

**Introduction to Genetics**  
**FALL 2024**  
**EXAM IV**

1. Which of the following populations are at Hardy-Weinberg equilibrium for the A locus?

- A)  $f(AA) = 1.00$        $f(Aa) = 0$        $f(aa) = 0$
- B)  $f(AA) = 0.25$        $f(Aa) = 0.50$        $f(aa) = 0.25$
- C)  $f(AA) = 0.10$        $f(Aa) = 0.80$        $f(aa) = 0.10$
- D) Both A and B
- E) Both B and C

**Questions 2 - 3 refer to the following allele:**

In a population, gene D has a frequency of 0.7 and mutates to d at a rate of  $1 \times 10^{-4}$ .

2. Assuming there is no selection, what would you expect the frequency of D to be in the next generation?

- A) 0.0001      B) 0.00007      C) 0.69993      D) 0.69990      E) 0.99993

3. Assuming there is no selection, what would you expect the frequency of D to be after 1,000 generations?

- A) 0.0700      B) 0.0952      C) 0.6334      D) 0.9090      E) 0.9048

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**Questions 4 - 10 refer to the following experiment:**

A tropical island population is in Hardy-Weinberg equilibrium for the autosomal locus determining the presence/absence of pigment in the skin. The frequency of albinism ( $aa$ ) on the island is 1 in 10,000.

4. What is the frequency of the  $a$  allele in the population?  
 A) 0.0001    **B) 0.0100**    C) 0.0198    D) 0.0199    E) 0.0250

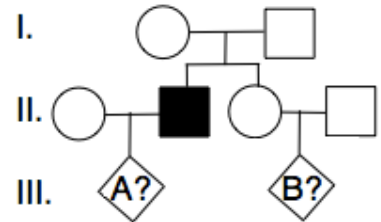
5. What is the frequency of heterozygotes in the population?  
 A) 0.0001    B) 0.0002    C) 0.0100    **D) 0.0198**    E) 0.9999

6. Knowing the frequency of albinism in this population, what is the probability that individual 'IIIA' will have albinism?

- A) 0.0100    **B) 0.0099**    C) 0.0198    D) 0.5000    E) 0.6667

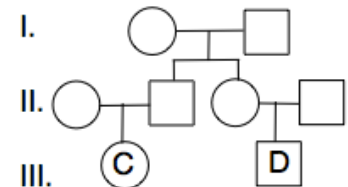
7. Knowing the frequency of albinism in this population, what is the probability that individual 'IIIB' will have albinism?

- A) 0.0033**    B) 0.0067    C) 0.0099    D) 0.0132    E) 0.33



8. What would the frequency of albinism be among the offspring of individual IIIC and IIID from this population, if the inbreeding coefficient among cousins equals 1/16?

- A) 0.0004    **B) 0.0007**    C) 0.0100    D) 0.0198    E) 0.0199



9. Suppose that the island experiences a rapid influx of immigrants so that the population doubles. If the frequency of albinism ( $aa$ ) among the arriving immigrants is 1 in 1,000. What would the new frequency of the 'a' allele be in the next generation?

- A) 0.0198    **B) 0.0208**    C) 0.0316    D) 0.0388    E) 0.0407

10. If after the immigrants arrive, all the parameters for maintaining Hardy-Weinberg equilibrium are met, what will the new frequency of heterozygotes be in the population when it reaches Hardy-Weinberg equilibrium?

- A) 0.0006    B) 0.0208    C) 0.0316    D) 0.0388    **E) 0.0407**

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**Questions 11 - 16 refer to the following experiment:**

You identify a population of mice (*Peromyscus maniculatus*) on an island. Their coat color is controlled by a single gene: *BB* mice are black, *Bb* mice are gray, and *bb* mice are white. You take a census of the population and record the following numbers of mice:

Black	80
Gray	240
White	180

11. What is the frequency of the 'B' allele?

- A) 0.09      B) 0.30      C) 0.40      D) 0.16      E) 0.20

12. What is the frequency of the 'b' allele?

- A) 0.81      B) 0.97      C) 0.60      D) 0.84      E) 0.80

13. What are the Hardy-Weinberg equilibrium frequencies for these three phenotypes?

- A) Black 0.08, Gray 0.24, White 0.18  
B) Black 0.16, Gray 0.48, White 0.36  
C) Black 0.40, Gray 0.24, White 0.60  
D) Black 0.64, Gray 0.32, White 0.04  
E) Black 0.81, Gray 0.18, White 0.01

14. A heat wave hits the island. All 80 mice with black fur die from heat stroke, but the other mice survive. What will be the approximate frequency of B in the next generation?

- A) 0      B) 0.24      C) 0.29      D) 0.43      E) 0.57

15. If the population suffers no further cataclysms after the heat wave, and the surviving animals mate randomly, what will be the frequency of mice with black fur when it returns to Hardy-Weinberg equilibrium?

- A) 0      B) 0.08      C) 0.24      D) 0.29      E) 0.41

16. If the climate is altered permanently, so that mice with black fur die before reproducing, which of the following statements are correct?

- A) At Hardy-Weinberg equilibrium,  $f(B)$  will equal 0.135.  
B) The fitness of mice with gray fur ( $W_{Bb}$ ) must be equal to 0.5.  
C) The fitness of the B allele ( $W_B$ ) is 0.  
D) The fitness of mice with black fur ( $W_{BB}$ ) is 0.  
E) The B allele will disappear from the population in one generation

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**Questions 17 - 21 refer to the following experiment:**

Four loci each with two alleles affect the quantitative phenotype of cucumber length in cucumber plants. A strain of cucumber plants makes cucumbers that are 12.0 cm long and has a genotype  $a/a ; b/b ; c/c ; d/d$ . Assume that the addition of each and any dominant allele (A, B, C, or D) adds 0.5 cm to the length.

17. How many different classes of cucumber lengths are possible?

- A) 4      B) 5      C) 8      **D) 9**      E) 16

18. What is the range in cucumber size that would be possible due to these loci?

- A) 2.0 cm      B) 2.5 cm      **C) 4.0 cm**      D) 4.5 cm      E) 8.0 cm

19. If two plants of genotype **Aa Bb Cc dd** were crossed, what proportion of the progeny would be expected to be 12.0 cm long?

- A) 1/8      B) 1/16      C) 1/32      **D) 1/64**      E) 1/256

20. If two plants of genotype **Aa Bb Cc dd** were crossed, how many different classes of cucumber lengths would be observed in the progeny?

- A) 4      B) 6      **C) 7**      D) 8      E) 9

21. If plants 12.5 cm long are crossed to plants 15.5 cm long, then the longest and shortest cucumbers possible from these crosses would be

- A) 8.0 cm and 20.0 cm.  
B) 12.0 cm and 16.0 cm.  
**C) 12.5 cm and 15.5 cm.**  
D) 13.5 cm and 14.5 cm.  
E) They would all be 14 cm

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**Questions 22 - 23 refer to the following population**

A heterogeneous population of beetles has a mean weight of 15 g.

22. Individuals of 25 g are collected and allowed to interbreed, and their progeny have a mean weight of 19 g. What is the narrow sense heritability ( $h^2$ ) for beetle weight?

- A) 0.16      **B) 0.40**      C) 0.60      D) 0.67      E) 0.80

23. The selective breeding is continued for a second generation. 25g beetles are again selected and from the new population that has a mean of 19g and allowed to breed. What will be the average weight of the beetles in the next generation?

- A) <21.4g**      B) 21.4g      C) 22.6g      D) 24g      E) 25g

**Questions 24 - 31 refer to the following experiment:**

Two inbred varieties of butternut squash are bred and the progeny are then self-fertilized. The mean length and variance of squash size for each generation is shown below. The growth conditions were kept the same in each generation.

	Mean Length (cm)	Variance (cm <sup>2</sup> )
Parent I	40	
Parent II	90	
F1	65	4
F2	65	49

24. What is the environmental variance (in cm<sup>2</sup>)?

- A) 0      B) 2      C) 4      D) 5      E) 7

25. What is the genetic variance (in cm<sup>2</sup>) in the F1 generation?

- A) 0      B) 2      C) 4      D) 7      E) 45

26. What is the genetic variance (in cm<sup>2</sup>) in the F2 generation?

- A) 4      B) 5      C) 7      D) 45      E) 49

27. If length is determined by additive alleles, what are largest butternut squash expected in the F2 generation (in cm)?

- A) 83      B) 88      C) 90      D) 92      E) 97

28. If the length is determined by additive alleles, what is the heritability of squash length in this population?

- A) 0.08      B) 0.71      C) 0.75      D) 0.92      E) 1.09

29. If the length is determined by additive alleles, approximately how many genes affect this trait?

- A) ~3      B) ~4      C) ~5      D) ~6      E) ~7

30. Assuming a normal distribution, 16% of the progeny in the **F2** would be expected to be longer than...

- A) 69 cm      B) 70 cm      C) 72 cm      D) 89.5 cm      E) 114 cm

31. Assuming a normal distribution, what percent of the population in the **F1** would be greater than 69 cm?

- A) 2.5%      B) 5%      C) 16%      D) 34%      E) 47.5%

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32. The broad sense and narrow sense heritability for several traits in domesticated cattle are:

Trait	$H^2$	$h^2$
percent protein in milk	0.80	0.56
feed efficiency	0.30	0.16
milk yield	0.70	0.60
calving interval	0.05	0.01

Which of these traits would be most responsive to artificial selection?

- A) percent protein in milk
- B) feed efficiency
- C) milk yield
- D) calving interval
- E) you need to know the environmental variance before this can be determined.

**Questions 33 - 34 refer to the following experiment:**

In pea plants, green peas (Y) are dominant to yellow peas (y). Suppose a large population of pea plants at Hardy-Weinberg equilibrium produces 1% yellow peas.

33. If the population was completely inbred during the next generation (all plants were self-fertilized), what would be the frequency of yellow peas in the next generation?

- A) 1.0%    B) 4.5%    C) 5.5%    D) 10%    E) 18%

34. If the population was continually inbred (all plants were self-fertilized) for many generations, what would be the frequency of yellow peas in the final population?

- A) 1.0%    B) 4.5%    C) 5.5%    D) 10%    E) 18%

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35. Which pair of hexameric primers could be used to amplify the DNA sequence shown below?

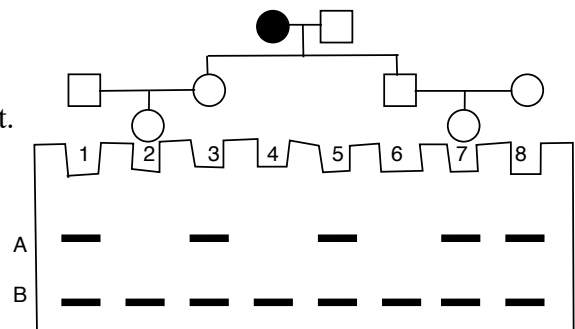
3' -TTTTTTGATTACATCGGCATTACCGATTTAAAGCCCTGGGGGG-5'  
 5' -AAAAAACTAATGTAGCCGTAATGGCTAAATTTTCGGGACCCCC-3'

- A) forward primer 5'-AAAAAA-3' and reverse primer 5'-GGGGGG-3'
- B) forward primer 5'-TTTTTT-3' and reverse primer 5'-CCCCCC-3'
- C) forward primer 5'-AAAAAA-3' and reverse primer 5'-CCCCCC-3'
- D) forward primer 5'-TTTTTT-3' and reverse primer 5'-GGGGGG-3'
- E) forward primer 5'-AAAAAA-3' and reverse primer 5'-TTTTTT-3'

36. The *E. coli* genome contains approximately 5 megabases of DNA. Assuming all base pairs are randomized in the genome, what is the minimum length of DNA (in bases) needed to design a sequence that is unique to that genome (ie found once or less throughout the genome)?

- A) 8
- B) 12
- C) 16
- D) 20
- E) 24

Questions 31-32 refer to the pedigree shown on the right.  
 A female has a rare recessive disease that is 90% linked to the AB locus.



37. The probability that female #2 is a carrier of the disease is

- A) 5%
- B) 10%
- C) 50%
- D) 90%
- E) 95%

38. The probability that female #7 is a carrier of the disease is

- A) 5%
- B) 10%
- C) 50%
- D) 90%
- E) 95%

Questions 33-34 refer to the following cross.

A plant of genotype *AA bb* is crossed to a plant of genotype *aa BB*. The  $F_1$  progeny is then testcrossed with a *aa bb* plant.

39. If the genes are unlinked, the percentage of plants with genotype *Aa bb* in the  $F_2$  progeny will be

- A) 12.5%
- B) 25%
- C) 37.5%
- D) 50%
- E) 75%

40. If the genes are 25 map units apart, the percentage of plants in the  $F_2$  progeny with genotype *Aa bb* progeny will be

- A) 12.5%
- B) 25%
- C) 37.5%
- D) 50%
- E) 75%

### Potentially Useful formulas

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

% 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. = Observed double recomb. / 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 =  $Cov(x,y) = \sum f_i (x_i - \bar{x})(y_i - \bar{y}) / N - 1$

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



**Potentially Useful formulas continued...**

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

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

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

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