UDC 575.
https://doi.org/10.2298/GENSR2101235P
Original scientific article

POPULATION GENETICS IN MULTIPLE SCALES: GENETIC MICROSTRUCTURE OF A CAT POPULATION IN COLOMBIA

Mauricio PEÑUELA[1], Angie PATIÑO-MONTOYA[2], Andrés PEÑA-CRUZ[3], Heiber CÁRDENAS[4]

[1]Posgrado en Ciencias-Biología, Facultad de Ciencias Naturales y Exactas, Universidad del Valle, Cali-Colombia
[2] Programa de Pós-graduação em Ecologia, Doutorado em Ecologia, Universidade de Brasília, Brasília D.F.-Brasil
[3]Gobernación del Valle del Cauca, Colombia
[4]Departamento de Biología, Facultad de Ciencias Naturales y Exactas, Universidad del Valle, Cali-Colombia

Peñuela M., A. Patiño-Montoya, A. Peña-Cruz, H. Cárdenas (2021). *Population genetics in multiple scales: genetic microstructure of a cat population in Colombia*.- Genetika, Vol 53, No.1, 235-246.

Considering of multiples research of genetic in cats, the objective of this study was to compare the genetic diversity of the domestic cat population at different spatial and temporal scales. According to the administrative division of the city of Cali, 8 colonies (localities) were chosen, which together form 5 subpopulations within the city for sampling. The phenotype from each individual's coat was recognized for the subsequent calculation of allele frequencies, Hardy-Weinberg (HW) equilibrium, genetic structure, and correlated genetic diversity and structure with antiquity in each neighborhood. The non-agouti allele obtained the highest frequencies, and the white allele had the lowest frequencies in all colonies and subpopulations; the manx allele was also reported. HW equilibrium was found in the orange locus, except for the Salomia, Sena and Santa Barbara colonies of the NW subpopulation. A significant association was found between the diversity of the tabby locus and antiquity and the differentiation of the colonies (F_{CT}) with antiquity of colonies. In conclusion, domestic cats in the city of Cali behave as a single population, with incipient genetic microstructure phenomena, which are part of the natural dynamics of the population in their interaction with the urban environment.

Keywords: *Felis catus*, dispersion, population genetics.

Corresponding author: Mauricio Peñuela, Posgrado en Ciencias-Biología, Facultad de Ciencias Naturales y Exactas, Universidad del Valle, Cali-Colombia, Email: mauricio.penuela@hotmail.com

INTRODUCTION

The domestic cat (*Felis catus*) is a model organism in population genetics due to the easy recognition of the genes responsible for color pattern, coat and tail length, and skeletal abnormalities (RUÍZ-GARCÍA, 1997; RUÍZ GARCÍA, 2000; KAELIN and BARSH, 2013). For the species, more than 400 populations from around the world have been genetically characterized, showing an association of genetic diversity with the history of human migrations (RUÍZ-GARCÍA and ÁLVAREZ, 2008). Although the strong association between cats and humans has been seen as a product of an artificial selection process (PONTIER *et al.*, 1995), it is known that domestic cat populations worldwide are in panmixia due to some attributes of their natural history, such as iteroparous reproduction and a complex social structure (RUÍZ-GARCÍA, 1994; RUÍZ-GARCÍA and KLEIN, 1997; PEÑUELA *et al.*, 2016). According to the above, the hypothesis of genetic stability was formulated, which postulates that domestic cat populations maintain their genetic diversity constant over time (PEÑA-CRUZ and PATIÑO-MONTOYA, 2017), relegating the hypothesis of novelty or artificial selection to a spatial scale and specific time as well as other stochastic processes.

A common assumption in population genetics in the analysis of phenotypic frequencies is that the sampled population is large and randomly mated. However, the natural populations of *Felis catus* are generally subdivided into smaller local populations, such as many populations of mammals that have populations divided with small effective numbers (SINNOCK, 1975; PATTON and FEDER, 1981; PEÑUELA and CÁRDENAS, 2012). This division promotes genetic heterogeneity or a higher rate of change in allele frequencies to a smaller geographic size (PEÑUELA and CÁRDENAS, 2012; PARDO *et al.*, 2016). However, the evolutionary force driving this change has not been precisely determined. When populations are subdivided, the observed number of homozygotes would be higher than expected, resulting in the Wahlund effect, a stochastic process generated by geographic isolation (SINNOCK, 1975). In this context, the introduction of immigrants by human dispersion seems to have an important influence on the social and reproductive structure of cats, preventing the high frequency of homozygotes (PARDO *et al.*, 2017a; 2017b).

These factors explain genetic heterogeneity, but it is possible that stochastic processes and selective differential agents have no significant effects (RUÍZ-GARCÍA, 1999). In this case, the genetic profile of the colonies would vary according to founder effects (PEÑA-CRUZ and PATIÑO-MONTOYA, 2017). In addition, dividing the size of the population for isolation would modify the genetic profiles of the populations, which would result in greater inbreeding and reduced genetic diversity (SCHWARTZ and ARMITAGE, 1980). However, several studies have shown that stochastic processes and consanguinity do not play an important role in the genetic composition of cats at micro and macrogeographic levels, especially in the urban context, where the estimation of gene flow is high (RUÍZ-GARCÍA, 1999).

Currently, the genetic profile of cats has been inventoried in many cities of Colombia (RUÍZ-GARCÍA and ÁLVAREZ, 1999; PEÑUELA and CÁRDENAS, 2012; PARDO *et al.*, 2015; PEÑA-CRUZ *et al*., 2015; PARDO *et al.*, 2016; PEÑUELA *et al.*, 2016; CAUSIL-VARGAS *et al.*, 2017; PARDO *et al.*, 2017a; PARDO *et al.*, 2017b; PARDO-PÉREZ *et al.*, 2017; LEMOS *et al.*, 2019). The city of Cali has been previously studied at the macrogeographic level by RUÍZ-GARCÍA and ÁLVAREZ (1999), and PEÑUELA *et al.* (2016). Nevertheless, at the microgeographic level, PEÑA-CRUZ *et al*.

(2015) found a Hardy-Weinberg (HW) imbalance due to the deficit of heterozygotes in the orange locus, which was explained by the differences in the length of time at the sampling sites. These findings suggest that in small populations with different times of antiquity, the genetic profile would be affected, which would lead to greater genetic heterogeneity among these small populations (SCHWARTZ and ARMITAGE, 1980; RUÍZ-GARCÍA, 1999; PEÑUELA and CÁRDENAS, 2012; PARDO *et al.*, 2016). The purpose of this study was to estimate allele frequencies based on coat markers and to know how genetic diversity varies at different spatial and temporal scales, with special emphasis on genetic heterogeneity at the microgeographic level.

MATERIALS AND METHODS

Phenotypic markers and sampling process

The standardized genetic nomenclature for cats was used to identify the genes. The 9 phenotypic markers used were orange vs. no-orange (*O, o*); agouti vs. non-agouti (*A, a*); tabby mackerel vs. tabby blotched (t^+, t^b); full color vs. dilution (*D, d*); short hair vs. long hair (*L, l*); white spotting vs. no spotting (*S, s*); white color dominate vs. wild color (*W, w*), wild vs. siamese (*C, cs*) and manx vs. long tail (*Mm, mm*) (Committee on Standardized Genetic Nomenclature for Cats 1968).

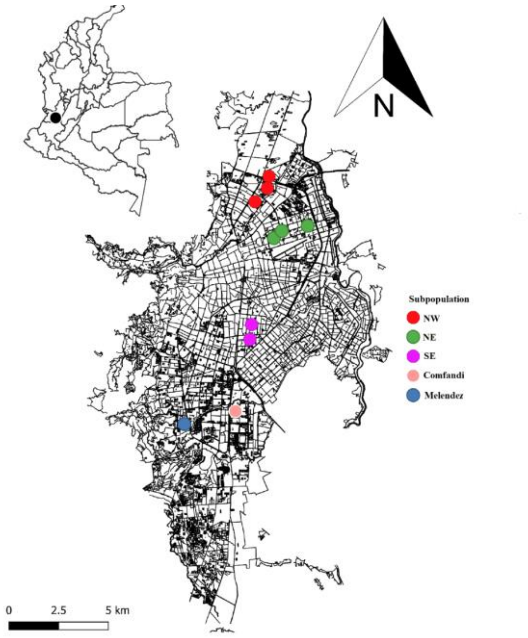

Figure 1. Location of colonies and subpopulations in the city of Cali for domestic cat sampling.

Cat sampling was performed using the PEÑA-CRUZ and PATIÑO-MONTOYA (2017) method, defining the subpopulations and colony levels according to the political organization of the city of Cali, with a colony being a neighborhood with a specific time of foundation and

geographically isolated from others. The set of neighborhoods forms a subpopulation. The colonies within each subpopulation are separated from each other by streets, avenues, and parks, while the subpopulations are separated by large distances between 4 and 12.7 km. In total, 5 subpopulations were selected: Northeast NE: [Sena (53 years), Salomia (60 years), Sta. Bárbara (18 years)], Northwest NW: [Álamos (42 years), Brisas-Álamos (19 years), La Merced (42 years)], Southeast SE: [San Carlos (50 years), Ciudad Modelo (46 years)], and Meléndez and Ciudad Comfandi. For the analysis, the urban variable "Antiquity" is expressed in years of colonial history reported by the "Plan de Ordenamiento Territorial de Cali" (Fig. 1).

Analysis of genetic diversity

HW equilibrium was performed for the orange locus in each colony and subpopulation because they allow phenotypically recognizing heterozygous individuals. After testing the HW equilibrium hypothesis, the allele frequencies were estimated for the rest of the loci. Different sample sizes were considered for each locus due to epistatic events.

The genetic analysis was performed using a model of genetic diversity in subdivided populations. This method is used for populations with hierarchical structures independent of mutation, selection, and migration (NEI, 1973). The G_{ST} parameter that measures genetic differentiation between subpopulations in relation to the total population was estimated. The G_{CS} parameter was also estimated, which measures the differentiation between colonies within each subpopulation and between the colonies in relation to the total population (G_{CT}) (NEI, 1973, CROW and AOKI, 1984). A correction for the sampling error was used, where $F_{ST}' = (F_{ST} - 1)/(2NT)$ and the significance was evaluated with the Chi-square test, $X^2_G' = 2NTF_{ST}'$. For each locus, F_{ST}' and X^2_G' were examined at all hierarchical levels. Finally, gene flow was estimated using an n-dimensional island model such as $Nm\alpha = [(1/F_{ST}') -1] / 4[n(n-1)]^2$, where n is the number of colonies or subpopulations. In this study, F_{ST}' was used instead of G_{ST} to estimate gene flow (NEI, 1973).

Association between genetic diversity and antiquity

Two regression analyses were performed to establish some association between the genetic diversity of the domestic cat population of the colonies in the city of Cali and antiquity of colonies. In the first analysis, the allele frequencies of each of the genes were associated with the antiquity of the colonies; in the second, the degree of differentiation of the colony with the total population (F_{CT}) was associated with the antiquity of each colony. For each regression, the equation describing the linear model, the coefficient of determination R^2 and the significance of the relationship using the F test, was determined using the software Statistica version7 (STATSOFT, 2004).

RESULTS

Genetic profile and HW equilibrium

The genetic profiles of subpopulations and colonies of Cali-Colombia show the manx allele and the non-agouti allele as the least common and the most common, respectively (Table 1). The manx allele was found at low frequencies in 2 colonies of the NW subpopulation (Álamos = 0.0132; Brisas-Álamos = 0.0109). At the colonial level, San Carlos had the highest frequency of the *O, d* and *S* alleles but the lowest frequency of the *cs* allele. In contrast, Santa

Barbara had the highest frequency of the *cs* allele and the lowest frequency of a allele, while Ciudad Modelo had the highest frequency of the *a* allele.

Table 1. Allele frequency and standard deviation of O = orange, a = non-agouti, t^b = tabby blotched, d = dilution, l = long hair, S = white spotting, W = dominant white, cs = siamese and M = manx; n = sample size of the colonies and subpopulations (NE, NW, SE, MEL, C. Comf.) defined from Cali, Colombia.

	n	*O*	*a*	t^b	*d*	*l*	*S*	*W*	*cs*	*M*
NE	**136**	0.23±0.026	0.72±0.035	0.24±0.036	0.38±0.033	0.42±0.030	0.36±0.030	0.02±0.008	0.44±0.030	0.00±0.000
Salomia	51	0.26±0.044	0.72±0.059	0.28±0.063	0.31±0.050	0.52±0.049	0.33±0.048	0.03±0.016	0.35±0.048	0.00±0.000
Sena	55	0.22±0.040	0.79±0.048	0.28±0.062	0.43±0.053	0.30±0.043	0.38±0.046	0.01±0.009	0.45±0.047	0.00±0.000
St.Barb	30	0.22±0.055	0.58±0.090	0.00±0.000	0.39±0.079	0.45±0.064	0.39±0.066	0.03±0.023	0.57±0.066	0.00±0.000
NW	**129**	0.22±0.026	0.69±0.034	0.28±0.036	0.31±0.031	0.49±0.031	0.30±0.029	0.02±0.008	0.36±0.030	0.01±0.005
Alamos	38	0.18±0.043	0.69±0.062	0.30±0.072	0.35±0.058	0.40±0.056	0.29±0.052	0.00±0.000	0.37±0.055	0.01±0.013
Bri.Ala	46	0.20±0.043	0.66±0.057	0.19±0.051	0.28±0.051	0.49±0.052	0.31±0.050	0.03±0.018	0.34±0.051	0.01±0.010
LaMer.	45	0.28±0.049	0.73±0.057	0.35±0.067	0.33±0.054	0.58±0.052	0.31±0.050	0.02±0.015	0.37±0.052	0.00±0.000
SE	**75**	0.23±0.034	0.76±0.041	0.26±0.046	0.55±0.043	0.42±0.040	0.37±0.040	0.01±0.006	0.31±0.037	0.00±0.000
SanCar.	35	0.29±0.053	0.64±0.065	0.20±0.058	0.55±0.061	0.45±0.059	0.43±0.059	0.00±0.000	0.24±0.050	0.00±0.000
C.Mod.	40	0.18±0.043	0.86±0.047	0.31±0.071	0.54±0.060	0.39±0.054	0.32±0.053	0.01±0.012	0.36±0.054	0.00±0.000
Mel.	**56**	0.27±0.043	0.76±0.048	0.33±0.064	0.34±0.050	0.52±0.047	0.35±0.047	0.03±0.015	0.39±0.047	0.00±0.000
C.Comf.	**31**	0.14±0.043	0.76±0.066	0.00±0.000	0.42±0.072	0.45±0.064	0.27±0.056	0.00±0.000	0.51±0.063	0.00±0.000

*Table 2. Statistical test for Hardy-Weinberg equilibrium at the orange locus (O, o) in colonies and subpopulations of cats from Cali. Subpopulations = NE, NW, SE, Meléndez, Ciudad Comfandi; Obs = Observed; Exp = Expected; **significant value of chi-squared test (X^2, $p < 0.05$).*

	Females						*males*				
	OO		*Oo*		*oo*		*Oy*		*oy*		
	Obs	Exp	Obs	Exp	Obs	Exp	Obs	Exp	Obs	Exp	X^2
NE	9.00	4.30	18.00	27.56	49.00	44.14	13.00	12.84	41.00	41.16	7.62**
Salomia	4.00	1.93	4.00	10.86	20.00	15.20	8.00	5.26	12.00	14.74	7.49**
Sena	3.00	1.55	10.00	10.76	18.00	18.69	3.00	5.14	20.00	17.86	1.27
Sta. Barbara	2.00	0.84	4.00	5.88	11.00	10.28	2.00	2.44	9.00	8.56	0.85
NW	1.00	3.06	21.00	21.65	41.00	38.29	18.00	13.23	42.00	46.77	2.86
Alamos	0.00	0.58	4.00	5.50	15.00	12.92	6.00	3.33	13.00	15.67	2.10
Bri.-Alamos	0.00	1.07	9.00	8.41	17.00	16.52	5.00	3.45	12.00	13.55	0.71
La Merced	1.00	1.45	8.00	7.31	9.00	9.25	7.00	6.80	17.00	17.20	0.03
SE	2.00	1.62	10.00	10.93	19.00	18.45	10.00	9.83	33.00	33.17	0.04
San Carlos	1.00	1.14	7.00	5.71	6.00	7.14	5.00	6.00	16.00	15.00	0.34
C. Modelo	1.00	0.54	3.00	4.99	13.00	11.47	5.00	3.93	17.00	18.07	0.64
Meléndez	1.00	2.07	10.00	11.08	17.00	14.86	10.00	6.79	15.00	18.21	1.85
Ciudad Comfandi	2.00	0.38	3.00	4.89	16.00	15.73	0.00	1.35	10.00	8.65	4.31

The *W* allele was not reported in San Carlos, Ciudad Comfandi and Álamos, and the t^b allele was also not reported in Santa Barbara and Ciudad Comfandi. The lowest frequencies of *d* and *l* were found in Brisas Álamos and Sena, respectively. At the subpopulation level, Meléndez had the highest frequency of *O*, *a*, t^b, *l* and *W*, while Ciudad Comfandi had the lowest frequency of *O*, t^b, *S* and *W* but had the highest frequency of *cs*. The SE subpopulation had the lowest frequency of *l* and *cs* but the highest frequency of *d* and *S*. The NW subpopulation showed the lowest frequency of the *a* and *d* alleles (Table 1). The HW equilibrium in the orange locus showed significant deviations in the Salomia colony and the NE subpopulation ($X^2 = 7.49$, $p = 0.0062$ and $X^2 = 7.62$, $p = 0.0058$, respectively, Table 2). When Salomia is removed from the NE subpopulation, the absence of HW equilibrium ($X^2 = 7.49$, $p = 0.0062$) continues due to the deficit of heterozygotes in female cats.

Analysis of genetic diversity

Table 3 shows the genetic diversity between colonies by subpopulation. The colonies within the NE and SE subpopulations presented significant heterogeneity ($F_{CS}' = 0.0221$, $p < 0.001$ and $F_{CS}' = 0.0140$, $p < 0.05$, respectively), with the NE being the subpopulation with the highest degree of genetic differentiation. However, the colonies within the NW subpopulation showed no genetic differentiation between them ($F_{CS}' = 0.0073$, $p > 0.05$). Significant heterogeneity in the NE subpopulation was attributable to loci *a* ($F_{CS}' = 0.0290$, $p < 0.05$), *t* ($F_{CS}' = 0.0753$, $p < 0.001$), *l* ($F_{CS}' = 0.0370$, $p < 0.05$) and *C* ($F_{CS}' = 0.0223$, $p < 0.05$), being the subpopulation with more loci with significant heterogeneity and a greater degree of genetic differentiation compared to the SE subpopulation, which only showed significant heterogeneity at locus *a*. Although estimates of gene flow in locus *S* of the NE subpopulation and locus *a* of the NW subpopulation were especially high ($Nm\alpha = 295$ and $Nm\alpha = 402.5$, respectively).

Table 3. Genetic diversity (Gcs, Fcs´) and gene flow (Nmα) within each subpopulation, O = orange, a = non-agouti, t = tabby, d = dilution, l = long hair, S = white spotting, W = dominant white, C = Color repart. 1. NE, 2. NW, 3. SE.

	G_{CS}			F_{CS}'			X^2			$Nm\alpha$		
Loci	1	2	3	1	2	3	1	2	3	1	2	3
O	0.00	0.01	0.02	0.00	0.01	0.01	0.43	2.10	1.43	70.40	13.60	6.50
a	0.03	0.00	0.07	0.03	0.00	0.06	7.89*	0.07	9.04*	3.70	402.50	1.00
t	0.08	0.02	0.01	0.08	0.02	0.01	20.49**	5.24	1.12	1.40	5.40	8.30
d	0.01	0.00	0.00	0.01	0.00	0.01	2.51	0.25	0.99	11.90	113.70	9.50
l	0.04	0.02	0.00	0.04	0.02	0.00	10.07*	4.34	0.45	2.90	6.50	21.00
S	0.00	0.00	0.01	0.00	0.00	0.01	0.10	0.90	0.97	295.00	31.90	9.70
W	0.01	0.01	0.02	0.00	0.01	0.01	0.50	1.43	1.37	60.80	20.00	6.80
C	0.03	0.00	0.02	0.02	0.00	0.01	6.07*	0.79	1.51	4.90	36.00	6.20
Mean	0.03	0.01	0.02	0.02	0.01	0.01	48.06**	15.12	16.85*	4.90	15.10	4.40

**significant value of chi-squared test (X^2 *p < 0.05 and **p < 0.001).*

In the analysis of genetic diversity between subpopulations (Table 3), the subpopulations within the Cali population have significant heterogeneity (F_{ST}' = 0.0112, p < 0.001), mainly due to the loci *t*, *d* and *C*. In this analysis, the estimation of gene flow (Nmα) with the loci evaluated varied between 5.2 and 61.8, with tabby and dilution being the loci with the lowest estimates ($Nm\alpha$ = 5.2 and $Nm\alpha$ = 6.2, respectively) and the greatest significant heterogeneity (F_{ST}' = 0.0296, p < 0.001 and F_{ST}' = 0.0252, p < 0.001, respectively). The white locus obtained the highest estimate of gene flow ($Nm\alpha$ = 61.8) and the lowest degree of genetic differentiation between the subpopulations (F_{ST}' = 0.0026).

Finally, significant heterogeneity was observed between the colonies of the Cali population (F_{CT}' = 0.0278, X^2 = 190.08, p < 0.001; Table 4). The genetic diversity attributable to the colonies within the subpopulations and the total population resulted from the analysis of the geographic structure with the most loci with significant heterogeneity. The F_{CT}' values were statistically significant for loci *a* (F_{CT}' = 0.0307, p < 0.05), *t* (F_{CT}' = 0.0458, p < 0.001), *d* (F_{CT}' = 0.0506, p <0.001), *l* (F_{CT}' = 0.0301, p < 0.05) and *C* (F_{CT}' = 0.0389, p < 0.001). It is important to highlight that the tabby locus (*t*) always had the greatest significant heterogeneity (p < 0.001) at all geographic levels (Tables 3, 4).

*Table 4. Genetic diversity (Gcs, Fcs´, F_{CT}') and gene flow (Nmα) between subpopulations and attributable to colonies within subpopulations and the total population, in O = orange, a = non-agouti, t = tabby, d = dilution, l = long hair, S = white spotting, W = dominant white, C = Color repart. *p < 0.05, **p < 0.001*

	Between subpopulations					**Colonies for total**					
Loci	G_{ST}	F_{ST}'	X^2	*df*	$Nm\alpha$	G_{CS}	G_{CT}	F_{CT}'	X^2	*df*	$Nm\alpha$
O	0.0053	0.0041	3.52	4	38.6	0.009	0.009	0.008	7	9	24.5
a	0.0053	0.0041	3.52	4	38.6	0.029	0.032	0.031	26.22*	9	6.4
t	0.0308	0.0296	25.27**	4	5.2	0.043	0.047	0.046	39.15**	9	4.2
d	0.0264	0.0252	21.52**	4	6.2	0.019	0.052	0.051	43.20**	9	3.8
l	0.0064	0.0052	4.46	4	30.5	0.025	0.031	0.03	25.70*	9	6.5
S	0.0048	0.0036	3.07	4	44.3	0.005	0.009	0.008	6.41	9	26.8
W	0.0038	0.0026	2.2	4	61.8	0.011	0.012	0.011	9.18	9	18.6
C	0.016	0.0148	12.65*	4	10.6	0.025	0.04	0.039	33.22**	9	5
Mean	0.0123	0.0112	76.22**	32	14.2	0.021	0.029	0.028	190.08**	72	7.1

Regression analysis

The regression analysis of the allele frequencies vs. antiquity of the colonies was significant only for the tabby blotched allele (R^2 = 0.42 p < 0.05), finding a positive association, that is, the allele frequencies increase with older colonies. On the other hand, in the relationship of the structure of each colony (F_{CT}) with antiquity, a significant relationship was found (R^2 = 0.53 p < 0.05), with the highest values of differentiation in the most recent colonies (Fig. 2).

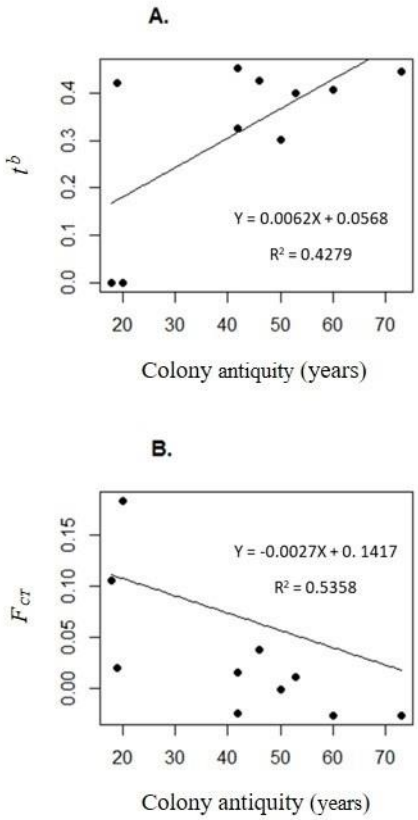

Figure 2. Regression analysis of the genetic diversity of the cat population in the city of Cali and the antiquity of colonies in years. A. Allele frequency of tabby blotched (t^b recessive form) vs. Colony antiquity, B. Genetic differentiation (F_{CT}) vs. Colony antiquity.

DISCUSSION

The genetic profile of the cat population described in this study does not differ significantly from the previous study by PEÑA-CRUZ *et al.* (2015), considering the city of Cali as a single population. The high gene flow, the low population structure, the high frequencies of the *a* allele and the low frequencies of the *W* allele are characteristics that it shares with the other Colombian cities despite the differences in size, number of inhabitants and climatic differences (RUÍZ-GARCÍA *et al.*, 1999; MONTES-DÍAZ *et al.*, 2015; PARDO *et al.*, 2015; PEÑUELA *et al.*, 2016; PARDO *et al.*, 2017a; 2017b). This is due to the European origin of the population of Colombian domestic cats, explained by the hypothesis of historical migration at the time of the conquest

(RUÍZ-GARCÍA *et al.*, 1999; PEÑUELA *et al.*, 2016; PARDO *et al.*, 2017a). In contrast to the stochastic processes at the microgeographic scale, which have been used as a tentative explanation for the configuration of the genetic profiles in each of the Colombian cities, the association with urban variables entails a greater presence of people, which directly influences the allele frequencies of coat genes in domestic cats (PEÑA-CRUZ and PATIÑO-MONTOYA, 2017).

Anthropic selection would be identified at different spatial and temporal scales; however, for the city of Cali, unlike most cities, HW equilibrium is found for the locus orange. In addition, the genetic structure found through time in previous temporal research do not provide sufficient evidence to support the novelty selection argument in a microgeographic scale (PEÑA-CRUZ and PATIÑO-MONTOYA, 2017). In the case of the Salomia colony and the NW subpopulation, the lack of HW equilibrium for the orange locus is due to an excess of heterozygotes probably caused by the difference in antiquity within the subpopulation, due to the colony of Santa Barbara was built 40 years after Sena and Salomia.

According to the above, the anthropic effect on the population of cats in the city of Cali would be the urban landscape, consisting of buildings, roads, and green areas. However, feline birth control in the city is quite scarce and there is a lack of care or customs of breeding with domestic cats, allowing them to cross with feral or street cats, keeping the population in panmixia (PEÑA-CRUZ and PATIÑO-MONTOYA, 2017). The significant relationship of the diversity of the tabby locus and the antiquity in this city, supports the hypothesis on the high frequencies of the gene in its recessive form (tabby blotched) in rural areas in the department of Córdoba (CAUSIL-VARGAS *et al.*, 2017). Therefore, the colony with less antiquity presents less genetic diversity of the locus. It takes time for cats carrying these less common alleles to migrate from other colonies or the nearest rural area.

Finally, for the city of Cali the genetic differentiation of the colonies with respect to the total population is correlated with the antiquity of the colonies, as proposed in the work of PEÑA-CRUZ *et al.* (2015). Although no evidence of subpopulations or metapopulations was found, it was observed that the recent colonies showed higher F_{CT} values with respect to the ancient colonies, indicating a different configuration of the genetic profile of domestic cats that, due to the high gene flow, quickly would homogenize the sector with its surroundings. There is no drift or selection force that causes a differentiation within the population to generate a system of patches or sink sources. For further studies evaluating cat populations in large cities, we recommend developing experimental designs that consider age and geographic distance between colonies, to obtain a detailed measure of what is happening at the sub-population level.

CONCLUSION

In conclusion, domestic cats in the city of Cali behave as a single population, with incipient gene microstructure phenomena, which are part of the natural dynamics of the population in their interaction with the urban environment, as evidenced by the relationship of the colonies. It is recommended to delve into the effect of urban variables other than artificial selection on the gene profile of domestic cat populations in Colombian cities at different spatial and temporal scales that would broaden the prospect of factors that modulate the genetic behavior of domestic cat populations.

ACKNOWLEDGMENTS

To the owners of the pets for allowing us to register their cats for this study.

Received, April 13en, 2020
Accepted January 30en, 2021

REFERENCES

CAUSIL-VARGAS, L.A., E., PARDO-PÉREZ, Y.M., HERRERA-BENAVIDES (2017): Evaluation of the genetics of domestic cats (Felis catus) through genes associated with coat in Sahagún, Córdoba, Colombia. Revista Tecnología en Marcha, *29*(4): 57-66.

COMMITTEE ON STANDARDIZED GENETIC NOMENCLATURE FOR CATS (1968): Standardized genetic nomenclature for the domestic cat. J Hered., *59*:39-49.

CROW, J., K., AOKI (1984): Group selection for a polygenic behavioral trait: Estimating the degree of population subdivision. P. Natl. Acad. Sci. USA, *81*:6073-6077.

KAELIN, C., G., BARSH (2013): Genetics of pigmentation in dogs and cats. Annu Rev Anim Biosci., *1*:125-156.

LEMOS, C., B., CÁRDENAS, J., GUZMÁN, C., BECERRA, D., CASTRO, S., CAÑÓN, A., ALMENDRA, J., VALENCIA, M., PEÑUELA (2019): Diferenciación genética de las poblaciones de *Felis catus* en los municipios de Restrepo y Darién del Valle del Cauca, Colombia. Rev. Asoc. Col. Cienc. (Col.), *31*: 36-44.

MONTES-DÍAZ, Y., Y.C., E., BARRIOS PARDO-PÉREZ (2015): Analysis of genetic variations in populations of domestic cats (*Felis catus*) by coat genes in Cartagena, Colombia. *RACCEFYN*, *39*(153): 503-513.

NEI, M. (1973): Analysis of gene diversity in subdivided populations. P. Nac. Acad. Sci. USA, *70*(12):3321-3323.

PARDO, E., L., CAUSIL, A., RODRÍGUEZ (2015): Study of the genetic diversity of domestic cat (*Felis catus*) by genes associated with coat color in Lorica-Córdoba, Colombia. Arch. Zootec., *64*(248): 389-395

PARDO, E., Y., MONTES, Y., CARDALES (2016): Genetic variability of the domestic cat (*Felis catus*) in Magangué, Bolívar, Colombia. Revista de Investigaciones Veterinarias del Perú., 27(2): 277-287.

PARDO PÉREZ, E., M.T., MARTÍNEZ BULA, J.D., ZAMBRANO CHARRASQUIEL (2017a): First report of genetic variability in cats (*Felis catus*), with phenotypic markers, in Coveñas, Sucre. Rev Med Vet., *36*: 27-36.

PARDO, E., L.A., CAUSIL VARGAS, B.L., MUÑOZ MASS (2017b): (Genetic profile of population of cats (*Felis catus*) in Riohacha, La Guajira, by coat genetic marks. Revista Facultad de Ciencias Básicas., *13*(2): 128-132.

PARDO-PÉREZ, E., T.I., CAVADÍA-MARTÍNEZ, J.L., BARRERA-VIOLETH (2017): Genetic diversity of the cat (*Felis catus*) through morphological markers in San Bernardo del Viento, Colombia. Rev Salud Anim., *39*(3): 1-10.

PATTON, J., J., FEDER (1981): Microspatial genetic heterogeneity in pocket gophers: Non-random breeding and drift. Evolution, *35*:912-920.

PEÑA-CRUZ, A.F., S., SANDOVAL, A., PATIÑO, M., BEDOYA, A., RODRÍGUEZ, J., ORJUELA *et al*. Genetic Analysis of the Cat Population of North and South of Cali, Colombia. Acta Biol., Colomb., *20*(1):111-118.

PEÑA-CRUZ, A.F., A., PATIÑO-MONTOYA (2017): Temporal differentiation of the genetic profiles of the cat population in Cali, Colombia, during the last decades. *RACCEFYN*., *41*(159): 187-191.

PEÑUELA, M., H., CÁRDENAS (2012): Marcadores genéticos del pelaje en gatos domésticos de Capurganá-Colombia (Coat genetics mark in domestic cats). Momentos de Ciencia., *9*(1):28-33.

PEÑUELA, M., E., PARDO, V.H., GARCÍA, H., CÁRDENAS (2016): Coat genetic markers of the domestic cat *Felis catus* (Felidae) from sotuhwestern Colombia. Rev. MVZ Córdoba, *21*(2):5390-5403.

PONTIER, D., N., RIOUX, A., HEIZMANN (1995): Evidence of selection on the orange allele in domestic cat *Felis catus*: the role of social structure. Oikos., *73*: 299-308.

RUIZ-GARCÍA, M., D., ÁLVAREZ, A., KAJON (1999): Spatial autocorrelation analysis of cat colonies at microgeographic level in three cities: Barcelona, Palma de Mallorca (Spain) and Buenos Aires (Argentina). Bol. R. Soc. Esp. Hist. Nat., *95*(1-2):193-211.

RUÍZ-GARCÍA, M., D., ÁLVAREZ (2008): A biogeographical population genetics perspective of the colonization of cats in Latin America and temporal genetic changes in Brazilian cat populations. Genet. Mol. Biol., *31*(3):772-782.

RUÍZ-GARCÍA, M., D., ÁLVAREZ (2000): Genetic microstructure in two Spanish cat populations. I: genic diversity, gene flow and selection. Genes Genet. Syst., *75*:269-280.

RUIZ-GARCÍA, M., D., ÁLVAREZ (1999): Phylogenetic analysis of 21 latin american cat populations with 10 morphologic loci using genetic distance matrix and maximum parsimony methods. Bol. R. Soc. Esp. Hist. Nat., *95*(3-4):139-164.

RUÍZ-GARCÍA, M., K., KLEIN (1997): Genetic structure of populations of the domestic cat in Catalonia (Spain) and upper Midwestern USA: a microgeographic and macrogeographic study. J. Genet., *76*(2):99-115.

RUIZ-GARCÍA, M. (1997): Genetic relationships among some new cat populations sampled in Europe: a spatial autocorrelation analysis. J. Genet., *76*: 1-24.

RUÍZ-GARCÍA, M. (1999): Genetic structure of different cat populations in Europe and South America at a microgeographical level: importance of the choice of an adequate sampling level in the accuracy of population genetics interpretations. Gen. Mol. Biol., *22*(4):493-505.

RUÍZ-GARCÍA, M. (1994): Genetic structure of the Marseilles cat population: is there really a strong founder effect? Gen. Sel. Evol., *26*: 317-331.

SCHWARTZ, O., K., ARMITAGE (1980): Genetic variation in social mammals: the marmot model. Science, *207*:665-667.

SINNOCK, P. (1975): The Wahlund effect for two-locus model. Am. Nat., *109*(969):565-570.

STATSOFT, INC. (2004): STATISTICA (data analysis software system), version 7. www.statsoft.com.

POPULACIONA GENETIKA U MULTIPLIM SKALAMA: GENETIČKA MIKROSTRUKTURA POPULACIJE MAČAKA U KULUMBIJI

Mauricio PEÑUELA[1], Angie PATIÑO-MONTOYA[2], Andrés PEÑA-CRUZ[3], Heiber CÁRDENAS[4]

[1]Prirodno-matematički fakultet, Univerzitet Vale, Kolumbija
[2]Univerzitet u Braziliji, Brazil
[3]Oblast Vale, Kolumbija
[4]Departaman za biologiju, Prirodno-matematički fakultet , Univerzitet Vale, Kolumbija

Izvod

Uzimajući u obzir istraživanja genetike mačaka, cilj ove studije bio je upoređivanje genetske raznolikosti domaće populacije mačaka u različitim prostornim i vremenskim razmerama. Prema administrativnoj podeli grada Kali, izabrano je 8 kolonija (lokaliteta), koje zajedno čine 5 subpopulacija za uzorkovanje unutar grada. Fenotip na osnovu dlake iz ogrtača svakog uzorka korišćen je za naknadno izračunavanje frekvencija alela, ravnoteže Hardi-Vejnberga (HV), genetske strukture i korelacije genetske raznolikosti i strukture u svakoj sredini. Non-aguti alel je pokazao najvišu frekvenciju, a beli alel je imao najniže frekvencije u svim kolonijama i subpopulacijama; prijavljen je i alel Manks. Ravnoteža HV pronađena je i za lokus bele pegavosti i za narandžasti, osim za kolonije Salomia, Sena i Santa Barbara iz subpopulacije SZ. Pronađena je značajna povezanost između raznolikosti tabbi lokusa i starosti i diferencijacije kolonija (FCT) na osnovu starosti. Može se zaključiti da se domaće mačke u gradu Kali ponašaju kao jedinstvena populacija, sa započetim fenomenima genetske mikrostrukture, koji su deo prirodne dinamike populacije u njihovoj interakciji sa urbanom sredinom.

Primljeno 13. IV.2020.
Odobreno 30. I. 2021.