

Molecular Genetics BSCI410 Final review, especially Lectures 18-23. Model Organisms

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This review sheet covers lectures 18-23, which will be covered on the final exam. Half of the points on the final exam will come from these lectures. The other half of the points are comprehensive. Review material for the earlier sections was provided on earlier homeworks and review sheets.

The final exam will be given on Thursday, December 14 at 8:00 am

**Vocabulary** Again, many of these words are in the glossary in Hartwell.

conditional lethal	multivulva	vulvaless
cell autonomous	yeast integrating plasmid	yeast centromeric plasmid
yeast episomal plasmid	<i>HO</i>	<i>MAT</i>
sporulation	tetrads	whorl
sepal	petal	stamen
carpel	pistil	T-DNA
<i>Agrobacterium</i>	RNA-mediated interference	imaginal disc
homeotic mutation	P element	enhancer trap
ectopic expression	chimeric embryo	ES cells
inbred strains	recombinant inbred strains	congenic lines
epistasis	spliced leader RNA	balancer chromosome
hybrid dysgenesis	M strains	

**Concepts.** Be sure to understand the following concepts.

yeast mating type	forward vs. reverse genetics
mosaic analysis	conservation of synteny
epistasis analysis	transgenic mice
ectopic expression vs. overexpression vs. antisense or dominant negative	
plasmid shuffle	

For each of the model organisms know

- Know the approximate size of the genome and the approximate number of genes.
- Be able to explain how one carries out reverse genetics in each of the model organisms.
- Be able to explain how one can determine the location of gene function in each of the multicellular model organisms. Be able to explain how GAL4 is used, and how FRTs are used, for this purpose.
- Be able to explain the advantages and disadvantages of each model organism.

**Study questions** (you may have questions like these on the exam).

Review solved problems at the end of chapters 19 and 21 and Refences A thru E

Question 19-4c. Is the phenotype of a null mutation in the *AGAMOUS* gene in *Arabidopsis* autonomous or nonautonomous?

Speculate on whether, among mutations **in the coding region of a gene**, a missense or a nonsense mutation is more likely to be dominant.

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Be able to explain the role of the TK gene in mammalian gene replacement. Is there a corresponding marker used in gene replacement in yeast? If so, which marker is normally used? If not, why not? What marker would you use if you did need to use such a marker?

In diagramming developmental signaling pathways, the symbol  $---|$  is used to indicate repression; the activity of one gene negatively regulates the activity of the next. For the pathway  $A \text{ ---| } B \text{ ---> } C$  if A is on, then B will be off. If B is on, then C will also be on. You are studying mutations that affect the sensory rays in the male tail development of *C. elegans* and you have defined two genes, *ray-1* and *ray-2*. Loss-of-function mutations in *ray-1* result in males with extra rays, more than the normal number. Loss-of-function mutations in *ray-2* result in males with no sensory rays in the tail. Which of the following regulatory pathways would be consistent with these results?

- ray-1*  $--->$  *ray-2*  $--->$  ray formation.
- ray-1*  $----|$  *ray-2*  $--->$  ray formation.
- ray-1*  $--->$  *ray-2*  $----|$  ray formation.
- ray-1*  $----|$  *ray-2*  $----|$  ray formation.
- ray-2*  $--->$  *ray-1*  $--->$  ray formation.
- ray-2*  $----|$  *ray-1*  $--->$  ray formation.
- ray-2*  $--->$  *ray-1*  $---|$  ray formation.
- ray-2*  $----|$  *ray-1*  $---|$  ray formation.

In further studies you find that a *ray-1*; *ray-2* double mutant looks identical to a *ray-2* single mutant (i.e. no rays are produced). Which of the pathways is most consistent with this result?

- ray-1*  $--->$  *ray-2*  $--->$  ray formation.
- ray-1*  $----|$  *ray-2*  $--->$  ray formation.
- ray-1*  $--->$  *ray-2*  $----|$  ray formation.
- ray-1*  $----|$  *ray-2*  $----|$  ray formation.
- ray-2*  $--->$  *ray-1*  $--->$  ray formation.
- ray-2*  $----|$  *ray-1*  $--->$  ray formation.
- ray-2*  $--->$  *ray-1*  $---|$  ray formation.
- ray-2*  $----|$  *ray-1*  $---|$  ray formation.

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