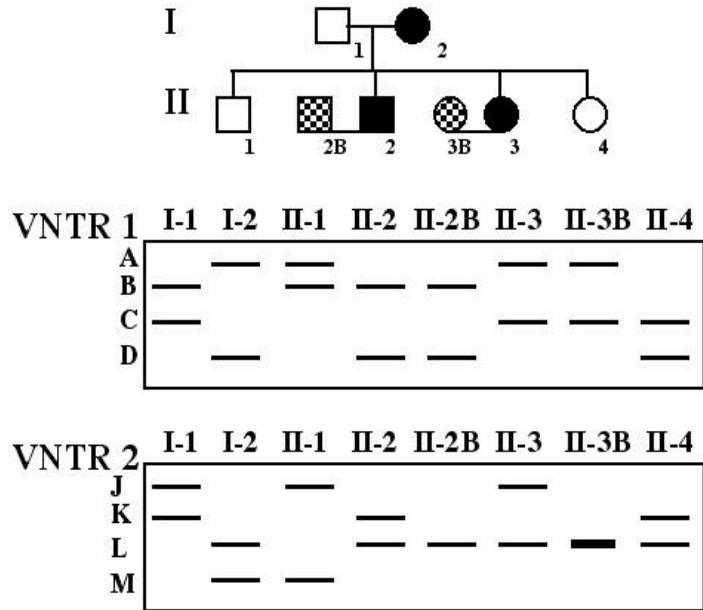


MCD Biology 2150 - Problem Set 11:

Due: **FRIDAY** May 5, 11:55 PM

Here is the pedigree for a family with an inherited predisposition to a form of cancer. The filled symbols indicate cases of cancer. The stippled symbols are tumor biopsies from the individual to which the symbol is connected. The biopsies are indicated by the individuals number followed by a "B." There is a dispute among the researchers studying this cancer. Some believe that the mutation leading to predisposition for the cancer is linked to VNTR1, whereas others believe that it is linked to VNTR2. To be safe, you have analyzed both VNTRs in the members of this family and in the available tumor biopsies. Those results are shown in the two gels. You are fortunate that the family is highly polymorphic for both VNTRs, allowing you to answer the following questions.



*Question 1.* In this family, are you looking at a mutation in a proto-oncogene or in a tumor suppressor gene?

- a. Proto-oncogene
- b. Tumor Suppressor gene
- c. Could be either
- d. Cannot be determined
- e. There's a difference?

*Question 2.* Which marker is linked to the mutation?

- a. Could be either
- b. Cannot be determined
- c. VNTR 1
- d. VNTR 2

*Question 3.* Which allele of the VNTR is on the same chromosome as the mutation (what is the haplotype with the mutation)?

- a. A
- b. B
- c. C
- d. D
- e. J
- f. K
- g. L
- h. M

*Question 4.* What genetic event has occurred in the tumor biopsies?

- a. A new mutation changing a proto-oncogene to an oncogene
- b. A new mutation activating a tumor suppressor gene
- c. A loss-of-heterozygosity event leaving the cell with only mutant allele(s) of a tumor suppressor gene
- d. A loss-of-heterozygosity event leaves the cell with at least one wild-type allele of a tumor suppressor gene
- e. A loss-of-heterozygosity event that made an oncogene homozygous.

*Question 5.* Which parent carries the mutation?

- a. Dad (I-1)
- b. Mom (I-2)
- c. Both parents
- d. Neither parent
- e. Could be either

*Question 6.* Is there a sibling of the two cancer patients in generation II who is at risk for the disease because of the mutation?

- a. Brother (II-1)
- b. Sister (II-4)
- c. Both siblings
- d. Neither siblings
- e. Could be either

*Question 7.* The *cdc* mutations in yeast are recessive, conditional mutations in genes that encode activators of the cell cycle. The wild-type alleles of the *CDC* genes are most similar to:

- a. Tumor suppressor genes
- b. Proto-oncogenes
- c. Oncogenes
- d. Could be either a or c
- e. Cannot be determined

*Question 8.* Checkpoint mutations in yeast can be recessive mutations in genes that encode negative regulators of the cell cycle needed for response to DNA damage. The wild-type alleles of the checkpoint genes are most similar to:

- a. Tumor suppressor genes
- b. Proto-oncogenes
- c. Oncogenes
- d. Could be either a or c
- e. Cannot be determined

*Question 9:* Why use the families that show early onset of a type of cancer when trying to identify mutations in tumor suppressor genes that cause predisposition to the given cancer?

- a. Because the families will be completely devoid of sporadic cases of the cancer.
- b. Because all of the early onset cases in the various families will arise from mutations in the same tumor suppressor gene.
- c. Because the early onset cases are unlikely to be sporadic cases, and more likely to be caused by a mutation in a tumor suppressor gene.
- d. Because you are assured that there will be an inherited genetic component to the cancer incidence in the families.

*Question 10.* A family with an apparent inherited predisposition to breast and ovarian cancer has been identified. Their genetic counselor suggests getting full sequence analysis of both *BRCA1* and *BRCA2*. Why should a family choose full sequence analysis? Answer all that are correct.

- a. Because the pedigree analysis has ruled out the other possible genes that when mutant contribute to predisposition to breast and ovarian cancer.
- b. Because full sequence analysis will detect nearly all mutations in *BRCA1* or *BRCA2*.
- c. Because ASOs or other techniques based on known alleles will not work.
- d. Because the pedigree analysis gives no information about which gene might be mutated in the family.