

Quantitative characters I: polygenes and environment

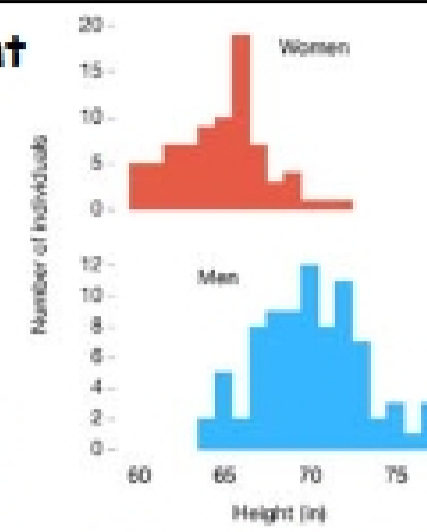
Most ecologically important quantitative traits (QTs) *vary*.

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*.



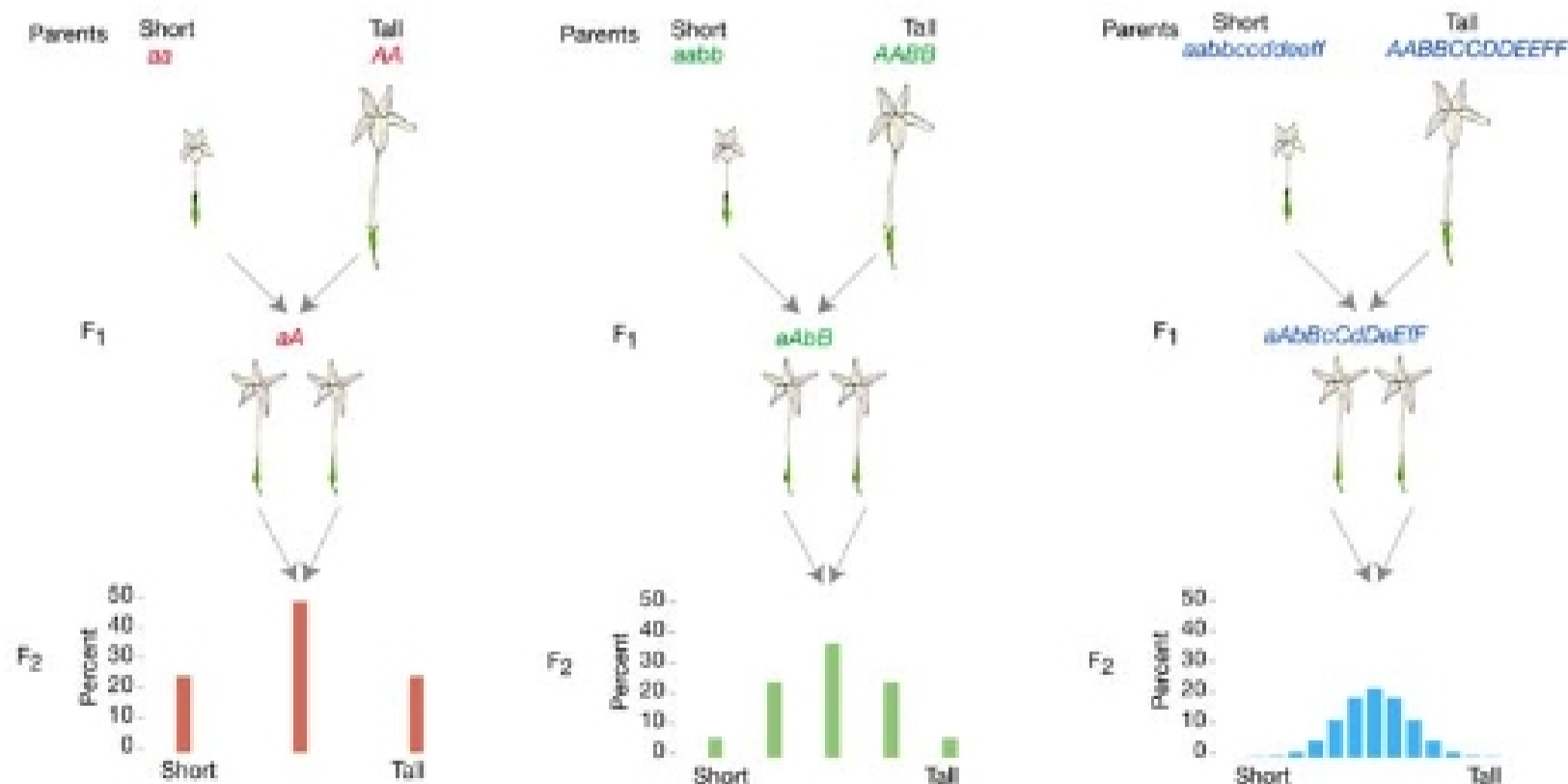
The simplest QT model: independent loci with "+" and "-" alleles

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.

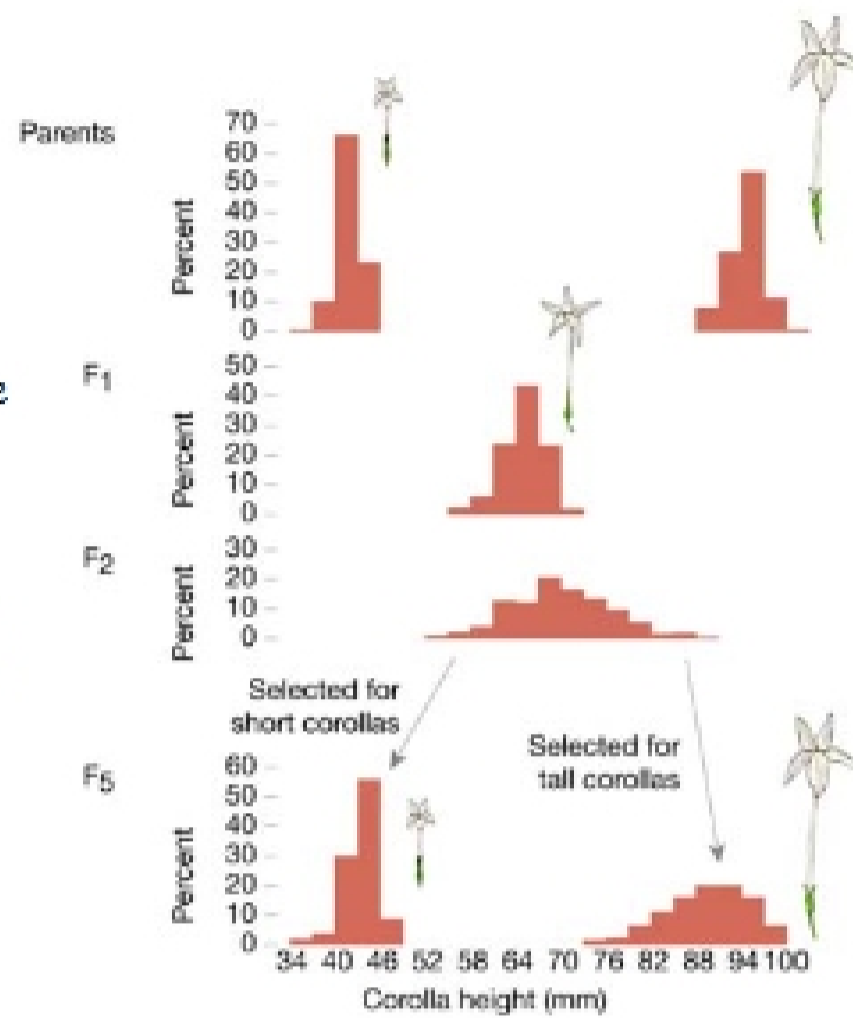
The F2s were also intermediate, but more variable.

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:

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

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

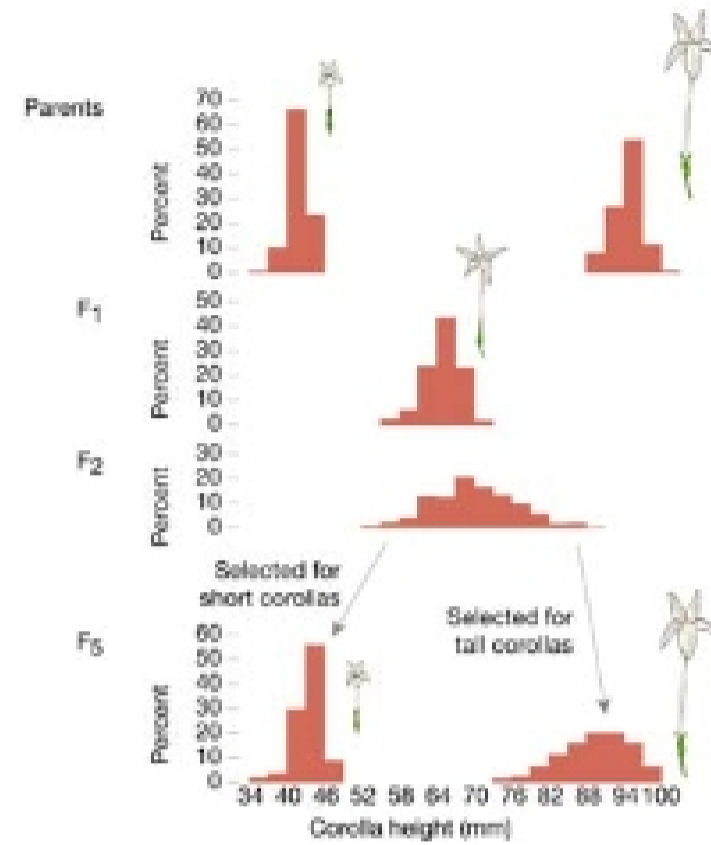
The broad-sense heritability is the fraction that's genetic:

$$H^2 = V_G / V_p$$

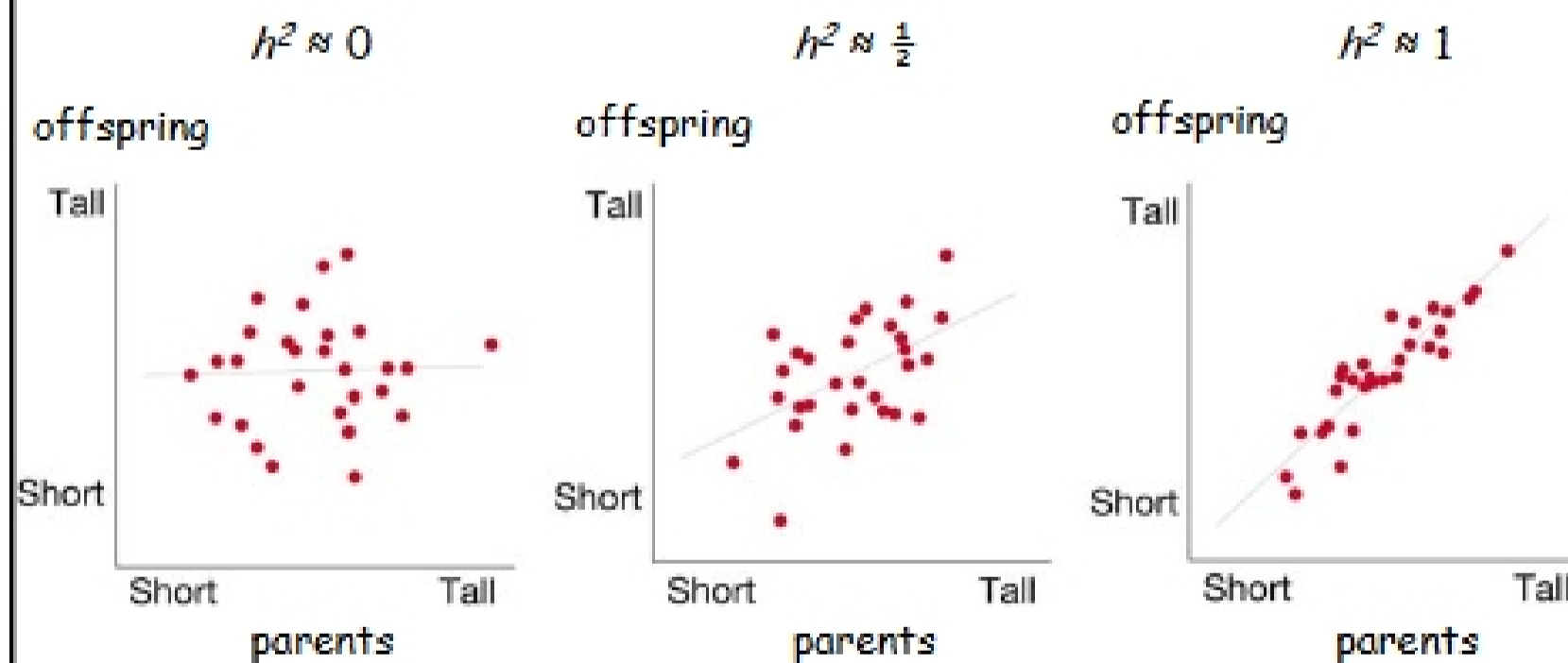
The narrow-sense heritability is the fraction that's *additive* genetic:

$$h^2 = V_A / V_p$$

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.