BIS101 Exam 1

Nov. 4, 2014

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I agree to allow my exam to be placed in a common location for return, and acknowledge that this mea other students can potentially see my exam score and student ID.

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1 Ng

Why would the sequencing approach of Ng. et al. have failed to discover the genetic basis of Miller syndrome if the syndrome was caused by mutations in more than one gene? (5pts)

2 Johnston

Why is single-locus overdominance or heterozygote advantage, as seen at the Ho^P locus in Soay sheep in Johnston *et al.*, unlikely to be common in populations? (5pts)

3 Schemske

Schemske and Bradshaw discovered that the a single locus, yup, explained a large proportion of the variation in flower color in Mimulus. They also showed that another single locus, which they called a "major nectar QTL" explained much of the variation in nectar abundance. Given these loci of large effect, is pollinator preference a quantitative trait? Why or why not? (5pt)

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4 Corn

4.1 Quantitaive Genetics

You are interested in breeding shorter ears of corn to use as projectiles in a giant corn cannon (patent pending). You have a set of 5 inbred lines of different genotypes. Each of these 5 lines is grown in two fields, and you measure the length of the ear of corn each produces. The lengths (in cm) are shown in the table below.

• The same genotypes are grown in both fields, and the broad sense heritability is $H^2 = 0.1$ in field 2. What is the broad sense heritability in field 1? (7pts)

Field 1	Field 2
3	3
4	6
3	3
2	1
3	2

• Assuming all of the genetic variance is additive, in which field is your selection experiment more likely to be successful and why? (6pts)

4.2 Gene Interaction

• In your field of otherwise yellow corn, you discover two purple kernels. You grow these seeds into adult plants (purple1 and purple2) and cross them, resulting in 300 dead kernels and 20 yellow kernels. When either purple1 or purple2 is self-pollinated, they produce kernels in the ratio of 1 yellow kernel for every 3 purple kernels. How many loci are involved? Write out the genotypes of the 1) purple1 and purple2 plants and 2) the live yellow kernels that result from the purple1 x purple2 cross. (5pts)

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5 Peppered moths

5.1 Population genetics

In a classic story of evolution, peppered moths in Britain shifted to being predominantly black during the industrial revolution, as soot darkened tree trunks, and acid rain killed off lichens living on the trees. Birds were able to see light colored moths on darker trees and at them. The allele responsible for black coloration is dominant to that for light coloration. In studying a population of moths you find that the allele frequency of the black allele is 0.8.

• What are the genotype frequencies if mating in the previous generation was random? (5pts)

• What are the phenotypic frequencies in these individuals? (5pts)

• If white moths survive and reproduce 50% as well as black moths, what will the allele frequencies be after one generation of selection? (7pts)

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5.2 Gene action

In one particular population of peppered moths, predation has completely removed all white moths from the population. After several generations in which no white moths are observed, you discover a single white moth among the new progeny.

• You capture this new mutant, and cross it to an inbred black moth. All of the F1 offspring are grey, but the F2 segregates for white, grey, and black in the ratios 1:2:1. What can you conclude about dominance of this new white allele? (6pts)

• You take one of these white F2 moths and cross it to a white moth from the original population. All of the F1 of this new cross are white. How many loci are involved in the the color polymorphisms described? (6pts)

6 Raghavan

One possible explanation for the similarities between the ancient Mal'ta genome and modern Europeans is contamination with modern DNA during extraction and processing. Explain some of the reasons why the authors could conclude this was not the case? (5pts)

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7 Ducks

7.1 Gene duplication

The Kaua'i mole duck (Anas carpitalpa), is blind and flightless, lives in caves, and uses its beak to rake through leaves to find invertebrates to eat. To compensate for being blind, the mole duck has expanded its repertoire of odorant receptor genes to use its sense of smell to explore its environment. One gene in particular, foetida, is known to be duplicated in the mole duck but not in its relative the Pacific black duck (Anas superciliosa). In the Pacific black duck, this gene is expressed in all tissues of the head including the nose and tongue, whereas in the mole duck one copy (foetida1) is expressed in the nose, while another (foetida2) is expressed only in the tongue.

• What kind of process describes the evolution of the two duplicates in the mole duck? (5pts)

7.2 Linkage

In Pacific black ducks, the foetida locus is linked to the turpis locus. You wish to know which of the two copies of foetida in the mole duck is in a syntenic position compared to Pacific black ducks. To do so, you perform some crosses. Mole ducks homozygous for the recessive allele at foetida1 (f_1) can't smell, and mole ducks homozygous for the recessive allele at foetida2 (f_2) can't taste. Ducks that are homozygous for the recessive allele at the turpis (t) locus are ugly. You cross an inbred duck that can't taste, is ugly, and can't smell, with an inbred duck that can taste, can smell, and is beautiful. The resulting offspring can all taste, can smell, and are beautiful as expected. One of these offspring is then crossed back to its ugly parent, and the phenotypes of the resulting ducklings are shown in the table below. Use t, f_1 , and f_2 for recessive alleles and T, F_1 , and F_2 for dominant alleles.

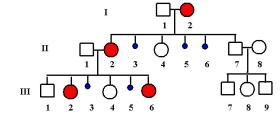
• Which copy of the *foetida* locus in mole ducks is syntenic to the *foetida* locus in Pacific black ducks and why? (6pts)

Phenotype	Count
ugly, can't smell, can't taste	40
beautiful, smells, tastes	41
beautiful, can't smell, tastes	40
beautiful, can't smell, can't taste	10
ugly, smells, tastes	9
ugly, smells, can't taste	40
ugly, can't smell, tastes	10
beautiful, smells, can't taste	10

• How far apart (in cM) is the linked copy from the turpis locus? (6pts)

8 Pedigree

Figure 1: The pedigree of a large family. Small dots are spontaneous abortions of unknown gender. Colored circles are females afflicted with a syndrome known by its French name *vraiment malade*.



Use the pedigree in Figure 1 above to answer the following questions.

• Careful sequencing studies have shown that a single mutation causes *vraiment malade*. What form of inheritance does this mutation show? (6pts)

• Why are there no afflicted males? (5pts)

• Individual III-2, an afflicted woman, decides to marry her cousin, individual III-7. Aside from telling her this is a bad idea for other reasons, what can you tell this woman about the probability that her daughters will have *vraiment malade?* (5pts)

Scratch Paper – will not be graded

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