

Population Genetics of Coat Characteristics in Domestic Cats

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Studies of free-ranging populations of domestic cats (*Felis domesticus*) provide excellent opportunities for students to learn and apply the principles of population genetics. Despite cats' domestic habits and interaction with humans, breeding in free-ranging populations is largely beyond human control. Thus, for genetic purposes, cats comprise essentially wild populations, with the distributions and frequencies of their genetic variations being determined by the natural processes of evolution. Variations in coat color and pattern are the focus of this exercise, since the genetic mechanisms underlying these traits are well known (Ellis, 1993), and the phenotypes may be easily observed and distinguished without handling or even closely approaching the animals (if binoculars are used).

To begin the exercise, students are taught to recognize the coat color and pattern phenotypes produced by alleles at seven distinct gene loci, using photographs of local cats, or pictures from cat calendars and magazines. Each student is then assigned to observe and record the sex, coat colors, and coat patterns of ten free-ranging cats. Students collect this data in the local community, on their own time, over a period of several weeks. Next, students determine and record the genotype at each locus for each cat in their sample (see Table 1).

Students' data is then pooled, so that the class has data for a random sample of 150 - 250 cats from the local population. The Hardy-Weinberg equation is used to determine allele frequencies at each locus, and a genetic profile for the local cat population is produced, consisting of the frequency of the mutant allele at each locus. In the final step of this study, students compare the genetic profile they have prepared with published genetic profiles for cat populations in other cities around the world (Chu, 1986; Halpine and Kerr, 1986; Todd et al., 1975). These comparisons lead to speculations, investigations, and discussions about the influences of environmental factors and migrations on the cat population's genetic profile.

Using the local cat population in our studies of population genetics and evolution has brought life and excitement to an area of biological study that formerly was perceived by many students as sterile and uninteresting. While the exercise described here emphasizes the determination of allele frequencies and the analysis of the genetic profile of the local cat population, it could be easily modified to focus on the study of autosomal and X-linked inheritance patterns, or on the effects of X-chromosome inactivation and epistasis.

TABLE 1. Relationships and phenotypic effects of the alleles at seven selected gene loci in domestic cats.

LOCUS	ALLELES	GENOTYPES	PHENOTYPES
W (autosomal)	W (mutant) w (wild-type)	W/_ w/w	completely non-pigmented (white) coat coat with at least some pigmented hair
D (autosomal)	D (wild-type) d (mutant)	D/_ d/d	dark pigmentation (black or orange) dilute pigmentation (gray or cream)
O (X-linked)	o (wild-type) o' (mutant)	o/o o/o' o/o'	black pigment orange pigment black & orange patches (females only)
A (autosomal)	A (wild-type) a (mutant)	A/_ a/a	agouti (partly pigmented individual hairs) nonagouti (uniformly pigmented hairs)
T (autosomal)	T (wild-type) t (mutant)	T/_ t/t	parallel 'tabby' stripes non-parallel 'blotched tabby' swirls
S (autosomal)	S (mutant) s (wild-type)	S/_ s/s	white 'piebald' spots no white spots at all
L (autosomal)	L (wild-type) l (mutant)	L/_ l/l	short hair long hair

References

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