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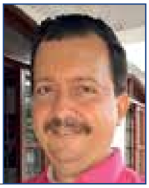
Genetic characterisation of the domestic cat population (*Felis catus*) in Valledupar – Cesar using coat markers



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Abstract

The domestic cat (*Felis catus*) is a small carnivorous mammal belonging to the feline family. It is characterised by significant variability in terms of breeds, with females commonly smaller than males. Cats are one of the most popular pet species worldwide, though there is growing evidence that their large populations are having negative effects on the environment. Cats exhibit noticeable polymorphisms, particularly related to the colour, pattern, and texture of their coat, which can be easily recognised by visual inspection. This makes data collection a straightforward procedure. Cats are an ideal species for population studies because they are cosmopolitan animals and form a panmictic population. Genetic population analyses of cats are essential for understanding the history of their evolution and for developing phylogenetic hypotheses about allele relationships. However, despite the importance of these studies, global information availability is limited and, in some areas, completely absent. The aim of this study was to determine the level of genetic diversity and structure in domestic cat populations using coat markers in Valledupar, Cesar. Random sampling was conducted between February and September 2022, and 365 adult animals were phenotypically identified in twelve neighbourhoods of the locality. The genes studied included *Orange*, *Agouti*, *Dilution*, *Tabby*, *Long Hair*, *Siamese*, *Manx*, *Spotting White*, and *Dominant White.* The *Non-agouti* marker showed the highest frequency (0.740), while the *Manx* gene exhibited the lowest value. Most of the genetic diversity was found within populations and was limited between populations. Additionally, high gene flow, an excess of heterozygotes, and reduced genetic differentiation between populations were observed. The *Spotting White* locus showed a departure from Hardy-Weinberg equilibrium. Genetic distance between populations and the obtained dendrogram revealed low significant values, indicating that the populations as a whole are closely related.

Key Words: *Felis catus; genetic diversity; homozygosity; genetic structure; dendrograms*

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Introduction

The domestic cat is found on all continents, including even the most remote or isolated regions, which is why its evolutionary success is unquestionable. While today it is one of the most beloved companion animals in the world, for ancient societies, barn cats, village cats, and ship cats provided essential protection against pests like rodents, which were responsible for economic losses and diseases (Ottoni et al., 2017).

The domestication of cats likely began as a symbiotic relationship between wild cats (*Felis silvestris*) and developing agricultural societies (Cameron-Beaumont et al., 2002). When humans transitioned from being hunter-gatherers to farmers approximately 12,000 years ago, cats probably took advantage of the increased density of prey (Nilson, 2022). Humans benefited from the predation of rodents, which caused crop damage, and they may have seen cats as a solution to the problems of that time.

Cats and humans have long benefited from these close associations, although the dynamics of the relationship have varied over time. It is evident that many people hold a reverent affinity for this species, which has likely been key and continues to persist despite the diminishing role of cats as pest controllers. These relationships have had a significant influence on cat movement patterns and how they have been distributed worldwide (Crowley et al., 2020).

Domestic cats are found in all human environments. They can live as pets in human homes or as free-roaming (stray) cats in cities, parking lots, farms, and other outdoor areas where resources like food, shelter, and mates are abundant. The social system of cats has been described as "facultative sociality," and they exhibit a great deal of flexibility in their social behaviour, living both solitarily and in groups. Cat groups can be found in high or low densities, ranging from 1 cat per square kilometre to more than 2500 cats per square kilometre (Vitale, 2022).

Cats are an excellent species for population genetic variability analysis due to their universal distribution and panmictic populations (Peñuela et al., 2016). The frequencies of wild-type and mutant coat gene markers in cats are specific to each population and reveal their genetic structure (Todd, 1977). Genetic profiles in cat populations for coat genes have been reported worldwide (Ruiz-García et al., 2005; Goncharenko and Zyat'kov, 2012). Population genetic studies in cats are essential for uncovering the evolutionary history of these animals and constructing phylogenetic hypotheses about the relationships between these markers.

Valledupar is considered the most important city in the department of Cesar in Columbia. It was founded in 1550 along the northeast Atlantic coast of the country. Valledupar is a significant centre for agricultural, agro-industrial, and livestock production with a rich history of human activity (Alcaldía de Valledupar, 2020). This historical human influence could have had an impact on the genetic variability of cat populations. Therefore, the aim of the present study was to determine the level of genetic diversity and structure in domestic cat populations (*Felis catus*) using coat markers in the municipality of Valledupar, Cesar, Colombia.

Materials and methods

Study Area

The study was conducted between May and December 2022 in the urban area of Valledupar (10° 27′ 55″ N and

73° 15′ 11″ W), a city located along the northeast Atlantic Coast of Columbia, in the department of Cesar. Currently, the urban area of Valledupar is divided into six districts spread across approximately 4,493 hectares, at an elevation of 169 metres, with an average annual air temperature of 34°C (Alcaldía de Valledupar, 2020).

Data Collection

Incidental sampling was conducted through direct observation in twelve neighbourhoods: El Prado, Santa Rosa, San Isidro, Fundadores, Loperena, Novalito, Doce de Octubre, Cañaguate, Los Cortijos, Primero de Mayo, Dangond, and El Carmen. A phenotypic classification of each of the 365 adult individuals found was carried out. Care was taken not to repeat individuals, and each route was traversed only once to confirm the presence or absence of each of the autosomal markers: *non-Agouti (a); Blotched tabby (Tb); Dilution (d); Long hair (l); Spotting white (S); Dominant white (W); Manx (X); Siamese (N); and the sex-linked Orange (O) locus* (Table 1). Additionally, photographic records of each animal were made.

Table 1. Description of the studied markers

Locus	Alleles	Characteristic
O (sex-linked gene)	*O*	Wild; non-orange pigmentation.
	O	Mutant; exhibits orange pigmentation; epistatic for the detection of locus A.
A (autosomal gene)	*A*	Wild; Agouti colour, the fur is divided into bands or stripes of different colours.
	A	Mutant; Non-agouti colour; uniform colour; no bands or stripes observed; epistatic for the observation of locus T
T (autosomal gene)	t^+	Wild; "*Mackerel tabby*"; recessive to a T^α, but dominant for t^b.
	t^b	Wild; "blotched tabby"; recessive.
	T^α	Wild; "Abyssinian tabby"; dominant.
D (autosomal gene)	*D*	Wild; Dense colour.
	D	Mutant; Dilute colour; recessive.
L (autosomal gene)	*L*	Wild; Short hair.
	L	Mutant; Long hair; recessive.
S (autosomal gene)	*S*	Wild; no white spots.
	S	Mutant; white spotting; dominant.
W (autosomal gene)	*W*	Wild; normal colour
	W	Mutant; White colour; epistatic to all other colorus
X (autosomal gene)	*X*	Wild; long tail.
	X	Mutant; short tail or no tail
N (autosomal gene)	*N*	Wild; Does not have dark coloration on the nose or paws.
	N	Mutant; Dark colouring on the tips of the paws and on the nose.

O: Orange; α: Non-agouti; t^b*: Blotched Tabby; d: Dilution; l: Long Hair; s: Spotting White; W: Dominant White; M: Manx; N: Siamese.*

Study Variables

To determine the genetic diversity of domestic cat populations (*Felis catus*) in Valledupar, the following phenotypic markers (Table 1) suggested by the Committee on Standardized Genetic Nomenclature for Cats (1968) were studied: *O* (*Orange*, sex-linked trait), and the autosomal *loci A (A, a; Agouti vs. non-Agouti), T (Ta, t+, tb; Abyssinian tabby vs. Mackerel or striped vs. Blotched tabby), D (D, d;* full colour *vs. Dilution), L (L, l; short hair vs. long hair), S (s+, S; non-spotted white vs. spotted white), W (w+, W;* normal colour *vs. Dominant White), X (x, X;* long tail vs. short tail or *tailless), N (n, N; not dark* on the nose *vs. dark* on the nose*).*

Population Analysis

The estimation of allele frequencies, and measures of genetic diversity such as total genetic diversity, diversity within populations, diversity between populations, the coefficient of genetic diversity, number of migrants, Hardy-Weinberg equilibrium (H-W), and genetic distance, were conducted using the program GenAlEx 6.503 (Peakall and Smouse, 2012). The genetic structure of the populations was analysed using the program FSTAT v. 2.9.3.2 (Goudet, 2002), and a dendrogram was constructed using the UPGMA clustering method with the program MEGA 11 (Tamura et al., 2021).

Results

Allelic Frequencies

In determining the allelic frequencies for each population, it was found that the *Non-agouti* gene had the highest frequency in the population (0.740), mainly in the Dangond, Doce de Octubre, and Primero de Mayo populations. On the other hand, the locus with the lowest frequency was *Manx*, which was only recorded in the populations of Santa Rosa, Doce de Octubre, and Primero de Mayo (Table 2).

Table 2. Allelic frequencies of *Felis catus* subpopulations in Valledupar

Populations	N°	O	α		d	l	S	W	M	N
El Prado	32	0.321	0.743	0.381	0.212	0.211	0.514	0.012	0,000	0,043
Santa Rosa	39	0.111	0.787	0.482	0.271	0.162	0.535	0.000	0,011	0,011
San Isidro	28	0.435	0.786	0.276	0.073	0.081	0.582	0.038	0,000	0,000
Fundadores	41	0.547	0.753	0.199	0.454	0.239	0.566	0.000	0,000	0,022
Loperena	47	0.787	0.638	0.401	0.051	0.126	0.421	0.000	0,000	0,002
Novalito	24	0.565	0.692	0.315	0.029	0.043	0.454	0.022	0,000	0,039
Doce de Octubre	26	0.233	0.809	0.240	0.409	0.391	0.601	0.000	0,013	0,012
Cañaguate	19	0.754	0.622	0.398	0.031	0.076	0.617	0.000	0,000	0,011
Los Cortijos	21	0.377	0.578	0.311	0.000	0.011	0.597	0.031	0,000	0,022
Primero de Mayo	26	0.151	0.801	0.289	0.329	0.261	0.681	0.000	0,009	0,000
Dangond	24	0.513	0.901	0.312	0.368	0.469	0.671	0.036	0,000	0,018
El Carmen	38	0.491	0.773	0.189	0.223	0.476	0.507	0.000	0,000	0,000
Promedio		0.440	0.740	0.316	0.204	0.212	0.562	0.012	0,002	0,014

N°: Number of sampled individuals; O: Orange; a: Non-agouti; T^b: Tabby blotched; d: Dilution; l: Long hair; s: Spotting White; W: Dominant White, M: Manx; N: Siamese.

Table 3. Distribution of genetic diversity in genetic markers in cats

	H_T	H_S	G_{ST}	D_{ST}	Nm
Orange	0.482	0.408	0.125	0.078	2.3
Non-Agouti	0.395	0.367	0.035	0.013	13.7
Tabby	0.000	0.000	0.000	0.000	0.0
Dilution	0.247	0.241	0.166	0.049	3.4
Long hair	0.312	0.262	0.199	0.048	2.7
Spotting white	0.491	0.466	0.024	0.014	16.3
White	0.011	0.012	0.003	0.000	32.2
Manx	0,005	0,006	0,012	0,000	28,6
Siamese	0,031	0,030	0,018	0,000	22,4
Media	0,225	0,208	0,091	0,012	3.5

H_T = Total genetic diversity; H_S = Diversity within populations D_{ST} = Diversity between populations; G_{ST}= Genetic diversity coefficient; Nm = Number of migrants

Table 4. F-statistic values for each marker in the global population.

Marcadores	F_{IT}	F_{ST}	F_{IS}
O	-0.4013	0.0041	-0.3389
A	-0.6971	0.0028	-0.7112
T^b	-0.2756	0.0013	-0.4796
D	-0.3948	0.0012	-0.2627
L	-0.2879	0.0008	-0.2934
S	-0.5391	0.0027	-0.5751
W	-0.0104	0.0079	-0.0309
M	-0.1388	0.0019	-0.0188
N	-0.2556	0.0035	-0.0864
Mean	-0.3294	0.0029	-0.3416

O: Orange; α: Non-agouti; t^b: Blotched Tabby; d: Dilution; l: Long Hair; s: Spotting White; W: Dominant White; M: Manx; N: Siamese.

Genetic Diversity

In the Valledupar population, the total heterozygosity (Table 3) showed an average of H_T = 0.225, with the markers *Spoting White* (H_T = 0.491), *Orange* (H_T = 0.482), and *Non-Agouti* (H_T = 0.395) exhibiting the highest diversity, while the marker *Manx* showed the lowest diversity (H_T = 0.005). The genetic diversity within populations revealed H_S = 0.208, and the diversity among populations was D_{ST} = 0.012. The coefficient of genetic diversity (G_{ST} = 0.091) indicated that 9.1% of the genetic diversity is found among populations, while 90.9% is within populations. The value of the number

Table 5. Hardy-Weinberg equilibrium analysis in the loci *Orange* and *Spotting White*

	Valledupar	El Prado	Santa Rosa	San sidro	Funda-dores	Loperena	Novalito	Doce de Octubre	Cañaguate	Los Cortijos	Primero de Mayo	Dangond	El Carmen
Orange	0,2212	0,767	0,2329	0,8715	0,1824	0,459	0,1582	0,7957	0,1945	0,6885	0,1642	0,3019	0.4432
Spotting White	0,0000	0,0385	0,7234	0,0847	0,2887	0,0032	0,0034	0,4951	0,6534	0,1284	0,4068	0,0043	0,3256

Table 6. Genetic distance matrix (D_{Nei}) between populations

	1	2	3	4	5	6	7	8	9	10	11	12
1	------											
2	0,010	------										
3	0,012	0,032	------									
4	0,016	0,052	0,038	------								
5	0,054	0,096	0,033	0,063	------							
6	0,025	0,048	0,007	0,044	0,014	------						
7	0,011	0,025	0,058	0,023	0,102	0,073	------					
8	0,038	0,078	0,016	0,046	0,011	0,007	0,088	------				
9	0,016	0,028	0,009	0,055	0,053	0,021	0,057	0,026	------			
10	0,006	0,013	0,030	0,033	0,104	0,056	0,010	0,077	0,033	------		
11	0,044	0,095	0,089	0,025	0,099	0,106	0,024	0,098	0,114	0,053	------	
12	0,013	0,035	0,037	0,026	0,044	0,043	0,021	0,052	0,054	0,034	0,028	------

1: El Prado, 2: Santa Rosa, 3: San Isidro, 4: Fundadores, 5: Loperena, 6: Novalito, 7: Doce de Octubre, 8: Cañaguate, 9: Los Cortijos, 10: Primero de Mayo, 11: Dangond, 12: El Carmen of migrants (3.5) ranged from 1 to 4, indicating a high gene flow among the studied local populations (Slatkin, 1981).

Population Structure

The F_{IS} and F_{IT} statistics for all genes showed negative values (Table 4), indicating a deficit of homozygotes among individuals within each population and among individuals in relation to the total population. On the other hand, the average F_{ST} value was low (0.0029), suggesting minimal genetic differentiation among the populations.

Hardy-Weinberg equilibrium

A nivel global en Valledupar, for the *Spotting White locus*, a lack of Hardy-Weinberg equilibrium was found (0.000). Additionally, a lack of equilibrium was observed in the El Prado (0.0385), Loperena (0.0032), Novalito (0.0034), and Dangond (0.0043) populations, while the *Orange* marker remained in Hardy-Weinberg equilibrium (Table 5).

Genetic Distances

The genetic distance between the populations of Valledupar showed that El Prado and Primero de Mayo are the closest populations (Table 6). In contrast, Los Cortijos and Dangond displayed the highest genetic divergence, although the values remain relatively low, not exceeding 11.5%.

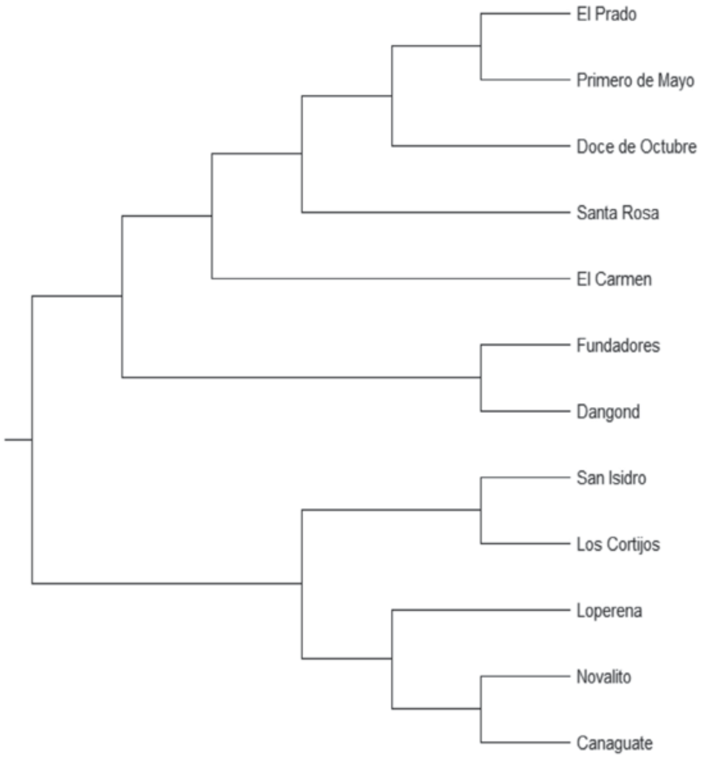

Figure 1. Dendrogram constructed using the UPGMA method based on Nei's genetic distance (1972) of Felis catus populations from Valledupar

The dendrogram obtained using the UPGMA method based on Nei's genetic distance (1972) revealed the genetic similarity (Figure 1) between the populations of El Prado and Primero de Mayo, which are also associated with the populations of Doce de Mayo, Santa Rosa, and El Carmen. Similarly, the populations of San Isidro, Los Cortijos, Novalito, Cañaguate, and Loperena were identified as the most distant, but with relatively low distance values. This suggests that the populations, as a whole, are closely related.

Discussion

Due to their domestication, the coat coloration of cats has undergone different selective pressures compared to other mammals, as they exhibit a wide range of colours and patterns. Unlike other domestic animals, artificial selection in cats primarily occurs based on colour patterns and less on other traits such as behaviour or sociability (Dubiner et al., 2023).

The high frequency of the *Non-agouti* and *Spotting White loci* in the Valledupar population could be related to environmental factors such as high temperatures, which can reach up to 39°C (Climate-data.org, 2022), and daily hours of sunlight, which can range from 9 to 10.5 hours (Climate-data.org, 2022). These factors may favour the presence and increase of individuals carrying these loci (Stelow et al., 2016; Kaelin et al., 2021).

Furthermore, the high prevalence of *Non Agouti* in this study could be explained by an enzymatic interaction that affects the colour pigmentation in most mammals. Corin is a transmembrane enzyme known for processing atrial natriuretic peptide (ANP) in cardiomyocytes to regulate electrolyte balance and blood pressure. Mutations that lead to loss of function in Corin impede ANP processing and result in lighter fur coloration in multiple species. The effects of Corin pigmentation depend on a locus (*Agouti*) that encodes the agouti signalling protein (ASIP). It has been confirmed that ASIP is a direct proteolytic substrate of the Corin enzyme (Ali et al., 2023). In contrast, loss-of-function mutations in ASIP result in the *Non-agouti* pattern caused by a deletion, leading to the loss of ASIP gene function (Eizirik and Trindade, 2021). The fact that melanism continuously emerged in cat populations, reaching appreciable frequencies in regional populations, supported the hypothesis that melanism could provide an adaptive advantage in certain environments.

Another factor to consider for the high frequency of the *Non-agouti* marker is "Gloger's rule," which states that mammals, including cats, tend to have elevated levels of melanin in tropical regions. This results in darker coloration, which has other consequences, such as being relatively insensitive to abrasion, antimicrobial benefits, protection against mutagenesis caused by UV rays, and improved heat absorption (Delhey, 2017, 2018). These findings are similar to those obtained in Tolú, Cartagena, Magangué, and Mompox (Montes et al., 2015; Pardo et al., 2016, 2018; Martínez et al., 2018;), and higher compared to reports from Lorica, Santa Marta, and Montería (Pardo et al., 2014, 2015; Causil et al., 2017).

The frequency of the *Dominant White* marker is similar to reports by Pardo et al. (2016) in Magangué and Ruiz-García and Álvarez (2008), who claim that the frequency of this gene is low in Latin America.

Coat colour is determined during embryonic development. Different types of melanin (eumelanin and pheomelanin) are synthesised and stored in melanosomes, which are large organelles in melanocytes. Melanocytes are not only present in the skin but also in the ears, eyes, brain, heart, lungs, and adipose tissue. Melanocyte precursor cells, originating from the neural crest, migrate to the skin, hair follicles, eyes, inner ear, and other organs (Charon and Lipka, 2015). Disruption in this migration can result in some areas of the skin lacking melanocytes, leading to partial or total depigmentation, which can result in entirely white individuals that may later exhibit deafness and lack of retinas (vision problems). This explains the low frequencies of these allelic variants in natural populations.

Likewise, the very low frequency of the *Manx* and *Siamese* alleles in Valledupar could be due to unsuitable climatic conditions for the evolution of these genes. It is expected that these genes would be more prevalent in locations with lower temperatures than those reported in this region, where temperatures range from 32-39°C (Pardo et al., 2014). Sacrocaudal dysgenesis observed in cats carrying the *Manx* allele is a series of congenital abnormalities that can affect the lumbar, sacral, or caudal vertebrae and is often associated with spinal malformations such as myelodysplasia, hydromyelia, syringomyelia, meningocele, and tethered spinal cord (López, 2019). This anomaly is caused by a mutation involving the substitution of cytosine with guanine at nucleotide 189 of the gene (C189G), resulting in an amino acid change from isoleucine to methionine at amino acid position 63 of the encoded protein. The transcription factor encoded by the T gene is crucial for the normal embryonic development of the posterior mesoderm, which gives rise to somite that later forms the vertebrae and tail (Haase et al., 2016).

Regarding the total genetic diversity (H_T) found in Valledupar, it was moderate, with most of the genetic diversity found within populations (H_S) and limited genetic differentiation among populations (D_{ST}). This suggests that the studied populations share a significant portion of their total diversity. The gene flow Nm was high, and in general, values of Nm close to or greater than 4 are considered sufficient to maintain relative genetic homogeneity (Slatkin, 1981). The high level of gene flow suggests that the populations are genetically related (Nilson et al., 2022). The results obtained indicate minimal differentiation among the analysed populations. The absence of genetic differentiation between populations is typically considered the result of adequate gene flow, often caused by migration, which helps mitigate the impact of selection or genetic drift. According to Lowe et al. (2018), when gene flow is greater than 1, populations are expected to retain genetic connections, as gene flow surpasses the effects of genetic drift and prevents population differentiation.

The deficit of homozygotes observed by various fixation indices (F_{IS} and F_{IT}) in each subpopulation suggests that these populations have a nearly uniform structure. This could be attributed to their geographic proximity, which can lead to a significant increase in gene flow between them. Increased gene flow prevents mating events between genetically related individuals within populations (Buchholz and Vella, 2016), resulting in a higher frequency of heterozygous genotypes. It is possible that the subpopulations analysed tend toward heterozygosity, possibly due to random mating within populations, indicating an absence of programmed mate selection for the analysed markers.

These fixation indices indirectly indicate levels of inbreeding and are consistent with the results obtained using the Hardy-Weinberg equilibrium test, where populations exhibited significant deviations from H-W equilibrium, revealing a deficit of homozygotes. In a population, such a deficit could be a consequence of possible genetic substructure, expressed as the Wahlund effect, or it could be that the studied genes are subject to natural selection, mutation, or genetic drift (Chen et al., 2017).

The low genetic distance values found among the studied populations are likely the result of their geographic proximity, as previously confirmed (Cruz-Salazar et al., 2016a). In the UPGMA dendrogram based on Nei's genetic distance values (1972) for the Valledupar populations, it is observed that genetic similarity correlates with geographical proximity and the history of neighbourhoods where it is presumed that the first cats arrived in Valledupar (Bonet and Ricciulli, 2020).

Conclusions

The gene with the highest frequency was *Non-agouti*, which could be related to environmental factors such as high temperatures, while the locus with the lowest frequency was *Manx*. The total genetic diversity found in Valledupar was moderate, with most found within populations and less differentiation among populations. This indicates that populations share a significant portion of the total diversity, and the high level of gene flow suggests that subpopulations are genetically closely related. The UPGMA dendrogram derived from Nei's genetic distance (1972) for the studied populations shows that genetic proximity corresponds to geographic proximity.

Acknowledgments

To the Universidad de Córdoba.

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Genetska karakterizacija populacije domaćih mačaka (*Felis catus*) u Valleduparu – Cesar uporabom markera krzna

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Domaća mačka (*Felis catus*) mali je sisavac, mesožder koji pripada porodici mačaka. Karakterizira ju značajna varijabilnost u smislu pasmine, s tim da su ženke obično veličinom manje od mužjaka. Mačke su jedna od najpopularnijih vrsta kućnih ljubimaca diljem svijeta, ali postoji sve više dokaza da njihove velike populacije imaju negativan učinak na okoliš. Mačke se odlikuju zamjetnim polimorfizmima, posebno bojom, uzorkom i teksturom njihovog krzna, što je lako moguće prepoznati vizualno. To čini prikupljanje podataka jednostavnim postupkom. Uz to, mačke su idealna vrsta za studije populacije, jer su to kozmopolitske životinje i čine panmiktičku populaciju. Genetske analize populacije mačaka ključne su za razumijevanje povijesti njihove evolucije i za razvoj filogenetskih hipoteza vezano uz odnosa alela. Međutim, unatoč važnosti ovih studija, globalna dostupnost informacija je ograničena pa čak i potpuno odsutna u nekim područjima. Cilj je ove studije bio je utvrditi razinu genetske raznolikosti i strukture u populacijama domaćih mačaka (*Felis catus*) uporabom markera krzna u Valleduparu, Cesar. Nasumično uzorkovanje je provedeno između veljače i rujna 2022. godine te je fenotipski identificirano 365 odraslih životinja u dvanaest kvartova lokaliteta. Proučavani geni uključivali su *Orange, Agouti, Dilution, Tabby, Long Hair, Siamese, Manx, Spotting White* i *Dominant White. Non-agouti* marker pokazao je najveću učestalost (0,740), dok je *Manx* gen pokazao najnižu vrijednost. Najviše genetske raznolikosti otkriveno je unutar populacija, a bilo je ograničeno između populacija. Uz to, zamijećen je i visoki genski tok, obilje heterozigota i smanjena genetska diferencijacija između populacija. *Spotting White locus* pokazao je otklon od Hardy-Weinberg ekvilibrija. Genetska udaljenost između populacija i dobiveni dendrogram otkrili su niske značajne vrijednosti, ukazujući da su populacije općenito u uskom srodstvu.

Ključne riječi: *Felis catus, genetska raznolikost, homozigotnost, genetska struktura, dendrogrami*