

**QUANTITATIVE GENETICS PROBLEMS- EVOLUTIONARY BIOLOGY FALL 2016**  
**(20 points total)(due November 4<sup>th</sup> 2016)**

1) Suppose that in a population of Peacocks the phenotypic variance for tail length is 2.5 and the slope of the father – offspring regression for this trait is 0.2. From a long-term captive population you also have data from a line of completely inbred individuals. In this line the phenotypic variance among individuals is 0.50. Assume that there are no shared environmental effects ( $V_{es}$ ) and no epistatic variance ( $V_I$ ) for this trait. (Note that these questions are not given in the order that you need to solve them)(6 points)

a) What is the total genetic variance for tail length?

**Given:**  
 $V_P = 3.0$

**Then  $V_P = V_G + V_E$**   
 $V_G = V_P - V_E = 2.5 - 0.5 = 2.0$

b) What is the additive genetic variance?

$h^2 = V_A / V_P$   
 $V_A = h^2 (V_P) = 0.4 (2.5) = 1.0$

c) What is the dominance genetic variance?

$V_G = V_A + V_D + V_{ES}$ ,  $V_{ES} = 0$  so  $V_D = V_G - V_A = 2.0 - 1.0 = 1.0$

d) What is the environmental variance?

**Since the inbred line has no genetic variance all the variance in the phenotypes must be due to environmental factors.**

**Variation within inbred lines = 0.5**  
 $V_P = V_G + V_E$ , since  $V_G = 0$ ,  $V_P = V_E = 0.5$

**This estimate of  $V_E$  can be used in part a to solve for  $V_G$**

e) What is the narrow-sense heritability ( $h^2$ )?

**Slope of the single parent – offspring regression = 0.2**  
 $0.2 = \frac{1}{2} h^2 \Rightarrow h^2 = 0.4$

f) What is the expected phenotypic covariance among full-sibs?

$COV_{FS} = \frac{1}{2}V_A + \frac{1}{4}V_D + V_{ES} = \frac{1}{2}(1.0) + \frac{1}{4}(1.0) + 0 = 0.75$

2) While Peacocks are great animals, they are large, noisy and difficult to work with. So, you switch to studying Barn Swallows. Suppose that you have estimates of tail length (**T in cm**) in Barn Swallows from a set of ten pairs of **paternal half-sibs** (denoted by the subscripts **x** and **y**) that share the same father, but have different mothers). For the first sib (denoted by **x** below), the number of offspring they produce over their lifetime ( $R_x$ ) is known as well. The number of offspring produced ( $R_x$ ) is a measure of absolute fitness. For each sib, first calculate the relative fitness value ( $W_x$ ). To estimate relative fitness, divide each  $R_x$  value by the mean absolute fitness value. (6 points)

Sibship	$T_x$	$T_y$	$R_x$
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1	17.00	18.00	23.00
2	16.00	25.00	29.00
3	23.00	15.00	43.00
4	13.00	13.00	19.00
5	15.00	16.00	29.00
6	11.00	19.00	37.00
7	24.00	23.00	31.00
8	19.00	12.00	49.00
9	17.00	18.00	35.00
10	21.00	15.00	53.00

### SEE SPREADSHEET FOR SOLUTIONS

Using these data:

- a) Compute the phenotypic mean and variance of tail length (use all the available data, i.e., both of the half-sibs).

$$\text{Mean} = 17.5$$

$$\text{Variance} = 15.65$$

- b) Compute the phenotypic covariance between paternal half-sibs, and estimate the heritability of tail length (remember that the denominator in a covariance equation is the number of pairs of observations).

$$\text{COV}(hs) = 0.76, \text{ Heritability} = 0.19$$

- c) Assuming that progeny production is the only way in which these individuals differ in fitness, use Price's Rule to estimate the directional selection differential on tail length.

$$S = 0.55$$

- d) What is the variance in relative fitness?

$$\text{VAR}(w) = 0.089$$

- e) Will relative fitness increase or decrease in the next generation? By how much?

**As long as there is additive genetic variance in relative fitness, it will always increase from one generation to the next. This is Fisher's fundamental Theorem. The increase will be equal the additive variance for fitness. We cannot estimate the  $V_a$  for fitness given the data we have, but we can make a statement on how big this could be. If all the phenotypic variance ( $V_p$ ) in the population is due entirely to additive effects (i.e., all other sources of variation are zero) then  $V_a = V_p$ . Thus,  $V_p$  is the upper limit to the rate of evolution of relative fitness. In this case  $V_p = 0.089$  is the upper limit.**

- 3) A striking feature of phenotypic change in the human lineage is a dramatic increase in brain size. This trait has increased from an average of approximately 500 cm<sup>3</sup> to 1200 cm<sup>3</sup> over the past 3 million years. Assume humans have an average generation time of 20 years and that the slope of a single parent-offspring regression for brain size is 0.20. (3 points)

- a) If this evolutionary change is a consequence of natural selection (and only natural selection) operating directly on brain size, what average **directional selection differential** per generation (**S**) is necessary to account for the observed change?

$$R = h^2 S$$

$$h^2 = b = 0.4$$

$$R = \text{Leg length} / \# \text{ of Generations}$$

$$\# \text{ Generations} = 3 \times 10^6 \text{ yrs.} / 20 \text{ yrs. per generation} = 1.5 \times 10^5 \text{ generations}$$

$$R = (1200 - 700) / 1.5 \times 10^5 = 4.7 \times 10^{-3} \text{ cm}^3/\text{generation}$$

$$S = R / h^2 = 4.7 \times 10^{-3} / 0.4 = 1.1 \times 10^{-2} \text{ cm}^3$$

b) If directional selection of this magnitude were to continue, what is the expected response to selection one generation from now?

$$R = 4.7 \times 10^{-3} \text{ cm}$$

$$\text{Mean Brain Size in the Next Generation} = \text{Mean in the last Generation} + \text{Response to Selection} = 1200 + 0.0047 = 1200.0047 \text{ cm}$$

c) How many additional years would be required for the average brain size of humans to reach  $1500 \text{ cm}^3$ ? (Assume the heritability remains constant).

$$R = 1500 - 1200 = 300 \text{ cm}^3$$

$$300 / 4.7 \times 10^{-3} \text{ cm per generation} = 64,286 \text{ Generations}$$

$$64,286 \times 20 = 1.285 \times 10^6 \text{ years}$$

4) On a recent trip to the Galapagos Islands some of your classmates were able to collect data on Darwin's finches. They measured data on beak size in a set of related individuals. Consider the following data on beak size. These quantitative trait values (in mm) are given for the mother, father and one of their offspring. (5 points)

Mother	Father	Offspring
8	11	10
7	13	11
14	9	10
9	11	10
11	10	13
14	15	14
8	12	11
9	10	8
11	6	10
13	7	12
8	9	11

### SEE SPREADSHEET FOR SOLUTIONS

a) Calculate the **midparent** values for each parent pair and use a midparent-offspring regression approach to calculate the **heritability ( $h^2$ )** of this trait. There is more than one way to do this, but it will be easiest if you use Microsoft Excel. You can use the **VARP** function to calculate the necessary variances and the **COVAR** function to calculate the covariance. Remember that the slope of the regression line is the  $\text{Cov}(\text{Midparent}, \text{Offspring}) / \text{Var}(\text{Midparent})$ . You can also calculate these by hand given the formulas from lecture, or use Excel to plot offspring value as a function of midparent value, and then have Excel fit a regression line.

$$\text{Midparent - offspring heritability estimate} = 0.615$$

b) Now calculate the heritability ( $h^2$ ) for the trait using a **mother-offspring regression** and a **father-offspring regression**. Are they the same?

$$\text{Mother-offspring heritability} = 0.554$$

$$\text{Father-offspring heritability} = 0.462$$

c) Maternal effects are nongenetic effects of the mother on the phenotype of the offspring, caused by things like the brooding environment, cytoplasmic factors and nutritional state of the mother. Do you see any evidence for maternal effects with respect to this trait? Explain your reasoning.

Since the mother-offspring comparison yields a higher heritability it suggests that there are some additional non-genetic effects that are increasing the phenotypic covariance between mother and offspring. Yes, there is some evidence for maternal effects for this trait.

- d) If the only individuals that could get sufficient resources to breed successfully are the five males and five females with the largest beak sizes what is the selection differential (**S**) on beak size? Assume the mean of the sample of the parents above represents the mean of the whole population of finches.

**S = 2.27**

- e) How much of an increase in beak size would expect to see in the next generation?

**R = 1.40 mm/generation**