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Morphological description and C-banding karyotype of Baladi Pigeon (*Columba livia*) occurring in Egypt

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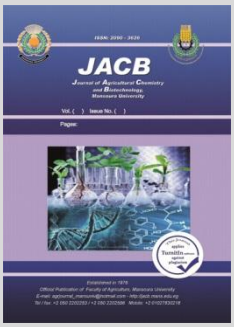

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ABSTRACT

The current work provides a detailed morphological and cytogenetic study of the Egyptian Baladi pigeon (*Columba livia)* collected from three localities (Maghagha, Samalout, Mallawy) of Minia, (Egypt) to describe its morphometric profiling and karyotype through conventional staining and C-banding techniques. Results showed that, Pigeon birds were morphologically diverse and exhibited variations in 15 studied traits particularly those of body size, head, beak size, and appendage length. Likewise, karyotype analysis showed a diploid number (2n=80) that made up of 9 macro-chromosome pairs (8 pairs of autosomes and ZW sex chromosomes) and 62 micro-chromosomes. Results also showed that the macrochromosomes no.1 was the largest one in the karyotype and it is metacentric, while chromosome no.2 is large meta- or submetacentric. Chromosome no.3 is large sub-telocentric. Chromosome nos.4 and 5 were medium sub-metacentrics, while chromosome nos.6, 7 and 8 are small telocentric. Z chromosome was medium sized submetacentric, while W was small submetacentric. The karyotype formula is 1m + 5sm + 1st + 3t or 2m + 2sm + 1st + 3t. Birds collected from the three localities likely possessed similar karyotypic parameters. For instance, the total haploid lengths of the chromosome set are 63.68, 35.21and 36.94. C-band variations are clearly found among 8 investigated macro-chromosomes. For instance, chromosomes 1, 2, 3, 4, and 6 mostly have large dark heterochromatin. It could be noted that twenty to thirty of the micro-chromosomes have clear c-banding blocks that were seen in almost all examined cells. Morphometric and cytogenetic significance of these results is discussed.

Keywords: *Pigeon – morphology –cytogenetic - karyotype – C-banding*

INTRODUCTION

The pigeon (*Columba livia*) which inhabits our backyards is considered as a member of the wild pigeon (Blasco *et al.,* 2014). The feral pigeon was probably domesticated in the Middle East and Mediterranean basins at least 5,000 years ago (Domyan and Shapiro 2017). It is belonging to the Kingdom: Animalia, Phylum: Chordata, Class: Aves, Order: Columbiformes, Family: Columbidae, Genus: Columba, and species is *Columba livia*, a feral ancestor of the domesticated pigeon. The pigeon is occurred everywhere due to simple domestication (Johnston and Janiga, 1995). This may grant it the honor of being the earliest winged bird to be domesticated and, perhaps, had its phenotypic variation most changeable (Price, 2002). Pigeons have filled some of man's needs (food source, communication tool, racing pigeon) for centuries. Wild-type pigeons possess blue-grey feathers with black wing bars. Selective breeding of domestic pigeons has introduced a wide range of plumage colors and patterns due to genetic reasons such as those regulated by the melanin-producing genes and sex-linked loci (Shapiro *et al.,* 2013). Wild-type ash-red, brown, and blue represent the primary colorations. These traits are due to genetic reasons, and ash-red is a dominant one (Shapiro *et al.,* 2013). Foot feathering in pigeon has been associated with the regulation of the PITX1 and Tbx5 genes, resulting in feathered hind feet and leg bone morphological changes (Domyan and Shapiro 2016).

Morphogenesis is a most valuable tool in developmental investigation of birds. Pigeons make an excellent model for morphological variation studies. For instance, wild rock pigeon ancestors were taken and as with all domesticates, selectively bred for numerous morphological and behavioral characteristics. Particularly, those of beak and head shape that have been intensely selected and resulted in pigeon breeds at the outskirts of distribution of width, length, depth, and curvature (Helms and Brugmann, 2022 and Çelik, 2022).

The karyotypes of an organism are normally arranged in order of their decreasing size, and they are highly informative regarding the organization and the genetic composition of an organism (Ata *et al*, 2007 and 2012). The domestic pigeon possesses a karyotype of 40 chromosome pairs, which are composed of 9 macro-chromosomes and 31 micro-chromosome pairs (Shibusawa *et al.,* 2001). One of the most distinct features of the domestic pigeon karyotype is the very large number of micro-chromosomes, which are much smaller than the macro-chromosomes. Micro-chromosomes were recently discovered to be of very significant importance in the genomic evolution and diversity of birds because they contain a high number of genes and are involved in very important biological processes such as sex determination (Ata *et al*, 2017 and 2021). For pigeons, micro-chromosomes have been thought to have evolved from their ancestral birds and have undergone some evolutionary adaptations to suit their current genomic organization (Burt, 2002). These gene-rich, highly conserved micro-chromosomes were seemingly present in the common ancestor of reptiles and modern birds, suggesting their ancient evolutionary origin (Osman *et al*., 2006 and Uno *et al.,* 2012). Micro-chromosomal

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conservation and periodic rearrangement in *Columba livia* both suggest species-specific genomic adaptation and old lineage traits (Kretschmer *et al.,* 2018).

C-banding is a cytogenetic technique used to highlight specific chromosome regions, and predominantly likely heterochromatin, that appears mainly in the centromere and pericentromere areas. In the case of *Columba livia* (domestic pigeon), C-banding has been used to study the chromosome organization and investigate the C-heterochromatic distribution along with the chromosomes. C-banding has also contributed to an understanding of variation in chromosomes as well as structural evolution in pigeon species (Kretschmer *et al,* 2020). Stock *et al.,* (2008) studied the avian genome evolution and organization, as well as chromosomal rearrangements that may cause speciation and adaptation. Early taxonomic studies of bird species tended most frequently to deal with the study of morphology, plumage and behavior (Livezey, 1986 and Johnsgard, 1961). Although much studies have been keen to outline the morophological and molecular characterization of domestic pigeon (*Columba livia*), a comparatively fewer literatures were concerned about the karyological analyses (normal and C- banding patterns). Therefore, this study aimed at characterize the morphological profile and analyze the conventional and c- banding karyotypes of the Baladi pigeon (*Columba livia*), occurring in Minia province, Egypt.

MATERIALS AND METHODS

This work was carried out at the Department of Genetics, Faculty of Agriculture, Minia University, Minia, Egypt to characterize the morphological profile and perform a karyotype analysis of the Egyptian Baladi pigeon (*Columba livia*), using both conventional and C-banding techniques.

1. Morphological description

For morphological description, a total of thirty adult individuals (15♂♂ and 15♀♀) with different color types of Egyptian Baladi pigeon (*Columba livia*) were collected from different localities in El-Minia governorate (Maghagha, Samaloot and Malawy), Egypt as shown in Fig. (1).

The collected pigeons were morphologically described and photographed (Fig.2). Several external morphological measurements were recorded for each specimen using digital calipers (RUPAC, Italy). The morphometric data were statistically analyzed using SPSS software, and the results were expressed as mean values with their corresponding standard errors (Mean ± SE) to evaluate the variation among the pigeon populations.

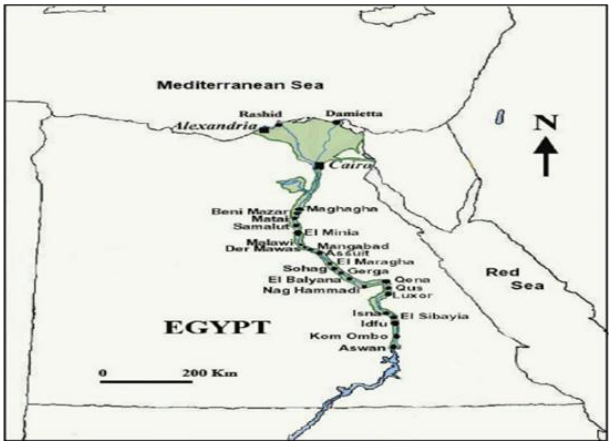

Figure 1. a map of Egypt showing the localities in Minia governorate from which the pigeon samples were collected.

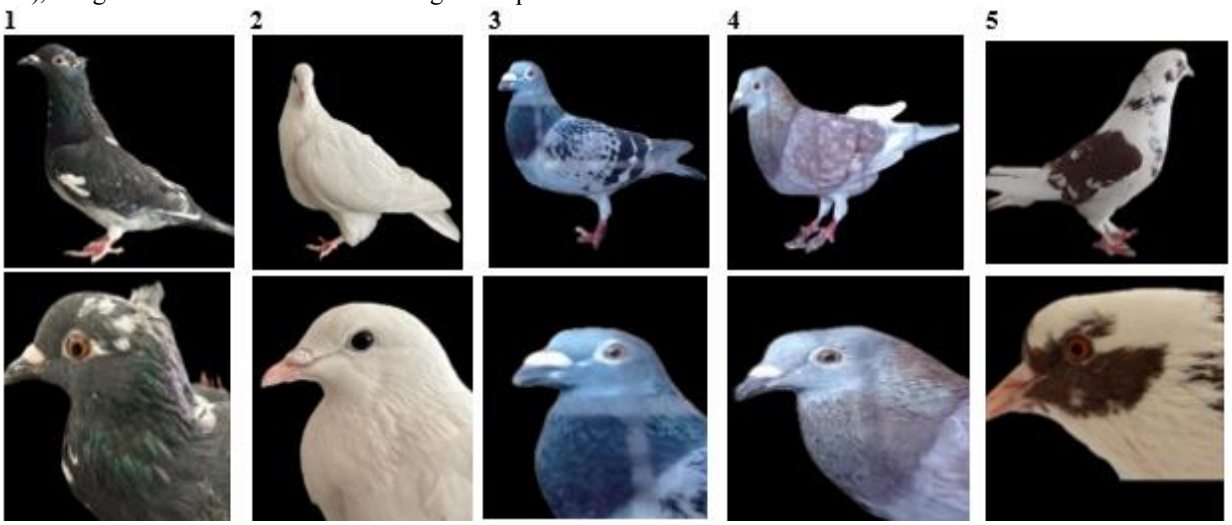

Figure 2. Illustrate some morphologically different color types (from 1-5) of Egyptian Baladi pigeon (Columba livia) collected from different localities in Minia province. Top is the whole body and the bottom is focusing on the head and beak picture of the same individual.

2. Conventional Karyotype analysis

Cytological preparations

The mitotic chromosome preparations were done according to Burt (2002) with some modifications by Ata *et al.,* (2021). The birds were injected intraperitoneally with 0.3 ml of 0.05% colchicine, 25 minutes after which the femurs and tibias were removed and washed out their bone marrow with 0.56% KCl in conical centrifuge tube. The cell suspension was incubated at 40 C° for 20 min and centrifuged at 5000 rpm for 10 min. Supernatant was decanted off and 5 ml of cold fresh prepared fixative solution (3 Methanol: 1 Acetic Acid) was added slowly without agitating the pellet and incubated at room temperature for 30 minutes. Centrifugation of re-suspended pellet was immediately performed. Supernatants were replaced with fresh fixative solution and centrifuged thrice. Minuscule drops of cell

suspension were added onto the dry clean surface of the slide using a Pasteur pipet and the cell spots were air dried at room temperature and stained with a 4% Giemsa.

Karyotype analysis

For conventional karyotyping, 30 good metaphase spreads per individual were enumerated and photographed using Olympus BX51 microscope fitted with a C-4040 zoom digital camera. Nine macro-chromosome pairs including the sex chromosomes were counted and measured using Soft Imaging System analysis software (SIS version 3.0). To approximate the total chromosome parameters such as total chromosome length, long (L), short (S) arm lengths, arm ratio (L / S) and centromere position, the rules of Levan *et al.,* (1964) were used for chromosome nomenclature and classifications. To determine the significance of variation between karyotypes of the five different color types of Egyptian Baladi pigeon (*Columba livia*), the means and standard error analysis of chromosome parameters were calculated. Karyotype ideogram was constructed using software developed by Altınordu *et al,* (2016). Karyotype software has the facility for the calculation of karyotype asymmetry indexes such as index of karyotype asymmetry (AsK) and Intra chromosomal asymmetry index (A). It can automatically or manually detect chromosome homology by chromosome length and arm ratio. The measurable parameters of karyotype are chromosome length (CL), arm ratio (AR), centromeric index (CI), relative length (RL) and karyotype measurements such as karyotype asymmetry index (AsK), Mean Centromeric Asymmetry (MCA), the total sum of haploid length of the chromosome set (THL) and Karyotype formula. The ideogram was established using Microsoft Excel 2010 software from karyological readings of white stork *Columba livia,* Baladi variety samples.

3. C-banding technique

C-banding technique was carried out following the procedure of Sumner (1972) with certain adjustments owing to our Lab. conditions (Ata *et al*.., 2005 and 2019). The slides were hydrolyzed in 0.2 N HCL at 10 o C for an hour, washed in distilled water, and stored in saturated Ba (OH) $2.8H_2O$ solution for 4-8 min at 60 C°. Slides were then washed in ethanol and incubated in 2 X SSC f or 30 minutes at 60 C°, then washed in 2X SSC. Slides were finally stained with 4 % Giemsa solution for 4-12 minutes at room temperature. A minimum of 20 metaphases spreads per bird with good quality were photographed using Olympus BX51 microscope with a C-4040 zoom digital camera. Sizes and distribution of C-band on macro-chromosomes were noted, the number of C-heterochromatin blocks per micro-chromosomes were also recorded.

RESULTS AND DISCUSSION

1. Morphological description

As shown in Table (1) a total of 15 morphological traits of Egyptian Baladi pigeons (*Columba livia*) were measured and presented as mean values with standard errors (Mean ± SE) reflecting the variation across three regions (Maghagha, Samalout, and Malawy) in Minia governorate.

Table 1. Measurements (cm) of 15 morphological characters of Egyptian Baladi pigeon (*Columba livia*) collected from different regions in Minia governorate.

Variable	Maghagha		Samalout		Malawy	
	Range	Mean± SE	Range	Mean± SE	Range	Mean± SE
Total beak length	2.1-2.5	2.37±0.13	2.4-2.8	2.60±0.12	2.4-2.6	2.47±0.07
Beak breadth	0.5-0.8	0.67±0.09	0.4-0.9	0.57±0.17	0.5-0.6	0.53±0.03
Nose length	0.5-0.6	0.53±0.03	0.5-0.7	0.53±0.03	0.3-0.7	0.60±0.15
Head length	5.4-5.5	5.47±0.03	5-5.6	5.23±0.19	5.6-6	5.73±0.13
Head breadth	1.5-1.7	1.2±0.03	1.3-1.9	1.53±0.19	1.3-1.7	1.53±0.12
Eye diameter	1.1-1.4	1.23±0.09	1.2-1.5	1.33±0.09	1.3-1.5	1.40±0.06
Distance between eye and beak	0.5-07	0.60±0.06	0.6-0.8	0.70±0.06	0.5-0.8	0.70±0.10
Neck length	5-6.4	5.80±0.42	5.5-7	6.20±0.44	5.6-5.9	6.03±0.24
Total body length without head	18.1-22	19.73±1.17	18-24.5	20.57±2.00	19.8-23	20.93±1.03
Total body length	23.4-27.5	25.17±1.22	23.6-29.5	25.97±1.80	25.4-29	26.67±1.17
Tarsus length	3.2-3.6	3.33±0.13	3.4-3.8	3.53±0.13	3.1-3.8	3.50±0.21
Foot length	6.2-7.5	6.73±0.39	6.1-6.5	6.33±0.12	5.6-6.5	6.33±0.17
Tail length	11.5-14.3	12.70±0.83	12.2-13.8	13.00±0.46	13.2-15	14.40±0.60
Number of tail feather	15-18	16.67±0.88	16-19	15.67±2.03	17-20	16.33±2.33
Thorax perimeter	4.1-6.8	5.67±0.81	5.1-7.2	6.23±0.61	4.9-6.8	6.07±0.59

Data showed subtle yet important variations in several traits, potentially linked to regional environmental conditions and genetic diversity. Beak length varied slightly across the regions, with the longest average recorded in Samalout (2.60 ± 0.12 cm). Beak breadth was widest in Maghagha (0.67 ± 0.09 cm). These differences could be associated with feeding behaviors and local environmental pressures, as beak morphology is known to be adaptive and functionally significant (Alkan *et al.,* 2013). Head length was the greatest in pigeon from Malawy (5.73 ± 0.13 cm), while eye diameter and the distance from eye to beak were also largest in this region. Larger eye size may enhance visual performance in variable light environments (Mitkus *et al.,* 2017), and regional cranial variation could reflect evolutionary divergence or adaptation (Yang *et al.,* 2020). Neck length and total body length (with and without head) tended to increase from north to south, with Malawy birds showing the highest values (e.g., body length: 26.67 ± 1.17 cm). These trends might indicate a clonal adaptation, with body size potentially playing a role in thermoregulation or mate selection (Thomas, 2004 and Padzil *et al.,* 2021). Such size differences have also been linked to flight efficiency and survival in variable landscapes. Foot length was slightly greater in Maghagha, while tail length reached its maximum in Malawy (14.40 ± 0.60 cm). Tail feather counts ranged between 15 and 20, with variability likely driven by genetic and functional factors. Tail structure in pigeons has been associated with maneuverability and sexual signaling (Johnston and Janiga, 2021). Thorax

perimeter was highest in Samalout (6.23 ± 0.61 cm), potentially indicating stronger pectoral musculature, which could enhance flight capacity. This may be associated with habitat structure or foraging range (Shafie *et al.,* 2020).

In summary, the morphological diversity observed among Baladi pigeons from different areas of El-Minia reflects possible environmental adaptation, selective pressures, and phenotypic plasticity. These findings align with previous reports on the adaptive variability of *Columba livia* in response to local ecological conditions (Thomas, 2004, Alkan *et al.*, 2013, Mitkus *et al*., 2017, Shafie *et al.,* 2020, Yang *et al*., 2020, Padzil *et al*., 2021 and Johnston and Janiga, 2021). Several studies on morphological traits of different pigeon taxa (Table 2) comparatively showed the phenomena of obvious diversity among them in different countries. The Baladi pigeon occurred in Egypt also showed quantitative and qualitative differences of 15 morphological traits reported herein. However, it could be concluded that the phenomena of the morphological divergences in pigeon lines were common and may due to outcross between genetically unknown parents.

Table 2. Morphological variations among pigeon species and their allies in different countries

Breed / Population	Head and Beak	Body Length	Color	Tail Feathers	Thorax perimeter	Reference
Angut Pigeon (Turkey)	Head crest present; beak ~18.7 mm length, ~8.6 mm depth	33.9 cm	Yellow, red, white, black variants	~13.3 cm tail length; ~12 feathers implied	Chest width 5.58 cm	Çelik, R. (2023)
Squadron Flyers (Turkey)	Bill ~17.4 mm length, ~6.8 mm depth	36.5 cm	Various	~15.2 cm tail length; ~15	Chest width ~5.60 cm	Özbaşer *et al.* (2016)
Hünkâri Pigeon (Turkey)	Mid-short beak; crested head	23 cm	Satinette / Blondinette color morphs	13.5 cm tail length; ~14	Chest width measured	Türkeş and Gündüz (2024)
Kırıkkale Tumblers (Turkey)	Beak depth significant differences (sex-linked)	Body length significant by sex (24-33) cm	Grey plumage dominant	Mostly 11, some 13–16)	Chest width by age	Özçelik *et al.* (2022)
Bangladesh Breeds (e.g., Strasser, Owl)	Bill ~28–28.8 mm; head length ~51.9 mm; depth ~10.7 mm	30.0–41.6 cm	Diverse	Mostly 12, some 11–14	Chest width not specified	Parvez *et al.* (2017)
Şanlıurfa Yapışan	Bill ~16.5 head length ~34.0 × 22.1	33.3	Diverse	Mostly 12, some 13–14	6.5	Çelik, (2022)

2. Karyotype analysis:

In general, the examined mitotic spreads of both males and females in Baladi pigeon occurring in Minia regions showed a diploid number of 2n = 80.

Data in Table (3) showed the measurements of nine macro-chromosomes including Z and W, while the remaining 31 pairs are so called micro-chromosomes. These measurements were lengths of both long (L) and short (S) arms, total length (L+S) and the arm ratio (L/S) of each macro-chromosome at metaphase spreads (Fig. 3) prepared from different color forms of pigeon collected from three localities of Minia, Egypt. Data in Table (3) also show graded macro-chromosomes size from 1 to 8. Therefore, chromosome nomenclature and karyotype could be constructed. Chromosome no.1 is the largest one with total length around 8 microns (µ) and arm ratio around 1.5 indicating that it is metacentric (M). The total length of chromosome no.2 is around 6.5 µ and its arm ratio nearly 1.5 and it is also (M). The size of chromosome no.3 is near 4.65 µ and it has arm ratio with 3.6 indicating that this chromosome is subtelocentric (sT). Chromosomes no.4 and 5 are medium sized with lengths around 3.0 µ and arm ratio near to 1.8 and classified as submetacentrics (sM). Chromosomes no.6, 7 and 8 are small sized with approximately 2.0 µ lengths and have arm ratio more than 7.0, indicating that they are telocentrics (T). Data also show that Z is medium sized submetacentric chromosome (sM) with length around 3 µ and W is small submetacentric (sM) with length 1.3 µ.

Table 3. Karyological parameters of macro-chromosomes (8 autosomes) and ZW sex chromosomes of the Egyptian Baladi pigeon (*Columba livia*), collected from different regions of Minia governorate.

parameters	localities	Chromosomes									
		1	2	3	4	5	6	7	8	Z	W
L	Maghagha	4.98	4.01	3.80	2.19	2.01	1.98	1.92	1.88	1.99	0.88
	Samalout	4.95	3.95	3.01	2.02	1.88	1.78	1.65	1.23	1.88	0.66
	Malawy	5.30	4.03	3.95	2.17	1.88	1.86	1.75	1.68	1.95	0.97
Mean ± SE		5.07±0.08	3.99±0.02	3.59±0.21	2.13±0.04	1.92±0.03	1.87±0.04	1.77±0.06	1.60±0.14	1.94±0.02	0.84±0.07
S	Maghagha	2.99	2.15	1.20	1.19	1.14	0.27	0.25	0.23	1.11	0.51
	Samalout	3.91	3.11	0.98	1.15	0.95	0.25	0.22	0.17	1.08	0.38
	Malaw	3.12	2.66	1.01	1.23	1.09	0.22	0.21	0.18	1.12	0.56
Mean ± SE		3.34±0.20	2.64±0.20	1.06±0.19	1.19±0.07	1.06±0.16	0.25±0.04	0.23±0.03	0.19±0.05	1.10±0.03	0.48±0.15
L+S	Maghagha	7.97	6.12	5	3.38	3.15	2.25	2.17	2.11	3.1	1.39
	Samalout	8.85	7.06	3.99	3.17	2.83	2.03	1.87	1.4	2.96	1.04
	Malawy	8.42	6.69	4.96	3.4	2.97	2.08	1.96	1.86	3.07	1.53
Mean ± SE		8.41±0.18	6.62±0.19	4.65±0.23	3.32±0.05	2.98±0.07	2.12±0.05	2.00±0.06	1.79±0.15	3.04±0.03	1.32±0.10
L/S	Maghagha	1.67	1.72	3.17	1.84	1.76	7.33	7.68	8.17	1.79	1.73
	Samalout	1.26	1.27	3.07	1.76	1.98	7.12	7.50	7.24	1.74	1.74
	Malawy	1.70	1.52	3.91	1.76	1.72	8.45	8.33	9.33	1.74	1.73
Mean ± SE		1.54±0.10	1.50±0.09	3.38±0.19	1.79±0.02	1.82±0.06	7.63±0.29	7.84±0.18	8.25±0.43	1.76±0.01	1.73±0.01

L= Long arm S= Short arm L+S= Total chromosome length L/S= Arm ratio

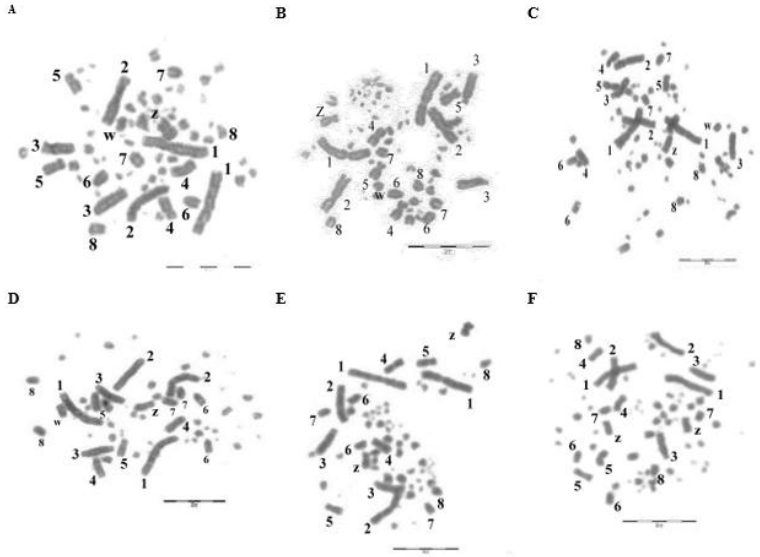

Figure 3. Metaphase spreads showing numbers of macro-chromosomes of both males and females of the Egyptian Baladi pigeon (Columba livia). A, B, C and D refers to female bird, E and F refers to male bird.

According to the software (so called KARYOTYPE) analysis, the karyotypic formula of pigeons collected from Maghagha is (1m + 5sm + 1st + 3t), while those collected from Samalout and Mallawy have Karyotypic formula (2m + 4sm + 1st + 3t) with slight difference that is represented in chromosome no.2 whether M or sM as shown in Table (4). In addition, birds collected from the three localities (Maghagha, Samalout, Mallawy) likely possessed similar other karyotypic parameters. For instance, the total haploid lengths of the chromosome set (THL) are 69.90, 65.65and 69.14. The karyograms resulted by the software are nearly similar as shown in (Fig.4) and assured the results of the karytypic formula.

The total haploid length of the chromosome set (Peruzzi *et al*., 2009), THL. Mean Centromeric Asymmetry (Peruzzi and Eroglu, 2013), MCA. Karyotype formula (Levan *et al*., 1964).

Table 4. The total haploid length of the chromosome set (THL), Mean Centromeric Asymmetry (MCA), karyotype formula, and karyotypic asymmetry (AsK) chromosomes of the Egyptian Baladi pigeon (*Columba livia*).

Birds	Parameters			
	THL	MCA	Formula	AsK%
Maghagha	36.68	40.05	2n = 1x = 1m + 5sm + 1st + 3t	69.90%
Samalout	35.21	41.63	2n = 1x = 2m + 4sm + 1st + 3t	65.65%
Malawy	36.94	45.18	2n = 1x = 2m + 4sm + 1st + 3t	69.14%

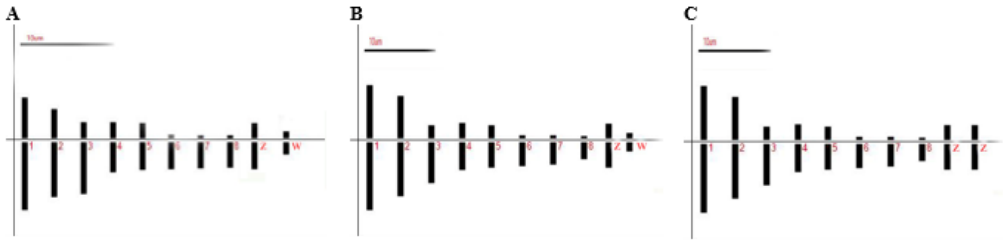

Figure 4. Karyograms showing the different categories of karyotypic formula in Egyptian Baladi pigeon (Columba livia). In A: 1m + 5sm + 1st + 3t, (B): 2m + 4sm + 1st + 3t and (C): 2m + 4sm + 1st + 3t, bar= 10 microns

The diploid number of *Columba livia* is now well established as 2n=80. Many works earlier couldn't establish the chromosome complement of pigeon particularly those linked with sex determination as suggested by Oguma (1927) and Makino *et al.* (1956). The work of De Lucca, (1984) ultimately finished the debate of this point. Thereafter, the advancement of methodological equipment and accumulative knowledge about chromosomes and genomes of family *Columbidae* were crucial.

As in Table (5) the karyotype of *Columba livia* reported herein is in agree with that reported by Kiazim, *et al* (2021) with a minute difference because its karyotype is clearly different in chromosome no.1 in addition to Z and W. Mis-karyotyping was also suggested by Makino *et al.* (1956) in which they couldn't clearly establish the centromere positions of chromosome nos.1, 4 and 6. They also couldn't find out W chromosome and counted a diploid number of 2n=79 in females leading to misunderstand in pigeon sex determining system. Another karytypic difference was also reported by Kretschmer, *et al* (2018) in which, chromosome no.1 is submetacentric while Z and W are metacentrics. It could be noted that karyotype differences within species *Columba livia* were in chromosome no.1 and sex chromosomes. The karyotypic asymmetry (AsK%) varied between 69.14% and 69.90%, indicating a moderately asymmetric karyotype, a phenomenon frequently documented in birds with well-differantiated macro- and micro-chromosomes (Waters *et al.,* 2021). Such slight differences may reflect adaptive chromosomal plasticity (O' Connor *et al.,* 2024). The moderate karyotypic asymmetry indicates a balance between structural rearrangements and conservatism of evolution, which may

impact recombination rates and genetic diversity (Zhou *et al.,* 2014). The rearrangements were the main factors affecting the intraspecific macro-chromosome variation (size and centromere position) as reported by several workers (Gunski *et al.,* 2019 Kiazim *et al*., 2021, De Boer *et al.,* 2021 and Garg 2022).

Table 5. Karyotype formula of *Columba livia* in the current study in comparison with some of those reported before.

Macro chromosome	*Columba livia*	*Columba livia var. domestica* 2n=79&80	*Columba livia* (2n = 80)	*Columba livia* (2n = 80)
1	L (M)	L (sM)	L (sM)	L (M)
2	L (M or sM)	L (sM)	L (sM)	L (M)
3	L (sT)	L (T or sT)	L (sT)	L (T or sT)
4	Medium (sM)	Medium (sM)	Medium (sM)	Medium (sM)
5	Medium (sM)	Medium (sM)	Medium (sM)	Medium (sM)
6	Small (T)	Small (T)	Small (T)	Small (T)
7	Small (T)	Small (T)	Small (T)	Small (T)
8	Small (T)	-	Small (T)	Small (T
Z	Medium (sM)	Fourth chromosome	Medium (M)	Medium (M)
W	Small (sM)	-	Small (M)	Small (M)
References	Running work	Makino *et al.,* (1956)	Kretschmer, *et al* (2018)	Kiazim, *et al* (2021)

The number and organization of the micro-chromosomes considered as cytogenetic and genomic quiz. It was difficult to count and identify them as distinct units. Modern methods of chromosome mapping and assembly facilitated the resolutions of many questions. Even some assembly errors are contemporary corrected. However, micro-chromosomes exhibit frequent recombination in addition to Robertsonian fusion and fission resulting in changes of number and structure. Micro-chromosomes exhibit a tendency towards decline in the number and in contrast increasing in the macro-chromosomes count (Tegelstrom and Ryttman, 1981 and Kretschmer *et al.,* 2020).

The submetacentric Z and W chromosomes are consistent with observation in other bird species, where Z is maintained and W tends to degenerate; the Z and W size confirms the hypothesis of progressive W chromosome degeneration, as with the mammalian Y chromosome (Zhou *et al.,* 2014). Since these are sex chromosomes, the proof shows that the metacentric/submetacentric form is predominantly preserved in all but some of the chromosomes, which suggests structural stability, desirable for successful segregation during meiosis (Kruger and Mueller, 2024).

3. C-banding patterns analysis

The distribution and quantity of heterochromatin within different chromosomes that fall into the heterochromatic regions: large dark, small dark, large faint, and small faint are shown in Fig. (5). C-band variations are clearly found among 8 investigated macro-chromosomes. Chromosomes 1, 2, 3, 4, and 6 mostly have large dark heterochromatin, and in this regard, the greatest proportions were found in Chromosome no.1 and 4. This means that these chromosomes contain large blocks of constitutive heterochromatin, commonly situated in the regions of centromeric and pericentromeric (John and Miklos, 1988).

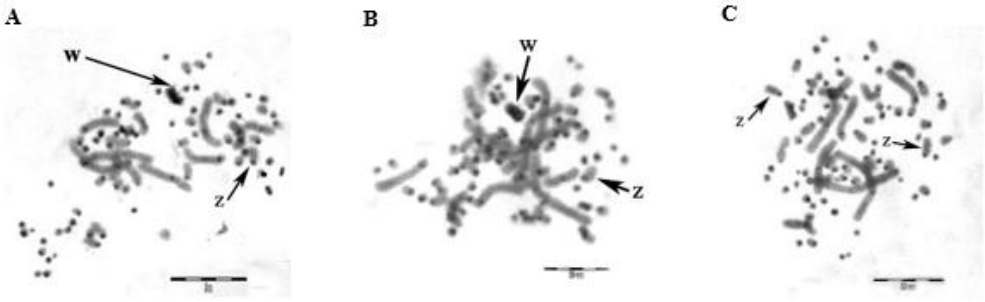

Figure 5. C-banding patterns of metaphase spreads of Egyptian Baladi pigeon (Columba livia), A and B refers to female and C refers to male arrows indicate to Z and W chromosomes).

Chromosomes 5 and 7, however, have large faint heterochromatin, which could be less compacted facultative heterochromatin, perhaps involved in gene regulation (Trojer and Reinberg, 2007). Chromosome 8 contains weak heterochromatin, indicating dispersed or less condensed heterochromatic regions, which can be linked to telomeric or interstitial heterochromatin (Pardue and DeBaryshe, 2003). The Z chromosome contains dark heterochromatin, which could indicate specialized function in sex chromosome differentiation (Charleswort *et al.,* 2005). The W chromosome is entirely heterochromatic, a shared characteristic in sex chromosomes from most species, in which heterochromatinization is linked with gene silencing and dosage compensation (Zhou *et al*., 2014). The differences in heterochromatin patterns between chromosomes imply evolutionary adaptations, perhaps connected to genome organization, recombination suppression, and epigenetic regulation (Grewal and Jia, 2007).

It could be noted that twenty to thirty of the micro-chromosomes have clear large and small dark c-banding blocks that were seen in almost all examined cells. It seems that the resemble numbers of c- banded micro-chromosomes were found in most of avian taxa (Ata *et al.,* 2005 and 2019 and Shahin *et al*., 2014). From the cytogenetic point of view c-banding methods have more difficult imposed due to the chromosome structure (Garg, 2022). So far, the identification of c-band size and situation on micro-chromosomes is still facing more complicated issues. Nowadays, the bioinformatics tools may share in resolving this problem.

CONCLUSION

Results of morphological and cytological studies of domestic pigeons revealed distinct variation among the studied

population. Hence, in the future, additional cytological and molecular studies need to be conducted, especially on pure Balady lines, as an effort to assess the genetic makeup of Balady varieties of domestic pigeons in Egypt.

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الوصف المورفولوجي والطراز الكروموسومي بتقنية C-banding للحمام البلدي (*Columba livia*) الموجود في مصر

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الملخص

يقدم هذا العمل دراسة تفصيلية للصفات المظهرية والخصائص الكروموسومية للحمام البلدي المصري (*Columba livia*) تم جمعه من ثلاث مناطق في محافظة المنيا (مغاغة، سمالوط، وملوي)، بهدف توصيف الخصائص المورفولوجية والتركيب الكروموسومي باستخدام الصبغات التقليدية وشرائط الجمزا من طراز C. أظهرت النتائج تنوعًا مورفولوجيًا ملحوظًا بين الطيور المدروسة، مع وجود اختلافات في ١٥ صفة مقاسة، خاصة في حجم الجسم، الرأس، المنقار، وطول الزوائد. وأشارت تحاليل النمط الكروموسومي إلى أن العدد الثنائي للكروموسومات(2n = 80) ، يتكون من ٩ أزواج من الكروموسومات الكبرى 8) أزواج جسمية وزوج جنسي Z و (Wو٦٢ ميكروكروموسومًا. الكروموسوم رقم ١ كان الأكبر وذو سنترومير وسطي، ورقم ٢ كبير ووسطى أو تحت وسطي، أما رقم ٣ فكان كبيرًا وتحت طرفي، في حين كانت الكروموسومات ٤ و٥ وسطية الحجم وتحت وسطية، بينما الكروموسومات ٦، ٧، و٨ صغيرة وطرفية. تميز الكروموسوم Z بكونه متوسط الحجم وتحت وسطي، أما W فكان صغير الحجم وتحت وسطي. صيغ الطرز الكروموسومي المقترحة كانت: ١ + m 5sm + 1st + 3t أو ٢ m + 2sm + 1st + 3t. أظهرت النتائج تشابهًا في الخصائص الكروموسومية للطيور من المناطق الثلاث، حيث بلغ الطول الكلي للكروموسومات الأحادية لمغاغة، سمالوط، وملوي: ٣٦,٦٨، ٣٥,٢١، و٣٦,٩٤ على التوالي. كما ظهرت اختلافات في أنماط الـ C-banding بين ٨ كروموسومات كبرى، واحتوت ٢٠–٣٠ ميكروكروموسومًا على كتل داكنة بدرجات متفاوتة، مما يعكس الأهمية الوراثية والمورفولوجية لهذه النتائج.