Problem Set 2

Due 2/14/2025

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Q1 As a plant breeder I want to fix an allele that provides resistance to an important crop disease. Unfortunately, I do not have the ability to directly genotype the causative mutation, but I have identified a genetic marker that is closely linked the causative mutation. Based on mapping experiments the recombination frequency between the marker (alleles: A & a) and the QTL (alleles: Q – resistant & q – susceptible) is r = .25

I have crossed a homozygous resistant line to a homozygous susceptible line to get an offspring with the genotype:

$$\begin{bmatrix} A \\ Q \end{bmatrix} \begin{bmatrix} a \\ q \end{bmatrix}$$

I will self this individual to generate offspring segregating for resistance.

A. If I select only lines with the genotype AA, what expected proportion of the **selected** lines that will be homozygous for the favorable QTL (QQ)? (2 pts)

Q2 Similar to Q1 I have identified markers linked to a QTL of interest and I now want to practice marker assisted selection to fix the favorable allele in a population. In this scenario I have 2 markers linked on either side of the QTL. Marker 1 (alleles A, a) has a recombination frequency $\mathbf{r} = .4$ with the QTL and Marker 2 (alleles B, b) has a recombination frequency $\mathbf{r} = .3$ with the QTL. As before I've crossed a line that is homozygous for the beneficial allele (Q) and a line that is homozygous for the unfavorable allele (q):

$$\begin{bmatrix} A \\ Q \\ B \end{bmatrix} \begin{bmatrix} a \\ q \\ b \end{bmatrix}$$

I selfed the heterozygous line above to generate many offspring.

The QQ genotype has a value of a = 5 for the trait of interest, the unfavorable genotype qq has a value of -a = -5 for the trait of interest. The trait is additive (no dominance)

- A. As a breeder I want to fix the resistance allele. If I select only lines with the genotype AABB, what is the expected proportion of the selected lines that will be homozygous for the favorable QTL (QQ)? (2 pts)
- B. What is the expected value for offspring with the genotype AABB? (3 pts)

- C. What is the expected value for lines with the genotype AA? (3 pts)
- D. What is the expected value for lines with the genotype BB? (3 pts)
- E. How close would a single marker need to be in order for marker assisted selection to as effective and the two marker example above? (2 pts)