

**Introduction to Genetics**  
**FALL 2023**  
**EXAM III**

1. In a mating between an F<sup>+</sup> donor and an F<sup>-</sup> recipient, the recipient

- A) receives a stable copy of the F plasmid
- B) may incorporate chromosomal genes from the donor into its genome
- C) receives a stable copy of the F plasmid that also contains a segment of chromosomal genes
- D) remains lysogenic
- E) induces the phage's lytic replication cycle

2. The process occurring above is referred to as

- A) transformation
- B) transjugation
- C) transduction
- D) conduction
- E) conjugation

**Questions 3 - 4 refer to the following experiment:**

In a generalized transduction experiment, donor *E. coli* cells have the genotype  $a^+b^-c^+$ , and recipient cells have the genotype  $a^-b^+c^-$ . P1-mediated transductants for  $a^+$  were selected, and their total genotypes were determined, with the following results:

<u>Genotype</u>	<u>Number of progeny</u>
$a^+b^-c^+$	390
$a^+b^-c^-$	410
$a^+b^+c^+$	10
$a^+b^+c^-$	<u>190</u>
	1000

3. What is the cotransduction frequency for  $a$  and  $b$ ?

- A) 0.20
- B) 0.40
- C) 0.60
- D) 0.80
- E) cannot be determined since they were not selected for

4. What is the cotransduction frequency for  $a$  and  $c$ ?

- A) 0.20
- B) 0.40
- C) 0.60
- D) 0.80
- E) cannot be determined since they were not selected for

5. In a generalized P1 transduction experiment using donor  $a^+ b^+ c^+ d^+$  *E. coli* cells and  $a^- b^- c^- d^-$  recipients, the following cotransduction frequencies are observed:

<u>Selecting for</u>	<u>Cotransduction percentage</u>
$a^+$ transductants	$b$ 30%, $c$ 10%, $d$ 50%
$b^+$ transductants	$c$ 0%, $d$ 40%
$c^+$ transductants	$d$ 3%

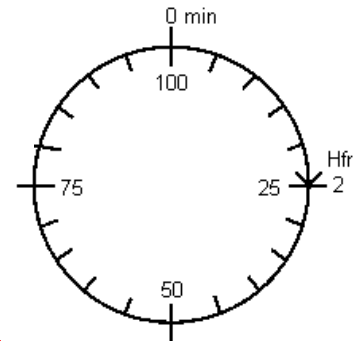
What is the order of the genes on the chromosome?

- A) abcd
- B) bdac
- C) cdab
- D) dabc
- E) bacd

**Questions 6 - 9 refer to the following experiment:**

An *E. coli* F<sup>-</sup> strain has the following genotype: A<sup>-</sup> B<sup>-</sup> C<sup>-</sup> D<sup>-</sup> E<sup>-</sup>. Three different Hfr strains, all carrying A<sup>+</sup> B<sup>+</sup> C<sup>+</sup> D<sup>+</sup> E<sup>+</sup> markers are mated with the F<sup>-</sup> strain in separate matings. The interrupted-mating results are given below. The numbers indicate time (in minutes) when different donor markers appeared in F<sup>-</sup> cells after mating began. Assume that the *E. coli* map consists of 100 minutes. Hfr 2 is known to have integrated at the 25min location on the chromosome and transfers in a counterclockwise direction.

Markers	Hfr 1	Hfr 2	Hfr 3
A	10	20	-
B	45	-	20
C	25	5	40
D	-	60	-
E	-	-	5



6. The gene order, starting from A and going clockwise is  
 A) ACBDE B) ADEBC C) AEDCB D) ABCED **E) ACBED**
7. What is the location of the origin for Hfr 1 and Hfr 3?  
 A) 95min; 30min **B) 95min; 60min** C) 15min; 35min D) 5min; 40min E) 85min; 30min
8. What is the direction of transfer for Hfr 1 and Hfr 3?  
 A) Both transfer in a clockwise direction  
 B) Both transfer in a counterclockwise direction  
**C) Hfr 1 transfers clockwise, Hfr 3 transfers counterclockwise**  
 D) Hfr 1 transfers counterclockwise, Hfr 3 transfers clockwise  
 E) Hfr 1 transfers counterclockwise, but Hfr 3 cannot be determined
9. What is the map location of the E marker?  
**A) 55min** B) 35min C) 95min D) 5min E) 70min

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Questions 10-6 refer to the following cross.

A plant of genotype CC dd is crossed to a plant of genotype cc DD. The F<sub>1</sub> progeny is then testcrossed with a cc dd plant.

10. If the genes are unlinked, the percentage of plants with genotype cc dd in the F<sub>2</sub> progeny will be  
 A) 12.5% **B) 25%** C) 37.5% D) 50% E) 75%
11. If the genes are 25 map units apart, the percentage of plants in the F<sub>2</sub> progeny with genotype cc dd progeny will be  
**A) 12.5%** B) 25% C) 37.5% D) 50% E) 75%
12. If the genes are 25 map units apart, the percentage of plants in the F<sub>2</sub> progeny with genotype Cc dd progeny will be  
 A) 12.5% B) 25% **C) 37.5%** D) 50% E) 75%

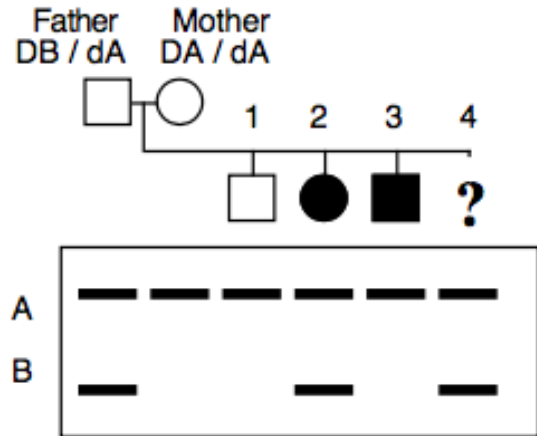
Questions 13-19 refer to the following cross.

Hobbits are legendary creatures from Middle Earth whose dominant traits are Large (L), Hairy (H), Tough (T) feet. Data from a testcross with a trihybrid individual of these three linked genes are shown below.

<b>Foot Phenotype</b>	<b>genotype</b>	<b>#</b>
Normal	LlHhTt	340
Small Hairless Soft	llhhtt	330
Small	llHhTt	120
Hairless Soft	Llhhtt	110
Small Hairless	llhhTt	40
Soft	LlHhtt	40
Hairless	LlhhTt	10
Small Soft	llHhtt	10
<b>Total</b>		<b>1000</b>

13. Which of the following represents a recombinant with respect to H and T  
 A) LlHhTt   B) LlHhtt   C) llhhtt   D) LlhhTt   E) llHhTt
14. What is the recombination frequency with respect to L and H?  
 A) 10%   B) 16%   C) 25%   D) 31%   E) 33%
15. The order of these three genes is?  
 A) LHT   B) HTL   C) TLH   D) A or B could be correct   E) B or C could be correct
16. Which of the following progeny represents a double recombinant?  
 A) llHhTt   B) LlHhtt   C) llhhTt   D) llhhtt   E) LlhhTt
17. How many double recombinants were observed in this cross?  
 A) 16   B) 20   C) 25   D) 31   E) 33
18. How many double recombinants were expected to occur in this cross?  
 A) 16   B) 20   C) 25   D) 31   E) 33
19. Based on the number of double recombinants you actually observed, what is the degree of interference for this region?  
 A) 0.2   B) ~0.4   C) 0.5   D) 0.6   E) 0.8

Questions 20-24 refer to the following cross.  
 A common recessive gene is associated with heart defects in dogs (d). The d locus is 90% linked to the SSR marker used in the analysis below. Two carriers of known genotypes had a litter of puppies and the puppies were tested for the linked marker as shown.



20. With respect to the SSR marker, puppy #1 inherited
- A) Allele A from the father and Allele A from the mother
  - B) Allele B from the father and Allele A from the mother
  - C) Both Allele A's came from the mother
  - D) An "A" Allele from the father but it is ambiguous in the mother
  - E) An "A" Allele from the mother but it is ambiguous in the father
21. With respect to the SSR marker, puppy #2 inherited
- A) Allele A from the mother and Allele A from the father
  - B) Allele B from the mother and Allele A from the father
  - C) Allele A from the mother and Allele B from the father
  - D) An "A" Allele from the father but it is ambiguous in the mother
  - E) Allele B from the father and Allele A could have been donated by either the mother or the father
22. If puppy #4 has not yet been tested for the heart defect, what is the probability that the mother passed on the disease allele to puppy #4?
- A) 10%      B) 25%      C) 50%      D) 81%      E) 90%
23. If puppy #4 has not yet been tested for the heart defect, what is the probability that the father passed on the disease allele to puppy #4?
- A) 10%      B) 25%      C) 50%      D) 81%      E) 90%
24. Which puppy(s) *must* be a recombinant with respect to the marker and disease locus?
- A) #1      B) #2      C) #3      D) #4      E) #3 & #4

Questions 25-28 refer to the following cross

Neurospora contain ordered tetrads. A cross is made between strains of genotype **Ab** and **aB** and the following ascii are observed.

Ascii	Genotypes of ascii	# of tetrads
Type 1	<i>ab ab aB aB Ab Ab AB AB</i>	160
Type 2	<i>aB aB AB AB Ab Ab ab ab</i>	60
Type 3	<i>aB aB aB aB Ab Ab Ab Ab</i>	180
	Total	400

25. Gene A is how far from its centromere

- A) 7.5 map units
- B) 15 map units
- C) 20 map units
- D) 22.5 map units
- E) 27.5 map units

26. Gene B is how far from its centromere

- A) 7.5 map units
- B) 15 map units
- C) 20 map units
- D) 22.5 map units
- E) 27.5 map units

27. Genes A and B are

- A) 15 map units apart
- B) 20 map units apart
- C) 22.5 map units apart
- D) 27.5 map units apart
- E) unlinked

28. The order of the three genes is

- A) A-centromere-B
- B) centromere-A-B
- C) centromere-B-A
- D) A and B are on different chromosomes
- E) unable to be determined since all three markers are unlinked

Questions 29-32 refer to the following cross

A female drosophila inherits a chromosome 12 that contains a paracentric inversion from their mother and a normal chromosome from their father. The inversion spans approximately one fourth of the total length of the chromosome.

29 A cross-over event occurring outside of the inversion on these chromatids during meiosis would result in

- A) a Robertsonian translocation.
- B) a dicentric and an acentric chromatid.
- C) two monocentric chromatids with deletions and duplications.
- D) two chromatids containing inversions
- E) two viable chromatids- one normal and one containing the inversion

30. A cross-over event occurring within the inversion region on these chromatids during meiosis would result in

- A) a Robertsonian translocation.
- B) a dicentric and an acentric chromatid.
- C) two monocentric chromatids with deletions and duplications.
- D) two chromatids containing inversions
- E) two viable chromatids- one normal and one containing the inversion

31. If each chromatid averages one crossover event per meiosis, what fraction of the total gametes produced would be expected to be viable?

- A) None of them
- B) 12.5%
- C) 75%
- D) 87.5%
- E) All of them

32. In male drosophila, crossovers (ie recombination between homologous chromosomes) do not occur during meiosis. What fraction of the total gametes produced by the male having these chromosomes would be expected to be viable?

- A) None of them
- B) 12.5%
- C) 75%
- D) 87.5%
- E) All of them

33. A diploid strain of watermelon  $2n=44$  is crossed with a tetraploid strain of watermelon. The progeny are viable, grow well, and produce tasty fruit. Which of the following is true?

- A) Half the progeny are diploid, half are tetraploid.
- B) All the progeny are triploid, and must be crossed with other triploid plants to reproduce
- C) All the progeny are triploid, but sterile.
- D) Half the progeny are diploid but their fertility would be reduced by ~50%.
- E) Half the progeny are triploid but their fertility would be reduced by ~50%.

### Potentially Useful formulas

the probability that, in  $n$  trials,  $A$  is realized  $s$  times and  $B$  is realized  $t$  times is equal to  $(n!)/(s!t!) \times (p^s q^t)$

% Recombinants =  $(\# \text{ recombinants}) / (\# \text{ total progeny}) \times 100\%$

map distance =  $(\# \text{ recombinants}) / (\# \text{ total progeny}) \times 100$

map distance =  $1/2 \times (\# \text{ tetratype tetrads}) / (\# \text{ total tetrads}) \times 100$

map distance =  $1/2 \times (\# \text{ ascii with 2nd division segregation}) / (\# \text{ total ascii}) \times 100$

Coeff. of coinc. =  $\text{Observed double recomb.} / \text{Expected double recomb.}$

Interference =  $1 - \text{Coefficient of coincidence}$

$\text{Chi}^2 = \sum (\text{observed} - \text{expected})^2 / \text{expected}$

if  $p$  = frequency of a dominant allele  $A$  and  $q$  = frequency of a recessive allele  $a$ , then  $p + q = 1$  and if the population is at Hardy-Weinberg equilibrium,  $p^2 : 2pq : q^2$

For a gene with a mutation rate  $\mu$  over  $n$  generations  $p_{(n)} = (1-\mu)^n p_{(0)}$

Average fitness of a population under selection,  $\bar{W} = W_{(AA)}p^2 + W_{(Aa)}2pq + W_{(aa)}q^2$

For an (i)sland population, where  $m$  fraction of the population has migrated in from the (m)ainland,  $p_{(i)}' = (1-m)p_{(i)} + mp_{(m)}$

Chance a new mutation becomes fixed  $1/2n$  or lost  $(2n-1)/2n$  from a pop. of size  $n$

Where  $F$  = the proportionate reduction in heterozygosity due to inbreeding

$f(AA) = p^2(1-F) + pF$

$f(Aa) = 2pq(1-F)$

$f(aa) = q^2(1-F) + qF$

Mean =  $\bar{x} = \sum x_i / N$

Variance =  $s^2 = \sum (x_i - \bar{x})^2 / N - 1$

Standard deviation =  $s = \sqrt{s^2}$

Covariance =  $\text{Cov}(x,y) = \sum f_i (x_i - \bar{x})(y_i - \bar{y}) / N - 1$

For a normal distribution,

~68% of the population falls within 1 standard deviation ( $s$ ) of the mean

~95% of the population falls within 2 standard deviation ( $s$ ) of the mean

~99.7% of the population falls within 3 standard deviation ( $s$ ) of the mean

$s_p^2 = s_g^2 + s_e^2$

where  $p$  = phenotype  $g$  = genotype  $e$  = environment

For additive alleles where  $n$  = # of additive loci,

$1/4^n$  = fraction in the population with the most extreme phenotype

$2n+1$  = the number of different phenotypes

**Formulas cont...**

$$n = D^2/8s_g^2$$

where n= number of genes, D= phenotypic difference between parental strains

$$s_p^2 = s_g^2 + s_e^2$$

$$H^2 = s_g^2 / s_p^2$$

where  $H^2$ =broad-sense heritability p=phenotype g= genotype e= environment

$$s_p^2 = s_a^2 + s_d^2 + s_e^2$$

$$h^2 = s_a^2 / s_p^2 = (M_N - M_O)/(M_E - M_O)$$

where  $h^2$ =narrow-sense heritability, d=dominant alleles, a= additive alleles, e= environment,

$M_O$ = original mean,  $M_N$ = new mean,  $M_E$ = mean of the bred population

