

Your name: \_\_\_\_\_

-----  
Define each of the following terms, explaining what it is and how it is used for molecular genetics research in one or more of the genetic model organisms we discussed (5 points each):

**recombinant inbred lines**

Inbred progeny (1 point) derived from a cross between two parental inbred strains (2 points), commonly created for the purpose of genetic analysis such as mapping genes.

**Balancer chromosomes**

Contain inversions, a dominant marker, and are lethal if carried homozygously (1 point each). Used in *Drosophila* (2 points).

**ES cells**

Embryonic stem cells (1 point) are totipotent (2 points). These cells are modified in vitro (gene replacements or knockouts) then re injected into another embryo (2 points) resulting in chimeras or hybrids.

**The cre site-specific recombinase**

Recognizes lox-P sites (1 point) and via recombination, removes the intervening sequence between two flanking lox-P sites. This is useful for loss of function experiments (2 points, remaining points awarded depending on description).

**T-DNA**

The portion of the Ti plasmid from *Agrobacterium* responsible for the creation of a tumor. T-DNA can be modified to include a gene of interest (as long as you maintain flanking T-DNA sequences ) that will be incorporated into the host genome (3 points awarded for a good representation of the explanation above). Used for transformation in *Arabidopsis* (2 points).

**GAL4 (in this case, explain how it is used in model organisms other than *S. cerevisiae*)**

A transcription factor that is commonly used as part of the enhancer trap technique. GAL4 binds to UAS<sub>G</sub> (upstream activator sequences), which is placed in front of your gene of interest and is turned on in the presence of GAL4.

GAL4 can be used in this manner for ectopic expression experiments, you can control the activation of your gene of interest by stimulating production of GAL4 (which can be placed under the control of a variety of genetic elements).

Your name: \_\_\_\_\_

1. (6 points) At a given locus, three alleles, 1, 2 and 3 are present in a population in Hardy-Weinberg equilibrium and no other alleles are present at appreciable frequencies. Homozygotes for allele 1 represent 25% of the population. Do you know what fraction of the population is heterozygous for allele 1? If so, what is that fraction?

Yes,  $p^2 = .25$ ,  $p = .5$ , therefore  $1 - p = q = 0.5$  (where  $q$  represents everything non- $p$ ).  
 $2pq = 2(0.5)2 = 0.5$

2. (4 points) Building on question 1, heterozygotes between alleles 1 and 2 represent 20% of the population. What fraction of the population is homozygous for allele 2?

$2pq = 20\% = 2(0.5)q$  (where  $q$  represents allele 2)  
 $q = 0.2$        $q^2 = 0.04$  or 4%

3. (4 points) Building on questions 1 and 2, what fraction of the population is homozygous for allele 3?

$1 - p - q = r$  (where  $r$  represents allele 3)  
 $r = 0.3$        $r^2 = 0.09$  or 9%

4. (4 points) You isolate DNA from a haploid strain of yeast and from a closely related and highly inbred diploid strain. In separate reactions of the same volume you allow 100 micrograms of DNA from each strain to denature and hybridize.

**c) DNA from the two strains would hybridize at the same rate**

5. (4 points) You repeat this experiment using DNA from the same number of cells rather than the same mass of DNA. This time

**d) DNA from the diploid strain would hybridize faster by a factor of 2**

You are studying a new mutation in the yeast *Saccharomyces cerevisiae* that is uv sensitive (no growth when irradiated  $30 \text{ Jm}^{-2}$  of ultraviolet light). You have named your mutation *mrd2*, for **my radiation sensitive 2** (although you anticipate re-naming it if it turns out to be allelic to an existing *RAD* gene). It may be a new gene, and you want to investigate.

First, you cross your haploid *mrd2* strain to a haploid strain of the opposite mating type carrying *can1* and *cup5*, both recessive markers on chromosome V. The phenotype of *can1* is resistance to canavanine. The phenotype of *cup5* is sensitivity to copper.

*CAN1* lies at position -50 cM (50 cM to the left of the centromere) and *CUP5* lies at -18 cM (32 map units to the right of *CAN1*, so the expected recombination frequency between *can1* and *cup5* is about 23.6%).

The resulting *mrd2/MRD2; can1 cup5 / CAN1 CUP5* diploids are wild-type (they grow after

Your name: \_\_\_\_\_

-----  
exposure to  $30 \text{ Jm}^{-2}$  of ultraviolet light) and sporulate normally.

You induce sporulation and examine the haploid spores.

6. Among the resulting haploid spores 50% are *cup5*. (5 points) What fraction of the *cup5* haploids are also resistant to canavanine?

Recombination rate is 23.6%, recombinants won't be resistant to canavanine, therefore the answer is **76.4% (the nonrecombinants)**.

You identify 20 colonies that are *can1 CUP5* using plates with canavanine and copper.

7. (5 points) If *MRD2* is unlinked (not on chromosome V), what fraction of these 20 colonies do you expect to continue growing after exposure to  $30 \text{ Jm}^{-2}$  of ultraviolet light?

**If it's unlinked, 50% (independent assortment)**.

8. (6 points) In this case (*MRD2* is unlinked) could you determine whether it is near the centromere of the chromosome that it is on? Is so, how would you do that?

**The fewer the number of tetratypes, the closer it is to the centromere**

9. (5 points) If *MRD2* is at -52 cM., 2 cM. to the left of *CAN1*, what fraction of these 20 colonies do you expect to continue growing after exposure to  $30 \text{ Jm}^{-2}$  of ultraviolet light?

**Recombination rate is 2%, 98% (nonrecombinants) or 19.6 (or all 20) will continue to grow.**

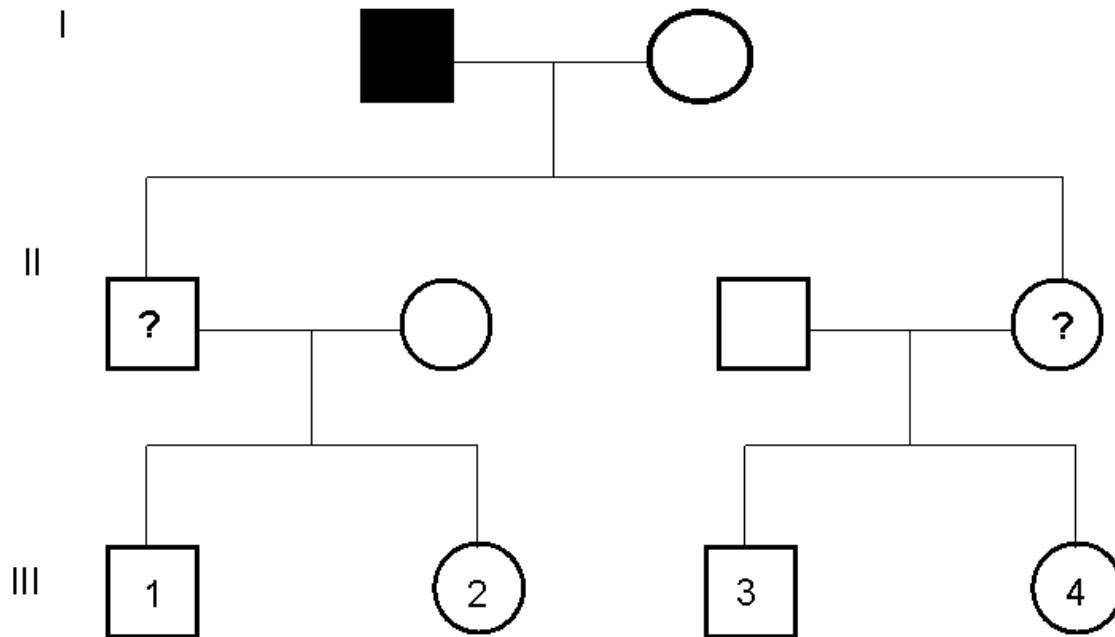
10. (5 points) If *MFT2* lies at -34 cM. (precisely between *CAN1* and *CUP5*) what fraction of these 20 colonies do you expect to continue growing after exposure to  $30 \text{ Jm}^{-2}$  of uv light?

**Recombination rate is 2%. Based on the passage of alleles, you would need to have a recombination even to grow, 2% (or 0.4 or 0 out of 20) will continue to grow .**

11. (5 points) If *MFT2* lies at -16, 2 cM. to the right of *CUP5*, what fraction of these 20 colonies do you expect to continue growing after exposure to  $30 \text{ Jm}^{-2}$  of ultraviolet light?

**Recombination rate is 2%. Based on the passage of alleles, you would need to have a recombination even to grow, 2% will continue to grow .**

Your name: \_\_\_\_\_



For each of the following types of inheritance indicate which progeny are at risk (circle the letter corresponding to all that apply). Assume that the trait is very rare (intermarrying partners are not affected and are not carriers).

12. (4 points) In the case of an autosomal dominant trait  
**a) 1**                      **b) 2**                      **c) 3**                      **d) 4**
13. (4 points) In the case of a maternally imprinted trait  
**a) 1**                      **b) 2**
14. (4 points) In the case of a paternally imprinted trait  
**c) 3**                      **d) 4**
15. (4 points) In the case of a recessive sex-linked trait  
**c) 3**
16. (4 points) In the case of a trait conferred by a mitochondrial gene
17. (4 points) In the case of a Y-linked trait  
**a) 1**

Your name: \_\_\_\_\_

(2 points per item; think of each question as multiple true/false statements). Circle, check or otherwise designate **each** correct statement (i.e. check all that apply). Again, ambiguous marks (checking both, placing a mark between the two statements, etc.) will be considered wrong.

18. The F plasmid

- b)** is a conjugative plasmid.
- c)** forms an **Hfr** bacterium upon integration into the *E. coli* chromosome.
- e)** contains genes for synthesizing connections between donor and recipient cells.
- f)** is the basis for the vector used in construction of BAC clones.

19. The fidelity of replication in vivo is increased about 100-fold by

- b)** mismatch repair
- c)** the 3'-to-5' exonuclease activity of DNA polymerase itself

For each of the following statements, indicate for which of the five model organisms (*Saccharomyces cerevisiae*, *Drosophila melanogaster*, *Caenorhabditis elegans*, *Arabidopsis thaliana*, *Mus musculus*) it is true. These are 25 true-false questions, worth 1 point each.

<b>Statement.</b>	<i>S. c.</i>	<i>D. m.</i>	<i>C. e.</i>	<i>A. t.</i>	<i>M. m.</i>
Gene disruption using homologous recombination is routinely used for reverse genetics.	<b>T</b>	<b>F</b>	<b>F</b>	<b>F</b>	<b>T</b>
XX individuals are females and XY individuals are males.	<b>F</b>	<b>T</b>	<b>F</b>	<b>F</b>	<b>T</b>
Self-fertilization allows a heterozygous allele in a single individual to be homozygous in the next generation.	<b>F</b>	<b>F</b>	<b>T</b>	<b>T</b>	<b>F</b>
The genome size is under 300 Mb..	<b>T</b>	<b>T</b>	<b>T</b>	<b>T</b>	<b>F</b>
The majority of genes have no introns.	<b>T</b>	<b>F</b>	<b>F</b>	<b>F</b>	<b>F</b>

Your name: \_\_\_\_\_

-----  
(4 points each). In each of the following there are two or more statements. One is true (generally, it is taken directly from your textbook) and the others have been modified so that to be untrue or misleading. Circle, check or otherwise designate the correct statement. Ambiguous marks (checking both, placing a mark between the two statements, etc.) will be considered wrong.

20. a) In reverse genetics, one starts with the gene sequence and determines the phenotype.

21. b) *FMR-1* alleles with an intermediate number of CGG triplet repeats (between 50 and 200) do not generate fragile X symptom in most carriers, but have an increased risk of mutation to alleles with a greater number of repeats that do show symptoms.

22. b) DNA methylation in mammals is specific for CG dinucleotides.

23. a) miRNAs are produced through processing from precursors that are encoded in non-protein-coding regions of plant and animal genomes.

24. b) Autozygosity is a term used to mean homozygosity for markers identical by descent and inherited from a recent common ancestor.

25. a) Wild-type yeast (*S. cerevisiae*) can grow vegetatively as either haploid or diploid cells.

26. b) Small regulatory RNAs like *lin-4* RNA may play a much larger role in development than originally suspected, and not only in nematodes.

27. a) Congenic mouse strains are identical except for a single locus and are generated by repeated backcrossing.

You are studying mutations that affect vulval development in *C. elegans* and you have defined two genes, *vuv-1* and *vuv-2*. Null alleles of *vuv-1* result in hermaphrodites with a vulvaless phenotype while loss-of-function mutations in *vuv-2* result in the multivulva phenotype.

28. (5 points) Which of the following regulatory pathways would be consistent with these results? List all that apply.

d) *vuv-1* ----| *vuv-2* ----| vulva formation.

f) *vuv-2* ----| *vuv-1* ---> vulva formation.

29. (5 points) In further studies you find that a *vuv-1*; *vuv-2* double mutant looks identical to a *vuv-2* single mutant (i.e. multivulva). Which of the pathways is most consistent with this result? Please refer to the options listed above (a through h), picking one.

d) *vuv-1* ----| *vuv-2* ----| vulva formation.

30. (6 points) You have a piece of DNA that includes the sequence:

5' - **CGTACCATGTACCTGT**TACCTGTACTATCTATCGGG**TGACTGCTTATCCA** - 3'

To amplify this DNA by PCR you would use a pair of primers containing which **two** of the following eight primers (you must get both primers right to get any credit -- circle **two** letters):

c) 5' - CGTACCATGTACCTG - 3'

e) 5' - TGGATAAGCAGTCAC - 3'