Webology (ISSN: 1735-188X)
Volume 19, Number 4, 2022

Genetic Variability Of The Domestic Cat (Felis Catus) By Genetic Markers From The Coat In The Department Of Sucre-Colombia

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Abstract

The objective of the research was to determine the genetic variability of the domestic cat Felis catus using ten genetic markers of hair coat in 13 subpopulations of the department of Sucre. A total of 1548 cats were genotyped for ten dominant hair markers in 13 subpopulations of Sucre. Allele frequencies per loci, percentage of polymorphic loci (%P) and expected heterozygosity (He) were estimated for each subpopulation. Hardy-Weinberg equilibrium (EHW) was calculated for the orange and spotted white loci. An analysis of molecular variance (AMOVA) was performed between subpopulations, estimating the coefficient of genetic differentiation (FST). A matrix of FST and geographic distances was constructed for the Mantel test. The GST (gene differentiation coefficient) was estimated from similar reports in 31 municipalities and 15 departments. The highest allelic frequency was at the spotted white locus and the lowest at the Abyssinian locus. Genetic diversity was moderate, with the lowest diversity found at the Abyssinian and Siamese loci. The most diverse loci were Inhibitor and Orange. Likewise, the most and least diverse subpopulations according to He and %P were Sincelejo and Buenavista, respectively. The dendrograms suggest that there is no population structure and that gene flow is high. In conclusions, the domestic cat of the department of Sucre has high genetic diversity, low population structure and high gene flow.

Keywords: dominant genes, genetic diversity, population genetics, population structure

Introduction

The domestic cat (Felis catus) is a carnivorous mammal of the felidae family, small in size and with a body weight of about 5 kg. It is an agile predator with a small head, short muzzle and abundant vibrissae, retractable claws, flexible and slender body, covered by fur, sharp teeth, forelegs with 5 digits and hind legs with 4 digits that can live up to 20 years in captivity [1]. It comes from five maternal lines of Near Eastern wildcats (Felis silvestris lybica) and would have been domesticated from wild cats (Felis libyca) more than 10,000 years ago. Today, due to their adaptive characteristics, they are globally distributed [2].

Cats are an ideal species for population studies of genetic diversity because they are cosmopolitan animals and their populations tend to panmixia [3]. Therefore, cats present evident polymorphisms, coherent with the color, pattern and texture of the coat, which present different inheritance patterns, feasible to recognize with the naked eye, which is why data collection is a simple procedure [4]. Genetic profiles for these traits have been reported in populations around the world [5-6]. Even so, similar studies are nonexistent in many places, despite their need to understand the evolutionary history and construction of phylogenetic hypotheses about their populations, it has been proposed that these relationships have been determined by human migrations [2-7].

In Colombia, the census of domestic cats amounted to 1,938,517 animals for 2019, of which 1.43% is located in the department of Sucre (Minsalud, 2020). In this department, there are previous reports in the municipalities of Coveñas [8] and Santiago de Tolú [9] on the variability of phenotypic markers in domestic cat coat genes. On this basis, the objective of this research was to determine the genetic variability of the domestic cat Felis catus by means of ten genetic markers of fur in 13 subpopulations of the department of Sucre.

Materials and methods

Study population. Taking into account the ethical, technical, scientific and administrative norms for animal research contained in Law 84 (National Congress of Colombia, 1989), 1548 cats (852 males and 692 females) were genotyped for fur markers by direct and photographic observation, belonging to the department of Sucre and the municipal capitals of Buenavista (BUE, n=60), Corozal (CLZ, n=140), Los Palmitos (LPA, n=60), Sampués (SAM, n=262), San Antonio de Palmito (SAP, n=60), San Marcos (SMA, n=90), San Onofre (SON, n=60), San Pedro (SPE, n=106), Santiago de Tolú (SDT, n=60), Sincé (SCE, n=76), Sincelejo (SJO, n=454), Sucre (SUC, n=60) and Toluviejo (TOL, n=60).

Collation routes were designed by neighborhood and/or commune within each municipality to avoid resampling. Inclusion criteria for the study were adult, clinically healthy, well-differentiated sex and unrelated individuals when more than one individual was genotyped in the same household. The genotypes were obtained by door-to-door visits, asking about the existence of feline pets, under consent, and the individuals were inspected and photographed. In addition, we asked whether the animals were sterilized or not. Finally, georeferencing data for each municipality was obtained from the web page of each of the corresponding municipalities.

Genetic markers studied. Ten dominant markers proposed by the Committee on Standardized Genetic Nomenclature for Cats [10], were genotyped and are described in Table 1. Nine markers were autosomal and only the Orange gene is sex-linked.

Table 1. Description of the ten genes genotyped in 1548 cats from the department of Sucre-Colombia.

Loci	Alleles	Characteristics	Gene/mutation
Orange (O)	o	Wild: not orange pigmentation	Not reported
	O	Mutant: all pigmentation is orange; epistatic for detection of the A locus. Heterozygous female can be identified.	
Agouti (A)	A	Wild: Agouti color	ASIP /deletion 2bp exon 2
	a	Mutant: color no-Agouti; un mismo color; color negro; epistático para la observación del locus T	
Abyssinian (Ti)	Ti(+)	Wild: Normal color, not Abyssinian	DKK4/ 188G>A/c.53C>T
	Ti(A)	Mutant: Abyssinian	
Tabby (Ta)	Ta(+)	Wild: Mackerel o or brindle	LVRN/c.176C>A
	Ta(b)	Mutant: Blotched tabby	
Dilution (D)	D	Wild: Dense color	MLPH
	d	Mutant: Dilute color	
Spotted white (S)	s	Wild: No stains	KIT/ insertion 617 pb intron 3 y 5
	S	Mutant: With white spots, incomplete dominant. The heterozygote can be identified.	
Inhibitor (I)	I	Wild: Normal color	Not reported
	I	Mutant: Basal part of the hair depigmented, pheomelanin discoloration, silvery appearance.	
	w	Wild: Color normal	

Dominant white (W)	W	Mutant: Completely white	KIT/ insertion completa del FERV1 intron 3 y 5
Long hair (L)	L l	Wild: Short hair Mutant: Long hair	FGF5/R136X
Siamese (C)	C c^s	Wild: Normal color Siamés: Concentrated color in places of the body more distant from the individual.	TYR exon 2 G > A G302R

Fuente: adaptado de [1,9]

Data analysis. In a first analysis, using GenAlEx software ver 6.5 [11], allele frequencies for dominant genes, assuming Hardy-Weinberg equilibrium (EHW), were estimated within each subpopulation (township). The percentage of polymorphic loci (%P) and the expected heterozygosity (He) were estimated within each municipality of the department. The theoretical deviations of EHW were calculated in the loci where heterozygous individuals could be distinguished (O and S locus). A molecular variance analysis was performed among the municipalities of Sucre, from which the coefficient of genetic differentiation (G_{ST}) was estimated. Nei's genetic distance and Wright's FST index between pairs of subpopulations were estimated. A Mantel test with 9999 replicates was performed between Wright's FST and georeference matrices. Finally, the MEGA X program [12] was used to construct a dendrogram from the genetic distance matrix using the Neighbor Joining algorithm.

In a second analysis, all literature reports of similar studies in Colombia were used, which included 7558 cats from 34 subpopulations, including Bogotá, Bucaramanga, Cali-1, Duitama, Ibagué, Leticia, Pasto, Popayan-1 [5], Leticia-Tabatinga [2], Capurganá [13], Montería [14] Cali-2 [15], Cartagena [16], Lorica [17], Buga, Bugalagrande, Cartago, Cali-3, Jamundí, Obando, Palmira, Pereira, Piendamó, Popayan-2, Santander de Quilichao ,Tuluá [3], Magangué [4], Rioacha [18], Santa Marta [19], Coveñas [8], Mompox [20], Santiago de Tolú [9], Calima and Restrepo [1] in 31 municipalities and 15 different departments, to estimate the G_{ST} genetic coefficient, from a molecular variance analysis grouped by subpopulation and by department using GenAlEx software ver 6. 5 [11]. With this same population structure, the genetic distance of Nei was estimated, which was used to construct a dendrogram by means of the Neighbor Joining algorithm, using the MEGA X program

Results

The table 2 shows the allelic frequencies for the ten loci evaluated in the 13 subpopulations. The O locus presented the highest frequency in the BUE subpopulation and the lowest in the SCE subpopulation. For the locus, the BUE and SUC subpopulations presented similar and the highest frequency, while the lowest frequency was in the SDT subpopulation. Only in the SJO subpopulation was the Ti(A) locus found with low frequency (1.68%). In the SON and BUE subpopulations, the highest and lowest frequencies were found for the Ta(b) locus, respectively. The d locus, presented the widest range in terms of frequency, the lowest was in the SAP subpopulation and the highest in the SON subpopulation. The SUC subpopulation showed the highest allele frequency in the S gene and the SDT subpopulation the lowest. In the SON and SUC subpopulations, the same and the lowest frequency were found for locus I, the highest frequency was present in LPA. The W gene was not present in the BUE, SON, SDT and SUC subpopulations. For this locus, the SAP subpopulation showed the highest frequency. The l locus was not found in BUE, SAP and SCE, while the highest frequency was in the SJO subpopulation. Finally, at locus c, the SON subpopulation showed the highest frequency, and it was absent in the BUE, SAP, SPE, SCE and TOL subpopulations.

Regarding genetic diversity indicators, the lowest values of expected heterozygosity (He) were found in the Ti(A) and c loci. Whereas, the most diverse loci were I and O. For the other loci, this value ranged from 25.8 to 38.9% (Table 3). Considering all subpopulations, the average %P was 81.5±10.7% and that of He was 0.339±0.012. The BUE subpopulation showed the lowest genetic diversity, reflected in the low %P and He values, on the contrary, the SJO subpopulation, presented the highest genetic diversity (Table 3).

At the O locus, the CLZ, SAM, SCE, SJO, SUC and TOL subpopulations showed significant deviations from Hardy-Weinberg equilibrium (Table 4). Although, the analysis of the whole population showed equilibrium. In contrast, for the S locus, the entire population and eight subpopulations showed deviations from the theoretical Hardy-Weinberg equilibrium.

Table 4. Hardy-Weinberg equilibrium for O and S loci in 13 subpopulations of the department of Sucre, Colombia.

subpopulations	**Locus O**		**Locus S**	
	Value X^2	**p- Value**	**Value X^2**	**p- Value**
BUE	4.214	0.332	34.166	0.000
CLZ	6.989	0.050	0.071	0.355
LPA	5.458	0.195	1.283	0.156
SAM	18.168	0.009	32.115	0.000
SAP	4.729	0.789	2.465	0.085
SMA	4.868	0.135	31.975	0.000
SON	3.100	0.517	1.327	0.145

SPE	8.205	0.055	13.510	0.046
SDT	2.287	0.382	39.777	0.000
SCE	12.984	0.010	28.393	0.000
SJO	32.726	0.002	17.353	0.000
SUC	12.983	0.010	0.133	0.876
TOL	10.805	0.039	33.277	0.000
All	5.809	0.194	22.807	0.000

BUE: Buenavista, CLZ: Corozal, LPA: Los Palmitos, SAM: Sampués, SAP: San Antonio de Palmito, SMA: San Marcos, SON: San Onofre, SPE: San Pedro, SDT: Santiago de Tolú, SCE: Sincé, SJO: Sincelejo, SUC: Sucre, TOL: Toluviejo

Table 2. Allelic frequencies for ten coat related loci in 13 subpopulations in the department of Sucre, Colombia.

Subpoblación	N	O	a	Ti(A)	Ta(b)	d	S	I	W	l	c
BUE	60	0.817±0.050	0.983±0.017	0.000±0.000	0.683±0.060	0.447±0.064	0.876±0.043	0.730±0.057	0.000±0.000	0.000±0.000	0.000±0.000
CLZ	140	0.697±0.039	0.892±0.033	0.000±0.000	0.759±0.042	0.802±0.044	0.845±0.039	0.667±0.049	0.337±0.050	0.239±0.036	0.120±0.028
LPA	60	0.606±0.063	0.753±0.056	0.000±0.000	0.817±0.050	0.753±0.056	0.796±0.052	0.796±0.052	0.365±0.062	0.258±0.057	0.258±0.057
SAM	262	0.648±0.029	0.781±0.026	0.000±0.000	0.763±0.027	0.774±0.027	0.770±0.027	0.654±0.030	0.221±0.026	0.262±0.027	0.087±0.017
SAP	60	0.775±0.054	0.674±0.099	0.000±0.000	0.686±0.079	0.316±0.104	0.817±0.079	0.577±0.090	0.408±0.100	0.000±0.000	0.000±0.000
SMA	90	0.633±0.051	0.803±0.042	0.000±0.000	0.803±0.042	0.745±0.046	0.830±0.039	0.667±0.049	0.211±0.043	0.149±0.038	0.149±0.038
SON	60	0.548±0.064	0.633±0.062	0.000±0.000	0.837±0.048	0.913±0.004	0.817±0.050	0.447±0.064	0.000±0.000	0.258±0.057	0.316±0.060
SPE	106	0.630±0.047	0.801±0.039	0.000±0.000	0.813±0.038	0.644±0.047	0.858±0.034	0.566±0.048	0.194±0.038	0.194±0.038	0.000±0.000
SDT	60	0.633±0.062	0.516±0.066	0.000±0.000	0.753±0.056	0.707±0.059	0.633±0.062	0.658±0.061	0.000±0.000	0.183±0.049	0.183±0.049
SCE	76	0.281±0.052	0.585±0.057	0.000±0.000	0.778±0.048	0.669±0.054	0.743±0.050	0.707±0.052	0.229±0.048	0.000±0.000	0.000±0.000
SJO	454	0.674±0.022	0.813±0.018	0.017±0.010	0.813±0.018	0.736±0.021	0.805±0.019	0.597±0.023	0.199±0.019	0.425±0.023	0.163±0.017

SUC	60	0.577±0.064	0.983±0.017	0.000±0.000	0.796±0.052	0.775±0.054	0.913±0.036	0.447±0.064	0.000±0.000	0.258±0.057	0.258±0.057
TOL	60	0.707±0.059	0.837±0.048	0.000±0.000	0.730±0.057	0.548±0.064	0.775±0.054	0.707±0.059	0.183±0.049	0.258±0.057	0.000±0.000
All	1548	0.633±0.050	0.773±0.045	0.001±0.001	0.772±0.047	0.679±0.052	0.806±0.045	0.632±0.054	0.181±0.034	0.191±0.034	0.118±0.025

BUE: Buenavista, CLZ: Corozal, LPA: Los Palmitos, SAM: Sampués, SAP: San Antonio de Palmito, SMA: San Marcos, SON: San Onofre, SPE: San Pedro, SDT: Santiago de Tolú, SCE: Sincé, SJO: Sincelejo, SUC: Sucre, TOL: Toluviejo. O: Orange, a: Agouti, Ti(A): Abyssinian, Ta(b): Tabby, d: Dilution, S: Spotted white, I: Inhibitor, W: Dominant white, L: Long hair, c: Siamese. All: Mean and Standard Deviation.

Table 3. Genetic diversity (He) and percentage of polymorphic loci for ten coat-related loci in 13 subpopulations in the department of Sucre, Colombia.

Subpoblación	**O**	**a**	**Ti(A)**	**Ta(b)**	**d**	**S**	**I**	**W**	**l**	**c**	**%P**	**He**
BUE	0.300	0.033	0.000	0.433	0.494	0.218	0.394	0.000	0.000	0.000	60%	0.234±0.066
CLZ	0.422	0.193	0.000	0.365	0.318	0.262	0.444	0.447	0.364	0.212	90%	0.337±0.029
LPA	0.478	0.372	0.000	0.300	0.372	0.325	0.325	0.464	0.383	0.383	90%	0.378±0.018
SAM	0.456	0.342	0.000	0.361	0.350	0.354	0.453	0.344	0.387	0.159	90%	0.365±0.027
SAP	0.349	0.439	0.000	0.431	0.432	0.300	0.488	0.483	0.000	0.000	70%	0.342±0.060

SMA	0.465	0.317	0.000	0.317	0.380	0.282	0.444	0.333	0.254	0.254	90%	0.330±0.024
SON	0.495	0.465	0.000	0.273	0.159	0.300	0.494	0.000	0.383	0.432	80%	0.347±0.052
SPE	0.466	0.319	0.000	0.305	0.458	0.244	0.491	0.313	0.313	0.000	80%	0.339±0.047
SDT	0.465	0.499	0.000	0.372	0.414	0.465	0.450	0.000	0.298	0.298	80%	0.370±0.046
SCE	0.404	0.486	0.000	0.345	0.443	0.382	0.414	0.354	0.000	0.000	70%	0.327±0.056
SJO	0.440	0.304	0.033	0.304	0.389	0.314	0.481	0.319	0.489	0.272	100%	0.380±0.028
SUC	0.488	0.033	0.000	0.325	0.349	0.159	0.494	0.000	0.383	0.383	80%	0.311±0.059
TOL	0.414	0.273	0.000	0.394	0.495	0.349	0.414	0.298	0.383	0.000	80%	0.352±0.045
All	0.434±0.057	0.314±0.153	0.003±0.009	0.348±0.050	0.389±0.089	0.304±0.077	0.445±.049	0.258±0.188	0.280±0.169	0.184±0.168	81.5±10.7%	0.339±0.012

BUE: Buenavista, CLZ: Corozal, LPA: Los Palmitos, SAM: Sampués, SAP: San Antonio de Palmito, SMA: San Marcos, SON: San Onofre, SPE: San Pedro, SDT: Santiago de Tolú, SCE: Sincé, SJO: Sincelejo, SUC: Sucre, TOL: Toluviejo. O: Orange, a: Agouti, Ti(A): Abyssinian, Ta(b): Tabby, d: Dilution, S: Spotted white, I: Inhibitor, W: Dominant white, L: Long hair, c: Siamese. %P: Percentage of polymorphic loci, He: expected heterozygosity. All: Mean and Standard Deviation

The analysis of molecular variance (Table 5) among the subpopulations of the department of Sucre showed a low percentage of variation (10%), as did the coefficient of genetic differentiation (p= 0.001). Likewise, the Mantel test between geographic distances and the FST index showed no correlation between the two (p= 0.493). In this sense, the dendrogram constructed using the Neighbor Joining algorithm from the genetic distance matrix (Figure 1) did not show genetic proximity between neighboring subpopulations.

Tabla 5. Analysis of molecular variance and population structure with different levels of organization from ten coat-related loci.

Between Sucre Municipalities					
Source of Variation	d.f.	Mean square	%	G_{ST}	p- value
Between Municipalities	12	12.734	10%		
Within Municipalities	1535	1.789	90%	0.0997	0.001
Total	1547		100%		
Between Colombian Municipalities					
Between Municipalities	46	32.270	28%		
Within Municipalities	9060	1.495	72%	0.2825	0.001
Total	9105		100%		
Between Departments					
Between Departments	14	82.929	28%		
Within departments	9091	1.574	72%	0.2754	0.001
Total	9105		100%		

d.f.: degree of freedom, G_{ST}: coefficient of gene differentiation

By including the literature reports of similar work in Colombia in the analysis of population structure, there were 47 subpopulations or municipalities. Thus, the analysis of molecular variance with this structure showed a high percentage of variation among the subpopulations, which meant a high and significant (p= 0.001) G_{ST} value (Table 5). Figure 2A corresponds to the dendrogram constructed using the Neighbor Joining algorithm with all the municipalities of Colombia. Its analysis shows that the subpopulations of Sucre behave as a single population, which is related to the cats of the municipality of Magangué. Then, it is clear the formation of two large groups, the first one formed by all the subpopulations belonging to the Caribbean region and the second one by the subpopulations of the center, south-west and south of Colombia. To simplify the analysis, each subpopulation was assigned to the corresponding department, thus, 15 populations represented in the same number of departments were obtained. The analysis of molecular variance (Table 5) showed a high population structure (G_{ST}= 0.2754, p= 0.001). Figure 2B shows the dendrogram constructed using the Neighbor Joining

algorithm for all the departments, where the grouping of the departments of the Caribbean region is clear.

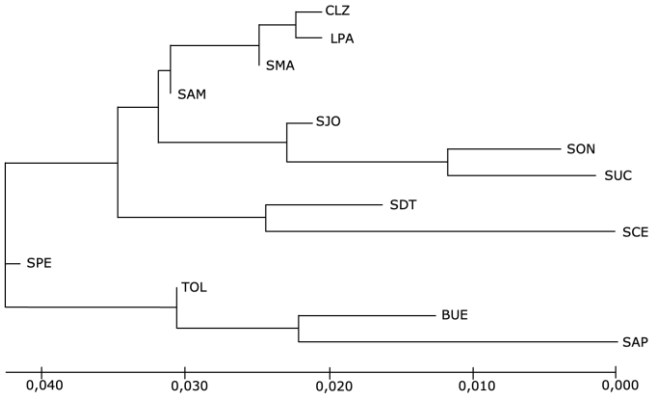

Figure 1. Dendrogram Neighbor Joining in 13 subpopulations of the department of Sucre, Colombia based on ten loci related to coat.. BUE: Buenavista, CLZ: Corozal, LPA: Los Palmitos, SAM: Sampués, SAP: San Antonio de Palmito, SMA: San Marcos, SON: San Onofre, SPE: San Pedro, SDT: Santiago de Tolú, SCE: Sincé, SJO: Sincelejo, SUC: Sucre, TOL: Toluviejo.

Discussion

Some authors suggest that allele frequencies from studies such as these should be interpreted with caution. This is because the data probably differ from populations of cats not kept in domestic conditions. However, during the process of collecting the phenotypes, little reproductive control by the human caretakers over the cats was evidenced, since only 10% of the females and 1% of the males that were genotyped were sterilized, which would favor panmixia [1, 3].

The high frequencies of the agouti and spotted white alleles could be related to the high environmental temperature and solar exposure in the study area, favoring the animals carrying these alleles, becoming a possible example of natural selection in situ [4, 21]. Likewise, the occurrence of selective processes associated with a progressive melanization of the coat is also possible [2], either due to high population densities or human interference. The latter is relevant, since a correlation has been demonstrated between coloration genes and behavioral traits; thus, more melanic animals are less fearful, less aggressive and less adaptable to urban environments [8, 20, 22].

On the other hand, the low frequencies found in the Ti(A) allele agree with those reported in studies carried out in the Colombian Caribbean region [4,8,19,10] and differ from those presented in feline populations in the southwestern part of the country [1,15]. It is affirmed that the frequencies of the Tabby locus are usually low in Latin America [2],

but high in Southeast Asia [3], where values of up to 30% are reported [5]. Likewise, it has been proposed that the W locus has pleiotropic effects on vision and hearing [23], which would explain the low frequency of this gene. The O, d and I loci presented the highest allelic variations, which is why they could be used as differentiators between subpopulations [3].

The presence of most of the markers studied in the subpopulations (%P) demonstrates the great variety of coat genes for Sucre cats. Likewise, the He values presented are in agreement with the majority of reports for Colombia, and are considered moderate [8,9,14,16]. In particular, the high genetic diversity found in the SJO subpopulation may be related to the larger population size, which surely favored the sampling of unrelated animals and a lower degree of inbreeding. On the contrary, in the BUE population, the low genetic diversity can be explained in principle by being the smallest municipality of the department and by its remoteness from the major population centers of the department, which could cause a lower genetic flow to and from the subpopulation.

The deviations from the Hardy-Weinberg equilibrium found in this study can be attributed to the deficit of heterozygotes for both loci in most of the subpopulations, which can be seen in the low He values. The latter could be attributed to evolutionary factors such as artificial selection, since people have a predilection for certain types of traits in cats, which has favored some phenotypic characteristics over others [4]. On the other hand, in other studies, EHW deviations have been attributed to excesses of heterozygous individuals [4], explained by the geographic proximity between the subpopulations analyzed. Since they are studies within a municipality, the geographic proximity causes an increase in gene flow between them, preventing inbreeding events and the increase of heterozygous genotypes in the population.

The population structure analysis allows inferring that the populations are genetically closely related and behave as a metapopulation, a situation that is attributed to the proximity of all the subpopulations and that is a reflection of a high genetic flow among them [4, 5]. In this regard, the population structure within Sucre was low, related to high gene flow. However, when the literature reports were included in the analysis of population structure, it increased considerably. This is evident in the dendrograms (Figure 2A and 2B), where the clustering between municipalities and neighboring departments is clear. This particular grouping may correspond to a common founding event of the Colombian Caribbean populations [5, 20], which originated from the Spanish populations during the process of colonization of America. Then, the relationship between these populations may be related to the vertiginous displacement of

the Spanish conquerors along the Magdalena River, where they established many cities in a short time [15].

In conclusion, the presence of all the markers studied in the Sucre cat population suggests a great genetic diversity available in the area, and the lack of human control over their reproduction considerably increased gene flow and panmixia. The highest allele frequencies corresponded to the Non-agouti and Spotting white alleles, while the Tabby bloched and Dominant white alleles presented the lowest frequencies. This could be related to factors such as high temperatures and anthropic preferences for aesthetic reasons. A possible effect of natural and/or artificial selection was evidenced in the Non-agouti and Spotting white markers. The genetic diversity found in this study was moderate. There was an absence of population structure in the department of Sucre, with greater variation within municipalities. The greatest population differentiation was achieved when other studies carried out in Colombia were included in the analysis, showing grouping according to the sampling region. It is recommended for future studies to include information on genetic polymorphisms of DNA, either in genomic studies and/or in mitochondrial DNA, to maximize the accuracy of the indicators of diversity, population genetic structure and genetic ancestry.

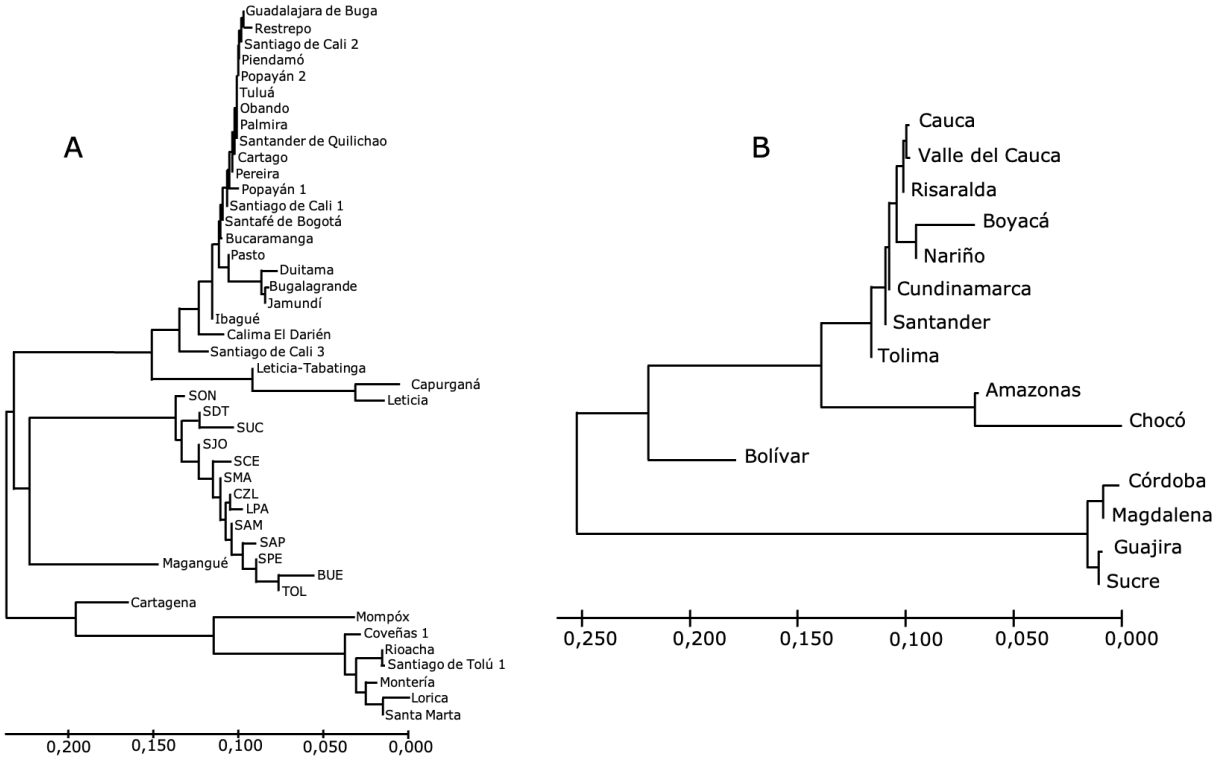

Figura 2. A. Dendrogram Neighbor Joining in 47 municipalities of Colombia from ten loci related to coat. B. Dendrogram Neighbor Joining in 15 departments of Colombia

from ten loci related to coat. BUE: Buenavista, CLZ: Corozal, LPA: Los Palmitos, SAM: Sampués, SAP: San Antonio de Palmito, SMA: San Marcos, SON: San Onofre, SPE: San Pedro, SDT: Santiago de Tolú, SCE: Sincé, SJO: Sincelejo, SUC: Sucre, TOL: Toluviejo.

Conflict of Interest

The authors declare that there are no potential conflicts of interest with respect to the research, authorship, or publication of this article.

Acknowledgments

The authors would like to thank the Universidad of Sucre for funding the research project, the "Student of the seedbed Animal Breeding and Reproduction Research" who participated in the collection of the phenotypes and the owners of the cats evaluated.

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