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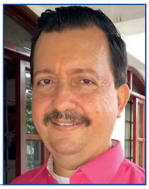
First report on the diversity of domestic pigeons (*Columba livia*) using plumage coloration and patterning in Saravena, Arauca, Colombia



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Abstract

The domestic pigeon (*Columba livia* Gmelin, 1789), native to Africa and Eurasia, is extensively found across Europe, Western Asia, Africa, and the Americas. The pigeon (*Columba livia*) was domesticated several centuries ago and holds a privileged place as a symbol of peace, love, fidelity, and ornamentation in parks. In recent decades, an increase in the populations of these pigeons has been detected. The Spanish brought *Columba livia* to Colombia in the 15th century. The objective of this study was to evaluate the genetic diversity of the domestic pigeon using loci related to plumage coloration and patterning in Saravena. Random sampling was conducted in six colonies between March and April 2024. Through urban visits, direct observation, and photographic records, a phenotypic classification of each of the 580 pigeons from the different flocks studied was carried out. Autosomal markers associated with coloration and plumage were analysed: *Grizzle, Spread, Checker*, and the sex-linked *locus Ash-Red*. Genetic profiles were calculated using indices: allele frequency, genetic diversity, and population structure, estimated with the PopGene 1.31 program. Diversity was assessed using the FSTAT program. The dendrogram was constructed with the MEGA X program. The marker with the highest allele frequency was *Grizzle* (*P*=0.1834), while the *Spread* marker had the lowest values (*P*=0.0300). The highest H_T value was 0.3002 for the Grizzle marker, G_{ST} showed figures of 0.0360, and gene flow was 20.6; the F_{IS} and F_{IT} statistics reported values of 0.2779 and 0.2848, and F_{IT} was 0.0091. Moderate genetic diversity, a deficit of heterozygotes, and an excess of homozygotes were observed, along with low interpopulation genetic differentiation and high gene flow between subpopulations. Low genetic distance values were also found between the studied subpopulations.

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The populations are closely related genetically, which may be due to their geographical proximity, which has favoured genetic exchange.

Key Words: *domestic pigeon; phenotypic markers; allele frequencies; genetic diversity; gene flow*

Introduction

The pigeon (*Columba livia*) was domesticated several centuries ago and holds a privileged place as a symbol of peace, love, fidelity, and ornamentation in parks. In recent decades, there has been a detected increase in the populations of these pigeons. One common characteristic in the natural populations of organisms, including the domestic pigeon, is phenotypic and morphological variation regarding different traits. *Columba livia* is a bird that has been domesticated for centuries. It originated in Europe, Africa, and Asia, but has since been introduced to many other parts of the world. This bird has a long history of domestication, which began about 5,000 years ago (Olalla et al., 2009). Since then, its range has expanded to much of the world due to human activities. Today, it is found in most countries, and according to global records, there are 19 subspecies, with an estimated population of hundreds of millions. This makes it one of the most successful species in terms of population size and geographic distribution (Olalla et al., 2009).

Pigeons, especially *Columba livia*, are extremely successful birds in colonising urban environments. Their remarkable adaptability makes them common inhabitants of streets, squares, and parks in cities around the world (Carlen et al., 2021). They are not demanding regarding their diet. They feed on a wide variety of foods, including grains, seeds, green leaves, invertebrates, and even food waste generated by humans (Priya et al., 2022).

Columba livia is a bird that varies widely in size and colouration. It has a robust build with a small head and bulky body, with a protuberance on the nose; it has a short, strong neck and legs, thick and silky plumage in a wide range of colours (Çelik, 2023). They typically have a grey body with a white rump, two black bars at the end of the wings, a wide black band on the tail, and red legs; however, body colouration can vary from grey to white, bronze, and black. The head is usually black, often with purple-green iridescence. It is a medium-sized bird, measuring 20 to 36 cm in length, and its weight ranges between 340 and 360 g (Olalla et al., 2009).

Many of these urban birds maintain the striking plumage variation of their ancestors and exhibit a series of social behaviours such as reduced breeding, sexual competition, dominance behaviours, mate preference, coloniality, and biparental cooperation in chick care (Stern and Dickinson, 2010). This species has opted for monogamy, forming lifelong pairs, and both parents actively share in the care of their chicks. There is no evidence of sexual dimorphism between males and females (Rose et al., 2006).

Birds are among the most studied animal groups in the field of urban biodiversity (Patankar et al., 2021). Their colouration is an important trait associated with biotic interactions and thermoregulation (Yu et al., 2024), which is closely linked to survival and reproductive success through mechanisms such as camouflage and signalling. Colouration patterns in birds are considered a result of natural selection exerted by urbanisation (Cuthill et al., 2017). Based on observed phenomena of melanism and urban opacity, urbanisation favours darker and less colourful bird species (Leveau, 2021). Terrill and Shultz (2023), in their research on the functions of feather patterns, reported how these patterns have allowed birds to adapt to an astonishing variety of environments in order to survive.

The use of phenotypic markers related to coloration emerges as an invaluable tool in the analysis of the genetic structure of populations. Their attributes, such as the abundance of information, affordability, ease of handling, and quick results, make them essential resources for field research (Pardo et al., 2015). In the Colombian Caribbean, genetic diversity in pigeon populations has been documented using markers associated with coloration and plumage design in the localities of Montería, Cotorra, Sincelejo, Ciénaga de Oro, and Lorica (Causil et al., 2016, 2017; Pardo et al., 2018; Rodríguez and Vargas, 2022; Pardo-Pérez et al., 2024). However, the same is not true for pigeon populations in other parts of Colombia, such as the Eastern Plains, where information is scarce. Therefore, it is important to develop research to understand population dynamics based on the study of plumage polymorphisms. The present study aimed to evaluate the diversity of domestic pigeon (*Columba livia*) populations in Saravena-Arauca, Eastern Plains of Colombia, using genes that code for colouration and plumage design.

Materials and methods

Study Area

The study was conducted between March and April 2024, in the urban area of the municipality of Saravena, Department of Arauca, located in the northeastern corner of the national territory, in the Eastern Cordillera, at 6°56′49″N and 71°53′18″W, at an altitude of 125 meters and temperature ranging between 24° and 26°C (Alcaldía de Saravena). Domestic pigeon samples were collected from 6 flocks located in the Alcaldía, Parque Principal, Plazoleta la Virgen, Barrio Chino, Veterinaria Sabana, and Veterinaria Santander.

Data Collection

Random sampling was conducted between March and April of 2024, between 06:00 and 08:00 hours, when the pigeons form flocks at foraging sites (Hetmañski and Jarosiewicz, 2008). Through urban visits, direct observation, and the support of photographic records, a phenotypic classification was performed for each of the individuals in the different flocks of pigeons found in Saravena (n=580). Each route was used only once to prevent repeated sampling.

Research Variables

The following autosomal genetic markers were analysed: *Grizzle* (*G*), *Spread* (*S*), *Checker* (*C*), and *Ash-Red* (*B*), to evaluate the genetic variation of the *Columba livia* populations in Saravena (Table 1).

Population Analysis

The genetic profiles of populations were determined using the following population genetic indices: allele frequencies, Nei's measures of genetic diversity corresponding to expected heterozygosity (H_S), total population expected heterozygosity (H_T), genetic differentiation coefficient (G_{ST}), gene flow (Nm), and Nei's genetic distances (1972). These indices were estimated using the PopGene 1.3113 program (Yeh et al., 1999). The fixation index (F) (Wright, 1951) was also calculated (F_{IS}, F_{IT}, and F_{ST}) and was determined using the program FSTAT v 2.9.3.2 (Goudet, 2002). Dendrogram construction based on the genetic distance data was performed using the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method, with the program MEGA 11 (Tamura et al., 2021).

Table 1. Description of the four markers studied.

Locus	Alleles	Characteristic
Ash-Red *(Sex linked gene)*	*B*	Mutant. Produces reddish plumage.
	b	Wild type. Produces non-red pigeons
Grizzle *(Autosomal gene)*	*G*	Mutant. Produces extended white patches around the head or body of the pigeon.
	g	Wild type. Pigeons without white patches.
Spread *(Autosomal gene)*	*S*	Mutant. Produces completely pigmented black pigeons.
	s	Wild type. Non-black pigeons.
Checker *(Autosomal gene)*	*C*	Mutant. Produces a pattern of light grey or blue triangular spots on a dark background on the back of the wings, complementing the wild type.
	c	Wild type. Without triangular spots.

Ash-Red (B); Grizzle (G); Spread (S) y Checker (C).

Table 2. Allelic frequencies of each marker in the subpopulations studied

Subpopulations	*N*	*Locus*			
		Ash-Red (B)	*Grizzle (G)*	*Spread (S)*	*Checker (C)*
Alcaldía	89	0.0513	0.1154	0.0128	0.1026
Parque Principal	113	0.0556	0.1508	0.0397	0.1349
Plazoleta la Virgen	115	0.0846	0.1769	0.0385	0.0692
Barrio Chino	95	0.0667	0.2778	0.0333	0.1556
Veterinaria Sabana	97	0.0638	0.2128	0.0319	0.0851
Veterinaria Santander	71	0.0238	0.1667	0.0238	0.1429
Mean		0.0576	0.1834	0.0300	0.1150

Table 3. Genetic diversity of the *Columba livia* population in Saravena

Locus	H_T	H_S	G_{ST}	D_{ST}	*Nm*
Ash-red	0.1174	0.1079	0.0809	0.0095	39.744
Grizzle	0.3002	0.2943	0.0196	0.0059	13.984
Spread	0.0622	0.0580	0.0675	0.0042	84.751
Checker	0.1969	0.2016	-0.0238	-0.0047	25.369
Mean	0.1694	0.1655	0.0360	0.0037	20.606

$\mathbf{H_T}$= Total genetic diversity; $\mathbf{H_S}$= Average genetic diversity within subpopulations; $\mathbf{G_{ST}}$= Genetic diversity coefficient; $\mathbf{D_{ST}}$= Genetic difference between subpopulations; **Nm**: Gene flow.

Results

Sampling

A total of 580 individuals were sampled, distributed across six colonies: Alcaldía (*n*=89), Parque Principal (*n*=113), Plazoleta la Virgen (*n*=115), Barrio Chino (*n*=95), Veterinaria Sabana (*n*=97), and Veterinaria Santander (*n*=71).

Allelic Frequencies

The allele frequencies for each colony in Saravena (Table 2) showed that the markers with the highest reported frequencies were *Grizzle* with an average of 0.1834, followed by *Checker* with an average of 0.1150. The least frequent *loci* were *Ash-Red* and *Spread*, with average frequencies of 0.0576 and 0.0300, respectively.

Genetic Diversity

Of the four analysed loci (Table 3), the total genetic diversity (H_T) had the highest index for the *Grizzle* marker with a value of 30.02%, and the lowest for the *Spread* gene with a value of 6.22%. The average genetic diversity within the colonies (H_S) revealed an average value of 16.55%, while the genetic differentiation coefficient (G_{ST}) showed that only 3.6% of the genetic variability was observed between colonies, while the remaining 96.4% was within colonies. The inter-population diversity (D_{ST}) revealed values of 0.003. The average gene flow (Nm) obtained was 20.6, a value higher than 4, indicating a high exchange of migrants between the analysed colonies in Saravena (Slatkin, 1994).

Population Structure

The F values (Table 4) for the Saravena population showed positive F_{IS} values ranging from 0.1666 to 0.3954 for the *Checker* and *Spread* markers, respectively, with an average of 0.2779. Similarly, the F_{IT} statistic presented positive values ranging from 0.1747 to 0.3972 for the *Checker* and *Spread* markers, respectively, with an average of 0.2848. These positive values for the F_{IS} and F_{IT} statistics in the four loci revealed an excess of homozygotes in the studied populations. The total F_{ST} statistic (0.009) calculated for all *loci*, and all analysed populations showed that 99.1% of the variance in allele frequencies is reported within each population, and only 0.9% of the variance is attributed to differences between populations.

Genetic Distances

The genetic distance obtained between colonies was small, with the closest populations being (Table 5): Parque Principal and Veterinaria Santander, followed by Plazoleta la Virgen and Veterinaria la Sabana. The populations of Alcaldía and Barrio Chino showed the greatest genetic difference, but this was not significant as it

Table 4. Values of the F statistics for each marker in the total population of Saravena

Locus	F_{IS}	F_{ST}	F_{IT}
Ash-red	0.3388	0.0063	0.3429
Grizzle	0.2108	0.0176	0.2246
Spread	0.3954	0.0029	0.3972
Checker	0.1666	0.0098	0.1747
Mean	0.2779	0.00915	0.2848

F_{IS}= Inbreeding coefficient; F_{ST}= Fixation index; F_{IT}= total inbreeding coefficient.

Table 5. Genetic distance matrix (Nei, 1972) between the subpopulations of Saravena

	A	B	C	D	E	F
A						
B	0.0006					
C	0.0017	0.0017				
D	0.0077	0.0048	0.0051			
E	0.0027	0.0019	0.0006	0.0025		
F	0.0014	0.0004	0.0028	0.0038	0.0021	

A: Alcaldía, B: Parque Principal, C: Plazoleta la Virgen, D: Barrio Chino, E: Veterinaria la Sabana, F: Veterinaria Santander.

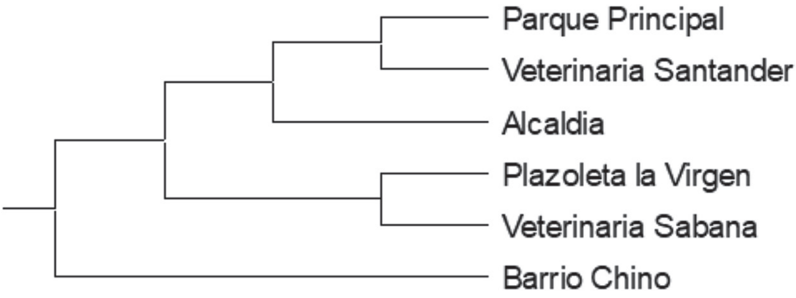

Figure 1. Dendrogram based on genetic distances (Nei, 1972) between subpopulations of domestic pigeon (*Columba livia*) in Saravena, Colombia, obtained using the UPGMA method

did not exceed 10%. The UPGMA dendrogram constructed from Nei's (1972) genetic distance values for the six populations of Saravena (Figure 1) indicates genetic similarity between the Parque Principal and Veterinaria Santander colonies. The Barrio Chino colony is the most distant, but with an insignificant distance value, suggesting that the populations are very closely related.

Discussion

The highest frequency of the *Grizzle* marker (Table 2) was found in the populations studied in Saravena, which could be due to specific conditions of this population, such as the small city area that is highly wooded, with low urban development, and without large companies, contributing to the maintenance of rural conditions. These results are like those obtained by Obukhova (2007), who reported that non-melanic colours in pigeons were better adapted to natural habitats. Haag-Wackernagel (1993) also noted that pigeon breeders prefer lighter colorations as they are more attractive, leading to an increase in the number of pigeons with light plumage. The higher presence of the *Grizzle* allele could also be due to a founder effect, resulting from the presence of pigeons with light phenotypes at the time of the pigeon population formation in

Saravena. These results differ from those reported by Pardo-Pérez et al. (2024), Csanády and Duranková (2021), Causil and Causil (2019), and Pardo et al. (2018), who reported a predominance of melanic phenotype pigeons in their studies.

The *Spread* allele (Table 2) showed the lowest frequencies, suggesting that this marker might be negatively selected, considering that dark feather surfaces absorb light and heat more than light-coloured feathers when exposed to the sun (Rogalla et al., 2022). Angelier (2020) reported that pigeons with the *Spread* mutation, when subjected to solar radiation, increased the temperature of their plumage, increasing the energetic costs for cooling compared to light-coloured pigeons. Additionally, Obukhova (2007) observed a latitudinal pattern where populations closer to the Equator reduced the number of *Spread* pigeons compared to populations closer to the poles. These conditions in Saravena could be influencing the population growth of these pigeons.

The present study revealed a low total genetic diversity value ($H_T = 0.169$), which was lower than reported by Pardo-Pérez et al., (2024) in Montería-Córdoba, Colombia, Rodríguez and Vargas (2022) in Cotorra-Córdoba, Colombia, and Pardo et al. (2018) in Sincelejo-Sucre, Colombia. Although the total expected heterozygosity is directly proportional to the number of alleles per marker, the low H_T value in Saravena pigeons may be due to the low variation among the analysed populations. The genetic differentiation coefficient in the total population ($G_{ST} = 0.036$) shows that 3.6% of the genetic diversity was between populations and 96.4% within populations, indicating that the six colonies share a large proportion of the total diversity (Hartl and Clark, 1997), generating a high gene flow among subpopulations (Nm = 20.6; Table 3).

The positive F_{IS} statistic values of 0.2779 for all markers indicated an excess of homozygotes among individuals compared to each colony, suggesting the presence of inbreeding within the colonies. The F_{ST} statistic result of 0.0091, calculated between populations and for all loci, reveals a slight degree of population structuring. According to this parameter, 99.09% of the variance in allele frequencies is observed within each colony, while 0.91% of the variance is due to differences between the studied colonies. Finally, the positive F_{IT} statistic values of 0.2848 also revealed an excess of homozygotes among individuals compared to the total population.

The similarity of genetic distances obtained between the studied colonies can be explained because this genetic closeness is related to geographical proximity (Siepielski et al., 2013; Gutiérrez-Cisneros et al., 2014). These subpopulations are geographically very close, resulting in similar demographic densities and significantly contributing to reducing genetic differences (Jacob et al., 2015). The small genetic distances observed between the six pigeon subpopulations, particularly between Parque Principal and Veterinaria Santander, as well as between Plazoleta la Virgen and Veterinaria la Sabana, can be attributed to a considerable exchange of genetic markers among colonies, generating a high gene flow within the general pigeon population. This suggests that individuals from these subpopulations are more likely to fly between nearby places, promoting a higher degree of familiarity and potentially influencing their local adaptation. This dynamic population structure is likely driven by the presence of non-ideal habitable areas within the municipality of Saravena, indicating that the domestic pigeon population in this region presents a mosaic pattern, potentially leading to a shared genetic profile among subpopulations.

The dendrogram further emphasises the genetic similarity among subpopulations, supporting the idea of continuous genetic exchange and reinforcing the genetic links among these populations (Causil et al., 2017). This close relationship could be explained by their geographical proximity, given that Saravena is a relatively small municipality.

Conclusions

In the populations studied in Saravena, Arauca, the highest allele frequencies were found for the *Grizzle* marker, while the *Spread* allele showed the lowest frequencies. The present study also revealed a low value of total genetic diversity and found an excess of homozygotes and a high similarity in relation to the genetic distances obtained between the analysed colonies.

Acknowledgments

To the Universidad de Córdoba.

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Prvo izvješće o raznolikosti gradskog goluba (*Columba livia*) uporabom boja i uzorka perja u Saraveni, Arauca, Kolumbija

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Gradski golub (*Columba livia* Gmelin, 1789.), podrijetlom iz Afrike i Euroazije, široko je rasprostranjen u Europi, Zapadnoj Aziji, Africi i Amerikama. Golub (*Columba livia*) je pripitomljen prije nekoliko stoljeća i ima posebno mjesto kao simbol mira, ljubavi, vjernosti i ukrasa u parkovima. Posljednjih desetljeća, zamijećeno je povećanje populacije tih golubova. Španjolci su donijeli *Columbu liviu* u Kolumbiju u 15. stoljeću. Cilj je ovog rada bio procijeniti genetičku raznolikost gradskog goluba uporabom lokusa povezanih s bojom i uzorcima perja u Saraveni. Provedeno je nasumično uzorkovanje u šest kolonija između ožujka i travnja 2024. Kroz posjete gradovima, izravno promatranje i fotografsku evidenciju, provedena je fenotipska klasifikacija svakog od 580 golubova iz različitih proučavanih jata. Analizirani su autosomalni markeri povezani s bojom i perjem: *Grizzle, Spread, Checker* i sa spolom povezani *lokus Ash-Red*. Genetski profili su izračunati uporabom sljedećih pokazatelja: frekvencija alela, genetska raznolikost i struktura populacije, procijenjeno pomoću PopGene 1.31 programa. Raznolikost je procijenjena uporabom FSTAT programa. Dendrogram je konstruiran pomoću MEGA X programa. Marker s najvećom frekvencijom alela bio je *Grizzle* (*P*=0,1834), dok je marker *Spread* imao najniže vrijednosti (*P*=0,0300). Najveća H_T vrijednost bila je 0,3002 za Grizzle marker, G_{ST} je pokazao brojku od 0,0360, a genski protok bio je 20,6; F_{IS} i F_{IT} statistika pokazala je vrijednosti od 0,2779 i 0,2848, a F_{IT} je bio 0,0091. Zamijećena je umjerena genetska raznolikost, deficit heterozigota i višak homozigota, uz nisku genetsku diferencijaciju među populacijama i visoki genski protok između subpopulacija. Niske vrijednosti genetske udaljenosti pronađene su i između proučavanih subpopulacija. Populacije su genetski u bliskom srodstvu, situacija kojoj uzrok može biti geografska blizina između njih, što je doprinijelo genetskoj razmjeni.

Ključne riječi: *gradski golub, fenotipski markeri, frekvencije alela, genetska raznolikost, genski tok*