Heritability and the response to selection

Resemblance between relatives in Quantitative traits

- A trait with L loci
- Each segregating an allele A_1 at freq. p_l

- Each copy of the A_1 allele at a locus increasing our phenotype by a_l, i.e. additively, around mean.
- An individual i's genotype at locus l is G_{il}=0,1,2
- w.p. p_l^2,$2p_l(1-p_l)$, $(1-p_l)^2$

- An individual's phenotype, X_p, is made up of
  - $X_P = X_A + X_E$

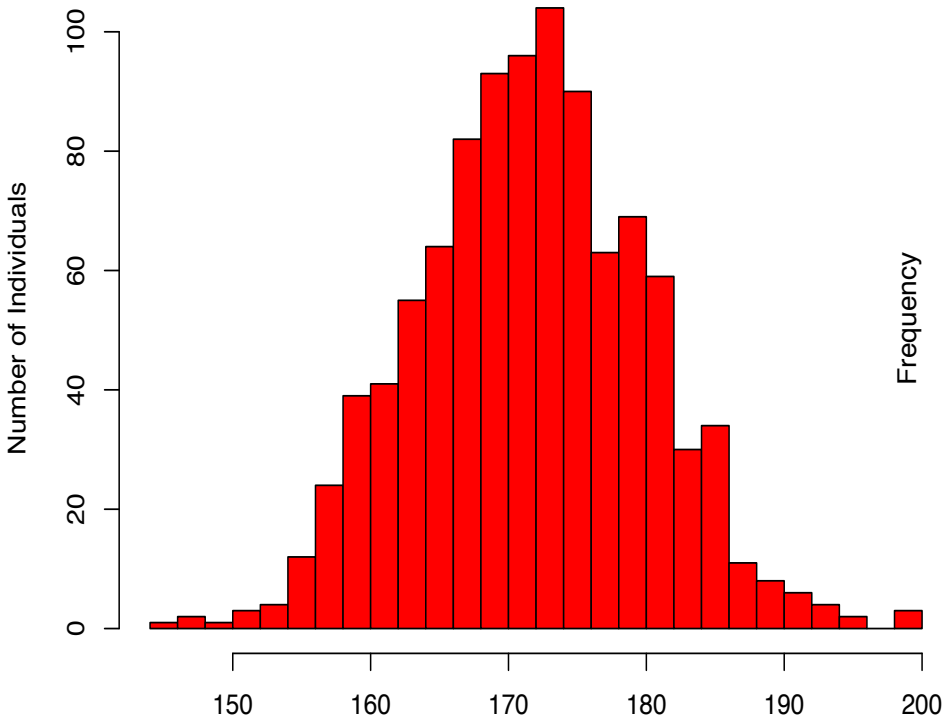
doi:10.1038/nature09410

163 loci
Mean additive
effect on height at a locus: 0.24cm

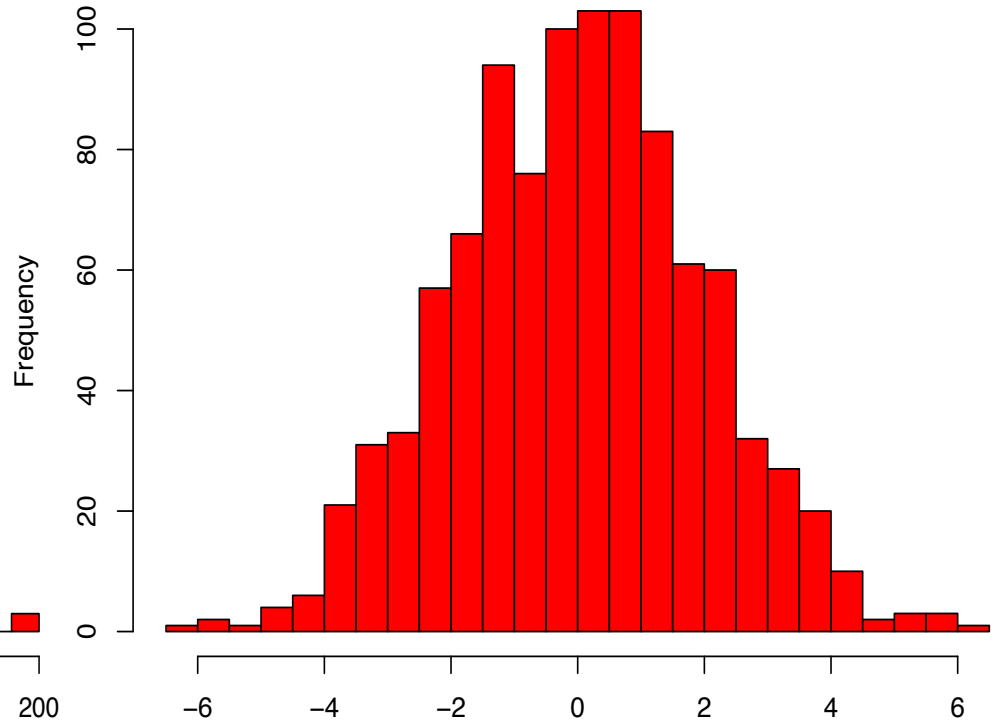
Mean allele frequency:
52% in French population

Hundreds of variants clustered in genomic loci and biological pathways affect human height

A full list of authors and their affiliations appears at the end of the paper.



Number of height increasing alleles



Genetic effect on height, cm

An individual's phenotype, X_p, is made up of

$X_P = X_A + X_E$

X_A Genetic contribution to phenotype has a normal distribution $N(0,V_A)$

--Follows from the Central Limit Theory

Assume that X_E has a normal distribution $N(\mu_E,V_E)$

Thus X_P has a normal distribution

$$N(\mu_A + \mu_E, V_P) \qquad V_P = V_E + V_A$$

$$*\text{Heritability} = h^2 = V_A/V_P$$

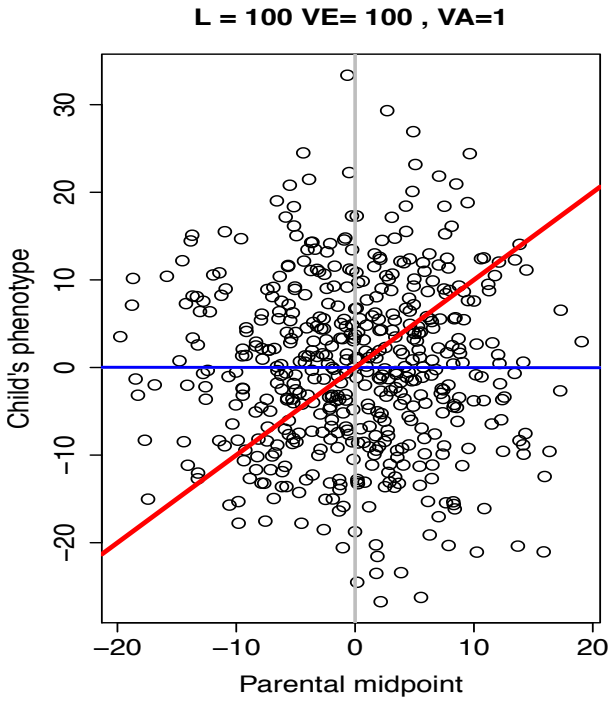
*NARROW SENSE

Resemblance between relatives in Quantitative traits

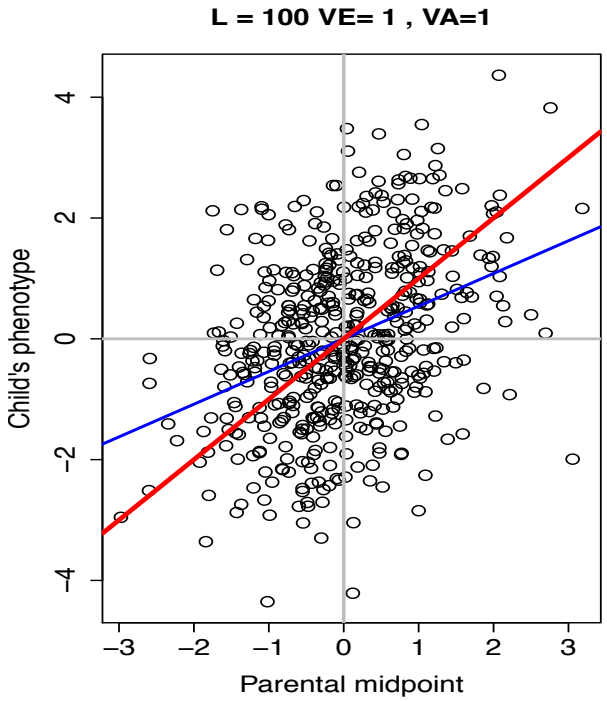
- Individual 1's phenotype = X_1
- Individual 2's phenotype =X_2
- Want to know the cov(X_1,X_2)
- = Cov((X_{1M}+X_{1P}+X_{1E}), (X_{2M}+X_{2P}+X_{2E}))

Heritability* is estimated from mid-parent-offspring analysis as the slope of the regression line

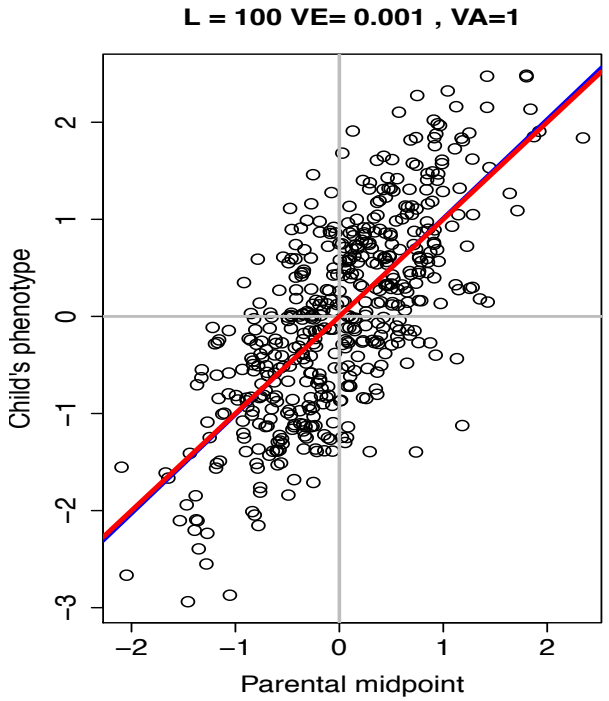
Slope=Cov(X,Y)/Var(X) =(V_A/2) /(V_P/2) = h^2



h^2=0



h^2=0.5

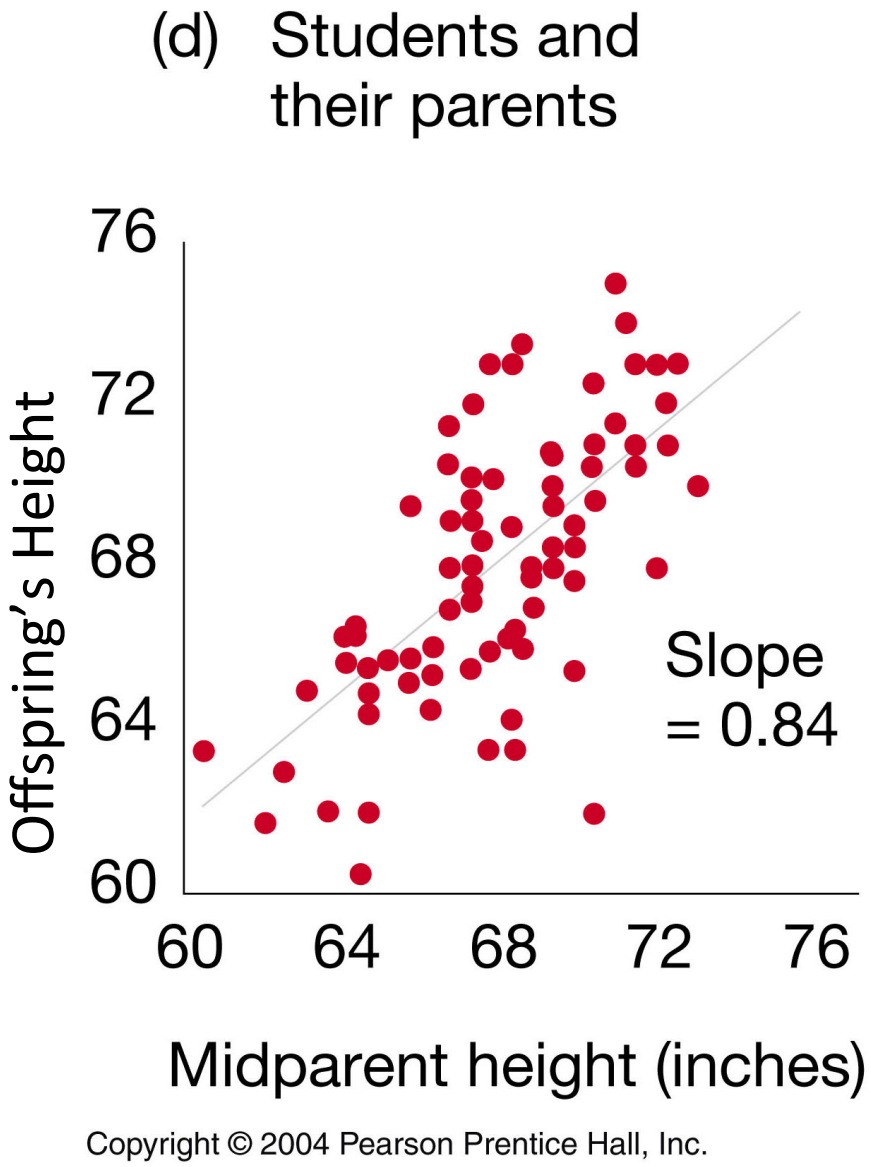


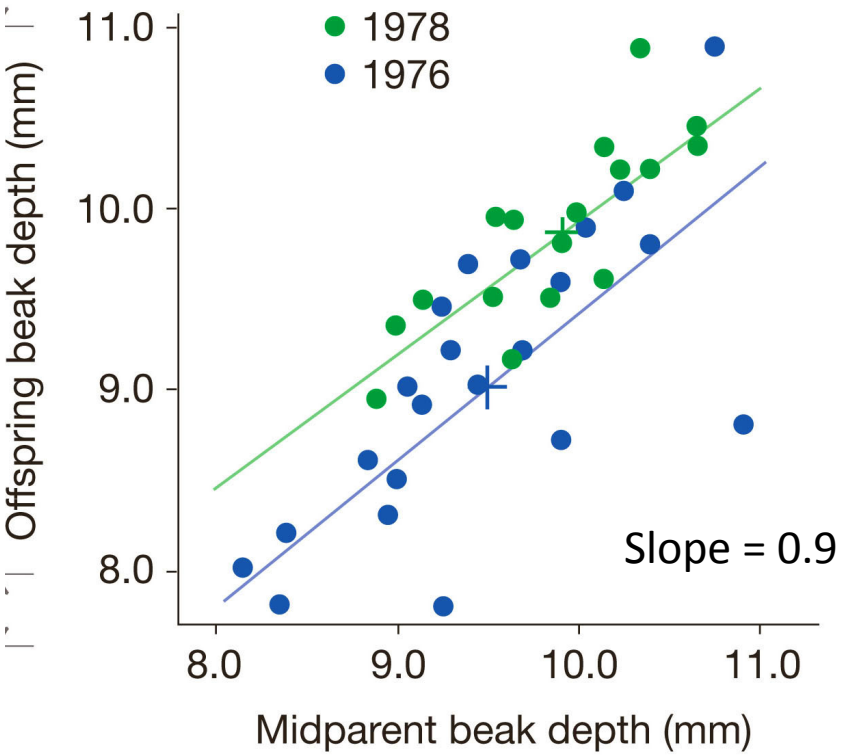
h^2=1

When mid-parental values does not influence offspring phenotype.

Offspring's phenotype predicted by parental mean

*narrow sense





the effect of shared environment

- Need to eliminate the covariance

of relatives due to shared environment.

- This is hard but doable

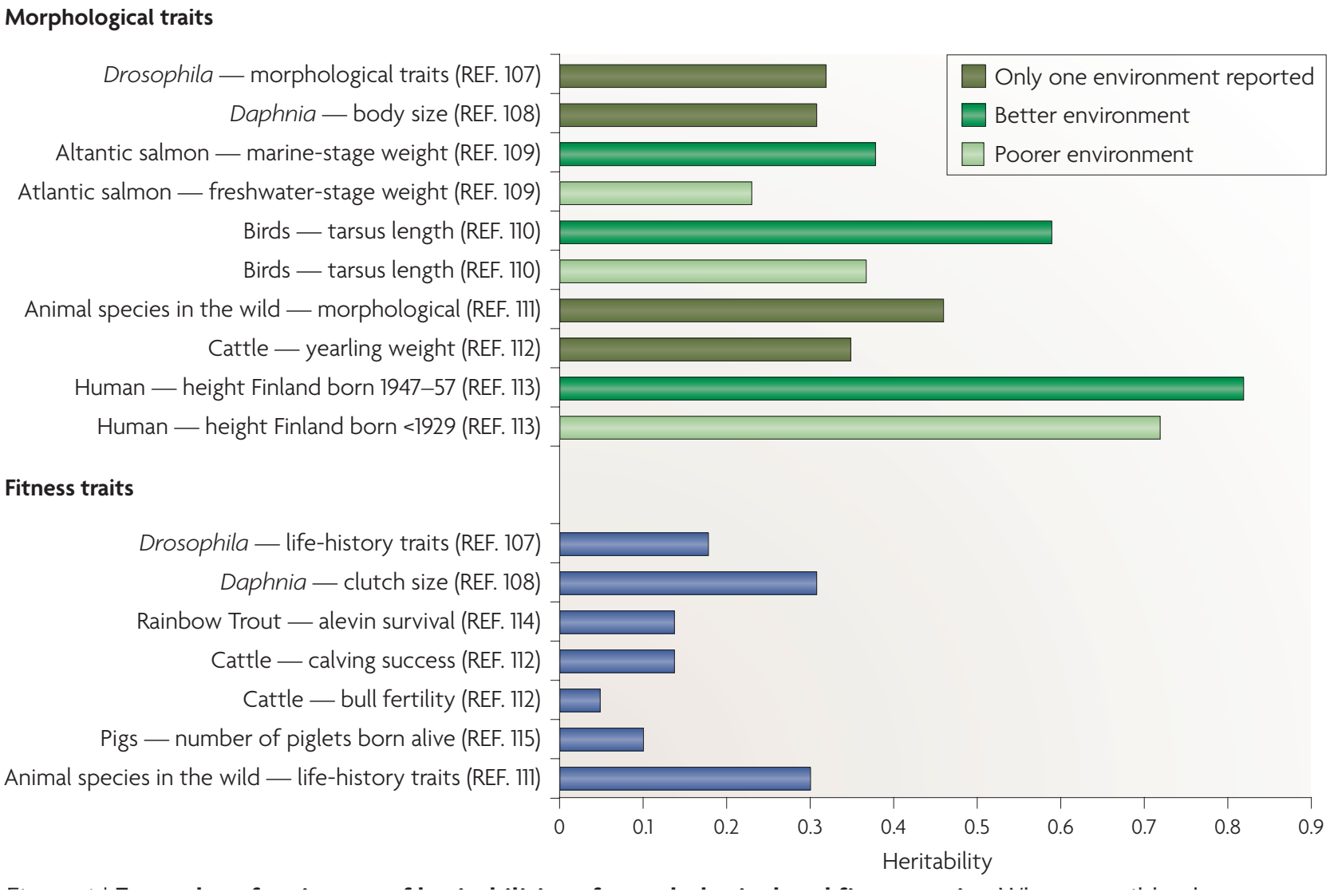
through careful experiments.

- E.g. cross fostering,

or common garden experiments

Or by use of other pairings of relatives.

Most traits show h^2 between 0.1 -- 0.9



- Easy to confuse genetic inheritance with shared environment
- Heritability measures are environment specific

- Differences between populations in a highly heritable phenotype, do not mean that the differences between populations are genetic.

- South Korean men 1.738 m (5 ft 8.5 in)
- North Korean men 1.65m (5 ft 5 in)

- English men mid-19th C. 1.66 m (5 ft 5.5 in)
- English men today. 1.772 m (5 ft 10 in)

Confusion over population differences in IQ are the worst cases of this

"…Owing to this struggle for life, any variation, however slight and from whatever cause proceeding, if it be in any degree profitable to an individual of any species, in its infinitely complex relations to other organic beings and to external nature, will tend to the preservation of that individual, and will generally be inherited by its offspring. The offspring, also, will thus have a better chance of surviving, for, of the many individuals of any species which are periodically born, but a small number can survive. I have called this principle, by which each slight variation, if useful, is preserved, by the term of Natural Selection…"

Charles Darwin, "The Origin of Species"

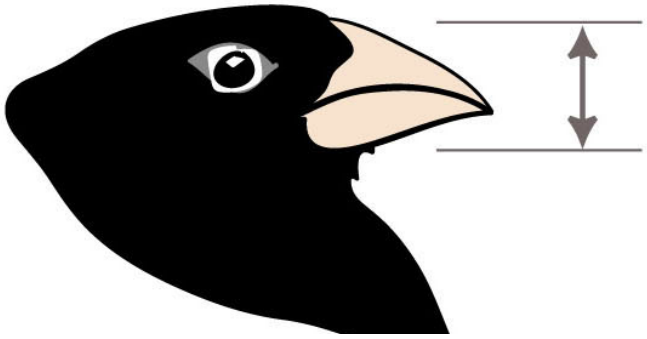
Conditions for evolution by natural selection

1. Variation must be present

2. This variation must affect the probability of survival and reproduction (fitness)

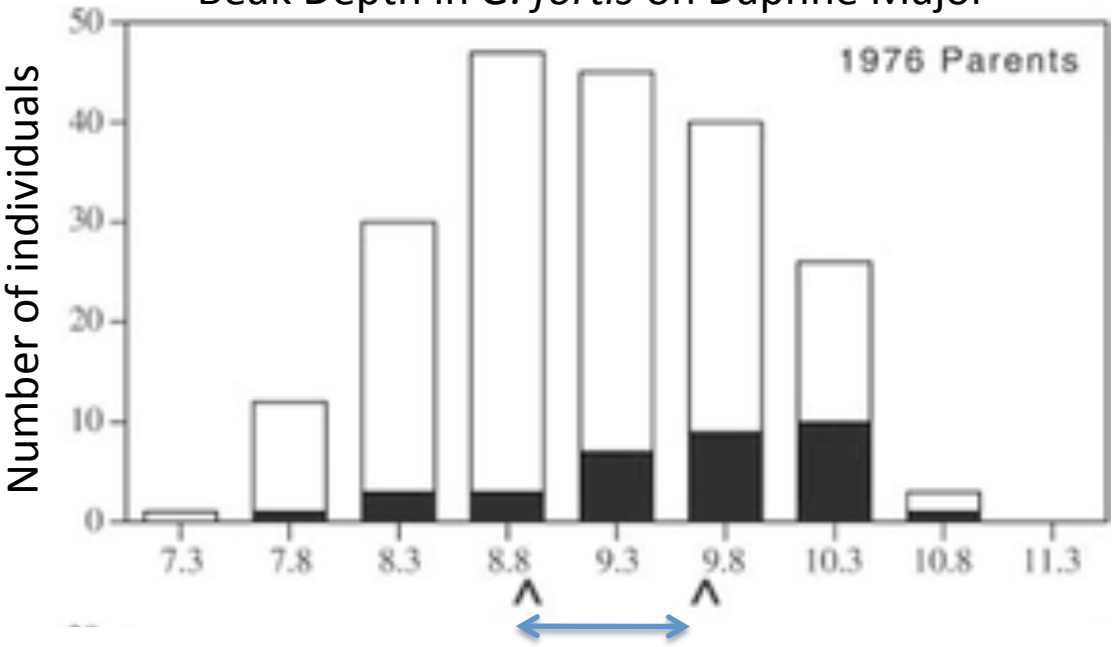
3. This variation must be heritable, i.e. genetic

Geospiza fortis



Drought in 1977 left only large seeds Available. Birds with deeper beaks were Better able to survive.

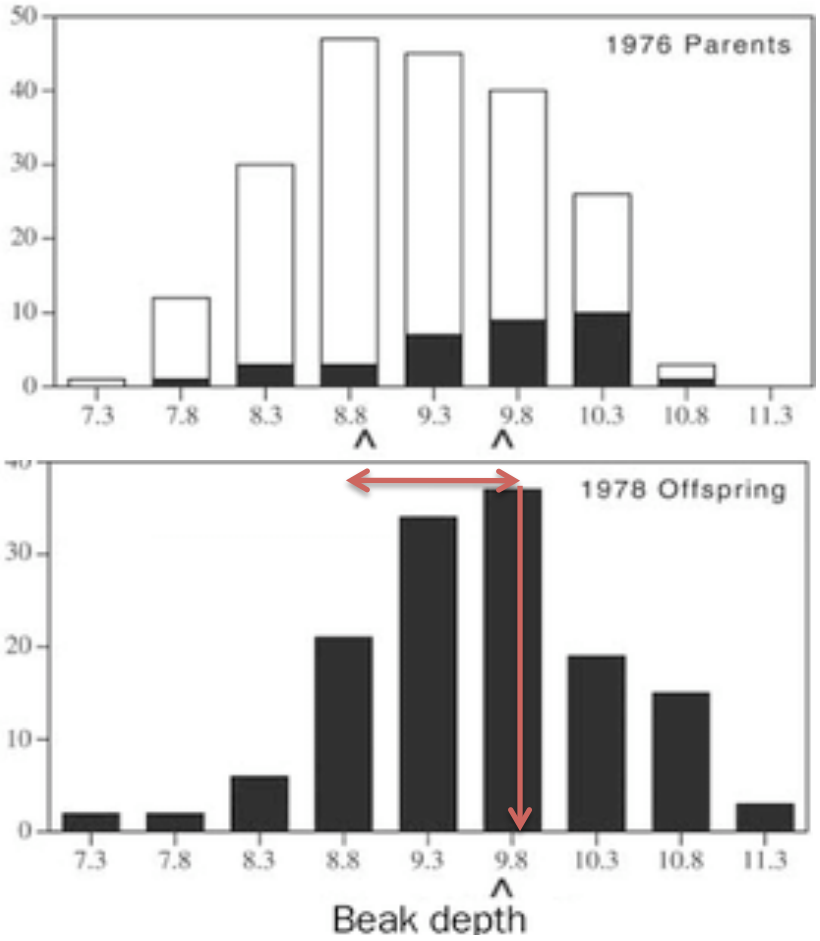
Beak Depth in *G. fortis* on Daphne Major



A change in mean phenotype within a generation due to natural selection

Grant and Grant 2002

- Evolution by natural selection will only occur if the change in mean phenotype caused by selection can be transmitted to next generation (i.e. it is heritable).

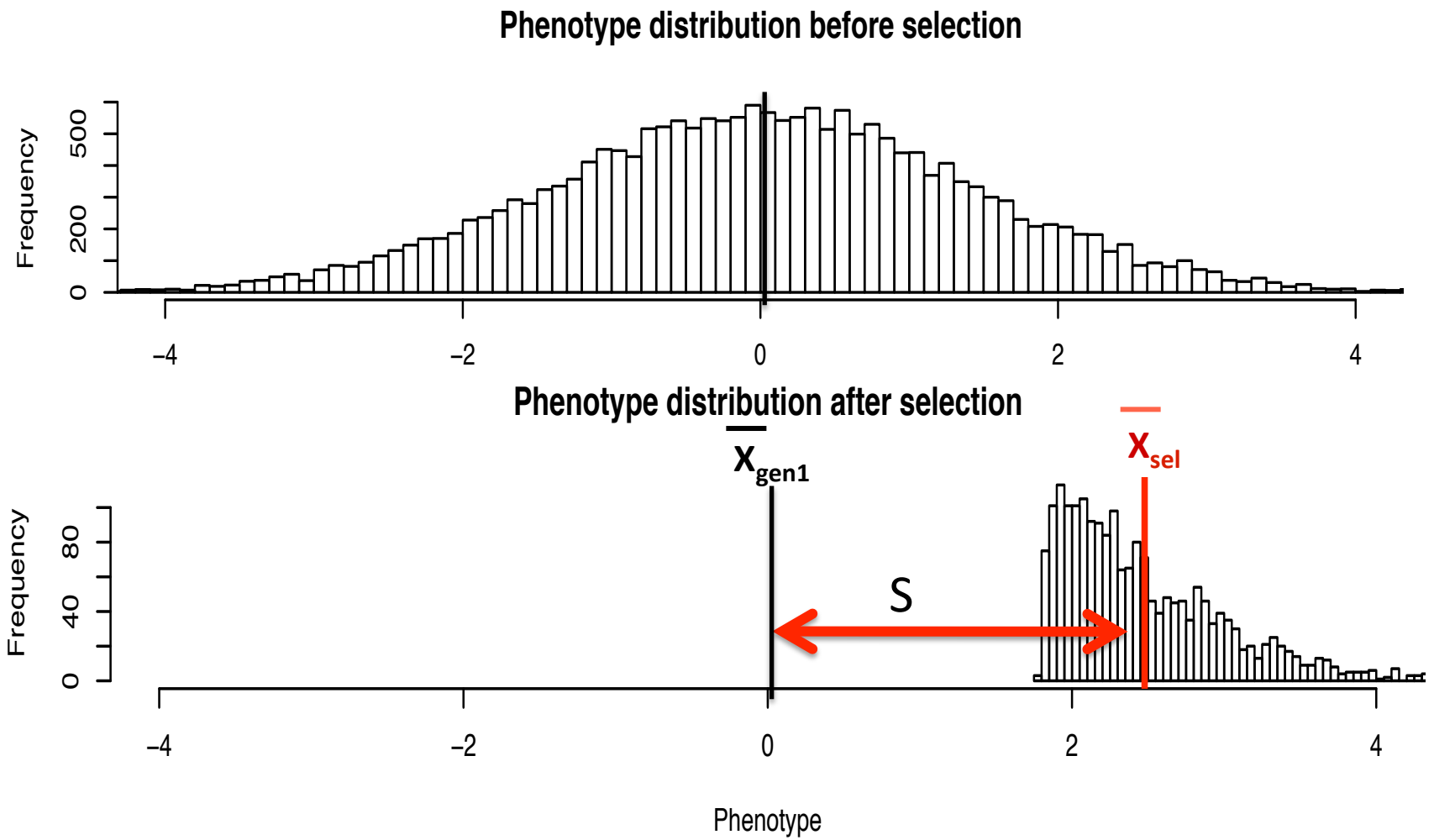


•Natural selection can act on a trait even in absence of genetic variation in that trait.

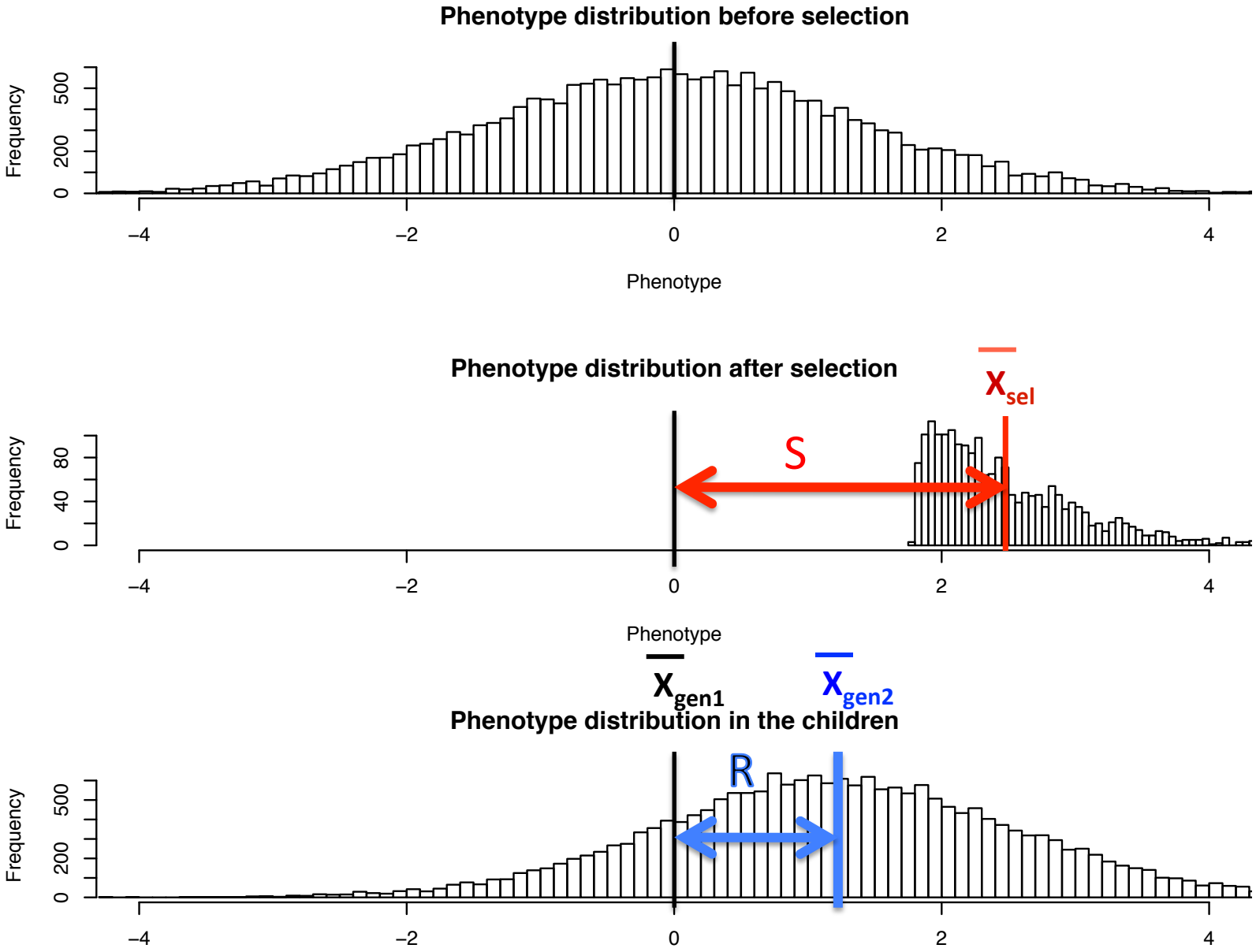
•However, no evolution due to natural selection will occur without genetic variation.

S, the selection differential, is the difference caused by selection in mean phenotype within a generation

$$= \bar{x}_{sel} - \bar{x}_{gen1}$$



R, the selection response, is the change in the trait mean across successive generations = $\overline{X}_{gen2} - \overline{X}_{gen1}$



The breeder's equation.

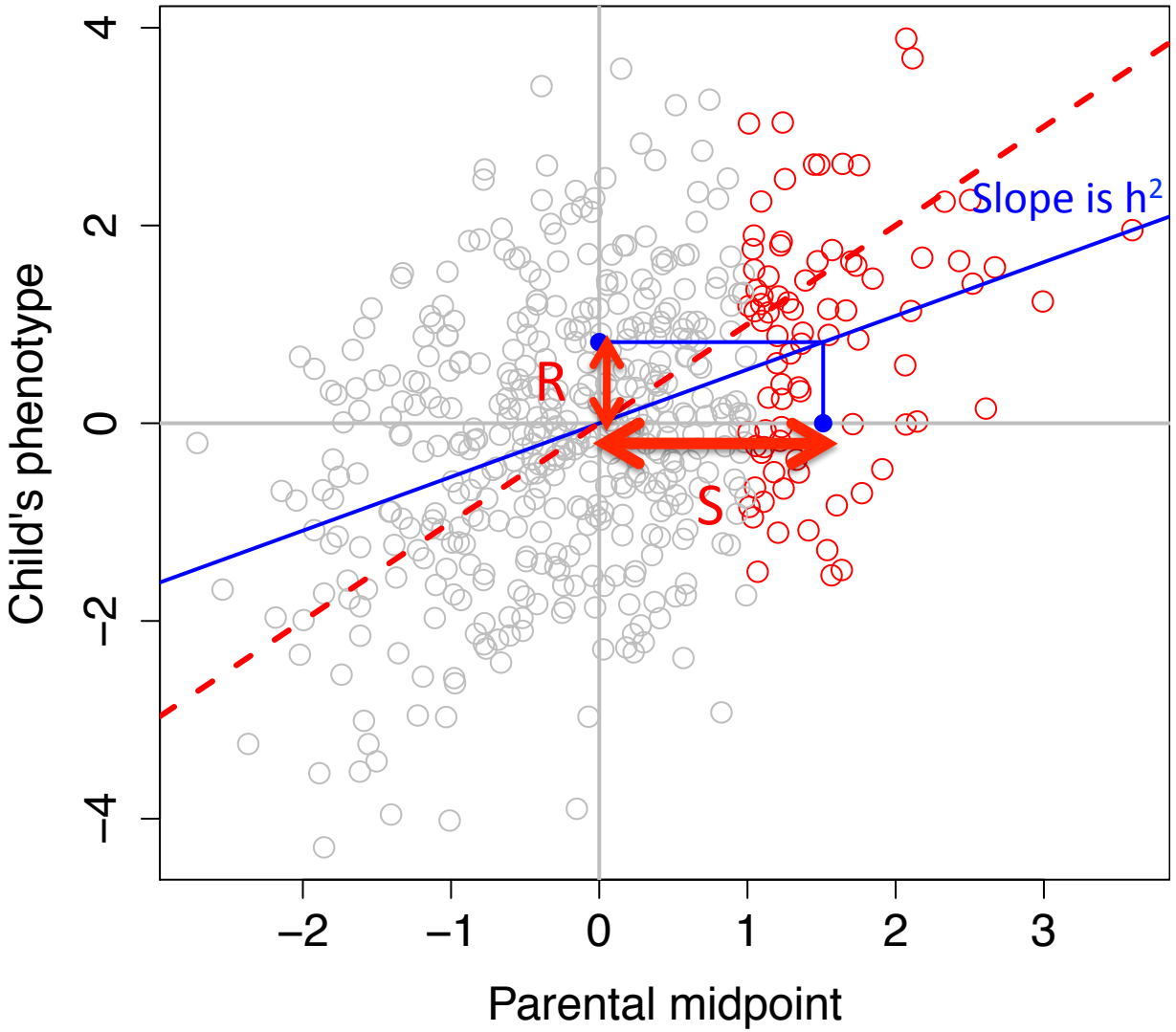
$$R = h^2 S$$

S – change in phenotypic mean in parental generation due to selection

R- Response: change in mean in offspring generation

h^2- Narrow sense heritability,

Rapid evolution
With strong selection pressures
Highly heritable traits.



The breeder's equation.

$$R = h^2 S$$

Mean flowering time before selection: 60 days

Selection due to drought in one generation

moved the mean flowering time to 53 days

S = -7 days

$h^2 = 0.46$

R = 0.46 x (-7)=-3.22 days.

Predicted change in next generation.

Mustard weed

Rapid evolution of flowering time by an annual plant in response to a climate fluctuation

Steven J. Franks*, Sheina Sim, and Arthur E. Weis

Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697

Edited by Barbara A. Schaal, Washington University, St. Louis, MO, and approved November 30, 2006 (received for review September 22, 2006)

Ongoing climate change has affected the ecological dynamics of populations remain unchanged (11). The second protocol in-

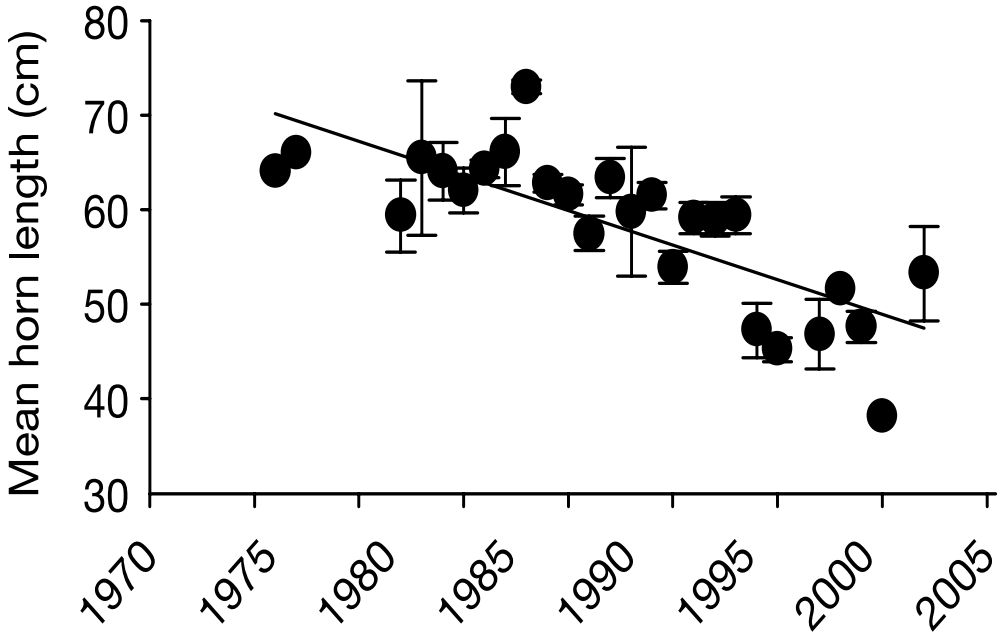
The breeders' equation can also be used to estimate heritability for a trait under selection

$$R = h^2 S$$

R=Change between successive generations = -6cm

S= Change within a generation = -8cm

What's h^2?



The breeder's equation.

- We can apply the breeder's equation over many generations:
- Change in mean over n discrete generations
- $R_n = n\, h^2\, S$

- If S is a constant each generation
- And h^2 remains constant. *

- *This may be a big if.