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Mutant Allele Frequencies and Genetic Distance Relationships in Domestic Cat Populations of Lower Egypt and the Eastern Mediterranean

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Summary. Gene frequency surveys conducted in Alexandria and Cairo reveal genetic profiles which are extensions of those that characterize the cat populations of European cities. For nine selected comparisons with Alexandria, regression analysis indicates that a linear function best describes the relationship between Nei's and Cavalli-Sforza's genetic distance indices and geographic distance.

Key words: Cat – Egypt – Genetic profile – Genetic distance

Introduction

During July 1974, surveys to ascertain mutant allele frequencies in domestic cats were conducted in Alexandria and Cairo. These data were sought for two reasons. 1) Such observations would be most valuable supplements to information previously gathered in Europe and the Middle East for the purpose of elucidating clines for several coat color polymorphisms (Dreux and Todd 1974; Todd and Kunz 1977; Todd and Todd 1976a). 2) The resultant genetic profile would reveal any unique features which might point towards an ancestral population and, in particular, any association of the Abyssinian phenotype with the region.

Methods

In Alexandria, 213 cats were tabulated from all geographic and socioeconomic areas of the city. By way of an internal check, the city was partitioned into two parts, approximating the 'Arab' and 'European' quarters. When the 116 animals of the Arab Quarter were compared to the 97 from other areas of the city, not a single mutant phenotype frequency approached a statistically significant difference. Such a finding of homogeneity leads to the conclusion that the sample is both representative and adequate for the purposes of estimating allele frequencies and for comparisons to other samples.

The Cairo survey, based upon 140 animals, cannot be held to be representative of the population of this huge urban complex. The sample was drawn almost exclusively from the central commercial district (within 1-2 miles of the Egyptian Museum). Most of the animals were seen in and around markets, cafes, etc. Here the sample may be characterized as highly urban and may, accordingly, be modified by 'urban factor' a phenomenon noted in other studies (Blumenberg 1977; Dreux and Legel 1973; Todd 1969; Todd, Fagen and Fagen 1975).

The genetic factors assessed in this survey include sexlinked nonorange, orange (O^+, O) and the autosomal factors controlling nonagouti, agouti (a^+, a); Abyssinian, striped, blotched tabby (T^A, t^+, t^b); intense, dilute (d^+, d); short hair, long hair (l^+, l); nonspotted, piebald spotting (s^+, S) and pigmented, dominant white (w^+, W). The modes of inheritance and interactions of these mutants have been reviewed in detail (Robinson 1977) and will not be repeated here. Recessive allele frequencies (q) are taken as the square root of phenotype frequencies and dominant allele frequencies (p) as 1-q. For O, maximum likelihood estimation has been employed (Robinson 1972). Standard errors are given by the formulae $\sqrt{1-q^2/4N}$ and $\sqrt{(2-p)p/4N}$ for recessive and dominant alleles respectively. Sample sizes for the various loci differ because orange is epistatic to agouti; nonagouti is epistatic to tabby and dominant white is epistatic to all other coat colors. In addition, certain diagnoses are occasionally difficult, or impossible, owing to high grades of piebald spotting and/or unfavorable viewing condition. Phenotypic observations were compared by means of two by two contingency tables.

The measures of genetic distance employed are those of Kidd and Cavalli-Sforza (1974) and Nei (1972; 1975). These indices are defined in the notes to Table 4. See also Blumenberg (1977), Blumenberg and Spikell (1978) and Spikell and Blumenberg (1977).

Results

In Table 1 are shown the observed and predicted phenotypes in Alexandria and Cairo controlled by the sex-linked nonorange, orange locus. As sex could not be, or was not, determined for most animals, allele frequencies have been calculated from maximum likelihood estimates and the χ^2

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test is based upon the assumption of a 1:1 sex ratio. The fit between observed and predicted is very close for these populations and both appear to conform to Hardy-Weinberg equilibrium.

In Table 2 are shown the phenotypes and mutant allele frequencies for the autosomal loci studied. The two values shown for blotched tabby (t^b) in Cairo represent the raw observation and a tentative correction for suspected consanguinity. The two values for *l* arise from shifting a number of equivocally diagnosed phenotypes from one category to another.

Discussion

Statistically significant differences at the .01 level exist between Alexandria and Cairo for the loci *O* (χ^2 = 29) and *S* (χ^2 = 7.3). The difference for *a* (χ^2 = 4.53) is significant at the .05 level and that for t^b(χ^2 = 4.92) reaches statistical significance only when the Cairo data is not corrected for possible consanguinity. There is little doubt that the differences in *O* are meaningful but they should not be exaggerated. An excess of males in the Alexandria sample would, for instance, elevate the esti-

Table 1. Observed and predicted phenotype frequencies for non-orange (+/?); tortoiseshell (+/0) and orange animals in Alexandria and Cairo

	Alexandria			Cairo		
	Observed	Predicted	χ^2	Observed	Predicted	χ^2
+/?	113	110.03	.0802	96	95.63	.0014
+/0	43	48.74	.6759	23	23.74	.0231
0/?	55	52.22	.1479	19	18.63	.0073
Totals	211	210.99	.9041	138	138	.0318

While each population appears to conform to Hardy-Weinberg Equilibrium (χ^2 = .904 and .032 respectively), the two populations differ greatly from one another (χ^2 = 29.63). See text for further discussion

Table 2. Phenotypes observed and mutant allele frequencies calculated therefrom in cats of Alexandria and Cairo

	Alexandria			Cairo		
+	86			51		
$a\bar{a}$	68		.667 ± 0.30	68		.736 ± .030
	154			119		
+_	126			56	(56)	.459 ± .053
t^bt^b	14		.317 ± .040	15	(11)	(.403 ± .057)
	140			71	(67)	
+	187			127		
$d\bar{d}$	23		.332 ± .065	11		.282 ± .041
	210			138		
+	210	(203)	.119 ± 034)	140	(130)	.0+
$l\bar{l}$	3	(10)	(.217 ± 0.33)	0	(10)	(.268 ± 0.41)
	213	213		140	140	
S	135			69		
$+\bar{+}$	74		.405 ± .028	69		.293 ± .030
	209			138		
W	2			2		
$+\bar{+}$	211		.005 ± .003	138		.007 ± .005
	213			140		

The values in parentheses for t^b represent a correction made for suspected consnguinity, and for *l* for equivocal phenotypic diagnosis. See text for further discussion and interpretation of symbols mate of O. Likewise, if 'urban factor' is operating in Cairo, this would tend to suppress the frequency of O, as well as a and S, while raising the frequency of t^b. Association tests suggest a deficit of agouti tortoiseshell individuals in the sample. One explanation for this is that some such phenotypes were inadvertently scored as wild type. If this were so, the frequency of O here reported might represent a slight underestimate.

Given the possibility of a bias in the Cairo sample it would be premature to attribute the difference between Cairo and Alexandria to any fundamental biological distinctions. More importantly, there are no striking differences between the cats of Egypt and those of several eastern Mediterranean populations (Table 3). The most remarkable feature of the genetic profile of modern Egyptian cats is that the major autosomal mutant allele frequencies are as low, or lower, than those found in most European populations. Sex-linked orange in Alexandria is at the highest level yet recorded in the Old World, but is only slightly above that of such disparate areas as the Shetland Islands, (Todd, Clark and Dreux 1974) and Singapore (Searle 1959) This issue of cats of the so-called Abyssinian tabby phenotype, which is controlled by an autosomal dominant allele T^A, is of particular interest. This mutant is rare in most localities but is relatively common in Budapest (Davis and Davis 1977) and in certain Asian populations (Saliternick and Mordokhovich 1975; Searle 1959). The absence from the present samples of any cats carrying the T^A allele (including about 175 additional animals seen in Upper Egypt and the Sudan) is another indication that Egyptian populations are simply extensions of those of Europe.

Thus it appears that no mutant has its focus in Egypt and for all alleles, Egyptian frequencies are peripheral to those of Europe. No matter how venerable cats may have been in Egypt, they are today very provincial in appearance. This suggests that mutants presently found there have penetrated from other areas. Perhaps the lack of distinguishing features can be attributed to the fact that Egyptian cat populations are, and probably long have been, relatively sparse when compared to those of Europe. Hence a kind of genetic swamping has occurred, for the

Table 3. Mutant allele frequencies in domestic cat populations of the Nile Valley, eastern Mediterranean and adjacent regions

Population	O	a	t^b	d	l	S	W
Alexandria	.36	.67	.32	.33	.12 – .22	.41	.005
Cairo	.22	.74	.41 – .46	.28	0 – .27	.29	.007
Upper Egypt	.29	.69	.25	.31	.0	.55	.026
Atbara	.25	.68	.21	.0	.0	.61	.0
Khartoum	.36	.82	.37	.0	0 – .12	.44	.0
Jerusalem	.17	.59	.11	.38	.57	.36	.0
Tel Aviv	.15	.71	.12	.20	.17	.49	.0
Istanbul (A)	.28	.60	.20	.28	.48	.37	.007
Istanbul (B)	.19	.63	.28	.35	.35	.39	.005
Izmir	.20	.59	.33	.19	.25	.39	.0
Ankara	.27	.57	.15	.29	.41	.40	.021
Cyprus	.21	.72	.25	.35	.50	.34	.001
Chios	.24	.68	.34	.26	.10	.41	.0
Samos	.12	.68	.38	.29	.21	.38	.0
Kerkyra	.18	.66	.25	.31	.06	.34	.0
Patras	.18	.74	.30	.24	.0	.45	.005
Argolis	.18	.74	.19	.21	.0	.22	.0
Athens	.12	.73	.31	.36	.10	.29	.007
Iraklion	.16	.64	.35	.27	.11	.45	.005
Rethimnon	.22	.62	.26	.11	.11	.46	.006
Chania	.23	.65	.26	.22	.08	.57	.017
Tunis	.18	.72	.0	.47	.11	.39	.0
Carthage	.22	.63	.19	.27	.10	.40	.0
Rome	.07	.65	.47	.32	–	–	.020
Venice	.06	.58	.48	.35	–	.27	.007
Marseille	.08	.72	.68	.34	.27	.29	.003

Data taken from Baxa (1973); Dreux (1975); Dyte (personal communication); Robinson (1972); Saliternick and Mordokhovich (1975); Saliternick, Schoenbaum and Ritte (1976); Searle (1966); Todd (1977b unpublished); Todd and Kunz (1977); Todd, Robinson and Clark (1974); Todd and Todd (1976a)

Table 4. Measures of genetic distance, protein identity and migration

Comparison	sep. dist. (km)	D_x[a]	D_y[b]	D_{xy}[c]	D[d]	I[e]	$\sqrt{f}$[f]	m x[g] 10^{-4}/gen
1. Alex-Cyprus	480	.603014	.515436	.570646	.011421	.988644	.122175	1.7
2. Alex-Irak	610	„	.535733	.585549	.016176	.983955	.148539	1.2
3. Alex-UE	730	„	.557708	.590952	.010591	.989465	.078987	1.9
4. Alex-Samos	780	„	.511026	.578462	.021442	.978786	.180653	.92
5. Alex-Izmir	840	„	.520741	.579461	.017584	.982570	.149902	1.1
6. Alex-Chios	875	„	.550745	.583611	.006732	.993291	.073887	3.0
7. Alex-Ist (E)	1080	„	.535323	.579176	.010007	.990043	.119090	2.0
8. Alex-Ist (A)	1080	„	.547490	.586627	.011375	.988689	.105439	1.7
9. Alex-Mars.	2475	„	.460830	.608880	.076696	.925929	.331259	.25

a) D_x is the excepted proportion of different genes between two randomly chosen genomes (individuals) in the 'first' population of the two being compared (i.e. Alexandria). In order to calculate D_x, one must compute j_x (each locus) = $x_1^2 + x_2^2$ where x_1 is the frequency of the mutant allele at the locus and x_2 is the frequency of the wild type allele. $j_{xi} = \Sigma x_i^2$ over all loci considered; J_x is the arithmetic mean of j_{xi}; and $D_x = -\log_e J_x$ (see Nei 1972, 1975).

b) As note a for the other population. If these populations meet the requirements for panmixia, D_x and/or D_y are also equal to the average proportion of heterozygous loci in an individual or average heterozygosity (Nei 1972, 1975).

c) D_{xy} is the expected proportion of different genes between two randomly chosen genomes (individuals), one chosen from the Alexandria population and the other individual chosen from the other population in the comparison. $j_{xy} = x_1 y_1 + x_2 y_2$; $j_{xiyi} = \Sigma x_i y_i$; J_{xy} is the arithmetic mean of j_{xy} and $D_{xy} = -\log_e J_x$ (Nei 1972, 1975).

d) The standard estimate of net codon differences per locus between the two populations when intrapopulational codon differences are subtracted; $D = D_{xy} - ((D_x + D_y) / 2)$. Nei (1975) believes that at least a dozen allele frequencies should be available from electrophoretic protein studies in order to have some confidence in the calculated value of D. In this study, five allele frequencies (*O*, *a*, t^b, *d*, *S*) are employed but these, of course, refer to gross morphological characteristics each of which is determined by a multi-enzyme pathway. In one sense, each of these frequencies represents an average of several different codon frequencies. It would be interesting to know the correlation between a D determined directly from an electrophoretic analysis of the enzyme pathways (which are not yet accessible for study) controlling each of these five traits vis à vis the D values arrived at in this paper.

e) The normalized identity of genes between two populations; $I = J_{xy} / \sqrt{(J_x)(J_y)}$ according to Nei (1972, 1975).

f) The measure of genetic distance derived in Kidd and Cavalli-Sforza (1974). The angular transformation of gene frequencies (subject to certain restrictions) is employed to calculate an estimate of the variance (f) for all k alleles at one locus. The $\sqrt{f}$ over several loci is a measure of genetic distance. See also Blumenberg (1977).

g) The maximum possible migration rate between the two populations assuming a mutation rate of 2×10^{-6} per locus. According to Nei (1975), $m = (2 \times 10^{-6} I) / (1 - I)$. These values do not reflect the overall migration rate but must reflect the number of individuals that migrate from one population to another and leave offspring in their new locality. These results seem to confirm a model which proposes that most cats migrating from one large and established population to another large and established population do not 'take'; i.e. they are killed or driven out (Todd unpublished). Another way of interpreting m is to say that if the maximum and effective (those individuals leaving offspring) migration rate between the two populations was higher than the particular value, they would not exhibit the differences in genetic profile that they do show

input of alleles into Egypt, almost exclusively through water transport of cats (Todd 1978), must far outweigh export.

It is likely that marine routes, as opposed to land contacts, were pre-eminent during the establishment of the Alexandria cat population. Therefore, the nine populations used for detailed comparisons with Alexandria were selected because migration from them to Alexandria would rarely, if ever, involve land travel. Table 4 gives indices of genetic distance, protein identity and migration. The magnitude of D is typical of values which define the separation between local races of *M. musculus* and *D. ordii*, and which also characterize the separation between subspecies of *T. talpoides* and *T. bottae* (Nei 1975). The magnitude of $\sqrt{f}$ for all paired comparisons is similar to that seen between *F. catus* populations in the United Kingdom and former British colonies where a relationship

Table 5. Regression Relationships

Linear regression			
D = .000033 g.d. – .012898		$\sqrt{f}$ = .000107 g.d. + .038653	
r = .905908	p < .001	r = .815606	.01 > p > .001
Power curve			
D = .000017 g.d.$^{.998751}$		$\sqrt{f}$ = .003069 g.d.$^{.55345}$	
r = .660618	.1 > p > .05	r = .563901	p > .1
Exponential curve			
lnD = .00921 g.d. – 5.10271		ln$\sqrt{f}$ = .000522 – 2.54595	
r = .777300	.02 > p > .01	r = .677897	.05 > p > .02
Logarithmic curve			
D = .037042 (lng.d.) – .23137		$\sqrt{f}$ = .11722 (lng.d.) – .65067	
r = .790002	.02 > p > .01	r = .697451	.05 > p > .02

For each equation, there are 7 degrees of freedom

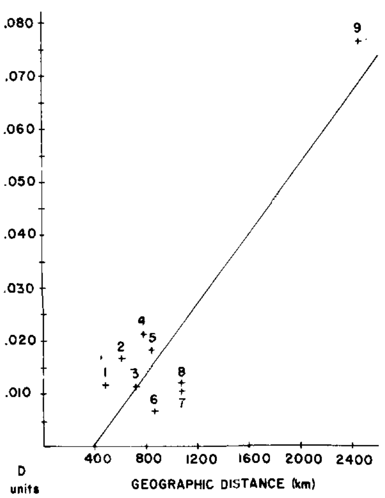

Fig. 1. Genetic distance (D) versus geographic distance. Arabic numerals refer to Table 4

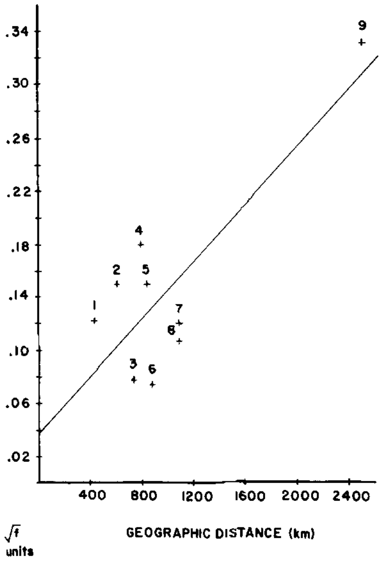

Fig. 2. Genetic distance ($\sqrt{f}$) versus geographic distance. Arabic numerals refer to Table 4

Table 6. Regression analysis of D upon $\sqrt{f}$

Linear regression $D = .268752\sqrt{f} - .018891$ $r = .963349 \quad p < .001$	Power curve $D = .298101\sqrt{f}^{1.46809}$ $r = .953065 \quad p < .001$
Exponential curve $\ln D = 8.82839\sqrt{f} - 5.47129$ $r = .981468 \quad p < .001$	Logarithmic curve $D = .041414 (\ln\sqrt{f}) + .104176$ $r = .866863 \quad .02 > p > .01$

For each equation, there are 7 degrees of freedom.

between f and separation time may be defined (Blumenberg 1977). Each of the latter group of populations is characterized by an origin in one major founding population whose arrival from the United Kingdom can be reliably documented historically (Blumenberg 1977; Blumenberg, Lowry and Blumenberg 1977; Costello and Blumenberg 1976; Dartnall and Todd 1975; Todd and Todd 1976b). A similar model for the founding of urban cat populations in the Mediterranean region cannot be established (Todd 1977a) and thus any attempt to define a relationship between genetic distance and separation time would rest upon faulty assumptions.

A relationship between D and $\sqrt{f}$ and geographic (separation) distance between populations may be defined for the eastern Mediterranean (Table 5). The data fit for Nei's D index is best described by a linear regression ($p < .001$) although the exponential and logarithmic relationships are significant at the .02 level. For Cavalli-Sforza's $\sqrt{f}$, the best fit is also linear ($.01 > p > .001$) although the exponential and logarithmic functions also meet the requirements for statistical significance ($p < .05$). A graphic representation of the relationship between D and $\sqrt{f}$ and geographic distance is presented in Figures 1 and 2 respectively. It is interesting to note that these data reveal a significant correlation between D and $\sqrt{f}$ (Table 6) but one cannot discriminate between the four models tested. Using *Drosophila* data Chakraborty and Tateno (1976) observed a significant, presumably simple, correlation between D and $\sqrt{f}$.

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