

Cat genetic profiles in Catalonia, Spain

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ABSTRACT

A study was made of three aspects of the genetic composition of some cat populations in Catalonia (Northeastern Iberian Peninsula, Spain). The allelic frequencies of the nine genes (O, A, T, D, L, S, W, C and I), which control color, tabby and length of coat, were investigated: 1) the cat population of Llansa only 8 km from the French frontier on the Mediterranean coast and a new sample obtained in the rural district of Castelldefels were shown to be in Hardy-Weinberg equilibrium for the O and S loci. 2) The second question concerned an analysis of the genetic relationships between the cat population of Llansa and other populations of Western Europe. Ruiz-Garcia *et al.* (*Mis. Zool.* 18: 169-196, 1995) looked for genetic similarity between cat populations in Northern Catalonia and France. Populations in central and Southern Catalonia had been found to be very distant from the French cat populations, genetically speaking. However, the cat population analyzed in Northern Catalonia did not show any increase in the genetic similarity with the French populations, and was found to be similar to the other cat populations in Catalonia, previously analyzed. A new sample of cats from Llansa, the northernmost of all populations in Catalonia sampled up to now, showed no increase in genetic similarity to French populations compared to other groups from Catalonia. The genic frequencies of the coat characteristics loci showed that the French and British cat populations were furthest away from the population of Llansa, among those of Western Europe. In general, the cat populations we sampled in Catalonia showed a greater genetic resemblance to Eastern Mediterranean and North African populations than to the cat populations found in Western Europe. 3) The third aspect concerns population change over time. In 1989, the genetic composition of a cat population from Castelldefels was analyzed. In 1994 this population was sampled again, and no significant differences were found in the eight allelic frequencies compared, which demonstrates great stability over time in the genetic profile of this cat population.

INTRODUCTION

The study of allelic frequencies of genes that control color, tabby and length of the coat in Catalan cat populations has, up to the present, given a pretty good idea of their genetic composition (Ruiz-Garcia, 1988,

1989, 1990a,b, 1991, 1993, 1994, 1997; Ruiz-Garcia *et al.*, 1995; Ruiz-Garcia and Klein, 1977).

Three basic genetic aspects were analyzed in the present study:

1) Two new samples of cats located in Llansa and in a rural area of Castelldefels were analyzed for possible Hardy-Weinberg equilibrium for two loci (O and S).

2) The study of Ruiz-Garcia *et al.* (1995) showed that: a) Northern Catalan populations (Girona, L'Estartit and Roses) were not more similar genetically to those of France, compared to cats from the rest of Catalonia, when Mendelian coat genes were studied. However, the northernmost of these populations,

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Roses, is located 20 km from the French frontier. We therefore sampled a small Catalan coast population further north and nearer to the French frontier (8 km), in Llansa.

3) Another question concerns with genetic population changes over time. In the few cat populations where this type of study has been conducted in London (Robinson, 1987), Lisbon (Todd, personal communication), Barcelona, Benidorm (Ruiz-Garcia, 1991; Robinson, 1971), Venice (Ruiz-Garcia, 1997), Athens (Todd *et al.*, 1974) and certain French populations (Pontier, 1989), the genetic stability over time has been very great. Nevertheless, it should be determined whether the stability of genetic profiles would also be maintained unchanged with passing generations in small rural populations or if stochastic and/or selective processes could alter, singly or together, the allele frequencies analyzed (Nei, 1987). Accordingly, in 1994 a sample of cats from the rural area of Castelldefels in Catalonia was analyzed, that had already been sampled in 1989. This time difference of five years could represent between 5 and 10 generations in the species analyzed, since, given the ecological conditions, this population can produce one or two generations each year (Natoli and De Vito, 1988).

MATERIAL AND METHODS

Seventy-five cats were sampled in Llansa (5000 inhabitants; Girona province) and 228 cats were examined in a rural area of Castelldefels (2000 inhabitants; Barcelona province) during July 1994. Each cat sampled was a stray, a feral cat or "pseudo-wild". Careful measures were taken in order not to repeat the observation of a cat previously examined in the different incursions made into these Catalan populations. The phenotypes of the cats were recorded directly from observation of the animals and the nomenclature used was that of the Committee on Standardized Genetic nomenclature for Cats (1968). The loci used were: the sex-linked *O* (*O*, *o*; Orange vs. Non-Orange) and the autosomal loci, *A* (*A*, *a*; Agouti vs. Non-Agouti), *T* (*T^a*, *t⁺*, *t^b*; Abyssinian vs. Mackerel vs. Blotched tabby), *D* (*D*, *d*; Intense color vs. Dilute color), *L* (*L*, *l*; Short hair vs. long hair), *S* (*S*, *s*; White spotting vs. Non-white spotting), *W* (*W*, *w*; Dominant White vs. Normal color), *C* (*C*, *c^s*; Full color vs. Siamese) and *I* (*I*, *i*; Inhibitor vs. Normal color). The inheritance of these genetic characteristics is Mendelian and they have complete or nearly complete penetrance (see Robinson, 1977; Wright and Walters, 1982; Ruiz-Garcia, 1994). Since the sex of all of the cats could not be determined,

a maximum likelihood approximation of Robinson and Silson (1969) and Robinson (1972) was used, assuming a 1:1 sex-ratio, to estimate the Orange allele frequency: $p(O) = (2a + b)/2N$, where *a* = number of Orange cats (*O/O* and *O/-*), *b* = number of tortoiseshell females (*O/o*) and *N* = total sample size for this locus. The standard error for the estimate of *p(O)* was:

$$\sqrt{p(2-3p)/(3-4p)}$$

(Robinson and Manchenko, 1981). With autosomal loci, recessive mutant frequencies (*q*) were taken as the square roots of observed phenotypic frequencies, while dominant mutant frequencies (*p*) were taken as $1 - q$. Standard errors were given by:

$$\sqrt{1-q^2/4N} \quad \text{and} \quad \sqrt{(2-p)p/4N}$$

for recessive and dominant alleles, respectively.

The *O* and *S* loci were used in order to be able to analyze Hardy-Weinberg equilibrium in the two population samples, because it is possible to distinguish the heterozygotes with them. In the case of the *S* locus, the white-spotted animals were classified on a scale from 1 to 9 (1 = 10% of the coat spotted white; 9 = 90% of the coat spotted white; Dreux, 1975). In different localities, it has been established that the heterozygotes for this characteristic have coat patterns that fall between 1 and 5. However, in other populations the heterozygotic individuals have oscillated between ranks 1-6. This could be due to the existence of different polygenes in the populations which alter the maximum phenotypic expression in the heterozygotes and/or to categorization which is not exactly identical among the different authors (Morrill and Todd, 1978; Ruiz-Garcia, 1991). For this reason, Hardy-Weinberg equilibrium was examined using both classifications of the heterozygotes at the *S* locus. The expected proportions for a Hardy-Weinberg equilibrium at the *O* locus were: O/O and $O/- = [p(1 + p)/2]N$; $O/o = p(1 - p)N$; o/o and $o/- = [(2 - p)(1 - p)/2]N$, where *p* is the frequency of *O* allele and *N* is the sample number at this locus. At the *S* locus, these proportions were calculated as follows: $ss = (1 - p)^2 N$; $Ss = 2p(1 - p)N$; $SS = p^2 N$, where *p* is the frequency of *S* allele and *N* the number of individuals sampled in this locus. The likelihood ratio criterion (Everitt, 1992) was used to analyze Hardy-Weinberg equilibrium at the *O* and *S* loci. Ku and Kullback (1974) and Williams (1976) showed that for a variety of reasons, this criterion is generally preferable to the classic chi-square test.

Allelic frequencies for seven loci (*O*, *A*, *T*, *D*, *L*, *S* and *W*) were used in the analytical work. *I* and *c^s* were not included in this analysis because they were rarely

found above trace levels, were exotic characters, or were not reported in other cat genetic population works. The genetic profiles of two groups of Catalan, Balearic, Italian, French and British populations were compared with the Llansa genetic profile reported here. The first group was composed of 15 populations (14 Western European populations plus Llansa). The second one was composed of 49 Western European localities (including Girona, L'Estartit, Roses and Llansa as representative populations from northern Catalonia). Additionally, an analysis grouped together a good part of the Western European populations used in previous analyses with populations from the Eastern Mediterranean basin and North Africa (a total of 35 populations). This was done in order to investigate whether, like other Catalan populations studied previously, those investigated here had greater genetic similarity to North African and Eastern Mediterranean cat populations than to Western European populations (Ruiz-Garcia, 1988, 1990a,b,c,d, 1991, 1994). The reasons for doing different classifications can be found in Sokal *et al.* (1984). The genetic profiles of all the cat populations used are in Lloyd and Todd (1989).

Genetic distances

To compare the genetic relationships between the cats of Llansa, the new rural Castelldefels sample and the other European cat populations, three genetic distances were used: Nei (1972) distance, the Cavalli-Sforza and Edwards (1967) chord distance and the Rogers (1972) distance. We used these genetic distance measures because each of them has different mathematical properties.

Dendrograms

Different algorithms were used to generate dendrograms with the two groups of Western European populations analyzed with the matrices obtained with these three genetic distances. To generate the clustering analysis, with the group of 15 European populations, UPGMA (Unweighted pair-group method), SINGLE (Single-linkage clustering) and COMPLETE (Complete-link method) algorithms were used (Sneath and Sokal, 1973; Crisci and Lopez-Armengol, 1983; Nei, 1987; Cuadras, 1991). In this study, we only show the UPGMA tree with the Nei (1972) distance for the 15 European population group. A strict consensus tree was also generated (Rohlf, 1982). This arose from the comparison between the nine trees obtained using UPGMA, SINGLE and COMPLETE, and the Nei, Cavalli-Sforza and Edwards and Rogers

distances. In addition, we used the neighbor-joining method (Saitou and Nei, 1987). This method generates unrooted trees. Because of this, we used the Llansa population as an outgroup element, to produce a tree with direction (Nei, 1987).

We obtained UPGMA trees with the Nei, Cavalli-Sforza and Edwards and Rogers distances with the 49 European population group. The UPGMA tree with the Nei distance (1972) is shown in Figure 2A. Also, a strict consensus tree produced by the comparison of three trees is shown in Figure 2B. As in the above case, trees with the neighbor-joining method and the three genetic distances used were obtained. Because this method does not generate rooted trees, the midpoint method was used to produce rooted trees (Farris, 1972).

We used the cophenetic correlation coefficient as a goodness-of-fit statistic for all those trees (Sneath and Sokal, 1973). We also calculated different indexes to establish the degree of similarity between the dendrograms that configure the consensus trees. These were the indexes of Colles, Mickevich (1980) and Schuh and Farris (1981).

Population canonic, principal coordinates and multidimensional scaling analyses

In order to investigate the genetic relationships between the Llansa population and other Western European cat populations from another analytical perspective, other multivariate techniques were used.

Two canonic analyses of populations were made using the Mahalanobis square distance (see Cuadras, 1991, and Ruiz-Garcia, 1997, for some theoretical aspects of this analysis). In the first one, Girona, L'Estartit, Roses and Llansa formed a group (northern Catalan populations). In the second analysis, each one of these populations was considered separately. The remaining four groups consisted of 13 Catalan and Balearic populations, six Italian populations, 17 French populations and nine British populations, respectively. As a complementary analysis, a principal coordinates analysis was developed (with the transformation of Gower, 1966), using the Rogers genetic distance matrix for the 15 European population group.

Also, it was investigated whether the samples described here retained the greater genetic similarity seen between the previously studied Catalan populations and North African and Eastern Mediterranean populations when compared to Western European populations. For this, a multidimensional scaling analysis with a monotone function was used (Kruskal, 1964a,b) coming from a space configuration of points at random using Nei's genetic distance matrix with 35

Western European, Eastern Mediterranean and North African populations. Fifty iterations were used to calculate the statistic called stress, which measured the goodness of fit of the distances in the configuration space to the monotone function of the original distances. A graphic matrix, "minimum spanning tree", was superimposed in order to see the probable local distortion generated by this process of dimensional reduction (Gower and Ross, 1969).

Temporal analysis of the rural Castelldefels cat population

In order to determine the existence of possible significant differences among the allele frequencies obtained in the rural population of Castelldefels sampled in 1989 and that sampled in 1994, the chi-square test was used. When the number of individuals compared was very small, Fisher's exact probability test was used.

RESULTS AND DISCUSSION

Hardy-Weinberg equilibrium

There was no significant statistical deviation between the observed and expected proportions in the Llansa and rural Castelldefels samples for the loci *O* and *S* (Tables I and II). Therefore, like many other cat populations, the two described here appear to be in Hardy-Weinberg equilibrium. Factors like consanguinity, Wahlund effect, selection for and/or against the homo and/or heterozygotes or different allele frequencies between the sexes apparently had no repercussions on these two cat populations for these two loci.

In Table III, we show the nine gene frequencies studied for these Catalan populations.

Table I - Likelihood ratio criterion for Hardy-Weinberg equilibrium at the Orange locus (*O*) in the Catalan cat populations of Llansa and rural Castelldefels. *O/O* = Orange females; *O/-* = orange males; *O/o* = heterozygote females; *o/o* = non-orange (wild) females; *o/-* = non-orange (wild) males. d.f. = Degree of freedom. NS = Not significant.

	<i>O/O</i> and <i>O/-</i>	<i>O/o</i>	<i>o/o</i> and <i>o/-</i>
Llansa			
Observed	13	13	48
Expected	12.32	14.36	47.32
		$\chi^2_L = 0.182$	1 d.f. NS
Rural Castelldefels			
Observed	26	35	156
Expected	26.10	34.78	156.11
		$\chi^2_L = 0.006$	1 d.f. NS

Table II - Likelihood ratio criterion for Hardy-Weinberg equilibrium at the White spotting locus (*S*) in the Catalan cat populations of Llansa and rural Castelldefels. *s/s* = Non-white spotting homozygotes; *S/s* = white spotting heterozygotes; *S/S* = white spotting homozygotes. 1-5 = Individuals up to 50% piebald white spotting were considered heterozygotes. 1-6 = Individuals up to 60% piebald white spotting were considered heterozygotes. d.f. = Degree of freedom. NS = Not significant.

Population	<i>s/s</i>	<i>S/s</i>	<i>S/S</i>	χ^2 (2 d.f.)
Llansa				
Expected	47.005	23.945	3.049	
Observed 1-5	47	22	5	$\chi^2_L = 0.604$, NS
Observed 1-6	47	25	2	$\chi^2_L = 0.459$, NS
Rural Castelldefels				
Expected	116.002	86.771	16.226	
Observed 1-5	116	80	23	$\chi^2_L = 3.045$, NS
Observed 1-6	116	85	18	$\chi^2_L = 0.226$, NS

Table III - Gene frequencies (*p*) and standard errors (SE) in the Catalan cat populations of Llansa and rural Castelldefels. The genetic profile of the 1989 rural Castelldefels is shown (Ruiz-Garcia, 1990b) for comparing with the profile of 1994 rural Castelldefels.

O = Orange; *a* = Non-Agouti; *t^b* = Blotched Tabby; *d* = Dilution; *l* = Long hair; *S* = White spotting; *W* = Dominant white; *c^s* = Siamese; *I* = Inhibitor. ^a*P* ± SE, ^bNumber of cats studied.

Population	<i>O</i>	<i>a</i>	<i>t^b</i>	<i>d</i>	<i>l</i>	<i>S</i>	<i>W</i>	<i>c^s</i>	<i>I</i>
Llansa	0.263 ± 0.047 ^a (74) ^b	0.742 ± 0.043 (60)	0.146 ± 0.072 (47)	0.236 ± 0.057 (72)	0.000 (74)	0.203 ± 0.035 (74)	0.000 (74)	0.115 ± 0.057 (75)	0.014 (73)
Rural Castelldefels (1994)	0.200 ± 0.024 (217)	0.781 ± 0.022 (192)	0.263 ± 0.047 (101)	0.263 ± 0.032 (217)	0.134 ± 0.033 (223)	0.272 ± 0.023 (219)	0.009 ± 0.004 (223)	0.149 ± 0.033 (224)	0.007 (218)
Rural Castelldefels (1989)	0.241 ± 0.022 (307)	0.798 ± 0.018 (262)	0.171 ± 0.042 (137)	0.221 ± 0.027 (307)	0.150 ± 0.028 (311)	0.283 ± 0.019 (307)	0.007 ± 0.003 (318)	0.186 ± 0.027 (311)	-

Dendrograms

1) With 15 European populations

The phenogram with the UPGMA algorithm and the Nei distance offered two principal groups (see Figure 1A), one composed of Catalan, Balearic and Italian populations and the other of French and British populations. On the other hand, the first cluster was composed of two other subgroups. In one of them, there were Catalan and Ciudadela (Balearics) populations. The other subgroup was composed of another Balearic population (Palma Majorca) and the Italian populations. The genetic relationship of Llansa, the new sampled population in the North of Catalonia, was shown to be closer to those in Barcelona and Ciudadela than to the other Catalan populations which were nearer geographically (like Girona and Roses and L'Estartit). The UPGMA tree with the Nei distance showed the highest cophenetic correlation coefficient, $r = 0.77277$ (approximate Mantel's t -test, $t = 8.251$, $P = 0.0000$; Monte Carlo simulation with 2000 permutations, $2000 < z$, $0 = z$, $0 > z$, $P = 0.0005$). However, as an example, with the SINGLE algorithm and with the Nei and Rogers distances, the Girona population showed more similarity to Llansa than to Rosas and L'Estartit. Nevertheless, and as a first approximation, Llansa, although only 8 km from the French frontier, did not have a greater genetic similarity to the French populations, and clearly belonged to the cluster of Catalan populations.

The strict consensus tree (see Figure 1B), coming from the comparison of nine trees (three different algorithms and three different distances), showed that there was a more constant relationship between French and British populations than in the case of Catalan, Balearic and Italian populations. The consensus indexes can be seen in Figure 1.

Figure 1C shows the analysis by the neighbor-joining method and by the Rogers distance, using the Llansa population as an outgroup element. It shows that the two populations genetically closest to Llansa were Girona and Rosas and L'Estartit, that is, the other two Catalan populations sampled in the north of Catalonia. The most genetically divergent populations with regard to Llansa were the French and British populations (especially the latter).

2) With 49 populations

As mentioned above, a way to analyze the stability of a classification is to include new OTUs. The UPGMA tree with the Nei distance (see Figure

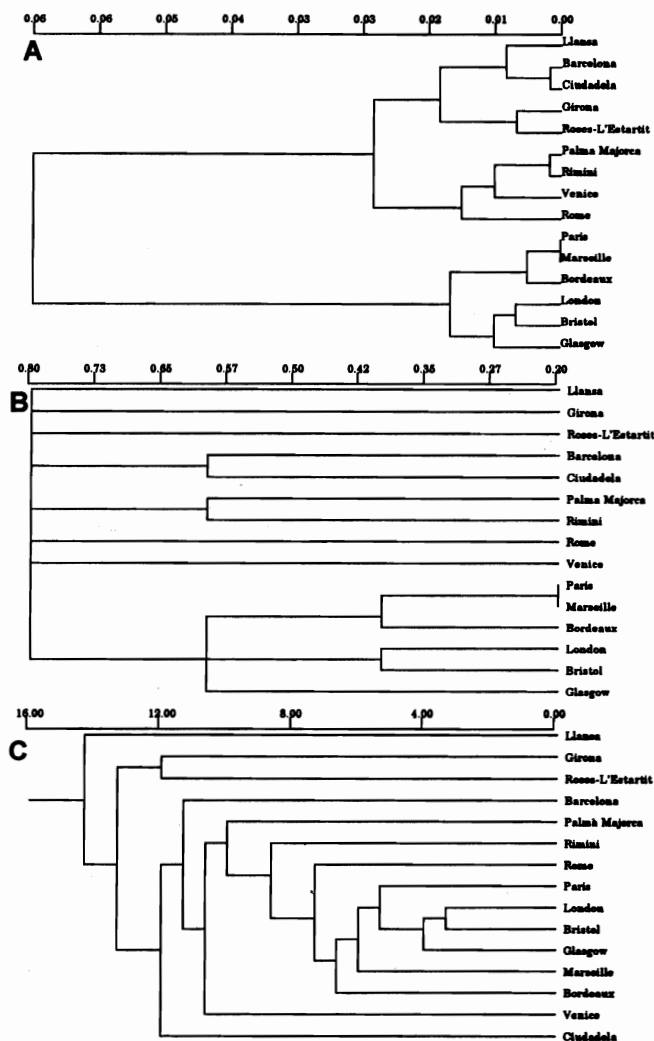


Figure 1 - Cluster analyses of 15 European cat populations. (A) UPGMA analysis with the Nei (1972) genetic distance. (B) Strict consensus tree using the UPGMA, SINGLE and COMPLETE algorithms with the Nei (1972), Cavalli-Sforza and Edwards (1967) and Rogers (1972) distances. Colles consensus index = 0.46154; Micevich consensus index = 0.22449; Schuh and Farris consensus index = 22. (C) Dendrogram using the neighbor-joining method (Saitou and Nei, 1987) using the Llansa cat population as an outgroup element.

2A; cophenetic correlation coefficient, $r = 0.70533$; approximate Mantel's t -test, $t = 16.311$, $P = 0.0000$ and a Monte Carlo simulation with 2000 permutations, where $2000 < z$, $0 = z$, $0 > z$, $P = 0.0005$) showed two large clusters. One of them only included Catalan and Balearic populations (with the exception of Palma Majorca). The other one contained all the Italian, French and British populations. Llansa was very similar to the Minorquinian populations (especially Ciudadela). Also, we observed that when Rosas and L'Estartit were treated as separate samples, the relationship between them with regard to the other Catalan and Balearic populations was different. L'Estartit was part of a cluster with two very near Catalan populations (Girona

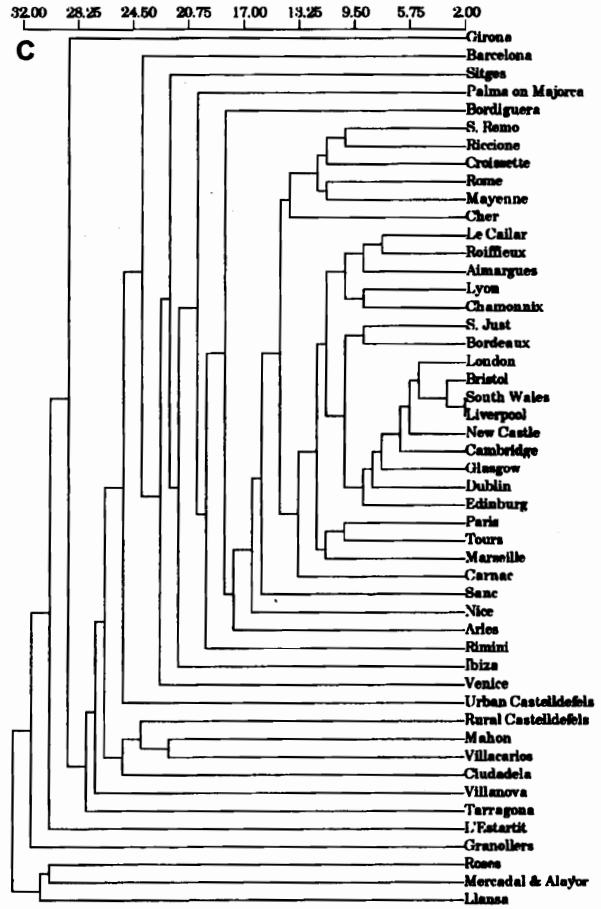
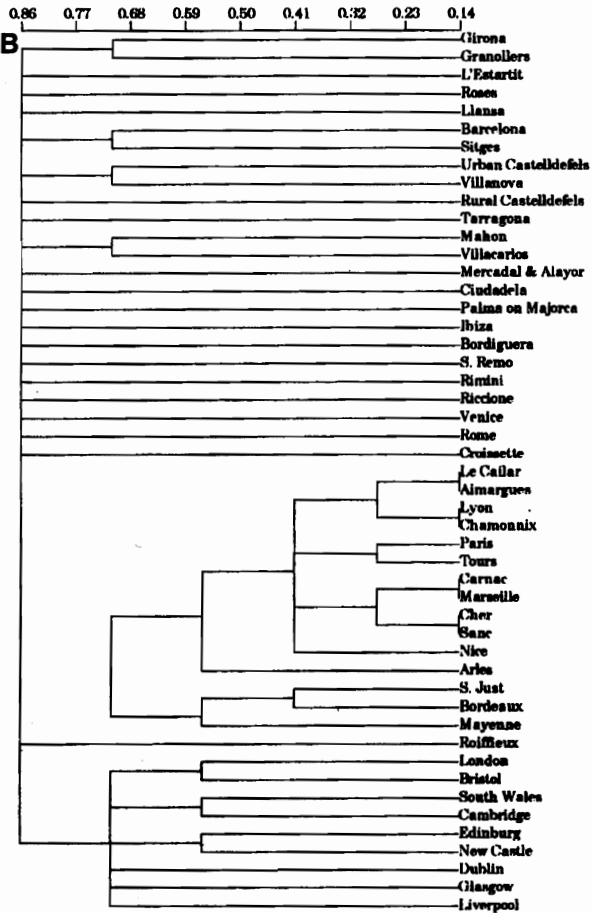
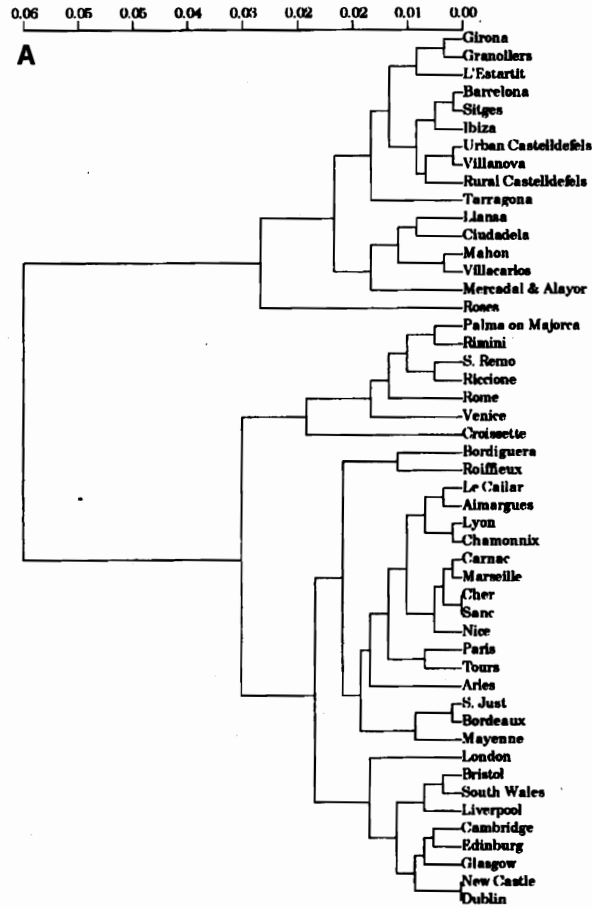


Figure 2 - Cluster analyses of 49 European cat populations. (A) UPGMA analysis with the Nei (1972) genetic distance. (B) Strict consensus tree using the UPGMA algorithm and the Nei, Cavalli-Sforza and Edwards and Rogers distances. Colles consensus index = 0.42553; Mickevich consensus index = 0.1111; Schuh and Farris consensus index = 290. (C) Dendrogram with the neighbor-joining method with the Cavalli-Sforza and Edwards (1967) chord genetic distance rotated by the midpoint rooting method.

and Granollers) while Roses was the most divergent sample from the Catalan-Balearic group.

The strict consensus tree using the UPGMA algorithm and the three genetic distances mentioned (Figure 2B) showed that the Catalan, Balearic and Italian populations were very different. The French and British populations were more similar no matter which genetic distance was used.

With the neighbor-joining method and with the Cavalli-Sforza and Edwards chord distance (Figure 2C), we obtained the best cophenetic correlation coefficient for this algorithm ($r = 0.66459$, approximate Mantel's t -test, $t = 6.327$, and Monte Carlo simulation with 2000 permutations, where $2000 < z$, $0 = z$, $0 > z$, $P = 0.0005$). However, this cophenetic correlation was notably lower than that obtained with other algorithms. In this tree we observed that the Llansa (Catalonia), Mercadal and Alayor (Minorca), Roses (Catalonia), Granollers (Catalonia), Girona (Catalonia) and L'Estartit (Catalonia) were the first ones that diverged from the tree. The most distant populations in relation to these were the French and British populations. That is, we observed again that the Llansa population, even though geographically very near to France, did not show greater genetic similarity to the French populations.

Population canonic and principal coordinate analyses

The results obtained with the two different canonic analyses of populations can be seen in Figures 3A and B. In the first, we observed that the critical region of the mean vector of the group consisting of Girona, L'Estartit, Roses and Llansa (all of them sampled in the north of Catalonia, that is, the nearest to France) widely superimposed the critical region of the mean vector corresponding to the other Catalan and Balearic populations. The remaining critical regions of the mean vectors of the other geographic groups (Italy, France, Great Britain) were very distant from the two Catalan population groups. In fact, this first population canonic analysis showed a $\lambda = 0.0149$ and $F = 10.6382$ with 28 and 134 degrees of freedom, with the Rao asymptotic approximation being $F = 1.5605$ for $\alpha = 0.05$. This meant that the mean vectors were significantly different between these geographic groups. In the second population canonic analysis, we considered the four North Catalan populations individually. It can be seen that the genetic profile of Girona was the most similar to the mean vector of Catalan and Balearic populations. The profiles of Llansa and L'Estartit were also near to the critical region of the Catalan and Balearic populations. The genetic profile of Roses was the most

divergent from the other Catalan and Balearic populations. Also, we can see, in this analysis, there were significant differences between the mean vectors of the four geographic groups considered, since $\lambda = 0.0069$ and $F = 6.1940$ with 49 and 182 degrees of freedom (F being $= 1.4243$ for $\alpha = 0.05$).

The principal coordinates analysis (three coordinates axis) with the Rogers distance and with 15 populations clearly showed that Llansa, even though it was population that was closest to France, was the Catalan population that had the lowest similarity to the French ones (Figure 4).

Some questions formulated by Ruiz-Garcia *et al.* (1995) can be answered with more detail in the present study: 1) though only 8 km from the French

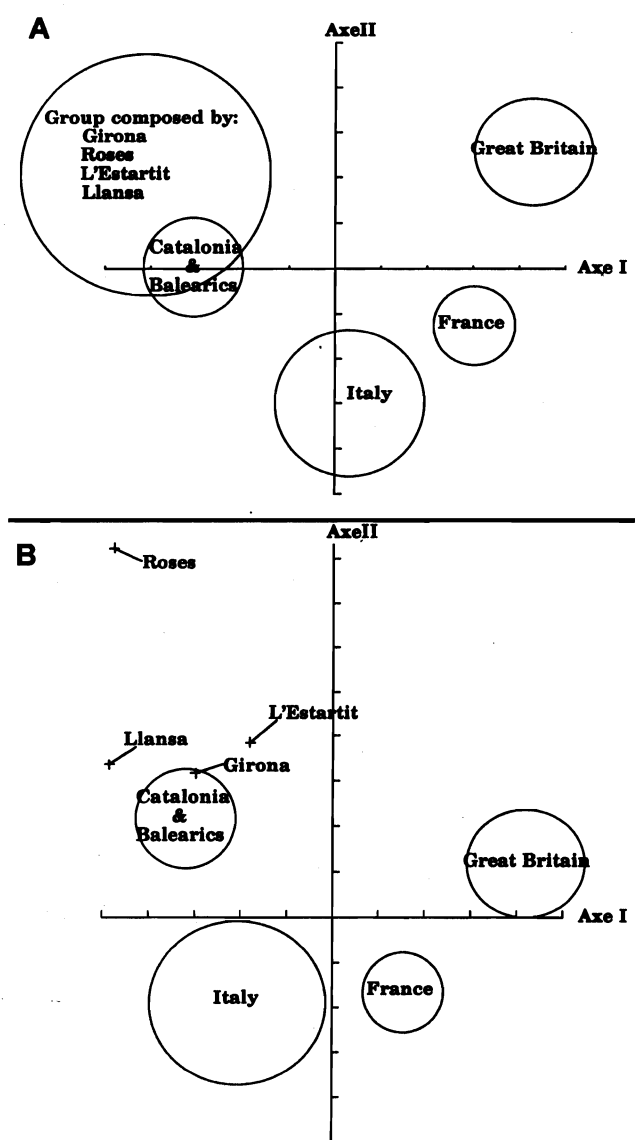


Figure 3 - Canonic population analyses (CPA). (A) CPA with Girona, L'Estartit, Roses and Llansa as the North Catalan cat group. (B) CPA where Girona, L'Estartit, Roses and Llansa were taken as individual populations.

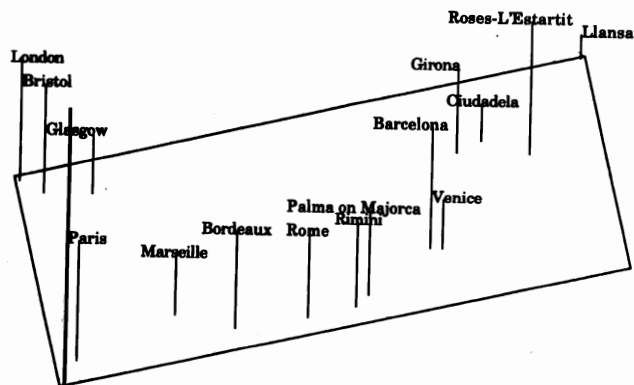


Figure 4 - Principal coordinates analysis with the Gower (1966) method using the Rogers genetic distance for 15 European cat populations.

frontier, there was no greater the genetic similarity with the French cat populations. It seems that in the Spanish Catalan coastal region there is no genetic influence coming from the French populations, although the cat population of Llansa (5000 inhabitants) is probably small and any gene flow from the nearby French populations could rapidly modify its genetic composition. 2) It seems that there is an abrupt gap between the gene pools of Spanish Catalan and French cats, and, if any kind of hybrid zone exists, it is in the south of France (French Catalonia).

Multidimensional scaling analysis

The nonmetric multidimensional scaling analysis, starting from Nei's distance matrix (Figure 5), clearly showed that the two new Catalan cat populations analyzed here maintained a close genetic relationship with other Catalan populations and with Eastern Mediterranean and North African populations, as has proven to be the case with other cat populations in this area of the Iberian Peninsula (Ruiz-Garcia, 1988, 1990b,c,d, 1991, 1994, 1997). This shows the relatively strong genetic homogeneity of all of the cat populations studied in Catalonia. The Llansa population showed the greatest genetic resemblance with the Greek population of Argolis (MST = 0.00199). The new sample from the rural area of Castelldefels most resembled three other Catalan populations, Barcelona (MST = 0.00169), Vilanova (MST = 0.00268) and the first sample obtained in the rural Castelldefels in 1989 (MST = 0.00249). The latter makes it manifest that the passage of 5-10 generations has introduced relatively few changes in the gene frequencies in the cat population of this rural locality. It also shows the strong influence of Barcelona cat populations on this rural population near the capital of Catalonia (about 25 km). Most inhabitants of this area originate from Barcelona, having country homes in this

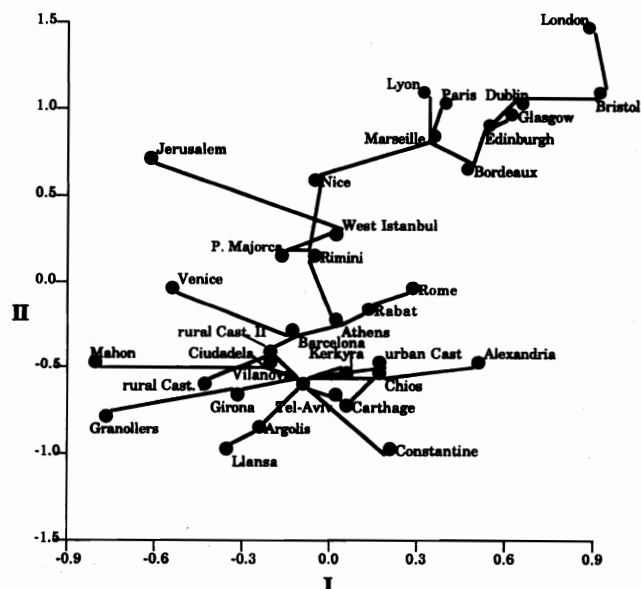


Figure 5 - Nonmetric multidimensional scaling analysis using the Nei genetic distance for 35 Western European, eastern Mediterranean and North African cat populations. Catalonia: Llansa, rural Castelldefels (1994), Barcelona, Granollers, urban Castelldefels, rural Castelldefels (1989), Girona, Vilanova. Balearics: Ciudadela (Minorca), Mahon (Minorca), Palma Majorca (Majorca). North-Africa: Rabat, Constantin, Carthage, Alexandria. Israel: Tel-Aviv, Jerusalem. Greece: Athens, Chios, Kerkyra, Argolis. Turkey: West Istanbul. Italy: Rome, Rimini, Venice. France: Nice, Paris, Lyon, Marseille, Bordeaux. Great Britain: London, Bristol, Glasgow, Edinburgh, Dublin.

region, which they use at certain times of the year, especially in summer. This could explain the close genetic similarity between this rural population and that of Barcelona. The multidimensional scaling analysis shown was obtained with 50 iterations and the final stress was 0.146. This means that the goodness of fit was "good".

Temporal comparison between the sample obtained in rural Castelldefels in 1989 and 1994

The comparison of eight allele frequencies in the rural population of Castelldefels showed that none of them changed significantly with the passage of 5-10 generations. The frequency that showed the greatest difference was $q(t^b)$ (0.17 in 1989 and 0.26 in 1994) which still was not statistically significant ($\chi^2 = 2.12$ 1 d.f. NS). However, more cat populations should be studied over time in order to prove whether the genetic stability found is a local or universal phenomenon.

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RESUMO

Foram estudados três aspectos da composição genética de algumas populações de gatos da Catalunha (nordeste da península Ibérica, Espanha). As frequências alélicas de nove gens (O, A, T, D, L, S, W, C e I), que controlam a cor, o comprimento e o aspecto malhado dos pêlos, foram investigadas: 1) a população de gatos de Llansa a apenas 8 km da fronteira francesa na costa mediterrânea e uma nova amostra obtida no distrito rural de Castelldefels, estavam em equilíbrio de Hardy-Weimberg para os loci O e S. 2) A segunda questão dizia respeito à análise da relação genética entre a população de gatos de Llansa e, outras populações da Europa ocidental. Ruiz-Garcia *et al.* (*Mis. Zool.* 18: 169-196, 1995) procuraram semelhanças genéticas entre as populações de gatos do norte catalão e da França. Populações no centro e no sul da Catalunha tinham-se mostrado muito distantes das populações da França, em termos genéticos. Contudo, a população de gatos analisada no norte da Catalunha não apresentou aumento na semelhança genética com as populações francesas e revelou-se semelhante às outras populações de gatos da Catalunha analisadas anteriormente. Uma nova amostra de gatos de Llansa, a população catalã mais ao norte entre todas as estudadas até agora, não apresentou aumento na semelhança genética com as populações francesas, comparado com outros grupos da Catalunha. As frequências gênicas dos loci das características do pêlo mostraram que as populações felinas francesas e britânicas estavam muito distantes da população Llansa, entre as da Europa ocidental. Em geral, as populações de gatos que nós estudamos na Catalunha mostraram uma semelhança genética maior com populações do leste do Mediterrâneo e do norte da África do que as populações da Europa ocidental. 3) O terceiro aspecto diz respeito a modificações das populações ao longo do tempo. Em 1989, a composição genética de uma população de gatos de Castelldefels foi analisada. Em 1994 esta população foi estudada novamente e não se encontraram diferenças significativas nas oito frequências alélicas comparadas, o que demonstra grande estabilidade ao longo do tempo no perfil genético desta população felina.

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