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Studying Gene Frequencies in a Natural Population

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ABSTRACT

Teaching population genetics presents difficulties because students often have a hard time thinking of a population in terms of a collection of alleles and with finding and using frequency calculations to determine whether a population is in equilibrium. Many of the activities that are used to demonstrate the Hardy-Weinberg principle are based on non-living models such M & M's®, coins or Goldfish® crackers. Models using real populations, such as squirrels tend to model only one locus. The domestic cat presents an easily observed population that allows students to gather information about multiple loci by simply noting the coat colour and patterning of the animals. Data can be recorded quickly and easily by photographing the animals and collated data can be used to calculate allele frequencies and to determine genetic equilibrium. There is, of course, a caveat: Unless one were to study a particular colony of cats, the "population" will not fit the Hardy-Weinberg definition, i.e. a large group of randomly interbreeding animals. In fact, in the absence of access to animals, data can be collected on a hypothetical population using photos of cats, such as the 365 examples found in one of those daily calendars. Population genetics is almost always taught at the end of a basic genetics course and a review of each of the loci in this activity serves to reinforce those basic genetic principles that students will have already studied.

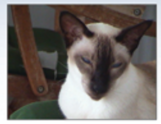
BACKGROUND INFORMATION

TABLE 1 - GENETICS OF COAT COLOUR IN THE CAT

LOCUS	INHERITANCE	FUNCTION	ALLELES
C - Albino	C > to all… c^a and c^b show incomplete dominance and c^b>c	Codes for tyrosinase, required for pigment production	C = full pigmentation c^a = blue-eyed albino c^s = Siamese c^b = Burmese c = pink-eyed albino
B - Black	Dominant	Codes for the pigment melanin	B = eumelanin, black b = brown b^l = cinnamon
O – mutant orange	X-Linked, expressed when present	Converts eumelanin to orange pheo-melanin	O^+O^+ or O^+Y = black OO or OY = orange O+O = orange & black
D - Dilute	Recessive	"Dilutes" black and orange to gray and buff	D = full color d = diluted colour
A – Agouti	Dominant	Results in agouti pattern on hair shaft	A = stripes a = solid coat color
T - Tabby	Dominant	Affects pattern of stripes	T = Mackerel tabby, symmetrical stripes t^b = Classic or blotched tabby t^a = spots on body
S - Pie-balding	Dominant	Results in white patches	S = white patches s = solid color
W - Dominant White	Dominant	Results in all white animal or pigmentation only on head & tail	W = solid white w = full pigmentation
I - Silver	Dominant	No pigment at base of hair shaft	I = "silver" appearance i = full pigmentation
L - Length	Recessive	Regulates length of hair	L = short hair l = long hair
M - Manx Dominant, recessive lethal		Regulates length of tail	Mm = short tail mm = normal tail length MM = lethal in utero

Alleles at the C Locus


Albino
c^ac^a


Siamese
c^sc^s


Burmese
c^bc^b


Burmese
c^bc^b

Allels at the T locus


C/_,B/_O^+Y,D/_,A/_,T/_
Mackerel tabby


C/_,B/_O^+Y,D/_,A/_,t^bt^b
Blotched tabby

Alleles at the S Locus

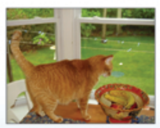

C/_,B/_O^+Y,D/_,aa,S/_
Genes at the T Locus cannot be determined in non-agouti.

Alleles at the B Locus


Black
C/_, B/_


Brown
C/_, b/b

Alleles at the O Locus


Female Ginger Cat
C/_, B/_,OO


Tortoise Shell
C/_, B/_O+O

Alleles at the W Locus

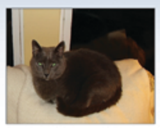

C/_,W/_
Dominant White


C/_,B/_O^+O^+,D/_,aa,W/_
Dominant White

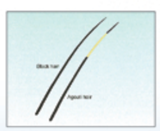
Alleles at the I Locus


C/_,B/_O^+Y,D/_,A/_,T/_,ss,ww,I/_
Silver Tabby

Alleles at the D locus


C/_, B/_,O+O+,dd

Alleles at the A Locus


A/_
Agouti Hair


C/_, B/_O+O,D/_aa
Stripes are always seen with X-linked O

Alleles at the L Locus


W/_ll

Alleles at the M Locus

MATERIALS AND METHODS

Using a digital (or phone) camera, each investigator should try to gather information on 6 cats. Using the photographs to document phenotypes, refer to the handout and assign a genotype to each of the various loci in the forms provided. Class data will be collated and frequencies of the alleles at each locus calculated.

RESULTS

TABLE 2 – INDIVIDUAL GENOTYPE DATA

CAT	C	B	O	D	A	T	S	W	L
1									
2									
3									
4									
5									
6									
Frequency of homozygous recessive animals			*						

*# X-linked orange /total number of alleles (females have 2, males only 1)

TABLE 3 – ANALYSIS OF CLASS DATA

N.B. For the X-linked O locus, count the number of O and O+ alleles and calculate frequency based on the number of alleles, not the number of animals. Omit the remaining calculations.

	C	B	O*	D	A	T**	S	W	L
Total number of homozygous recessive animals at each locus									
Total number of animals surveyed									
Frequency of homozygous recessive animals (q^2)									
Frequency of recessive allele (q)									
Frequency of dominant allele (p)									
Calculated frequency of heterozygotes ($2pq$)									

*Calculate p and q using the number of each allele/total number of alleles. Omit the rest of the calculations.

**It is not possible to learn the genotype at this locus if the animal is non-agouti. The same is true for an all white animal at several other loci. Calculate frequency based on the number of animals expressing each trait.

DISCUSSION QUESTIONS

1. Based on the class data for gene frequencies, how many cats in a sample of 500 from this population would you expect to be long-haired.
2. How does the frequency of homozygous recessive animals at each locus in your data compare to the frequency found when the class data was used.
3. How might a population pick up the mutant c^s allele at the C locus that is seen in the Siamese cat?
4. Why might you expect the dominant allele at the W locus to
   a. Increase?
   b. Decrease?
5. Explain how the "founders' effect" could explain unusually high or low frequencies of certain alleles within a population.
6. The gene responsible for the short tail seen in the Manx cat is dominant, but lethal when homozygous. How can you account for the continuing presence of the allele in a population?
7. Explain how selection pressures contribute to changes in gene frequencies and therefore to evolution.

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