

Quantitative Genetics II: Estimating and using heritability

OUTLINE

Thus far, we have shown how heritability is derived and related to certain types of genetic variation.

In this lecture, we will look at how heritability is estimated and used in non-agricultural systems (including humans and other species).

We will also examine how quantitative genetics approaches allow us to determine the number and magnitude of effect of genetic loci affecting quantitative traits (i.e., via quantitative trait locus (QTL) analysis).

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Sample Heritabilities

Humans	h^2
Stature	0.65
Serum immunoglobulin level	0.45
Pig	
Back fat thickness	0.60
Daily gain	0.30
Poultry	
Egg mass	0.55
Sexual maturity	0.45

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Sample Heritabilities

Human Birth Weight		
Source of Variation	% of variation	
<u>Genetic</u>	18	$H =$
Additive	15	$h^2 =$
Non-additive	1	
Gender	2	
<u>Environmental</u>	82	
Maternal genotype	20	Most of the variation is environmental
Maternal environment	24	
Age of mother	1	
Parity (birth order)	7	
Intangible	30	

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Approaches to Estimating Heritability (h^2)

1. Analysis of related individuals
 - parent-offspring regression
 - analysis of covariance among relatives
2. Measuring a population's response to selection, across generations.

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Estimating Heritability (h^2): Analysis of related individuals

The covariance between the phenotype of a parent and its offspring equals

$$\text{Cov}(O,P) = 1/2 V_A$$

More importantly, the **regression** of the phenotypic value of offspring on that of their parents equals

$$\text{Cov}(O,P)/V_P = 1/2 V_A / V_P = 1/2 h^2$$

$$h^2 = 2 [\text{Regression}(\text{offspring,parent})]$$

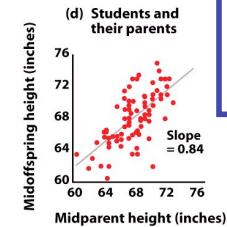
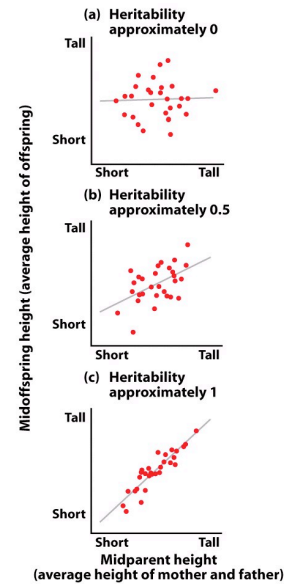
If both parents are measured:

$$\text{Regression}(\text{Offspring, mid-parent})/V_P = V_A / V_P$$

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Approaches to Estimating Heritability (h^2): Parent-offspring regression



Note: midparent value = average of the phenotypic value of the parents
Midoffspring value: mean phenotypic value of the offspring

Figure 9-13 Evolutionary Analysis, 4/e
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Estimating Heritability (h^2): Analysis of related individuals

Note that the expected correlation between many other types of relatives has also been derived.

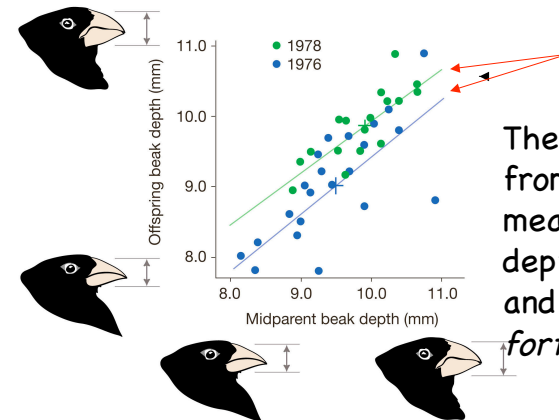
For example, the expected correlation between full siblings is:

$$\text{Cov}(\text{fullsib,fullsib}) = \frac{1/2 V_A + 1/4 V_D}{V_P}$$

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h^2 from analysis of relatives: Darwin's finches



$$h^2 = 0.65$$

These data come from capturing and measuring beak depth in parents and offspring of *G. fortis* in the field

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Estimating Heritability (h^2): Using the response to selection

Recall the fundamental formula of quantitative genetics (the breeder's equation):

$$R = h^2 S$$

Given knowledge of the selection differential, and the response to selection, it is possible to estimate the heritability of a trait.

Selection differential (S): The phenotypic mean of parents chosen to breed minus the population mean.

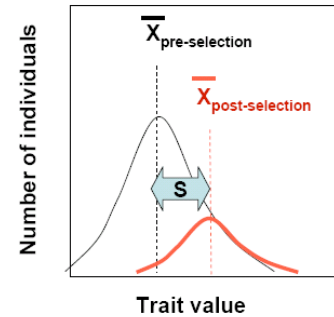
Response to selection (R): The phenotypic mean of offspring of these parents minus the population mean.]

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Estimating heritability using the response to selection

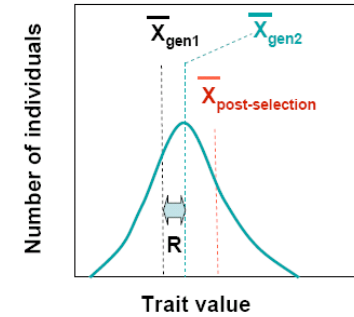
Selection within generation 1



S = selection differential

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Response in generation 2

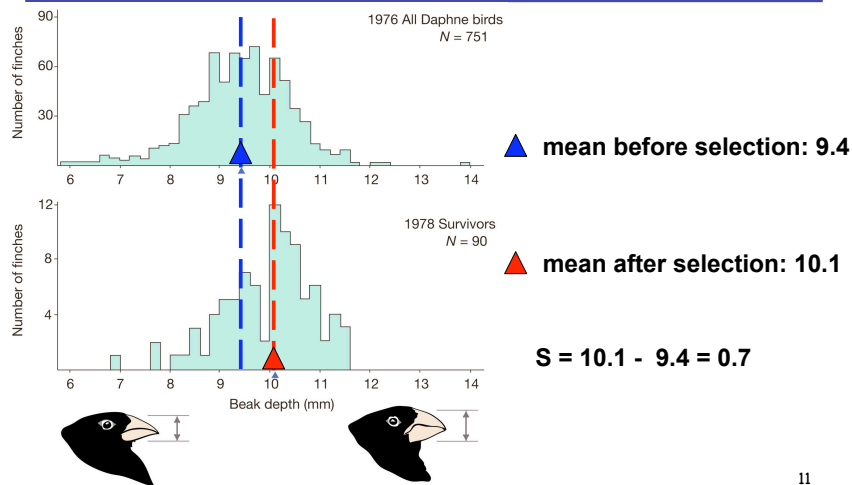


S = selection differential

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Breeder's equation: $R = h^2 S$

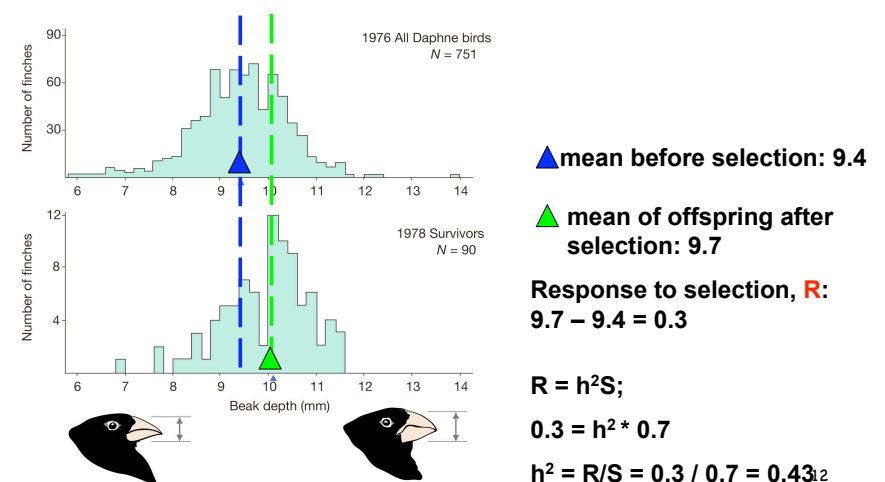
h^2 from the response to selection: Darwin's finches



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h^2 from the response to selection: Darwin's finches II



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Predicting the response to selection: Abdominal bristle number in *Drosophila*

(Clayton, Morris and Robertson, 1957)

The estimate of narrow-sense heritability of abdominal bristle number in *Drosophila* was $h^2 = 0.52$

Parental mean: **35.3 bristles**

Among those allowed to breed (those selected), the mean number of bristles was **40.6**

The selection differential was $S = 40.6 - 35.3 = 5.3$

Predicted response to selection: $R = h^2 S$
 $= 0.52 \times 5.3 = 2.8$

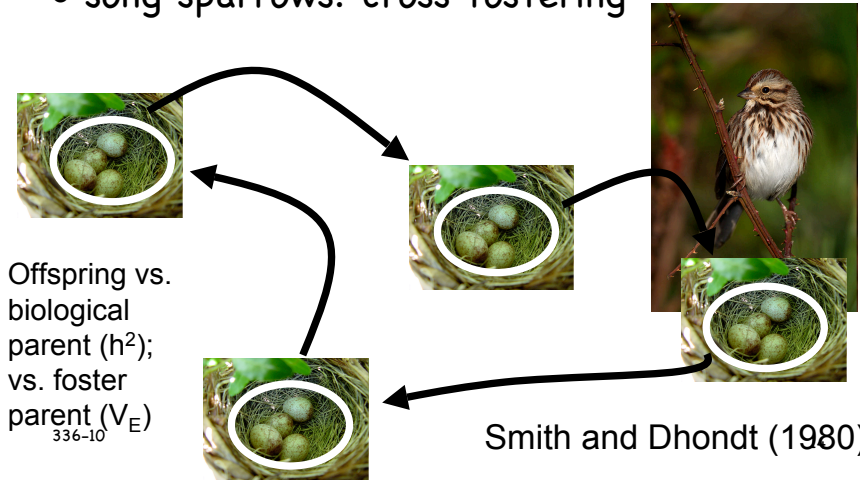
Actual mean in next generation: **37.9 bristles**

Actual response to selection: $R = 37.9 - 35.3 = 2.6$

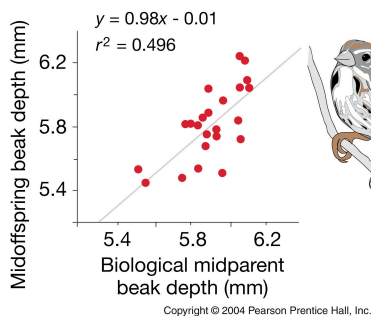
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Controlling for environmental effects on beak size

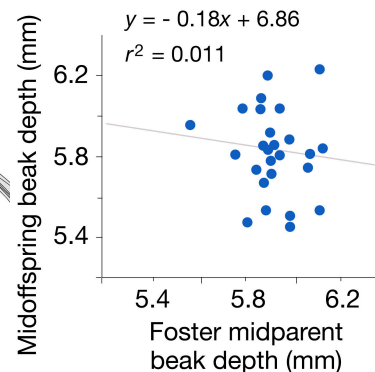
- song sparrows: cross fostering



Cross fostering in song sparrows



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Heritability and the long term response to selection

Heritability is not a constant attribute of a population.

Over time, the heritability of a trait will change as:

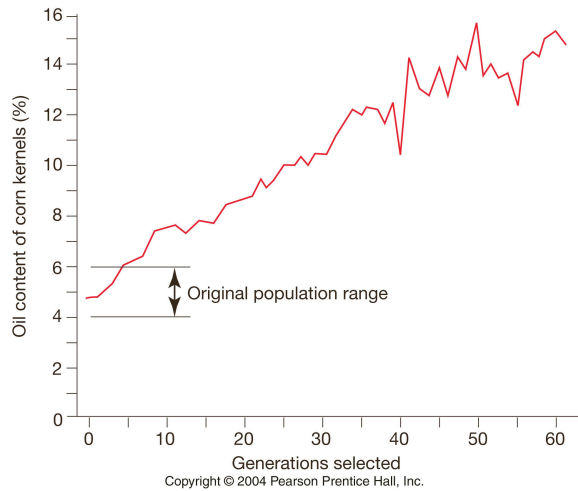
- allele frequencies change
- disequilibria change
- variance is reduced

$$R = h^2 S$$

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Heritability and the long term response to selection



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Heritability and the long term response to selection

Factors affecting the total response before a plateau is reached:

- (1) The total response will be less when few individuals are chosen to breed, since less genetic variation is preserved among these individuals.
- (2) The total response will be less when selection occurs rapidly because of genetic hitchhiking (some alleles that act in the opposite direction may get dragged along and fix, especially when S is high).
- (3) The total response will be less if few loci contribute to the trait, since those few loci will go to fixation and since the array of possible combinations of alleles is much more limited.

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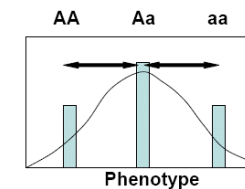
Detecting loci affecting quantitative traits (QTL)



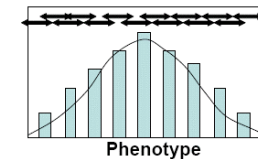
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QTLs and genes of major effects



H. Allen Orr, Jerry Coyne, others



Ronald Fisher + most evolutionary geneticists of the Modern Synthesis

How important are genes of major effect in adaptation?

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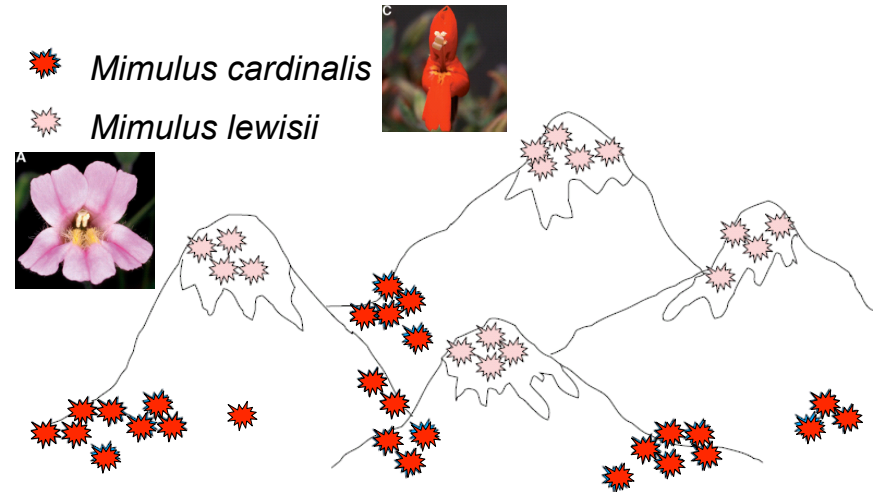
QTL analysis: Quantitative Trait Loci – where are the genes contributing to quantitative traits?

- Approach
 - two lineages consistently differing for trait of interest (preferably inbred for homozygosity)
 - Identify genetic markers specific to each lineage (eg microsatellite markers)
 - make crosses to form F1
 - generate F2s and measure trait of interest
 - test for association between markers and trait
 - Estimate the effect on the phenotype of each marker

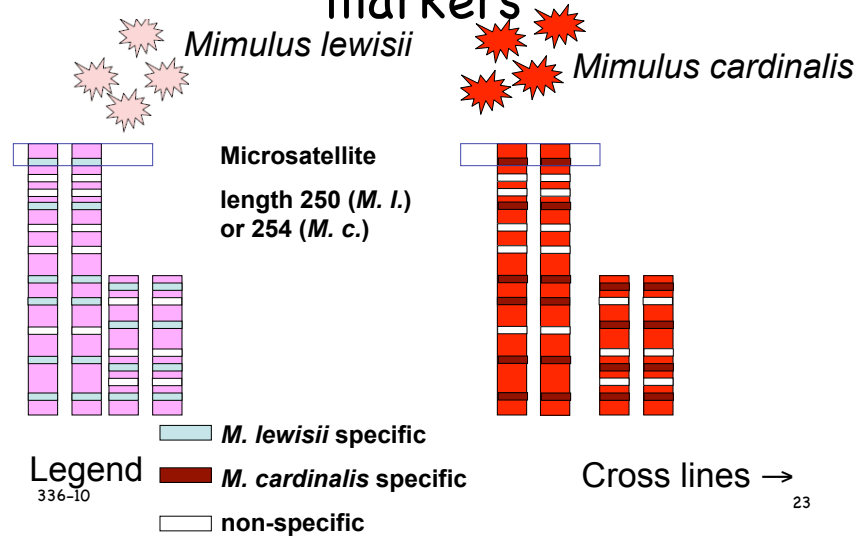
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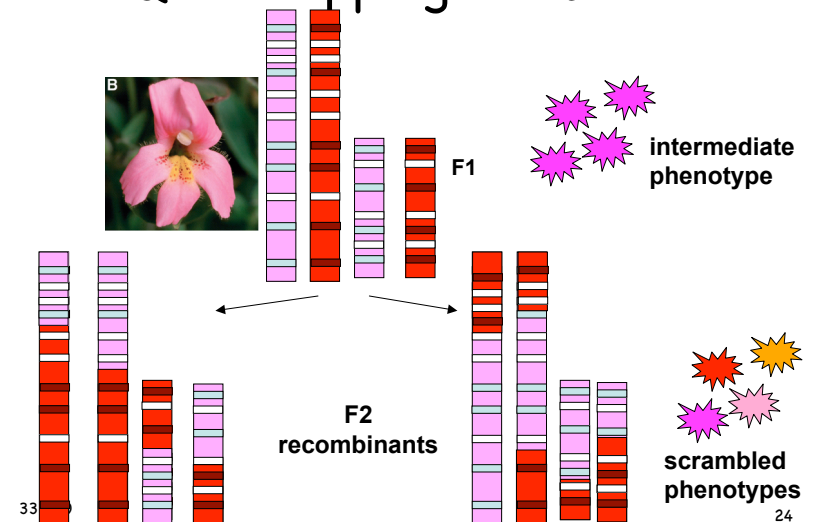
Example: *Mimulus cardinalis* and *Mimulus lewisii*



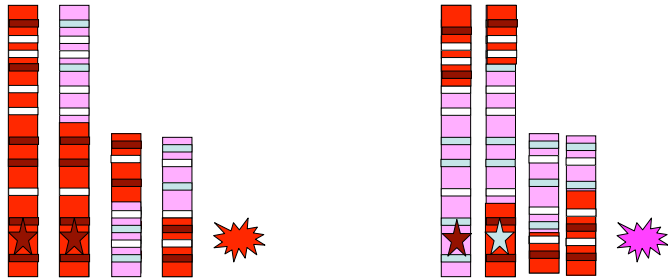
Locate lineage-specific markers



QTL Mapping: crosses



QTL analysis: trait associations



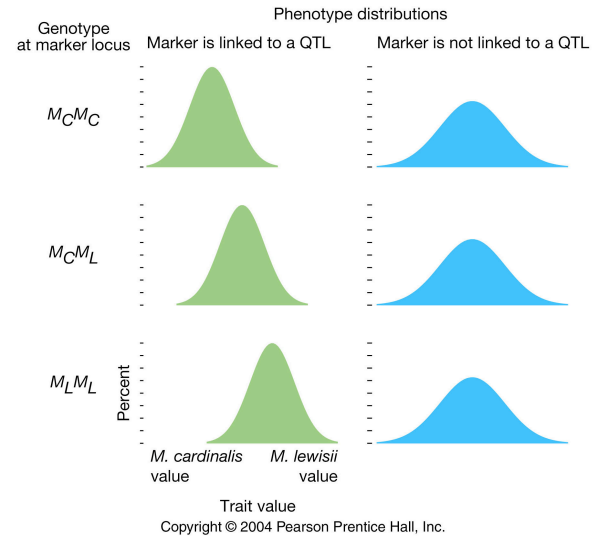
Homozygotes at marker 2 are closer to one parent

Heterozygotes at marker 2 are intermediate in trait values

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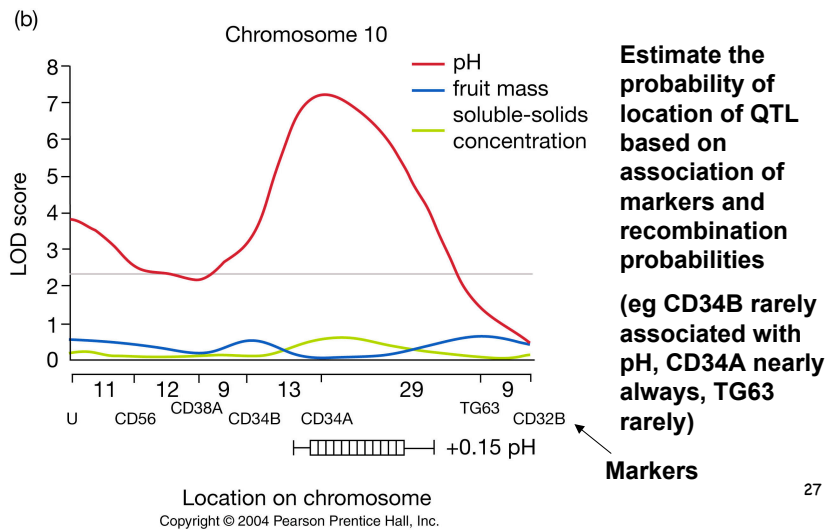
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Trait analysis



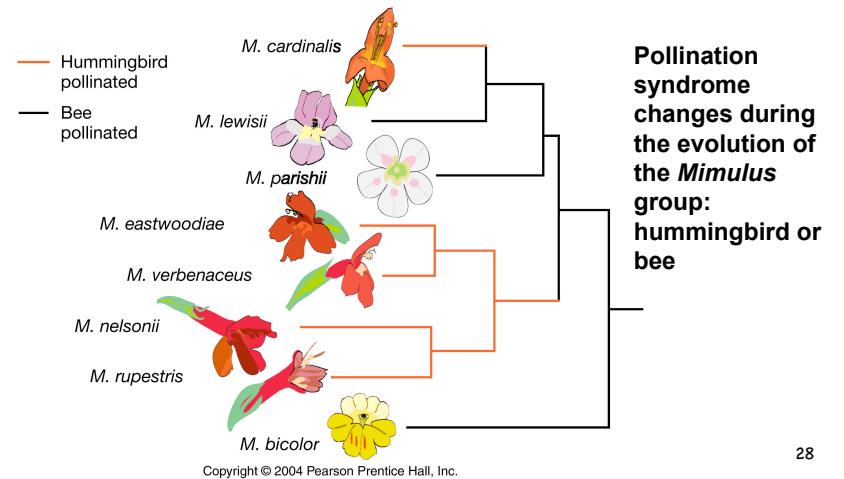
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QTL probabilities



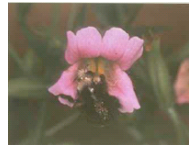
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Example study: basis of floral traits in two *Mimulus* species (Schemske and Bradshaw, PNAS 1999)



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F2 plants showed variation for most floral traits



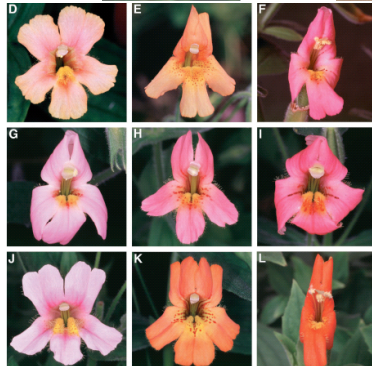
M. lewisii



F1



M. cardinalis



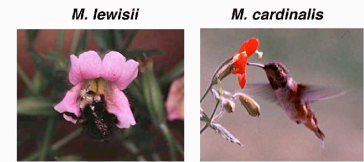
F2 plants

Most traits had multiple QTL but one explaining > 25% of variation

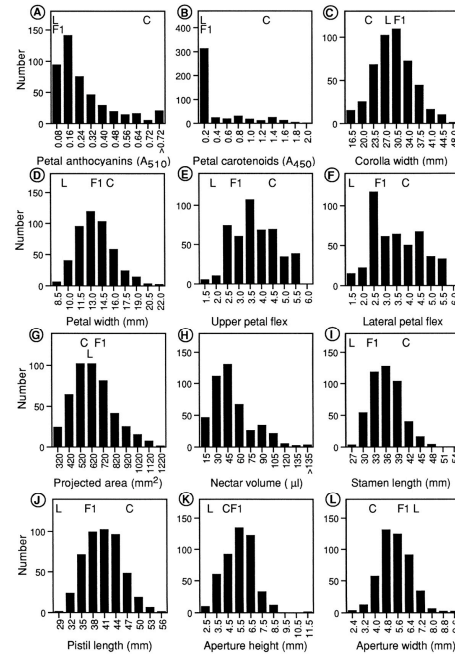
→ Few genes of large effect important in this case

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Quantitative Trait Inheritance in monkeyflowers

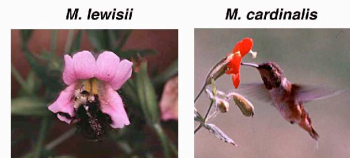


These panels show traits measured in a set of F2 plants from a cross between the two plants shown above. Most traits show continuous variation.



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Quantitative Trait Inheritance in monkeyflowers



For example, for petal anthocyanin (a measure of how much yellow is present in the flowers), the phenotypes seen in the F₂ are skewed towards one side, suggesting that alleles for low anthocyanin tend to be dominant.

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Recap: quantitative genetics

- Are traits heritable?
 - Usually find heritability
 - However, environmental effects can be large
- Are genes controlling quantitative traits of large effect or small effect?
 - Some important genes for adaptation of large effect (will revisit when we talk about adaptation and speciation).
 - Overall pattern still unclear.

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