Molecular characterization of genetic biodiversity in ducks, using RAPD-PCR analysis

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ABSTRACT

This study aimed at elucidating the genetic variation within and between duck populations and estimating the phylogenetic relationships among them. Five duck breeds of two species, Muscovy and Sudani of Cairina species, and White Pekin, Damietti and Khaki Campbell of Anas species, were used. The technique of random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR) was applied using five random primers. Individual DNA samples within breed and also a bulk of DNA samples for each breed were used. Primers amplified bands with an overall mean of 8.45 and 8.68 bands for individual and pooled samples, respectively. No significant difference was observed between pooled and individual samples indicating the reliability of mixing DNA samples within breed. High levels of polymorphism and heterozygosity between breeds were obtained. Two primers (OPC-08 and OPC-11), resulted in highly polymorphic markers for duck genomes. Specific bands were obtained for species and also for breeds. The overall mean of genetic variability indices within breed was low to moderate and averaged 0.38, whereas band sharing levels within breed were high and averaged 0.73. Variability estimates between breeds were 0.47 and 0.35 for individual and pooled samples respectively, whereas band sharing estimates were 0.63 and 0.74. Genetic distance indices between breeds ranged between 0.264 and 0.728.

***Keywords**: RAPD-PCR, duck genome, polymorphism, genetic distance.*

INTRODUCTION

Some livestocks, which have been occasionally consumed in the past, are presently raised intensively and commercially. Ducks are among these livestocks. Because of the steady increase of duck meat consumption, duck farming and production currently receive much attention. Therefore, there is a recent interest in research and development of duck production, and thus in duck breeding. Breeding needs information on genetic background about ducks, particularly the genetic variation. In fact, very few reports are available about genetic information on duck populations (Pingel, 1990; Knust *et al.* 1995; Romboli, 1995). With the recent advances in techniques in molecular genetics, the detailed genetic information of animals is available with high accuracy compared to the information obtained by pedigree relationship and trait phenotypes. Such techniques have been successfully employed to address the genetic variation and, in turn, the genetic diversity among different

populations, which can help in breeding programs.

The association between molecular techniques and conventional animal breeding methods to identify animals with higher genetic potential tends to maximize the genetic gain for the traits of interest (Schmidt *et al*., 2000). Few studies have been recently performed to assess the genetic polymorphism in ducks using DNA fingerprinting technique. Maak *et al.* (2000) developed microsatellite markers for White Pekin and Muscovy ducks. Also, Dolmatova *et al.* (2000b) studied the possibility of using RAPD markers for the detection of differences among lines of White Pekin ducks. It was reported that genetic distances precisely reflected even the slight changes that occurred in the genetic structure during breeding. The polymorphism in DNA bands for six duck breeds was also studied by TianFang *et al.* (2002), using RAPD procedure. The results showed that nine out of 40 arbitrary primers amplified clear and reproducible bands. The phylogenetic distance between Muscovy and the domesticated ducks was high. Dolmatova *et al.* (2000a) studied the genetic polymorphism in ducks using RAPD-PCR analysis to differentiate between White Pekin and Muscovy ducks. The obtained pattern of breed clustering adequately reflected the actual genetic background known from the history and genealogy of breeds. The RAPD procedure was applied to DNA of fowls, ducks and geese by Shiau *et al.* (1996), using 40 primers. Most of the primers identified DNA polymorphism in the three species. Also, female-specific bands, by species, were observed.

In Egypt, local breeds of ducks are adapted to living in the subtropical conditions. Such breeds should therefore be considered important resources for agricultural development, when their genetic compositions are accurately studied and properly used. The objectives of the present study were to evaluate the genetic variation within and between breeds of ducks and the molecular characterization for the local breeds of ducks, and its relationship with tolerance to subtropical conditions.

MATERIALS AND METHODS

Twenty five mature individuals of five duck closed populations, five individuals for each, were used in this study. The populations were of two exotic breeds, Muscovy (M) and White Pekin (P); two local breeds, Sudani (S) and Damietti (D); and a breed for table egg production, Khaki Campbell (K). Mature birds were weighed, and 10 ml of blood were collected from the wing venous in plastic autoclaved tubes containing ethylenediamine tetra acetic acid (EDTA) as anticoagulant. Blood samples were then refrigerated at -20°C until use.

Extraction of DNA, RAPD-PCR procedures and Gel electrophoresis

DNA extraction was carried out on each individual sample, using Puregene blood kit (Gentra systems, Minneapolis, Minnesota, USA). Equal amounts of the individual DNA samples, by breed, were drawn and mixed together to get a mixed (pooled) DNA sample.

The RAPD-PCR analysis was carried out on a mix composed of 5 µl of 10X buffer, 5 µl dNTPs, 10 µl primer, 2 µl $MgCl_2$, 10 çg genomic DNA, and 0.2 unit Gold-Taq DNA polymerase, and sdH_2O was added to the mix to get a total volume of 50 µl. The PCR program was carried out using Gene Amp PCR system 2400 (Perkin-Elmer corp., Norwalk, CT., USA). Five random 10-mer primers, with GC contents of 60-70%, were used in this study. The sequences of primers are shown in Table (1). The primers were synthesized on an ABI392 DNA/RNA

synthesizer (Applied Biosystems, Foster City, CA., USA). The RAPD-PCR analysis was applied to the individual and pooled samples, by breed. The amplified DNA fragments were separated to their molecular weights using electrophoresis on 1.7 % agarose gel prepared in 1X TAE buffer. Two standard molecular markers, 1-Kb and 100-bp ladders, were used to determine the molecular weights of the amplified bands. Gels were visually examined under UV light using ethidium bromide. All successful agarose gels were exposed to Polaroid films.

Parameters and statistical analysis

The gel photographs were then developed and used to estimate the following parameters:

1. Heterozygosity (H): Heterozygosity was calculated according to Ott (1992) as:

$$H = 1 - \sum P_i^2$$

where, P_i is the frequency of i^{th} allele among a total of *l* alleles.

2. Band sharing (BS): All possible pairwise comparisons of amplified bands of any two individual or pooled samples on the same gel were made. The following formula of Jeffreys and Morton (1987) and Lynch (1990) was used:

$$BS = \frac{2(B_{ab})}{B_a + B_b}$$

where, BS indicates band sharing level, B_{ab} indicates number of bands shared by samples a and b, B_a and B_b are the total numbers of bands of samples a and b.

3. Genetic variability (GV): According to Kuhnlein *et al.* (1989), genetic variability indices within and between breeds were estimated, using the following equation:

$$GV = 1 - \frac{1}{N} \sum_{i=1}^{N} v_i$$

where, v_i is the frequency of band *i* in all individuals within or between breeds and *N* is the total number of bands scored within or between breeds.

4. Genetic distance (D): The indices of genetic distance between breeds were calculated according to the following formula of Kuhnlein *et al*. (1989) as:

$$D = -\ln (I)$$

where I is the genetic identity index computed according to the equation:

$$I = \frac{1}{N} \sum_{i=1}^{N} \frac{2\ V_i^{(1)} \cdot V_i^{(2)}}{(V_i^{(1)})^2 + (V_i^{(2)})^2}$$

where, *N* is the number of different bands in two given breeds and $V_i^{(1)}$ and $V_i^{(2)}$ are the frequencies of band *i* in the two breeds, respectively.

5. Phylogenetic analysis: The dendograms of phylogenetic relationships between different breeds were constructed. The computer program "PhyloDraw", designed by Choi *et al.* (2000), was used based on the genetic distance indices.

The statistical analysis system (SAS, 1999) was applied to the data set for analyzing breed effect on body weight, genetic variability and band sharing levels. Multiple-range test of Duncan (1955) was used to separate means, whenever significance of breed effect was shown.

RESULTS AND DISCUSSION

Number of bands and molecular size

All primers showed successful amplification of DNA fragments in all individual genomes. Primers amplified 1056 bands with an overall mean of 8.45 bands/individual (Table 1). The number of bands varied among breeds between 4 and 13 bands. The molecular size ranged between 150 and 2800 bp. TianFang *et al.* (2002) used RAPD analysis and 40 primers on the genomes of six duck breeds, and reported band number averaging 3 to 13 bands/primer, with

band sizes varying between 200 and 2000 bp. Individual band numbers within breed significantly differed by using different primers, and this was obvious in Muscovy, Damietti and Khaki Campbell breeds. When pooled DNA samples were used, the average of band numbers, overall breeds and primers, was 8.68 band/pooled sample, with band sizes of 230 to 2800 bp (Table 2). The band numbers obtained using pooled samples were statistically examined for reliability (Table 2). The degree of accuracy of mixing individual DNA samples was obtained. It indicated the probability that any band, appearing in individual samples could be denied in pooled samples, was extremely low with an overall average of 0.005757. Also, no significant difference was observed between the averages of band numbers obtained by individual samples and those of pooled samples, using the t statistical test. Mixing DNA samples of individuals of the same population or even pooled blood samples has been successfully used in studying chicken genomes (Ponsuksili *et al.,* 1996; El-Gendy *et al.,* 2000; Lipkin *et al*., 2002).

Table (1): Total and average number of DNA bands, by breed and primer (Individual samples).

Primer	Sequence (5'-3')	% of total bands	Molecular weight range (bp)	Average of DNA band numbers					Summary		
				Muscovy	Sudani	White Pekin	Damietti	Khaki Campbell	Average overall individuals±SE	*Cairina* sp.	*Anas* sp.
OPC-06	GAACGGACTC	24.24	230-2150	10.60^{a}	10.40	9.40	10.80 ^{a}	10.00^{a}	10.24±0.25	10.50	10.06
OPC-08	TGGACCGGTG	20.08	270-2800	9.80^{ab}	8.40	7.40	7.60 ^{bc}	9.20^{ab}	8.48±0.46	9.10	8.06
OPC-11	AAAGCTGCGG	18.47	150-2400	8.20^{bc}	9.40	8.00	6.60 ^{c}	6.80^{bc}	7.80±0.51	8.80	7.13
OPC-16	CACACTCCAG	19.70	220-2100	9.40^{abc}	9.20	7.60	9.00 ^{ab}	6.40^{c}	8.32±0.57	9.30	7.66
OPC-19	GTTGCCAGCC	17.52	400-1800	7.60 ^{c}	7.40	6.40	7.80 ^{bc}	7.80^{abc}	7.40±0.26	7.50	7.37
Total		100		45.60	44.80	38.60	41.60	40.20	42.16±1.34	45.20	40.30
Average				9.12	8.96	7.76	8.36	8.04	8.45±0.26	9.04^{X}	8.06 ^{Y}

$^{a, b, c}$, means with different superscripts within the same column are significantly different ($P \leq 0.05$).
$^{X, Y}$, means of different species with different superscripts are significantly different ($P \leq 0.05$).

Table (2): Average number of DNA bands, by breed and primer (Pooled samples).

Primer	**% of total bands**	**Molecular weight range (bp)**	**Average of DNA band numbers**					**Summary**		
			Muscovy	Sudani	White Pekin	Damietti	Khaki Campbell	Average overall individuals ± SE	*Cairina* sp.	*Anas* sp.
OPC-06	20.74	230-1800	9	10	8	10	8	9.00±0.45	9.5	8.7
OPC-08	23.50	270-2800	11	9	10	12	9	10.20±0.58	10.0	10.3
OPC-11	22.58	270-2100	11	11	10	9	8	9.80±0.58	11.0	9.0
OPC-16	20.28	230-1800	10	10	8	8	8	8.80±0.48	10.0	8.0
OPC-19	12.90	400-1600	5	4	6	6	7	5.60±0.51	4.5	6.3
Total	100.00		46.0	44.0	42.0	45.0	40.0		45.0	42.3
Average			9.2	8.8	8.4	9.0	8.0	8.68±0.22	9.0	8.5

Reliability of the patterns of DNA fingerprints obtained from pooled samples

Accuracy degree analysis		t statistical analysis[1]		
Primer	Accuracy degree ($\bar{X}$ ± SE)	Breed	Individual Samples	Pooled samples
OPC-06	0.000092±0.000045		M	9.12	9.2
OPC-08	0.008240±0.003427		S	8.69	8.8
OPC-11	0.016872±0.005583		D	7.76	8.4
OPC-16	0.003229±0.001317		P	8.36	9.0
OPC-19	0.000354±0.000181		K	8.04	8.0
			df = 4		
$\bar{X}$ ± SE	0.005757±0.013933		P (T ≤ t) = 0.1230 (not significant)		

[1] , t statistical analysis was for the comparisons between number of bands, overall primers and by breed, generated form individual samples and those of pooled samples.
M, S, P, D and K indicate Muscovy, Sudani, White Pekin, Damietti and Khaki Campbell breeds, respectively.

Polymorphism

Summary of the polymorphic information between and within species is presented in Table (3). All primers amplified bands with polymorphic patterns between species. The number of polymorphic loci varied between 83% to 100% of the total bands. The average heterozygosity overall detected loci in individual birds of both species varied between 0.52 to 0.81. Ott

(1992) considered a genetic marker highly polymorphic when it amplifies bands with a heterozygosity estimate of more than 0.70. Accordingly, primers OPC-08 and OPC-11 resulted in highly polymorphic markers, where they amplified bands with average heterozygosity levels of 0.73 and 0.81, respectively. The high percentage of polymorphic bands and high heterozygosity levels, are expected since individual birds are of five different breeds of two different species. Polymorphism in distant species was reported by Shiau *et al.* (1996), where DNA bands were produced by RAPD procedure and successfully used to differentiate between chickens, ducks and geese. Also, Siripholvat and Tragoonrung (1998) and TianFang *et al.* (2002) reported polymorphic patterns in DNA bands of different duck breeds, belonging to both species *Cairina* and *Anas*.

Species-specific bands were also amplified by different primers (Table 3). Primer OPC-06 classified one band with molecular size of 2150 bp as a *Cairina*-specific band (Fig. 1). However, primer OPC-11 detected two bands of 450 and 400 bp specific for individuals of *Cairina* species versus a specific band of 500 bp for individuals of *Anas* species (Fig. 2). Also, primer OPC-16 amplified three bands of 1000, 530 and 220 bp specific for individuals of *Cairina* species versus a band of 300 bp specific for individuals of *Anas* species (Fig. 3). Huang *et al.* (2003) recognized DNA bands specific for female Chinese geese, which could be used for sex determination. The primers also detected monomorphic alleles specific for species (Table 3). Primer OPC-06 amplified a monomorphic band with molecular size of 360 bp in individuals of *Cairina* species. However, primer OPC-16 detected a monomorphic allele of 760 bp in individual birds of *Cairina* species versus a monomorphic allele at 800 bp in individuals of *Anas* species. On the other hand, two loci with monomorphic patterns were detected in individuals of the native breeds; Sudani and Damietti. One locus was detected at 1400 bp by primer OPC-08 and another at 900 bp by primer OPC-11. The significance of both loci to adaptation to local environmental conditions is, therefore, probable. Such results indicate the genetic specificity of different species and breeds. In chickens, Sharma *et al.* (2001) demonstrated the presence of monomorphic bands characterizing different breeds. The average heterozygosity estimates were, in general, less within either *Cairina* or *Anas* species than those estimated between species, revealing the less variation within species compared to that between species (Table 3). Several breed-specific monomorphic alleles were also shown within *Cairina* or *Anas* species.

The allele frequency in some loci varied between breeds in a trend that seemed to be related to the classification of breeds according to type of production. For instance, the frequency of the band of 230 bp primed by primer OPC-06 was 1.0 (monomorphic) in Muscovy, and reached 0.8 in Sudani, less frequent in each of Damietti and White Pekin (0.2) and was 0.0 in Khaki Campbell birds (Fig. 1). Muscovy is classified as a meat breed, Sudani and White Pekin are also meat breeds but gain less, Damietti is a light breed, and Khaki Campbell is a breed for egg production. Similar trends of allele frequency were also observed for bands amplified by primer OPC-08 at 2100 and 400 bp, and for bands amplified by primer OPC-16 at 2100, 1900, 1700 and 270 bp (Fig. 3). Furthermore, some alleles were polymorphic in local breeds only, but monomorphic in the other breeds. Primer OPC-08 amplified a band of 530 bp with polymorphic pattern in only Sudani and Damietti breeds. This pattern may express the relationship of the locus to the survival under local conditions, too. Appropriate trials are

perhaps needed to precisely assess the relationship between band frequency and type of production or surviving local conditions.

The polymorphic nature of many bands amplified by the primers was also obvious within breeds. The percentage of polymorphic bands greatly varied by primers and breeds. It ranged between 18.2% within Khaki Campbells using primer OPC-06 and 94.4% within White Pekins using primer OPC-11. The average heterozygosity estimates within different breeds were apparently less than those estimated within or between species. The primers also detected alleles specific for certain breeds. Primer OPC-06 detected a polymorphic band with molecular size of 1850 bp specific for Muscovy ducks, and another polymorphic band of 1400 bp specific for Damietti ducks (Fig. 1). The results obtained from pooled samples were, in general, in agreement with the results obtained from individual samples. The primers, except primer OPC-19, amplified a variety of bands at different molecular sizes specific for *Cairina* species. Whereas, only the two primers OPC-11 and OPC-19 amplified bands specific for *Anas* species (Fig. 4). The results of polymorphism demonstrate the efficiency of the used primers to assess the genetic specificity and reflect the genetic diversity in duck breeds. In the study of Maak *et al.* (2000), microsatellite markers were developed for ducks and used successfully to study biodiversity and population structure.

Table (3): Summary of between-, and within-species polymorphism generated by the primers (Individual samples).

Parameter		Primers				
		OPC-06	OPC-08	OPC-11	OPC-16	OPC-19
				Between species		
# bands		17	19	21	17	12
# polymorphic bands		15	19	21	15	10
% polymorphic bands		88.20	100.00	100.00	88.20	83.30
$\bar{X}$ heterozygosity [1]		0.53	0.73	0.81	0.67	0.52
Species specific band:	*Cairina*	1	-	2	3	-
	Anas	-	-	1	1	-
Monomorphic band:	*Cairina*	1	2	1	1	-
	Anas	-	-	-	1	1
	Natives	-	1	1	-	-
				Within *Cairina* species		
# bands		16	15	18	16	11
# polymorphic bands		10	13	17	13	9
$\bar{X}$ heterozygosity [1]		0.42	0.50	0.68	0.55	0.42
Monomorphic band:	M	3	4	3	3	4
	S	-	1	2	-	1
				Within *Anas* species		
# bands		15	18	19	14	12
# polymorphic bands		13	18	19	11	9
$\bar{X}$ heterozygosity [1]		0.39	0.78	0.77	0.50	0.52
Monomorphic band:	P	3	2	1	-	-
	D	5	1	1	2	1
	K	5	3	2	-	3

[1], average heterozygosity overall amplified bands.
M, S, P, D and K indicate Muscovy, Sudani, White Pekin, Damietti and Khaki Campbell breeds, respectively.

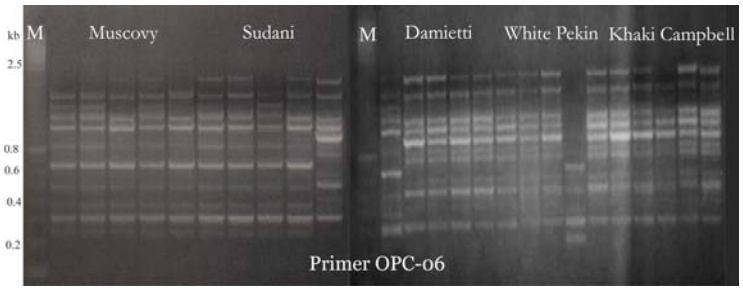

Fig. (1): RAPD profile of individual samples generated by primer OPC-06.

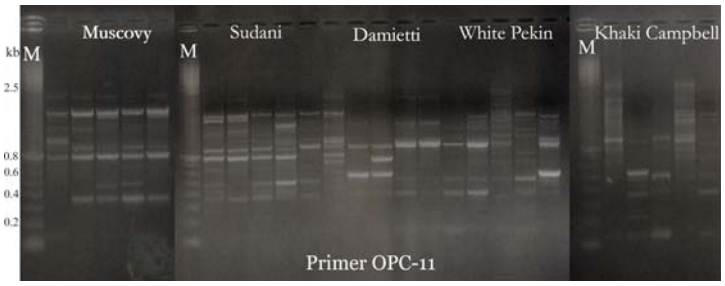

Fig. (2): RAPD profile of individual samples generated by primer OPC-11.

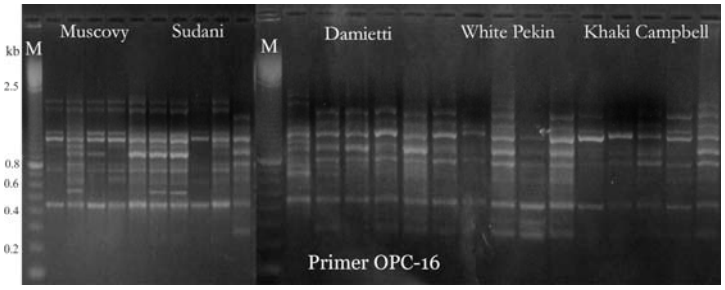

Fig. (3): RAPD profile of individual samples generated by primer OPC-16.

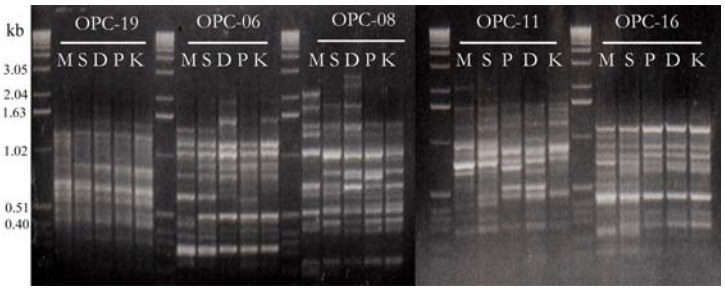

Fig. (4): RAPD profile of pooled samples of Muscovy (M), Sudani (S), Damietti (D), White Pekin (P) and Khaki Campbell ducks (K).

Genetic variability and band sharing estimates

1- Within breeds: The Genetic variability and band sharing indices within breeds using different primers are presented in Table (4). The genetic variability within breeds were in general low to moderate. The averages, overall primers, significantly differed and ranged between 0.27 in Muscovy ducks to 0.44 in White Pekin and Damietti ducks. The levels of band sharing were in general high, and were the highest for Muscovy ducks with an average, overall primers, of 0.83, and were the lowest within White Pekin and Damietti breeds with an average of 0.68 for each. The fairly low to moderate genetic variability and high similarity observed within each breed, may reflect keeping breeds as small closed populations. Thus some degree of inbreeding may be expected, increasing homozygosity within breeds. It can therefore be concluded that breeding history of the populations can be studied using the patterns of RAPD fingerprints. Such conclusion agree with Dolmatova *et al.* (2000b), Maak *et al*. (2000) and Singh and Sharma (2002), about the possibility of using genetic markers and estimates of genetic variability to reflect the changes in genetic structure of duck and chicken populations.

2- Between Breeds: Using individual samples, the genetic variability index between Muscovy and Sudani breeds averaged 0.35 overall primers. However, higher genetic variability estimates with an average of 0.53 were observed between Muscovies and each of the breeds White Pekin, Damietti and Khaki Campbell. Also, genetic variability estimates of high magnitude were obtained between Sudani ducks and any of White Pekin, Damietti and Khaki Campbell breeds, with an average of 0.51 overall estimates. However, the genetic variability indices among White Pekin, Damietti and Khaki Campbell breeds were somewhat similar to that obtained between Muscovy and Sudani breeds with an average of 0.39. The same tendency was found for the genetic variability and band sharing indices obtained among different breeds using pooled samples.

High levels of band sharing were found between Muscovy and Sudani breeds with the highest average of 0.74 overall primers. The band sharing levels among White Pekin, Damietti and Khaki Campbell breeds were also high and averaged 0.67. However, those between Muscovy or Sudani breeds and any of White Pekin, Damietti and Khaki Campbell breeds averaged 0.57 or 0.59, respectively. The average band sharing level between Muscovy and White Pekin breeds was the smallest (0.53). Similar trend of band sharing levels among different breeds, with higher magnitude, was also found using pooled samples. The results indicate the presence of less variation between breeds of *Cairina* species and also between breeds of *Anas* species, compared to the variation obtained between breeds of different species. Such results agree with the expectation that birds of different species show distinct differences among them. These differences are ascribed to the differences in their genetic backgrounds, and influence the overall performance of birds in meat and egg production. The efficiency of RAPD markers to assess the genetic variability and similarity within and between populations of different strains, breeds or species was reported in chickens (Wei *et al.,* 1997; Singh and Sharma, 2002), and in chickens, quail and guinea fowl (Hoshi *et al.,* 2002).

Table (4): Genetic variability and band sharing indices within breeds, by primer (Individual samples).

Primer	Muscovy	Sudani	White Pekin	Damietti	Khaki Campbell	$\bar{X}$ ± SE
			Genetic Variability			
OPC-06	0.15	0.27	0.25	0.26	0.08	0.20 ± 0.04
OPC-08	0.25	0.50	0.59	0.58	0.51	0.49 ± 0.06
OPC-11	0.47	0.47	0.62	0.65	0.58	0.56 ± 0.04
OPC16	0.35	0.48	0.35	0.37	0.40	0.39 ± 0.02
OPC-19	0.15	0.31	0.38	0.36	0.20	0.28 ± 0.05
$\bar{X}$ ± SE	0.27 ± 0.61[b]	0.41 ± 0.05[a]	0.44 ± 0.07[a]	0.44 ± 0.07[a]	0.35±0.09[ab]	0.38 ± 0.03
			Band Sharing			
OPC-06	0.92	0.81	0.84	0.84	0.96	0.87 ± 0.02
OPC-08	0.84	0.61	0.66	0.54	0.63	0.66 ± 0.05
OPC-11	0.67	0.68	0.51	0.51	0.54	0.58 ± 0.04
OPC16	0.80	0.68	0.62	0.74	0.68	0.70 ± 0.03
OPC-19	0.91	0.81	0.75	0.78	0.89	0.83 ± 0.03
$\bar{X}$ ± SE	0.83 ±0.05[a]	0.72 ± 0.04[b]	0.68 ± 0.06[b]	0.68 ± 0.07[b]	0.74 ± 0.08[b]	0.73 ± 0.03

[a, b], means with different superscripts within a raw are significantly different ($P \leq 0.05$).

Genetic distance and phylogenetic analysis

Genetic distance indices between breeds are presented in Table (5). Breeds of *Cairina* species (Muscovy and Sudani) showed more distances to each other (0.405), compared to the distances between breeds of *Anas* species (White Pekin, Damietti and Khaki Campbell), which ranged from 0.264 to 0.383. However,

Muscovy and Sudani breeds were more distant from White Pekin, Damietti and Khaki Campbell breeds, where the genetic distance indices ranged between 0.477 and 0.728. These results confirm the results of the estimations of genetic variability and band sharing between species. Ruane (1999) and Nagamine and Higuchi (2001) reported the usefulness of genetic distances to classify and elucidate the evolutionary relationship between populations, level of genetic variation as well as history of animals. The significance of using the genetic distance estimates to assess biodiversity, population structure and genetic changes in White Pekin and Muscovy ducks was reported by Dolmatova *et al.* (2000a; 2000b) and Maak *et al.* (2000). A dendogram of phylogenetic relationships, was constructed based on the genetic distance indices (Fig. 5). It appears that Sudani breed is the closest to Muscovy. Also, Muscovy breed was most distant from the other breeds. The large distance between Muscovy and Khaki Campbell may reflect their different production trends. The narrow distance between Sudani and Damietti breeds may reflect their being native breeds. It is expected that they share specific genetic composition which interacts favorably with the environmental conditions. TianFang *et al.* (2002) revealed the distant phylogenetic relationship between Muscovy ducks and domesticated ducks and the close relationships between Chinese native breeds of ducks. Also, Dolmatova *et al.* (2000a) reported similar dendogram patterns among different duck populations using different primers and methods of population construction. It was reported that the dendograms adequately reflected the actual genetic backgrounds of duck populations.

Table (5): Genetic distance indices between different breeds, by primer (Individual samples).

Species	Breed	OPC-06	OPC-08	OPC-11	OPC-16	OPC-19	$\bar{X}$ ± SE
Within *Cairina* species	M↔S	0.645	0.313	0.446	0.216	0.403	0.405 ± 0.719
Between breeds of different Species	M↔P	0.792	0.645	0.689	1.003	0.512	0.728 ± 0.082
	M↔D	0.739	0.759	0.783	0.559	0.435	0.655 ± 0.068
	M↔K	0.831	0.479	0.894	0.897	0.251	0.670 ± 0.130
	S↔P	0.451	0.379	0.634	0.783	0.377	0.525 ± 0.080
	S↔D	0.490	0.267	0.604	0.611	0.411	0.477 ± 0.064
	S↔K	0.490	0.509	0.942	0.734	0.726	0.680 ± 0.083
Within *Anas* species	P↔D	0.274	0.509	0.469	0.374	0.204	0.366 ± 0.057
	P↔K	0.100	0.414	0.438	0.092	0.278	0.264 ± 0.074
	D↔K	0.352	0.407	0.493	0.396	0.267	0.383 ± 0.037

M, S, P, D and K indicate Muscovy, Sudani, White Pekin, Damietti and Khaki Campbell breeds, respectively.

Banding patterns and quantitative trait interaction

The significant effect of breed on adult body weight was observed. It may be worth to state that significant phenotypic correlation coefficients (0.61 and 0.44) were obtained between adult body weight and band sharing levels for bands amplified by primers OPC-11 and OPC-16 respectively, regardless of breed. This implies that many of the bands amplified by both markers certainly influence body weight in ducks. Accordingly, both primers may be used to identify alleles for body weight in ducks, regardless of the genetic background. The association of DNA bands and genes coding for quantitative traits were reported by Dunnington *et al.* (1993), in chickens. Dunnington *et al.* (1992) detected a DNA band in chickens associated with shank length and body weight and was an effective predictor of phenotype of both traits.

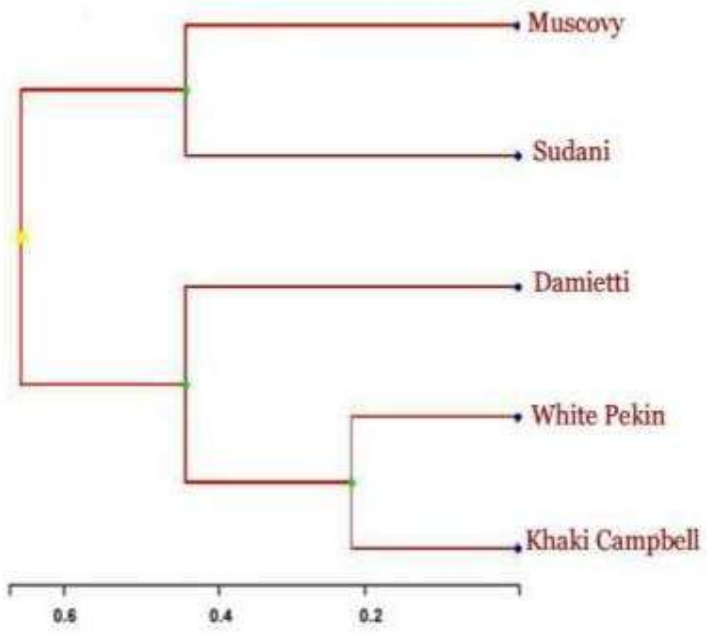

Fig. (5): Dendogram of the phylogenetic relationships between duck breeds using individual samples.

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الملخص العربي

التوصيف الجزيئي للتنوع الوراثي في سلالات البط باستخدام طريقة RAPD-PCR

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أجريت هذه الدراسة بهدف تقييم التباين الوراثي داخل وبين سلالات البط، حيث استخدمت خمس سلالات تتبع نوعين مختلفين وراثياً: المسكوفي والسوداني وهما نوعان من الجنس *Cairina*، والبكيني الأبيض والدمياطي والكاكي كامبل وهي أنواع تتبع الجنس *Anas* . وباستخدام خمس بادئات تم تضخيم المادة الوراثية (الدنا) للسلالات المختلفة بطريقة RAPD-PCR، وقد كان التضخيم بشكل فردي داخل كل سلالة، كما تم خلط العينات الفردية لتكوين عينة واحدة ممثلة لكل سلالة.

كان متوسط عدد شرائط الدنا التي تم تضخيمها ٨,٤٥ و ٨,٦٨ شريطاً في العينات الفردية والمخلوطة علي التوالي، ولم تكن الاختلافات بين الطريقتين معنوية، وكانت قيم تعدد المظهر (Polymorphism) ونسبة الخلط (Heterozygosity) عالية جداً، وتم اعتبار البادئين OPC-08, OPC-11 من البادئات متعددة المظهر في المواقع الوراثية الخاصة بجينوم البط بشكل كبير، كما تم تحديد الشرائط المميزة سواءاً للسلالات أو الأنواع المختلفة.

كان متوسط قيم التباين الوراثي داخل السلالات هو ٠,٣٨ ، بينما ارتفعت نسبة المشاركة في شرائط الدنا المتشابهة لتصل إلي ٠,٧٣، أما عن قيم التباين الوراثي بين السلالات فقد كانت ٠,٤٧ و ٠,٣٥ في العينات الفردية والمخلوطة علي التوالي، بينما كانت قيم المشاركة في شرائط الدنا بين السلالات ٠,٦٣ و ٠,٧٤ ، وتراوحت المسافة الوراثية بين ٠,٢٦٤ و ٠,٧٢٨ ، وأظهرت النتائج أن المسافة الوراثية بين المسكوفي وهي سلالة إنتاج لحم والكاكي كامبل وهي سلالة إنتاج بيض كانت كبيرة (٠,٦٧٠) وهو ما قد يعكس بقدر كبير ما بين السلالتين من اختلافات وراثية تؤثر علي الصفات الإنتاجية .