Biology 352 Practice Exam #2G

ANSWER KEY

Many *Yucca* plants are pollinated by specialized moths. There is a polymorphism in a *Yucca* gene that leads to variation in pollination success. Genotype *PP* has a 80% pollination success, genotype *Pp* has a 40% pollination success, and genotype *pp* has a 0% pollination success

1. What model of natural selection fits these data?
   a. Selection for a completely dominant trait.
   b. Selection for a completely recessive trait.
   c. Partial dominance
   d. Overdominance
   e. Underdominance

   The heterozygote has an intermediate fitness.

2. What is the selection coefficient against genotype *pp*?
   a. 0.00 b. 0.20 c. 0.40 d. 0.80 e. 1.00

3. If 49% of the gene pool is the dominant allele right now, and natural selection occurs as described above, what will happen to the gene pool? (Assume random mating, and that no other microevolutionary forces are acting.)
   a. Eventually the dominant allele will be extinct.
   b. Eventually the dominant allele will be fixed.
   c. Eventually the frequency of the dominant allele will stabilize somewhere between 0 and 1, but it won't be fixed.
   d. The dominant allele will reach a stable cycle where it will fluctuate up and down in frequency over time.
   e. There is no way to know, since this selection model is completely unpredictable.

   For partial dominance (= incomplete dominance), the equilibrium is fixation for the dominant allele.

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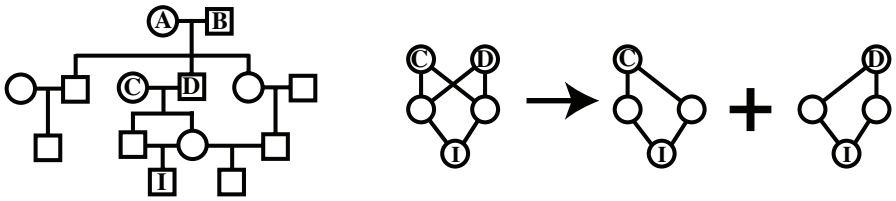
4. Prior to equilibrium in a polymorphic population, natural selection _____ the average population fitness every generation.
   a. always increases
   b. always keeps constant
   c. always decreases
   d. sometimes increases, sometimes decreases

5. What is the inbreeding coefficient for individual I in this pedigree? Assume that A and B are not inbred. Also use the standard assumption that if no information is available about an individual's ancestry, that individual is not inbred.
   a. 0.031 b. 0.063 c. 0.125 d. 0.250 e. 0.313



Individual I is inbred because its parents are full siblings. Grandparents C and D are unrelated, so D's parents A and B do not contribute any additional inbreeding. A and B do not need to be included in the path diagram. The fact that I has a half-sibling is also irrelevant. F_C and F_D are equal to 0.

$$F_I = (0.5)^2(0.5)(1+F_C) + (0.5)^2(0.5)(1+F_D) = (0.5)^3 + (0.5)^3 = 0.25$$

6. Coffin–Lowry syndrome is a dominant X-linked disease in humans. It causes severe mental retardation and a variety of other abnormalities. At birth, the frequency of Coffin–Lowry syndrome in males is one in 40,000 males. Assuming Hardy-Weinberg genotype frequencies, what should the frequency be in females at birth? (Use 6 decimal places in your calculations.)
   a. 0.000000
   b. 0.000025
   c. 0.000040
   d. 0.000050
   e. 0.005000

Males only have one X chromosome, so the frequency of the disease in males is the same as the frequency of the allele in males. $p = f(\text{Coffin - Lowry allele}) = \frac{1}{40{,}000} = 0.000025$

This is a dominant disease, so females who get the disease either have genotype X_CX_C or genotype X_CX_{normal}. Assuming Hardy Weinberg, the frequencies of these two genotypes are

$$p^2 + 2pq = (0.000025)^2 + 2(0.000025)(0.999975)$$

$$= 6.25 \times 10^{-10} + 0.000050 = 0.000050$$

7. In a population that follows the Hardy Weinberg model, the frequency of the recessive phenotype will always be _____, if the two alleles are present.
   a. 0.25
   b. 0.50
   c. less than the frequency of the recessive allele
   d. equal to the frequency of the recessive allele
   e. greater than the frequency of the recessive allele

There are always some recessive alleles in heterozygotes, so C is correct.

Imagine how ancient peoples might have domesticated crops. When a new generation was planted in the field, only the plants with desirable characteristics (such as bigger seeds) would have been used. The remainder of the plants from the previous generation would not have been allowed to reproduce.

8. This process of starting the next generation with only the desirable phenotypes is best characterized as
   a. inbreeding.
   b. one-way mutation.
   c. random drift.
   d. migration
   e. natural selection

9. Although not intended, this process also created _____ every generation.
   a. new alleles
   b. population bottlenecks
   c. negative assortative mating
   d. excessive environmental variance
   e. Hardy Weinberg gene pools

Starting each generation with gametes from a smaller number of individuals than are in the gene pool creates a bottleneck. It does not create new alleles – only mutations can create new alleles.

10. A sample of 10 diploid individuals has 8 with genotype *AA*, 1 with genotype *Aa* and 1 with genotype *aa*. What is the frequency of allele *A* in this sample?
    a. 0.150
    b. 0.170
    c. 0.450
    d. 0.850
    e. 0.894

11. Speciation can occur when different populations accumulate enough genetic differences that they become unable to reproduce with one another. The evolutionary force called _____ is thought to greatly retard this process.
    a. gene flow
    b. genetic drift
    c. inbreeding
    d. natural selection
    e. mutation

See lecture notes.

Ectrodactyly is an autosomal recessive condition in humans in which the fingers and toes are fused. Suppose the frequency of the ectrodactyly allele is 0.01.

12. What is the frequency of heterozygous carriers for the disease, if we can assume Hardy Weinberg genotype frequencies?
    a. 0.0001
    b. 0.0099
    c. 0.0198
    d. 0.1800
    e. 0.9999

$2pq = 2(0.01)(0.99) = 0.0198$

13. What is the frequency of people with ectrodactyly in a Hardy Weinberg population with a small amount of inbreeding (F = 0.01)?
    a. 0.0000010
    b. 0.0000990
    c. 0.0001000
    d. 0.0001990
    e. 0.0002980

$f(aa) = q^2 + Fpq = 0.01^2 + (0.01)(0.01)(0.99) = 0.000199$

Twenty-two gene that code for blood proteins were studied in 42 chimpanzees (*Pan troglodytes*). For 21 loci, all individuals were homozygous for the same allele. For the 22nd locus (PGM-1), there were 16 heterozygotes (*Aa*), 26 homozygotes (*AA*), and no *aa* individuals.

14. What is P, the proportion of loci that is polymorphic?
    a. 0.024
    b. 0.045
    c. 0.190
    d. 0.308
    e. 0.810

$P = \frac{1}{22} = 0.045$

15. What is the inbreeding coefficient (*F*) at the PGM-1 locus for this population?
    a. -1.154
    b. 0.071
    c. 0.154
    d. 0.536
    e. 1.154

$p = \frac{(2*26)+16}{2(42)} = \frac{68}{84} = 0.8095;\ \ q = 0.1905$

$F = 1 - H_o / H_e = 1 - \left(\frac{16}{42} / 2(0.8095)(0.1905) \right) = 1 - \left(0.3810 / 0.3084 \right) = -0.2353$

No correct answer was provided, everyone will get credit. There is an excess of heterozygotes in this example, so the inbreeding coefficient is negative. That could be indicative of outbreeding.

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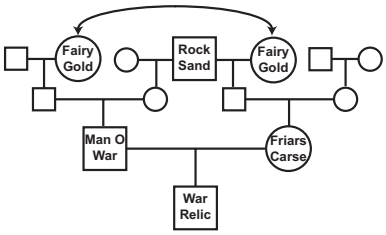
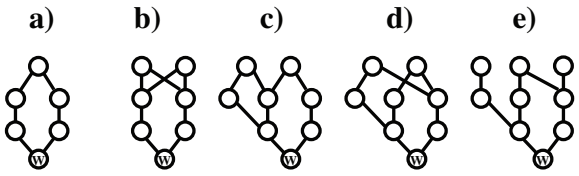
16. If allele *A* and allele *a* are both present in a diploid population, then which of the following is false?
    a. Expected heterozygosity must be greater than zero.
    b. The expected Hardy Weinberg genotype frequencies can be calculated.
    c. The inbreeding coefficient *F* can be calculated.
    d. The population can evolve.
    e. There is no correct answer; A-D are all true.

17. War Relic was a famous racehorse that won many notable races in 1941. His sire (father) was the famous Man o' War, and his dam (mother) was Friar's Carse, the United States' champion 2-year old filly of 1925. Looking back through 5 generations of War Relic's pedigree, one can find 9 different ancestors that are represented multiple times! These 9 ancestors led to a high degree of inbreeding. Below is a small part of War Relic's pedigree going back only 3 generations. Note that Fairy Gold is the mother of both his grandfathers, although it is difficult to draw this into the pedigree without crossing lines. Which path diagram matches the pedigree?





The correct answer is D, since War Relic can be inbred through either Rock Sand, or through Fairy Gold. Man o' War's parents are not related, but Man o' War's father is the half brother of Friar Carse's father.

18. The total amount of variance for a quantitative trait can be subdivided into many components. Which of the following is <u>not</u> a variance component that is used for these analyses?
    a. V_M, the Mendelian variance
    b. V_E, the environmental variance
    c. V_A, the additive component of genetic variance
    d. V_I, the interactions among different genes
    e. A-D are all variance components, so there is no correct answer above.

19. You plan to study hybridization between bluegills and pumpkinseeds (two species of fish). The number of scales below the lateral line in these fish ranges from 13 to 17. This trait is best classified as _____ trait.
    a. an epistatic
    b. a continuous
    c. a variance
    d. a Mendelian
    e. a meristic

Table 1. Individuals classified according to their X values

Sample	X (no. of scales below the lateral line)					Total no. individuals
	13	14	15	16	17	
Pumpkinseed	2	35	45	2	0	84
Bluegill	0	0	21	55	15	91
Hybrid	0	14	63	14	0	91

20. In cichlid fish from Lake Victoria, Africa, mate choice is based on coloration. Males and females with similar colors mate with each other more often than you would expect based on chance encounters. This is an example of
    a. positive assortative mating
    b. negative assortative mating
    c. outbreeding
    d. sexual selection
    e. fertility selection

21. Experiments designed to measure heritability in lizard tail length is conducted in two places: the laboratory, and a very large field enclosure. The two sets of experiments are identical, except that the laboratory conditions are constant, and every lizard is fed as many lizard chow pellets as they can eat. In the field cage, the diet is natural and temperature varies from spot to spot. What do we expect to find?
    a. $h^2_{\text{laboratory}} > h^2_{\text{field}}$
    b. $h^2_{\text{laboratory}} = h^2_{\text{field}}$
    c. $h^2_{\text{laboratory}} < h^2_{\text{field}}$

$$h^2 = \frac{V_A}{V_A + V_D + V_I + V_E + V_{GE}}$$

If an experiment is conducted in the field, where the environmental variance V_E is greater, then the denominator increases. The fraction becomes a smaller number. So heritability measured in the field will be less than heritability measured in the lab.

22. Which of the following models of evolution can maintain polymorphism indefinitely in a single gene pool, if more than one allele is present at $t = 0$?
    a. a model with natural selection in the form of incomplete dominance (and no other evolutionary forces)
    b. an ideal Hardy-Weinberg population model
    c. a model with drift (and no other evolutionary forces)
    d. A and B only.
    e. A, B and C are all true.

For partial dominance (= incomplete dominance), the equilibrium is fixation for the dominant allele, unless the recessive allele is replenished with mutations. Under drift, the population will become monomorphic unless mutations create new alleles.

23. Resistance to anticoagulant rodenticides (such as warfarin in the Norway rat *Rattus norvegicus*) is a well documented example of an evolutionary response to natural selection. Resistance has a simple genetic basis, and the following selective coefficients have been suggested. Genotype *SS* corresponds to rats that are killed by the poison warfarin, with a mortality rate of 90%. In the same population, genotype *RR* is resistant to warfarin, but has a very high vitamin K requirement. Because *RR* rats can not always get enough vitamin K, their mortality rate is 50%. The heterozygotes *SR* are resistant to warfarin, but have more modest vitamin K requirements than *RR*. Mortality rates for heterozygotes are only 25%. Assuming that only natural selection is important, what should the frequency of the *R* allele be at equilibrium?
    a. 0.278
    b. 0.385
    c. 0.643
    d. 0.667
    e. 0.723

The absolute fitness is the survival rate. $\text{Abs}_{SS} = 0.10$ $\text{Abs}_{RS} = 0.75$ $\text{Abs}_{RR} = 0.50$

$w_{SS} = \frac{0.10}{0.75} = 0.133$ $w_{RS} = \frac{0.75}{0.75} = 1.000$ $w_{RR} = \frac{0.50}{0.75} = 0.667$

$s_{SS} = 0.867$ $s_{RS} = 0.000$ $s_{RR} = \frac{0.50}{0.75} = 0.333$

$\hat{q} = f(\hat{r}) = \frac{0.867}{0.867+0.333} = 0.7225$

24. For evolution in natural populations, migration is usually a more important factor than mutation because
    a. Mutations do not occur in natural populations.
    b. Migration in natural populations always results in the rapid loss of alleles.
    c. Migration rates are usually many orders of magnitude higher than mutation rates for the genes that are studied.
    d. No population genetic models have been developed to deal with mutations.
    e. Migration between gene pools tends to lead to the formation of new species.

25. In *Tribolium* flour beetles, elytra length is a polygenic trait controlled by 6 genes. A standard hybrid cross experiment is conducted, beginning with two true breeding lines: one line has the longest possible elytras, and the other line has the shortest possible. Assuming that environmental variance can be eliminated, and that there are only 2 alleles per gene, we should see _____ discrete phenotypic classes in the F2 generation of this experiment.
    a. 1
    b. 3
    c. 11
    d. 12
    e. 13

$2(6)+1=13$

26. For a gene undergoing one-way mutation (and no other evolutionary forces), its eventual fate is
    a. complete loss of the dominant allele.
    b. reduction of the dominant allele to frequencies so low that it is only found in heterozygotes.
    c. coexistence of the dominant and recessive alleles at intermediate frequencies.
    d. reduction of the recessive allele to frequencies so low that it is only found in heterozygotes.
    e. complete loss of the recessive allele.

27. In a polymorphic population, which microevolutionary force(s) cause a predictable change in the frequency of an allele from one generation to the next?
    a. mutation
    b. natural selection (complete dominance)
    c. drift
    d. A and B only.
    e. A, B and C are all true.

On practice exam 2C #18. Similar to practice exam 2E #19. The mutation models that we studied both provide an exact equation to predict allele frequencies each generation. The same is true for the natural selection models. However drift may cause allele frequencies to increase , decrease or stay the same from one generation to the next.

28. Genetic variation can be studied in natural populations of a single species using which techniques?
    a. chromosomal mutations
    b. a technique developed in the 1960's called protein electrophoresis
    c. morphological characters (if they have a genetic basis)
    d. A and B only.
    e. A, B and C are all true.

29. In a population of 100 diploid individuals, a particular gene is fixed for allele G_1. A new mutation produces one individual in the next generation that is heterozygous $G_1\ G_2$. The other 99 are $G_1\ G_1$. If drift is the only evolutionary factor in all future generations, what is the probability that the entire population will some day have genotype $G_2\ G_2$?
    a. 0
    b. 0.000025
    c. 0.001
    d. 0.005
    e. 0.01

The new mutation is at a frequency of 1/200 in the gene pool, which is 0.005. The probability that the entire population will someday be fixed for G_2 is 0.005. When it is fixed (meaning that its frequency q = 1.0), every individual will have genotype $G_2\ G_2$.

30. Thirty experimental gene pools of *Drosophila* are set up in the lab in separate jars. Each contains 20 males and 20 females. Population size is kept constant every generation. The jars are allowed to evolve independently of one another for 20 generations. At the beginning, they all had the same allele frequencies for a particular gene: $p = 0.1$ and $q = 0.9$. After the 30 generation experiment is over, what would you expect to find?
    a. $p = 0.0$ in every population
    b. $p = 0.1$ in every population
    c. $p = 0.5$ in every population
    d. $p = 1.0$ in every population
    e. The allele frequencies will be different from population to population.

Drift causes each isolated population to evolve independently, with its own allele frequencies.

31. In a field of sunflowers, flowers with genotype *MM* produce an average of 800 seeds. Genotype *Mm* produces an average of 600 seeds. Genotype *mm* produces an average of 100 seeds. What is the relative fitness of the heterozygote?
    a. 0.125
    b. 0.391
    c. 0.400
    d. 0.600
    e. 0.750

600/800 = 0.75

In a particular species of beetle, blue coloration is dominant to gray. A sample of 300 beetles from a single population finds that 100 of them are gray. The blue beetles are screened genetically for the gene that controls coloration, and half of the blue beetles are determined to be heterozygous.

32. Does this locus depart from Hardy-Weinberg genotype frequencies? (For 1 degree of freedom $\chi^2 >$ 3.84 is significant.)
    a. Yes
    b. No

33. What is the χ^2 value for this test? Use three decimal places in all your calculations.

G = gray, B = blue

Observed	**GG**	**BG**	**BB**	**Sum**
Observed genotype counts	**100**	**100**	**100**	**300**
Allele frequencies:	G	B		
	0.500	0.500		
Expected	**GG**	**BG**	**BB**	**Sum**
Expected genotype freq	0.250	0.500	0.250	
Expected genotype counts	**75.000**	**150.000**	**75.000**	
O-E	25.000	-50.000	25.000	
Chi-square calculation	8.333	16.667	8.333	33.333
Chi-square =	**33.333**			