

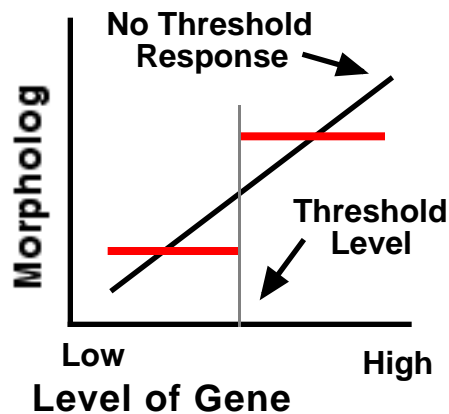
Polygenetic Traits

I) Quantative Genetics

- Study of morphological traits that are controlled by several different genes.
- Often have multifactoral influences
 - ✓ epistasis
 - ✓ environment
 - ✓ genotype environment interactions
 - ✓ stochastic

A) Types of Quantative Traits

- 1) Continuous (metric) – height, weight, growth rate, etc.
- 2) Meristic – integral class characters (i.e., counts) such as number of offspring, hairs, toes, etc.
- 3) Discrete – presence or absence such as eye color, schizophrenia. Often associated with thresholds



B) Regression Analysis

- **Key tool in the analysis of quantitative traits is a regression analysis and covariance estimation.**
- **Parents and offspring co-vary (in part) because of genetic relatedness. The higher the co-variation the higher the genetic basis of the character.**

OH 14.1A and 14.1B

- **Use regression against male phenotype to remove maternal effects. Can use mid-parent (i.e., average between father and mother) if maternal effects are minimal (i.e., broadcast spawning, etc).**

$$\text{cov}(\mathbf{x}, \mathbf{y}) = \frac{\sum_{i=1}^n (\mathbf{x}_i - \bar{\mathbf{x}})(\mathbf{y}_i - \bar{\mathbf{y}})}{n}$$

The regression coefficient is the slope of the best-fit line (i.e., the smallest sum of the squared deviation of the points to the line):

$$\mathbf{b} = \frac{\text{cov}(\mathbf{x}, \mathbf{y})}{\text{var}(\mathbf{x})}$$

The correlation coefficient (i.e., how close is the fit):

$$\mathbf{R} = \frac{\text{cov}(\mathbf{x}, \mathbf{y})}{\sqrt{\text{var}(\mathbf{x})\text{var}(\mathbf{y})}}$$

C) Heritability of Characters

- **How much of the observed variation in phenotype is explained by variation in the genotype alone is considered the heritability of a character.**

$$\mathbf{V}_P = \mathbf{V}_G + \mathbf{V}_E + 2\text{cov}(\mathbf{G}, \mathbf{E})$$

- 1) **Broad Sense Heritability** – describes the proportion of the phenotypic variation that is due to the genetic variation.

$$H^2 = \frac{V_G}{V_P}$$

BUT:

$$V_G = V_A + V_D + V_I$$

V_G = Total genetic variation

V_A = Additive genetic variation

V_D = Dominance genetic variation

V_I = Epistatic genetic variation

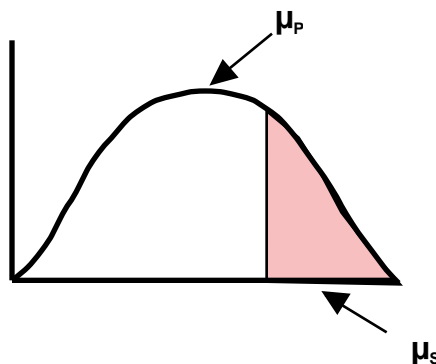
OH 14.2 (The effect of epistasis is similar to dominance)

- 2) **Narrow Sense Heritability** – describes the proportion of the phenotype variation that is due to the additive genetic variation only (natural selection can only operate on additive genetic variation not dominance).

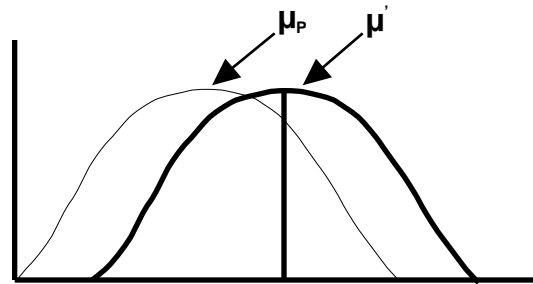
$$h^2 = \frac{V_A}{V_P} = \text{regression coefficient (b)}$$

D) Artificial Selection and Quantative Traits – it is often easier to understand selection on quantative traits by considering artificial selection.

- 1) **Truncation Selection** – only a certain fraction of the phenotypic distribution (i.e., V_P) is allowed to reproduce.



After selection the offspring generation:



$$S = \text{selection differential} = \mu_S - \mu_P$$

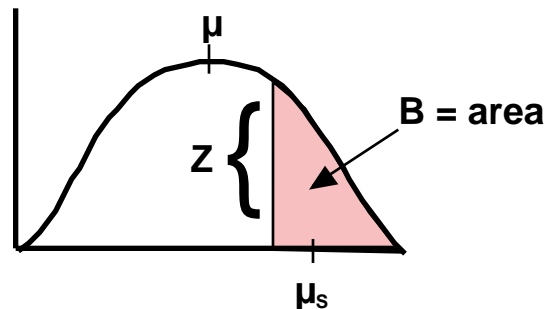
$$R = \text{Response to Selection} = \mu' - \mu_P$$

generally $\mu' \neq \mu_S$

$$R = h^2 S \text{ or } h^2 = \frac{R}{S}$$

E) Genetic Models of Quantitative Trait Selection

We know that for a standard normal distribution:



$$\frac{Z}{B} = \frac{\mu_S - \mu}{\sigma^2}$$

Assume a single gene with two alleles (A and A') and

$d = a$ if A is dominant

$d = 0$ if additive

$d = -a$ if A' is dominant

$-a \leq d \leq a$ and measure of dominance = $\frac{d}{a}$

OH 14.3 and 14.4

Fitness can then be defined as the area difference between the genotypes.

OH 14.5

We know from classical model:

$$\Delta p = \frac{pq[p(W_{11} - W_{12}) + q(W_{12} - W_{22})]}{\bar{W}}$$

and from overheads:

$$\bar{W} = B, W_{11} - W_{12} = Z(a - d), \text{ and } W_{12} - W_{22} = Z(a + d)$$

Substituting and rearranging:

$$\Delta p = \frac{pq[p(Z(a - d)) + q(Z(a + d))]}{B}$$

$$\Delta p = \frac{Z}{B} pq[a + (q - p)d]$$

The mean value of the trait after selection is:

$$F(A) = p + \Delta p \text{ and } F(A') = q - \Delta q$$

Then:

$$\mu' = (p + \Delta p)^2(\mu^* + a) + 2(p + \Delta p)(q - \Delta q)(\mu^* + d) + (q - \Delta q)^2(\mu^* - a)$$

ignoring Δp^2 and Δq^2 since they are very small

$$\mu \quad \mu + 2[a + (p - q)d] \quad p$$

$$\mu' - \mu = 2[a + (p - q)d] \quad p$$

substituting in Δp

$$\mu' - \mu = \frac{Z}{B} 2pq[a + (q - p)d]^2$$

And:

$$\frac{Z}{B} = \frac{\mu_s - \mu}{\sigma^2} \text{ (from general normal curve)}$$

And:

$$\mu' - \mu = \frac{(\mu_s - \mu)2pq[a + (q - p)d]^2}{\sigma^2}$$

Since: $\mu_s - \mu = S$, $\mu' - \mu = R$, and $h^2 = \frac{R}{S}$

$$h^2 = \frac{2pq[a + (q - p)d]^2}{\sigma^2}$$

Since this is for a single gene, for a quantitative trait:

Additive
Genetic
Variance

$$h^2 = \frac{2pq[a + (q - p)d]^2}{\sigma^2}$$

F) Genotype – Environment Interaction – sometimes genotypes act differently in different environments.

Phenotype Value = population mean + Δ genes + Δ environment

$$V_P = \mu + G_i + E_i$$

Genotype Δ genes Δ environment

AA G₁ E₁

AA G₁ E₂

AA G₁ E₃

AA' G₂ E₄

AA' G₂ E₅

AA' G₂ E₆

A'A' G₃ E₇

A'A' G₃ E₈

A'A' G₃ E₉

$$\begin{aligned}\text{Variance in Phenotype } (V_P) &= (P - \mu)^2 = (\mu + G + E - \mu)^2 \\ &= (G + E)^2 \\ &= G^2 + 2GE + E^2\end{aligned}$$

And: $G^2 = V_G$, $E^2 = V_E$, AND $2GE = \text{cov}(G, E)$ [often assumed to = 0]

Remember:

$$\begin{aligned}\mu &= p^2(\mu^* + a) + 2pq(\mu^* + d) + q^2(\mu^* - a) \\ &= \mu^* + (p - q)a + 2pqd\end{aligned}$$

| <u>Genotype</u> | <u>Freq.</u> | <u>μ Pheno</u> | <u>Genetic deviation from μ</u> |
|-----------------|--------------|-------------------------------|-------------------------------------------------------------|
| AA | p^2 | $\mu^* + a$ | $G_1 = \mu^* + a - \mu$ $= 2q[a + (q - p)d] - 2q^2d$ |
| AA' | $2pq$ | $\mu^* + d$ | $G_2 = \mu^* + d - \mu$ $= (q - p)[a + (q - p)d] - 2pqd$ |
| A'A' | q^2 | $\mu^* - a$ | $G_3 = \mu^* - a - \mu$ $= -2p[a + (q - p)d] - 2q^2d$ |

$$\begin{aligned}V_G &= p^2 G_1^2 + 2pq G_2^2 + q^2 G_3^2 \\ &= \underline{2pq[a + (q - p)d]^2} + \underline{(2pqd)^2}\end{aligned}$$

Remember:

$$V_G = V_A + V_D$$

So:

$$V_A = 2pq[a + (q - p)d]^2$$

and

$$V_D = (2pqd)^2$$

Also remember by a different way:

$$h^2 = \frac{2pq[a + (q - p)d]^2}{\sigma^2}$$

and

$$h^2 = \frac{V_A}{V_P}$$

Natural selection, therefore, will only act on the additive genetic variation of a trait.

$$R = \frac{V_A}{V_P} S$$

OH 14.6

G) Norm of Reaction – for the most part, we have been ignoring (or assuming is zero) the genotype–environment interaction terms. This is not usually true.

- 1) Variance in Phenotype across environment is called the Norm of Reaction**

OH 16.2

- a) Additive and dominance genetic variation therefore have environmental components.**
- b) Phenotypic plasticity may itself be acted upon by natural selection (i.e., genes for phenotypic plasticity).**