QTL

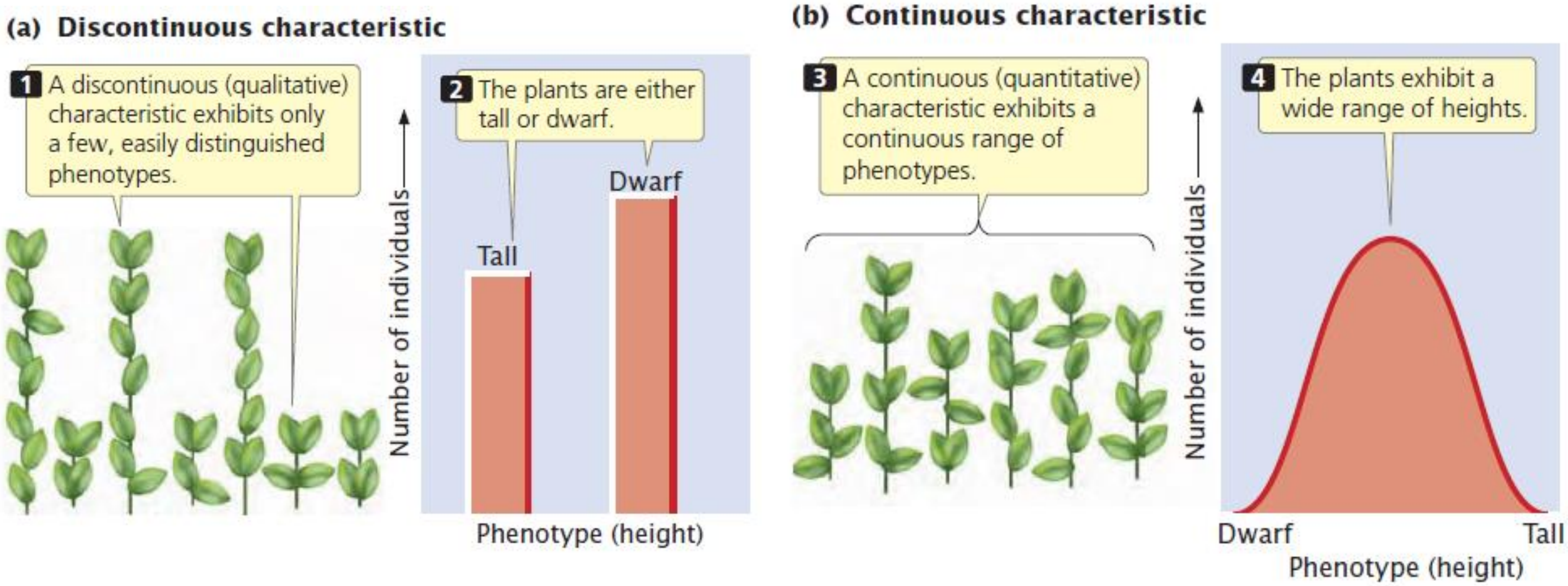
BIOS 0802

2017

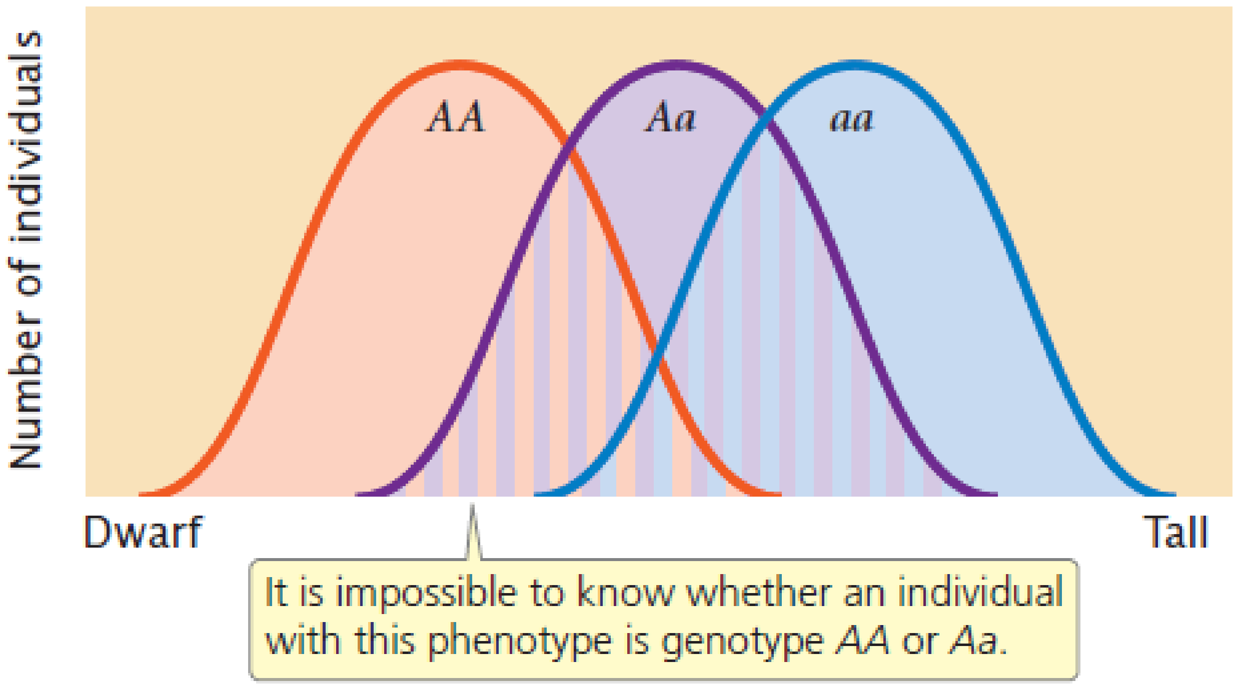
QTL

In 2008, geneticists used a combination of quantitative genetics and molecular techniques to identify a key gene that controls oil content in corn. First, they conducted crosses between high-oil corn plants and low-oil plants to identify chromosomal regions that play an important role in determining oil production. Chromosome regions containing genes that influence a quantitative trait are termed **quantitative trait loci** (QTLs).

Quantitative genetics



Genotype and phenotype



Same example

Table 24.1 Hypothetical example of plant height determined by pairs of alleles at each of three loci

Plant Genotype	Doses of Hormone	Height (cm)
$A^-A^-\ B^-B^-\ C^-C^-$	0	10
$A^+A^-\ B^-B^-\ C^-C^-$	1	11
$A^-A^-\ B^+B^-\ C^-C^-$		
$A^-A^-\ B^-B^-\ C^-C^+$		
$A^+A^+\ B^-B^-\ C^-C^-$	2	12
$A^-A^-\ B^+B^+\ C^-C^-$		
$A^-A^-\ B^-B^-\ C^+C^+$		
$A^+A^-\ B^+B^-\ C^-C^-$		
$A^+A^-\ B^-B^-\ C^+C^-$		
$A^-A^-\ B^+B^-\ C^+C^-$		
$A^+A^+\ B^+B^-\ C^-C^-$	3	13
$A^+A^+\ B^-B^-\ C^+C^-$		
$A^+A^-\ B^+B^+\ C^-C^-$		
$A^-A^-\ B^+B^+\ C^+C^-$		
$A^+A^-\ B^-B^-\ C^+C^+$		
$A^-A^-\ B^+B^-\ C^+C^+$		
$A^+A^-\ B^+B^-\ C^+C^-$		
$A^+A^+\ B^+B^+\ C^-C^-$	4	14
$A^+A^+\ B^+B^-\ C^+C^-$		
$A^+A^-\ B^+B^+\ C^+C^-$		
$A^-A^-\ B^+B^+\ C^+C^+$		
$A^+A^+\ B^-B^-\ C^+C^+$		
$A^+A^-\ B^+B^-\ C^+C^+$		
$A^+A^+\ B^+B^+\ C^+C^-$	5	15
$A^+A^-\ B^+B^+\ C^+C^+$		
$A^+A^+\ B^+B^-\ C^+C^+$		
$A^+A^+\ B^+B^+\ C^+C^+$	6	16

Types of quantitative characterestics

- **Meristic characteristics**, for instance, are measured in whole numbers. An example is litter size: a female mouse may have 4, 5, or 6 pups but not 4.13 pups.
- **Threshold characteristic**, which is simply present or absent. For example, the presence of some diseases can be considered a threshold characteristic. Although threshold characteristics exhibit only two phenotypes, they are considered quantitative because they, too, are determined by multiple genetic and environmental factors.

Nilsson-Ehle's cross (1908-11)

P Plants with white kernels × Plants with purple kernels

↓

F_1 Plants with red kernels

↓

F_2

$^1/_{16}$ plants with purple kernels
$^4/_{16}$ plants with dark-red kernels
$^6/_{16}$ plants with red kernels
$^4/_{16}$ plants with light-red kernels
$^1/_{16}$ plants with white kernels

The logic

Genotype	Doses of pigment	Phenotype
$A^+A^+\ B^+B^+$	4	Purple
$A^+A^+\ B^+B^-$ $A^+A^-\ B^+B^+$	3	Dark red
$A^+A^+\ B^-B^-$ $A^-A^-\ B^+B^+$ $A^+A^-\ B^+B^-$	2	Red
$A^+A^-\ B^-B^-$ $A^-A^-\ B^+B^-$	1	Light red
$A^-A^-\ B^-B^-$	0	White

The math

- Assume we are crossing in the first locus A^+A^- X A^+A^-
  - Probability of getting A^+A^+ is ¼ ; A^+A^- is ½ ; A^-A^- is ¼ [¼ + ½ + ¼ = 1]
- Using the same logic
  - Probability of getting B^+B^+ is ¼ ; B^+B^- is ½ ; B^-B^- is ¼ [¼ + ½ + ¼ = 1]
- Therefore the probability of having $A^+A^+B^+B^+$ is ¼ x ¼ = 1/16
- So if we to look for red kernel then the genotypes would be
  - $A^+A^+ B^-B^-$ 1/16
  - $A^-A^- B^+B^+$ 1/16
  - $A^+A^- B^+B^-$ ¼
- So, the total probability of finding red is 1/16 + 1/16 + ¼ = 6/16

Nilsson-Ehle's cross (1908-11)

P: Plants with white kernels × Plants with purple kernels

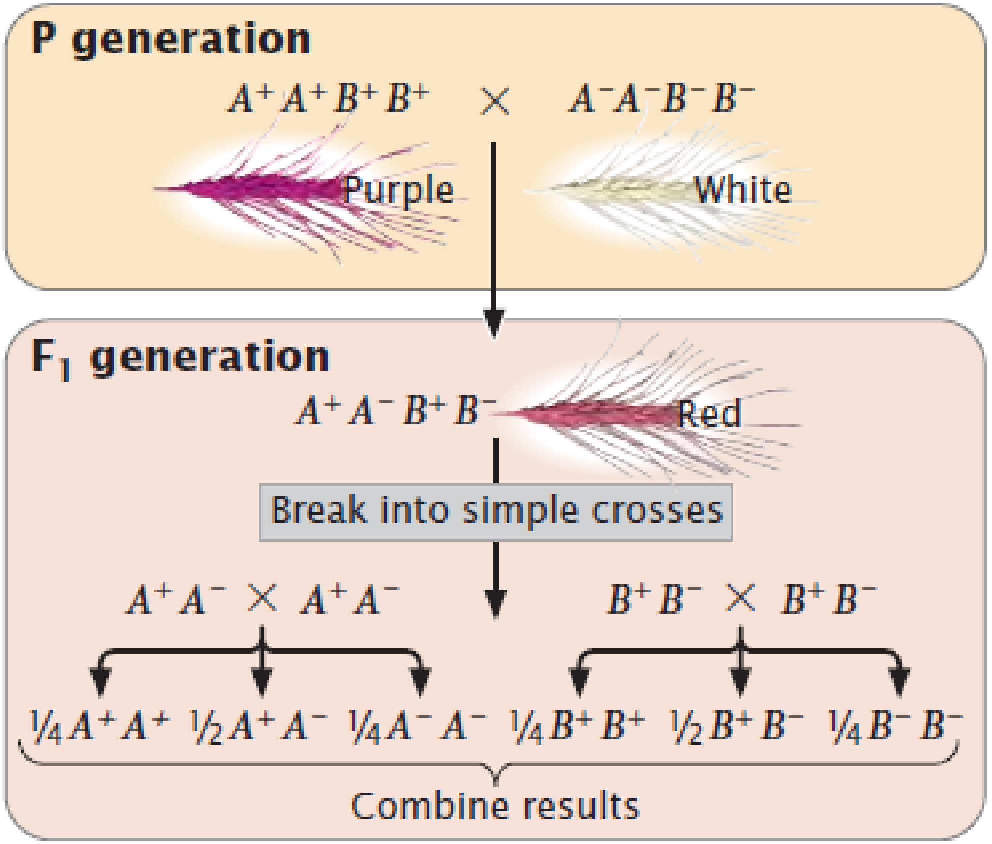
↓

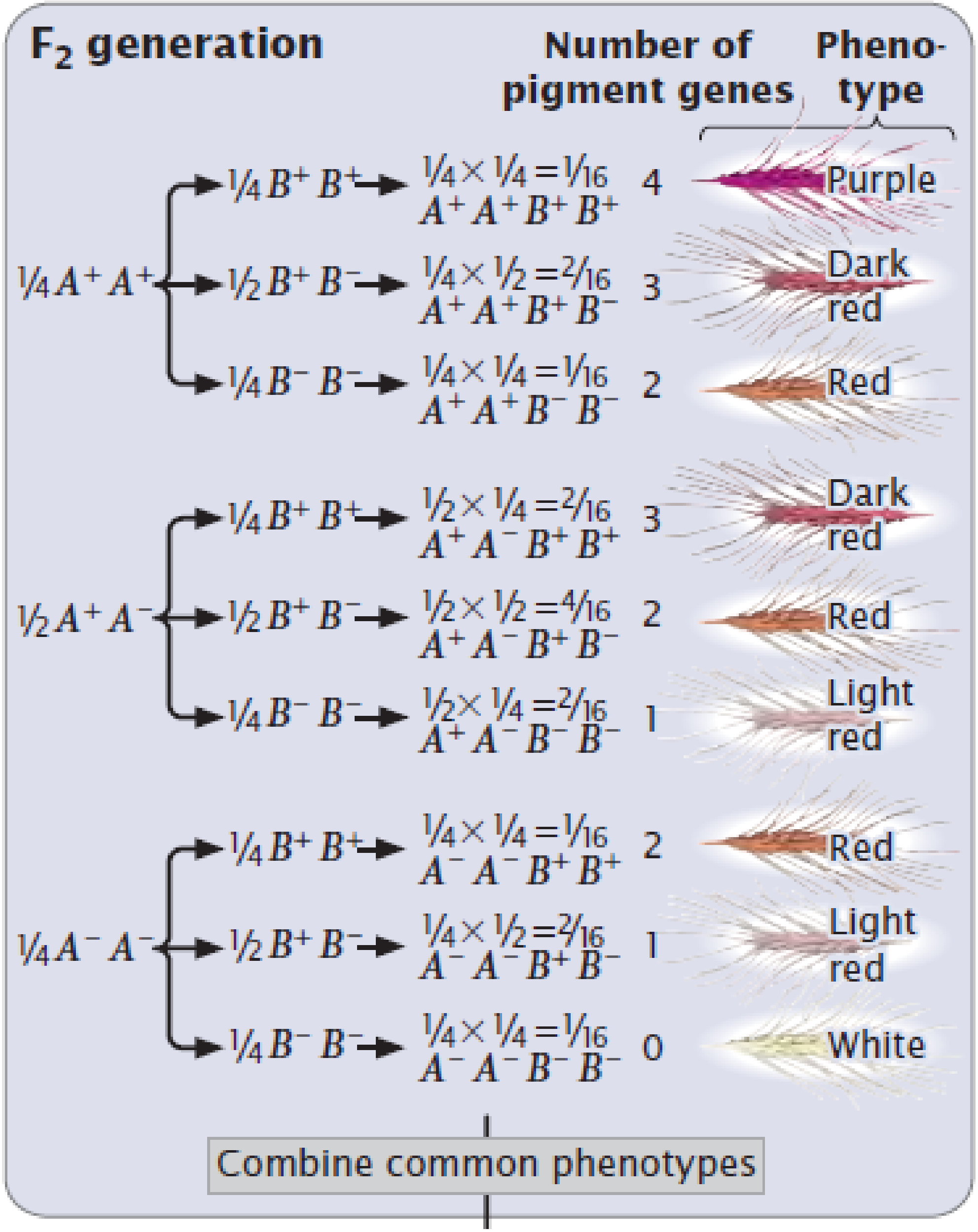
F_1: Plants with red kernels

↓

F_2:
- $^{1}/_{16}$ plants with purple kernels
- $^{4}/_{16}$ plants with dark-red kernels
- $^{6}/_{16}$ plants with red kernels
- $^{4}/_{16}$ plants with light-red kernels
- $^{1}/_{16}$ plants with white kernels

Visually

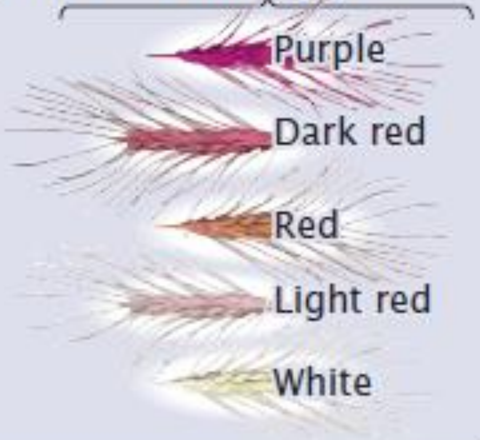

P generation
A+A+B+B+ × A−A−B−B−
Purple
White
F1 generation
A+A−B+B−
Red
Break into simple crosses
A+A− × A+A−
B+B− × B+B−
1/4 A+A+ 1/2 A+A− 1/4 A−A− 1/4 B+B+ 1/2 B+B− 1/4 B−B−
Combine results


F2 generation
Number of pigment genes
Pheno-type
1/4 A+A+
1/4 B+B+ 1/4 × 1/4 = 1/16 A+A+B+B+ 4 Purple
1/2 B+B− 1/4 × 1/2 = 2/16 A+A+B+B− 3 Dark red
1/4 B−B− 1/4 × 1/4 = 1/16 A+A+B−B− 2 Red
1/2 A+A−
1/4 B+B+ 1/2 × 1/4 = 2/16 A+A−B+B+ 3 Dark red
1/2 B+B− 1/2 × 1/2 = 4/16 A+A−B+B− 2 Red
1/4 B−B− 1/2 × 1/4 = 2/16 A+A−B−B− 1 Light red
1/4 A−A−
1/4 B+B+ 1/4 × 1/4 = 1/16 A−A−B+B+ 2 Red
1/2 B+B− 1/4 × 1/2 = 2/16 A−A−B+B− 1 Light red
1/4 B−B− 1/4 × 1/4 = 1/16 A−A−B−B− 0 White
Combine common phenotypes

Sum up

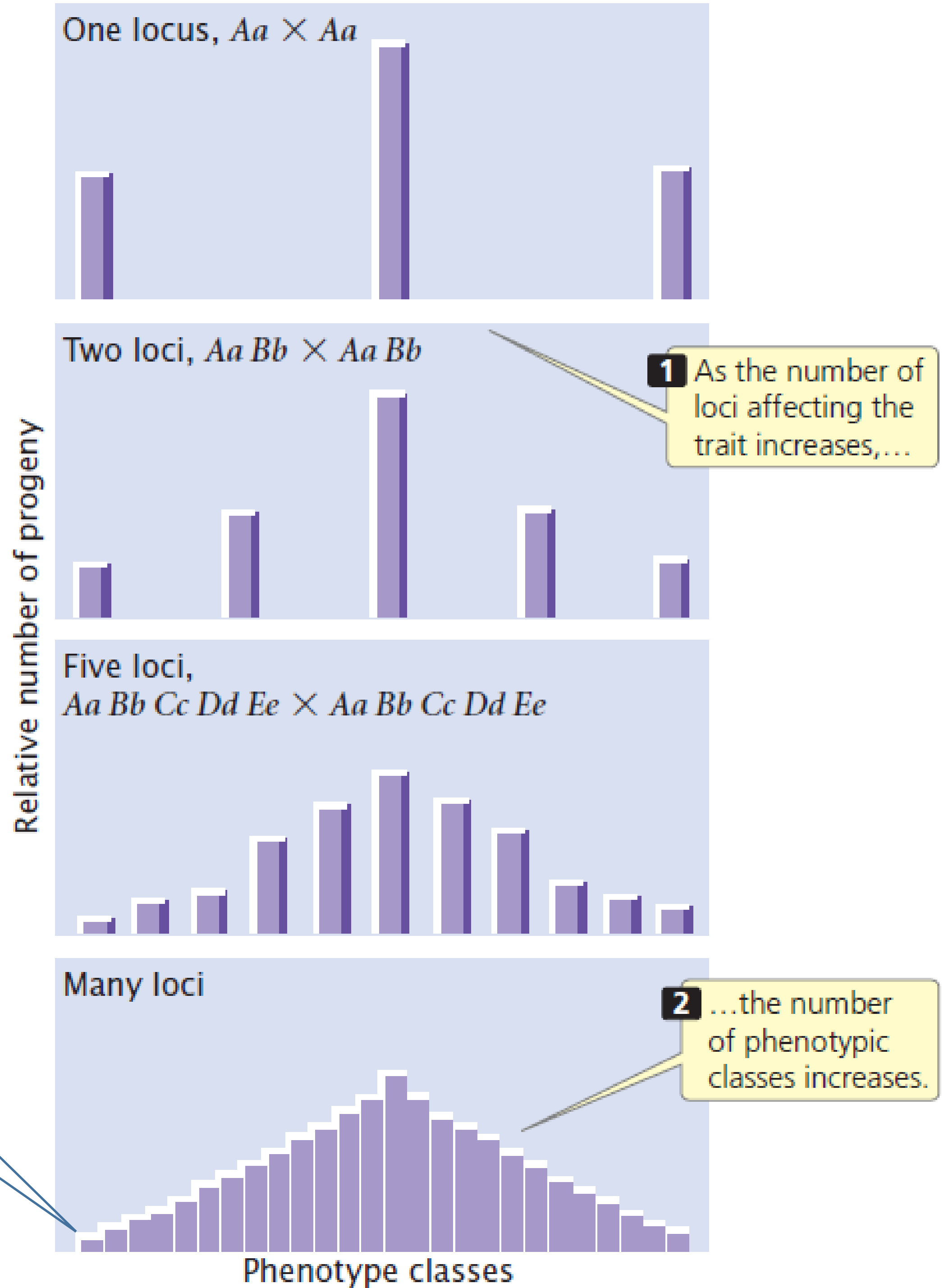
F_2 ratio

Frequency	Number of pigment genes	Phenotype
1/16	4	Purple
4/16	3	Dark red
6/16	2	Red
4/16	1	Light red
1/16	0	White

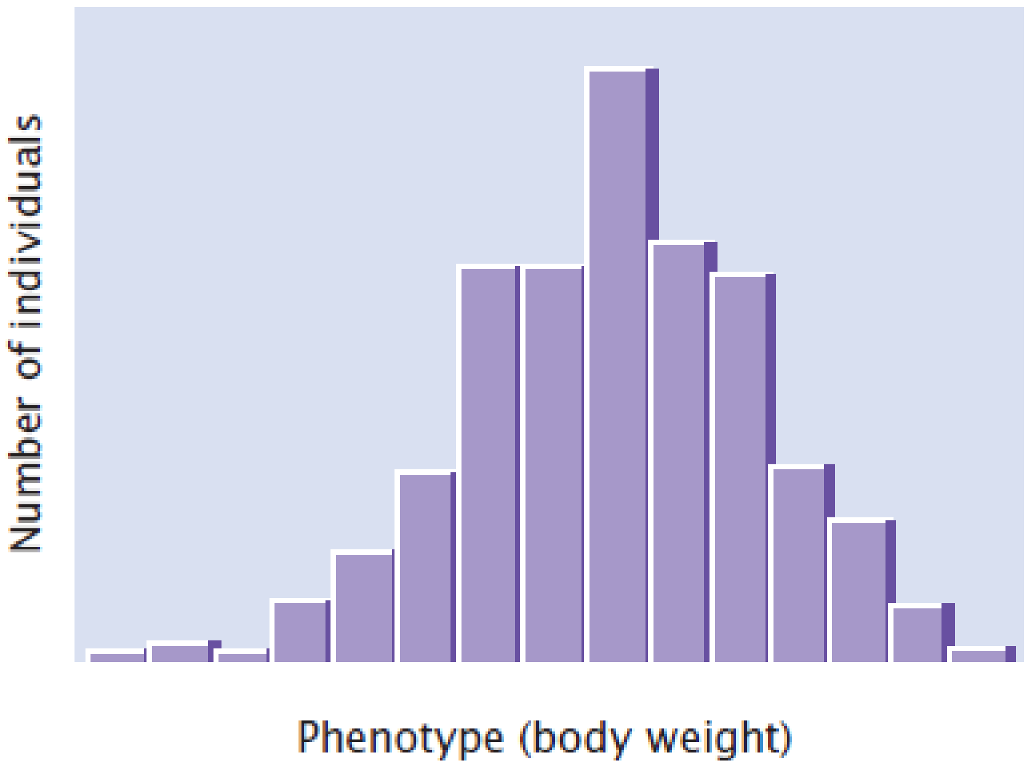


Expanding the math

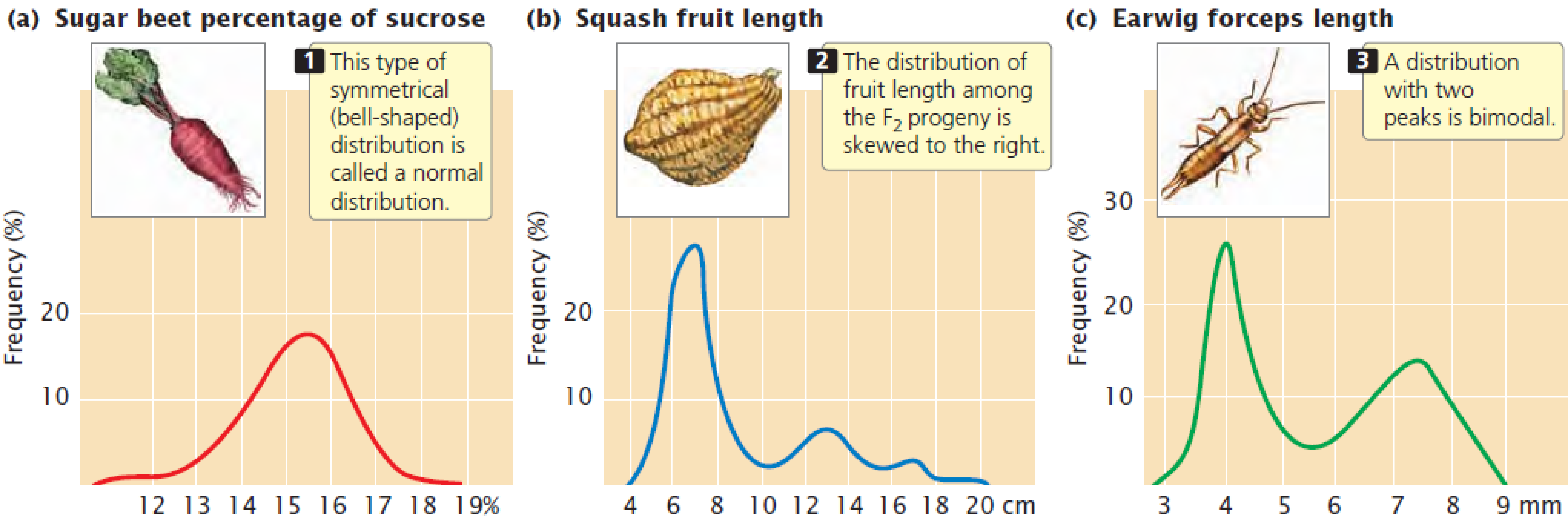
In a population homozygotes are always minority



Now statistics
Frequency Distribution



Examples

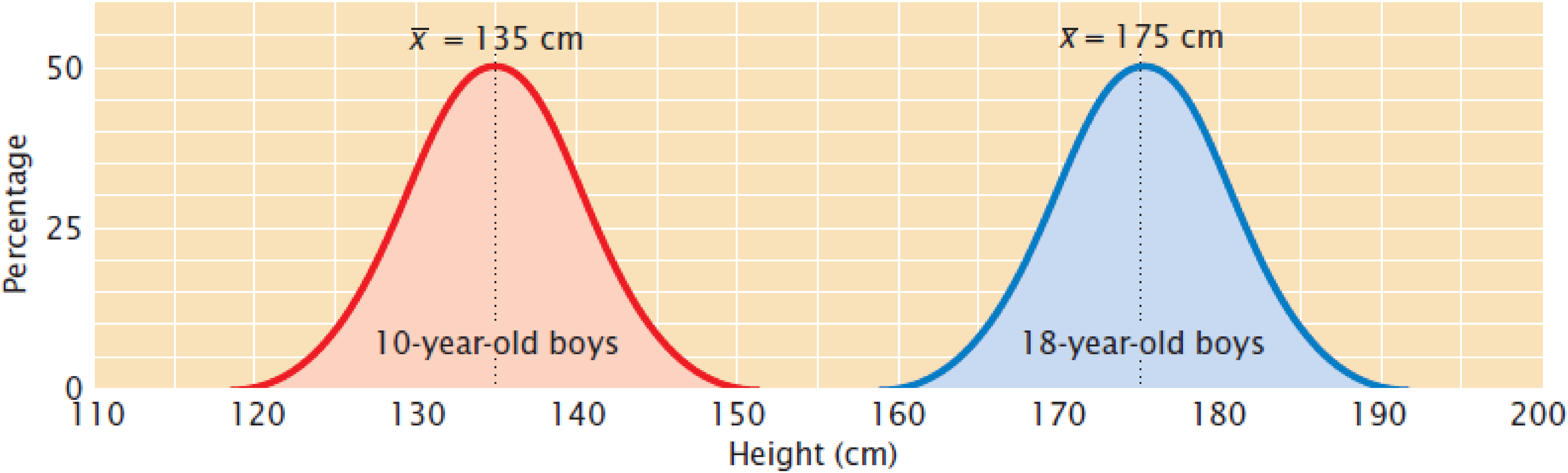


Many quantitative characteristics exhibit a symmetrical curve: Normal distribution or bell shaped curve

But they can also be skewed

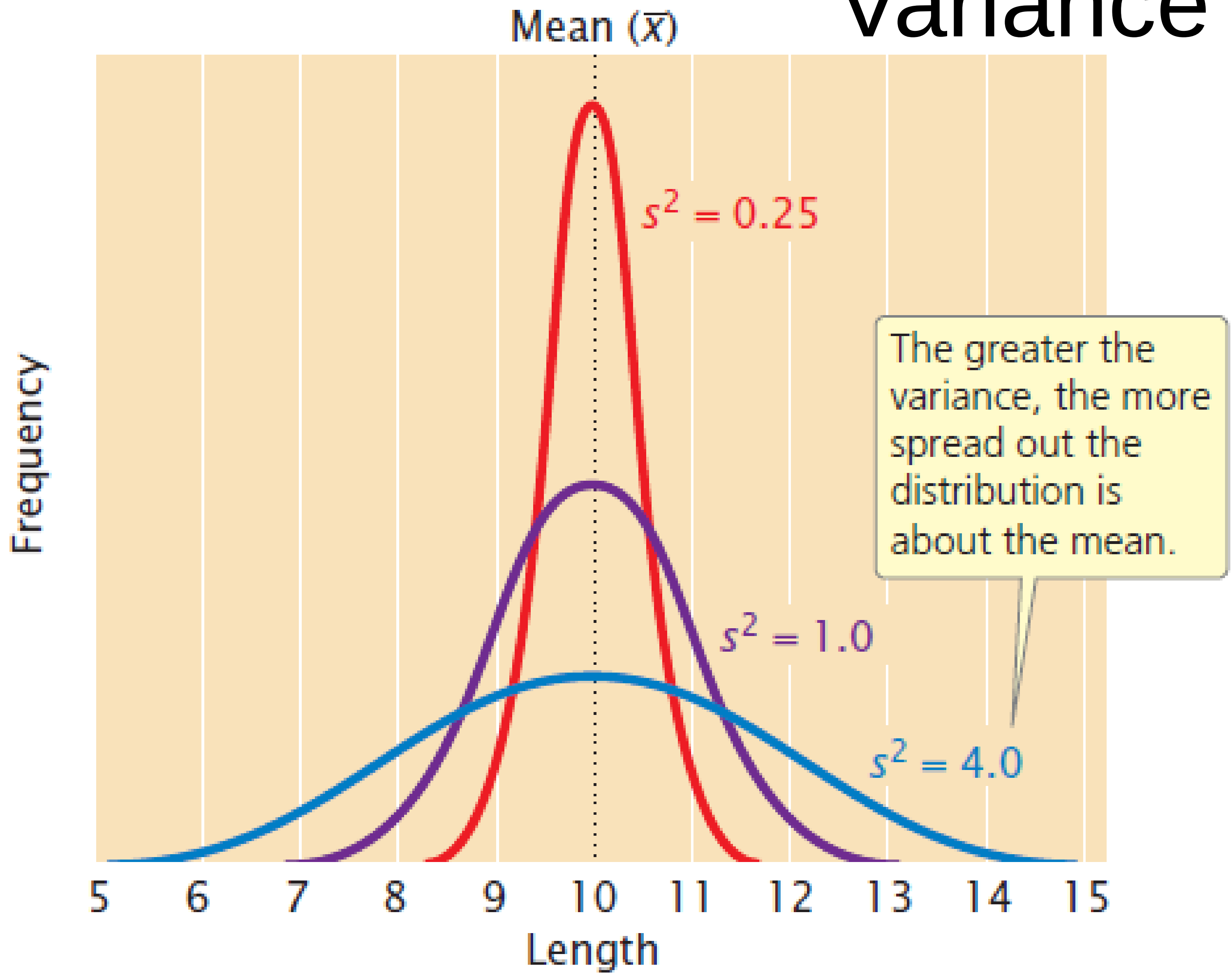
Or bimodal

The mean



$$\bar{x} = \frac{1}{n} \sum x_i$$

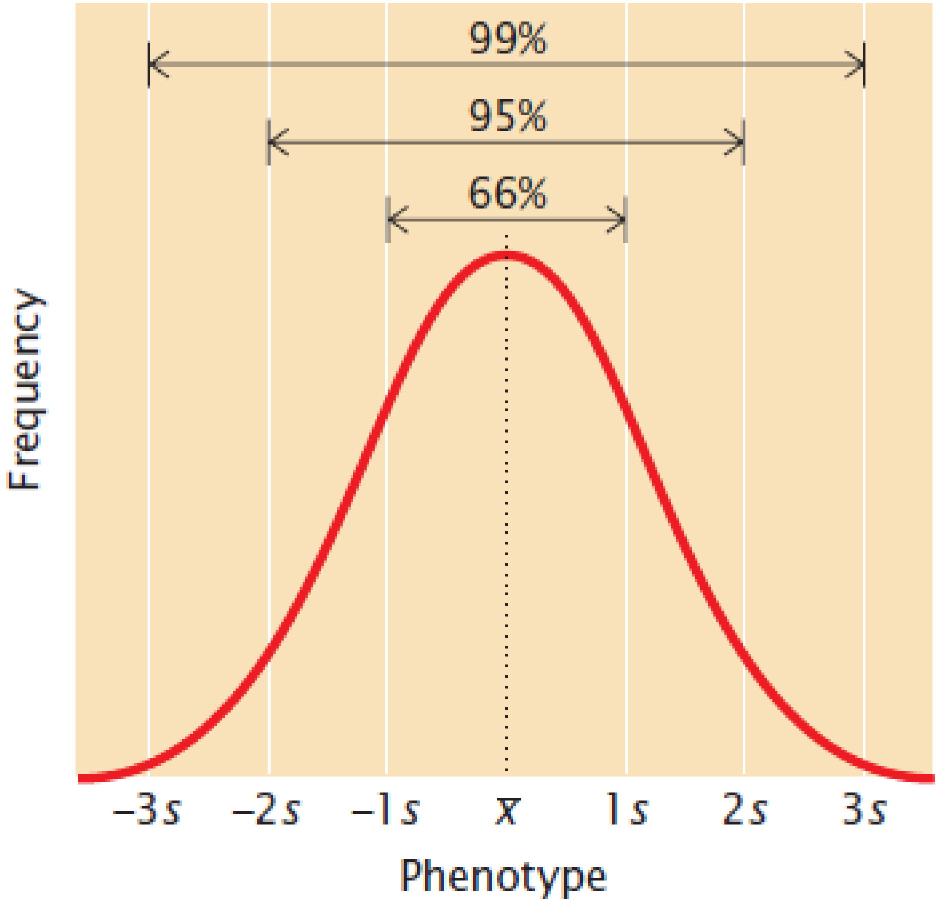
Variance



$$s^2 = \frac{\sum (x_i - \bar{x})^2}{n-1}$$

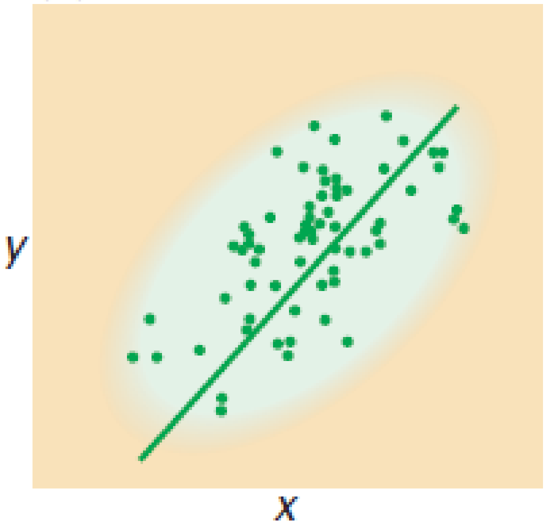
$$s = \sqrt{s^2}$$

Standard Deviation



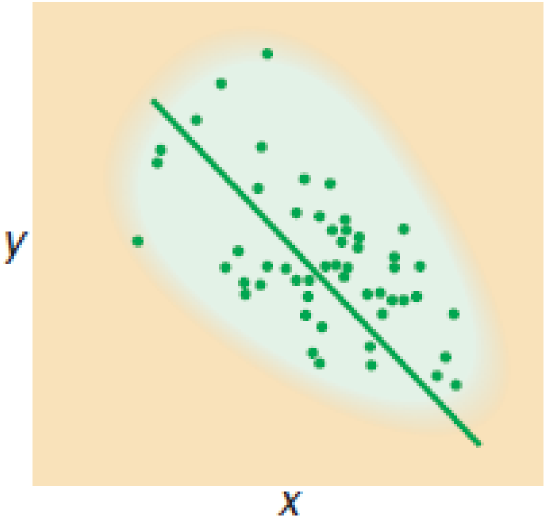
Correlation

(a) $r = 0.7$



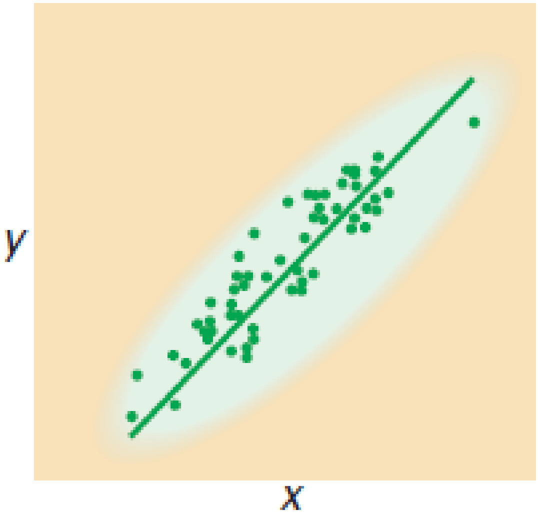
A positive correlation indicates that there is a direct association between variables.

(b) $r = -0.7$



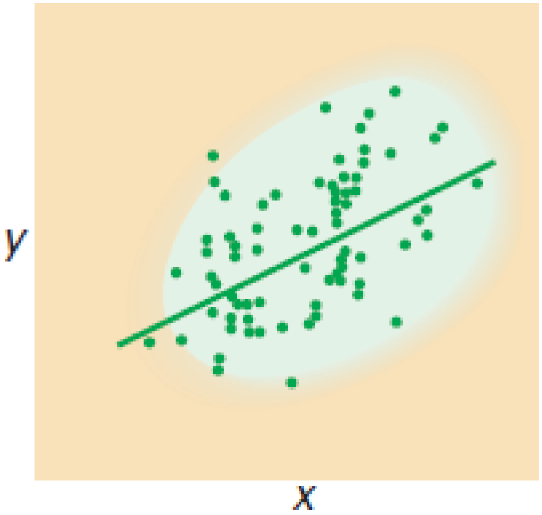
A negative correlation indicates that there is an inverse association between variables.

(c) $r = 0.9$



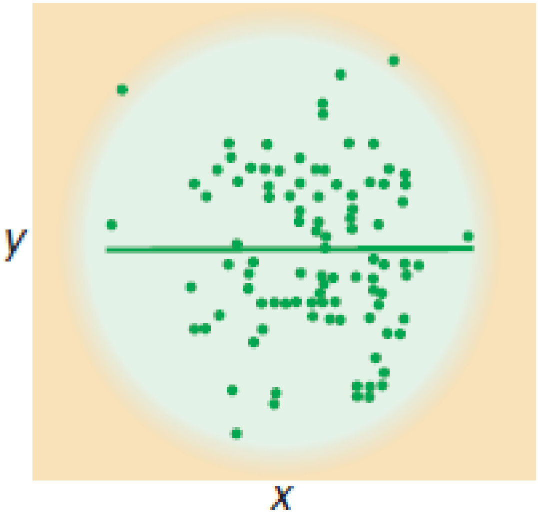
A strong positive correlation

(d) $r = 0.3$



A weak positive correlation.

(e) $r = 0$

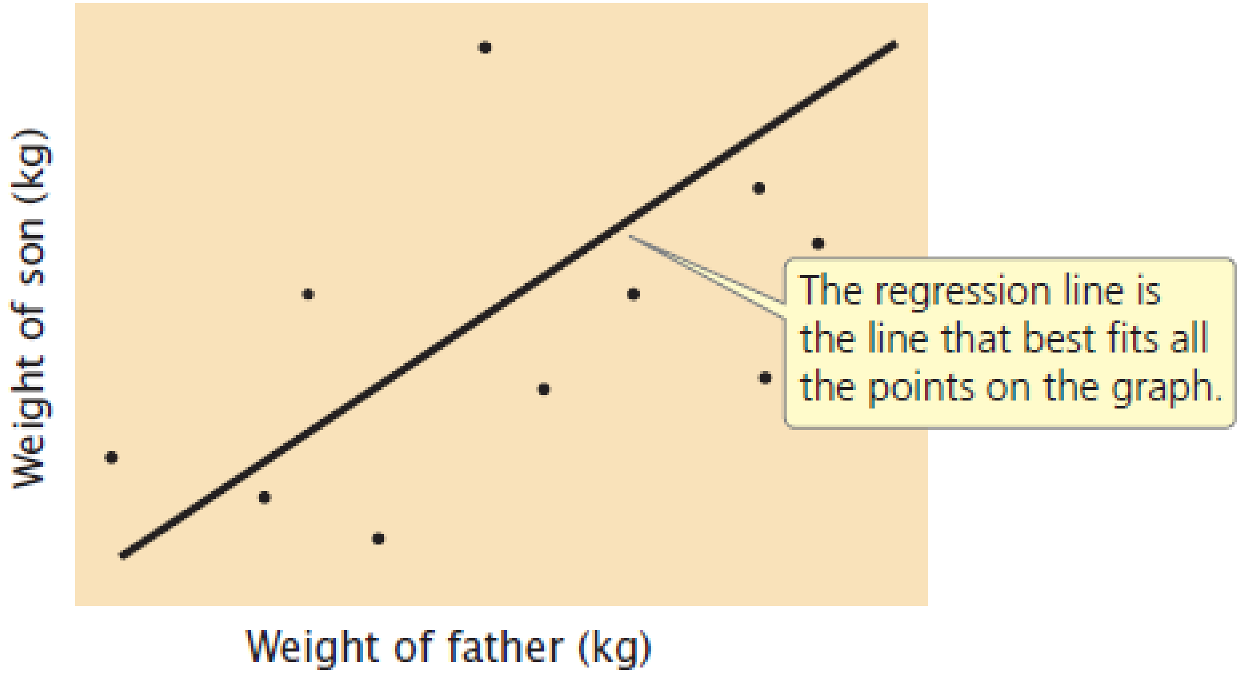


A correlation of zero indicates that there is no association between variables.

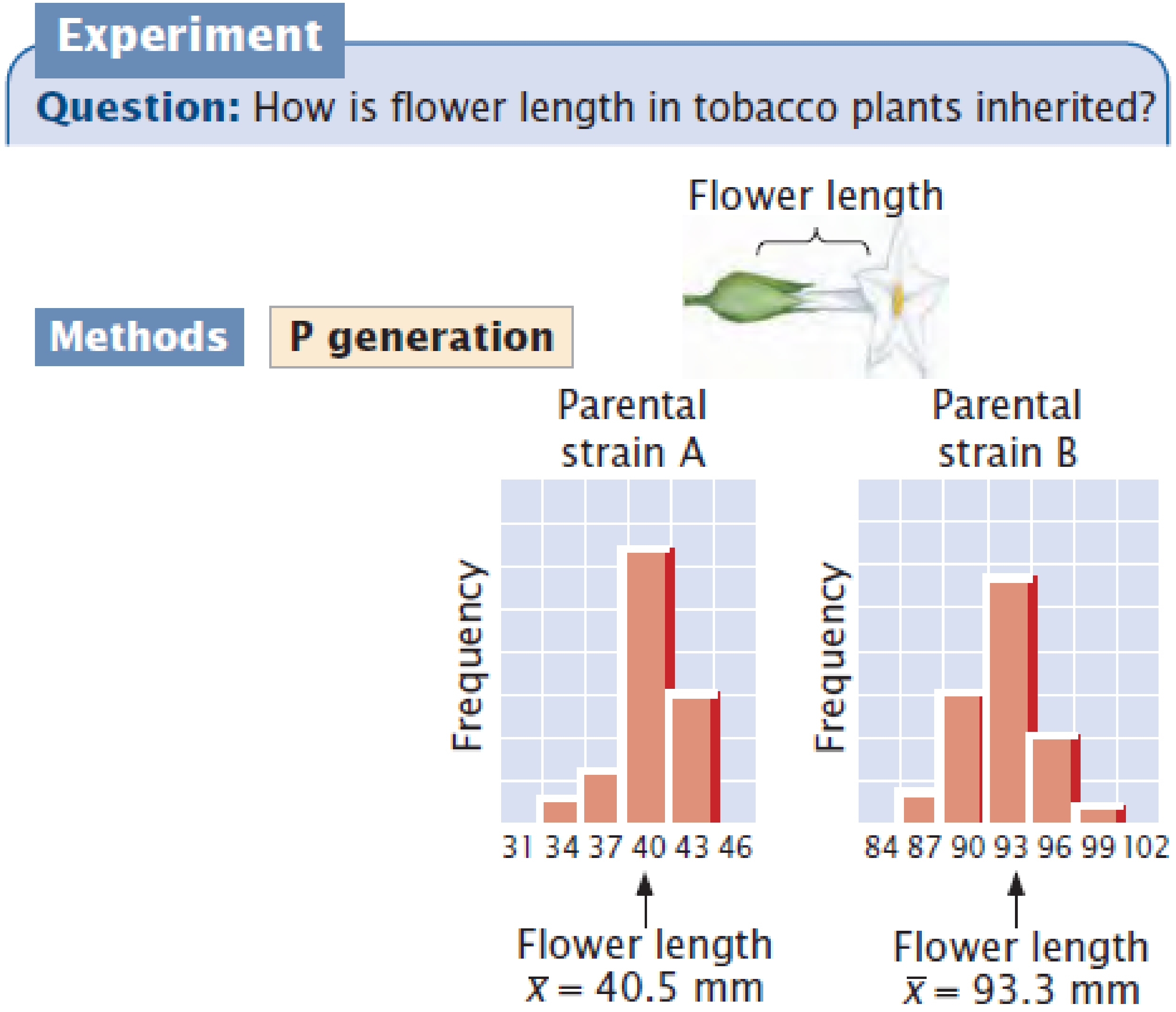
$$COV_{xy} = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{n-1}$$

$$r = \frac{COV_{xy}}{s_x s_y}$$

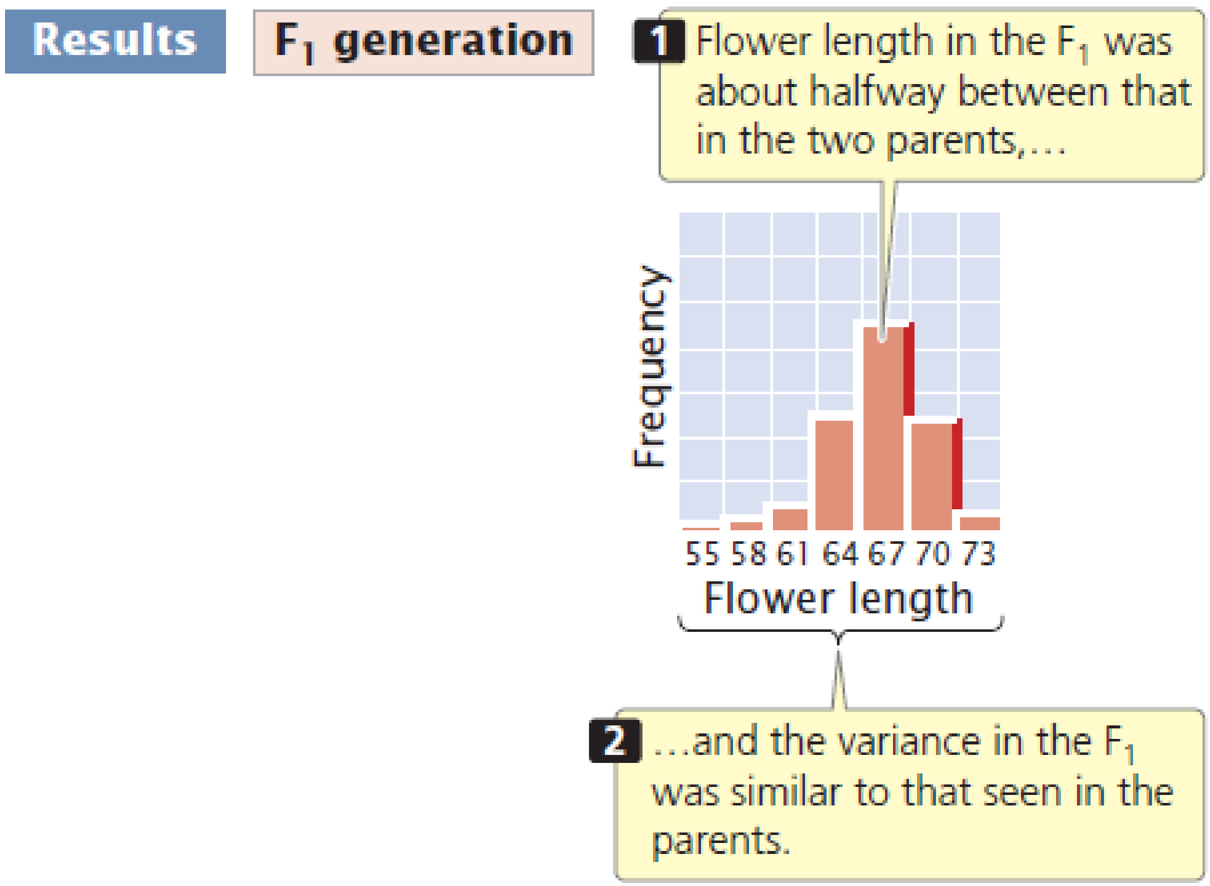
Regression


Weight of son (kg)
The regression line is the line that best fits all the points on the graph.
Weight of father (kg)

First study

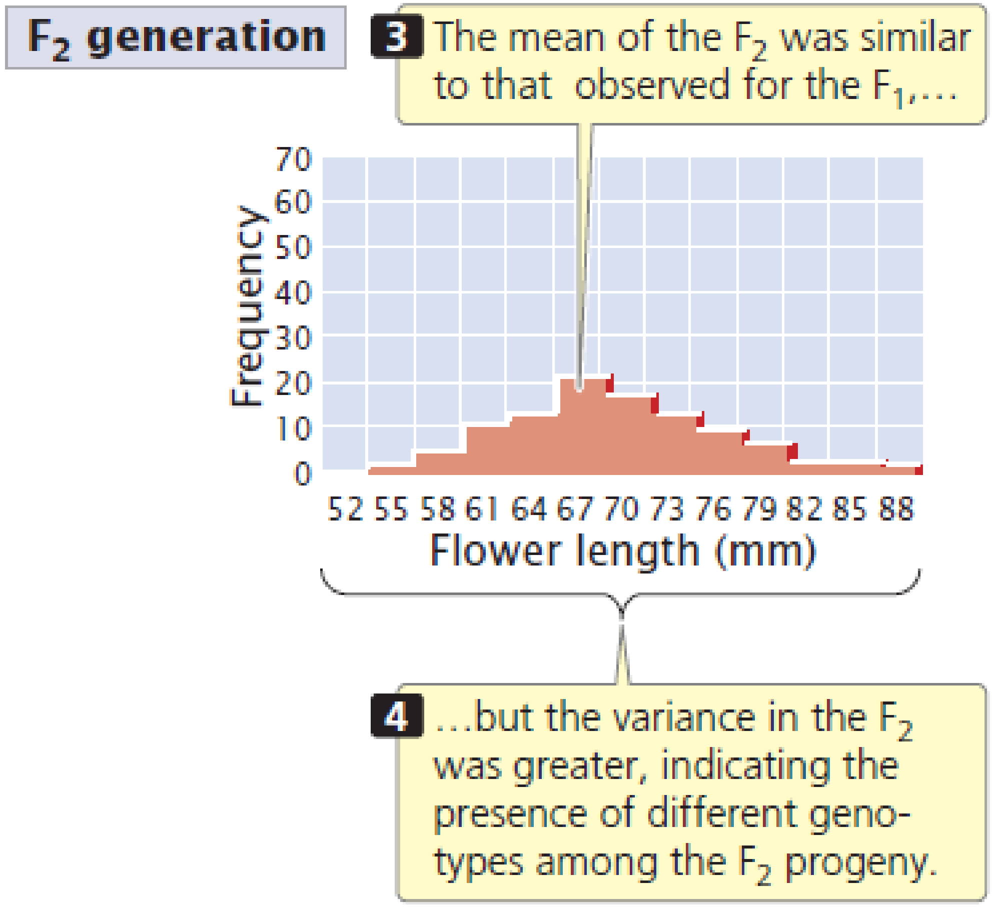

Experiment
Question: How is flower length in tobacco plants inherited?
Flower length
Methods
P generation
Parental strain A
Parental strain B
Frequency
31 34 37 40 43 46
Flower length
$\bar{x}$ = 40.5 mm
Frequency
84 87 90 93 96 99 102
Flower length
$\bar{x}$ = 93.3 mm

Results



Results
F1 generation
1 Flower length in the F1 was about halfway between that in the two parents,...
Frequency
55 58 61 64 67 70 73
Flower length
2 ...and the variance in the F1 was similar to that seen in the parents.

Results



Conclusion: Flower length of the F_1 and F_2 is consistent with the hypothesis that the characteristic is determined by several genes that are additive in their effects.

Working problem

Weight (mg)	Eggs (thousands)
x	y
14	61
17	37
24	65
25	69
27	54
33	93
34	87
37	89
40	100
41	90
42	97

What are the correlation coefficient for body weight and egg number in these 11 fishes?

Solution

1. Find the means $\bar{x} = \frac{1}{n}\sum x_i$

2. Find the deviations $s^2 = \frac{\sum (x_i - \bar{x})^2}{n-1}$ And Standard deviations $s = \sqrt{s^2}$

3. Find the covariance $\text{cov}_{xy} = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{n-1}$ And regression $r = \frac{\text{cov}_{xy}}{s_x s_y}$

What is regression coefficient

- The regression coefficient indicates how much *y* increases, on average, per increase in *x*.

$$b = \frac{\text{cov}_{xy}}{s_x^{\;2}}$$

- Now calculate Regression coefficient