100**	0	1	0	1	0	0	0	0
	100	1	0	0	0	0	0	0	0		**900**	0	0	0	0	0	0	1	1
OPA-10	1750	0	1	0	0	0	0	0	0		**750**	0	0	0	1	1	1	0	0
	600	0	0	0	1	0	0	0	0		**490**	0	0	0	0	0	1	1	1
	260	1	0	1	1	0	0	0	0		**300**	0	0	0	1	0	0	0	0
	240	0	0	0	1	0	1	0	1		**260**	0	0	1	0	0	0	1	1
OPA -18	500	1	0	0	0	0	0	0	0		**240**	0	0	0	0	0	0	1	0
	300	0	1	1	0	0	0	0	0	OPC-08	**4900**	0	0	1	0	0	0	0	0
	250	0	0	0	1	1	1	1	1		**4500**	0	0	0	0	0	1	0	0
	240	0	0	0	0	0	0	0	0		**2600**	0	0	0	0	1	1	0	0
OPB-02	**2250**	0	0	0	0	0	0	0	1		**2400**	1	0	1	0	0	0	0	0
	2100	0	0	0	1	0	0	0	0		**2250**	0	0	0	1	1	0	0	0
	1500	0	0	0	0	0	0	0	1		**1800**	0	0	0	0	0	1	0	0
	1250	0	0	0	0	0	0	0	1		**1500**	0	0	1	0	0	0	0	0
	1000	1	1	1	0	0	0	0	1		**1250**	1	1	0	0	0	0	0	0
	750	0	0	0	1	0	0	0	0		**900**	0	0	0	1	0	1	0	0
	600	1	1	1	0	0	0	0	0		**740**	0	0	0	0	1	1	0	0
	510	0	0	0	0	0	0	0	1		**500**	0	0	1	1	1	1	0	0
	500	0	0	0	1	0	0	0	0		**250**	0	0	0	0	0	0	0	1
	450	1	1	1	1	0	0	0	0		**110**	0	0	0	0	0	0	1	0
	300	0	0	0	0	0	0	0	1										
	250	1	1	1	1	0	0	0	0										

Phylogenetic relationship between quail genotypes based on RAPD primers

The sharing of bands between quail varieties results in genetic resemblance. Accordingly, there is a highest genetic similarity (0.8537) between males and females of the cross (L×U), while the lowest genetic similarity (0.5244) is most noticeable between females of the cross hybrids (L×U) and local males (L). The genetic similarity between the remaining genetic groups, on the other hand, ranged from (0.5732 to 0.8293) Table (5). These results greed with (Abdulrazaq, *et al*., 2020).

Table (4): Total number of amplified, polymorphic, and unique bands for each primer, as well as the efficiency (%) and discriminatory power (%).

	Total No. amplified bands	Unique bands	Polymorphic bands	Efficiency (%)	Discriminatory power (%)
OPA-11	10	3	7	7.19	7.53
OPL-07	10	3	7	7.19	7.53
OPA-13	14	7	7	10.07	7.53
OPA-10	8	2	6	5.76	6.45
OPA-18	8	1	7	5.76	7.53
OPB-02	23	8	13	16.55	16.13
OPB-10	16	6	10	11.51	10.75
OPE-06	8	3	5	5.76	5.38
OPE-19	20	7	13	14.39	13.98
OPC-08	22	6	14	15.83	17.20
Total	139	46	93	100	100

Table (5): Similarity matrix between the Ukrainian and local brown quail and their cross and reciprocal cross on the basis of RAPD-PCR analysis.

	U-M	U-F	L×U-M	L×U-F	U×L-M	U×L-F	L-M	L-F
U-M	1							
U-F	0.8293	1						
L×U-M	0.8171	0.8171	1					
L×U-F	0.5732	0.622	0.6341	1				
U×L-M	0.5976	0.6463	0.6585	0.6585	1			
U×L-F	0.5976	0.6463	0.6585	0.6829	0.8537	1		
L-M	0.6098	0.6341	0.6707	0.5244	0.6707	0.6707	1	
L-F	0.5854	0.6341	0.622	0.5732	0.5976	0.6463	0.6341	1

Results from Table (6) show information about genetic distance, the genetic distance between males and females of the cross (U×L) was found to be 0.1582 cM, while the genetic distance between female of the cross (L×U) and local male (L) was (0.6455). Every group's genetic distance ranged from 0.1872 to 0.5565 overall, These results greed with (Abdulrazaq, et al., 2020 and Omarbly *et al.,* 2021).

Table (6): Genetic distance between the Ukrainian and local brown quail and their cross and reciprocal cross.

	U-M	U-F	L×U-M	L×U-F	U×L-M	U×L-F	L-M	L-F
U-M	0							
U-F	0.1872	0						
L×U-M	0.2020	0.2020	0					
L×U-F	0.5565	0.4748	0.4555	0				
U×L-M	0.5148	0.4365	0.4178	0.4178	0			
U×L-F	0.5148	0.4365	0.4178	0.3814	0.1582	0		
L-M	0.4946	0.4555	0.3994	0.6455	0.3994	0.3994	0	
L-F	0.5355	0.4555	0.4748	0.5565	0.5148	0.4365	0.4555	0

The genetic patterns of Ukrainian and local quail are grouped into two main groupings, as seen by the dendrogram Figure (7). A distinct cluster was formed by dividing the female reciprocal cross (L×U) into the first group. Two subgroups emerged from the second main group. The first subgroup included only local quail females. The second subgroup was divided into two secondary subgroups; the initial subgroup included two clusters: the first cluster was exclusively composed of male local quail, while the second cluster was composed of the cross's most akin males and females (U×L). In the second secondary subgroup, there were two clusters: male reciprocal cross (L×U) in the first cluster, the second cluster included both male and female Ukrainian quail (the second most similar group).

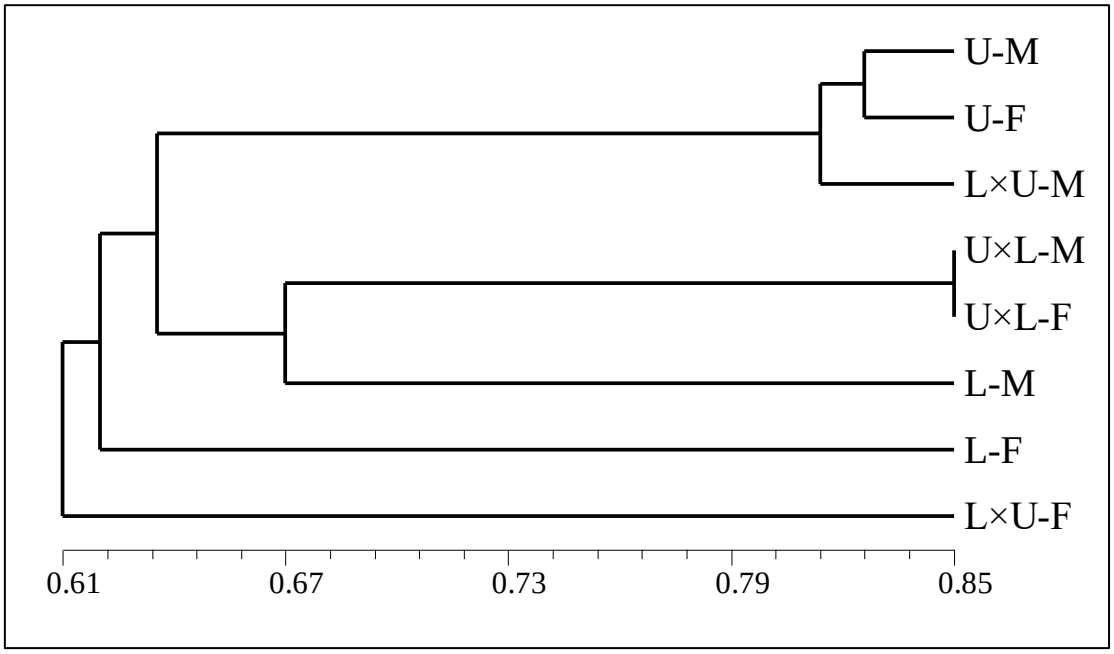


Figure (7): Eight distinct quails made from RAPDs were represented in the dendrogram data using UPGMA and a similarity matrix

CONCLUSIONS

According to the results of these study, the productive and genetic performance of Ukrainian quail and reciprocal crossbreeding (L×U) was superior to that of local quail and crossbreeding (U×L). The CEW, HDP, and FCR of the reciprocal crossbreeding (L×U) and Ukrainian quail were significantly greater than those of the local quail and crossbreeding (U×L) quails. When it came to genetic similarity, the male and female of reciprocal crossbreeding (L×U) had the lowest genetic similarity, while the male and female of crossbreeding (U×L) had the highest. The results of the genetic distance analysis confirmed the previous conclusions. The local reciprocal crossbreeding male and female (L×U) had the greatest genetic distance, while the crossbreeding male and female (U×L) had the lowest. According to these results, local poultry production systems may benefit from increased quail productivity and genetic performance through reciprocal crossbreeding (L×U) with Ukrainian quails. To evaluate these results and create breeding plans that will enhance quail performance in regional settings, more research is required.

ACKNOWLEDGMENT

The author would like to thank the University of Mosul / College of Agriculture and Forestry and Nineveh Research Department for their provided facilities in this research.

CONFLICT OF INTEREST

The authors state that there are no conflicts of interest with the publication of this work.

الأداء الإنتاجي والتشابه الوراثي في السمان الاوكراني والمحلي البني اللون

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الخلاصة

نفذت هذه الدراسة للتعرف على الأداء الإنتاجي والوراثي في خطين من السمان الاوكراني (U) والمحلي (L) البني اللون والتضريب (U×L) والتضريب التبادلي (L×U) الناتج في حقول دائرة البحوث الزراعية للفترة من 1-3-2023 ولغاية 1-6-2023. إذ قدر أداء الطيور المختلفة لمدة 8 أسابيع لنسبة انتاج البيض / أنثى الكلي ووزن البيض التراكمي وكفاءة التحويل الغذائي غم علف / غم كتلة بيض. كما قدر التشابه الوراثي والمسافة الوراثية بين ذكور واناث المجموعات تحت الدراسة. أظهرت النتائج وجود زيادة معنوية (أ < 0.05) للسمان الاوكراني والتضريب التبادلي (L×U) في وزن البيض التراكمي (589.37، 560.25) g ونسبة انتاج البيض (74.86 و72.77) % وتحسن معنوي (أ < 0.05) في كفاءة التحويل الغذائي (4.38 و3.93) غم علف / غم كتلة بيض مقارنة بالسمان المحلي والسمان الناتج من التضريب (U×L). وأظهرت نتائج التحليل الوراثي اعلى تشابه (0.8537) بين ذكور واناث التضريب (U×L) واقل تشابه وراثي (0.5244) بين الذكور المحلية واناث التضريب التبادلي (L ×U) وجاءت نتائج المسافة الوراثية مؤكدة لما سبق إذ كانت اقل مسافة وراثية بين بين ذكور واناث التضريب (U×L) (0.1582) واعلى مسافة وراثية (0.6455) بين الذكور المحلية واناث التضريب التبادلي (L ×U).

الكلمات المفتاحية: السمان الاوكراني والمحلي، الأداء الإنتاجي، التشابه والمسافة الوراثية.

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