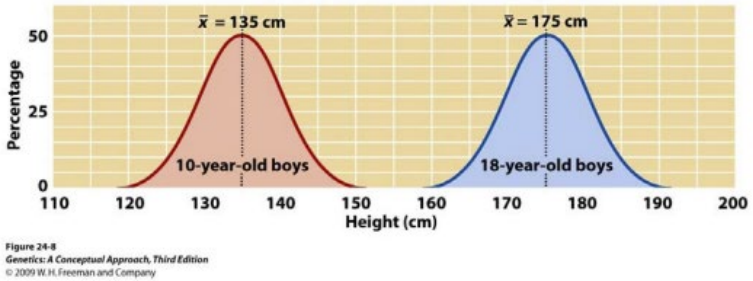
Unit 6 | QUANTITATIVE GENETICS



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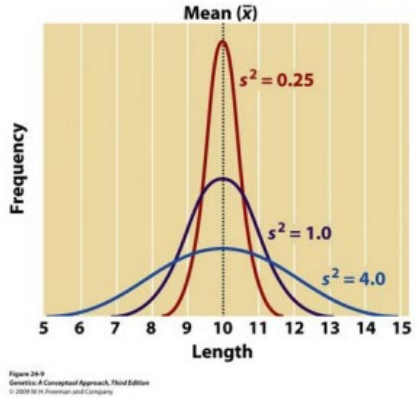

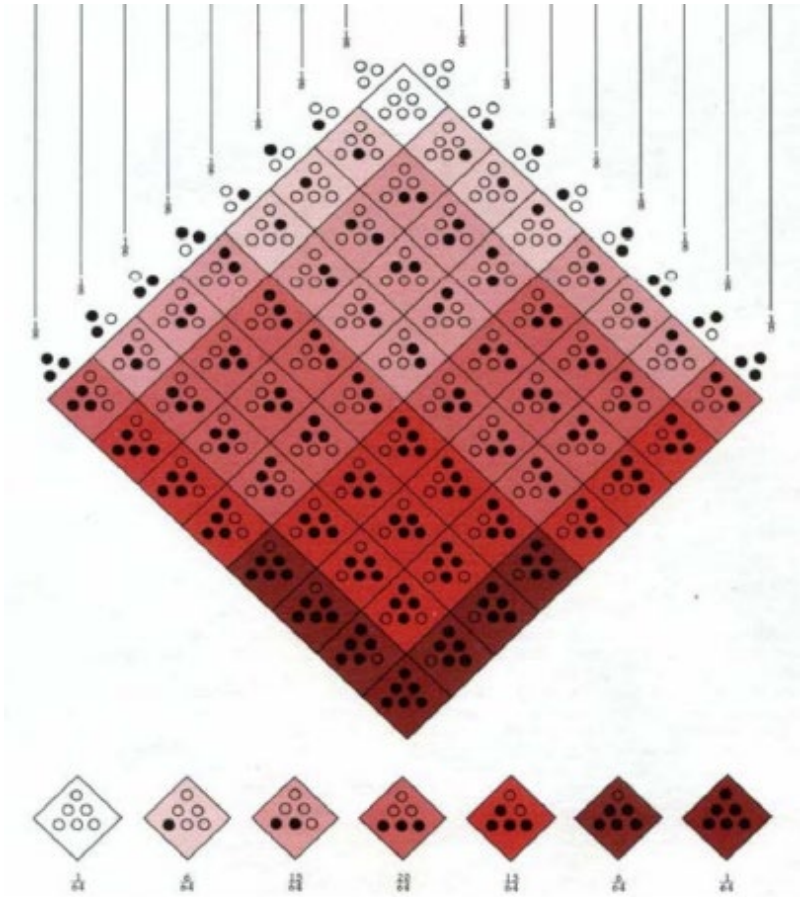

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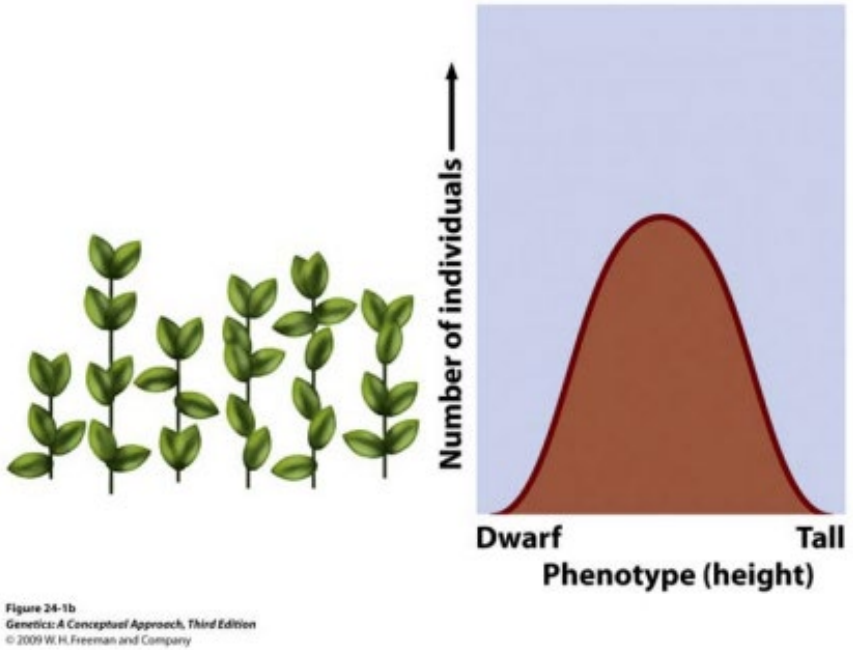
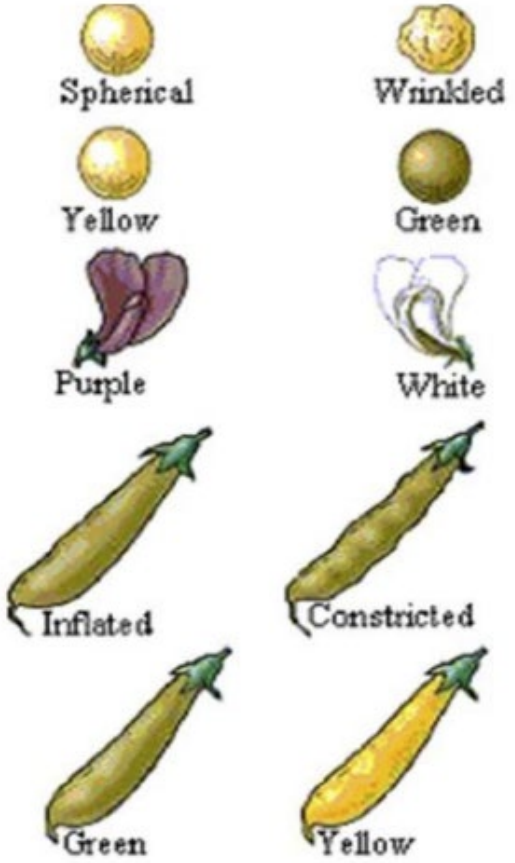
Biometry vs Mendelian Genetics

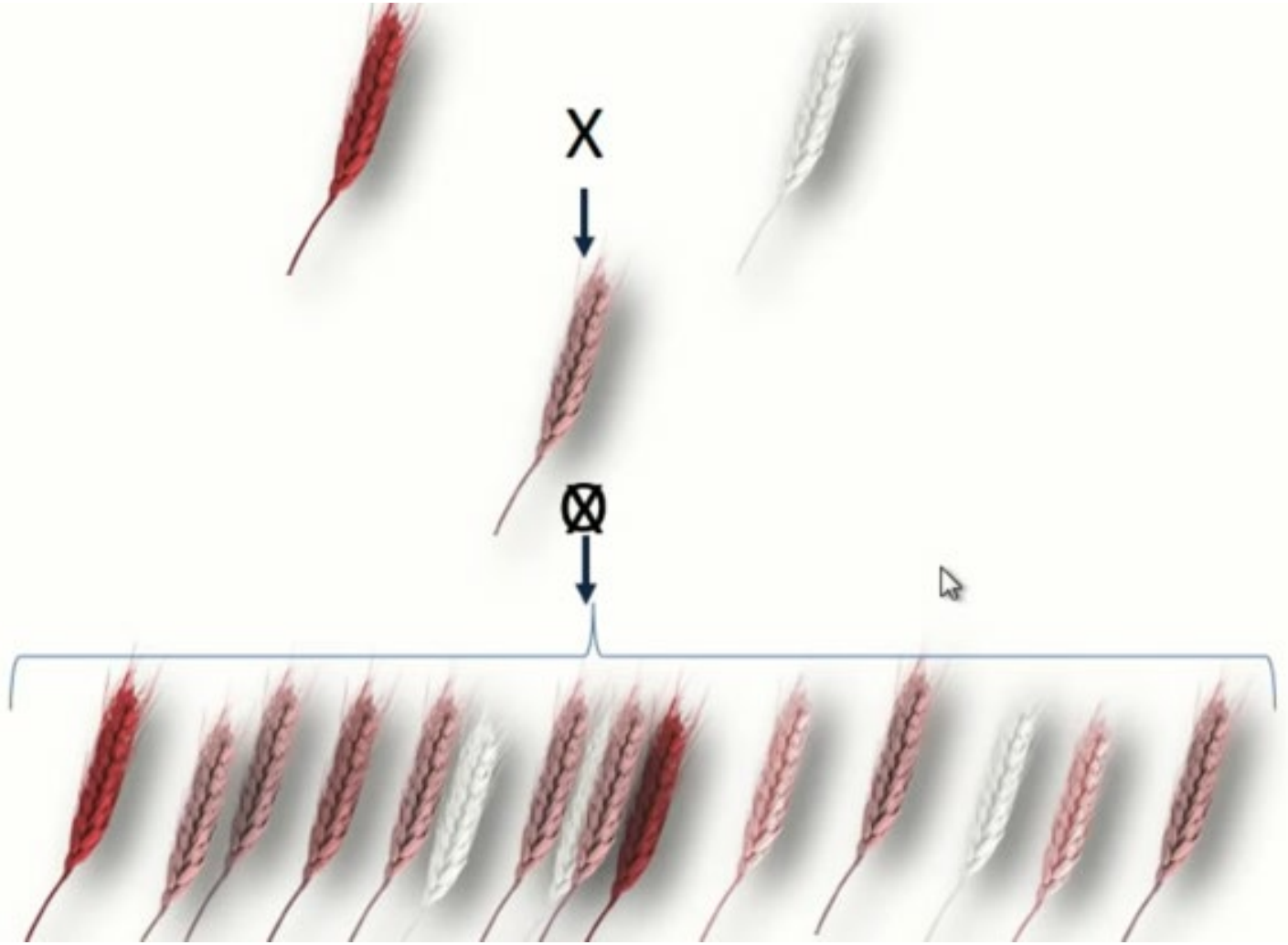


Continuous variation



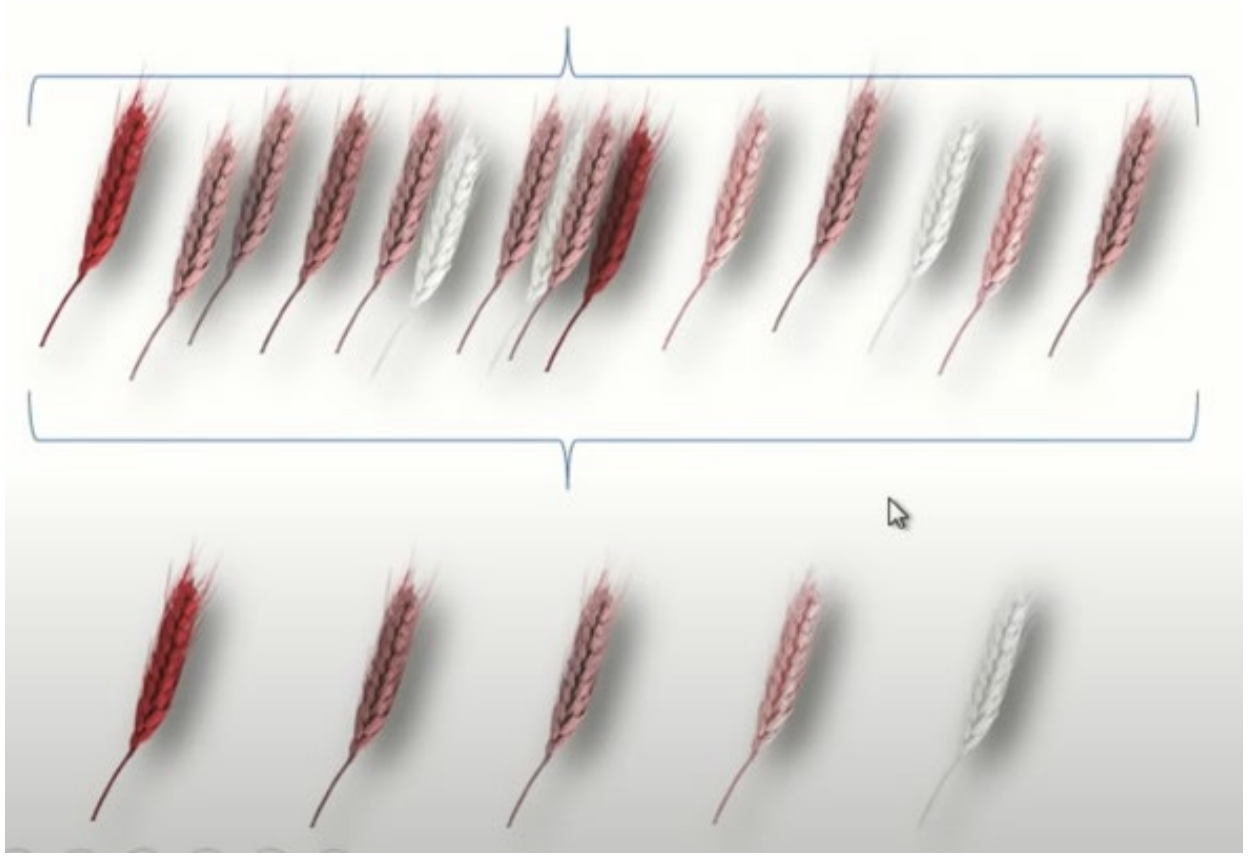
Discontinuous variation

Nilsson-Ehle Experiment (1909)



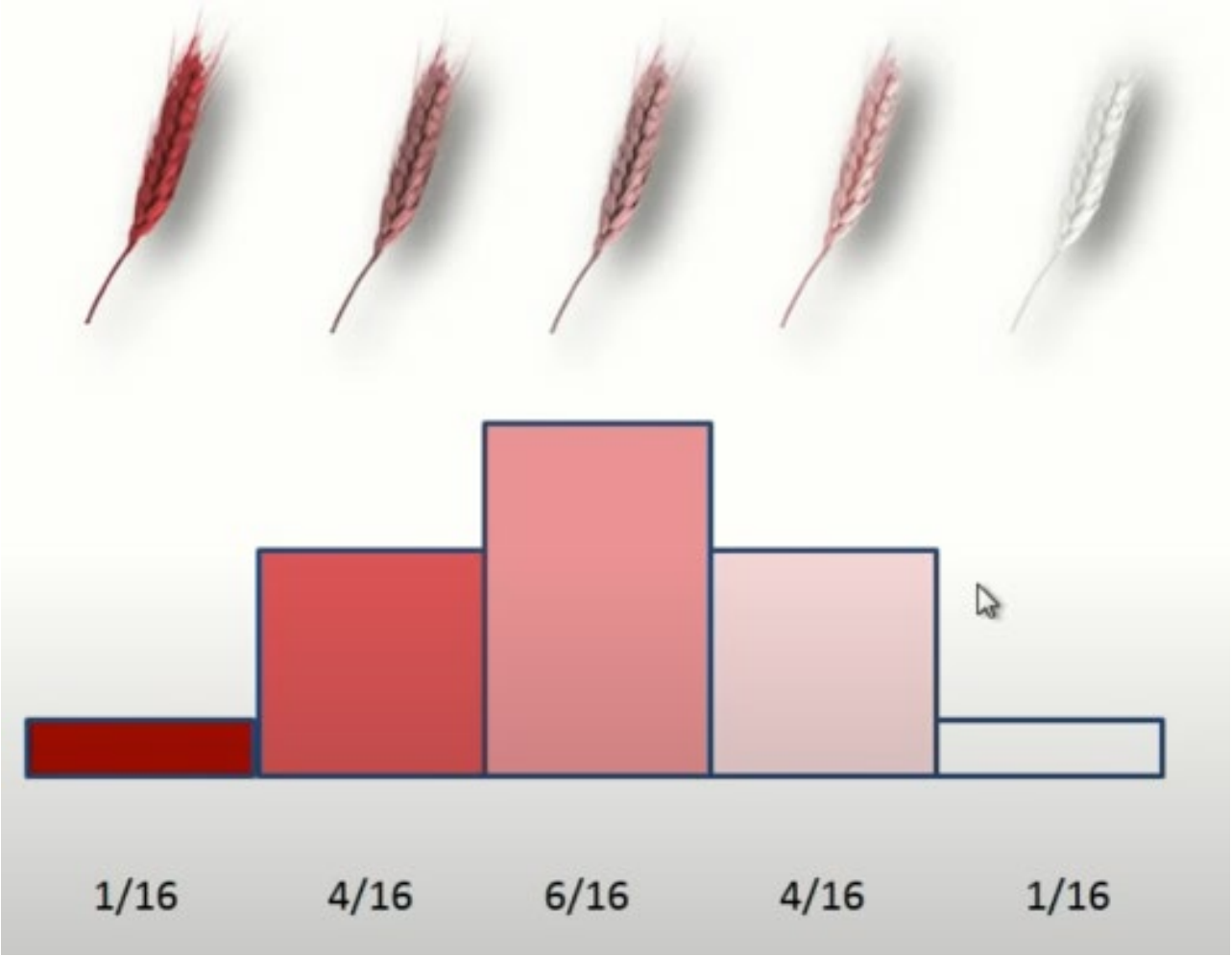
Source: https://youtu.be/6yzSbXlZNuU

Nilsson-Ehle Experiment (1909)



Source: https://youtu.be/6yzSbXlZNuU

Nilsson-Ehle Experiment (1909)

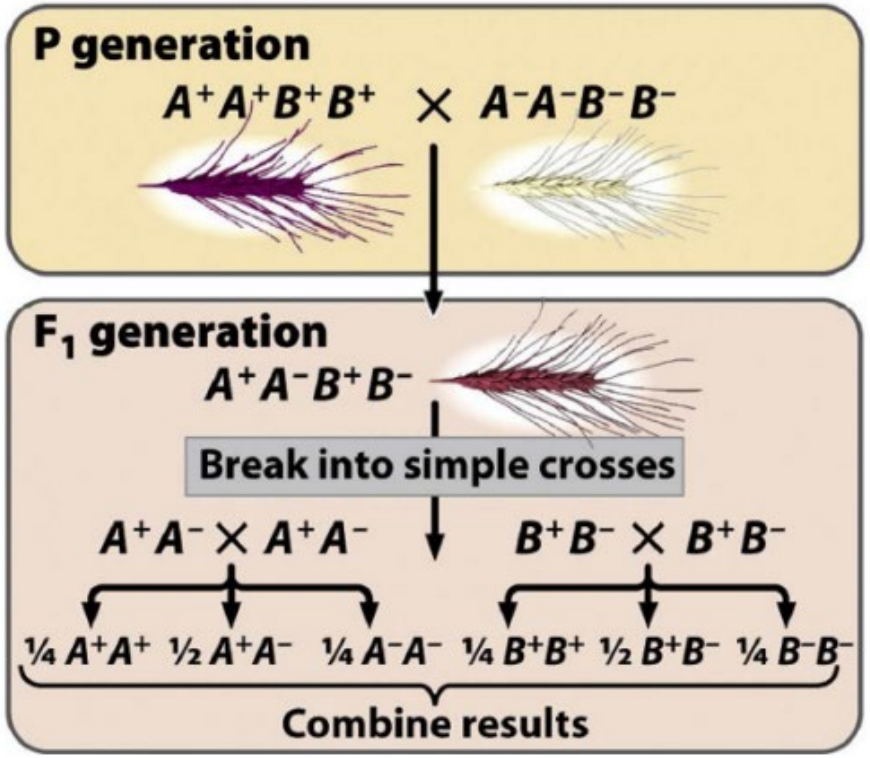


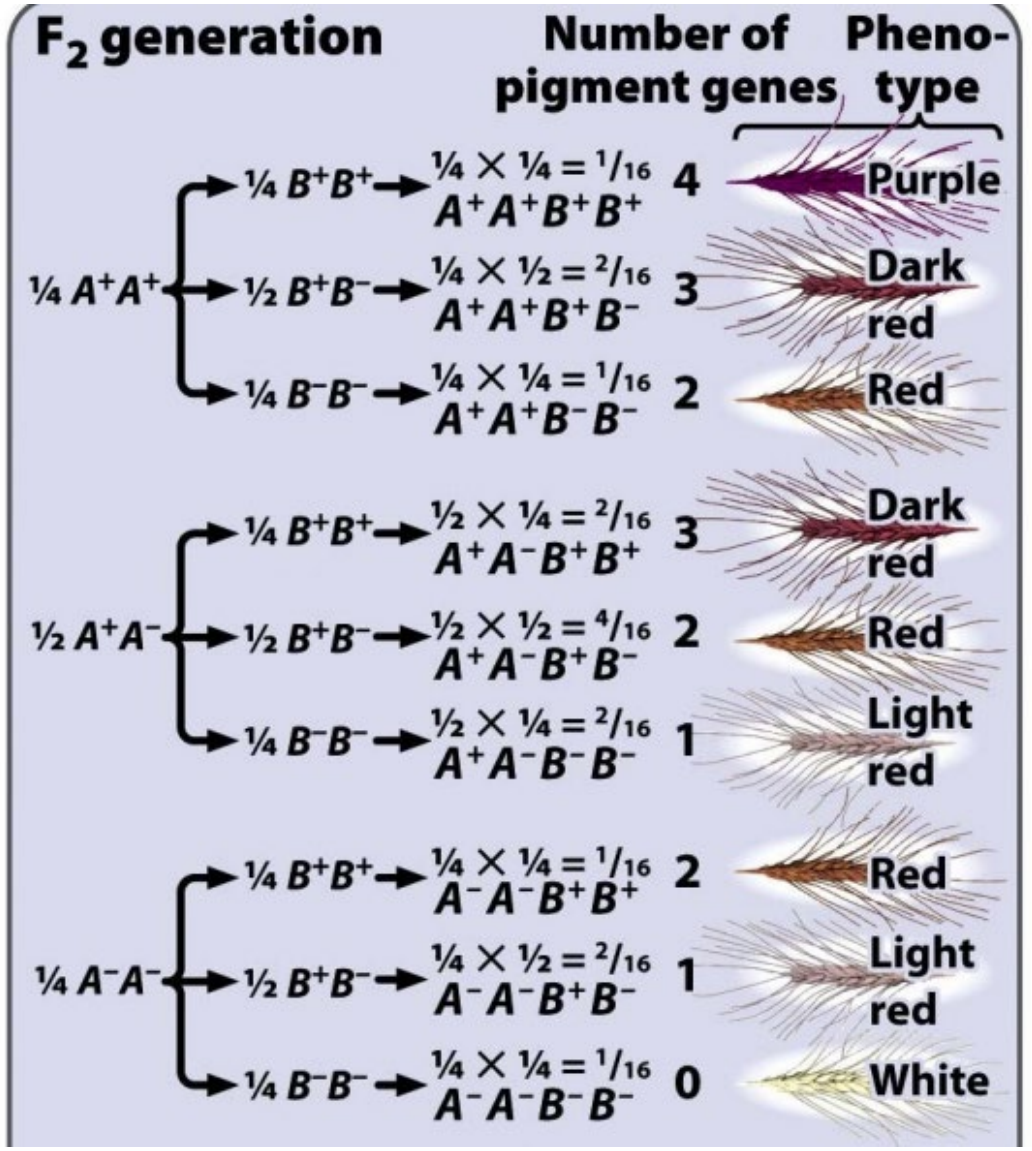
Source: https://youtu.be/6yzSbXlZNuU

Nilsson-Ehle Experiment (1909)

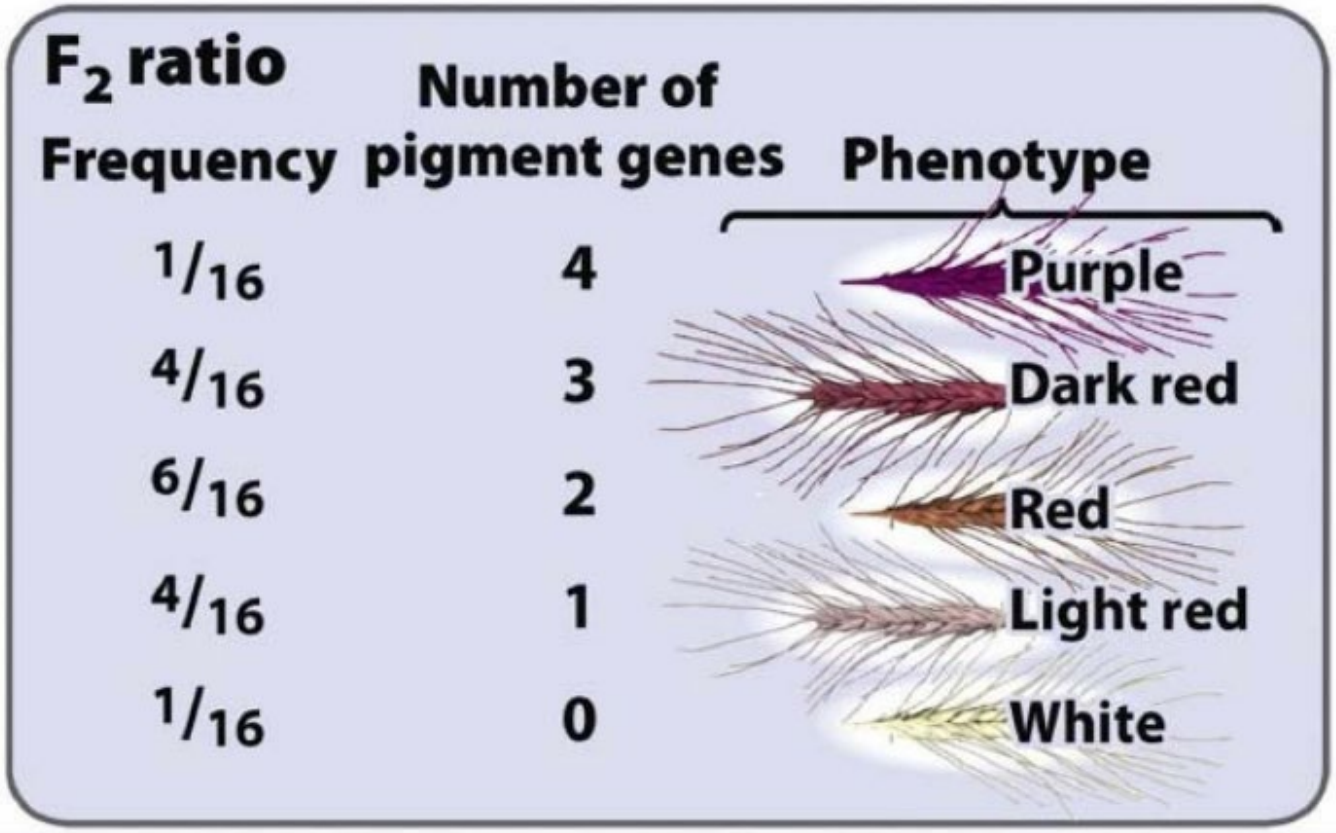
Methods Cross wheat having white kernels and wheat having purple kernels. Intercross the F_1 to produce F_2.

Results

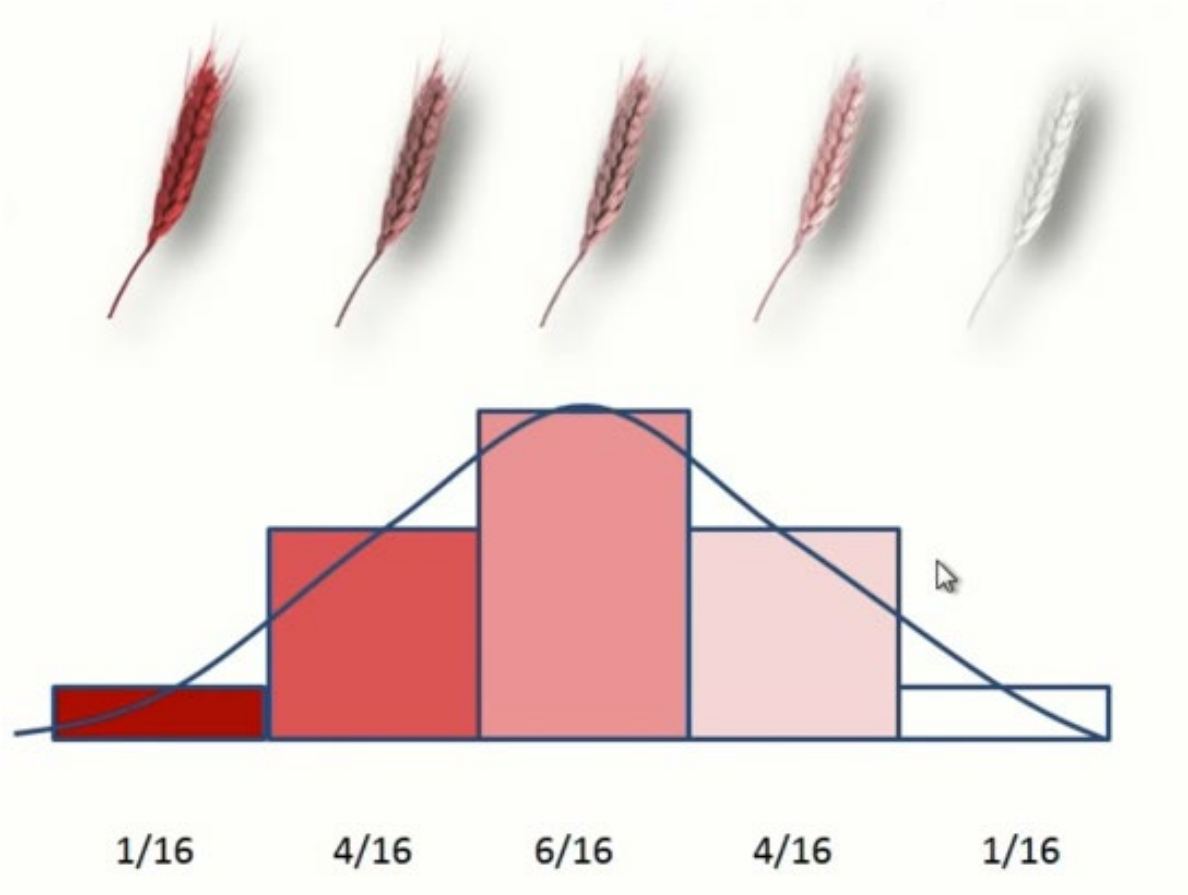




Nilsson-Ehle Experiment (1909)



Nilsson-Ehle Experiment (1909)



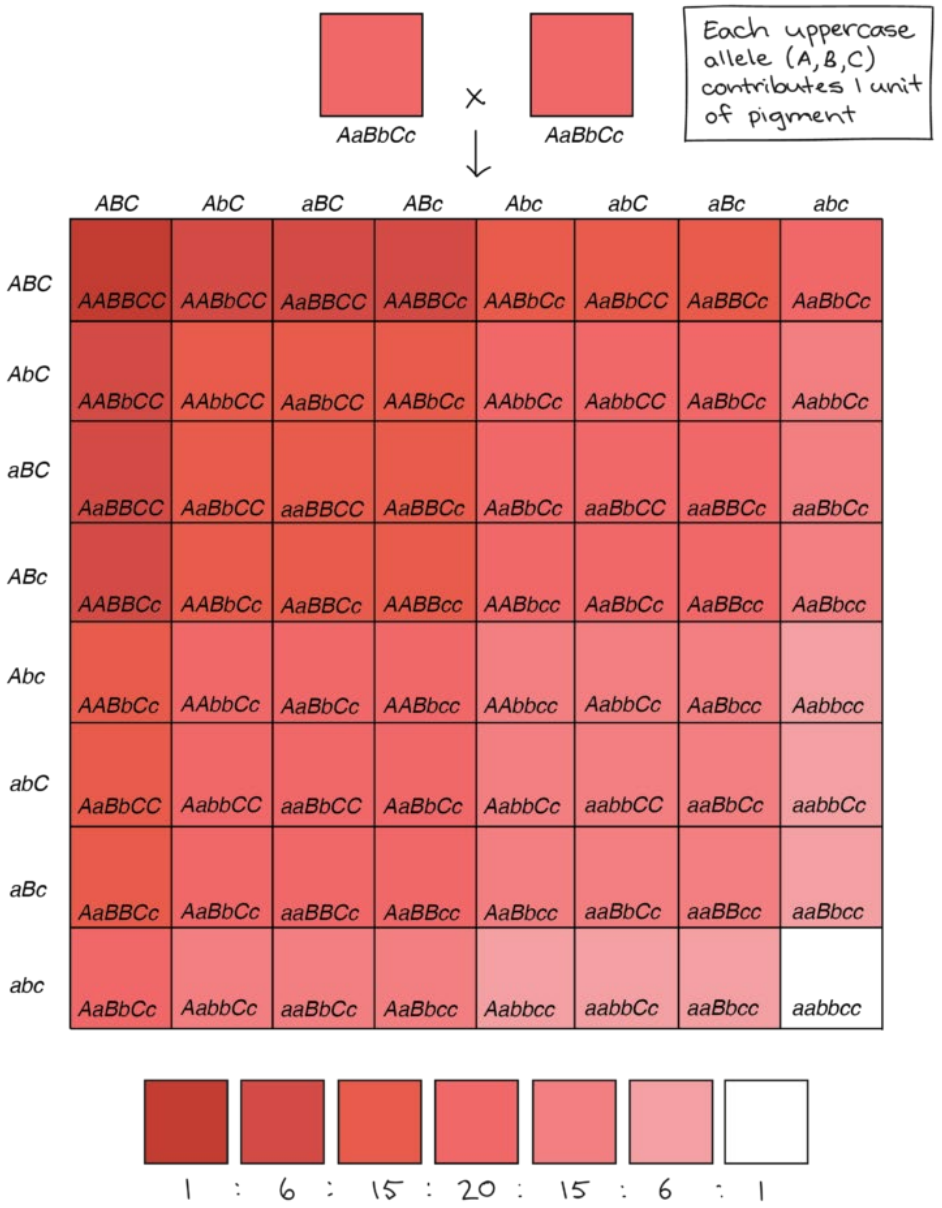
Source: https://youtu.be/6yzSbXlZNuU

Additive Model:

- Trait due to several genes: polygenic.

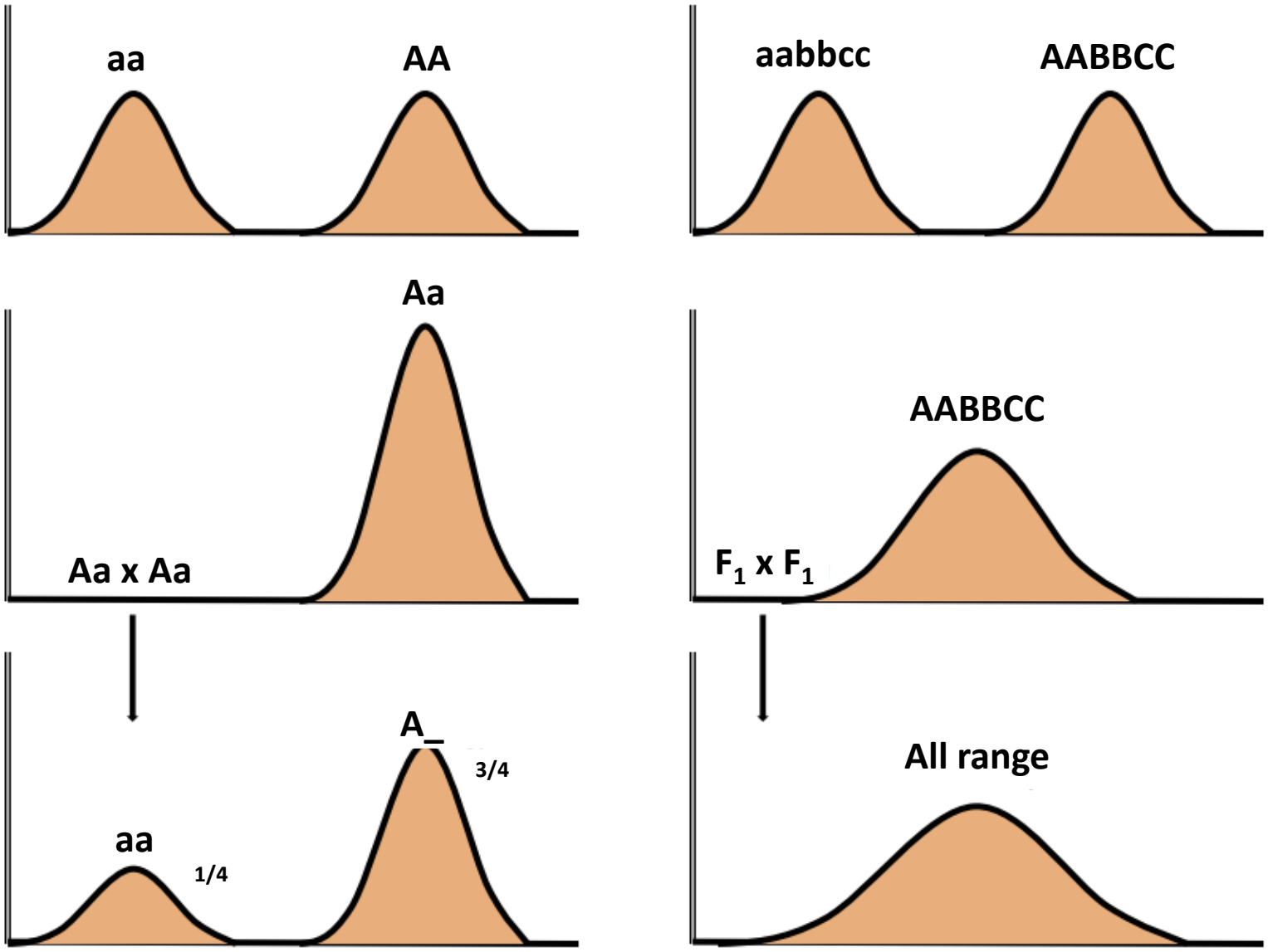
- There are additive and non-additive alleles (**additive alleles** contribute to the expression of the trait; **non-additive alleles** don't).

- The contribution of additive alleles is similar and small.



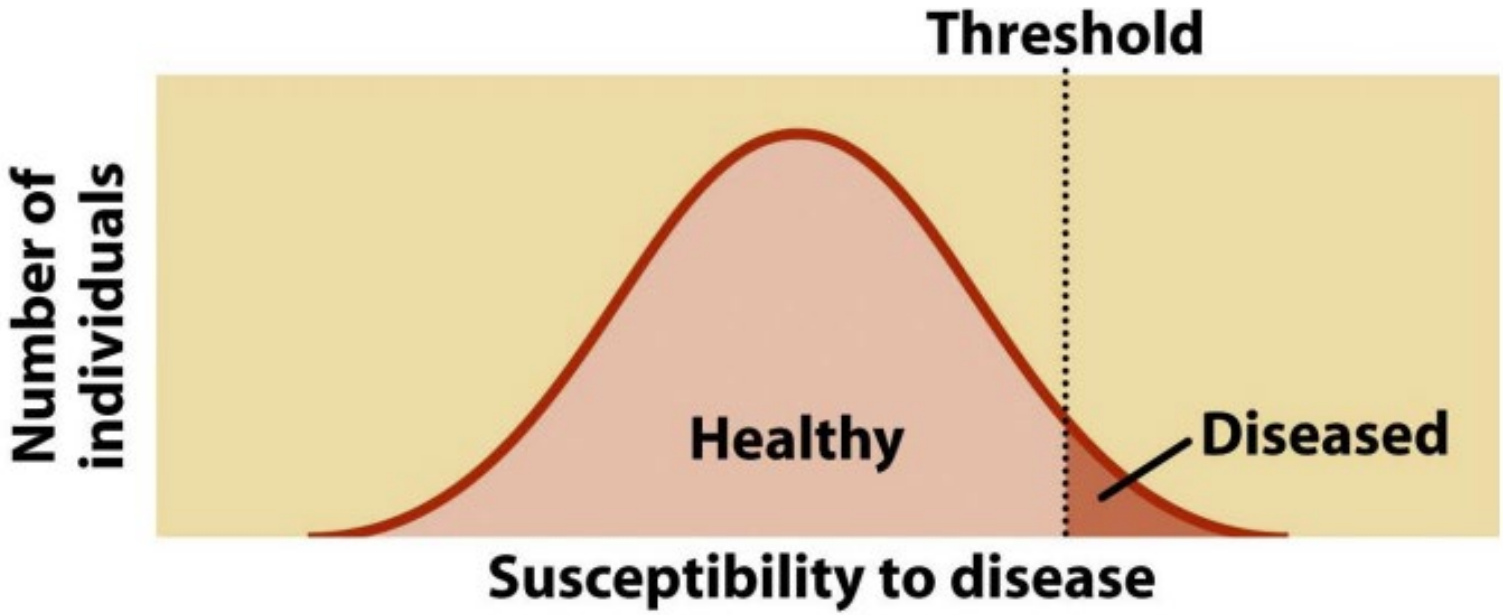
Source: https://courses.lumenlearning.com/

Qualitative vs Quantitative



Meristic Traits: quantitative traits depending on polygenes but organised in closed categories.

Threshold Traits: quantitative traits that are discretely expressed in a limited number of phenotypes (usually two).



Questions of Quantitative Genetics

- **Can we make predictions** on how many individuals with a particular phenotype we might expect?

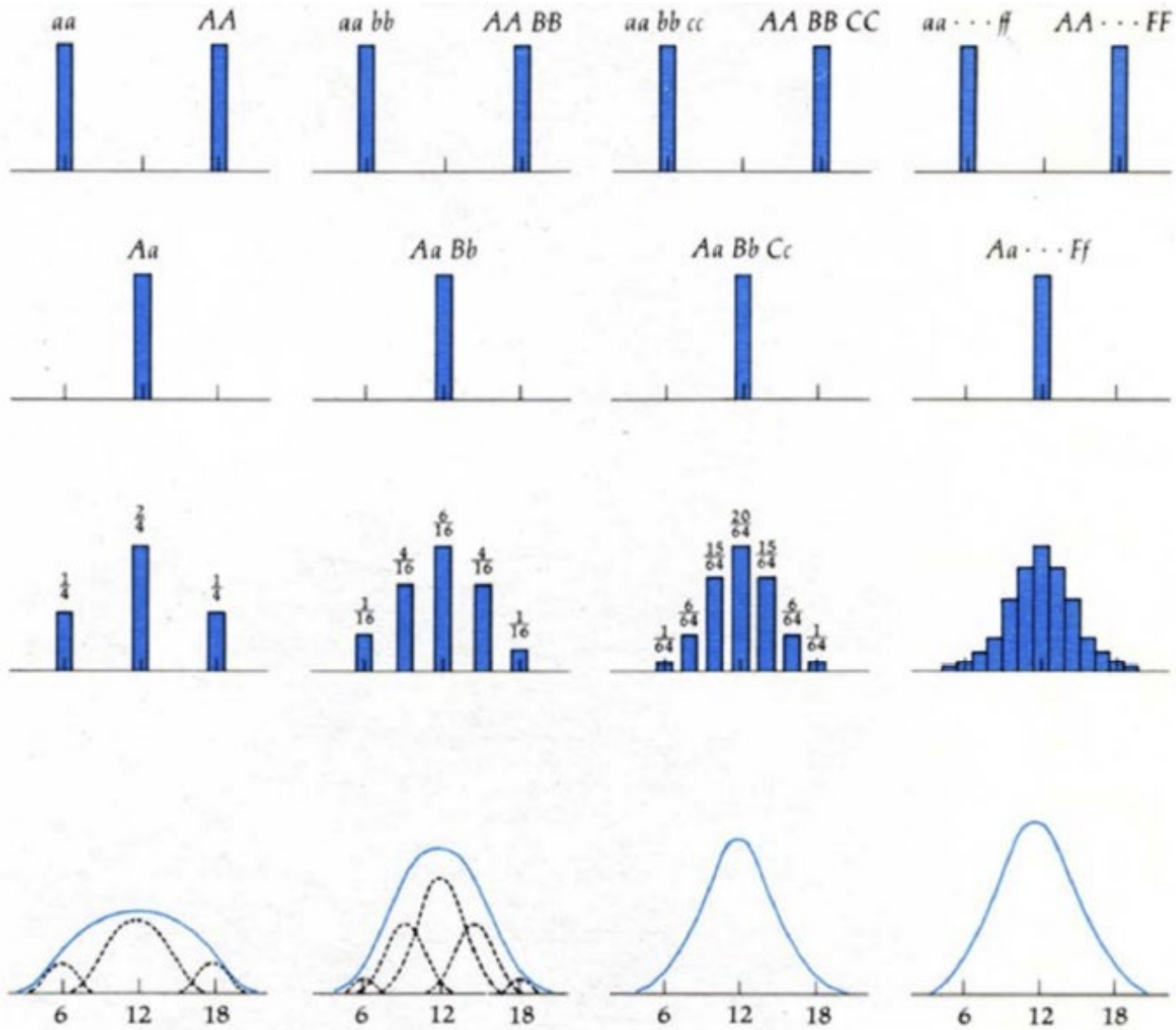
- **How many genes** are involved in a particular trait?

- What portion of observed variability is due to a **genetic differences** between individuals? What portion is due to **environmental factors**?

- Where are these genes **located in the genome**?

Questions of Quantitative Genetics

- **Can we make predictions** on how many individuals with a particular phenotype we might expect?


aa
AA
aa bb
AA BB
aa bb cc
AA BB CC
aa · · · ff
AA · · · FF
Aa
Aa Bb
Aa Bb Cc
Aa · · · Ff
1/4
2/4
1/4
1/16
4/16
6/16
4/16
1/16
1/64
6/64
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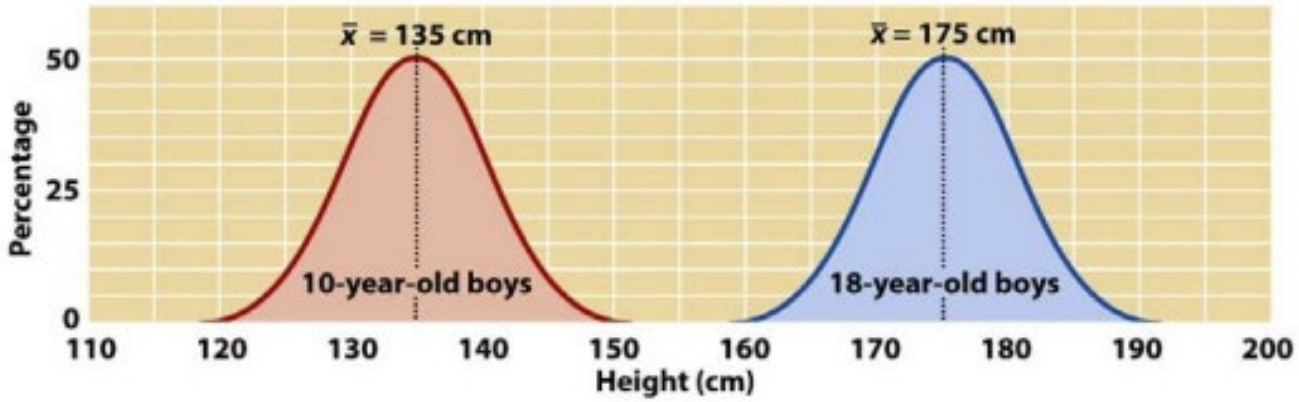
12
18



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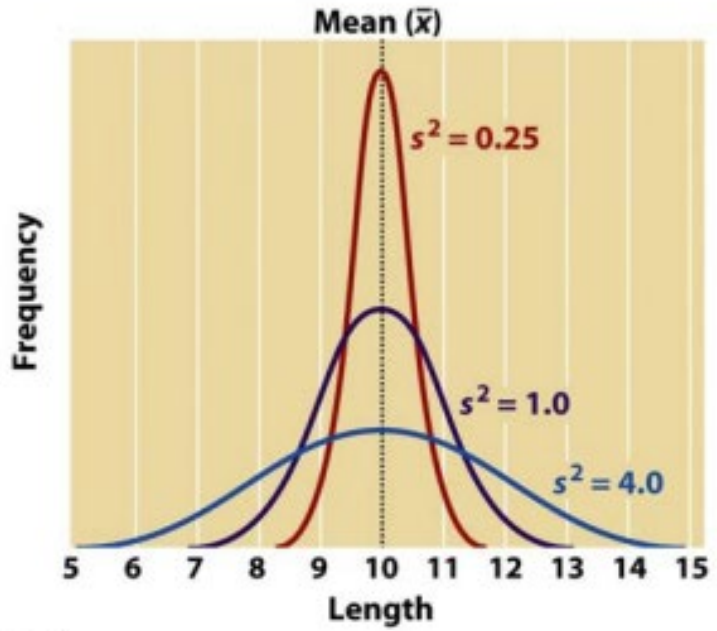

Figure 24-9
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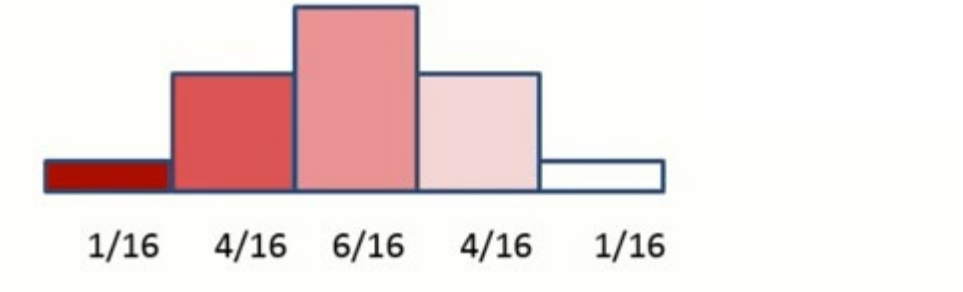
Mean: sum of a collection of numbers divided by the count of numbers in the collection

Variance: measure of data dispersion (how far a set of numbers is spread out from their average value).

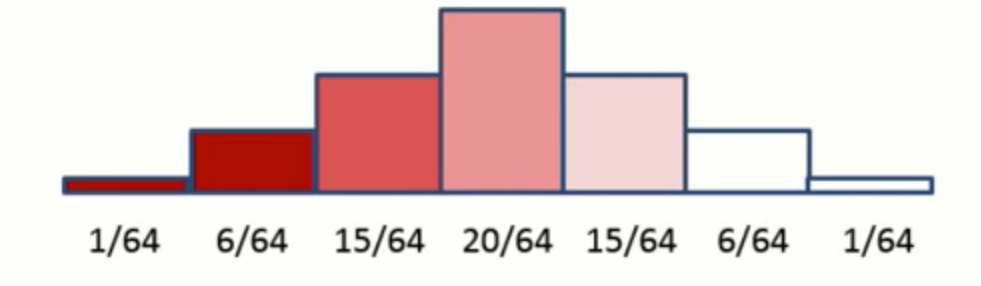
	1 locus	*2 loci*	*3 loci*	*n loci*
Number of gametes produced in the F_1 polyhybrid	**2** (A,a)	**4** (AB, ab, Ab, aB)	**8** (ABC, ABc, Abc, abc, aBC, abC, AbC, aBc)	**2^n**
Number of genotypes expected in F_2	**3** (AA, Aa, aa)	**9** (AABB, AaBB, aaBB, AABb, AaBb, Aabb, aaBB, AAbb, aabb)	**27** (AABBCC, …, aaabbbccc)	**3^n**
Number of phenotypes expected in F_2	**3**	**5**	**7**	**2n+1**
Number of individuals with parental phenotype expected in F_2	**1/4** (AA/aa)	**1/16** (AABB/aabb)	**1/64** (AABBCC/aabbcc)	**$1/4^n$**

Calculating the number of genes involved in a quantitative trait

1 gene



2 genes



3 genes

Source: https://youtu.be/6yzSbXlZNuU

AABBCCDDEE x aabbccddee

25 cm 15 cm

AaBbCcDdEe

20 cm

In a F_2 of 512, how many of them will have 19 cm?

AABBCCDDEE x aabbccddee

25 cm | 15 cm

AaBbCcDdEe

20 cm

NUMBER OF ADDITIVE ALLELES	PHENOTYPE
0	15
1	16
2	17
3	18
4	19
5	20
6	21
7	22
8	23
9	24
10	25

AABBCCDDEE x aabbccddee

25 cm 15 cm

AaBbCcDdEe

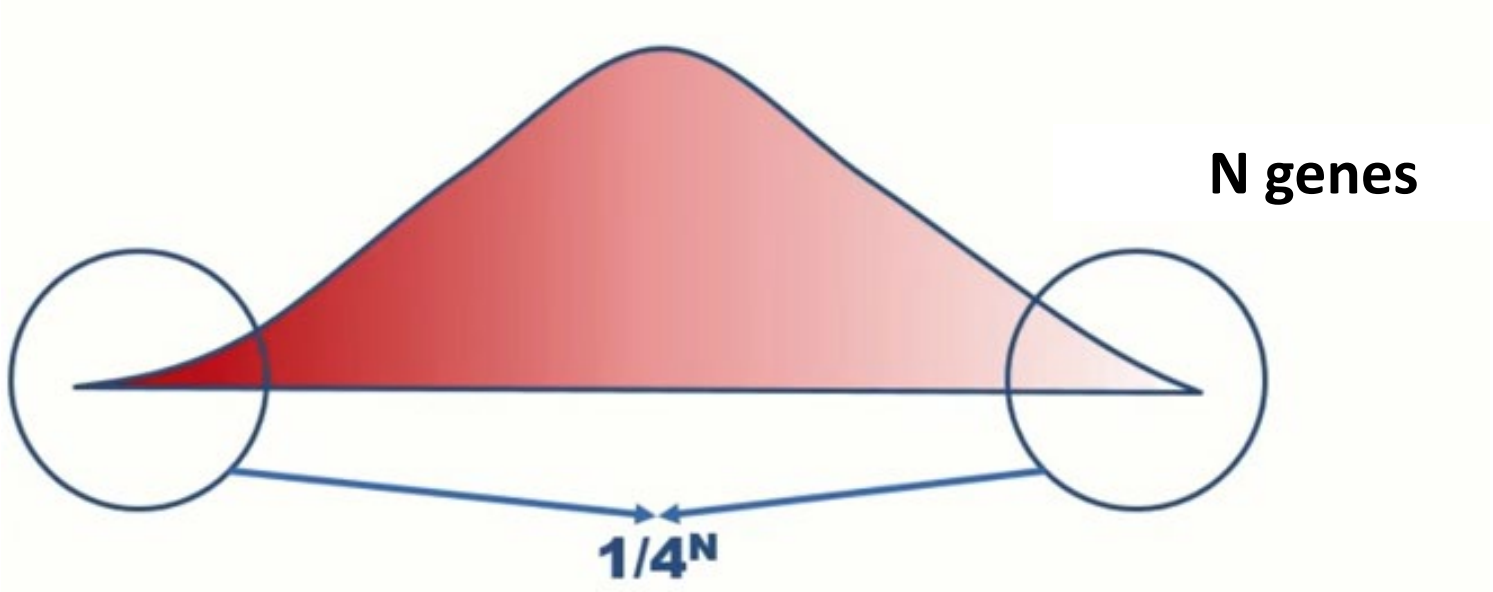
20 cm

$$\frac{10!}{4!\,6!}(1/2)^4 \times (1/2)^8 = \frac{210}{1024} \times 512 = 105$$

Questions of Quantitative Genetics

- **How many genes** are involved in a particular trait?

Calculating the number of genes involved in a quantitative trait



$$p = 1/4^N$$

$$\rightarrow \text{Log}(p) = \log(1/4^N) \rightarrow \text{Log}(p) = N \log(1/4) \rightarrow$$

$$\rightarrow N = \text{Log}(p) / \log(1/4)$$

Source: https://youtu.be/6yzSbXlZNuU

Calculating the number of genes involved in a quantitative trait

We have two purebreds plants producing fruits of 50g and 100g each.
F_1 is uniform and produces in average fruits of 75g.
F_2 is highly variable. 1 out of 1030 plants produces fruits of 50g.

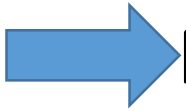
N = Log (p) / log(1/4) → N = Log (1/1030) / log(1/4) →

→ N =-3,013 / -0,602 → N = 5,005

Source: https://youtu.be/6yzSbXlZNuU

Questions of Quantitative Genetics

- What portion of observed variability is due to a **genetic differences** between individuals? What portion is due to **environmental factors**?

GENOTYPE (G) + ENVIRONMENT (E)  **PHENOTYPE (P)**

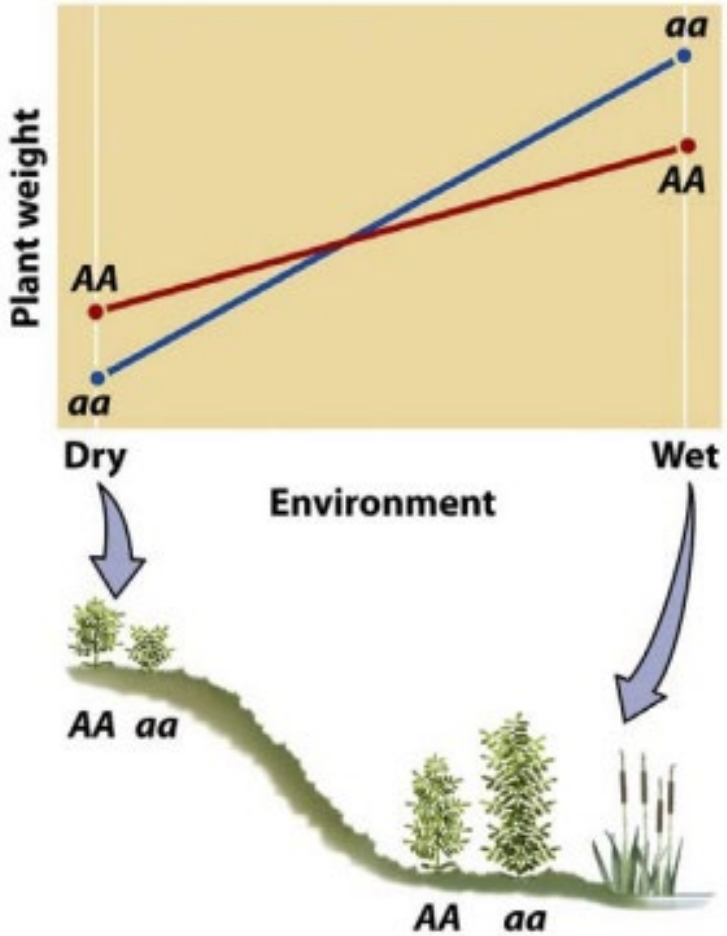
Heritability: estimates the degree of variation in a phenotypic trait in a population that is due to genetic variation between individuals in that population.

GENOTYPE (G) + ENVIRONMENT (E) → **PHENOTYPE (P)**

$$VAR(P) = VAR(G) + VAR(E) + VAR(G/E)$$

Additive variance
Dominance variance
Gene-interaction variance

VAR(G/E): the expression of some genes relies on environmental factors.



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Broad-sense heritability *(H^2)*

Reflects all the genetic contributions to a population's phenotypic variance including additive, dominant, and the one due to gene interactions.

$$H^2 = \frac{\mathrm{Var}(G)}{\mathrm{Var}(P)}$$

Calculating broad-sense heritability *(H^2)*

by elimination of some components of the equation.

VAR(P) = VAR(G) + VAR(E)

If all individuals are bred in an identical and controlled environment

VAR(E) = 0

VAR(P) = VAR(G)

$$H^2 = \frac{\mathrm{Var}(G)}{\mathrm{Var}(P)}$$

Calculating broad-sense heritability *(H^2)*

by elimination of some components of the equation.

VAR(P) = VAR(G) + VAR(E)

If all individuals are clones (genetically identical)

VAR(G) = 0

VAR(P) = VAR(E)

$$H^2 = \frac{\mathrm{Var}(G)}{\mathrm{Var}(P)}$$

Calculating broad-sense heritability *(H^2)*

by elimination of some components of the equation.

Experiment 1

We cultivate a type of plant and observe the size of the fruits. All variance will be considered VAR(P)

VAR(P) = VAR(G) + VAR(E) = 573

Experiment 2

We reproduce an individual asexually and observe the size of the fruits. All variance will be considered VAR(E)

VAR(P) = VAR(E) = 340

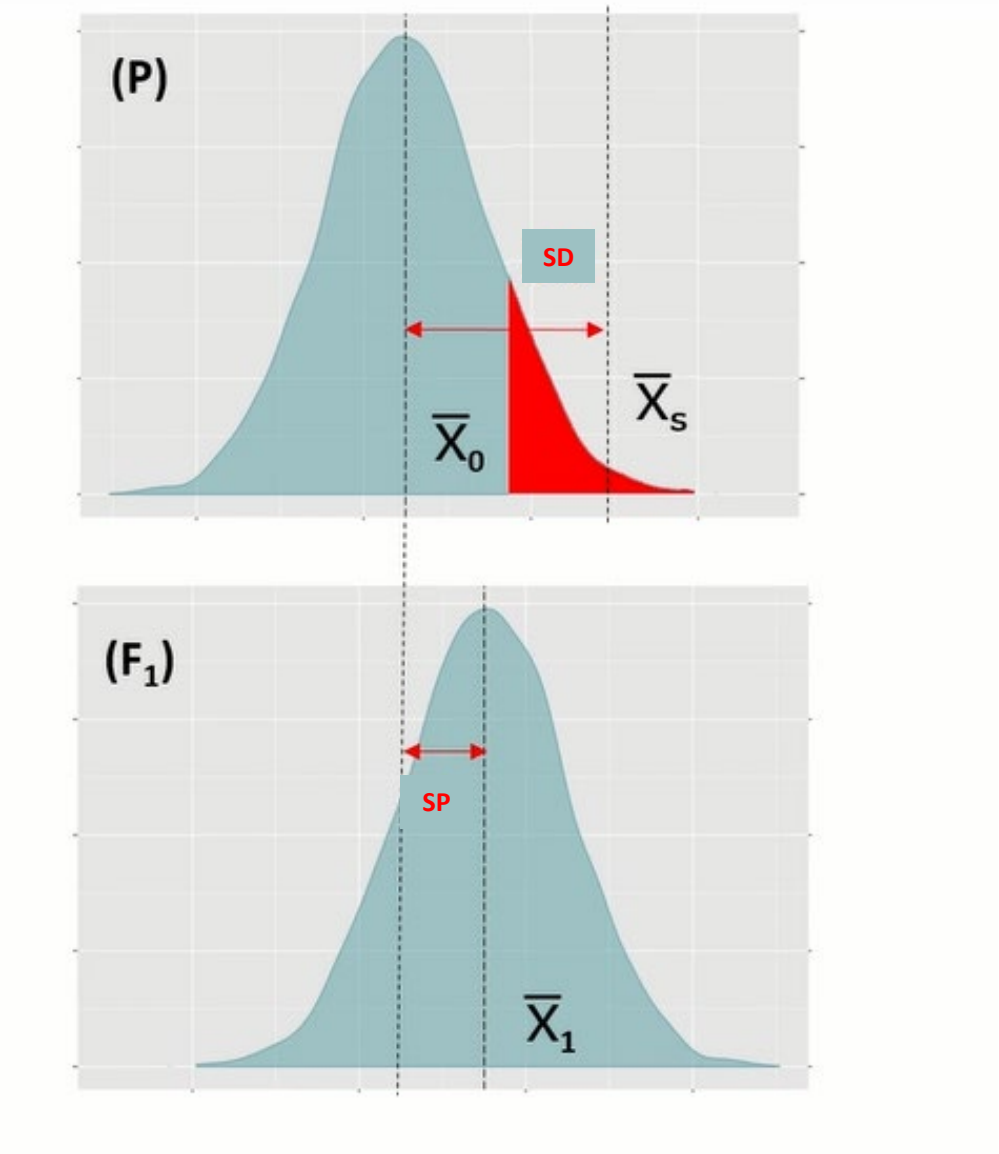
VAR(G) = VAR(P) - VAR(E) = 573 - 340 = 233

$$H^2 = \frac{\mathrm{Var}(G)}{\mathrm{Var}(P)} = \frac{233}{573} = 0.41$$

Narrow-sense heritability *(h^2)*

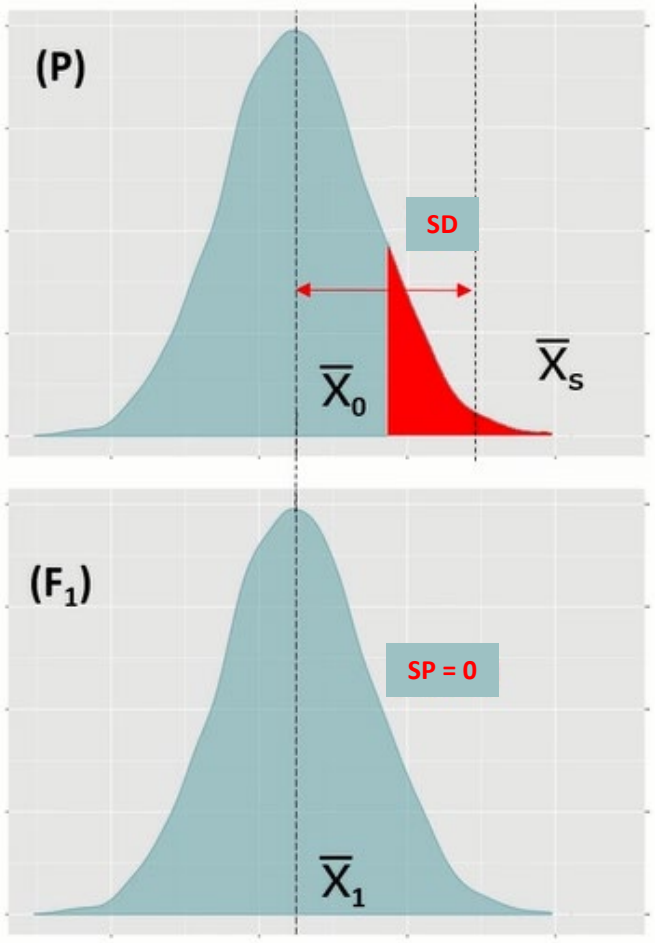
Reflects the genetic contribution of additive alleles to a population's phenotypic variance.

$$h^2 = \frac{\mathrm{Var}(A)}{\mathrm{Var}(P)}$$



$$h^2 = \frac{selection\ progress}{selection\ differential} = \frac{|x_1 - x_0|}{|x_s - x_0|}$$

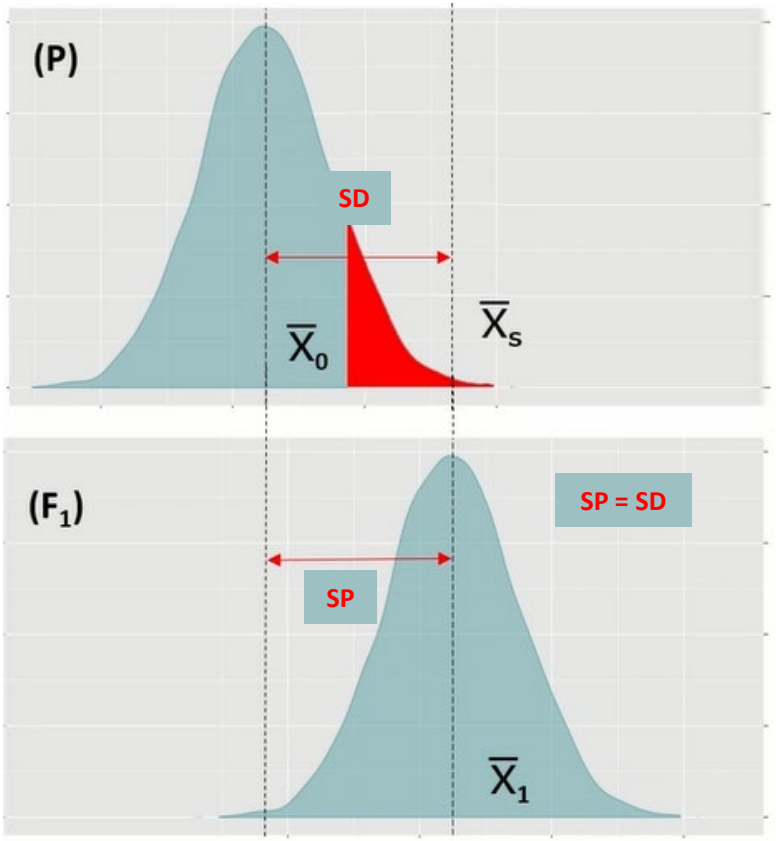
Source: https://youtu.be/BaC37Qa6LKE



$$h^2 = \frac{selection\ progress}{selection\ differential} = \frac{|x_1 - x_0|}{|x_s - x_0|}$$

$$\frac{\overline{X}_1 - \overline{X}_0}{\overline{X}_S - \overline{X}_0} \quad (\overline{X}_1 = \overline{X}_0) \quad \overline{X}_1 - \overline{X}_0 = 0 \quad = 0$$

Source: https://youtu.be/BaC37Qa6LKE

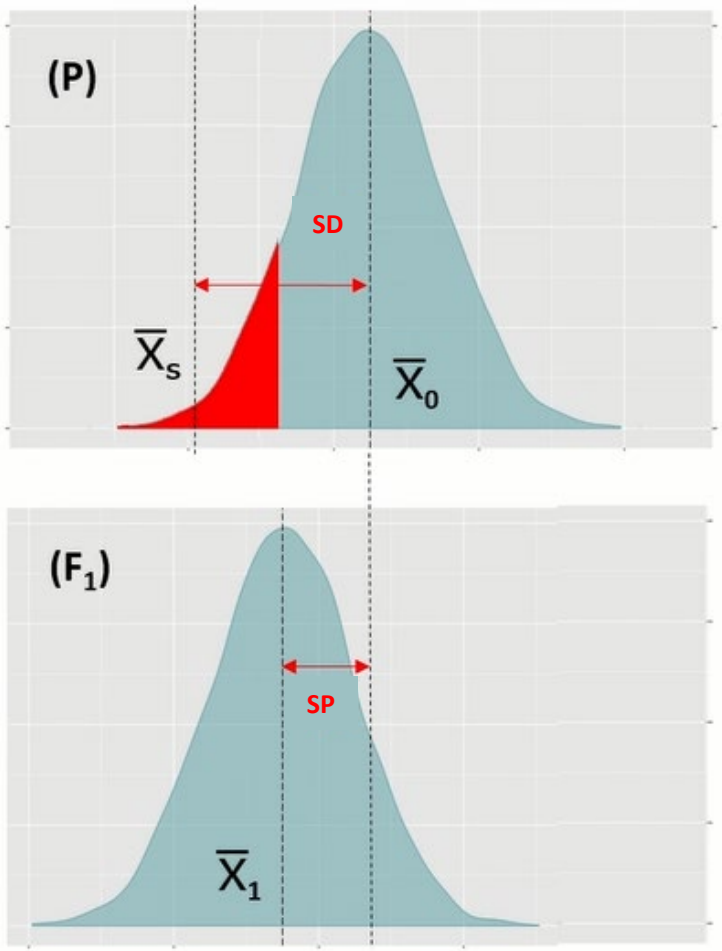


$$h^2 = \frac{selection\ progress}{selection\ differential} = \frac{|x_1 - x_0|}{|x_s - x_0|}$$

$(\overline{X}_1 = \overline{X}_S)$

$$\frac{\overline{X}_1 - \overline{X}_0}{\overline{X}_S - \overline{X}_0} = 1$$

Source: https://youtu.be/BaC37Qa6LKE



$$h^2 = \frac{selection\ progress}{selection\ differential} = \frac{|x_1 - x_0|}{|x_s - x_0|}$$

$(\overline{X}_1 < \overline{X}_0)$

$$\frac{\overline{X}_1 - \overline{X}_0}{\overline{X}_S - \overline{X}_0}$$

$(\overline{X}_s < \overline{X}_0)$

Source: https://youtu.be/BaC37Qa6LKE

Heritability

$0 < h^2 > 0.25$	**Low**
$0.25 < h^2 > 0.5$	**Medium**
$0.5 < h^2 > 1$	**High**

In traits with **high heritability**, additive genetic component is predominant. They are easily improved.

In traits with **low heritability**, non-genetic components are more important in the expression of the character (environment). They are not easily improved.

Genetic Improvement

Can we improve a trait indefinitely?

- After many generations of selection, selection response stabilizes and the trait do not longer respond to selection.

- Genetic variability decreases in the population. Additive alleles get fixed. Heritability tends to 0.

Limitations of the heritability

- It is not individual but it refers to a specific population.
- There is no universal value of heritability for a particular trait.
- Even though heritability is high, influence of environment can still be important.

Questions of Quantitative Genetics

- Where are these genes **located in the genome**?

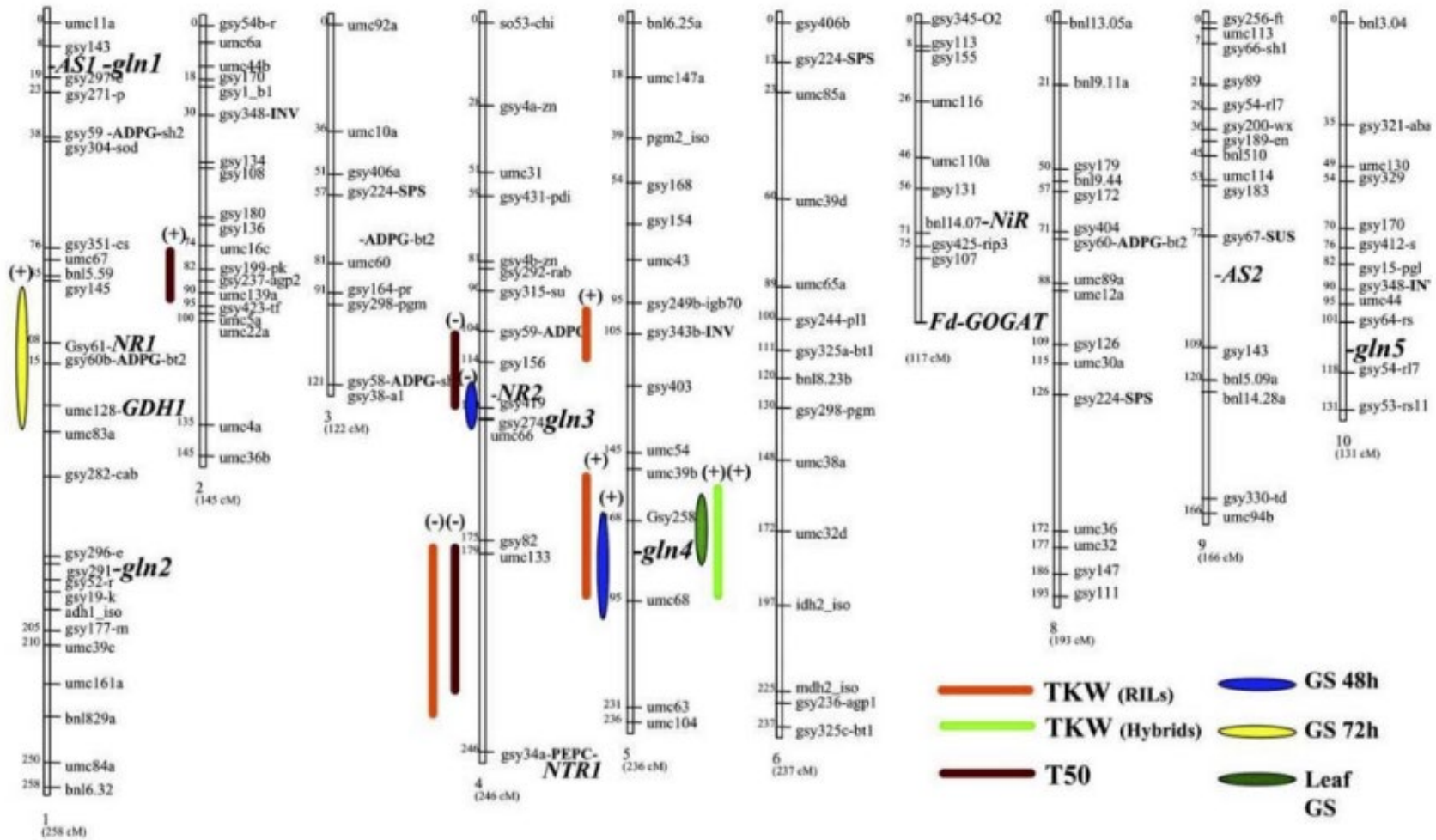
QTLs (Quantitative Trait Loci)

Chromosome regions involved in the expression of a polygenic trait.

If we find a molecular marker systematically inherited with a trait, this is most probably associated to a QTL.

Table 24.2 Quantitative characteristics for which QTLs have been detected

Organism	Quantitative Characteristic	Number of QTLs Detected
Tomato	Soluble solids	7
	Fruit mass	13
	Fruit pH	9
	Growth	5
	Leaflet shape	9
	Height	9
Corn	Height	11
	Leaf length	7
	Tiller number	1
	Glume hardness	5
	Grain yield	18
	Number of ears	9
	Thermotolerance	6
Common bean	Number of nodules	4
Mung bean	Seed weight	4
Cow pea	Seed weight	2
Wheat	Preharvest sprout	4
Pig	Growth	2
	Length of small intestine	1
	Average back fat	1
	Abdominal fat	1
Mouse	Epilepsy	2
Rat	Hypertension	2


umc11a
gsy143
-AS1-gln1
gsy297-e
gsy271-p
gsy59 -ADPG-sh2
gsy304-sod
gsy351-cs
umc67
bnl5.59
gsy145
Gsy61-NR1
gsy60b-ADPG-bt2
umc128-GDH1
umc83a
gsy282-cab
gsy296-e
gsy291-gln2
gsy52-r
gsy19-k
adh1_iso
gsy177-m
umc39c
umc161a
bnl829a
umc84a
bnl6.32
1
(258 cM)
gsy54b-r
umc6a
umc44b
gsy170
gsy1_b1
gsy348-INV
gsy134
gsy108
gsy180
gsy136
umc16c
gsy199-pk
gsy237-agp2
umc139a
gsy423-tf
umc59a
umc22a
umc4a
umc36b
2
(145 cM)
umc92a
umc10a
gsy406a
gsy224-SPS
-ADPG-bt2
umc60
gsy164-pr
gsy298-pgm
gsy58-ADPG-st
gsy38-a1
3
(122 cM)
so53-chi
gsy4a-zn
umc31
gsy431-pdi
gsy4b-zn
gsy292-rab
gsy315-su
gsy59-ADP
gsy156
-NR2
gsy274
gln3
umc66
gsy82
umc133
gsy34a-PEPC-
NTR1
4
(246 cM)
bnl6.25a
umc147a
pgm2_iso
gsy168
gsy154
umc43
gsy249b-igb70
gsy343b-INV
gsy403
umc54
umc39b
Gsy258
-gln4
umc68
umc63
umc104
5
(236 cM)
gsy406b
gsy224-SPS
umc85a
umc39d
umc65a
gsy244-pl1
gsy325a-bt1
bnl8.23b
gsy298-pgm
umc38a
umc32d
idh2_iso
mdh2_iso
gsy236-agp1
gsy325c-bt1
6
(237 cM)
gsy345-O2
gsy113
gsy155
umc116
umc110a
gsy131
bnl14.07-NiR
gsy425-rip3
gsy107
Fd-GOGAT
(117 cM)
bnl13.05a
bnl9.11a
gsy179
bnl9.44
gsy172
gsy404
gsy60-ADPG-bt2
umc89a
umc12a
gsy126
umc30a
gsy224-SPS
umc36
umc32
gsy147
gsy111
8
(193 cM)
gsy256-ft
umc113
gsy66-sh1
gsy89
gsy54-rl7
gsy200-wx
gsy189-en
bnl510
umc114
gsy183
gsy67-SUS
-AS2
gsy143
bnl5.09a
bnl14.28a
gsy330-td
umc94b
9
(166 cM)
bnl3.04
gsy321-aba
umc130
gsy329
gsy170
gsy412-s
gsy15-pgl
gsy348-IN'
umc44
gsy64-rs
-gln5
gsy54-rl7
gsy53-rs11
10
(131 cM)
TKW (RILs)
TKW (Hybrids)
T50
GS 48h
GS 72h
Leaf GS