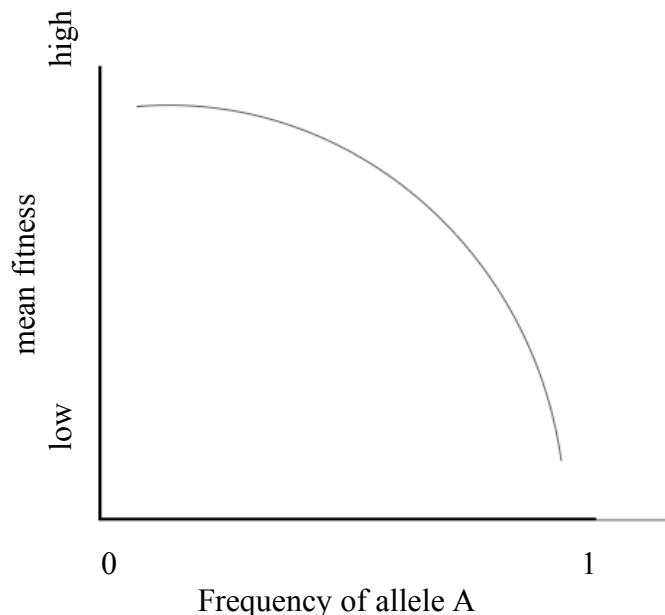


Evolutionary Biology EEB 2245/2245W
Spring 2011
Problem Set 3

- 1- a. AA 10, Aa 60, aa 30
b. Before selection $40+100+60 = 200$ eggs total
 Freq AA = $40/200 = 0.2$
 Freq Aa = $100/200 = 0.5$
 Freq aa = $60/200 = 0.3$
 After selection $10+60+30 = 100$ adults total
 Freq AA = $10/100 = 0.1$
 Freq Aa = $60/100 = 0.6$
 Freq aa = $30/100 = 0.3$
c. Before selection Freq of A = $0.2 + (0.5/2) = 0.45$
 After selection Freq of A = $0.1 + (0.6/2) = 0.4$
d. Genotype freq of adult's offspring assuming HWE
 Freq of A = 0.4, so Freq of a = $1-0.4 = 0.6$
 Freq AA = $0.4^2 = 0.16$
 Freq Aa = $2 \times 0.4 \times 0.6 = 0.48$
 Freq aa = $0.6^2 = 0.36$

2- a. Fisher's Fundamental Theorem says the mean fitness of the offspring generation is greater than or equal to the mean fitness of the parent generation. Because AA is the genotype with the lowest fitness, and the heterozygote is intermediate in fitness the A allele will become lost in this population. Freq of A = 0

b.



3- It is helpful to organize the data for this question in a table.

a. Allele Freq = $D = 0.2$ and $d = 1 - 0.2 = 0.8$

	DD	Dd	dd
Genotype Freq of zygotes 1	$0.2^2 = 0.04$	$2 \times 0.2 \times 0.8 = 0.32$	$0.8^2 = 0.64$
Survival probability	1	1	.22
Number of adults	$0.04 \times 100 \times 1 = 4$	$0.32 \times 100 \times 1 = 32$	$0.64 \times 100 \times 0.22 = 14$
Genotype Freq of adults 1	$4/50 = 0.08$	$32/50 = 0.64$	$14/50 = 0.28$
Freq of zygotes 2	0.08	0.64	0.28
Survival probability (same as before)	1	1	0.22
Number of adults 2	$0.08 \times 100 \times 1 = 8$	$0.64 \times 100 \times 1 = 64$	$0.28 \times 100 \times 0.22 = 6$
Genotype Freq of adults 2	$8/78 = 0.10$	$64/78 = 0.82$	$6/78 = 0.08$

- a. Average fitness of a population = $DD \times w_{11} + Dd \times w_{12} + dd \times w_{22}$
 Calculate genotype frequencies of the zygotes, assuming HWE.
 Average fitness of zygotes = $(0.04 \times 1) + (0.32 \times 1) + (0.64 \times 0.22) = 0.5008$
- b. Assume that there are 100 zygotes and calculate the number of surviving adults.
 Determine the total number of surviving adults = $4 + 14 + 32 = 50$. Calculate the genotype frequencies of the adults. Assuming that there are no HWE violations, the allele freq of the zygotes in the next generation will be the same as the adults.
 Freq of $D = 0.08 + (0.64/2) = 0.4$
 Freq of $d = 0.28 + (0.64/2) = 1 - 0.4 = 0.6$
- c. Assume the zygotes of this second generation undergo selection as well, then repeat step b for the next generation of adults. Total number of surviving adults = $8 + 64 + 6 = 78$. Then calculate allele frequencies of the second generation of surviving adults
 Freq of $D = 0.10 + (0.82/2) = 0.51$
 Freq of $d = 0.08 + (0.82/2) = 0.49$
- d. Average fitness of the next generation = the average fitness of zygotes in the second generation = $(0.08 \times 1) + (0.64 \times 1) + (0.28 \times 0.22) = 0.7816$

4- a. Allele Frequencies are $L = 0.1$, so $V = 1 - 0.1 = 0.9$

Calculate genotype frequencies assuming HWE

Freq $VV = 0.9^2 = 81$

Freq $VL = 2 \times 0.9 \times 0.1 = 0.18$

Freq $LL = 0.1^2 = 0.01$

To find number of individuals = genotype freq x number of individuals

$VV = 0.81 \times 1000 = 810$

$VL = 0.18 \times 1000 = 180$

$LL = 0.01 \times 1000 = 10$

b. Calculate the number of surviving individuals after selection. Total individuals in population = 810 + 180 = 990. Calculate Genotype frequencies, then allele frequencies. $V = 0.82 + (0.18/2) = 0.91$ $L = (0.18/2) + 0 = 0.09$

	VV	VL	LL
Number of individuals BEFORE	810	180	10
Survival Probability	1	1	0
Number of individuals AFTER	810	180	0
Freq of individuals after selection	$810/990 = 0.82$	$180/990 = 0.18$	0

c. Because the heterozygotes show the dominant phenotype, selection only affects homozygous recessive individuals. Therefore, the rate at which the lethal allele is lost in the population is very slow once the allele becomes rare because the chance that a homozygous recessive genotype is produced becomes infrequent. In this case, even though very strong selection is acting, the frequency of the lethal allele decreased only from 10% to 9% in one generation.

5- a. Total individuals in population = 90 + 60 + 150 = 300

$$\text{Freq BB} = 90/300 = 0.3$$

$$\text{Freq BT} = 60/300 = 0.2$$

$$\text{Freq TT} = 150/300 = 0.5$$

$$\text{Freq B} = 0.3 + (0.2/2) = 0.4$$

$$\text{Freq T} = 0.5 + (0.2/2) = 0.6$$

b. The expected genotype frequencies assuming HWE

$$\text{Freq BB} = 0.4^2 = 0.16$$

$$\text{Freq BT} = 2 \times 0.4 \times 0.6 = 0.48$$

$$\text{Freq TT} = 0.6^2 = 0.36$$

There are far fewer heterozygotes than expected in this population so heterozygotes are underrepresented. The TT and BB genotypes are overrepresented in this population compared to the genotype frequencies under HWE.

c. Inbreeding, assortative mating or disruptive selection could produce this pattern. Geographic variation in allele frequencies along with random mating within subpopulations (but not between them) could also produce this pattern.

d. If it was inbreeding you would expect mating individuals would be closely related. If it was assortative mating then individuals in the population would be mating with individuals that have the same genotype. If you examined other loci than you could determine if inbreeding or assortative mating was occurring because other loci would have the same pattern as this in inbreeding but be random for assortative mating.

If it was disruptive selection then you would expect heterozygotes to have a low fitness compared to either homozygote, and you'd expect to see a difference in genotype frequencies between zygotes and adults (with the expected HW proportions before selection acts)

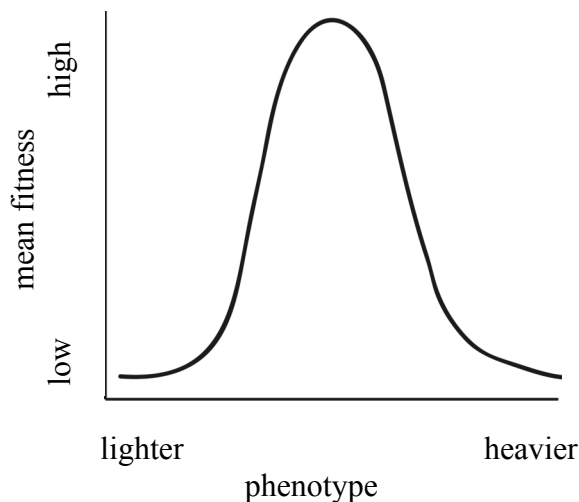
If it were geographic variation you would expect to be able to identify two populations with different allele frequencies, each of which was in HWE

6- a. Inbreeding depression because a small population implies that related individuals are reproducing. Every individual is likely to harbor recessive lethal alleles and when related individuals reproduce it is more likely for their offspring to have two copies of the same deleterious allele which could produce the pattern of snakes with stillborn and deformed offspring. Genetic drift could also produce this pattern because in small populations deleterious alleles can be fixed in the population due to random chance even though selection favors the loss of those alleles.

b. The researchers could build corridors of suitable adder habitat between populations to allow for migration between populations. They could also purposefully move individuals from other adder populations into this very small population to add genetic diversity and increase the population size.

7- a. Stabilizing selection which favors the average phenotype

b.



c. This question should have said “Give a scenario where the ABOVE average weight of the dogs was beneficial.” Any scenario that shows the heavier dogs to be more adapted to the environment would work. A scenario could be it would be beneficial to be heavier if all the snow melted and so the dogs didn’t sink into the snow and heavier dogs were more powerful. This was an example of directional selection.

8- a. It would be an evolutionary change if the change in flower color is due to a genetic trait and an evolutionary process is affecting which flowers are present in the populations. You could test if the trait is genetic by doing a common garden experiment in which you grew plants from both populations under the same conditions. If the plants have the same color flowers the difference in flower color between the two populations is due to

environmental factors. If both populations of plants retain their differently colored flowers even in the same environment, then it is probable the flower colors are genetically inherited.

b. The two types of pollinators are moths and bees, not two types of bees. To conduct an experiment to test whether or not the prevalent color in each population is due to the pollinator, moths or bees, you would select equal numbers of plants from each population which represent how many plants from each colored flower. You would then set up conditions where plants were pollinated by either moths, bees, or hand pollinated as a control

c. After many generations if the flower colors are due to which pollinator is present you would expect the color patterns of the experimental plants to resemble the color patterns found in nature.

If the flower colors are not due to which pollinator is present you would expect the color patterns to be the same as the initial generation of experimental plants

9-a. $S = \text{average trait after selection} - \text{average trait before selection}$

$$S = 30 \text{ cm} - 40 \text{ cm} = -10 \text{ cm}$$

$$R = S \times h^2 = -10 \times 0.8 = -8 \text{ cm}$$

b. The average trait after reproduction = average trait before selection + R

$$\text{For 1}^{\text{st}} \text{ generation after selection event} = 40 \text{ cm} + (-8 \text{ cm}) = 32 \text{ cm}$$

$$\text{For 2}^{\text{nd}} \text{ generation assume that } S \text{ remains the same} = -10 \text{ cm}$$

$$R = -10 \text{ cm} \times 0.8 = -8, \text{ then } 32 \text{ cm} + (-8 \text{ cm}) = 24 \text{ cm}$$

$$\text{For 3}^{\text{rd}} \text{ generation after another selection event} = S = -10 \text{ cm}$$

$$R = -10 \text{ cm} \times 0.8 = -8 \text{ cm}, \text{ then } 24 \text{ cm} + (-8 \text{ cm}) = 16 \text{ cm}$$

10- a. $h^2 = V_G / (V_G + V_E) = 1.5 \text{ g}^2 / (1.5 \text{ g}^2 + 0.5 \text{ g}^2) = 0.75$

$$h^2 = R/S \text{ so } R = h^2 \times S = 0.75 \times 3 \text{ g} = 2.25 \text{ g}$$

$$R = 2.25 \text{ g}$$

b. $h^2 = 1 \text{ g}^2 / (1 \text{ g}^2 + 1 \text{ g}^2) = 0.5, R = 0.5 \times 5 \text{ g} = 2.5 \text{ g}$

$$R = 2.5 \text{ g}$$

c. $h^2 = 2 \text{ g}^2 / (2 \text{ g}^2 + 8 \text{ g}^2) = 0.2, R = 0.2 \times 5 \text{ g} = 1 \text{ g}$

$$R = 1 \text{ g}$$

d. Assuming parameters are the same as in part c:

$$\text{Initial mean of trait} = 10 \text{ g}, S = 5 \text{ g}, h^2 = 0.2$$

$$R = 5 \text{ g} \times 0.2 = 1 \text{ g}, \text{ then } 10 \text{ g} + 1 \text{ g} = 11 \text{ g}$$

$$\text{after 2}^{\text{nd}} \text{ generations } R = 5 \text{ g} \times 0.2 = 1 \text{ g}, \text{ then } 11 \text{ g} + 1 \text{ g} = 12 \text{ g}$$

11- a. $h^2 = R/S = 0.3$ which is the slope of the regression line

$$\text{b. } S = 14.5 - 13 \text{ kg} = 1.5 \text{ kg}, R = h^2 \times S = 1.5 \text{ kg} \times 0.3 = 0.45 \text{ kg}$$

$$13 \text{ kg} + 0.45 \text{ kg} = 13.45 \text{ kg}$$

12- Information that is necessary to answer this question was omitted. To calculate S you need to know the number of individual that were eaten by birds and whether the 10 cm antenna length was observed before or after selection had acted. The following is what the question should say:

A researcher is studying long-horned beetle antennal length in New England. 550 individuals that survived predation by birds have an average antennae length of 10 cm. The average antennae length of the 450 beetles that were eaten by birds in the spring was estimated to be 12cm.

a. $S = \text{average trait after selection} - \text{average trait before selection}$

To calculate the average trait before selection = $([550 \text{ individuals} \times 10\text{cm}] + [450 \text{ individuals} \times 12 \text{ cm}]) / (550 + 450) = 10.9 \text{ cm}$

$$S = 10 \text{ cm} - 10.9\text{cm} = -0.9\text{cm}$$

b. Directional selection

c. $R = 11 \text{ cm} - 10.9 \text{ cm} = 0.1 \text{ cm}$, $S = -0.9 \text{ cm}$,

$$h^2 = R/S = 0.1/-0.9 = 0.11$$

13- a. seven phenotypes ranging from white to black. There are six alleles so if a 2 allele is present at any of the alleles then it is darker than white, which is when all of the alleles are of the 1 type

b. 3 genotypes possible for 1st locus x 3 genotypes of 2nd locus x 3 genotypes of 3rd locus = 27 genotypes

c. There are 6 possible alleles and all have to be a '2' allele for the mice to be jet black. If a '1' allele occurs at any of the 6 places then a shade lighter than jet black would be produced = 6 genotypes

d. Freq A1 = 0.9, then Freq A2 = 0.1

Freq A2A2 = $0.1^2 = 0.01$, which is going to be the same freq of B2B2 and C2C2

The probability of seeing a jet black mouse would be $0.01 \times 0.01 \times 0.01 = 0.000001$

e. Freq A1 = 0.9, then Freq A1A1 = $0.9^2 = 0.81$, which would be the same for B1B1 and C1C1

The probability of seeing a white mouse would be $0.81 \times 0.81 \times 0.81 = 0.53$

f. Because this population has the exact opposite allele frequencies as the first population then the probability of seeing a jet black mouse would be 0.53

g. Strong directional selection for darker coat color, which has led to an increase in the frequency of the '2' alleles

h. In this example, the jet black phenotype would be a new phenotype, observed in the lava population (frequency 53%) but not observed (or very unlikely to be observed) in the white sands population from which the lava population originated. The appearance of the jet black phenotype in the population occurred because of the increased frequency of alleles causing darker coat color at many loci independently, rather than because of mutations introducing new alleles into the population. As a result of these increased frequencies, new genetic combinations (and hence new phenotypes) occurred in the lava population.

i. Fixed for the '2' allele at each locus.