Tentamentsskrivning i **TMS106/MSA610: Population genetics, 7.5 hp**

Tid: Måndagen den 26 maj 2008 kl 8.30-12.30.

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Hjälpmedel: Räknedosa utan manualer och med tömda minnen, egen formelsamlingen fyra A4 sidor, utdelade tabeller

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Grading system (CTH):	marks	0-11	12-17	18-23	24-30
	grade	U	3	4	5

Grading system (GU):	marks	0-11	12-20	21-30
	grade	U	G	VG

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1. (5 marks) The genotype aa is lethal and yet the population has an equilibrium frequency for a of .40. If the fitness of Aa is 1, what is the fitness of the AA genotype?

2. (5 marks) A wildflower native to California, the dwarf lupin (Lupinus nanus) normally bears blue flowers. Occasionally, plants with pink flowers are observed in wild populations. Flower color is controlled at a single locus, with the pink allele completely recessive to the blue allele. Harding (1970) censused several lupin populations in the California Coast Ranges. In one population of lupins at Spanish Flat, California, he found 25 pink flowers and 3291 blue flowers, for a total of 3316 flowers.

   a) Calculate the expected allele frequencies and genotype frequencies if the population were in Hardy-Weinberg equilibrium.

   b) Harding studied the fertility of lupins by counting number of seed pods produced per plant in a subsample of the Spanish Flat population. He found the following:

	mean number of pods	number of plants examined
blue	19.33	39
pink	13.08	24

   Assume that heterozygotes are as fit as homozygous blue lupins, and that seeds from both pink and blue lupins all suffer about the same mortality rate after germinating. Calculate the relative fitness of each genotype.

   c) Predict quantitatively the effect of natural selection on the frequencies of phenotypes in the next generation of lupins.

3. (5 marks) Carefully explain why Tajima's D statistic is sensitive to population expansion. To illustrate, draw a gene tree of a relevant shape and mark mutations uniformly over the branches.

4. (5 marks) A certain disease is caused by a dominant allele, H. This disease typically doesn't affect people until between the ages of 35 and 45. Assume that the frequency of the H allele is 0.00005. Assume that the mutation rate for this locus is 0.00001, with the h allele changing to the H allele at a rate of 0.00001 per generation. Assuming that the fitness of HH, Hh,and hh individuals is equal, what will the frequencies of h and H be in the next generation? Show your work.

5. (5 marks) Below I give three excerpts from Wikipedia describing different key concepts of population genetics. Your task is to name these concepts and present your understanding of them.

   a. ... is an influential theory that was introduced with provocative effect by Motoo Kimura in the late 1960s and early 1970s. Although the theory was received by some as an argument against Darwin's theory of evolution by natural selection, Kimura maintained, and most modern evolutionary biologists agree, that the two theories are compatible.

   b. The concept was first introduced by Sewall Wright in the 1920s, and is now held to be one of the primary mechanisms of biological evolution. It is distinct from natural selection, a non-random evolutionary selection process in which the tendency of alleles to become more or less widespread in a population over time is due to the alleles' effects on adaptive and reproductive success.

   c. The notion of the existence of a so-called ... was first attributed to Emile Zuckerkandl and Linus Pauling who, in 1962, noticed that the number of amino acid differences in hemoglobin between lineages scales roughly with divergence times, as estimated from fossil evidence.

6. (5 marks) Suppose that we have a trait that shows a mean of 105.2, a variance of 30.6, and a father-offspring correlation of 0.45.

   a. Draw a scatter plot with a regression line illustrating such a relationship.

   b. What is the heritability of the trait?

   c. If we choose fathers that measure exactly 110 on the scale, what trait value of their offspring should be expected, if they each mate with a randomly chosen female?

Tables and data supplied

1. Normal distibution table

Partial answers and solutions are also welcome. Good luck!

Numerical answers

Problem 1.

Recall that if the genotypes AA: Aa: aa have fitnesses $1-s:1:1-t$, then the equilibrium frequency of A is $t/(s+t)$. Here, $t=1$ (as aa is lethal), so that freq(A) = 1 – freq(a) = 0.6 = 1/(1+s). Solving gives $s = 1/0.6 - 1 = 2/3$. Hence fitness of AA is $1-s = 1-2/3 = 1/3$.

Problem 2a.

Let B be the blue allele and b be the pink allele, so that p is frequency (B) and q is frequency (b). Assuming HWE

$R = 25/3316 = q^2$, so $q = \sqrt{0.00754} = 0.0868$.

Thus $p = 0.913$, and we now obtain

$D = p^2 = 0.834, H = 2pq = 0.158, R = 0.00754$.

Problem 2b.

Relative fitnesses reflect the ratio among numbers of pods (fertility) of different genotypes

$$w_{BB} = 1, w_{Bb} = 1, w_{bb} = 13.08/19.33 = 0.677.$$

Problem 2c. First, calculate the average fitness:

$$\bar{w} = p^2 w_{BB} + 2pq w_{Bb} + q^2 w_{bb} = 0.997.$$

Now divide all terms through by w-bar to get the predictions for the genotype frequencies after one round of selection:

$$D' = \frac{0.913^2 \cdot 1}{0.997} = 0.836, H' = \frac{2 \cdot 0.913 \cdot 0.0868 \cdot 1}{0.997} = 0.159,$$
$$R' = \frac{0.0868 * 0.0868 * 0.677}{0.997} = 0.00512.$$

So that next genegeration phenotype frequences are: Blue flowers 0.9949 and pink flowers 0.0051. Moral of the story: Natural selection isn't all that efficient at eliminating rare alleles.

Problem 4.

This is a no selection one-way mutation case. Any h allele mutates till H with probability 0.00001 so the increase of H frequency due to h→H mutation will be $0.99995 \cdot 0.00001 = 0.00001$. Thus the next generation allele frequencies will be 99.994% and 0.006%.

Problem 6b. The slope of the regression line for the father-osspring relationship is $b = Cov(P_o, P_f)/Var(P_f) = Cov(P_o, P_f)/\sqrt{Var(P_o)Var(P_f)} = 0.45$. Thus the narrow sense heritability coefficient can be estimates as $h^2 = 2b = 90\%$.

Problem 6c. Applying the linear regression model $P_o = 105.2 + b(P_f - 105.2)$ with $P_f = 110$ we obtain the expected offspring trait value 107.4.