

Quantitative characters I: polygenes and environment

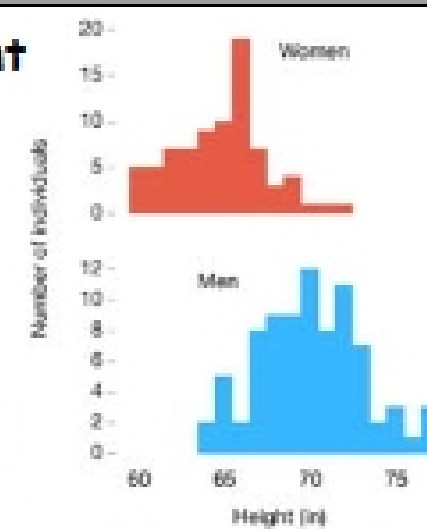
Most ecologically important quantitative traits (QTs) *vary*.

Distributions are often *unimodal* and approximately *normal*.

Offspring and parents are *correlated*.

What's the explanation?

Independent contributions by genotypes at *many loci*, and by *random environmental influences*.



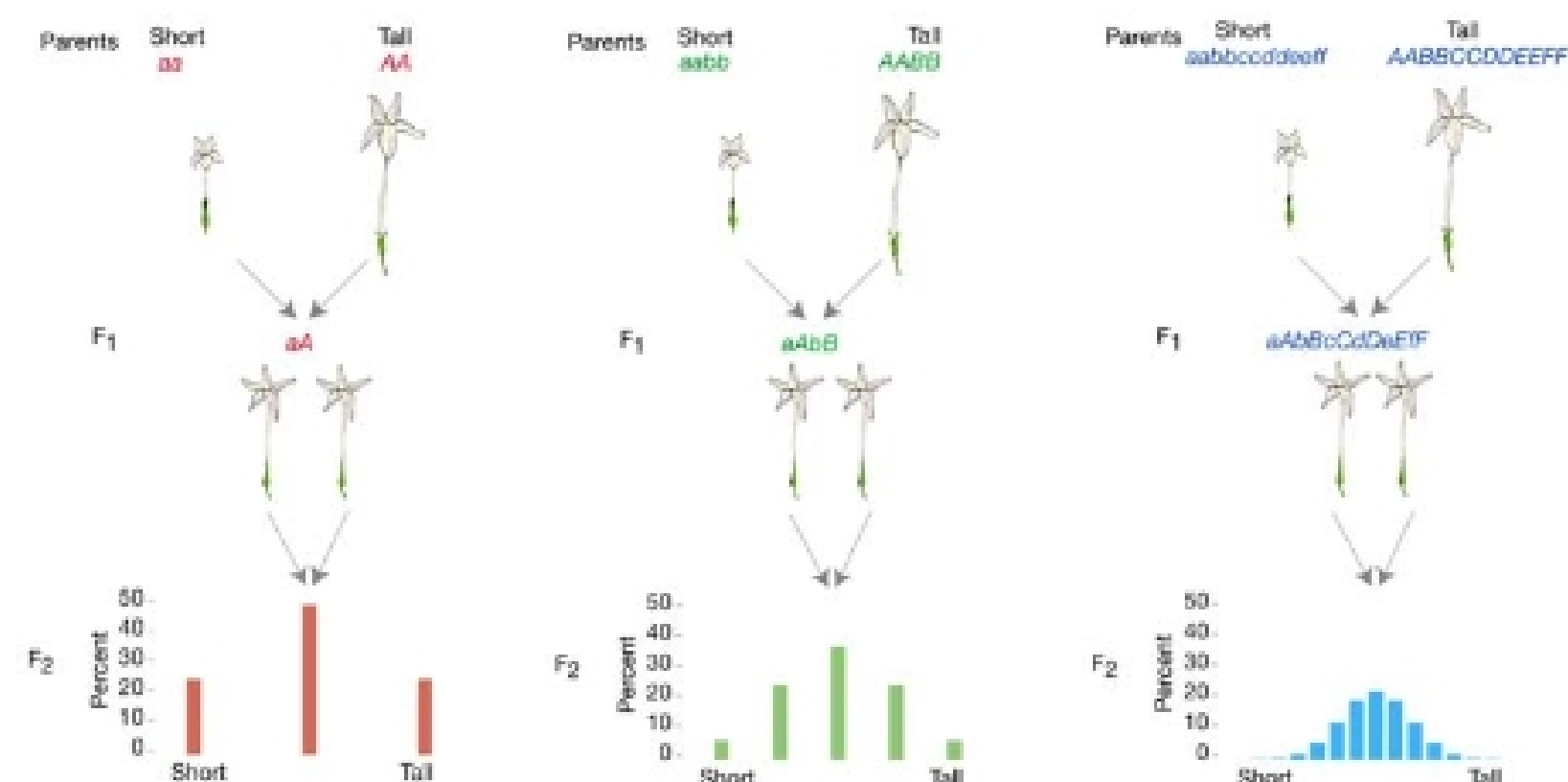
The simplest QT model: independent loci with "+" and "-" alleles

Assume each individual's trait value is the *sum* of its "+" alleles at all loci.

That is, a "+" allele at locus A has the *same* effect as a "+" at locus B.

Then with random mating and free recombination, we get *binomial* distributions.

As the *number of loci* increases, these distributions become *smooth* and *normal*.



Nice theory. Is it true? (Classical test: breeding experiments)

Edward East (1916) crossed pure breeding (inbred) lines of tobacco (*Nicotiana longiflora*) that differed in corolla height.

The F₁s were intermediate, but not significantly more variable than the parental lines.

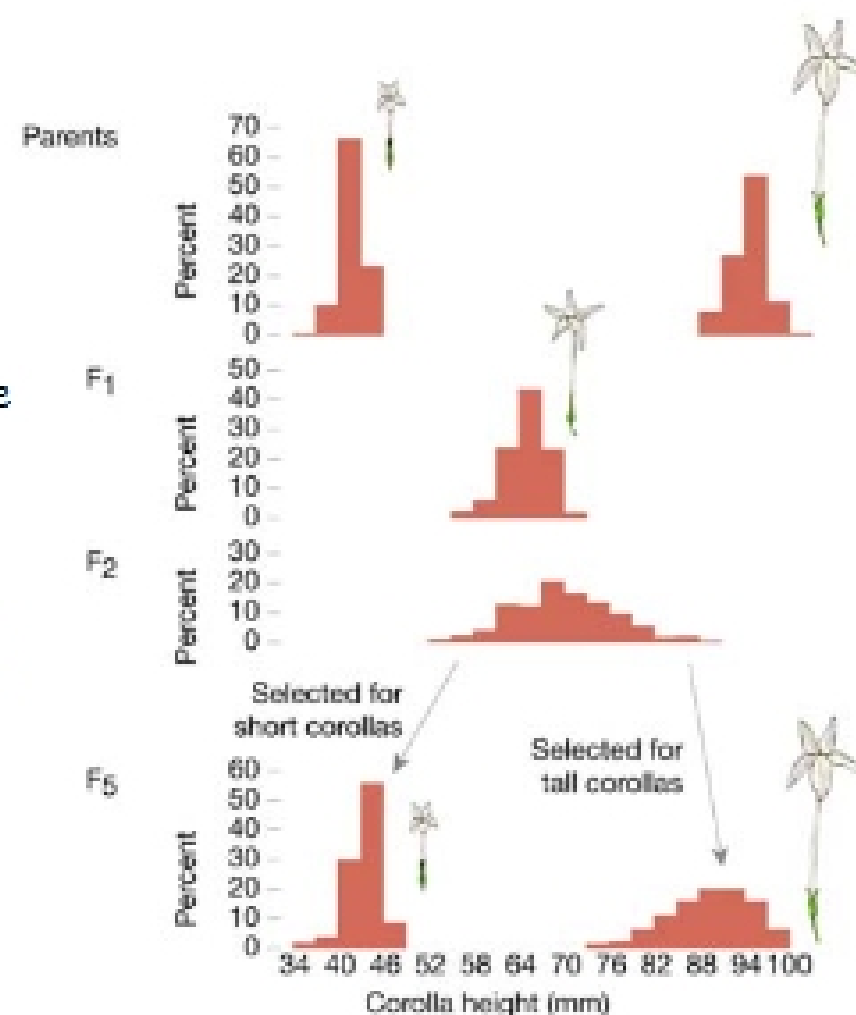
The F₂s were also intermediate, but more variable.

By breeding selectively from the smallest-flowered and largest-flowered F₂, F₃, and F₄ individuals, East was able to reconstitute lines nearly as different and uniform as his original parental lines.

Implications:

Many polymorphic loci contribute to corolla length in *N. longiflora*.

And there is *environmentally induced variation* even among the genetically identical parental plants.



Total phenotypic variance = genetic variance + environmental variance

What you *see* is what you get from two distinct sources that can be separated.

1. *Genetic variance* is the variance among phenotypes caused by *genotypic* differences among individuals (holding their *environments* constant).
2. *Environmental variance* is the variance among *phenotypes* caused by differences in the *experiences* of individuals (holding *genotypes* constant).

Example: Suppose the *average* trait values of AA, Aa and aa individuals are -1, 0, and +1 units, and $p = q = 0.5$.

Then the *genetic variance* (average squared deviation from the population mean) is 0.5.

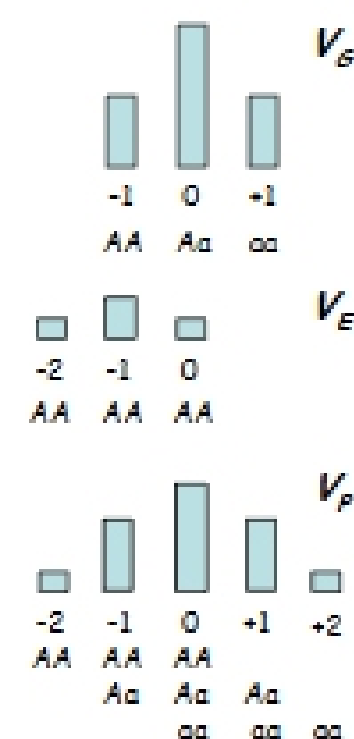
But suppose 25% of each genotype deviates one unit above or below its average trait value, because of the environment.

Then the *environmental variance* is also 0.5.

The resulting *phenotypic variance* is $0.5 + 0.5 = 1.0$.

In general, $V_p = V_G + V_E$.

This matters because a trait's *heritability* is the *fraction* of V_p that is *genetic* (actually, *additive genetic*, as we will see).



Quantitative characters II: components of the variance

The *variance* of a trait (x) is the average squared deviation of x from its mean:

$$V_p = (1/n) \sum (x - m_x)^2$$

This total phenotypic variance can be partitioned into components:

$$V_p = V_G + V_E \text{ (genetic and environmental)}$$

$$V_G = V_A + V_D \text{ (additive and dominance)}$$

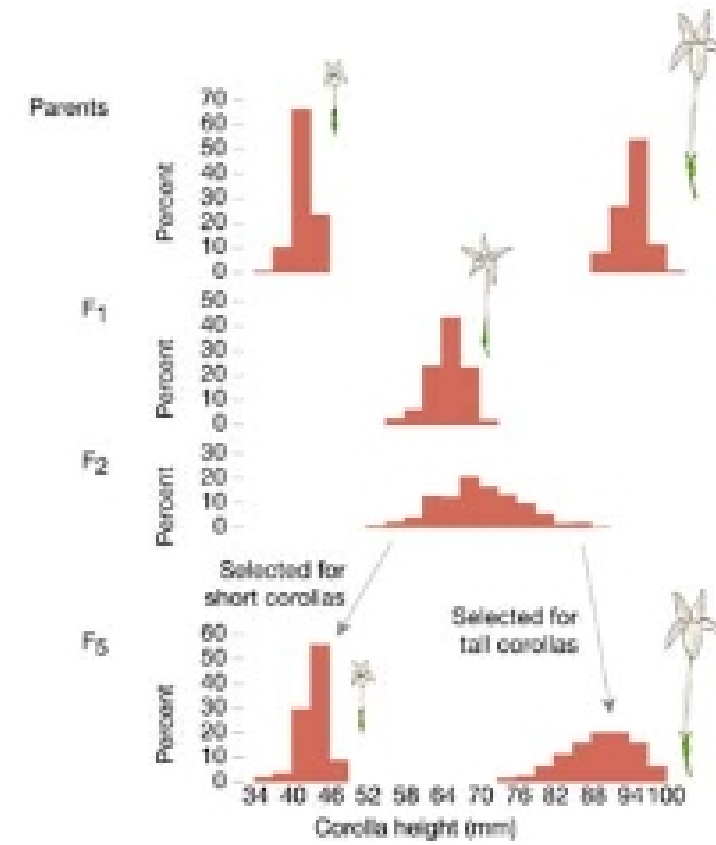
The broad-sense heritability is the fraction that's genetic:

$$H^2 = V_G / V_p$$

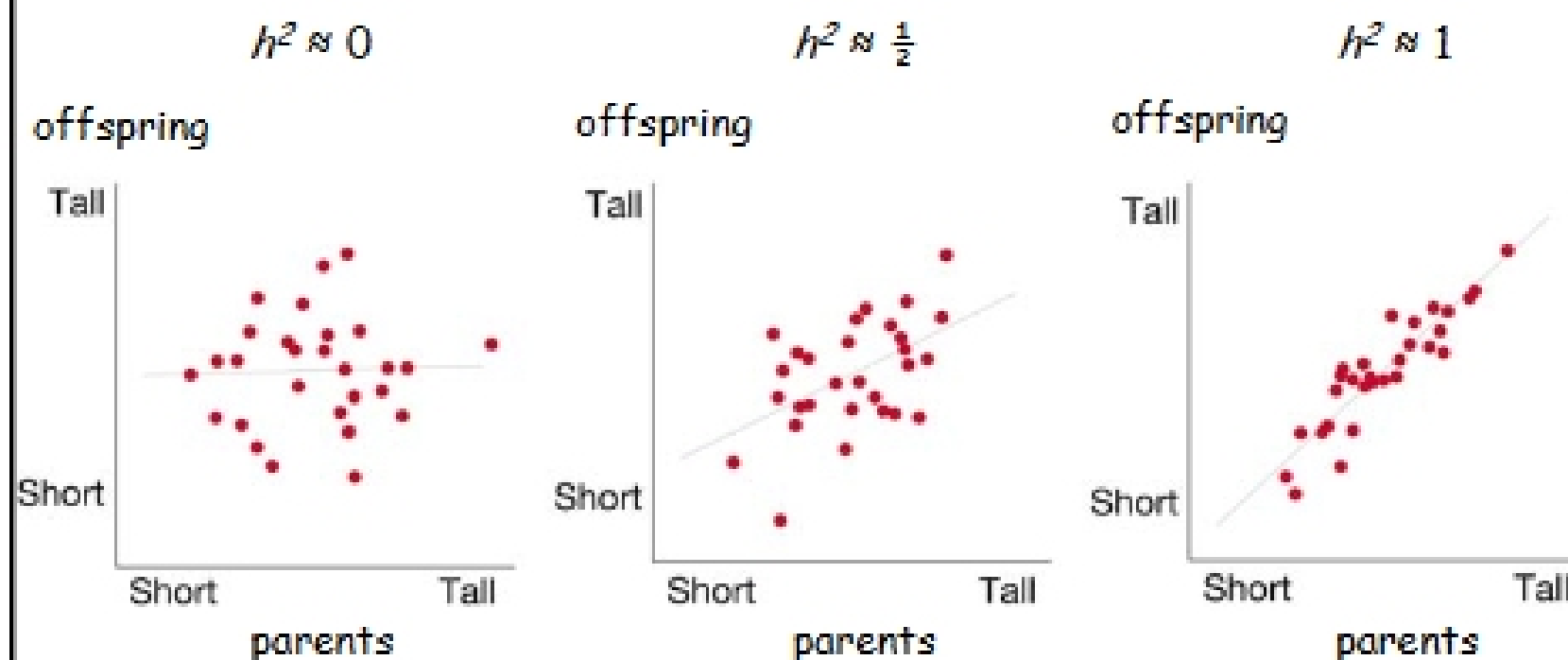
The narrow-sense heritability is the fraction that's *additive* genetic:

$$h^2 = V_A / V_p$$

h^2 determines (1) the *resemblance of offspring to their parents*, and (2) the *population's evolutionary response to selection*.



h^2 is the regression (slope) of offspring on parents



The higher the slope, the better offspring resemble their parents.

In other words, the higher the heritability, the better offspring trait values are *predicted* by parental trait values.