Evolution of Quantitative Traits 1

Outline

- what are quantitative traits
- how many genes
- heritability and additive variance
- measuring selection
- forms of selection

B&D Ch. 9, pp. 294-297, 318-325; box 9.3, 9.4

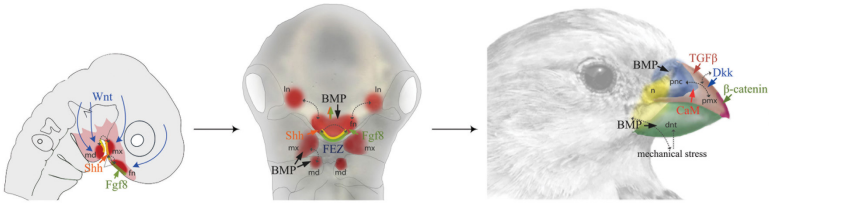
Quantitative Traits

continuous traits

meristic traits

threshold traits

Evolution of Quantitative Traits



Badyaev 2011 Auk 128:467

several to many genes may affect phenotype
-- number, location, identity of genes unknown

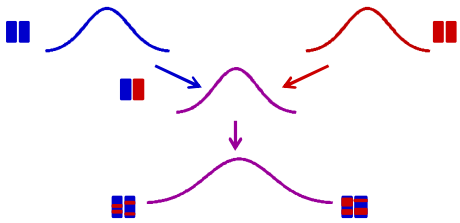
environmental variation

developmental noise

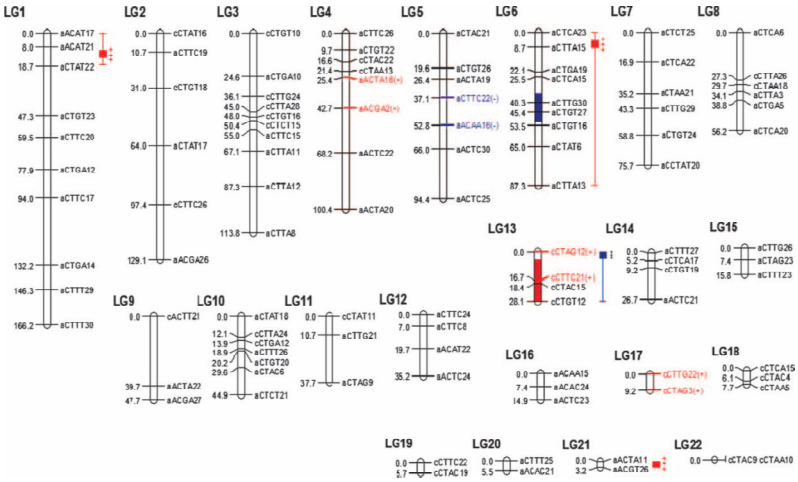
genetic architecture of quantitative traits

Quantitative Trait Locus (QTL) mapping

- cross of inbred lines (species) to generate F_1
- backcross or F_1 cross to produce recombinant progeny
- genotyping of BC or F_2 progeny that are "parental-like"
- subsequent fine-scale mapping



QTL analysis of Louisiana Iris

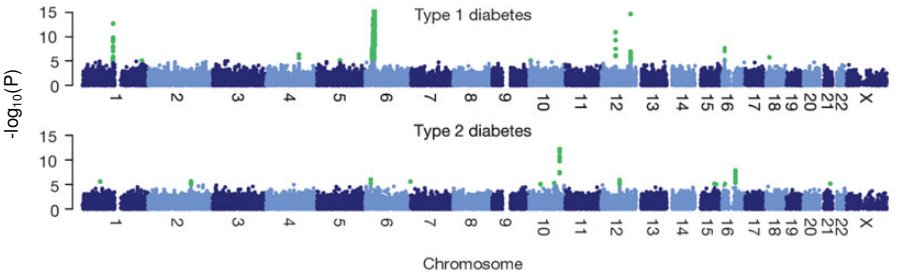


Martin et al 2006 Genetics 172:2481

genetic architecture of quantitative traits

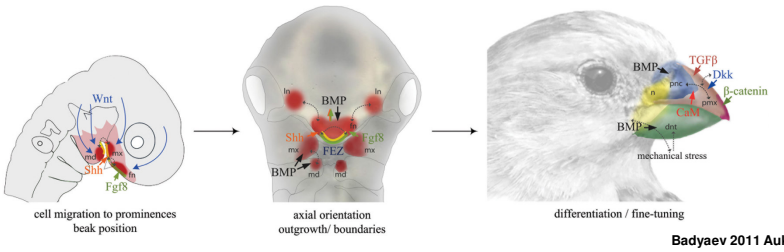
Genome-Wide Association studies

- genomic SNP map; high throughput sequencing
- survey of large sample from randomly-mating population
- compare affected group (w/disease) and control group



Wellcome Trust Consortium
Nature 447:661 (2007)

Evolution of Quantitative Traits



Badyaev 2011 Auk 128:467

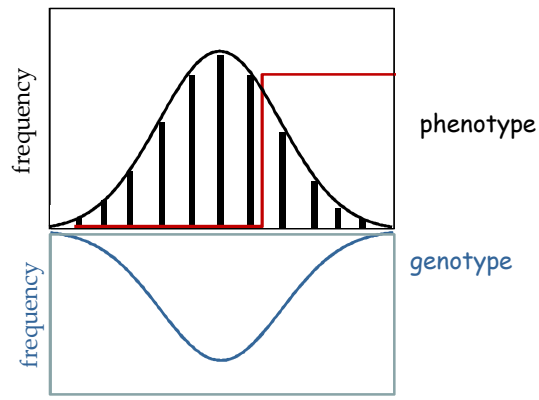
$$P = G + E$$

P = phenotype value (what is measured)

G = genotypic value = expected phenotypic value of a given genotype

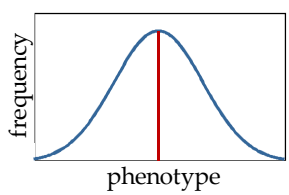
E = environmental deviation

relating phenotypic variation to genetic variation

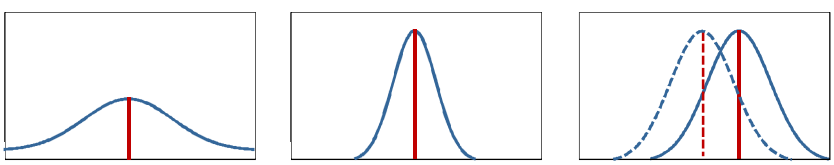


$$P = G + E \rightarrow V_P = V_G + V_E$$

Variance = $\frac{1}{N}\Sigma (x_i - x)^2$



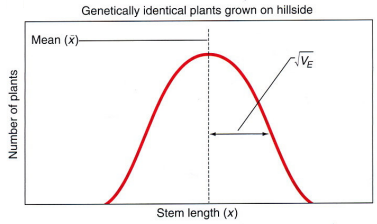
Mean = $\frac{1}{N}\Sigma n_i$

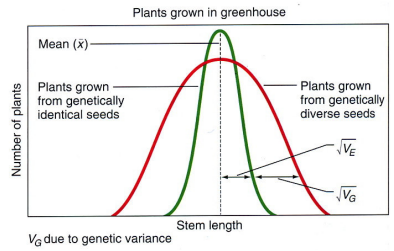


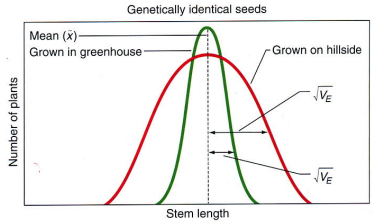
same mean, larger variance | same mean, smaller variance | different mean, same variance

$$V_P = V_G + V_E$$

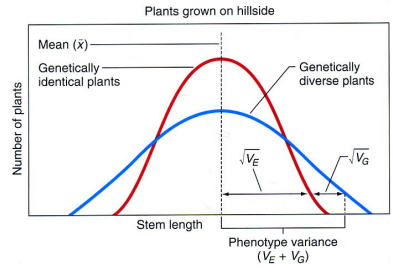
$$V_P = V_G + V_E$$







V_E is smaller among greenhouse-grown plants.



heritability and additive genetic variance:

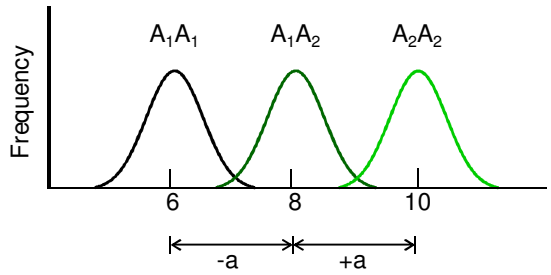
$$V_P = V_G + V_E$$

genetic variance (V_G) components:

- V_A - additive genetic variance
- V_D - dominance variance
- V_I - epistatic variance
- V_M - maternal variance

additive genetic variance, V_A

effect of an allele on the phenotype is independent of what other alleles are present

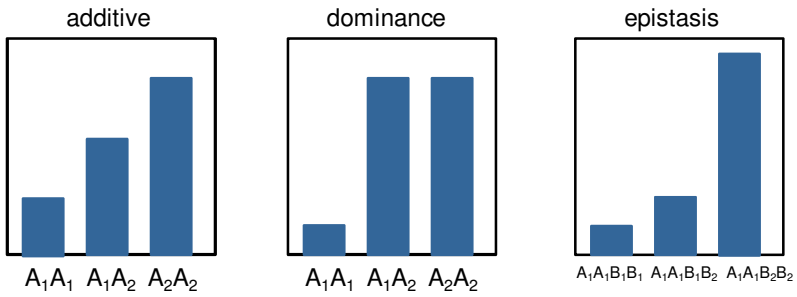


the *HMGA2* locus in human affects height: one allele increases height by 0.5 cm
(Weedon et al 2007 Nature Genetics 39:1245)

**differences due to additive alleles are transmitted from parents to offspring*

dominance variance (V_D) and epistatic variance (V_I)

dominance and epistasis are interactions between alleles - effect of an allele on the phenotype depends on what allele(s) it is paired with



**effects of dominance and epistasis are not inherited*

how can we measure additive genetic variance (V_A)?

heritability, h^2 is:
the proportion of phenotypic variance
that is due to additive genetic variance

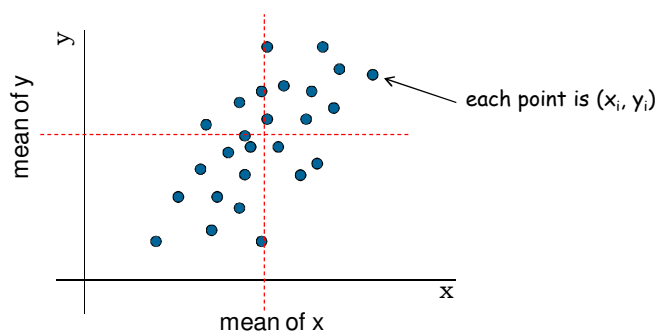
$$\frac{V_A}{V_P} = h^2$$

compare trait values in close relatives (parents and offspring)

rear under same environmental conditions – minimize V_E

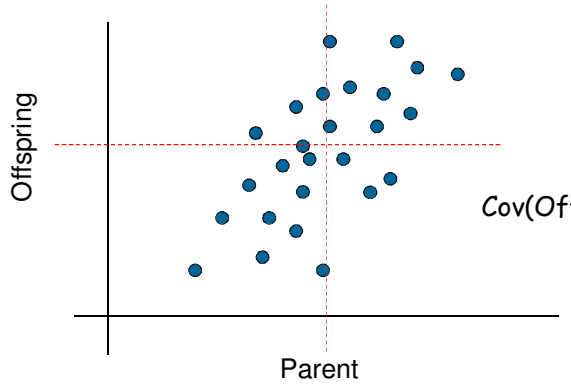
estimate the strength of similarity: P-O regression

Covariance

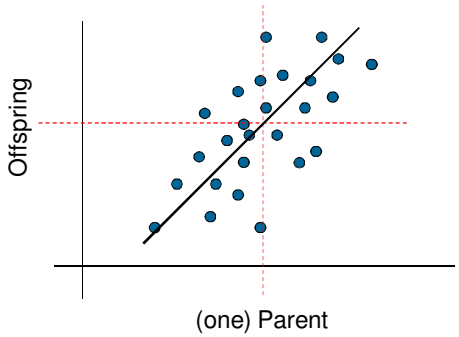


$$\frac{1}{n}\sum_i (x_i - \bar{x})(y_i - \bar{y}) \equiv Cov(x, y)$$

when offspring resemble parents their phenotypes covary



Cov(Offspring, <u>one</u> Parent)
$= \frac{1}{2}V_A$



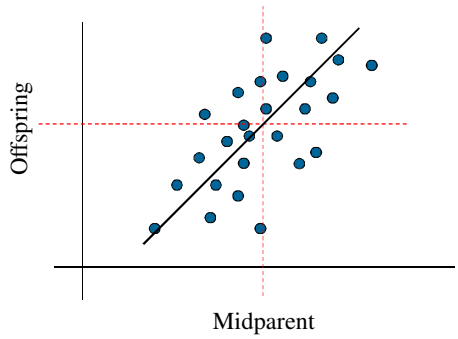
Can we predict the phenotype of the offspring from the phenotype of the parents?

Regression: want to predict **y** from **x**

We produce a regression coefficient or slope for a line

The line goes through the mean **x** and mean **y**

$$\text{Regression coefficient} = \frac{\text{Cov}(x, y)}{\text{Var}(x)} = \frac{\frac{1}{2}V_A}{V_P} = \frac{1}{2}h^2$$



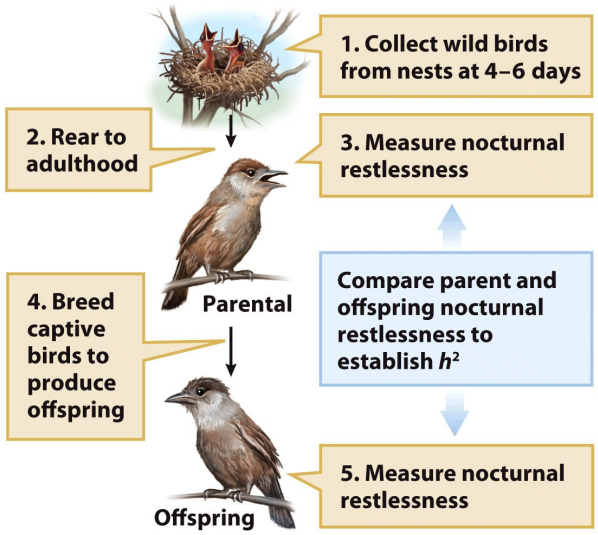
offspring have two parents

Midparent Value = average parental phenotype

Variance of midparents is less than variance of one parent (the variance of an average is always less): $V_{Midparent} = \frac{1}{2}V_P$

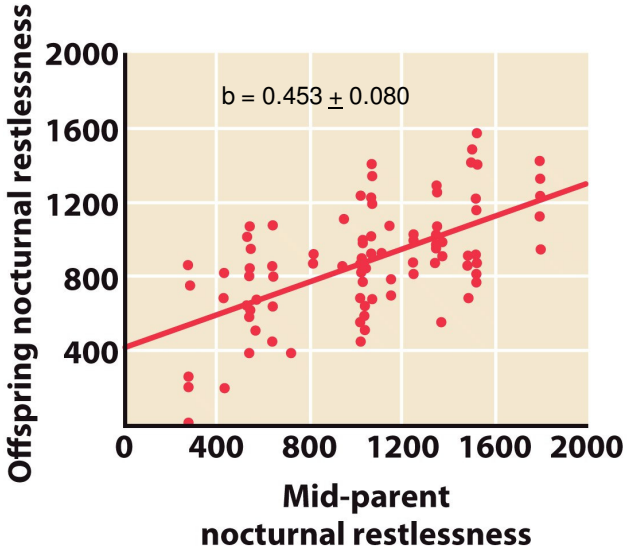
regression of offspring on midparent $= \frac{Cov(o, m)}{Var(m)} = \frac{\frac{1}{2} V_A}{\frac{1}{2} V_P} = h^2$

estimating h^2 of behavior in the blackcap



Evolution, 1/e Figure 9.35b

estimating h^2 of behavior in the blackcap



Evolution, 1/e Figure 9.35c
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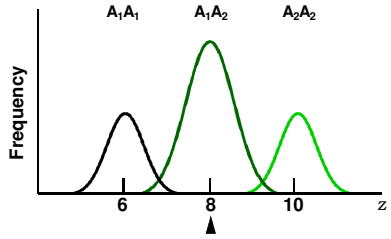
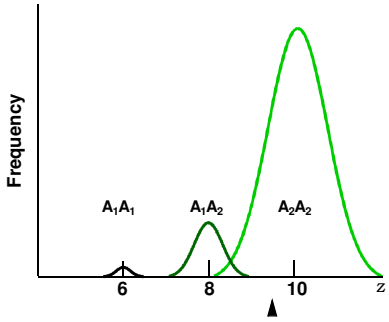


q = p =0.5

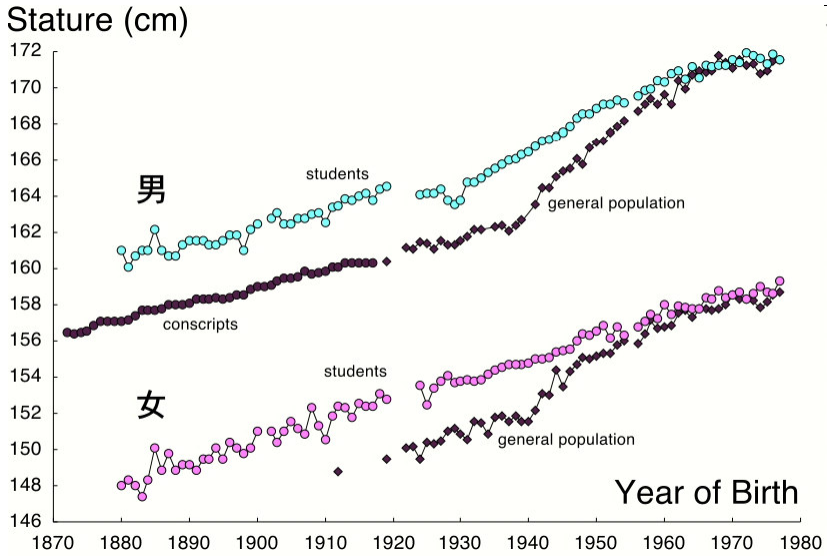


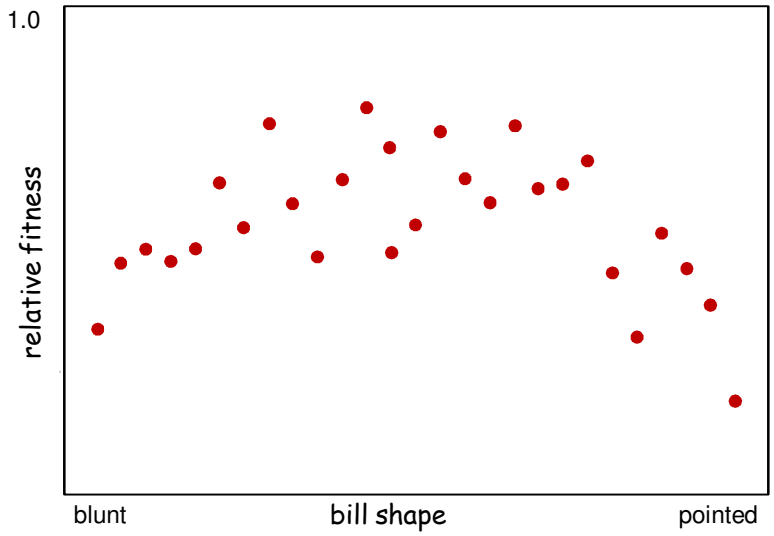
q = 0.1, p = 0.9

**heritability is a property of a population*

measuring selection on quantitative traits

temporal changes in the height of Japanese men and women





the fitness (w) of a trait (z) can be estimated as:

$$w = \alpha + \beta z + (\gamma/2)z^2$$

α is the *y*-intercept of the fitness function

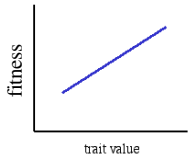
β is the fitness function's slope

γ measures the amount of curvature in the fitness function

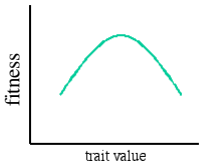
β and γ are the selection gradients

patterns of selection on quantitative traits

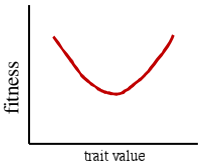
directional

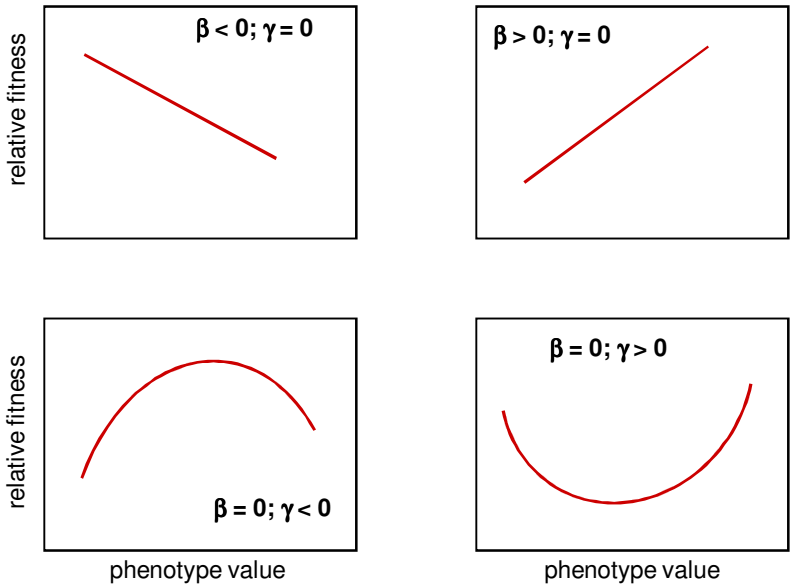


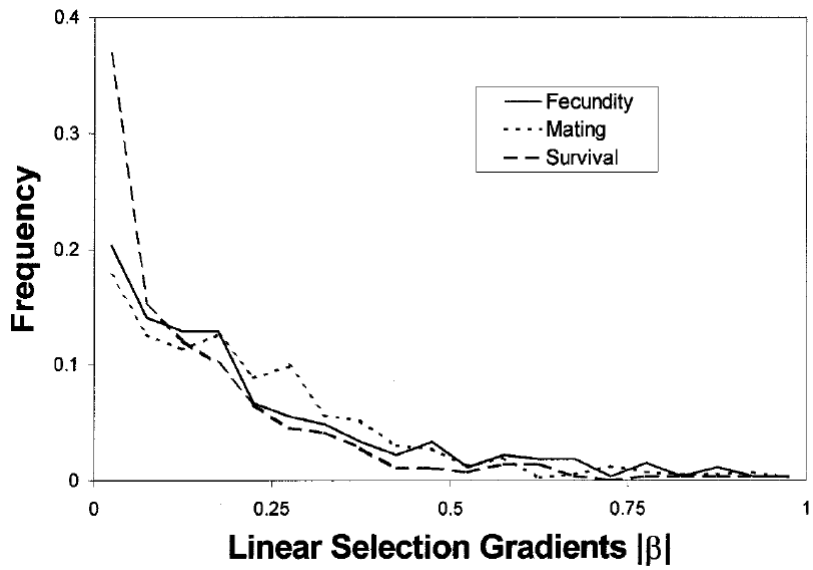
stabilizing



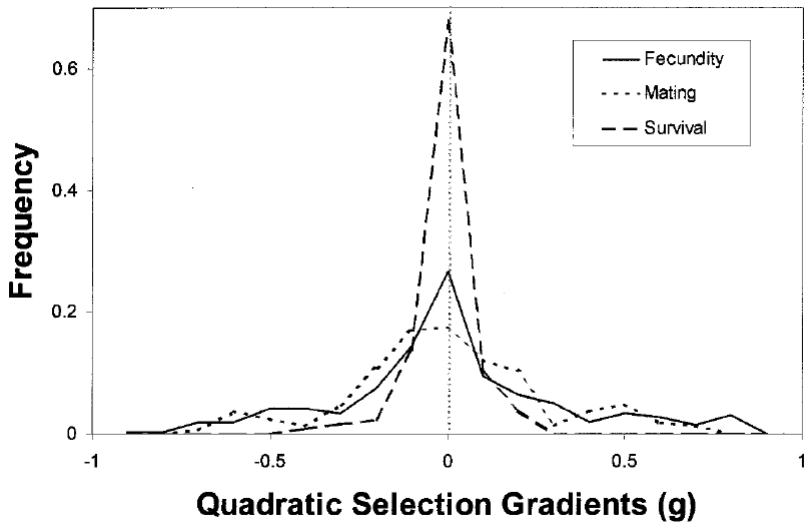
disruptive







Kingsolver et al 2001 Am Nat 157:245



Kingsolver et al 2001 Am Nat 157:245

Evolution of quantitative characters

phenotypic variance in a trait can be partitioned into several genetic variance components

additive genetic variance (V_A) represents the heritable component of the phenotype

selection will change the genetic variation in a quantitative trait in a manner similar to one with simpler genetics

heritability can be estimated from breeding studies

heritability is a property of a population