Unit 6 - Week 4

Course outline

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Assignment 4

The due date for submitting this assignment has passed.
As per our records you have not submitted this assignment.

Due on 2020-10-14, 23:59 IST.

1) Which of the following methods can help you identify multiple/additional genes functioning in a single pathway? *1 point*

- Suppressor screen
- Blue-white screen
- Chromosome walking
- Synthetic screen

No, the answer is incorrect.
Score: 0
Accepted Answers:
Suppressor screen
Synthetic screen

2) Assume that you have identified a new gene called *gene-*X. About 10 % of progeny from animals homozygous for a null allele of *gene-*X do not survive. You suspect *gene-*X functions redundantly with another gene (*gene-*Y). Which of the following methods is most suitable for identifying *gene-*Y *1 point*

- Two-factor analysis
- Three-factor analysis
- Synthetic screen
- Cosmid rescue

No, the answer is incorrect.
Score: 0
Accepted Answers:
Synthetic screen

3) Which of the following points would you keep in mind while designing and performing a suppressor screen? *1 point*

- The mutant phenotype should be readily visible.
- The number of progeny at the F2 generation should be large.
- The number of progeny at the F2 generation should be small.
- The new mutation must follow Mendelian Inheritance pattern.

No, the answer is incorrect.
Score: 0
Accepted Answers:
The mutant phenotype should be readily visible.
The number of progeny at the F2 generation should be large.
The new mutation must follow Mendelian Inheritance pattern.

4) Following are some of the steps followed (not in order) to identify a gene's chromosomal location and function. Choose the correct order. *1 point*

1. Transgenic rescue with cosmids
2. Correlation of genetic map and physical map near the gene of interest
3. Identification of DNA lesions in the gene of interest in the mutant
4. Identification of the chromosomal interval
5. Transgenic rescue with wild-type DNA clones

- 2,4,3,5,1
- 4,5,2,3,1
- 5,3,1,2,4
- 4,1,2,5,3

No, the answer is incorrect.
Score: 0
Accepted Answers:
4,1,2,5,3

The two general mutant phenotypes observed with regards to the vulval development in $C.$ *elegans* are (i)_____ and (ii)_____. [Do not abbreviate your answer. Example, write "lethal", instead of "let"]

5) (i)_____

No, the answer is incorrect.
Score: 0
Accepted Answers:
(Type: String) Multivulva
(Type: String) Vulvaless

0.5 points

6) ii)_____

No, the answer is incorrect.
Score: 0
Accepted Answers:
(Type: String) Vulvaless
(Type: String) Multivulva

0.5 points

7) Lineage analysis is suitable for identifying which of the following? *1 point*

- Cell-cell interactions
- Duration of cell cycle
- Phenotypes of a wild-type cell
- Developmental potentials of a cell

No, the answer is incorrect.
Score: 0
Accepted Answers:
Cell-cell interactions
Developmental potentials of a cell

8) Which of the following statement(s) are false? *1 point*

- AC induces vulval development.
- Pnps are pluripotent.
- Tertiary fate is the ground or uninduced fate.
- Hypermorph, neomorph and antimorph are types of recessive mutations.

No, the answer is incorrect.
Score: 0
Accepted Answers:
Pnps are pluripotent.
Hypermorph, neomorph and antimorph are types of recessive mutations.

9) Which of the following is TRUE with respect to mutations that affect genes encoding enzymes of a metabolic pathway? *1 point*

- Upstream mutations will be epistatic over downstream mutations
- Downstream mutations will be epistatic over upstream mutations
- Downstream mutations will suppress the effect of upstream mutations
- None of the other options listed here are true.

No, the answer is incorrect.
Score: 0
Accepted Answers:
Upstream mutations will be epistatic over downstream mutations

10) Mosaic analysis is used to primarily study the: *1 point*

- Spatial patterning of cells
- Anatomical focus of gene function
- Anatomical focus of gene expression
- Gene-Gene interactions

No, the answer is incorrect.
Score: 0
Accepted Answers:
Anatomical focus of gene function

11) Assume a new recessive mutation was obtained by mutagenizing strain A. In this species, strain B is used for crossing with strain A for SNP-based gene mapping, as several SNPs have been well established between these two strains. Among the F2 progenies displaying the mutant phenotype, *1 point*

- Strain A SNP will predominate if the SNP is close to the mutant allele's locus.
- Strain B SNP will predominate if the SNP is far from the mutant allele's locus.
- Both SNPs will be equally represented if the SNP is far from the mutant allele's locus.
- Strain B SNP will predominate if the SNP is close to the mutant allele's locus

No, the answer is incorrect.
Score: 0
Accepted Answers:
Strain A SNP will predominate if the SNP is close to the mutant allele's locus.
Both SNPs will be equally represented if the SNP is far from the mutant allele's locus.