Quiz 4

1. There is a region of the genome with a three base pair repeat (CAG)n and unique primers are designed flanking this region. PCR is used to amplify the repetitive region and gel electrophoresis is used to determine the number of repeats in Bob and Jane.

Jane

Bob

(CAG)25

Larger

(CAG)5

Smaller

a) What type of molecular marker is this?

*SSR or microsatellite*

b) What is the genotype of Bob at the repeat locus? What is the genotype of Jane at the repeat locus?

*Bob is (CAG)25  and (CAG)5. Jane is homozygous (CAG)­5.*

c) Bob and Jane have a daughter named Sue. PCR is used to amplify the repetitive region and gel electrophoresis is used to determine the number of repeats in Sue. Draw out all possible PCR products in Sue assuming no new mutations have occurred. Note: You may not need to use all the spaces provided.

Sue

Sue

Sue

(CAG)30

Larger

Sue

(CAG)25

(CAG)5

Smaller

c) Assume there was a mutation in one of the repeats from (CAG)5 to (CAG)3CA**T**CAG. Would this mutation be detected by the 2-step (PCR and electrophoresis) technique used in this question? Why or why not?

*No, because this technique is only recognizing the length of the repeat.*

2. The recurrence risk of heart disease in the monozygotic twin of a proband is 38%; in a dizygotic twin it is 16%; and in a full sibling it is 7%.

a) Why is the recurrence risk less for a dizygotic twin then it is for a monozygotic twin?

*Because heart disease has a genetic component, and monozygotic twins share 100% of their genes, while dizygotic share only 50%.*

b) Why is the recurrence risk less for a full sibling then it is for a dizygotic twin?

*Because heart disease has an environmental component. Although dizygotic twins share the same number of genes as full siblings, twins have a more similar environment than other siblings, both in the womb and throughout their childhoods.*

3. A case control study was done to find loci responsible for pancreatic cancer, using 100,000 genetic markers. A given allele for a SNP was found to be highly associated with the occurrence of pancreatic cancer, p= 0.0001.

a) What are two possible explanations for this very low p-value?

*1) A gene responsible for pancreatic cancer is tightly linked to the genetic marker.*

*2) Since you looked at 100,000 genetic markers you expect to get p-values this small 10 times, just at random.*

b) How would you distinguish between those hypotheses?

*Do another study with more individuals and fewer markers. Only look at the markers that had very low p-values in the first study. If this marker is still highly associated with pancreatic cancer, then it is likely that it is in fact linked to an important gene.*