KEY

QUANTITATIVE GENETICS PROBLEMS- EVOLUTIONARY BIOLOGY FALL 2017
(20 points total)(due October 27th 2017)

1) Cichlid fishes in the African Rift lakes form one of the most iconic adaptive radiations. Male Cichlids are challenged by predators and completion from other males for mates. Males of many species have wildly colored fins and engage in elaborate courtship displays. Use the data below showing a performance trait related to escape ability (swim burst speed), two morphological traits (body size, and an index of color intensity), and a measure of relative fitness (probability of mating success) to estimate quantitative genetic parameters related to these traits. (You can use Excel to calculate means, variances and covariances, or you can calculate these by hand given the formulas from lecture) (7 points)

	Trait				
Male	**Burst Speed (M/sec)**	**Body Size (mm)**	**Intensity of color**	**Intensity of son's color**	**Probability of mating success**
1	22	180	6.8	5.5	0.89
2	32	152	5.3	7.7	0.67
3	22	168	5.7	3.8	0.75
4	9	144	4.8	1.2	0.34
5	20	148	3.2	4.2	0.43
6	8	160	7.1	4.2	0.79
7	17	184	6.9	2.5	0.92
8	16	136	0.6	4.6	0.14
9	10	176	8.7	9.3	0.96
10	20	164	3.7	5.5	0.55

SEE pg. 4 FOR SOLUTIONS TO #1

a) Compute the phenotypic mean and variance of Burst Speed, Body Size, and intensity of color in this set of males. (1 pt)

b) Use Price's Rule to estimate the Selection Differential (**S**) for these performance and morphological traits. Which of the three traits is under the strongest directional selection? (2 pt)

c) What is the heritability of the trait Intensity of Color (**h^2**) in this population? (1 pt)

d) From a different experiment, you have an estimate of heritability (**h^2**) generated from a set of full-sib brothers. This estimate is 0.65. Explain why is the estimate generated from fathers and sons is different than the estimate generated from full-sibs pairs. (1 pt)

e) Assuming that the mean trait value of the males in this table is a good estimate of the mean in the population, and that selection via mating success is the only selection on body size, if the heritability of body size is 0.42, what would you expect the body size to be in the next generation? (1 pt)

f) Will relative fitness increase or decrease in the next generation? What is the upper limit to a change in fitness in the next generation? (1 pt)

2) Suppose that in a population of African Cichlids the phenotypic variance for Burst Speed is 40.0 and the slope of a parent – offspring regression for this trait is 0.2. You also have data from a long-term captive population with a line of completely inbred individuals. In this line the phenotypic variance for Burst Speed is 20. 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 (V_G) for Burst Speed?

Given:
$V_P = 40$

Then $V_P = V_G + V_E$
$V_G = V_P – V_E = 40 – 20 = 20$ (V_E comes from part d)

b) What is the additive genetic variance (V_A)?

$h^2 = V_A / V_P$
$V_A = h^2 (V_P) = 0.4 (40) = 16$

c) What is the dominance genetic variance (V_D)?

$V_G = V_A + V_D + V_I$, $V_I = 0$ so $V_D = V_G – V_A = 20 – 16 = 4$

d) What is the environmental variance (V_E)?

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

Variation within inbred lines = 20
$V_P = V_G + V_E$, since $V_G = 0$, $V_P = V_E = 20$

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

e) What is the heritability (h^2)?

Slope of the parent - offspring regression = 0.2
$h^2 = 2b = 2(0.2) = 0.4$

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

$COV_{FS} = ½V_A + ¼V_D + V_{ES} = ½(16) + ¼(4) + 0 = 9$

3) One classic example of phenotypic evolution from the fossil record is evolutionary change in Woolly Mammoths. Towards the end of their era there was a dramatic decrease in body size. In addition to these changes in body size, there was also a decrease in Tusk length. Tusk length decreased from an average of approximately **300 cm** to **150 cm** over a period of 500,000 years. Assume that Mammoths have an average generation time of 10 years and that the slope of the midparent-offspring regression for Tusk length is 0.40. (3 points)

a) If this evolutionary change is a consequence of natural selection (and only natural selection) operating directly on tusk length, what average **directional selection differential** per generation (**S**) is necessary to account for the observed change? (1 pt)

$R = h^2 S$
$h^2 = b = 0.4$
R = Change is Tusk Length / # of Generations
 # Generations = 500,000 yrs. / 10 yrs. per generation = 5×10^4 generations
$R = (300 - 150) / 5 \times 10^4 = 3 \times 10^{-3}$ cm / generation
$S = R / h^2 = 3 \times 10^{-3}$ cm $/ 0.4 = 7.5 \times 10^{-3}$ cm

b) How many additional years would be required for the average tusk length of Mammoths to reach 50 cm? (Assume the heritability remains constant). (2 pt)

R =150 – 50 = 100 cm
100 / 3 x 10^{-3} cm cm per generation = 3.33 x 10^{4} Generations
(3.33 x 10^{4}) x 10 = 3.33 x 10^{5} 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. (4 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 pg. 5 FOR SOLUTIONS

a) Calculate the **midparen**t 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 Cov(Midparent,Offspring)/Var(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 fit a regression line. (1 pt)

Midparent – offspring heritability estimate = 0.62

b) Now calculate the heritability **(h^2)** for the trait using a **mother-offspring regression** and a **father-offspring regression**. Are they the same? (1 pt)

Mother-offspring heritability = 0.55

Father-offspring heritability = 0.46

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. (1 pt)

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 there is no sexual dimorphism and that the mean of the sample of all the parents above represents the mean of the whole population of finches. (1 pt)

S = 2.27

Problem Set #3 F2017 Problem #1

#1

	Trait				
Male	Burst Speed (M/sec)	Body size (mm)	Intensity of color	Intensity of son's color	Probability of mating success
1	22	180	6.8	5.5	0.89
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		Burst Speed	Body Size	Color	Probability of mating success
a)	**Mean**	17.60	161.20	5.28	
	Var (VAR.P)	48.44	233.76	4.91	0.07
	Var (VAR.S)	53.82	259.73	5.45	
b)	**S=Cov(phenotype, fitness)**	0.06	3.64	0.53	

c)

COV(P,O)	1.41	
Vp	4.91	
h^2=2b==2Cov(P,O)/VAR(P)		0.57

d)

Because the phenotypic covariance among full-sibs includes 1/4V_D and some shared environmental effects (V_{es}). This extra variance inflates the numerator in an estimate of heritability and causes a larger estimate of heritability. For this reason most estimates of heirtability are based on parent-offspring or half-sib regressions.

e)

R = h^2S = (0.42)(3.64) = 1.53

X_1=X_0+R = 161.2 + 1.53 = 162.73

f)

Relative fitness will increase in the next generation.

From Fisher's Fundemental Threrom, the rate of change in fitness is equal to the additive variance in fitness (V_a). If the only source of variation in a population is from the additive effects of alleles, and all other sources of variation are = 0, then Va = Vp. The upper limit to Va is Vp. Of course this will never be the case in a real population. In our sample the phenotypic variance in fitness is 0.07.

Problem Set #3 F2017 Problem #4

Mother	Father	Offspring	Midparent
8	11	10	9.5
7	13	11	10
14	9	10	11.5
9	11	10	10
11	10	13	10.5
14	15	14	14.5
8	12	11	10
9	10	8	9.5
11	6	10	8.5
13	7	12	10
8	9	11	8.5

a)

Midparent-offspring regression	Using VAR.p	Using VAR.s
Cov(MP-O)	1.52	
Var(MP)	2.47	2.72
b	0.62	0.56
h2 = b	0.62	0.56

b)

Mother-Offspring regression	Using VAR.p	Using VAR.s
Cov(M-O)	1.65	
V(M)	5.97	6.56
b	0.28	0.25
h2 = 2b	0.55	0.50

Father-Offspring regression	Using VAR.p	Using VAR.s
Cov(F-O)	1.39	
V(F)	6.02	6.62
b	0.23	0.21
h2 = 2b	0.46	0.42

c)

d) Top five Males and Females

Mother	Father
14	11
14	15
13	13
11	12
11	11

Mean of all Males and Females	10.23
Mean of top 5 Male and Females	12.5
S=	12.5 - 10.23
S=	2.27