Introduction to Genetics
FALL 2023
EXAM IV

Questions 1 - 2 refer to the following experiment:
In beetles, red eye color is determined by a single dominant allele (R). A large population is created by mixing 50% (RR) red-eyed beetles with 50% (rr) white-eyed beetles. If all the conditions of Hardy-Weinberg equilibrium are met,

1. What fraction of beetles will have red eyes in the next generation?

A) 25% B) 50% C) 62.5% [✓ D) 75%] E) 100

2. What fraction of beetles will have red eyes when the population reaches Hardy-Weinberg equilibrium?

A) 25% B) 50% C) 62.5% [✓ D) 75%] E) 100

Questions 3 - 4 refer to the following population:
A human virus has a mutation rate of $5*10^{-3}$. Gene D, encodes a capsid protein that is recognized by the immune system and important for clearing viral infections. Assume that 90% of the population of viral genomes have a wild type copy of D at the time of infection.

3. Assuming there is no selection, what fraction of the viral population would have the wild type copy of the D gene after it replicates once (ie one generation)?

A) 0.0045 B) 0.0050 [✓ C) 0. 8955] D) 0.8995 E) 0.9995

4. Assuming there is no selection, what fraction of the viral population would have the wild type copy of the D gene after 1,000 rounds of replication (ie 1,000 generations)?

A) 0.0045 [✓ B) 0.0060] C) 0.0067 D) 0.0452 E) 0.4520

Questions 5 - 11 refer to the following population:

A population of frogs in a large pond is in Hardy-Weinberg equilibrium for an autosomal locus that determines the presence or absence of a forked tongue. The frequency of forked tongues (*ff*) in the population is 5 in 1,000.

5. What is the frequency of the *f* allele in the population?

A) $2.5*10^{-5}$ B) 0.00498 C) 0.00500 [✓ D) 0.07070] E) 0.00995

6. What is the frequency of carriers of the forked tongue allele in the population?

A) 0.0050 B) 0.0010 C) 0.0657 D) 0.07070 [✓ E) 0.1314]

7. A frog with an <u>unforked</u> tongue, has parents with <u>unforked</u> tongues. However, some of his siblings have forked tongues. What is the probability that this frog is a carrier of the *f* allele?

A) 0.0657 B) 0.0876 C) 0.1314 [✓ D) 0.66667] E) 0.75000

8. The frog from question 7 mates with another frog from this population. They lay 500 eggs. What is the approximate probability that some of the tadpoles will have forked tongues when they hatch?

A) 0.04 [✓ B) 0.09] C) 0.13 D) 0.67 E) 0.75

9. What would the expected frequency of forked tongued frogs be among the offspring of any siblings that mated within this frog population? The inbreeding coefficient among siblings is 1/4.

A) 0.0013 [✓ B) 0.0215] C) 0.0376 D) 0.0441 E) 0. 0568

10. Suppose that a flood brings in a new population of frogs from a nearby pond where the frequency of forked tongues (*ff*) is 5 in 100. If after the flood, 50 percent of the frogs in the population are from the nearby pond, what will be the new frequency of the *f* allele?

A) 0.0275 B) 0.0866 [✓ C) 0.1472] D) 0.2236 E) 0.2943

11. If after the flood, all the parameters for maintaining Hardy-Weinberg equilibrium are met, what will the new frequency of forked tongued frogs be in the population when it reaches Hardy-Weinberg equilibrium?

[✓ A) 0.0217] B) 0.0866 C) 0.1118 D) 0.2236 E) 0.2943

Questions 12 - 15 refer to the following experiment:
You identify a population of rabbits from a dark forest whose coat color is controlled by a single gene: *BB* rabbits are black, *Bb* rabbits are gray, and *bb* rabbit are white. You take a census of the population and record the following numbers of rabbits:

Black	490
Gray	420
White	90

12. What are the allele frequencies of B and b?

A) f(*B*)=0.490, f(*b*)=0.090
[✓ B) f(*B*)=0.700, f(*b*)=0.300]
C) f(*B*)=0.465, f(*b*)=0.255
D) f(*B*)=0.910, f(*b*)=0.510
E) f(*B*)=0.900, f(*b*)=0.100

13. A rare snow hits the region making it advantageous to have white fur. Before the spring mating season arrives, 245 black rabbits and 105 gray rabbits have been eaten by wolves. All the other rabbits survive. What is the average fitness of the rabbit population in the spring?

A) 0. 245 B) 0.403 C) 0.620 [✓ D) 0.650] E) 0.750

14. What will be the frequency of the *B* allele among rabbits born in the spring?

A) 0. 245 B) 0.403 [✓ C) 0.620] D) 0.650 E) 0.750

15. If it doesn't snow anymore and all rabbits are again equally fit, what will the new Hardy-Weinberg frequencies be for the offspring of the spring generation of rabbits?

A) Black 245, Gray 315, White 90
B) Black 377, Gray 485, White 138
[✓ C) Black 384, Gray 471, White 145]
D) Black 245, Gray 315, White 440
E) Black 490, Gray 420, White 90

+_+_*+_*+_*+_*+_*+_*+_*

16. With random genetic drift, the probability of ultimate fixation of a particular allele is

A) dependent on the degree of dominance of the allele.
B) lower than the frequency of the allele in the original population.
C) higher than the frequency of the allele in the original population.
[✓ D) equal to the frequency of the allele in the original population.]
E) inversely proportionate to the frequency of the allele in the original population

17. Inbreeding results in

A) increased frequency of heterozygotes.
[✓ B) increased frequency of homozygotes.]
C) increased frequency of rare recessive alleles.
D) increased frequency of dominant alleles.
E) increased frequency of mutations

Questions 18 - 21 refer to the following experiment:
Pumpkin weight is controlled by additive alleles at three loci (genes). A pumpkin plant with a genotype a/a ; b/b ; c/c makes pumpkins that average 3 lbs. A pumpkin plant with a genotype A/A ; B/B ; C/C makes pumpkins that average 12 lbs.

18. How many different classes of pumpkin weights are possible?

A) 3   B) 5   C) 6   [✓ D) 7]   E) 9

19. How much does each dominant additive allele add to the weight of the pumpkin?

A) 1.0 lb   [✓ B) 1.5 lbs]   C) 2.0 lbs   D) 2.5 lbs   E) 3.0 lbs

20. Two parents of genotype **aaBBcc** and **AABBCC** are crossed. The resulting F1 progeny are then selfed to generate the F2. What is the average weight of the F2 pumpkins?

A) 1.0 lb   B) 6.0 lbs   C) 7.5 lbs   D) 8.0 lbs   [✓ E) 9.0 lbs]

21. Two parents of genotype **aaBBcc** and **AABBCC** are crossed. The resulting F1 progeny are then selfed to generate the F2. What fraction of the F2 pumpkins are expected to be 12lbs?

A) 1/4   B) 3/8   C) 3/16   [✓ D) 1/16]   E) 1/32

****

22. A genetically heterogeneous population of rice has a mean number of 30 days to maturation. Selection for decreased period of maturation is carried out for one generation. The average period to maturation among the plants selected as parents for the next generation is 25 days. F_1 plants mature on average in 27 days. Estimate the narrow sense heritability.

A) 0.100   B) 0.833   [✓ C) 0.600]   D) 0.400   E) 0.900

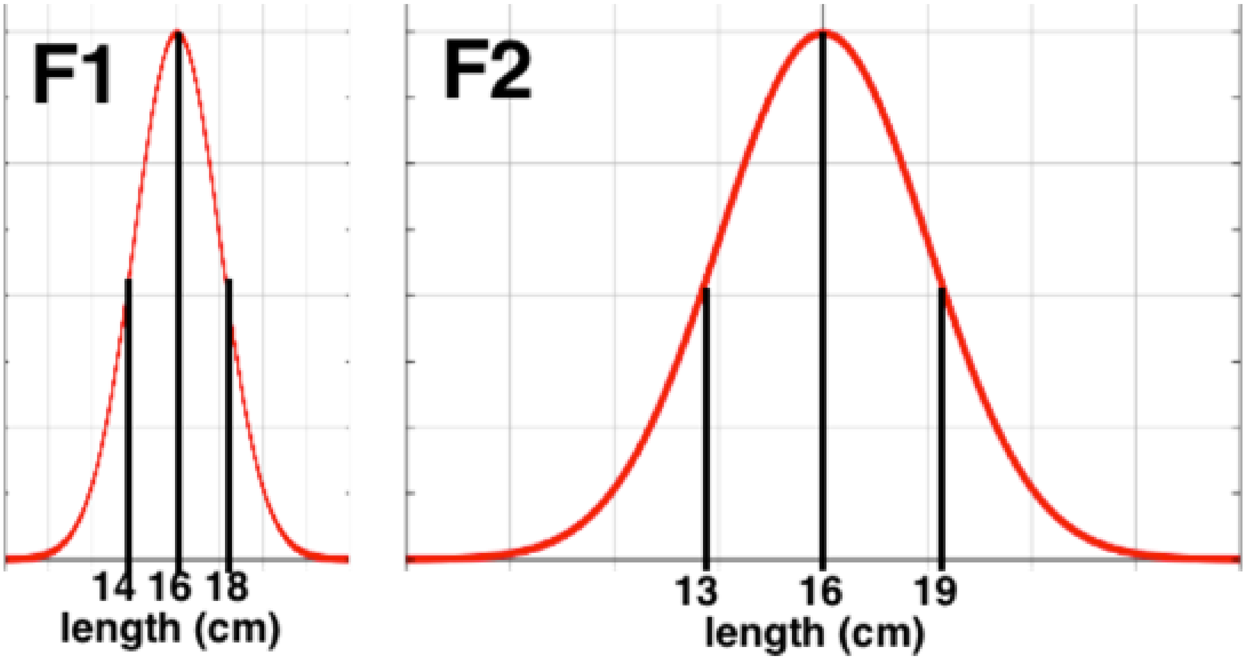
23. The broad sense and narrow sense heritabilities for several traits in domesticated cattle are:

Trait	H^2	h^2
percent protein in milk	0.56	0.44
feed efficiency	0.30	0.16
milk yield	0.80	0.24
calving interval	0.04	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 24 - 28 refer to the following experiment:
Two inbred varieties of long beans, with averages measuring 10.5 cm and 21.5 cm, are bred and the progeny are then self-fertilized. The distribution of long bean length among the F1 and F2 populations is shown below. The length of the <u>average</u> bean, and the length of beans <u>one standard deviation</u> above and below the average is plotted on the graph.



24. What is the genetic *variance* (cm^2) in the F1 population?

[✓ A) 0] B) 1 C) 2 D) 4 E) 5

25 What is the genetic *variance* (cm^2) in the F2 population?

A) 0 B) 1 C) 1.5 [✓ D) 5] E) 9

26. Calculate the broad-sense heritability.

A) 0.33 B) 0.44 [✓ C) 0.56] D) 0.67 E) 0.75

27. If the narrow sense heritability is equal to the broad sense heritability, approximately how many genes contribute to long bean length?

A) 2 [✓ B) 3] C) 4 D) 5 E) 6

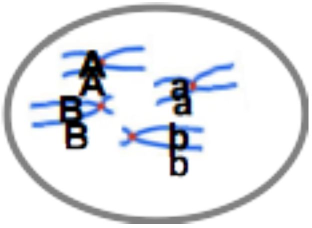
28. Assuming a normal distribution, what proportion of the progeny in the **<u>F2</u>** would be expected to be longer than 19cm.

A) 2.5% B) 5% [✓ C) 16%] D) 32% E) 34%

29. The DNA content of an organism contains 80% GC basepairs. On average, how frequently would you expect to find the sequence 5´ TCGA 3´?

A) once every 16 bases
B) once every 39 bases
C) once every 256 bases
[✓ D) once every 625 bases]
E) once every 4096 bases

30. The cell shown on the right is from a diploid organism, 2n=4. If there is only one gene on each chromosome, and the organism is hybrid at all loci, how many genotypically distinct gametes can this organism produce?



A) 1 B) 2 [✓ C) 4] D) 8 E) 16

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

`3'-TTTTTGATTACATCGGCATTACCGATTTAAAGCCCTCCCCC-5'`
`5'-AAAAACTAATGTAGCCGTAATGGCTAAATTTCGGGAGGGGG-3'`

A) forward primer 5'-AAAAA-3' and reverse primer 5'-GGGGG-3'
B) forward primer 5'-TTTTT-3' and reverse primer 5'-CCCCC-3'
[✓ C) forward primer 5'-AAAAA-3' and reverse primer 5'-CCCCC-3']
D) forward primer 5'-TTTTT-3' and reverse primer 5'-GGGGG-3'
E) forward primer 5'-AAAAA-3' and reverse primer 5'-TTTTT-3'

H U G E are four dominant genes controlling tomato size that are located on different chromosomes. A cross is carried out between Plant 1 with genotype-Hh UU gg ee and Plant 2 of genotype-Hh Uu GG Ee.

32. What percentage of the progeny are expected to be phenotypically identical to Plant 2?

A) 0 [✓ B) 3/8] C) 1/16 D) 9/32 E) 9/128

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.

33. 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%

34. If the genes are 20 map units apart, the percentage of plants in the F_2 progeny with genotype *Aa bb* progeny will be

A) 10 % B) 20 % [✓ C) 40%] D) 60% E) 80%

Questions **35-37** 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.

Foot Phenotpye	**genotype**	**#**
Normal	LlHhTt	340
Small Hairless Soft	llhhtt	330
Small	llHhTt	120
Hairlesss Soft	Llhhtt	110
Small Hairless	llhhTt	40
Soft	LlHhtt	40
Hairless	LlhhTt	10
Small Soft	llHhtt	10
	Total	**1000**

35. Which of the following represents a recombinant with respect to H and T

`A)LlHhTt` [✓ `B)LlHhtt`] `C)llhhtt` `D)Llhhtt` `E)llHhTt`

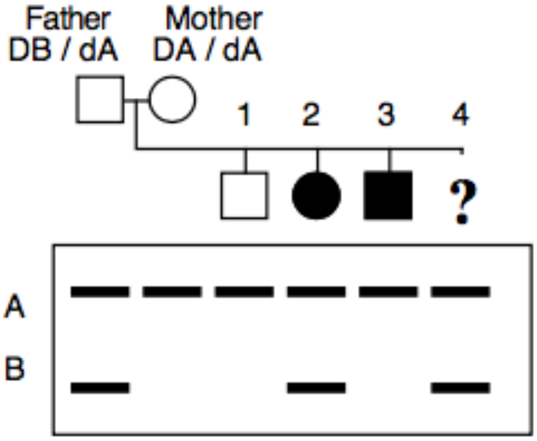
36. What is the recombination frequency with respect to H and T?

[✓ A) 10%] B) 16% C) 25% D) 31% E) 33%

37. The order of these three genes is?

A) TLH B) HTL [✓ C) LHT] D) A or B could be correct E) B or C could be correct

Questions **38-39** refer to the following cross.
A common recessive gene is associated with heart defects in dogs (d). The d locus is 75% 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 below.



38. 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) 6.25% B) 12.5% C) 25% [✓ D) 50%] E) 75%

39. If puppy #4 has not yet been tested for the heart defect, what is the probability that puppy #4 will have the disease?

A) 6.25% [✓ B) 12.5%] C) 25% D) 50% E) 75%

+!+!*+!*+!*+!*+!*+!*+!*!+!*+

40. 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!) x ($p^s q^t$)

% Recombinants = (# recombinants) / (# total progeny) x 100%
map distance = (# recombinants) / (# total progeny) x 100
map distance = 1⁄2 x (# tetratype tetrads) / (# total tetrads) x 100
map distance = 1⁄2 x (# ascii with 2nd division segregation) / (# total ascii) x 100
Coeff. of coinc. = Observed double recomb. / Expected double recomb.
Interference = 1 – 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 μ over n generations $p_{(n)} = (1-\mu)^n p_{(0)}$
Average fitness of a population under selection, $\overline{W} = W_{(AA)}p^2 + W_{(Aa)}2pq + W_{(aa)}q^2$
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 heterozygousity due to inbreeding
$f(AA) = p^2(1-F) + pF$
$f(Aa) = 2pq(1-F)$
$f(aa) = q^2(1-F) + qF$

Mean = $\overline{x} = \sum x_i / N$
Variance = $s^2 = \sum (x_i - \overline{x})^2 / N-1$
Standard deviation = $s = \sqrt{s^2}$
Covariance = $Cov(x,y) = \sum f_i (x_i - \overline{x})(y_i - \overline{y}) / N-1$

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