1. Show that in a large population, the mean phenotypic value is equal to the mean genotypic value.

Start with $P = G + E$. Then the mean phenotypic value is

$\bar{P} = \bar{G} + \bar{E}$. But in a large population, $\bar{E}$ will be approximately 0 because by definition the expected value of E is 0. Hence, in a large population, $\bar{P} = \bar{G} + 0 = \bar{G}$.

Q.E.D.

2. In a recent set of observations on a species of Galapagos finch, bill length of several males was measured, as was the bill length of those males' offspring. These offspring were sired over a five-year period. Females lay one egg per year. Males are not monogamous and pair with different mates each year. The following data was obtained

Male	Male bill length (mm)	Offspring bill lengths (mm)
1	10	10, 10.5, 11
2	12	11, 11.25, 11.25, 11.5
3	15	12, 12, 12.25, 12.5

Calculate the heritability of bill length from this data using both parent-offspring regression and from the variance in breeding values. Do you get similar results? Comment.

First, caluculate the heritability using P-O regression:

$$h^2 = 2 \times \text{slope of regression} = 2 \times \frac{\text{Cov}(P,\bar{O})}{\text{Var}(P)}.$$

To calculate $\text{Cov}(P,\bar{O})$, set up the following table:

Male	Bill length	Mean offspring bill length
1	10	10.5
2	12	11.25
3	15	12.19

Then $\bar{P} = \frac{10+12+15}{3} = 12.3$ and $\bar{\bar{O}} = \frac{10.5+11.25+12.19}{3} = 11.31$

Then, $\text{Cov}(P,\bar{O}) = \frac{(10-12.3)(10.5-11.31)+(12-12.3)(11.25-11.31)+(15-12.3)(12.19-11.31)}{3} = 1.43.$

And $\text{Var(P)} = \dfrac{\sum(\text{P}-\bar{\text{P}})^2}{n} = \dfrac{[(10-12.3)^2+(12-12.3)^2+(15-12.3)^2]}{3} = 4.2$

Consequently, $h^2 = 2 \times \frac{1.43}{4.2} = 0.68$

Next, calculate the heritability as the variance of the breeding values:

For each male, the breeding value is $2 \times (\bar{\text{P}} - \bar{\bar{\text{O}}})$, giving

Male	Breeding Value
1	$2 \times (10.5 - 11.31) = -1.62$
2	$2 \times (11.25 - 11.31) = -0.12$
3	$2 \times (12.19 - 11.31) = 1.76$

Then, the variance of the breeding values is:

$$\text{Var (BV)} = \text{V}_\text{A} = \frac{[(-1.62)^2+(-0.12)^2+(1.76)^2]}{3} = 1.90$$

Then,

$$h^2 = \frac{\text{V}_\text{A}}{\text{V}_\text{P}} = \frac{1.90}{4.2} = 0.45 \ .$$

Although the two estimates are not exactly the same, they are in reasonably good agreement, given the small sample size.

3. Show that the slope of a regression of mean offspring phenotype on mid-parent phenotype equals h^2.

Let P_1 and P_2 be the phenotypic values of the two parents of a pair. Then the midparent value is $\text{P}_\text{m} = \frac{1}{2}(\text{P}_1 + \text{P}_2)$.

Now, the slope of the regression is just

$$\text{slope} = \frac{\text{Cov}(\text{P}_\text{m},\bar{\text{O}})}{\text{Var}(\text{P}_\text{m})} \ .$$

First, calculate $\text{Cov}(\text{P}_\text{m},\bar{\text{O}}) = \text{Cov}[\frac{1}{2}(\text{P}_1 + \text{P}_2), \bar{\text{O}}] = \frac{1}{2}[\text{Cov}(\text{P}_1\bar{\text{O}}) + \text{Cov}(\text{P}_2\bar{\text{O}})]$
But because male and female parents, on average, contribute the same genetic material to offspring,

$\text{Cov}(\text{P}_1\bar{\text{O}}) = \text{Cov}(\text{P}_2\bar{\text{O}})$, so

$$\mathrm{Cov}(P_m,\bar{O}) = \mathrm{Cov}(P_1\bar{O}) = \tfrac{1}{2}V_A.$$

Next, $\mathrm{Var}(P_m) = \mathrm{Var}[\tfrac{1}{2}(P_1 + P_2)] = \tfrac{1}{4}[\mathrm{Var}(P_1) + \mathrm{Var}(P_2)]$.
But again, we can assume that the phenotypic variance for the trait is the same for both parents, so

$$\mathrm{Var}(P_1) + \mathrm{Var}(P_2) = 2\ \mathrm{Var}(P_1), \text{ and hence}$$

$$\mathrm{Var}(P_m) = \tfrac{1}{4} \times 2\ \mathrm{Var}(P_1) = \tfrac{1}{2}\mathrm{Var}(P_1) = \tfrac{1}{2}V_P\ .$$

Thus, $\text{slope} = \dfrac{\mathrm{Cov}(P_m,\bar{O})}{\mathrm{Var}(P_m)} = \dfrac{\frac{1}{2}V_A}{\frac{1}{2}V_P} = \dfrac{V_A}{V_P} = h^2$.

Q.E.D.