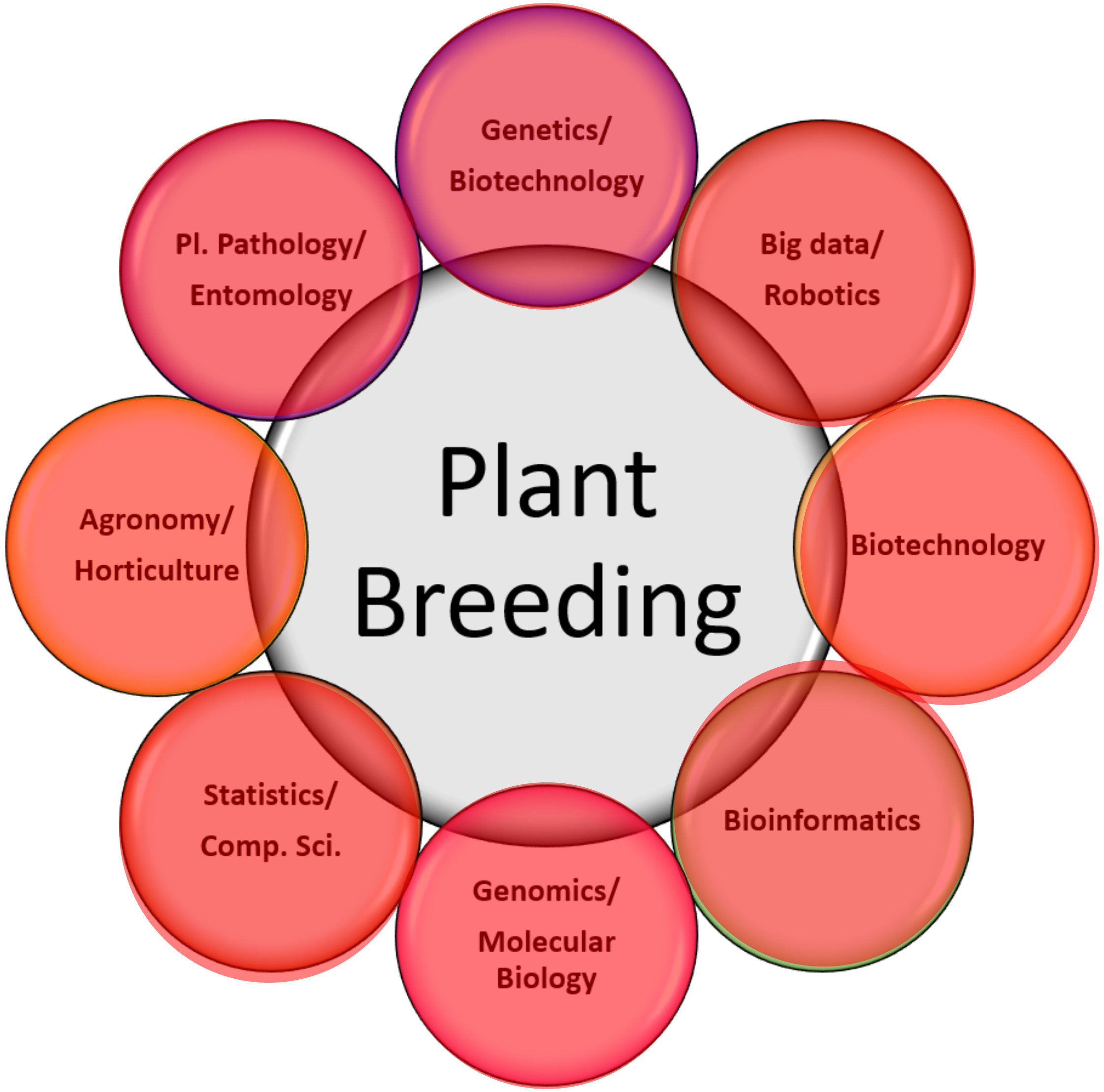
Quantitative Genetics



Plant Breeding

Genetics/ Biotechnology

Big data/ Robotics

Biotechnology

Bioinformatics

Genomics/ Molecular Biology

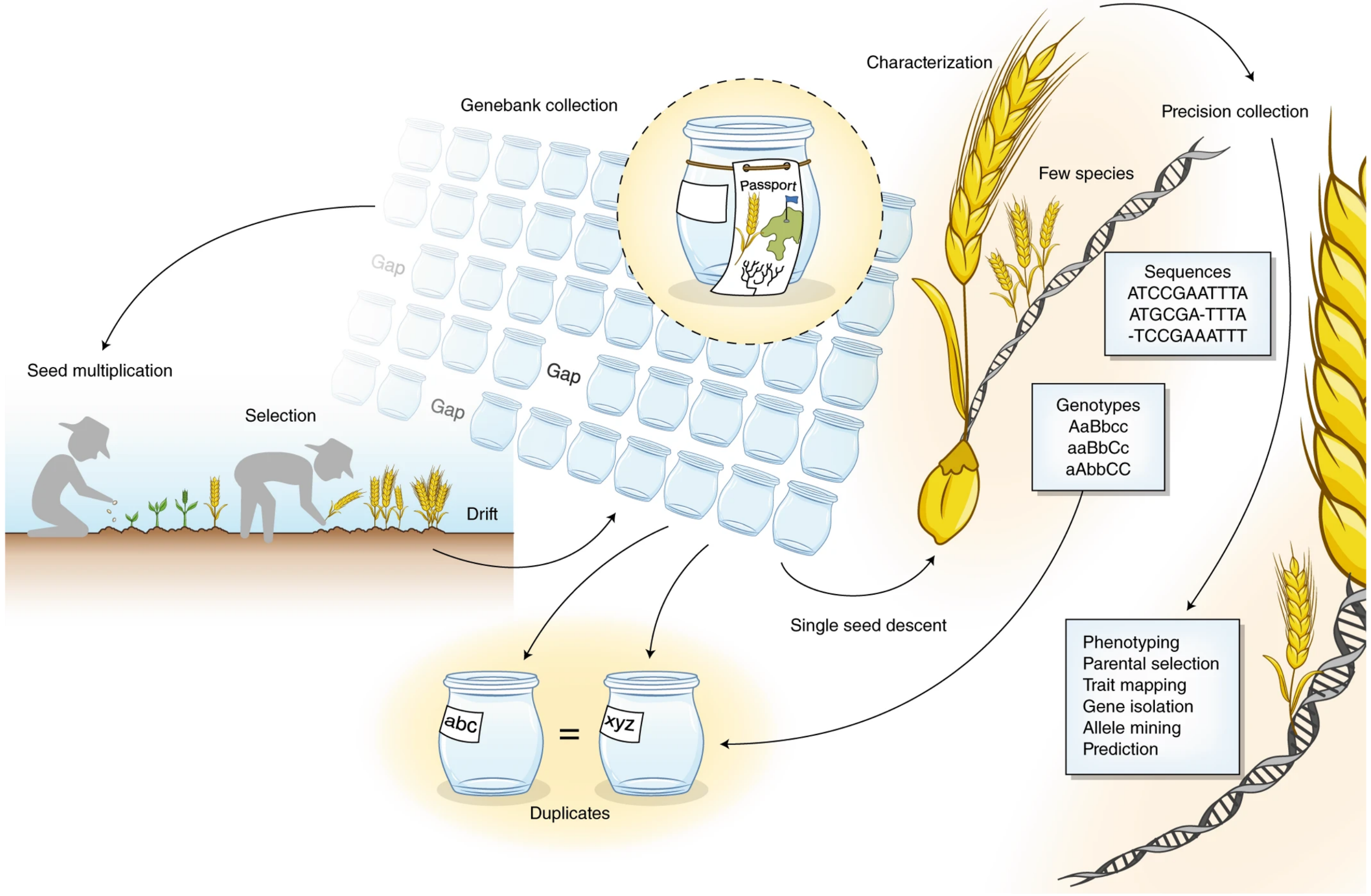
Statistics/ Comp. Sci.

Agronomy/ Horticulture

Pl. Pathology/ Entomology

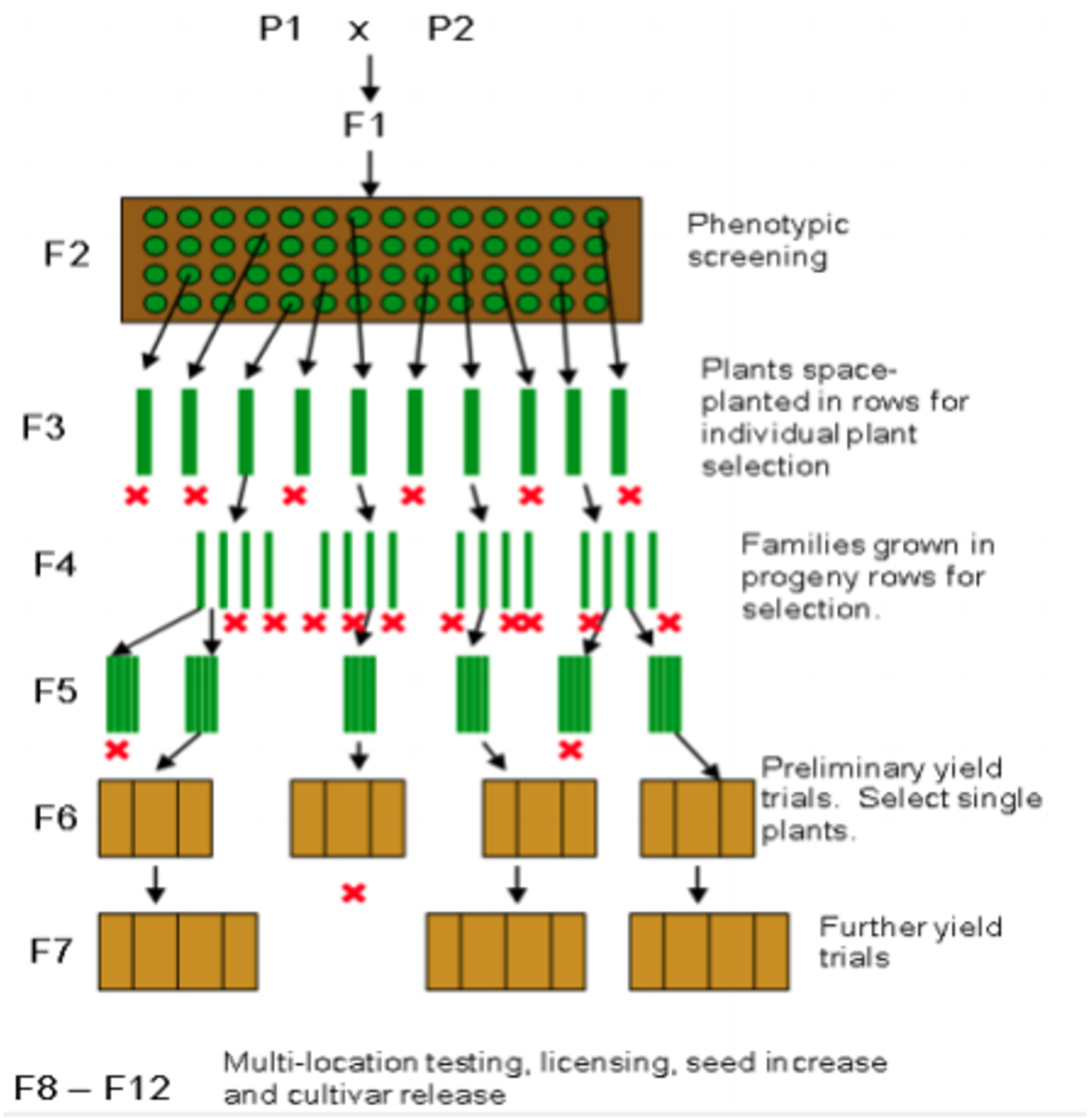
Where are we and where do we want to go?

- Conventional breeding
- Marker Assisted Selection
- Genomic Selection



Mascher et al 2019

Conventional Plant Breeding



Phenotypic screening

Plants space-planted in rows for individual plant selection

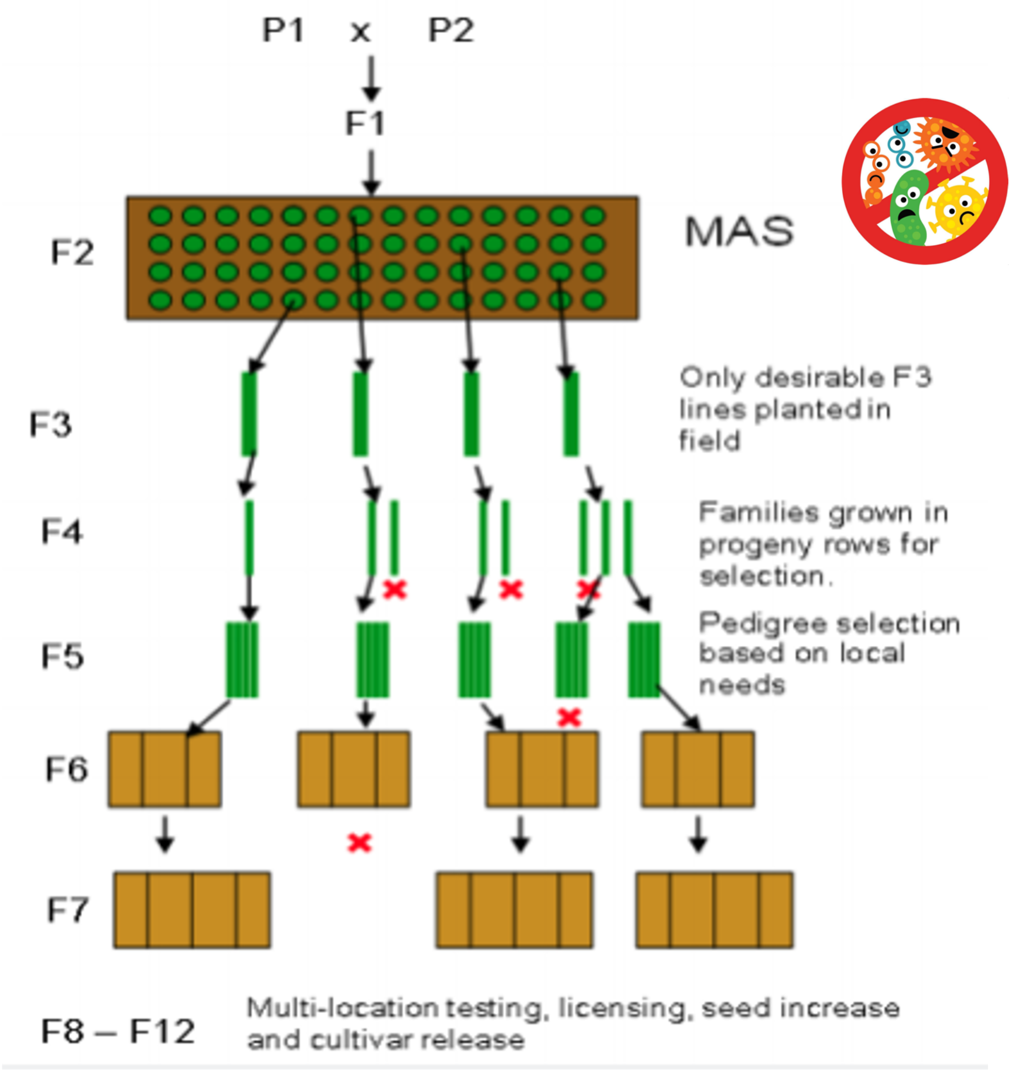
Families grown in progeny rows for selection.

Preliminary yield trials. Select single plants.

Further yield trials

Multi-location testing, licensing, seed increase and cultivar release

Marker Assisted Selection



Only desirable F3 lines planted in field

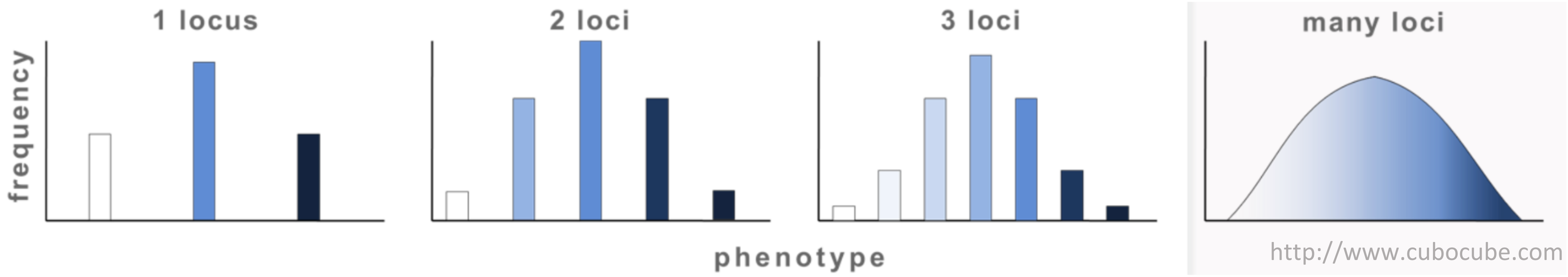
Families grown in progeny rows for selection.

Pedigree selection based on local needs

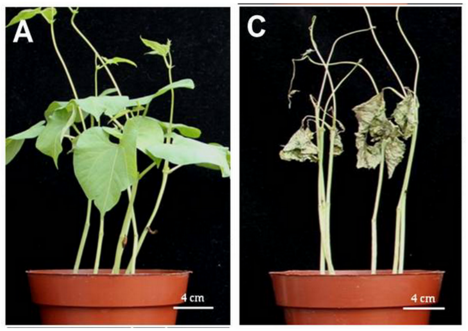
Multi-location testing, licensing, seed increase and cultivar release

Lema 2018

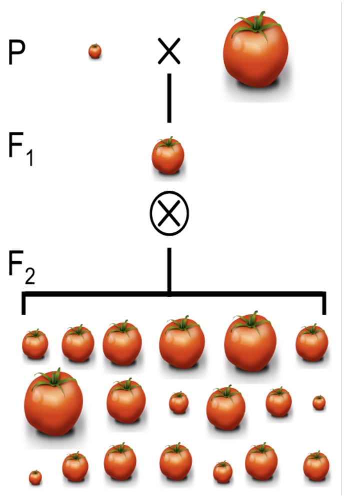
What are quantitative traits?



http://www.cubocube.com

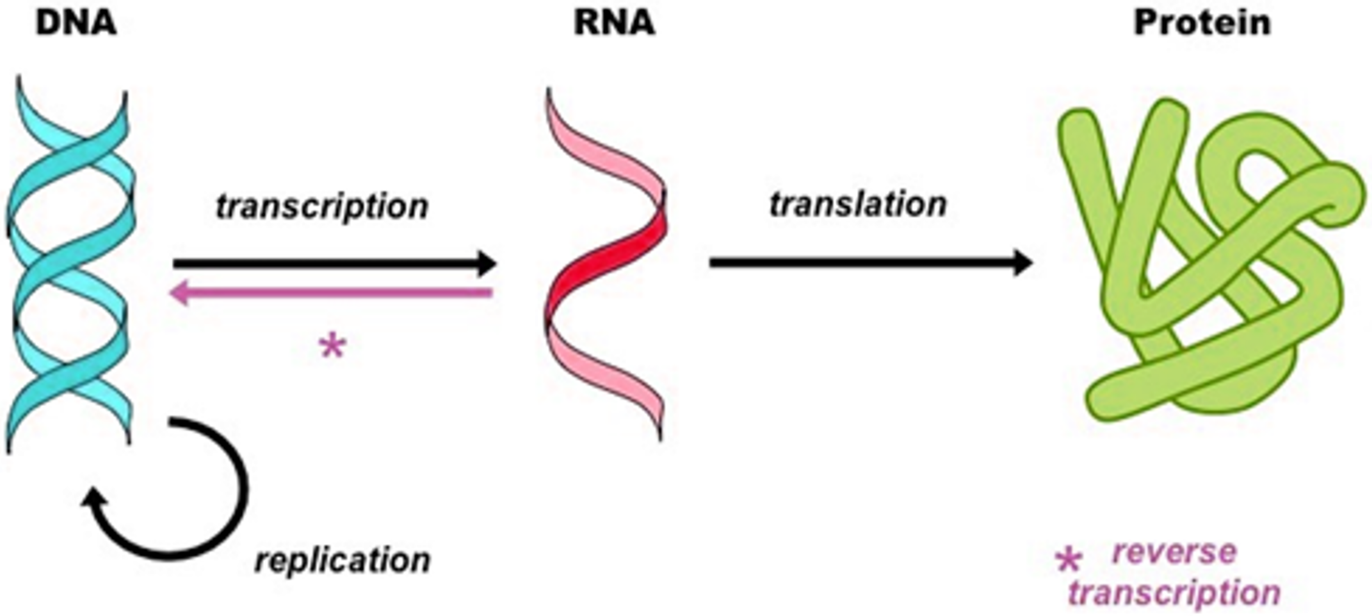


Chen *et al* 2017



Important concepts

CENTRAL DOGMA



DNA

RNA

Protein

transcription

translation

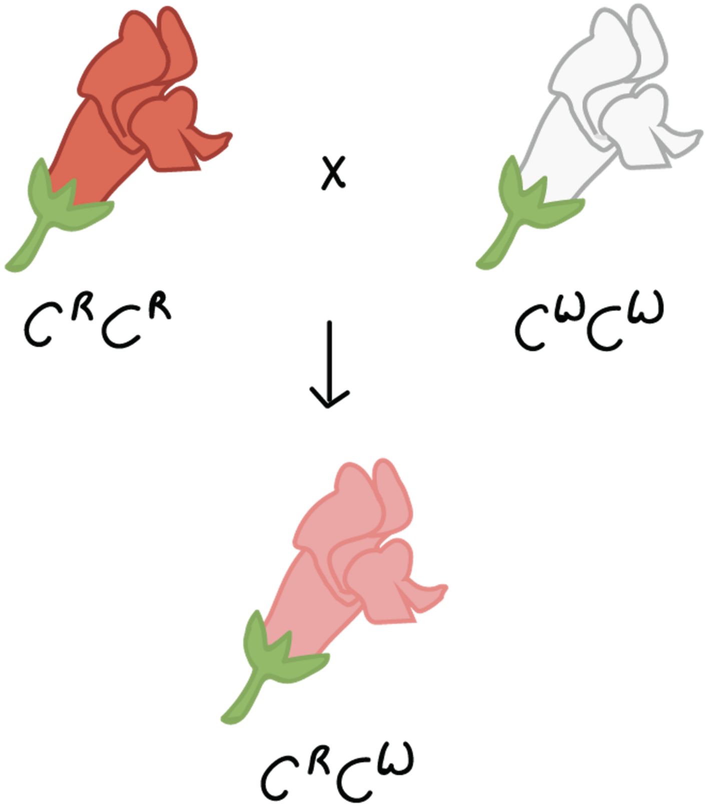
*

replication

* reverse transcription

Alleles

- An allele is one of two or more versions of a gene.
- If two alleles are the same, the individual is homozygous for that gene.
- If the alleles are different, the individual is heterozygous.
- The use of the allele also refers to variation among non-coding DNA sequences.



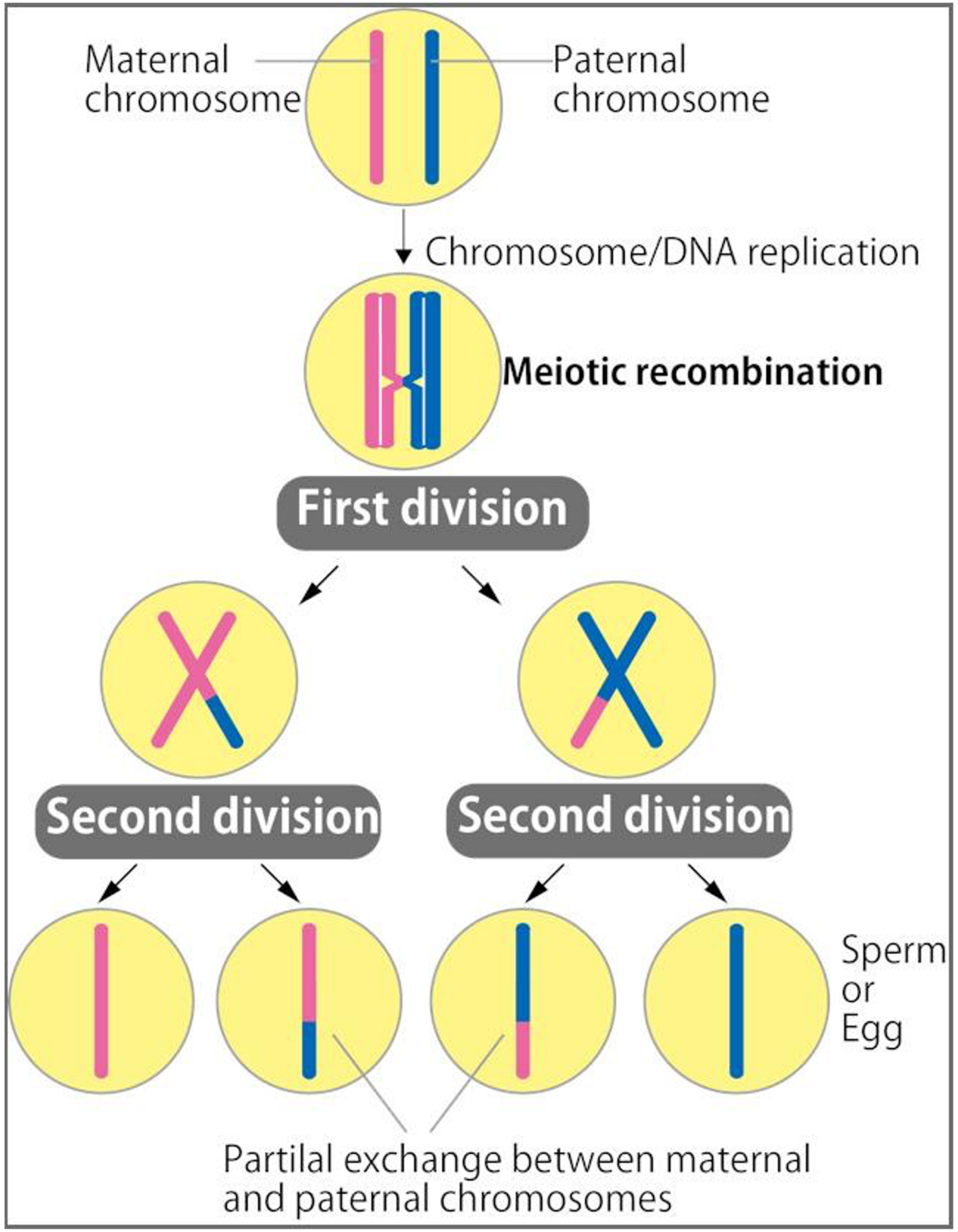
https://www.khanacademy.org

Meiosis

During meiosis, diploid cells undergo DNA replication, followed by two rounds of cell division in germ cells, producing four haploid sex cells.

Meiosis maintains genetic continuity from generation to generation and gives rise to genetic variation in gametes through:

- Crossing over of homologous chromosomes.
- Unique combinations of maternal/paternal chromosomes.



Population genetics

Allele Frequencies

- Consider a locus with two possible alleles (A and a)

$$A = p \,,\ a = q$$

- We can estimate the frequency of AA genotype by dividing the number of AA individuals by total number of individuals in the population.

$$AA + Aa + aa = 1$$

- Allele Frequencies:

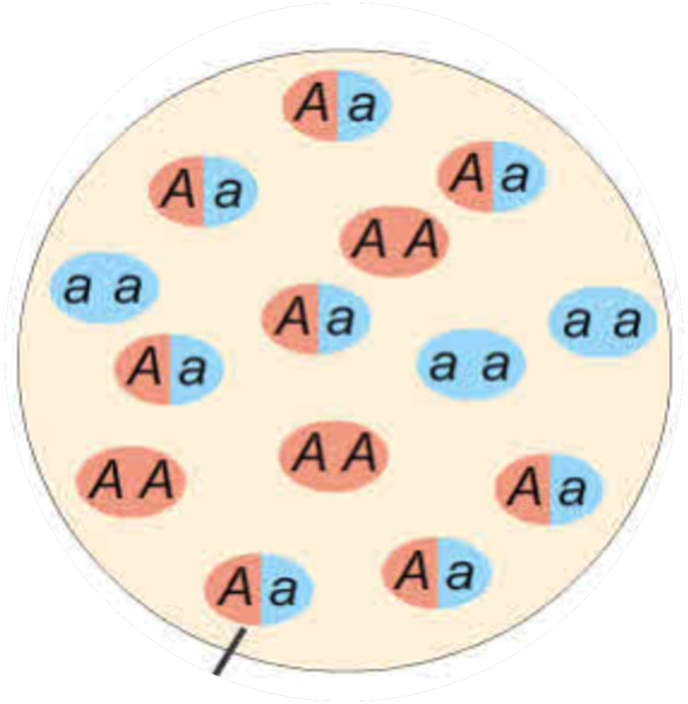
$p = f(AA) + \frac{1}{2} f\,(Aa)$ = frequency of A

$q = f(aa) + \frac{1}{2}\ f(Aa) = 1 - p$ frequency of a

$$p + q = 1$$

Hardy-Weinberg Equilibrium

HWE law, states that allele and genotype frequencies in a population will remain constant from generation to generation in the absence of other evolutionary influences.

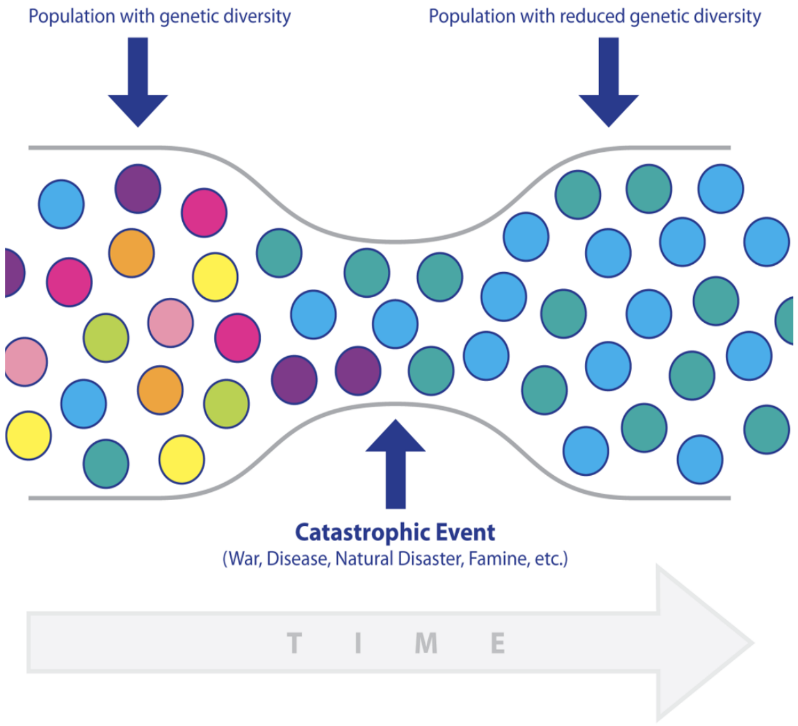


Meiosis:

- Aa produces gametes A and a (in equal frequency)
- The homozygous AA only produce one gamete: A
- Likewise aa only produce one gamete: a

Hardy-Weinberg assumptions

- Random mating
- Genotypes have same viability
- Population must not be divided into subpopulations
- Apply only to large populations
- No migration
- No mutation
- No selection
- No drift

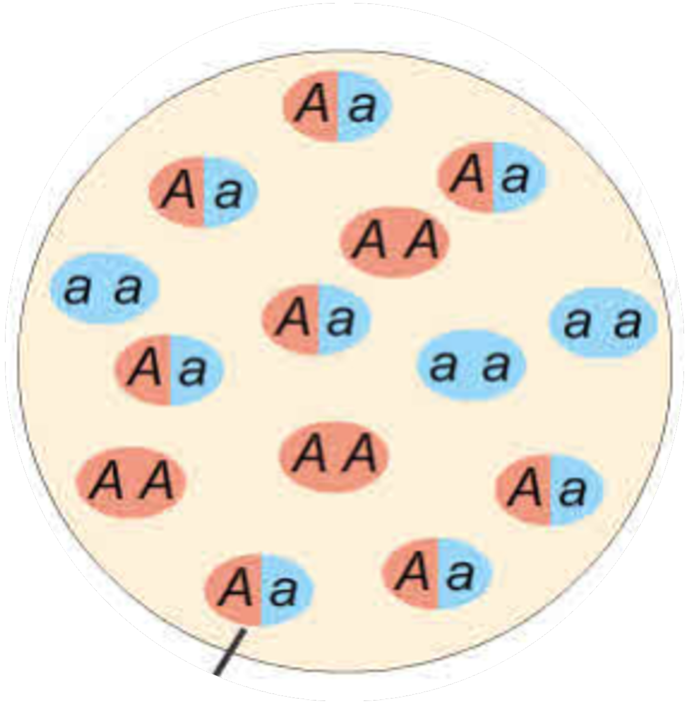


https://co.pinterest.com/

If any of these assumptions is not true, the population could departure from HWE.

These departures in most cases manifest as an excess of homozygosity relative to HWE.

Hardy-Weinberg Equilibrium



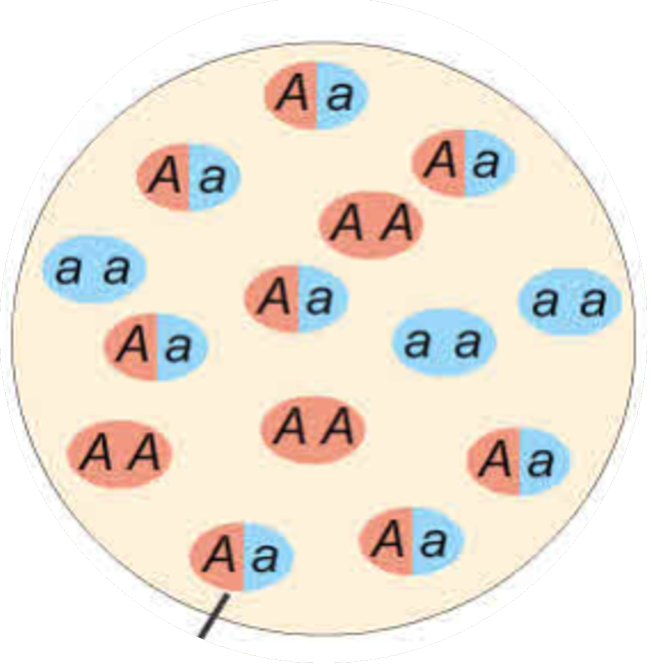
Random sampling of gametes (random sampling of parents + **no mutation**)

p(A)=p   p(a) = q = (1-p)

Expected genotype frequencies (**random mating**)

AA=p^2 ,   aa=q^2 ,   Aa=2pq

Hardy-Weinberg Equilibrium



N = 14

AA = 3

Aa = 8

aa = 3

p(A)=p   p(a) = q = (1-p)

p= f(AA) + $\frac{1}{2}$ f (Aa) = frequency of A

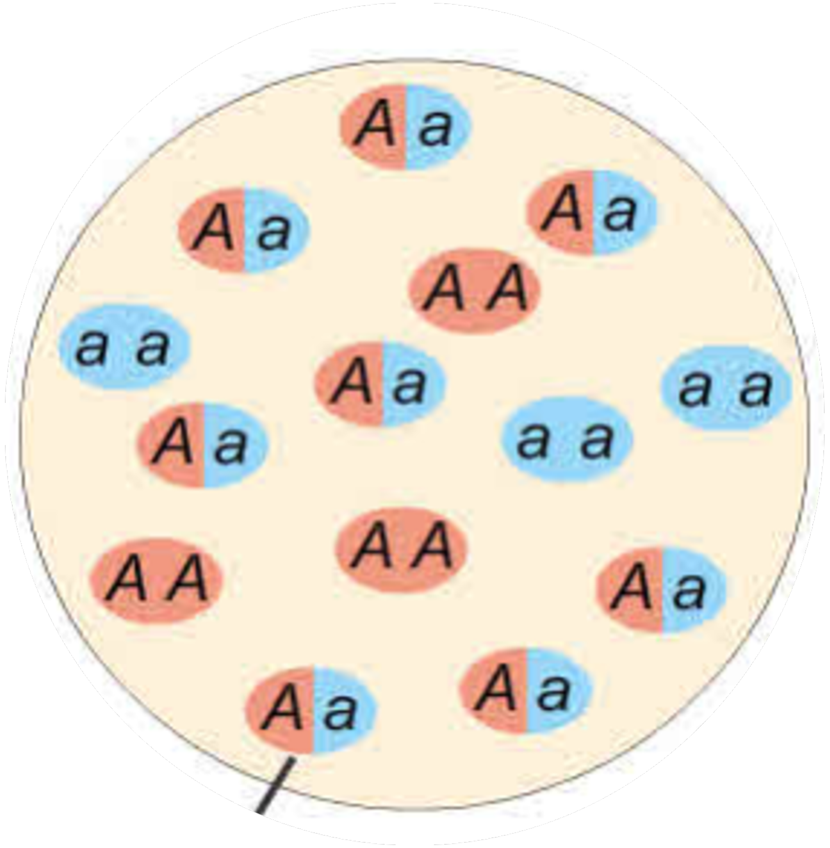
p = (3/14) + $\frac{1}{2}$(8/14) = 0.5

q = (1-p)

q = 1– 0.5 = 0.5

Hardy-Weinberg Equilibrium

N = 14, AA = 3 , Aa = 8, aa = 3



$p = 0.5$
$q = 0.5$

Expected genotype frequencies :

$p(AA)=p^2$, $p(Aa)=2pq$, $p(aa)=q^2$

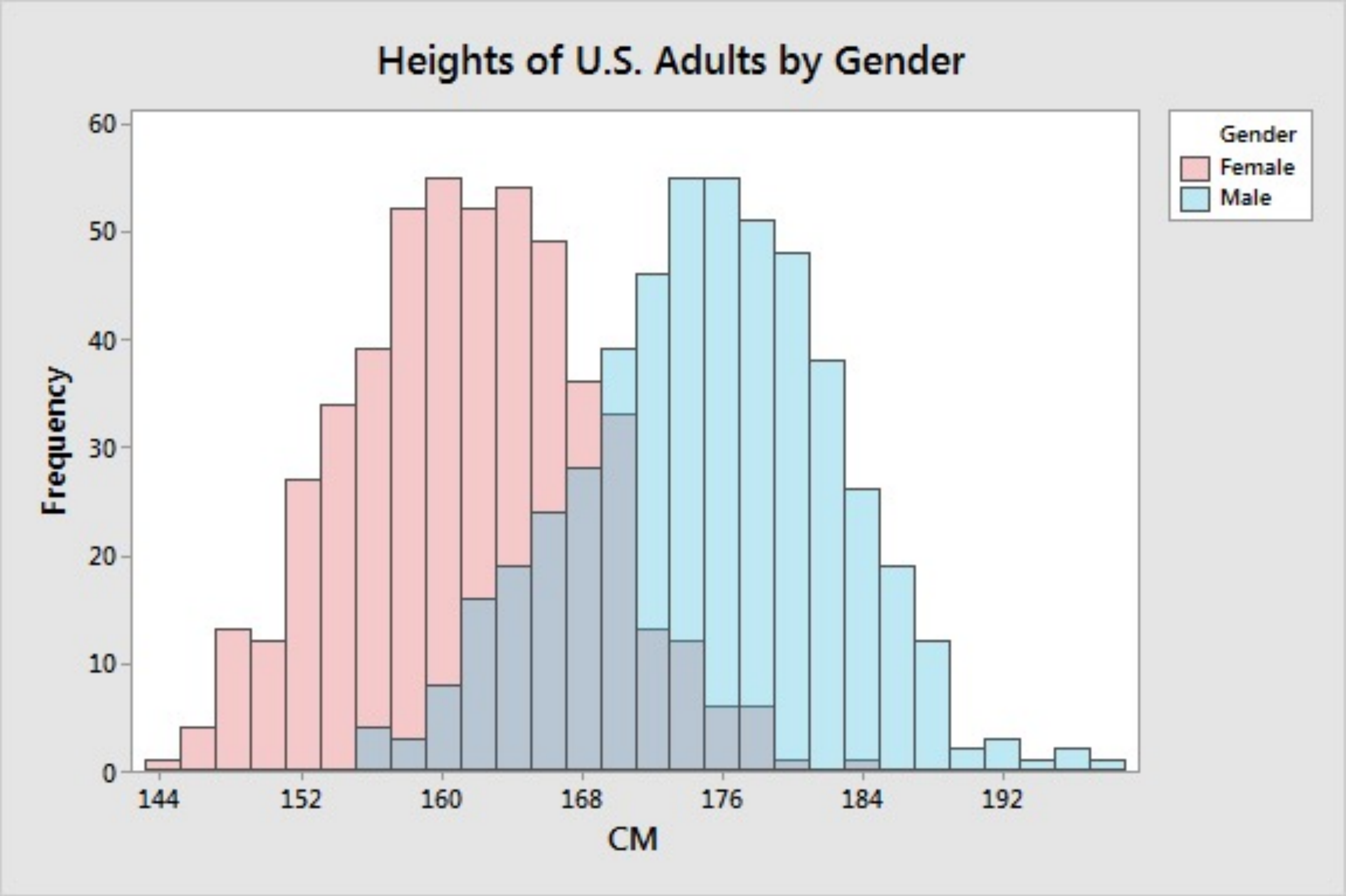
$p^2 + 2pq + q^2$

$0.5^2 + 2(0.5*0.5) + 0.5^2 =$ 0.25, 0.5, 0.25

Review

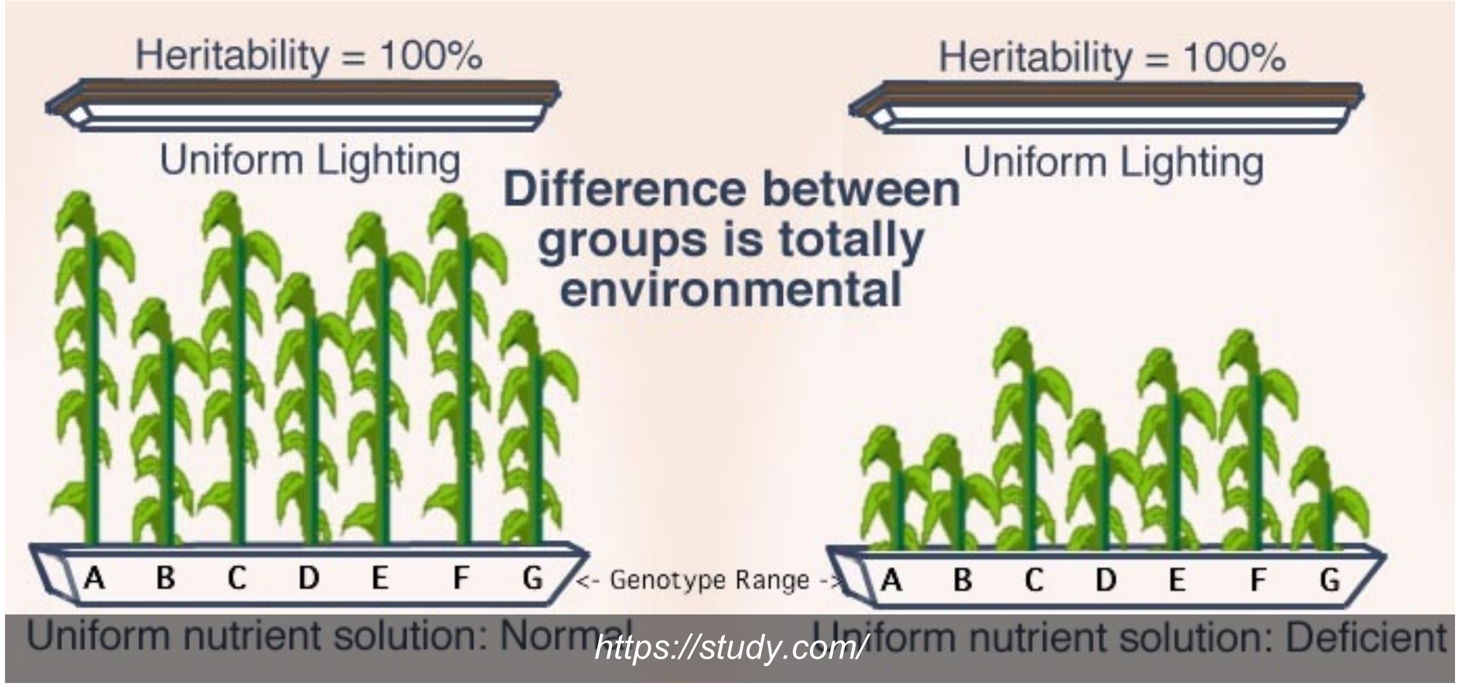
- Central dogma
- Meiosis
- Allele frequencies
- genotype frequencies
- HWE

Quantitative Genetics



The inheritance of complex traits

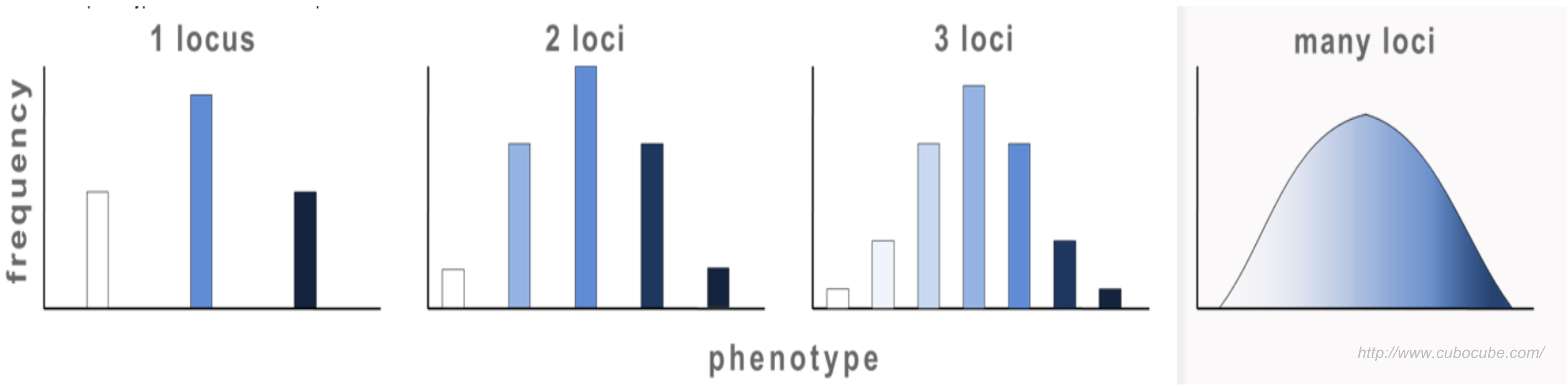
- Quantitative variation: Mean, variance, standard deviation
- Genetic model
- Genetic and environmental variances



https://study.com/

Quantitative variation

Traits that show a continuous range of variation and don’t behave in simple Mendelian fashion are known as quantitative or complex traits



http://www.cubocube.com/

Quantitative genetics!

Basic statistical concepts

Mean

$$\overline{X} = \frac{1}{n}\sum_{i=1}^{n} X_i$$

$$\bar{X} = \frac{X_1 + X_1 + X_{1\ldots}X_n}{n}$$

Where

$\bar{X}$ = mean

X_1 = first value

X_2 = second value

X_3 = third value

X_n = last value

n = number of samples

Basic statistical concepts

Mean

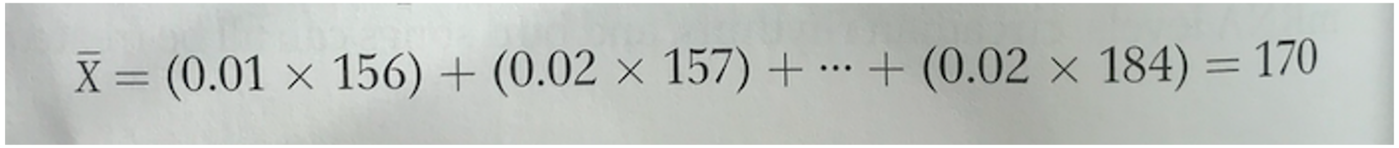
$$\bar{X} = \sum_{i=1}^{k} f_i X_i$$

Where
$\bar{X}$ = mean
k = classes
f = frequency

Height (cm)	Count	Frequency x Height
156	1	1.56
157	2	3.14
158	1	1.58
…	…	…
184	2	3.68
sum	100	170

Griffiths et al 2012

$\bar{X} = (X_1 * f_1) + (X_2 * f_2) + (X_3 * f_3)$



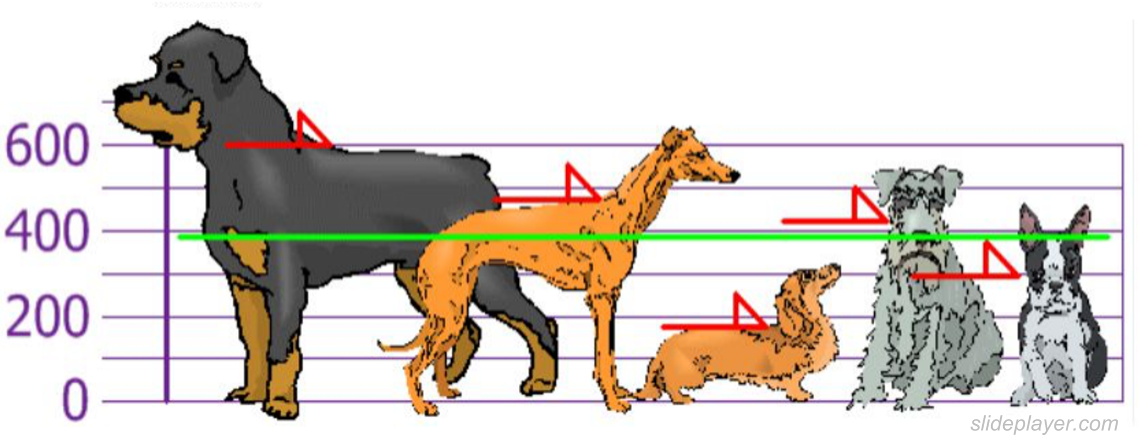
$\bar{X} = (0.01 \times 156) + (0.02 \times 157) + \cdots + (0.02 \times 184) = 170$

Basic statistical concepts

Variance:

Measure of dispersion around the mean.

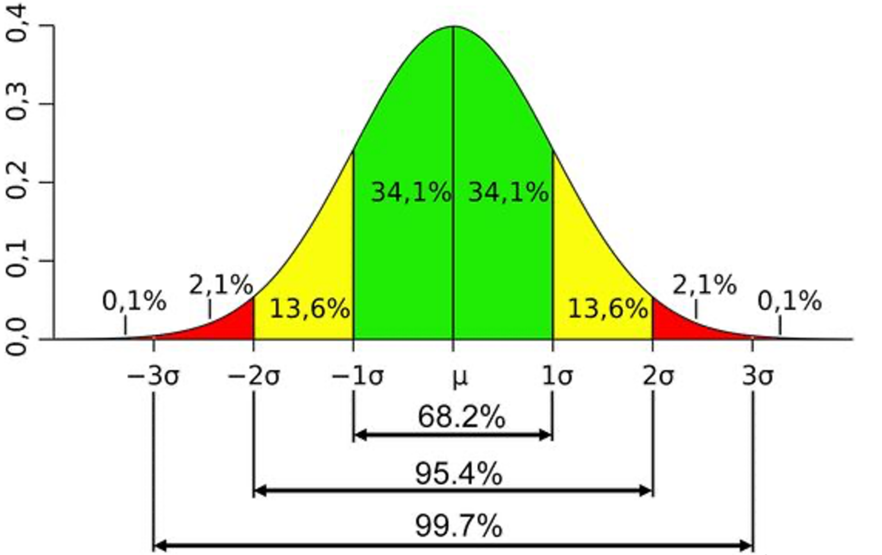
$$s^2 = \frac{1}{n-1}\sum_i (X_i - \bar{X})^2$$



slideplayer.com

Standard deviation:

$$s = \sqrt{\frac{1}{n}\sum_i (X_i - \bar{X})}$$
$$= \sqrt{s^2}$$



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Basic statistical concepts

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Standard deviation:

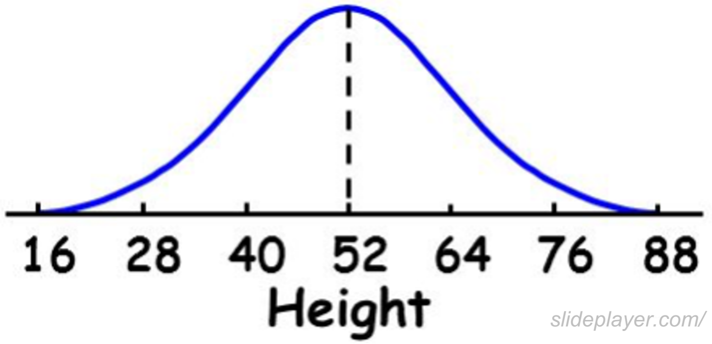
$$s = \sqrt{\frac{1}{n}\sum_i (X_i - \bar{X})}$$

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

pinterest.com

Simple genetic model

- $X = \bar{X} + g + e$



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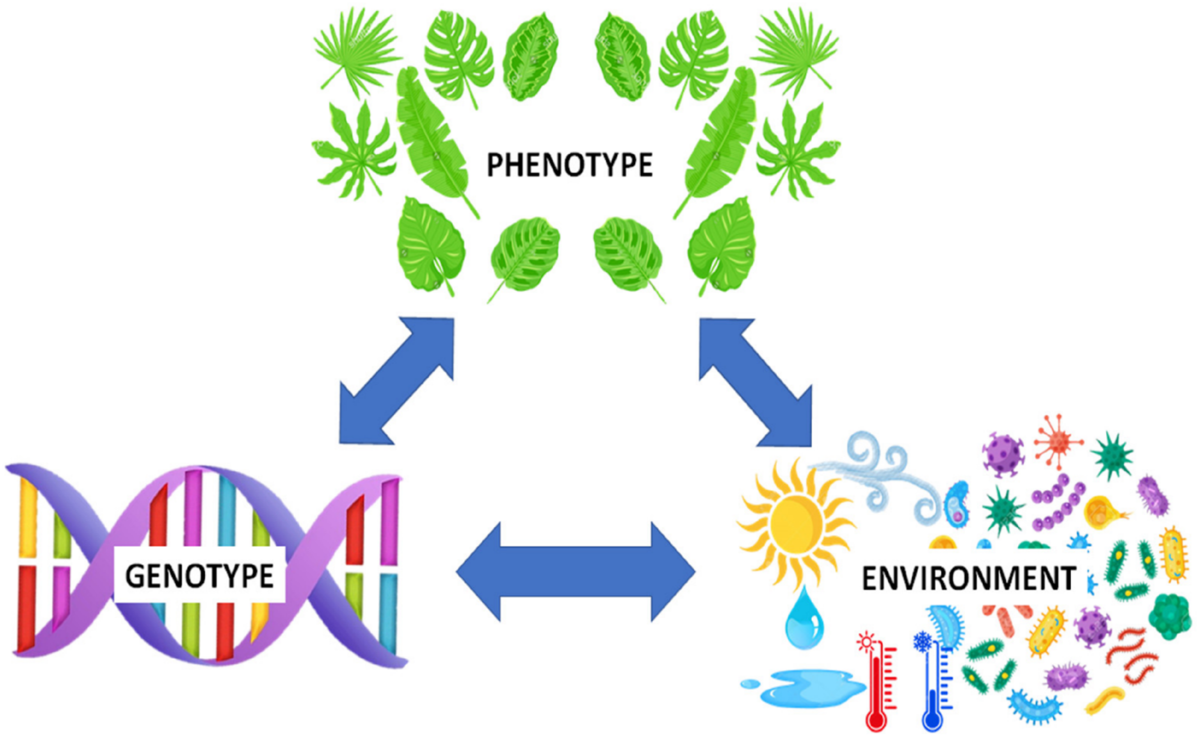


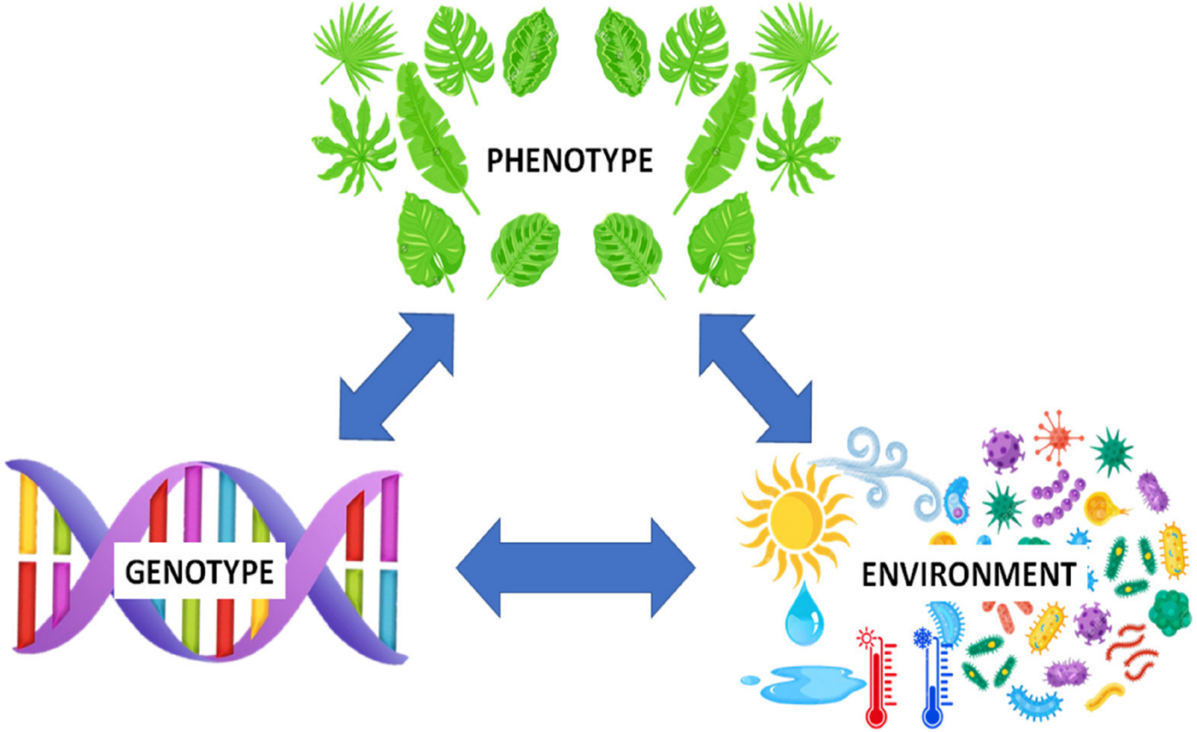
Djande et al 2020

Simple genetic model

$$X = \bar{X} + g + e$$

- $$x = g + e$$

x is the individual's phenotypic deviation.



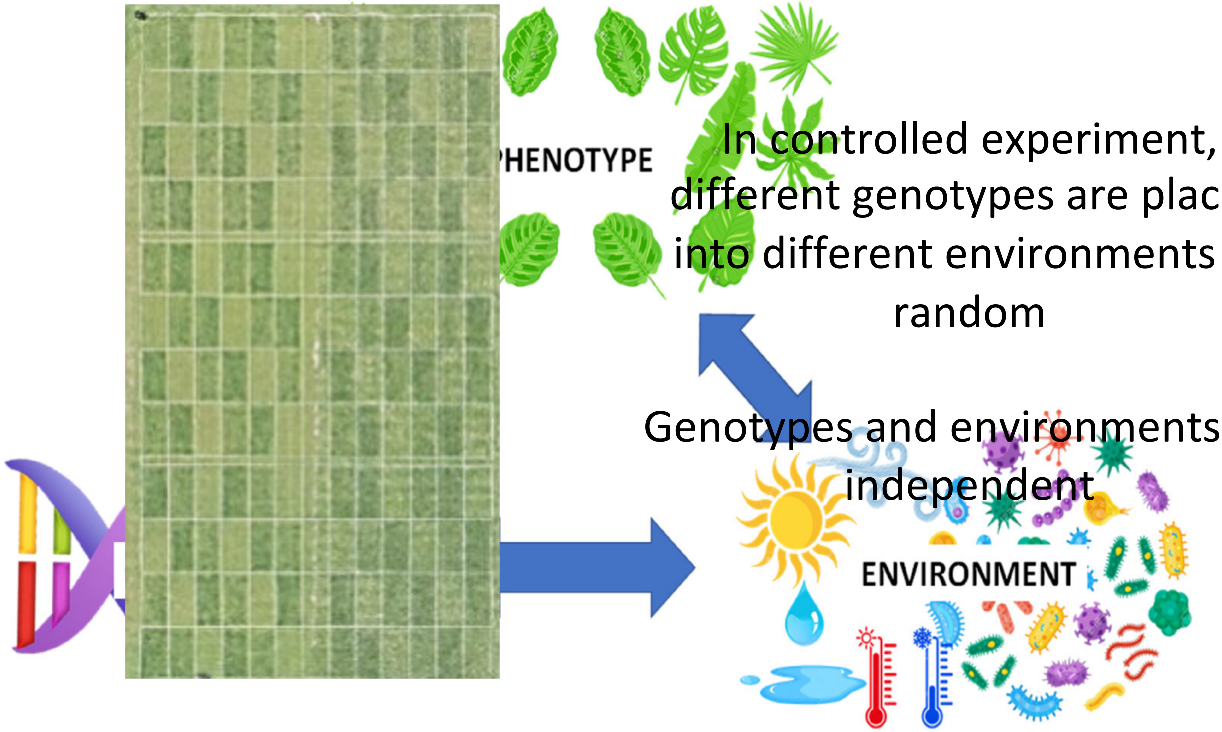
Djande et al 2020

Genetic and environmental variances

$$x = g + e$$

$$V_x = Vg + Ve + 2cov_{ge}$$

$$V_x = Vg + Ve$$



In controlled experiment, different genotypes are placed into different environments at random

Genotypes and environments are independent

Djande et al 2020

Review

- $\bar{X} = \sum_{i=1}^{k} f_i X_i$
- $s^2 = \frac{1}{n-1} \sum_{i} (X_i - \bar{X})^2$
- $s = \sqrt{s^2}$
- $x = g + e$
- $V_x = Vg + Ve + 2cov_{ge}$

Heritability

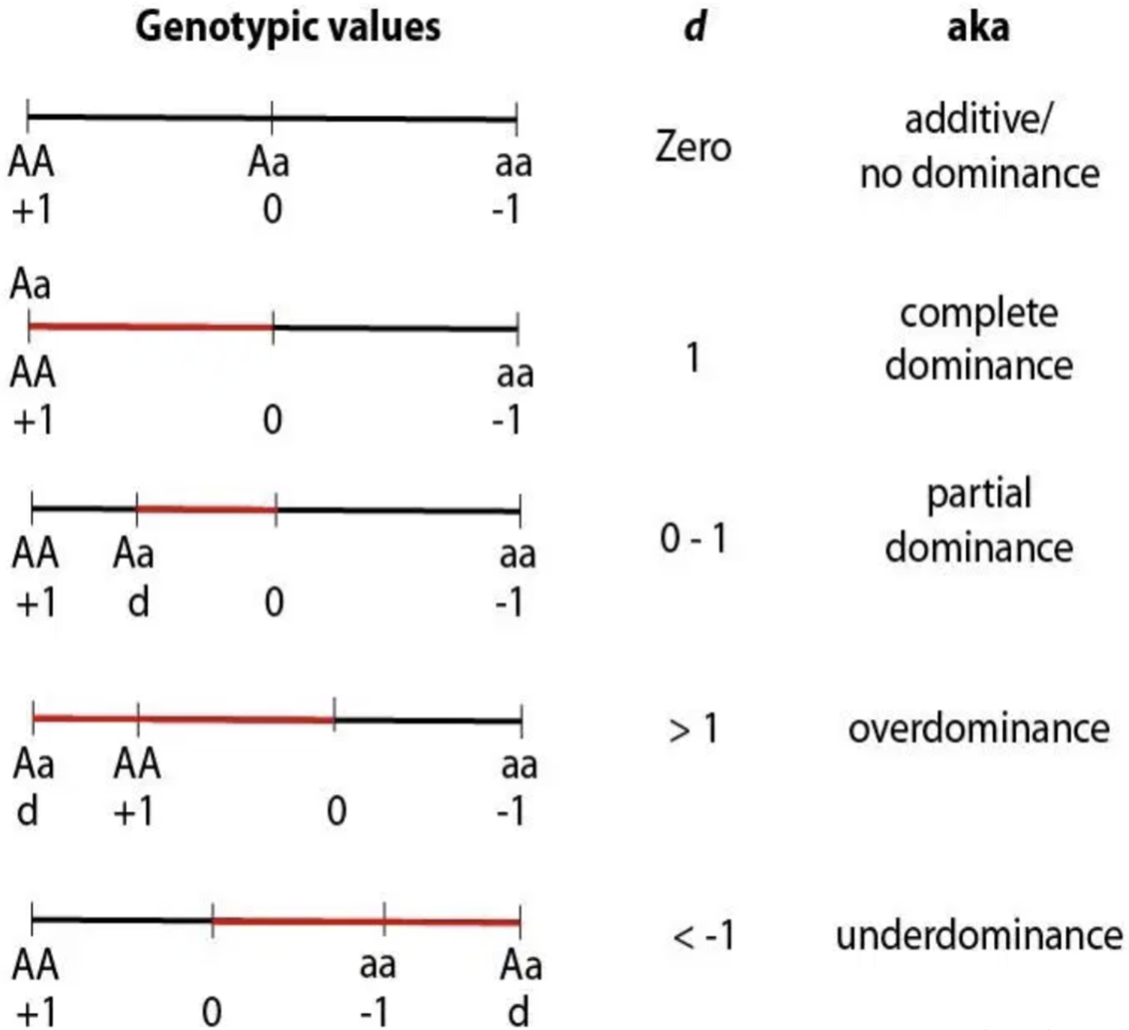
The degree of variation in a phenotypic trait in a population that is due to genetic variation between individuals in that population.

$$V_x = Vg + Ve$$

Broad-sense heritability (H^2)

$$H^2 = \frac{Vg}{Vx}$$

$$V_g = V_A + V_D + V_I$$



genewiz.wordpress.com

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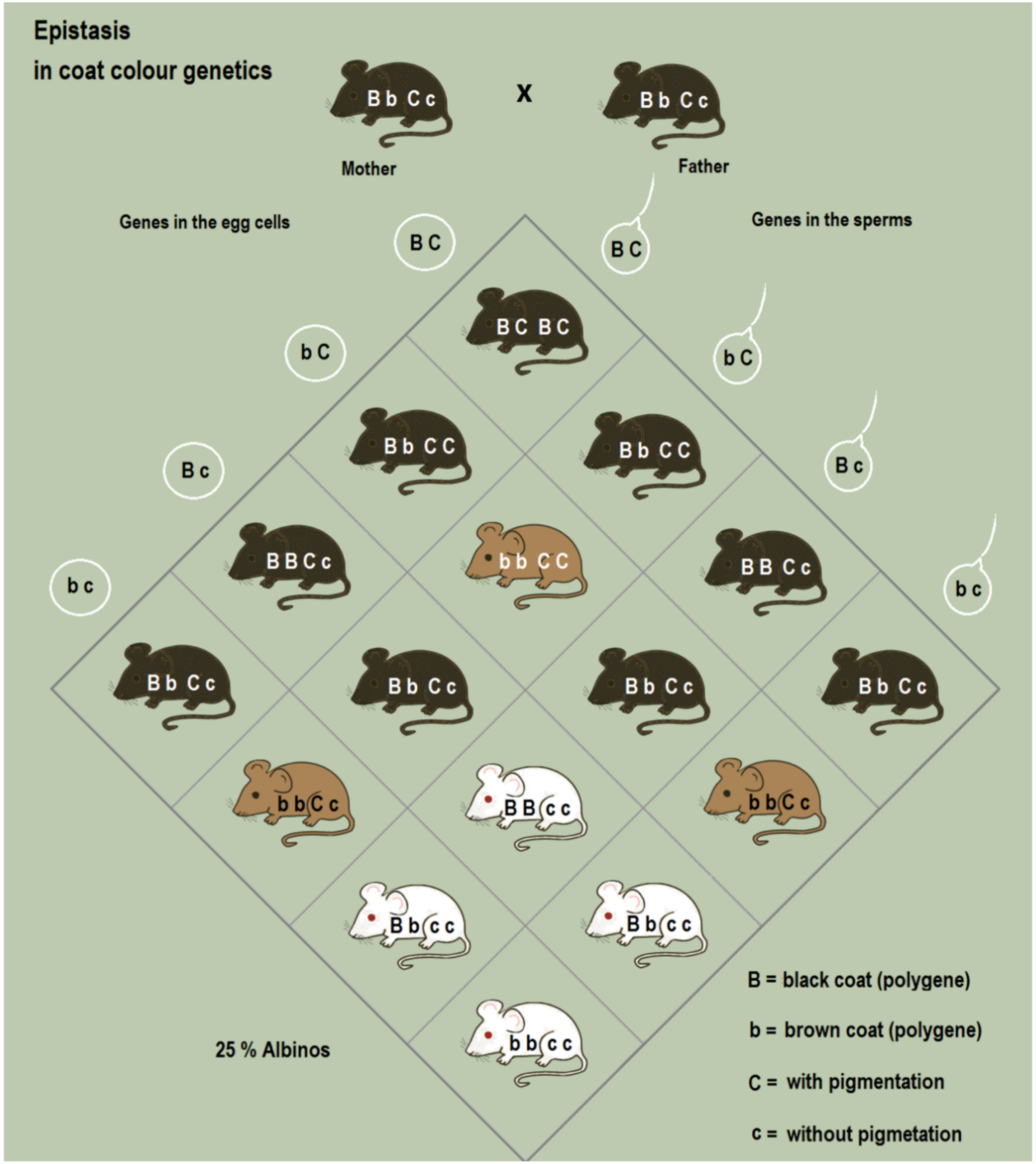


en.wikipedia.org

Heritability

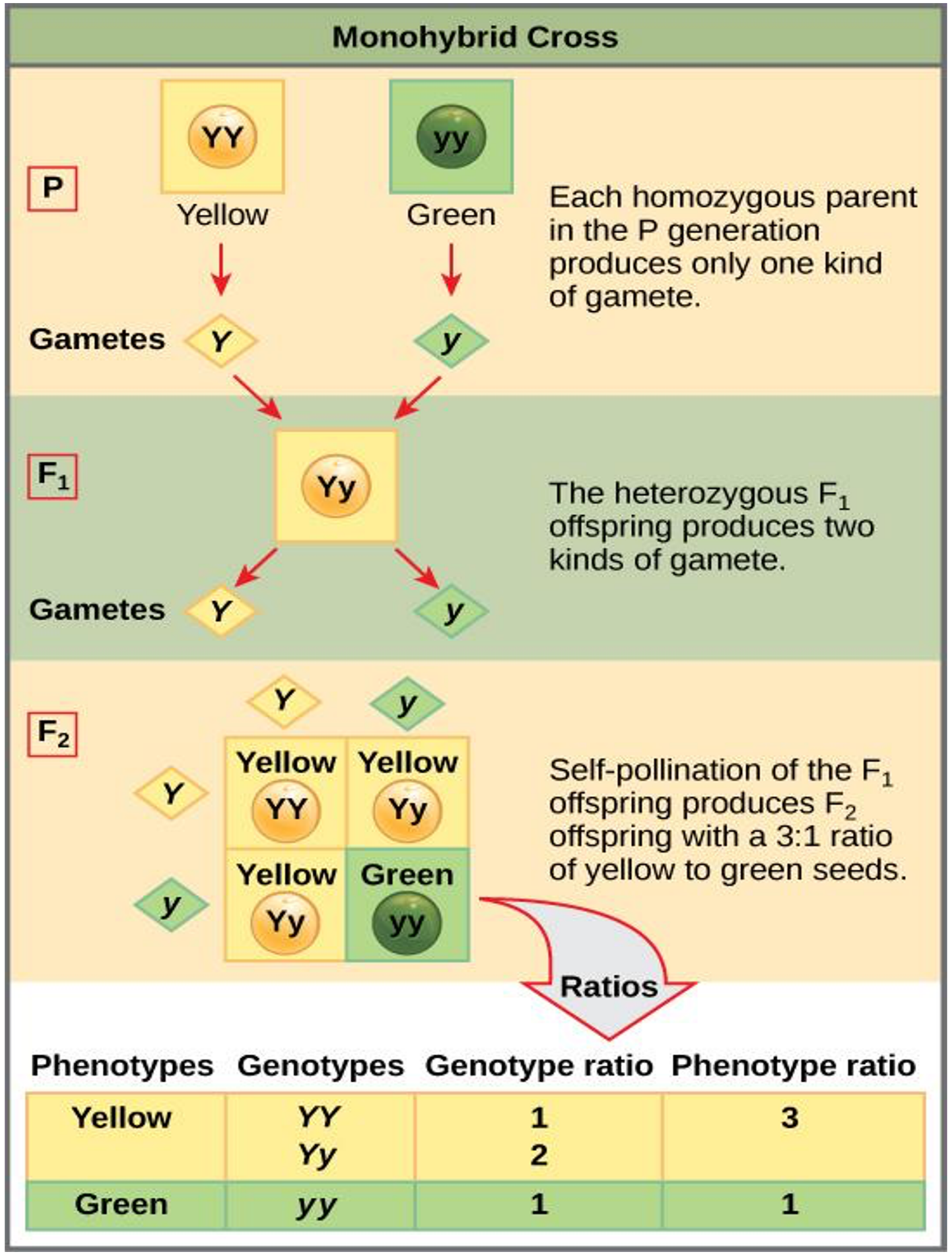
Broad-sense heritability (H^2)

$$H^2 = \frac{Vg}{Vx}$$

$$V_g = V_a + V_d + V_i$$

H^2 is not transmissible to the next generation in a predictive way!

Parents transmit their genes **but not** their genotypes!



Each homozygous parent in the P generation produces only one kind of gamete.

The heterozygous F$_1$ offspring produces two kinds of gamete.

Self-pollination of the F$_1$ offspring produces F$_2$ offspring with a 3:1 ratio of yellow to green seeds.

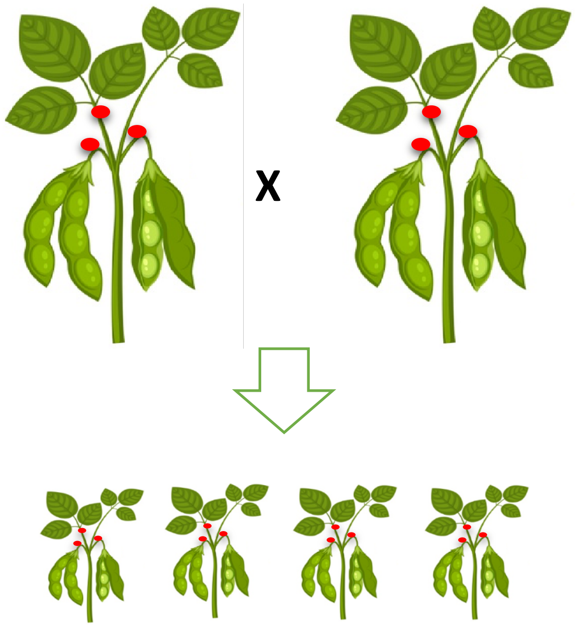
Phenotypes	Genotypes	Genotype ratio	Phenotype ratio
Yellow	*YY* *Yy*	1 2	3
Green	*yy*	1	1

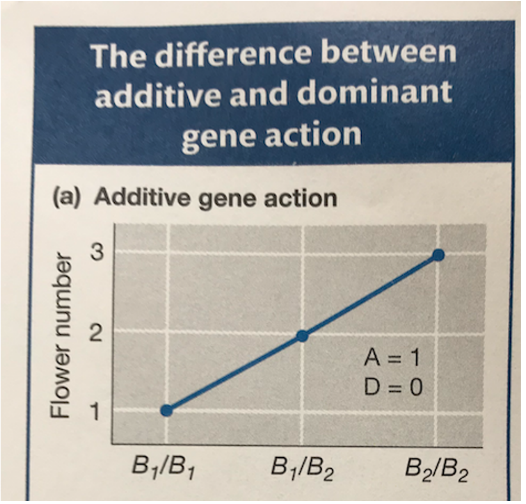
Heritability

Narrow-sense heritability (h^2)

$$h^2 = \frac{Va}{Vx} = \frac{Va}{Va+Vd+Vi+Ve}$$

h^2 is transmissible to the next generation in a predictive way!

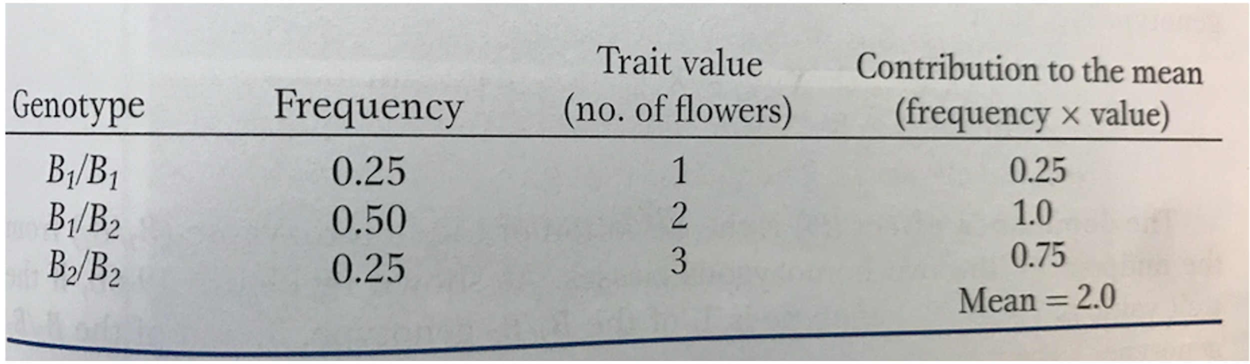




The difference between additive and dominant gene action

(a) Additive gene action

Griffiths et al 2012



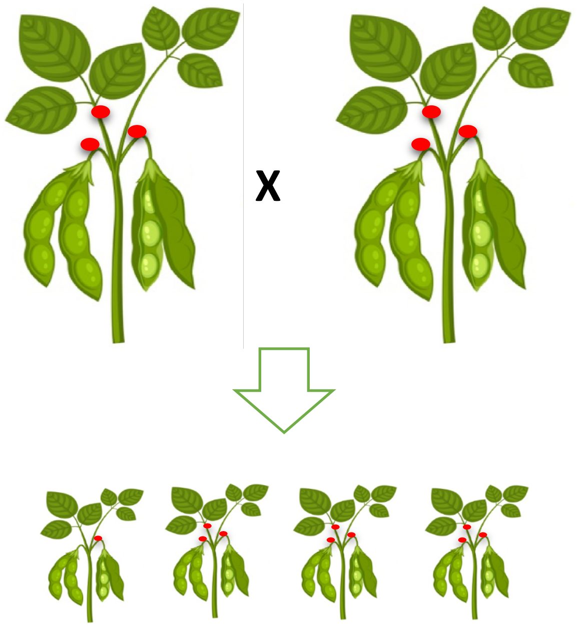
Genotype	Frequency	Trait value (no. of flowers)	Contribution to the mean (frequency × value)
B_1/B_1	0.25	1	0.25
B_1/B_2	0.50	2	1.0
B_2/B_2	0.25	3	0.75
			Mean = 2.0

Heritability

Narrow-sense heritability (h^2)

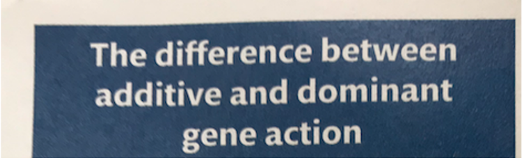
$$h^2 = \frac{Va}{Vx} = \frac{Va}{Va+Vd+Vi+Ve}$$

parents = 3



Offspring < 3 (2.78)

The phenotype is not fully heritable!



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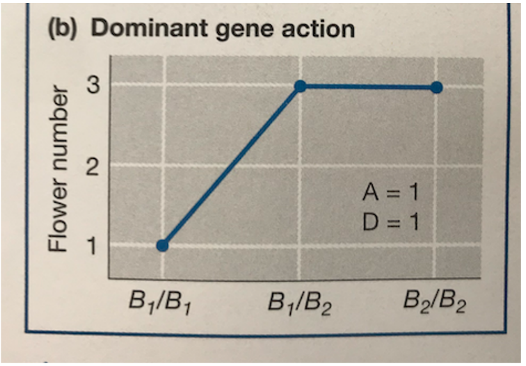
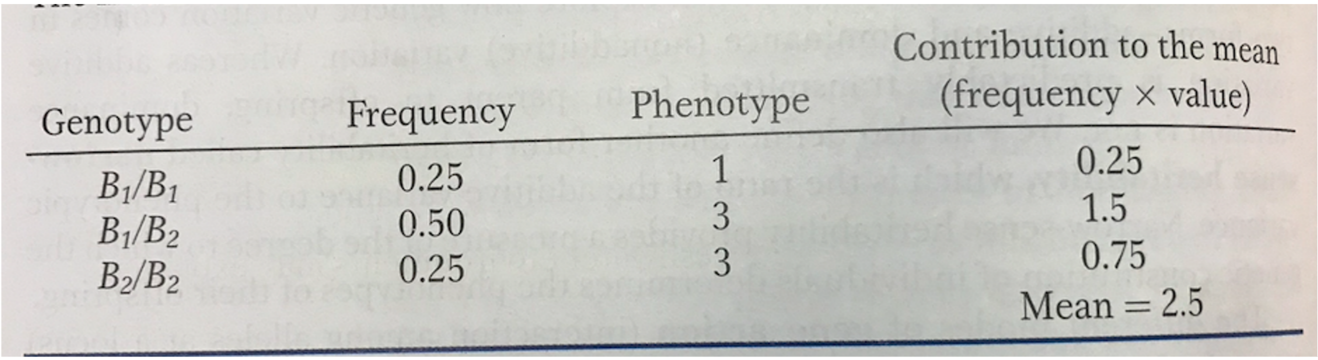


Griffiths et al 2012

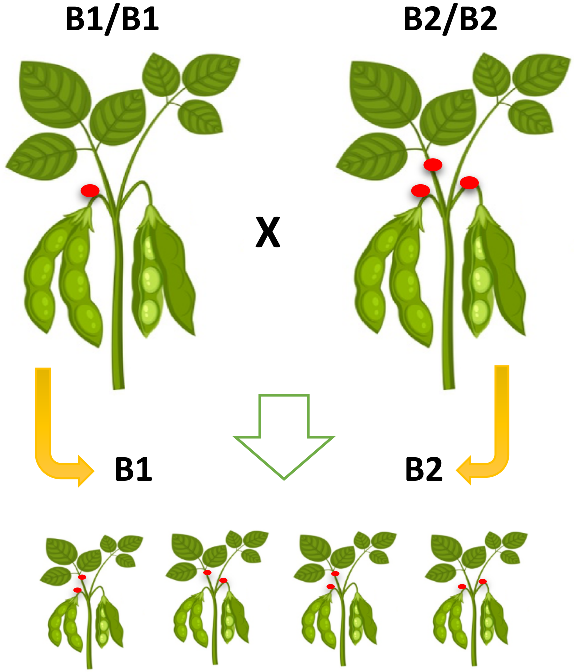


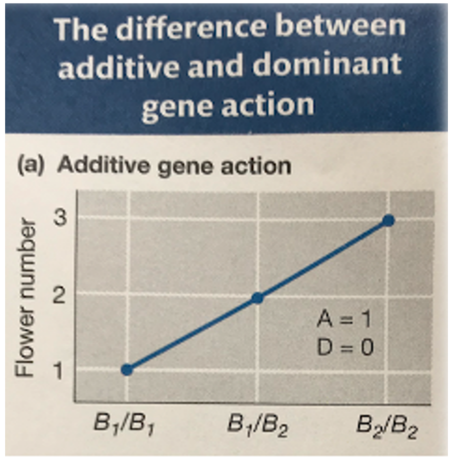
Genotype	Frequency	Phenotype	Contribution to the mean (frequency × value)
B_1/B_1	0.25	1	0.25
B_1/B_2	0.50	3	1.5
B_2/B_2	0.25	3	0.75
			Mean = 2.5

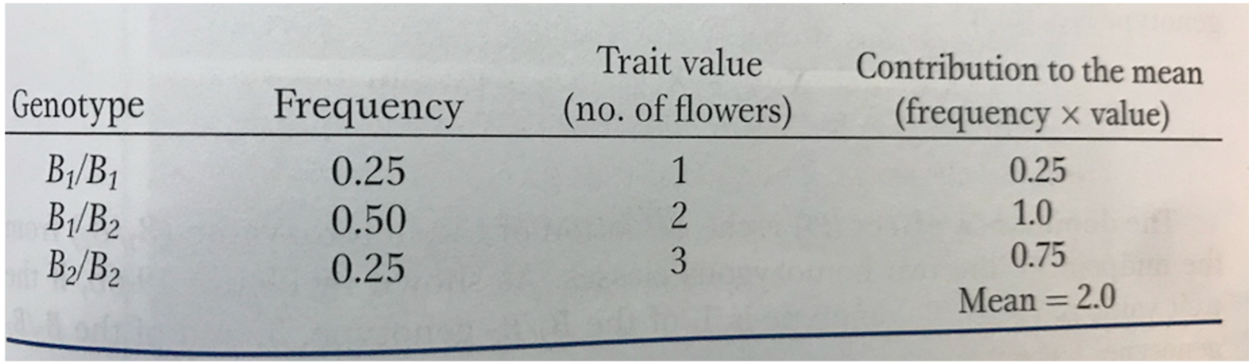
Heritability

Narrow-sense heritability (h^2)

$$\beta_{O\sim Mp} = \frac{Cov(u_{ih},u_i)}{Var(y_i)} = \frac{\sigma_a^2}{\sigma_p^2} = h^2$$







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Griffiths et al 2012

Review

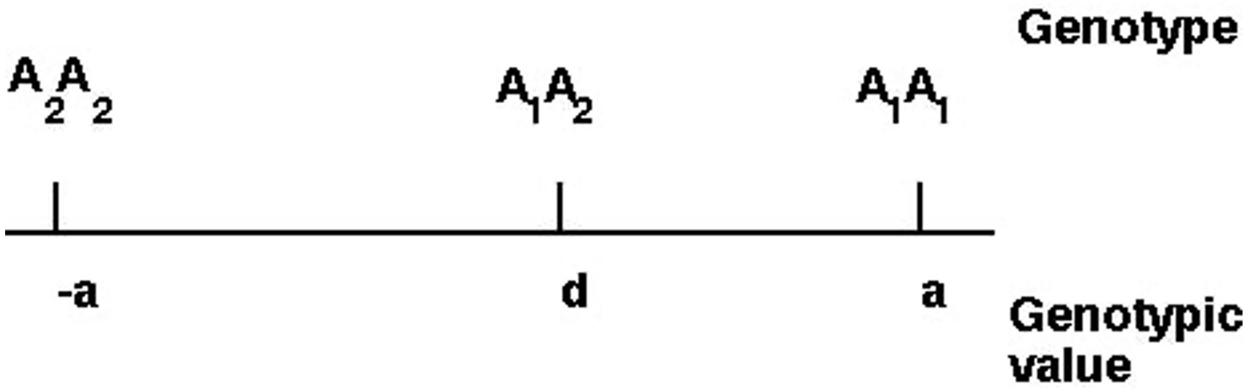
- $V_g = V_a + V_d + V_i$
- $H^2 = \frac{Vg}{Vx}$
- $h^2 = \frac{Va}{Vx}$

Values and means in a single locus

Values and means in a single locus

- Genetic values
- Population mean
- Average allele effect
- Average allele substitution effect

$$\overline{X} = \sum_{i=1}^{k} f_i X_i$$



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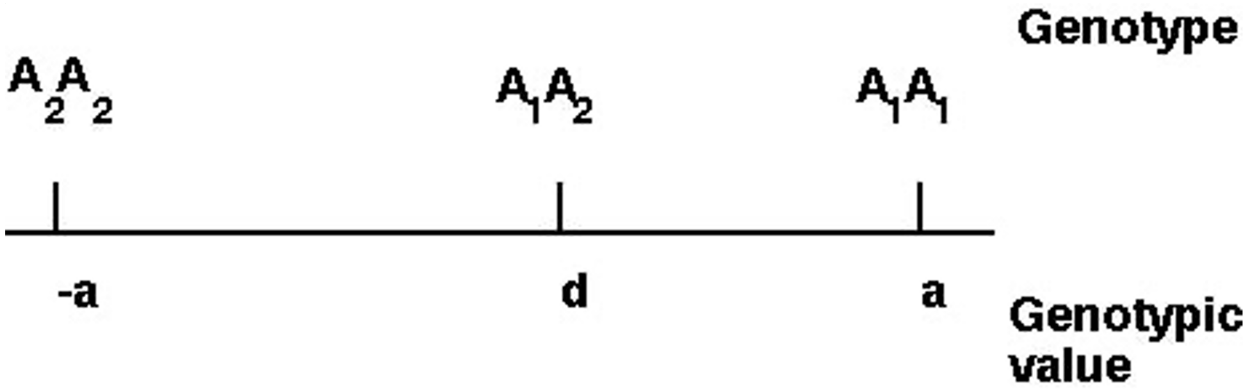
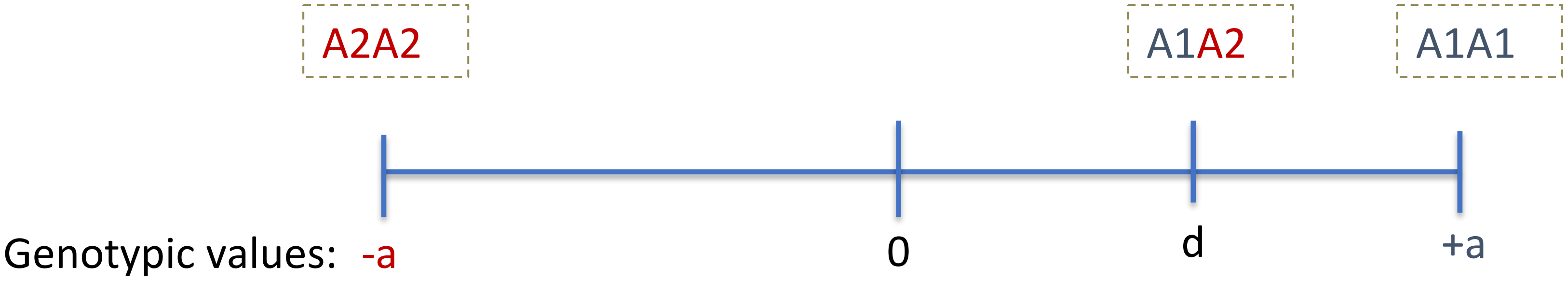
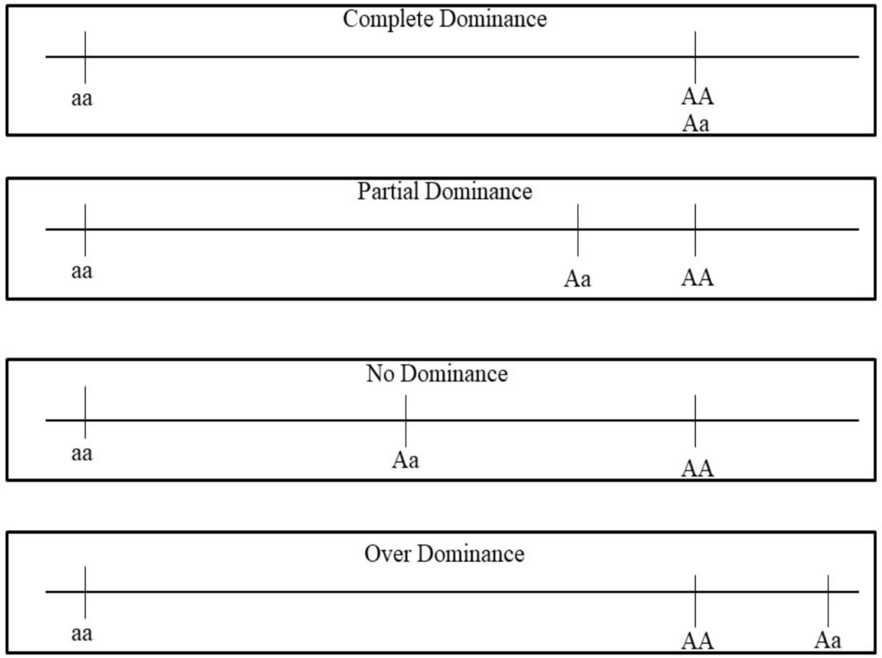


Genetic values

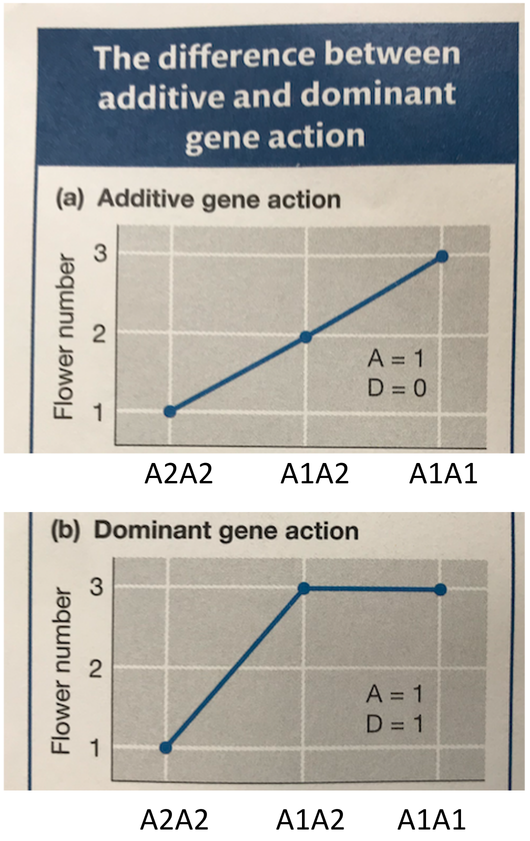


A2A2 A1A2 A1A1

Genotypic values: -a 0 d +a



simmental.org



Griffiths et al 2012

Values and means in a single locus

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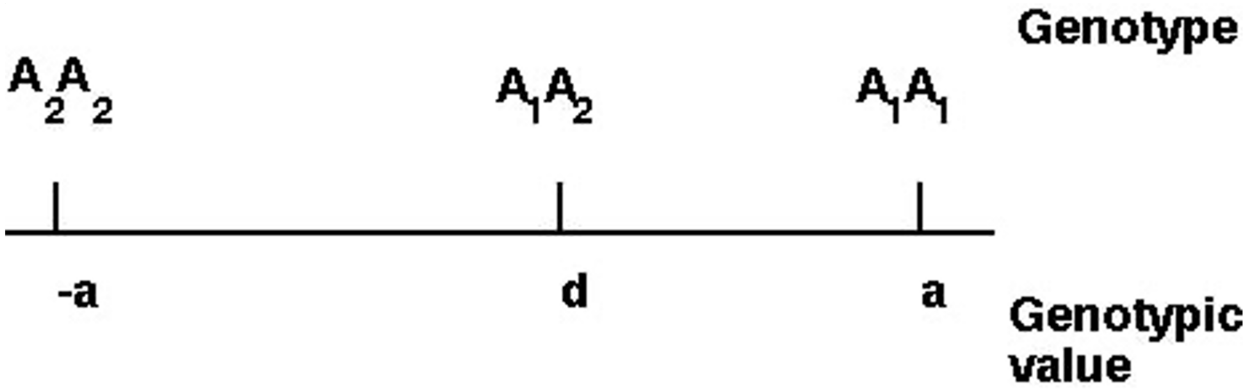
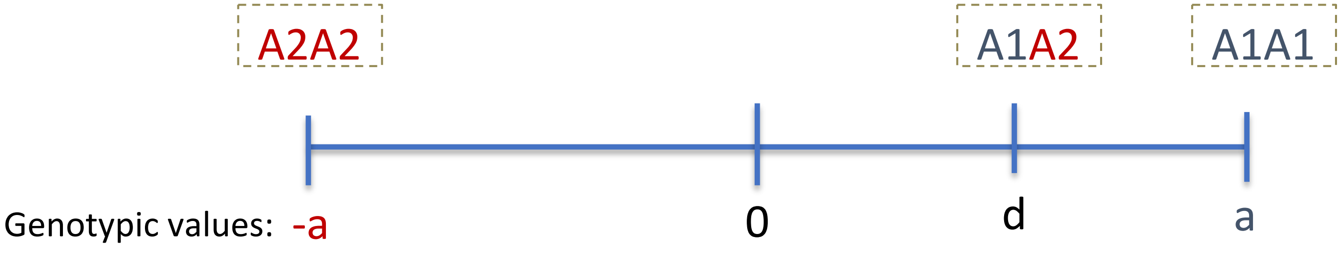


Population mean



A2A2 A1A2 A1A1

Genotypic values: -a 0 d a

Genotype	Freq	Value	Freq × Value
A1A1	p^2	a	p^2a
A1A2	$2pq$	d	$2pqd$
A2A2	q^2	-a	$-q^2a$
Sum	1		$a(p-q)+2pqd$

$$\overline{X} = \sum_{i=1}^{k} f_i X_i$$

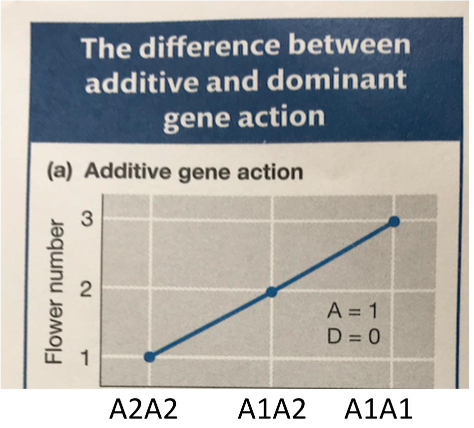
$$E[u] = a(p-q) + 2pqd$$

$$E[u] = a(p-q)$$

Population mean

$$u = \sum_{i=1}^{k} f_i X_i$$

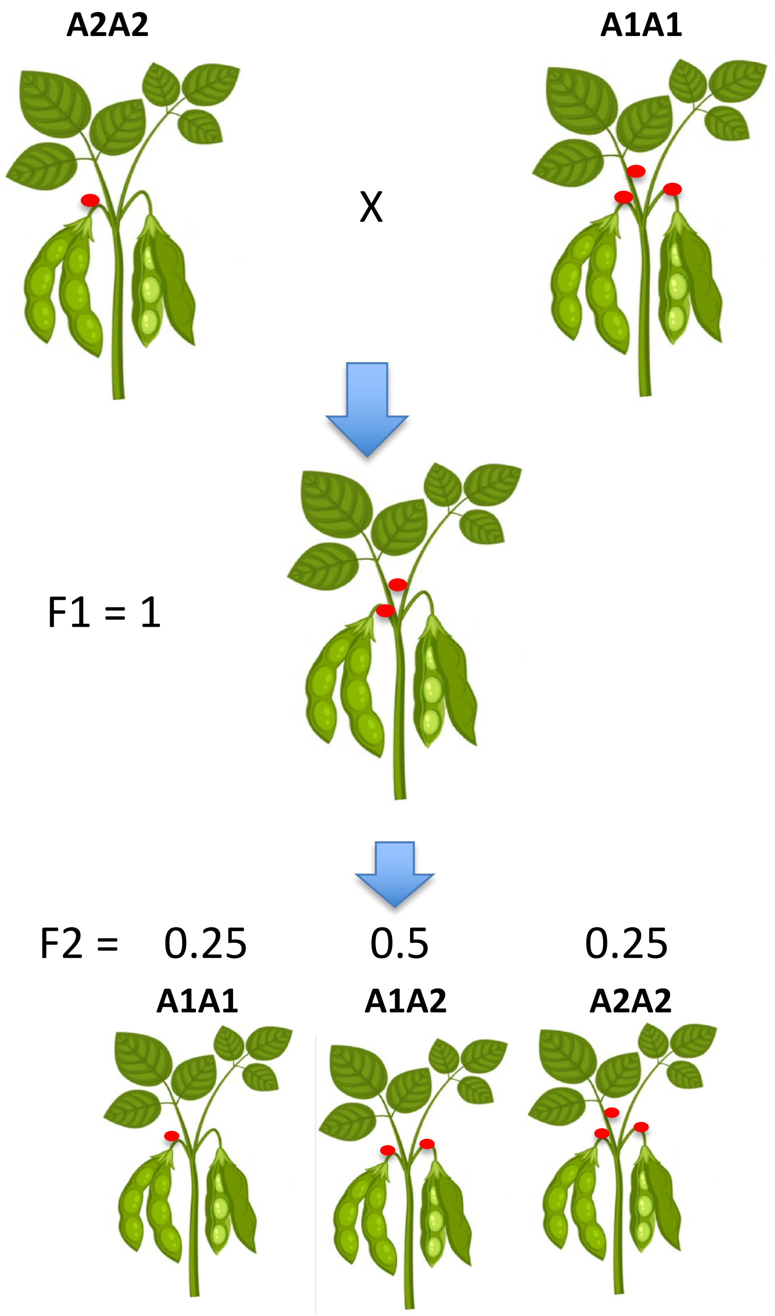
Genotype	Freq	Value	Freq × Value
A1A1	p^2	a	p^2a
A1A2	2pq	d	2pqd
A2A2	q^2	-a	$-q^2a$
Sum	1		a(p-q)+2pqd



The difference between additive and dominant gene action

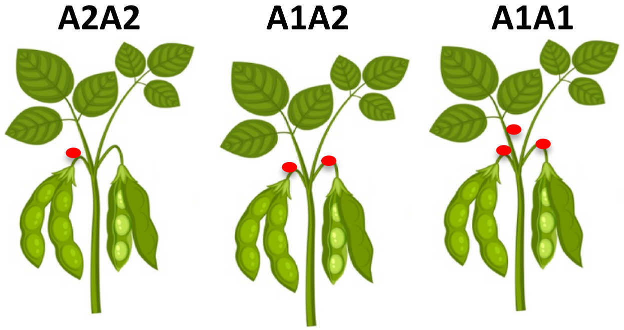
(a) Additive gene action

Griffiths et al 2012

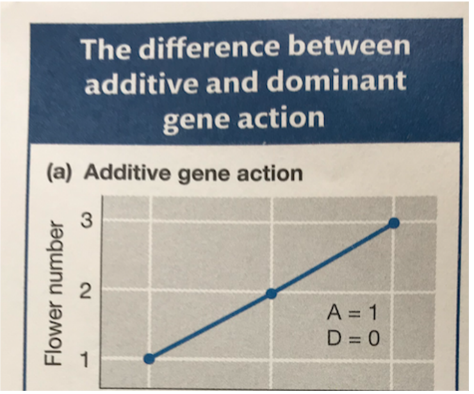


Population mean

F2 = 0.25 0.5 0.25



Genotype	Freq	Value	Freq × Value
A1A1	p^2	a	p^2a
A1A2	$2pq$	d	$2pqd$
A2A2	q^2	-a	$-q^2a$
Sum	1		$a(p-q)+2pqd$

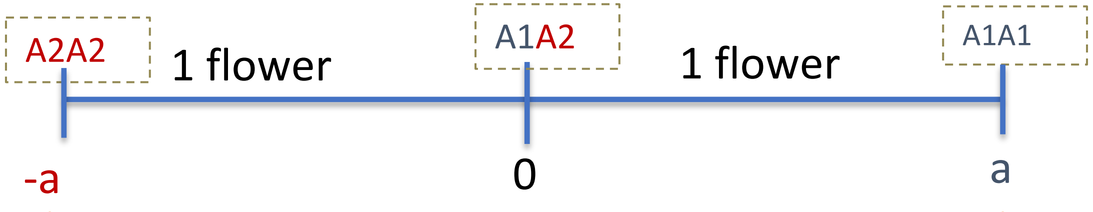


The difference between additive and dominant gene action

(a) Additive gene action

Griffiths et al 2012

$$p = \sqrt{0.25} = 0.5$$
$$q = 1 - p = 0.5$$



A2A2

1 flower

A1A2

1 flower

A1A1

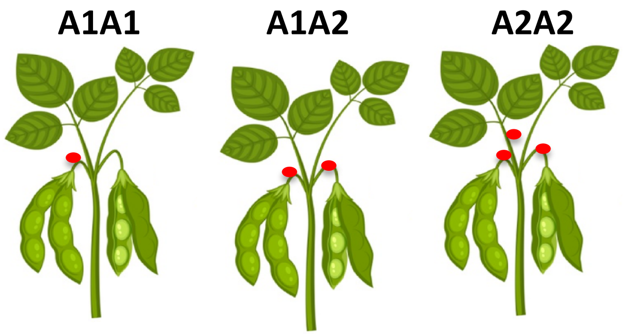
-a

0

a

2 flowers

F2 = 0.25 0.5 0.25

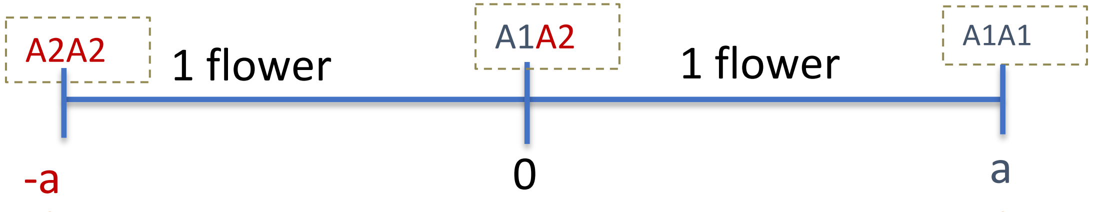


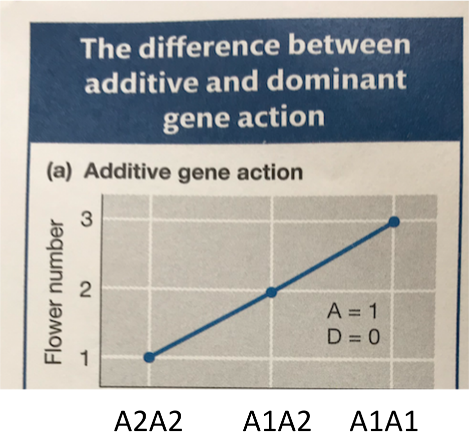
Population mean

Genotype	Freq	Value	Freq × Value
A1A1	0.5^2	1	0.25*1
A1A2	2*0.5*0.5	0	2*0.5*0.5*0
A2A2	0.5^2	-1	-0.25*1
Sum	1		1(0.5-0.5)+2*0.5*0.5*0

a(p-q)+2pqd = 0

$$p = \sqrt{0.25} = 0.5$$
$$q = 1 - p = 0.5$$



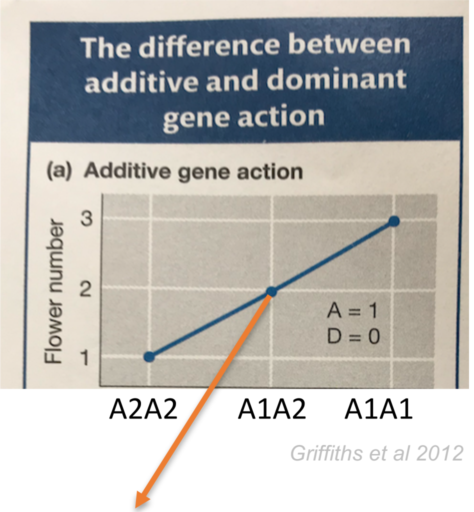


Griffiths et al 2012

Population mean

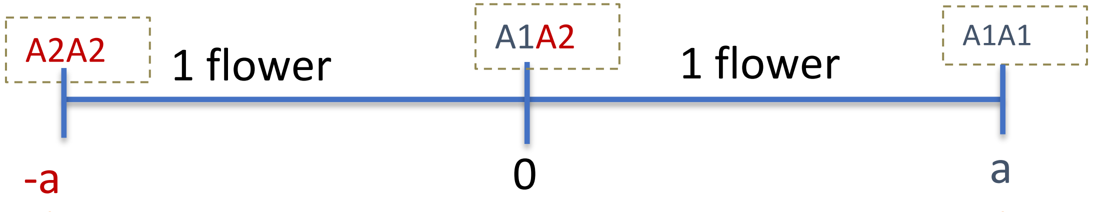
Genotype	Freq	Value	Freq × Value
A1A1	0.5^2	1	0.25*1
A1A2	2*0.5*0.5	0	2*0.5*0.5*0
A2A2	0.5^2	-1	-0.25*1
Sum	1		1(0.5-0.5)+2*0.5*0.5*0

$a(p-q)+2pqd = 0$



Griffiths et al 2012

This value of mean is measure from the mid-homozygote point, which is 2 flowers


A2A2

1 flower

A1A2

1 flower

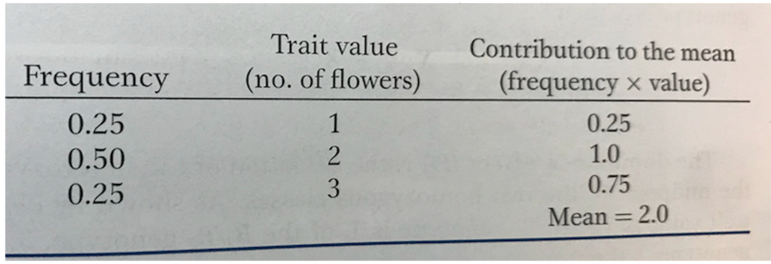
A1A1

-a

0

a

2 flowers



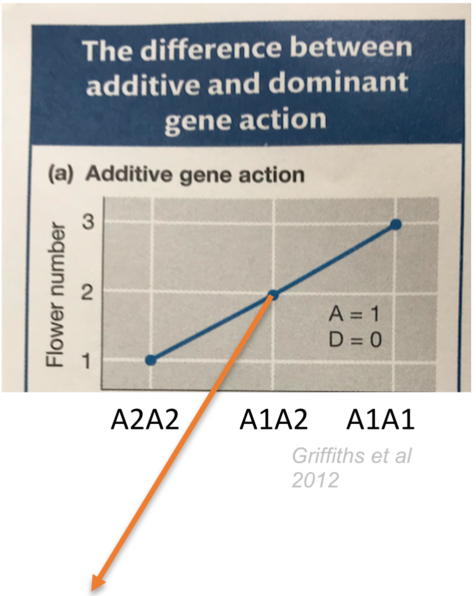
	Frequency	Trait value (no. of flowers)	Contribution to the mean (frequency × value)
A2A2	0.25	1	0.25
A1A2	0.50	2	1.0
A1A1	0.25	3	0.75
			Mean = 2.0

Population mean

Genotype	Freq	Value	Freq × Value
A1A1	0.9^2	1	0.81*1
A1A2	2*0.9*0.1	0	0.18*0
A2A2	0.1^2	-1	-0.01*1
Sum	1		1(0.8)+2*0.09*0

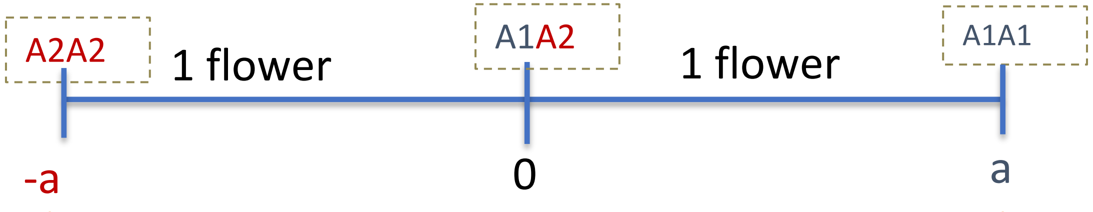
$a(p-q)+2pqd = 0.8$

$$p = 0.9$$
$$q = 0.1$$



Griffiths et al 2012

2 + 0.8 = 2.8 flowers



A2A2

1 flower

A1A2

1 flower

A1A1

-a

0

a

2 flowers

Population mean

Genotype	Freq	Value	Freq × Value
A1A1	p^2	a	p^2a
A1A2	2pq	d	2pqd
A2A2	q^2	-a	$-q^2a$
Sum	1		a(p-q)+2pqd

$$E[u] = a(p-q) + 2pqd$$

Single locus

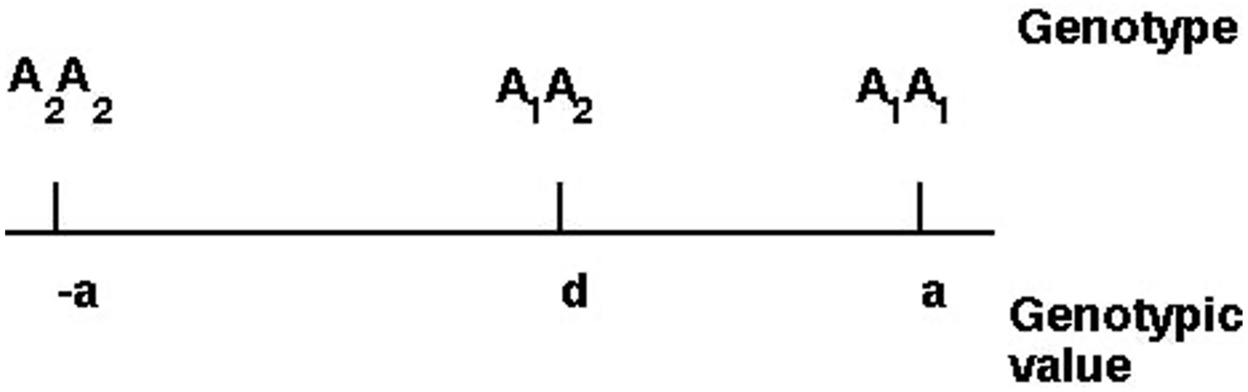
The population mean resulting from joint effects of several loci is the sum of the contributions of each of separate loci

$$E[u] = \sum a(p-q) + 2\sum dpq$$

Several loci

Values and means in a single locus

- Genetic values
- Population mean
- Average allele effect
- Average allele substitution effect



Average allele effect

Deviation from the population mean of individuals which received an allele (A1 or A2) from one parent when the other allele come at random from the population

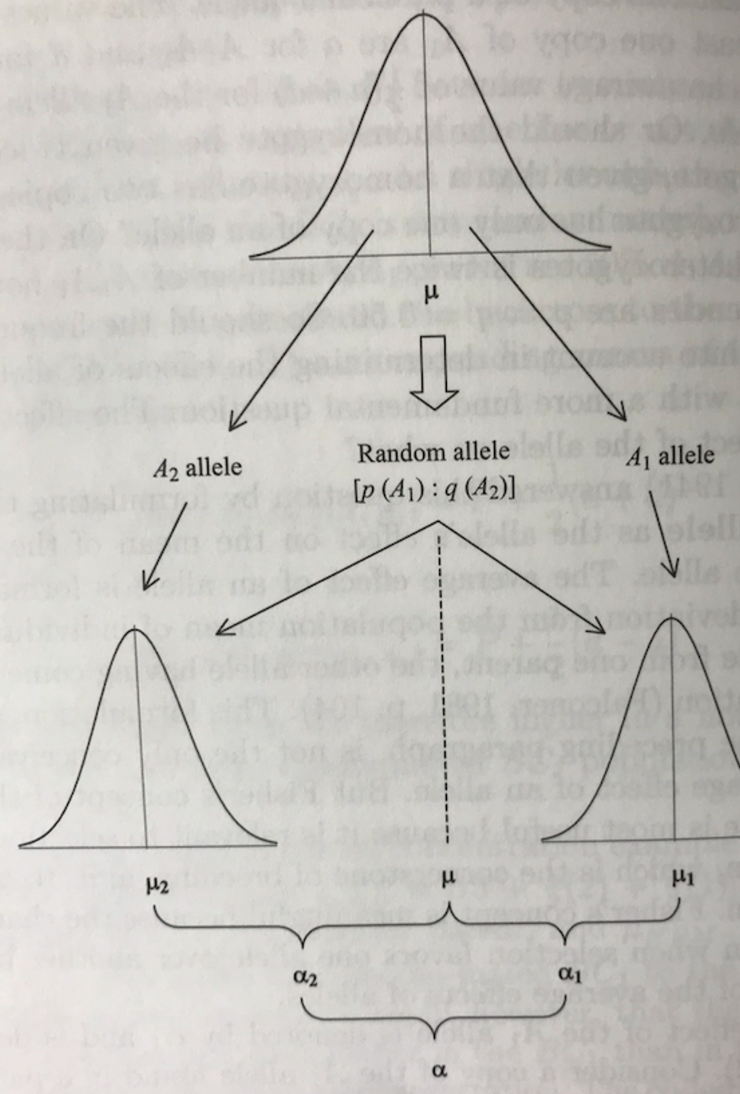


FIGURE 3.2. Average effects of alleles.

Average allele effect

Type of gamete	Values and frequencies of genotypes produced			Mean value of genotypes	Population mean to be deducted	Average effect of gene
	A1A1	A1A2	A2A2			
	a	d	-a		a(p-q) + 2pqd	
A1	p	q		pa + qd	-[a(p-q) + 2dpq]	q[a+d(q-p)]
A2		p	q	-qa + pd	-[a(p-q) + 2dpq]	-p[a+d(q-p)]

Falconer & Mackay 1996

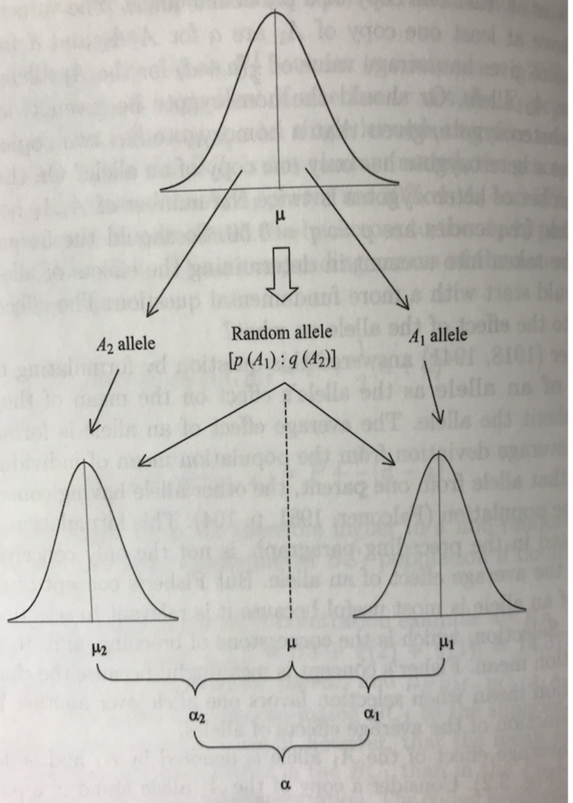


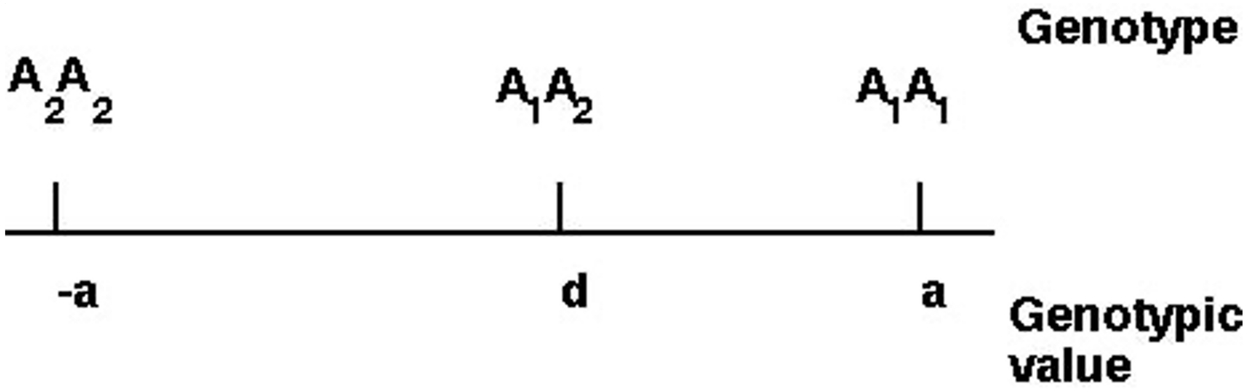
FIGURE 3.2. Average effects of alleles.

Average effects of the alleles: $\alpha_1 = q[a + d(q - p)]$ $\alpha_2 = -p[a + d(q - p)]$

Average effects of the gene substitution: $\alpha = \alpha_1 - \alpha_2 = \mathrm{a} + \mathrm{d}(\mathrm{q} - \mathrm{p})$

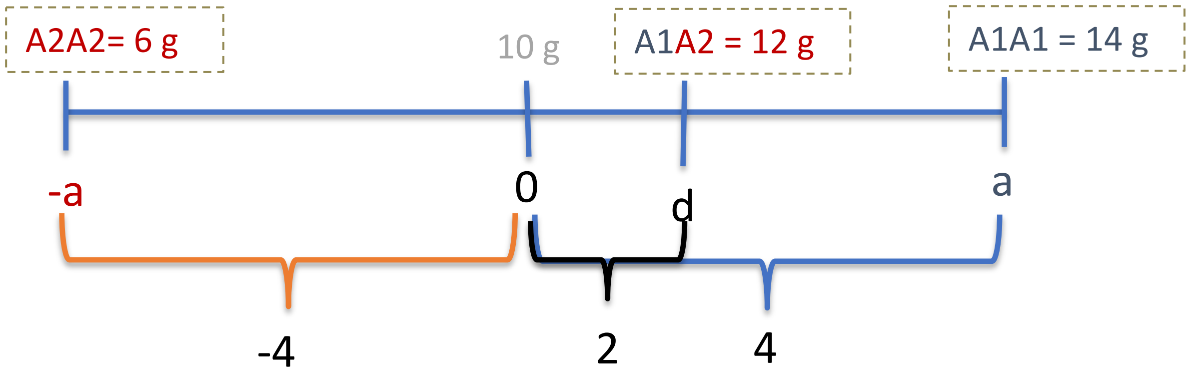
Values and means in a single locus

- Genetic values
- Population mean
- Average allele effect
- Average allele substitution effect



Average effects of gene substitution

$$\begin{aligned}\alpha &= \alpha_1 - \alpha_2 \\ &= \mathrm{a} + \mathrm{d}(\mathrm{q} - \mathrm{p})\end{aligned}$$



$$\alpha = \mathrm{a} + \mathrm{d}(\mathrm{q} - \mathrm{p})$$

Populations	p	q
Pop 1	0.9	0.1
Pop 2	0.6	0.4

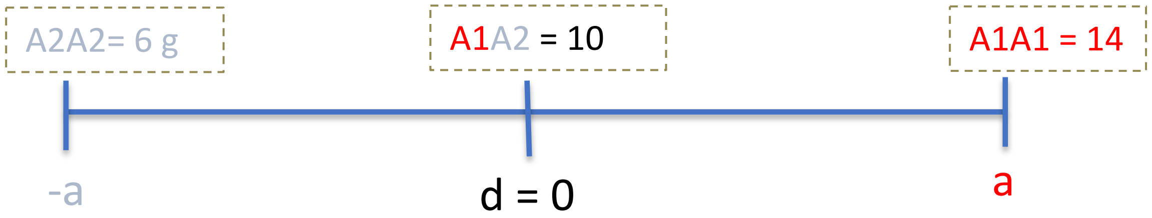
$$\alpha = 4 + 2(0.1 - 0.9) = 2.4$$

$$\alpha = 4 + 2(0.4 - 0.6) = 3.6$$

Average effects of gene substitution

Type of gamete	Values and frequencies of genotypes produced			Mean value of genotypes	Population mean to be deducted	Average effect of gene
	A1A1	A1A2	A2A2			
	a	d	-a			
A1	p	q		pa + qd	-[a(p-q) + 2dpq]	q[a+d(q-p)]
A2		p	q	-qa + pd	-[a(p-q) + 2dpq]	-p[a+d(q-p)]

Falconer & Mackay 1996



Populations	p	q
Pop 1	0.5	0.5

$$\alpha = a + d(q - p)$$

$$\alpha_1 = q[a + d(q - p)] = q\alpha$$

$$\alpha_2 = -p[a + d(q - p)] = -p\alpha$$

α = 4 + 0 (0.5 - 0.5) = 4

α_1 = 0.5 * 4 = 2
α_2 = -0.5 * 4 = -2

α = α_1 - α_2 = 2 – (-2) = 4

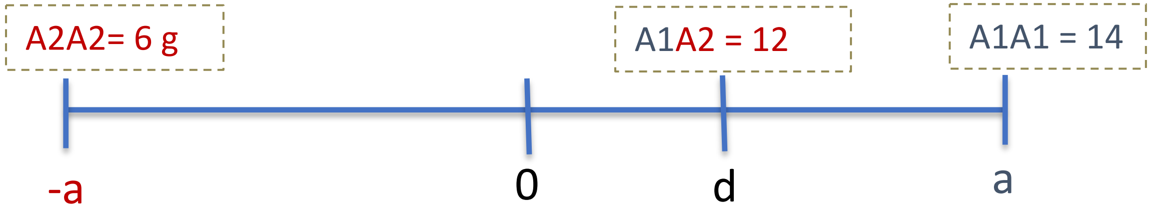
Average effects of gene substitution

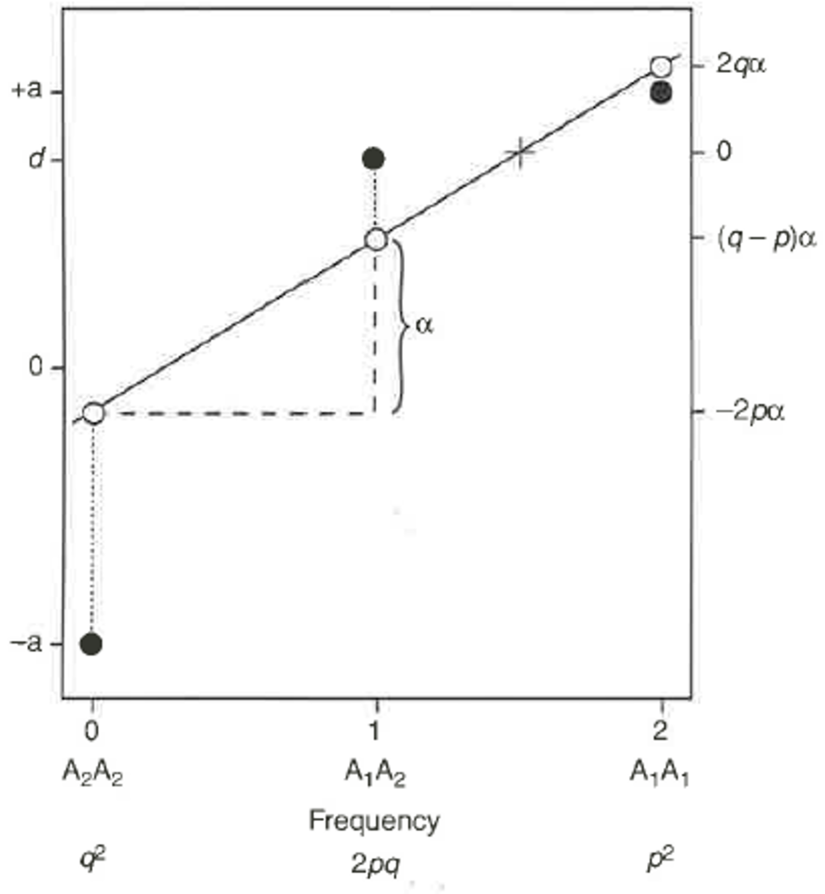
$$\alpha = a + d(q - p)$$

One half of the difference between the two homozygous

Deviation due to dominance

Breeding value
$2\alpha_1 = 2q\alpha$
$\alpha_1 + \alpha_2 = (q - p)\,\alpha$
$2\alpha_2 = -2p\alpha$



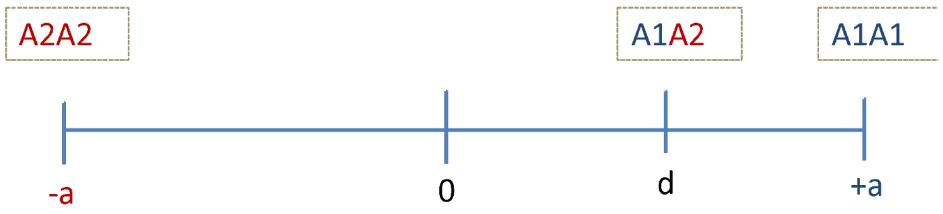


Genotypic values: ● and breeding values: ○

Falconer & Mackay 1996

Review:

Genotypic values:

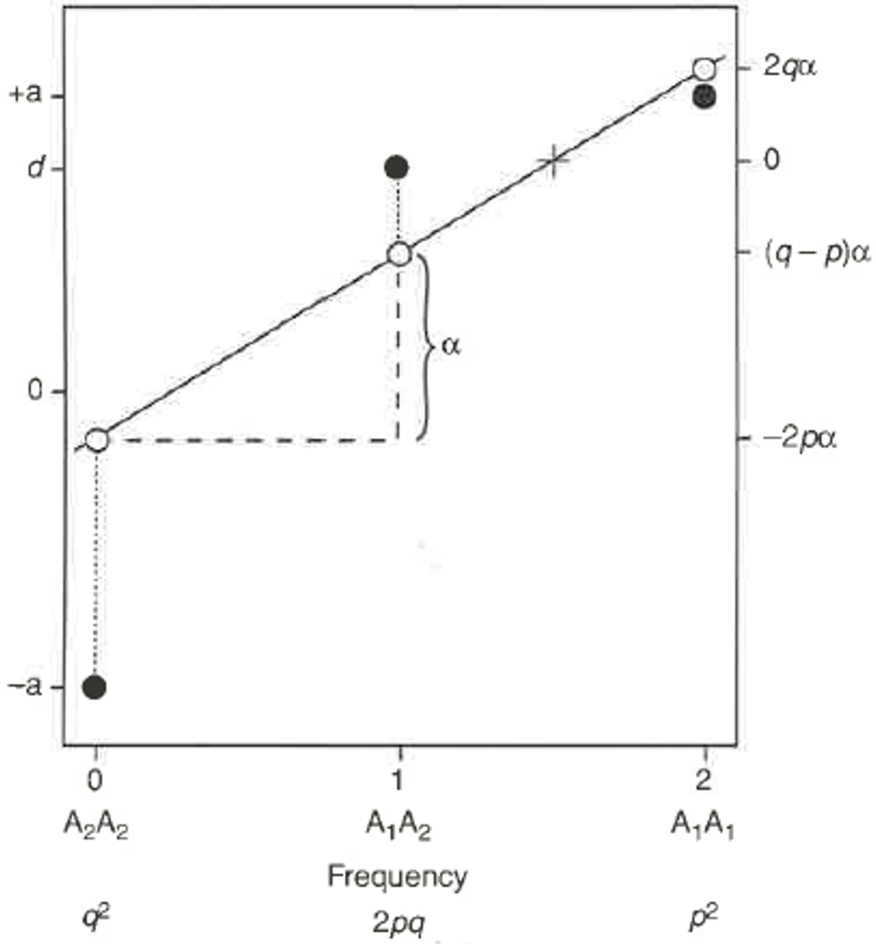


Average effects of the gene substitution:

$$\alpha = \alpha_1 - \alpha_2 = \mathrm{a} + \mathrm{d}(\mathrm{q} - \mathrm{p})$$

Average effects of alleles:

$$\alpha_1 = q[a + d(q - p)]$$
$$\alpha_2 = -p[a + d(q - p)]$$



Genotypic values: ● and breeding values: ○

Super review!!!

1

- Central dogma
- Mexiosis
- Allele frequencies
- genotype frequencies
- HWE

2

$$\bar{X} = \sum_{i=1}^{k} f_i X_i$$

$$s^2 = \frac{1}{n-1}\sum_{i} (X_i - \bar{X})^2$$

$$x = g + e$$

$$V_x = Vg + Ve + 2cov_{ge}$$

3

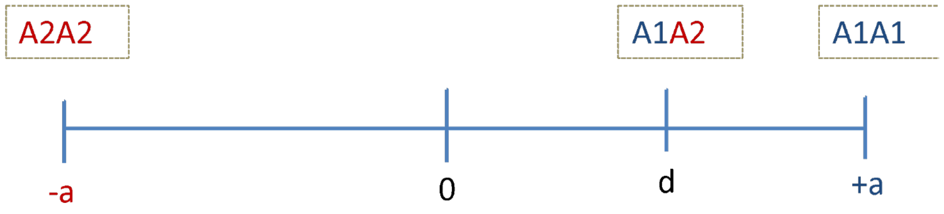
$$V_g = V_a + V_d + V_i$$

$$H^2 = \frac{Vg}{Vx}$$

$$h^2 = \frac{Va}{Vx}$$

4

Genotypic values

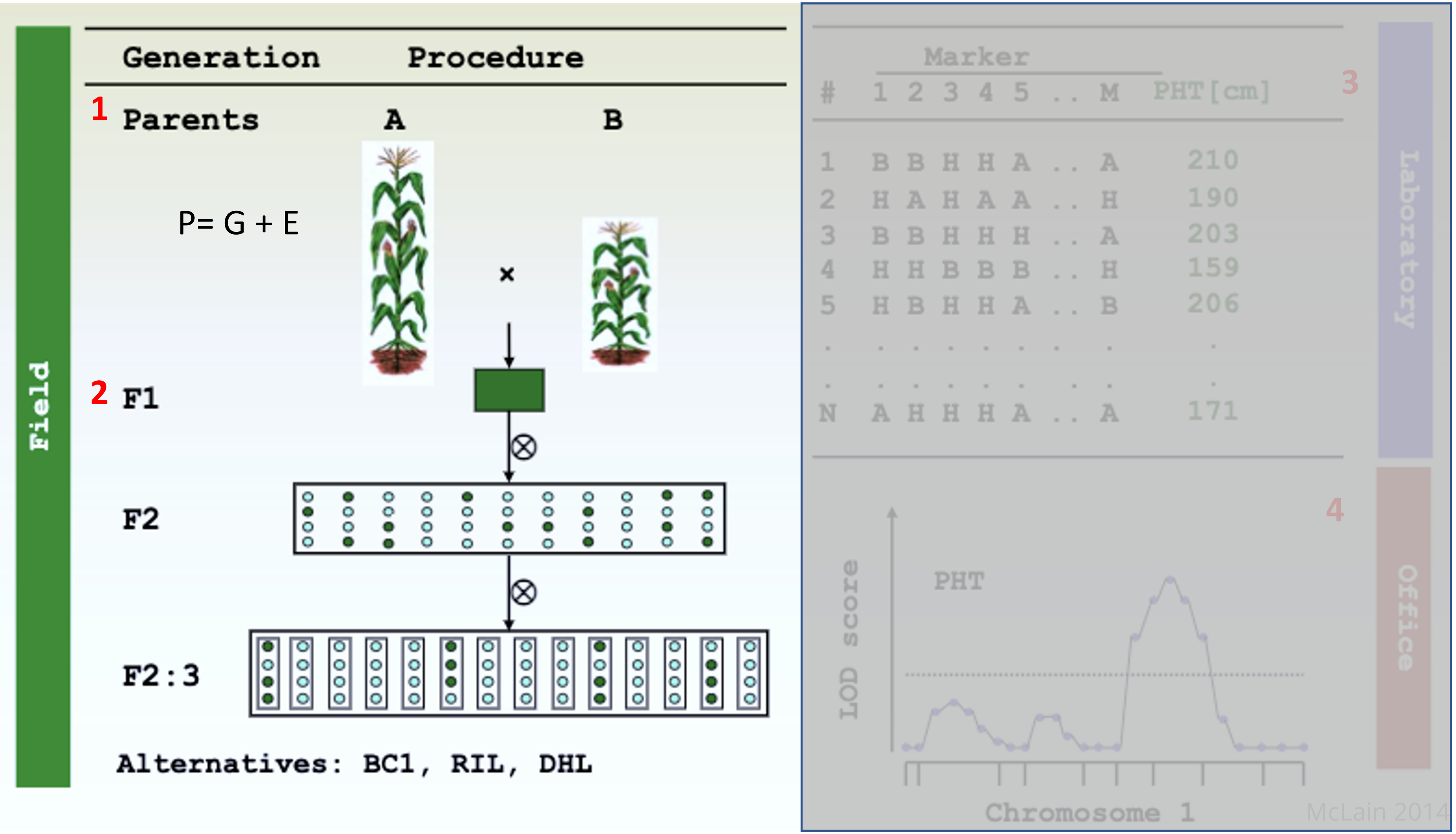


Average effects of the gene substitution:

$$\alpha = \alpha_1 - \alpha_2 = a + d(q - p)$$

Quantitative Trait Loci (QTL)

Quantitative trait loci



Field

Generation **Procedure**

1 **Parents** A B

P= G + E

×

2 **F1**

F2

F2:3

Alternatives: BC1, RIL, DHL

3

	Marker							
#	1	2	3	4	5	..	M	PHT[cm]
1	B	B	H	H	A	..	A	210
2	H	A	H	A	A	..	H	190
3	B	B	H	H	H	..	A	203
4	H	H	B	B	B	..	H	159
5	H	B	H	H	A	..	B	206
.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.
N	A	H	H	H	A	..	A	171

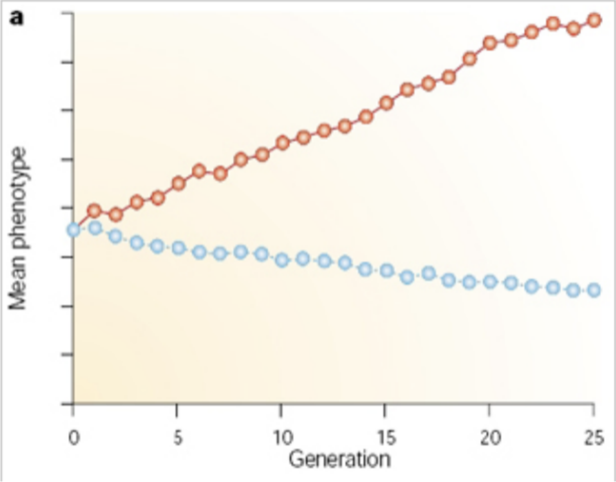
Laboratory

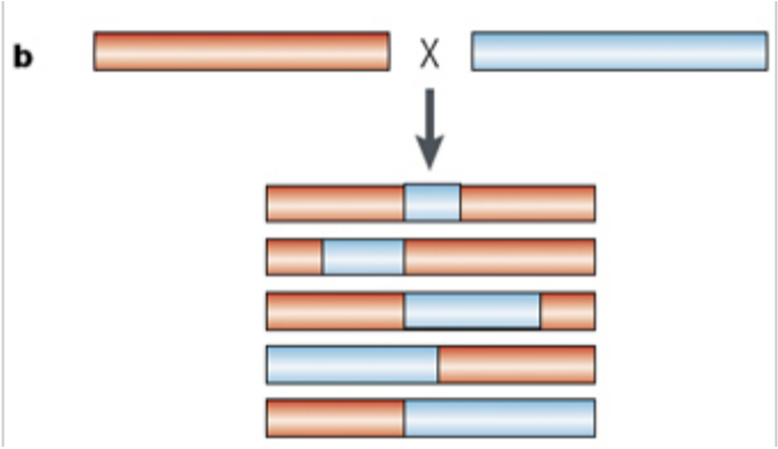
McLain 2014

1 – 2. Parents and Population

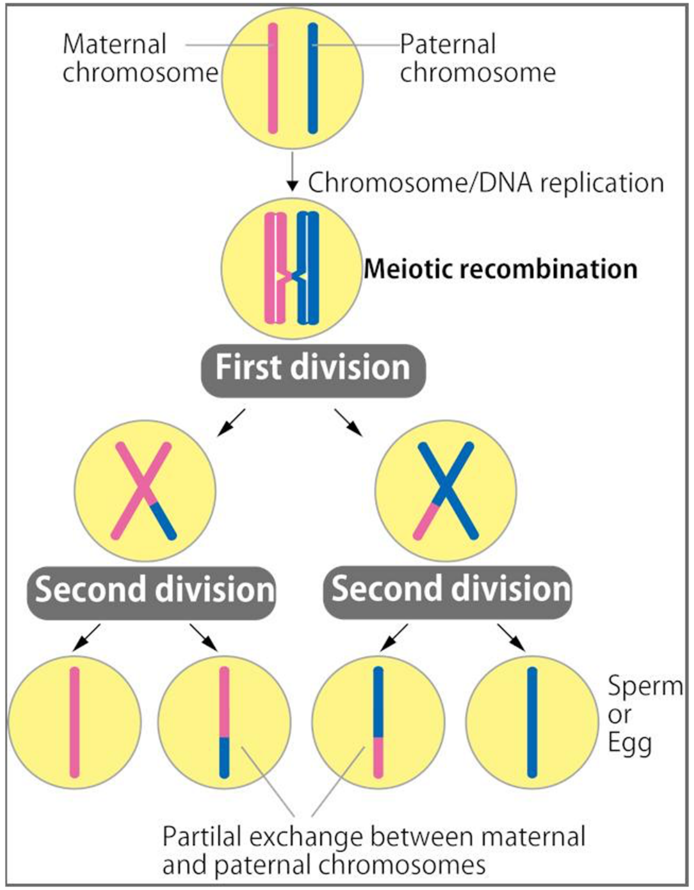
Select parents

bi-parental populations

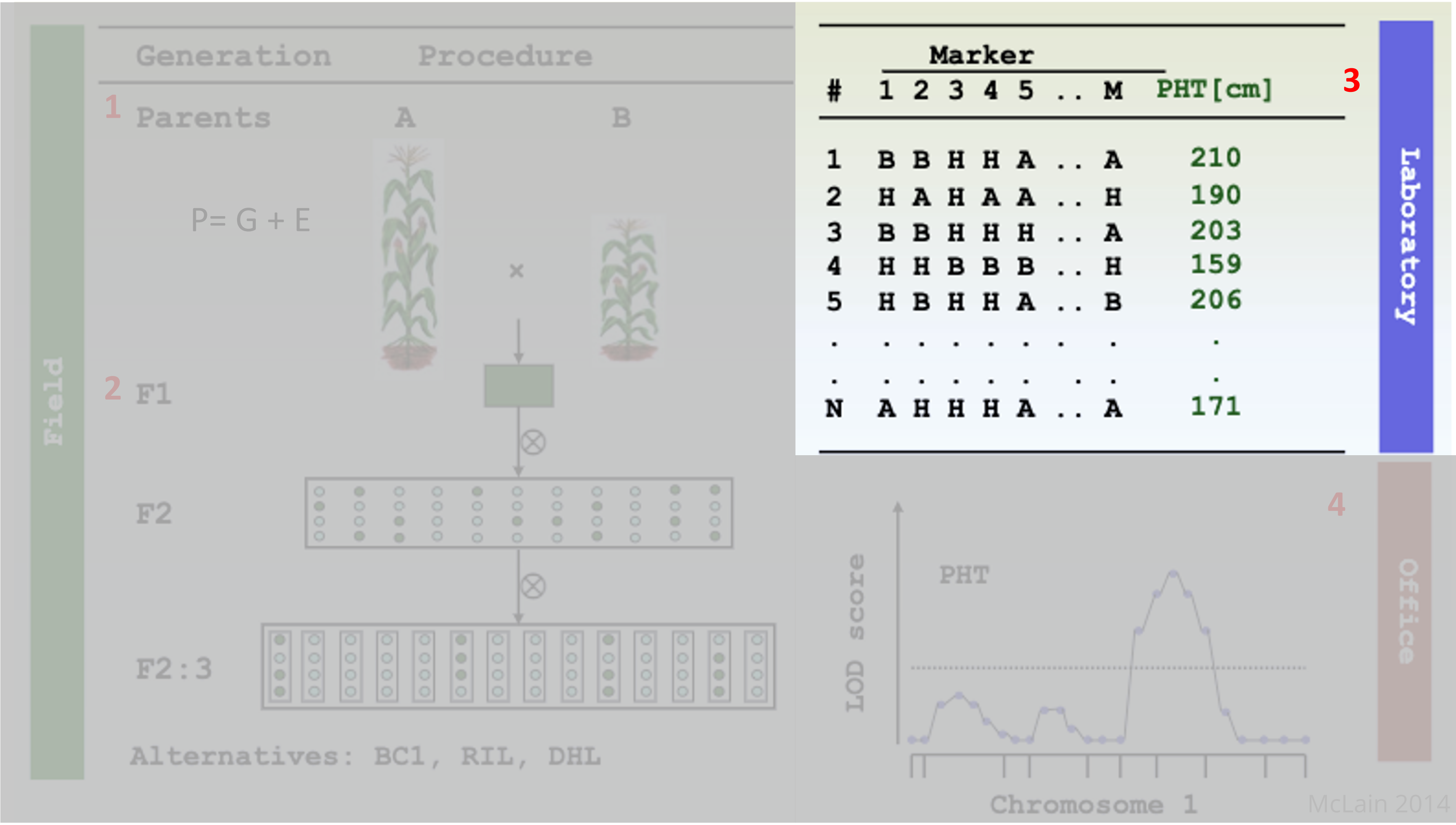




Miles & Wayne 2008



Quantitative trait loci

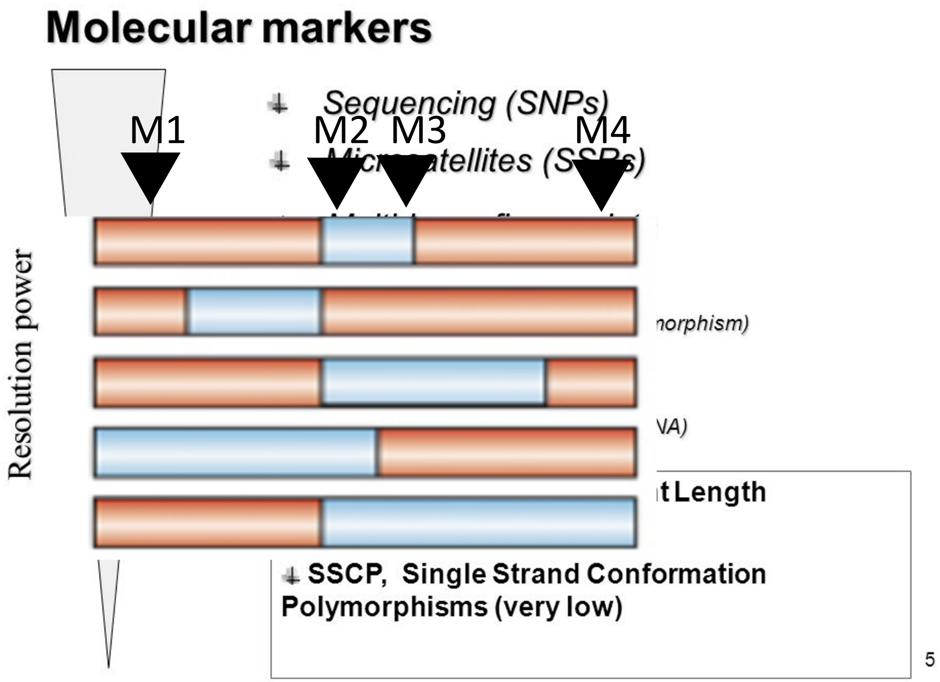


	Marker							
#	1	2	3	4	5	..	M	PHT[cm]
1	B	B	H	H	A	..	A	210
2	H	A	H	A	A	..	H	190
3	B	B	H	H	H	..	A	203
4	H	H	B	B	B	..	H	159
5	H	B	H	H	A	..	B	206
.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.
N	A	H	H	H	A	..	A	171

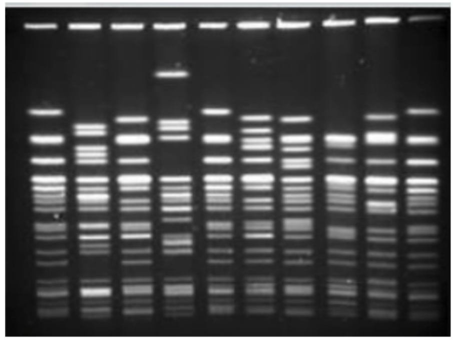
McLain 2014

3. Markers and linkage maps

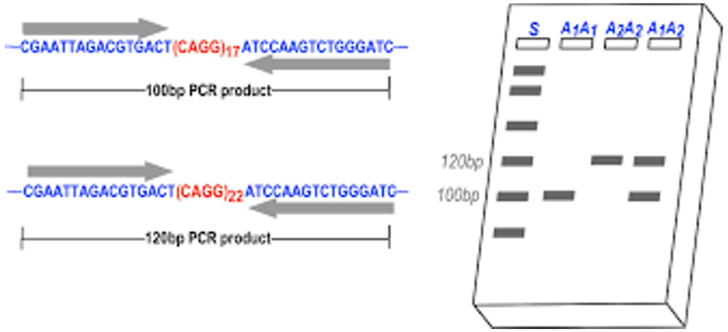
- In genetics, a **molecular marker** is a fragment of DNA that is associated with a certain location within the genome.



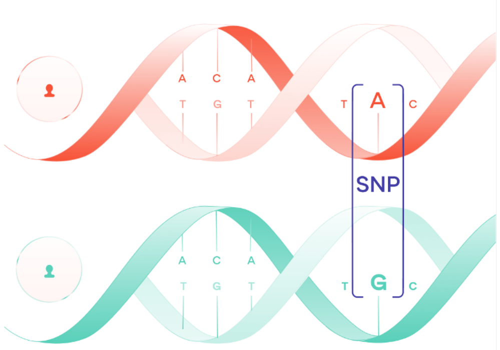
AFLP



SSR



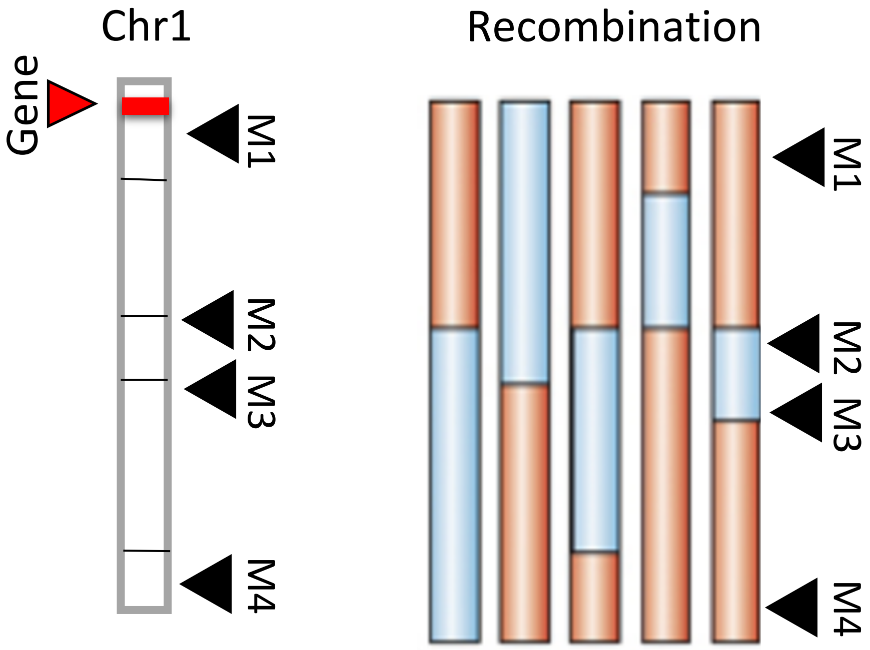
SNP



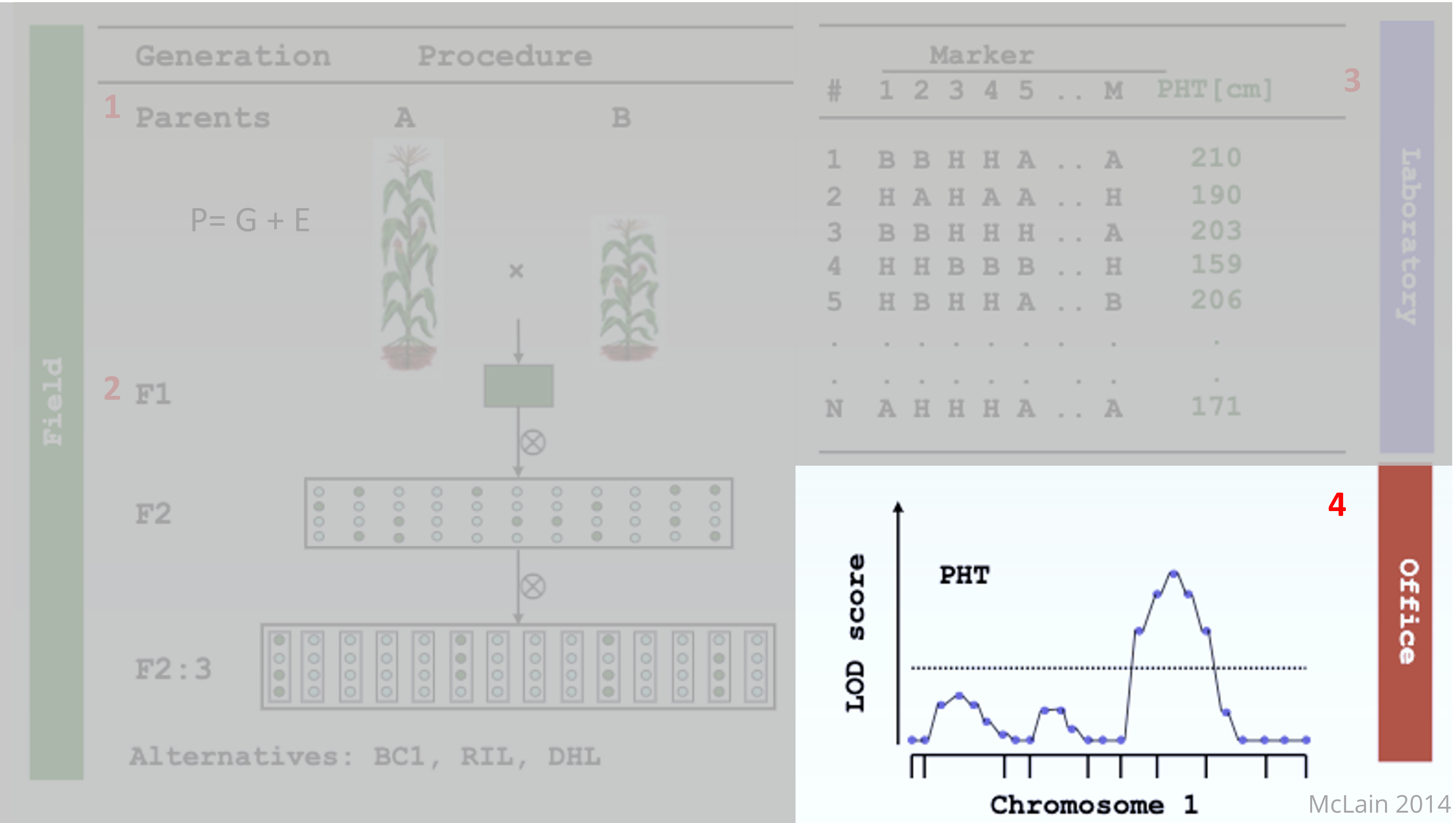
3. Markers and linkage maps

- Linkage maps indicate the position and relative genetic distances between markers along chromosomes.

- QTL mapping is based on the principle that genes and markers segregate via chromosome recombination during meiosis.



Quantitative trait loci



#	1	2	3	4	5	..	M	PHT [cm]
1	B	B	H	H	A	..	A	210
2	H	A	H	A	A	..	H	190
3	B	B	H	H	H	..	A	203
4	H	H	B	B	B	..	H	159
5	H	B	H	H	A	..	B	206
.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.
N	A	H	H	H	A	..	A	171

McLain 2014

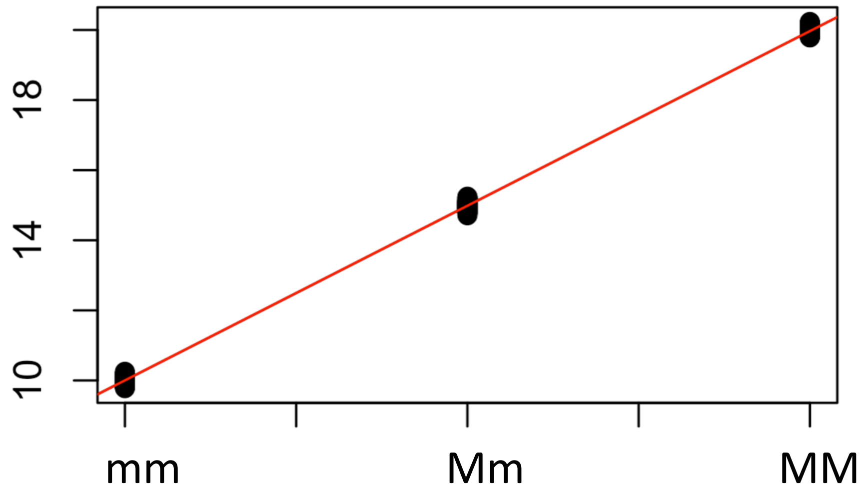
4. QTL detection

The statistical methods used for single-marker analysis include t-tests, analysis of variance (ANOVA) and linear regression.

$$t = \frac{\overline{MM} - \overline{mm}}{\sqrt{\frac{\hat{V}(MM)}{N} + \frac{\hat{V}(mm)}{N} +}}$$

T-test: compare the mean of 2 groups. To compare 3 or more groups, one must use an ANOVA.

$$\overset{\text{Estimated (or predicted) y value}}{y_i} = \overset{\text{Estimate of the regression intercept}}{b_0} + \overset{\text{Estimate of the regression slope}}{b_1}\overset{\text{Independent variable}}{x} + \underset{\text{Error term}}{e}$$



4. QTL detection

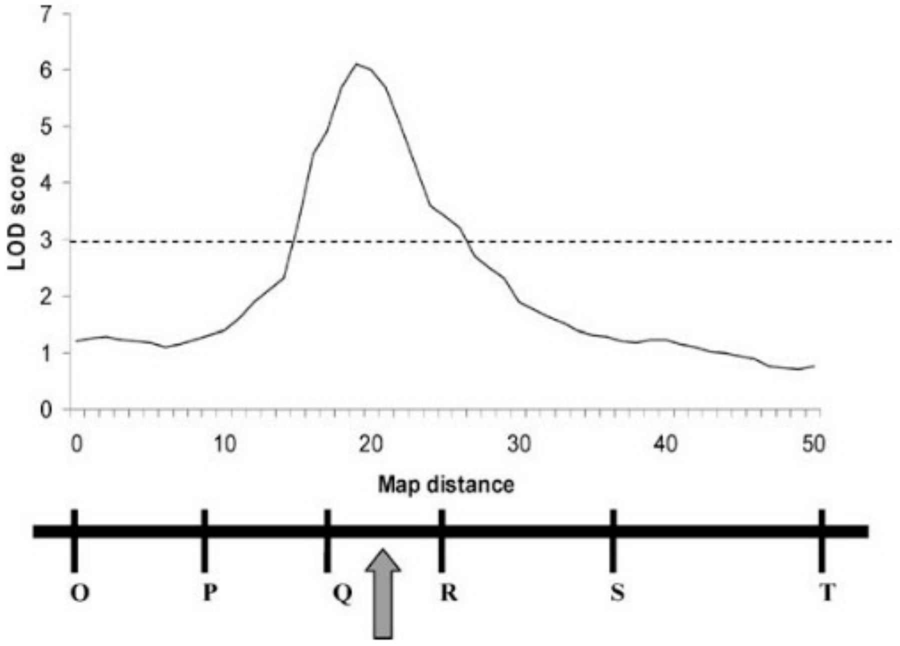
Interval mapping

- **Simple Interval Mapping (SIM)**

SIM uses adjacent markers to estimate a QTL location.

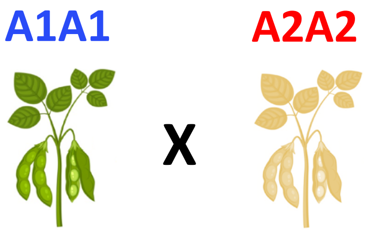
- **Composite Interval Mapping (CIM)**

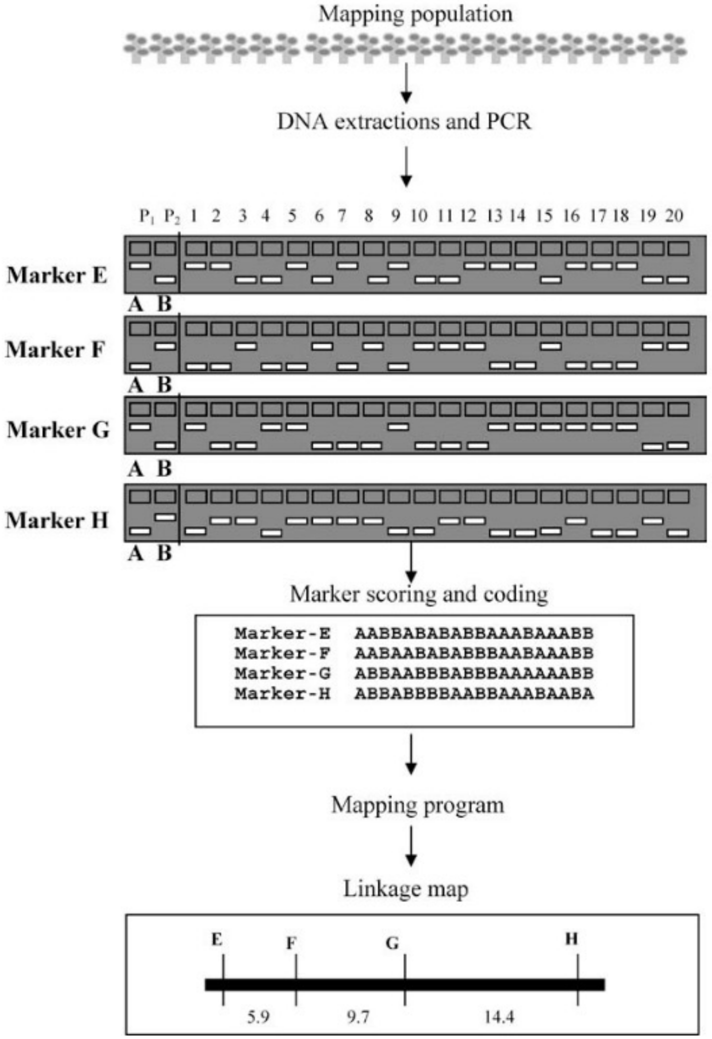
CIM uses interval mapping and includes genetic markers in the statistical model in addition to an adjacent pair of linked markers for interval mapping.



Collard *et al* 2005

Review:




Mapping population

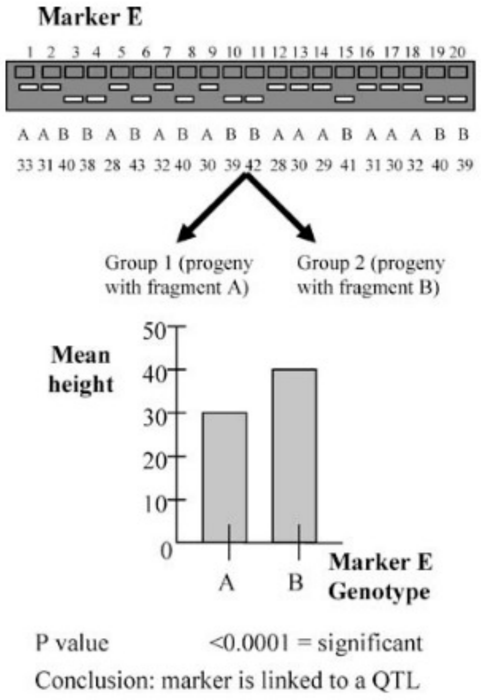
DNA extractions and PCR

Marker scoring and coding

```
Marker-E  AABBABABABBAAABAAABB
Marker-F  AABAABABABBBAABAAABB
Marker-G  ABBAABBBABBBAAAAAABB
Marker-H  ABBABBBBAABBAAABAABA
```

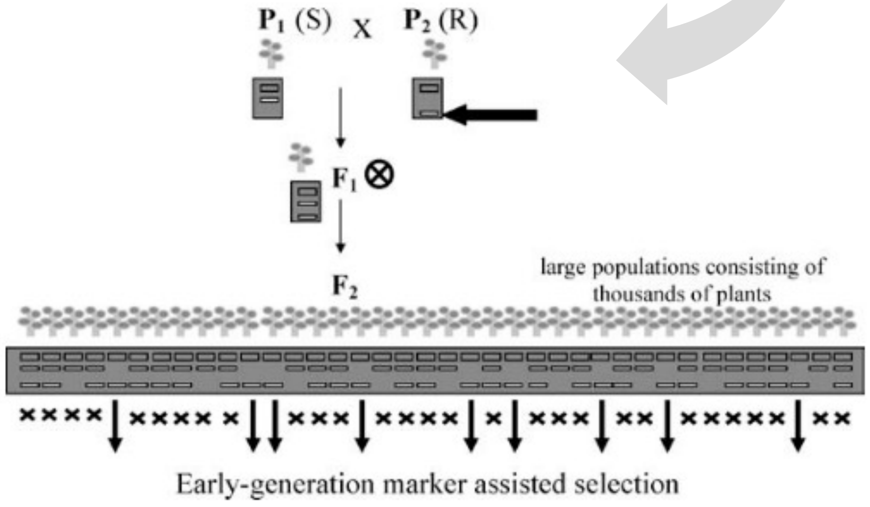
Mapping program

Linkage map



P value <0.0001 = significant

Conclusion: marker is linked to a QTL



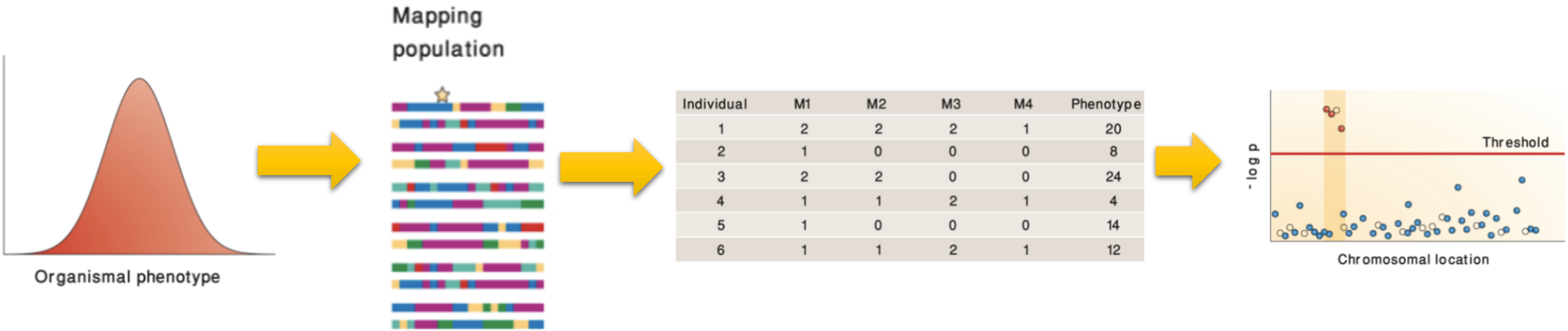
Early-generation marker assisted selection

Collard *et al* 2005

Association mapping

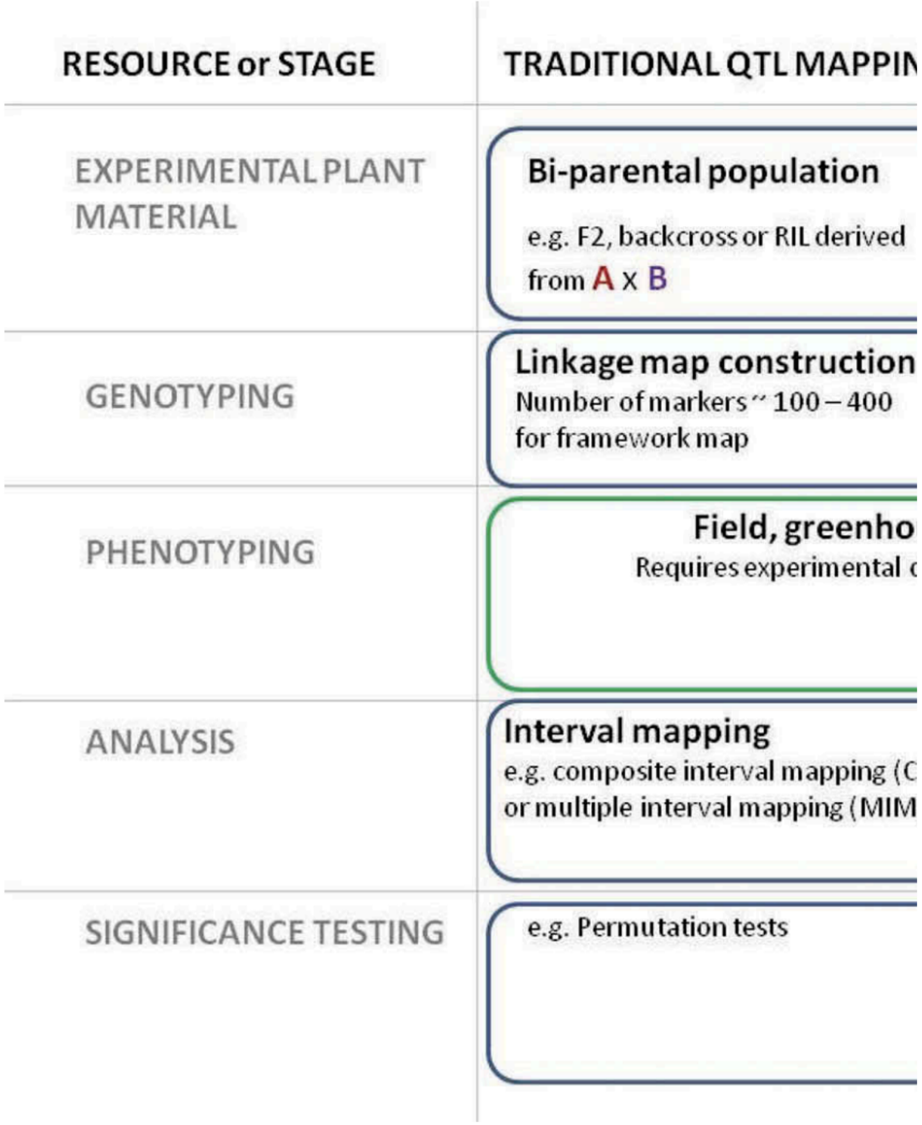
Association mapping

- Association analysis uses historical recombination events over many generations within a short interval surrounding a trait locus
- Association analysis is advantageous for the identification of relatively small genomic regions, in which only few genes may reside.



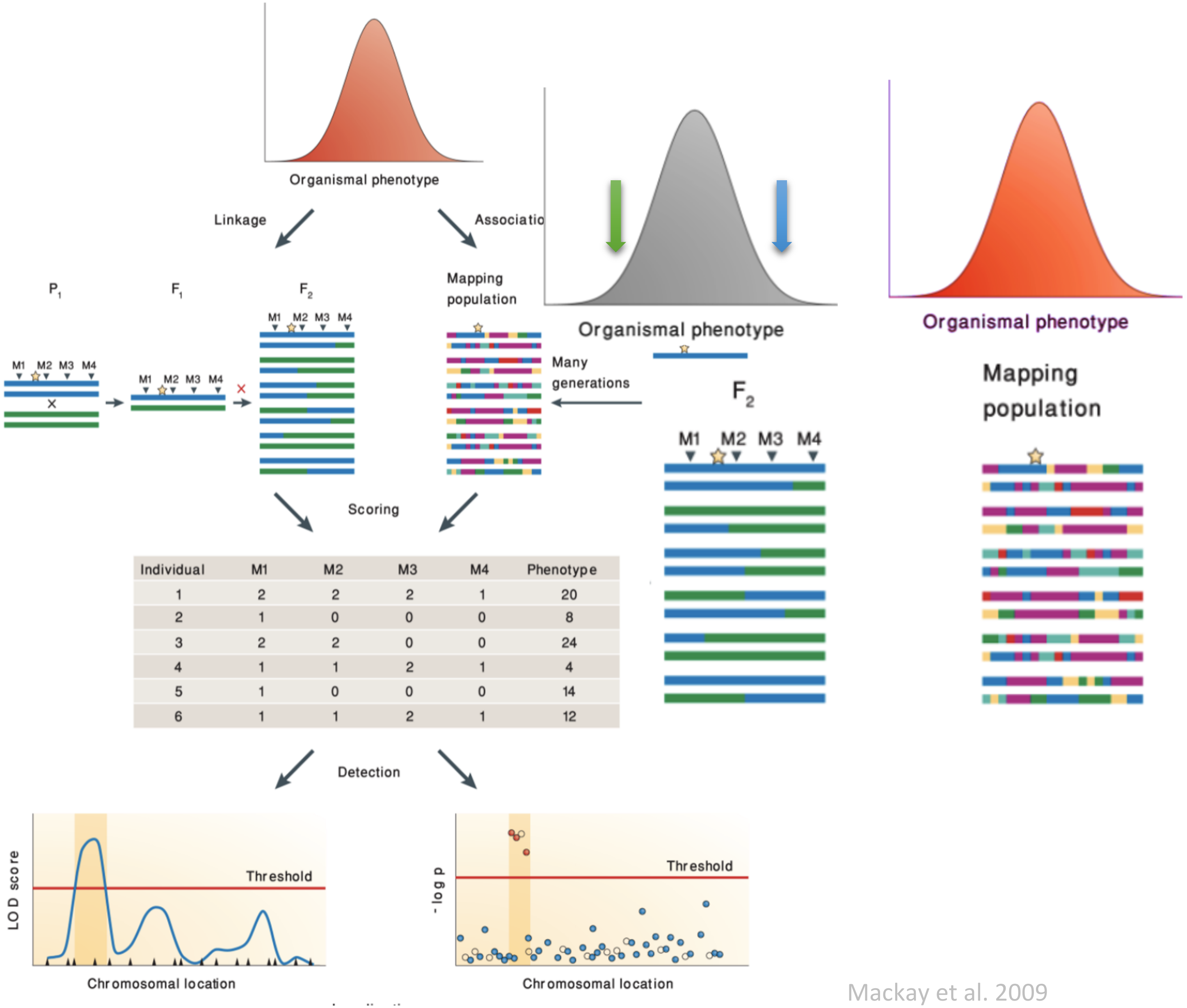
Individual	M1	M2	M3	M4	Phenotype
1	2	2	2	1	20
2	1	0	0	0	8
3	2	2	0	0	24
4	1	1	2	1	4
5	1	0	0	0	14
6	1	1	2	1	12

Mapping population vs Association mapping



RESOURCE or STAGE	TRADITIONAL QTL MAPPIN
EXPERIMENTAL PLANT MATERIAL	**Bi-parental population** e.g. F2, backcross or RIL derived from A x B
GENOTYPING	**Linkage map construction** Number of markers ~ 100 – 400 for framework map
PHENOTYPING	**Field, greenho** Requires experimental
ANALYSIS	**Interval mapping** e.g. composite interval mapping (C or multiple interval mapping (MIM
SIGNIFICANCE TESTING	e.g. Permutation tests

Verdep



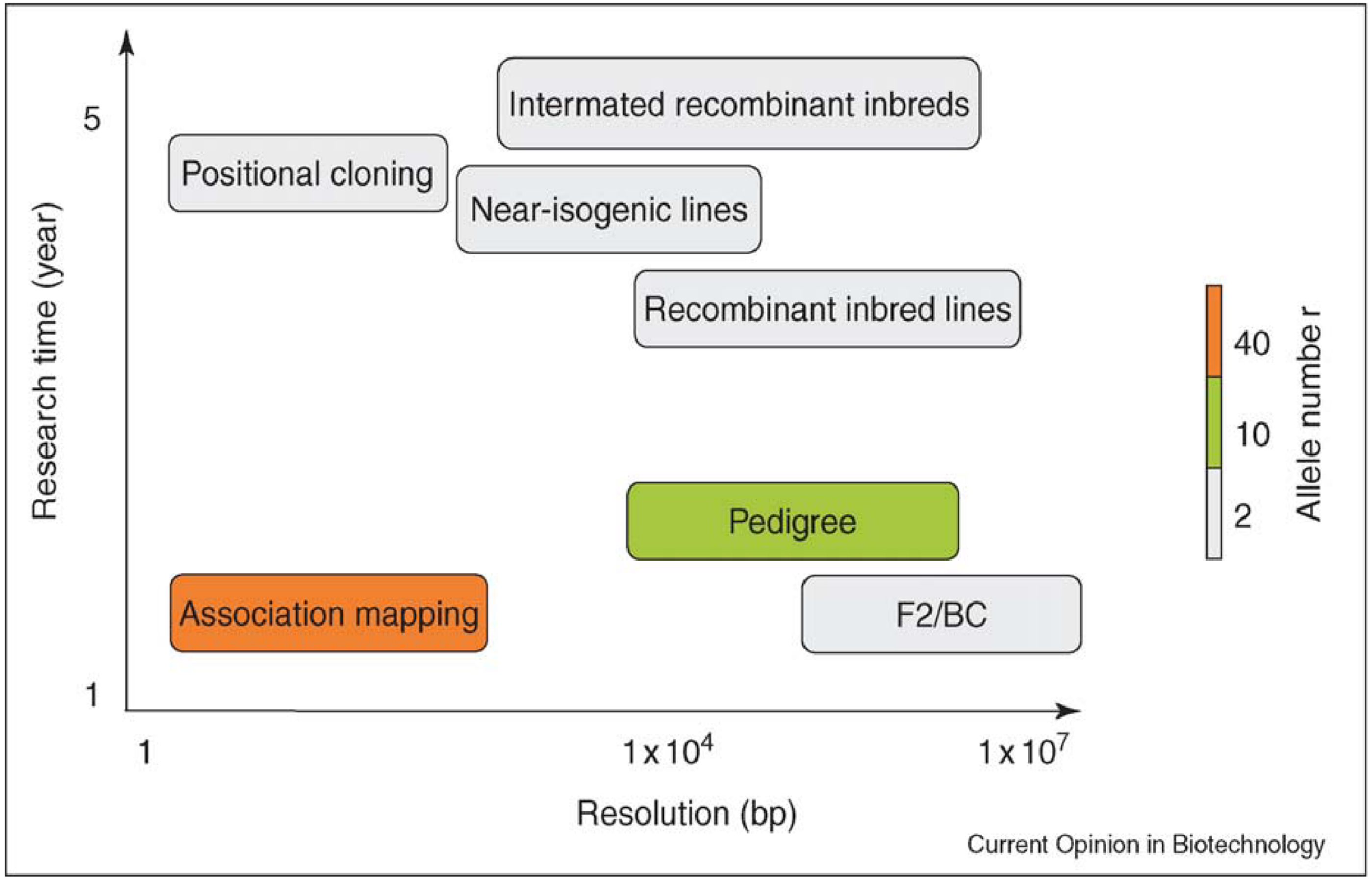
Individual	M1	M2	M3	M4	Phenotype
1	2	2	2	1	20
2	1	0	0	0	8
3	2	2	0	0	24
4	1	1	2	1	4
5	1	0	0	0	14
6	1	1	2	1	12

Mackay et al. 2009

Mapping population vs Association mapping

Association mapping offers three advantages over linkage analysis:

- Higher mapping resolution
- Greater allele number
- Less research time in establishing an association

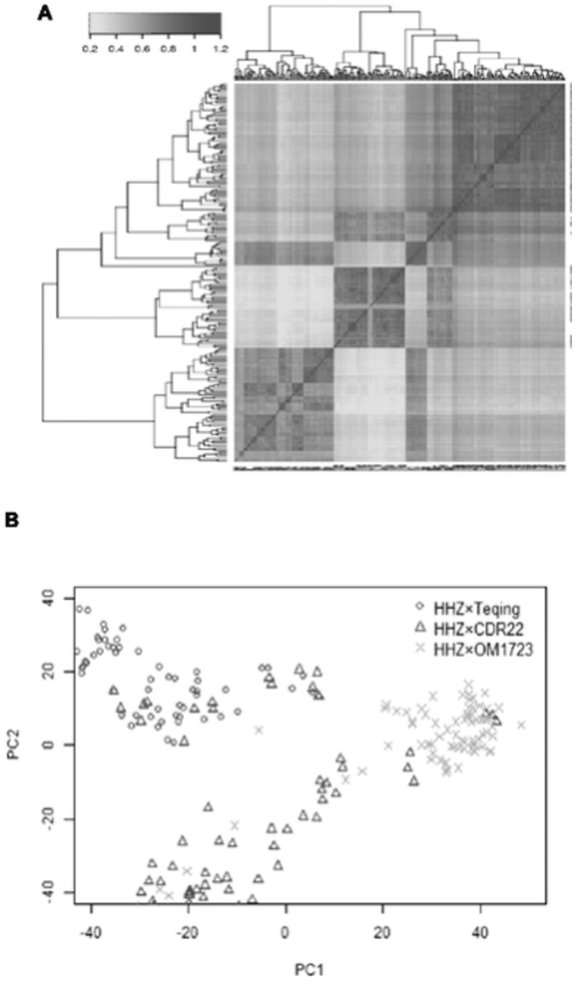


Yu & Buckler 2005

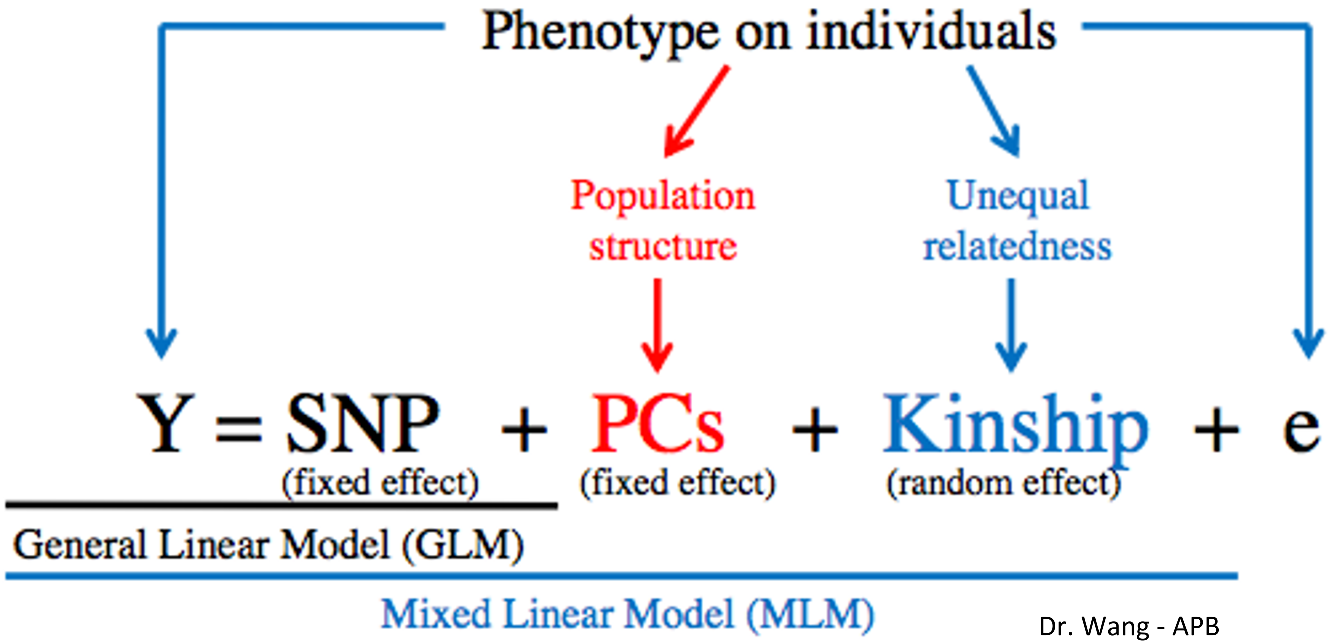
Statistical approaches

Kinship

PCA



Feng *et al* 2018



Phenotype on individuals

Population structure

Unequal relatedness

$$Y = SNP + PCs + Kinship + e$$

SNP (fixed effect)

PCs (fixed effect)

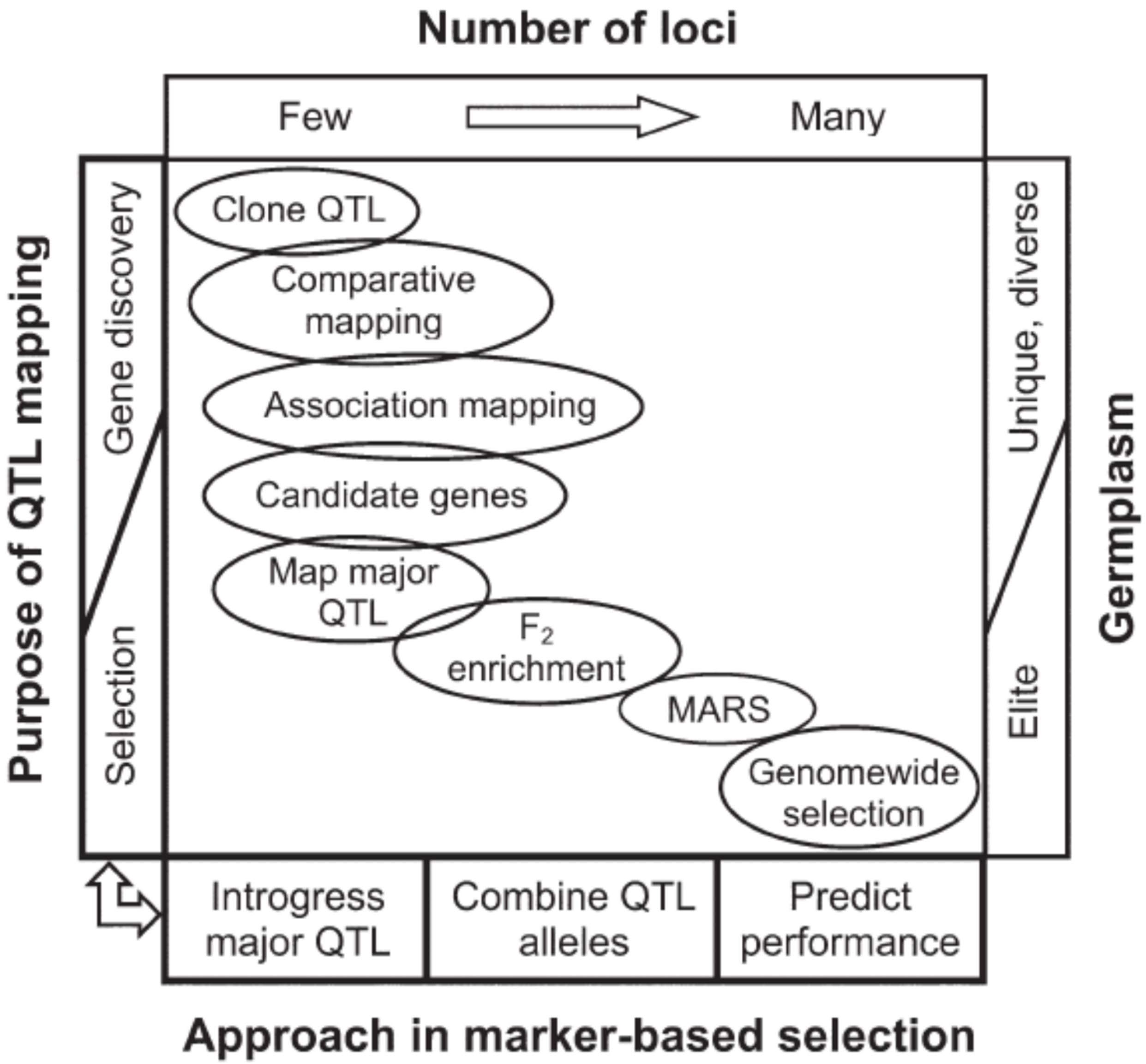
Kinship (random effect)

General Linear Model (GLM)

Mixed Linear Model (MLM)

Dr. Wang - APB

Genomic selection



Number of loci

Few

Many

Purpose of QTL mapping

Gene discovery

Selection

Clone QTL

Comparative mapping

Association mapping

Candidate genes

Map major QTL

F_2 enrichment

MARS

Genomewide selection

Germplasm

Unique, diverse

Elite

Introgress major QTL

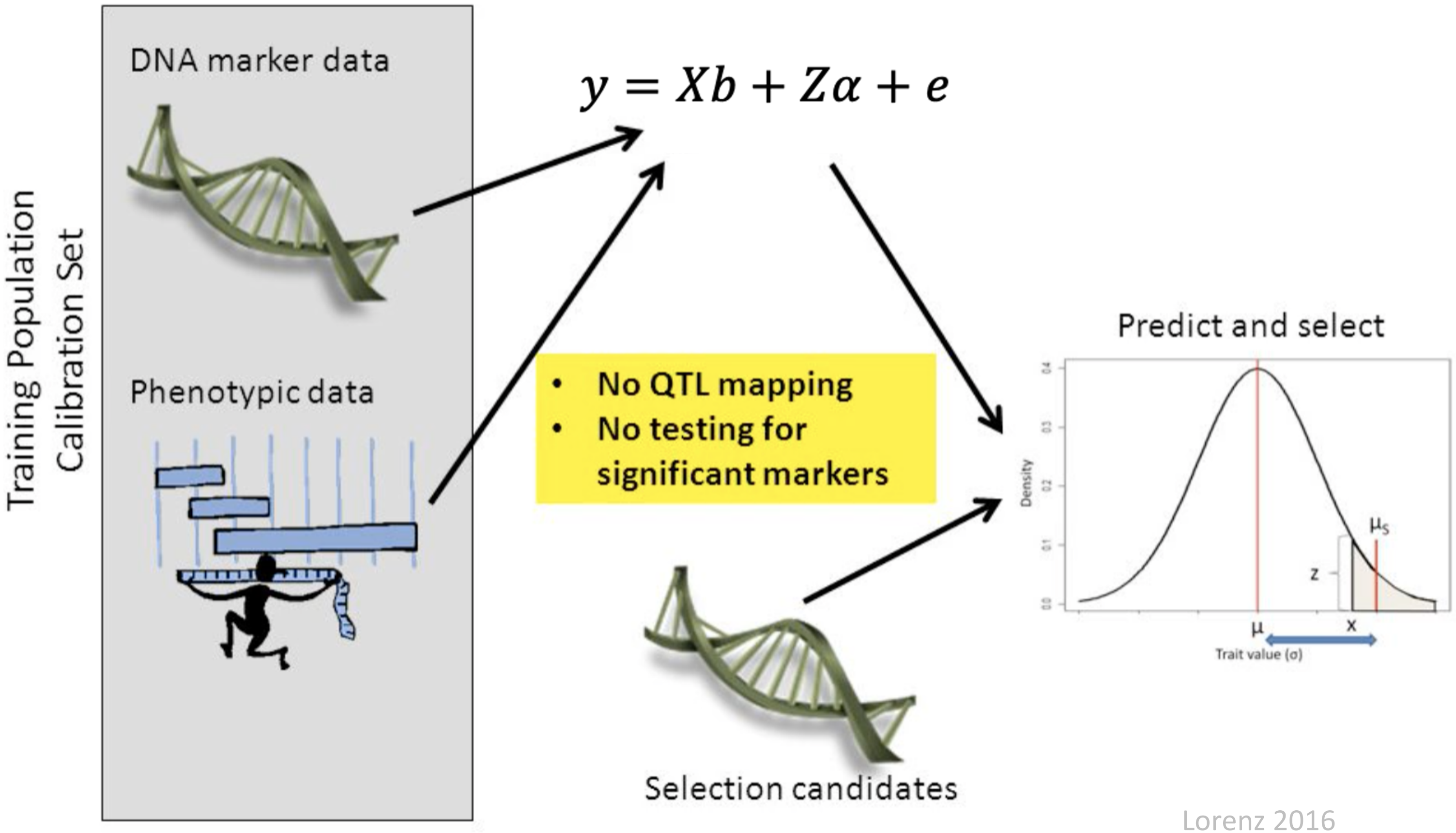
Combine QTL alleles

Predict performance

Approach in marker-based selection

Bernardo 2008

Genomic selection



$$y = Xb + Z\alpha + e$$

- No QTL mapping
- No testing for significant markers

Lorenz 2016

Trait

Incidence matrix

Effects for fixed effects

$$y = Xb + Z\alpha + e$$

Incidence matrix

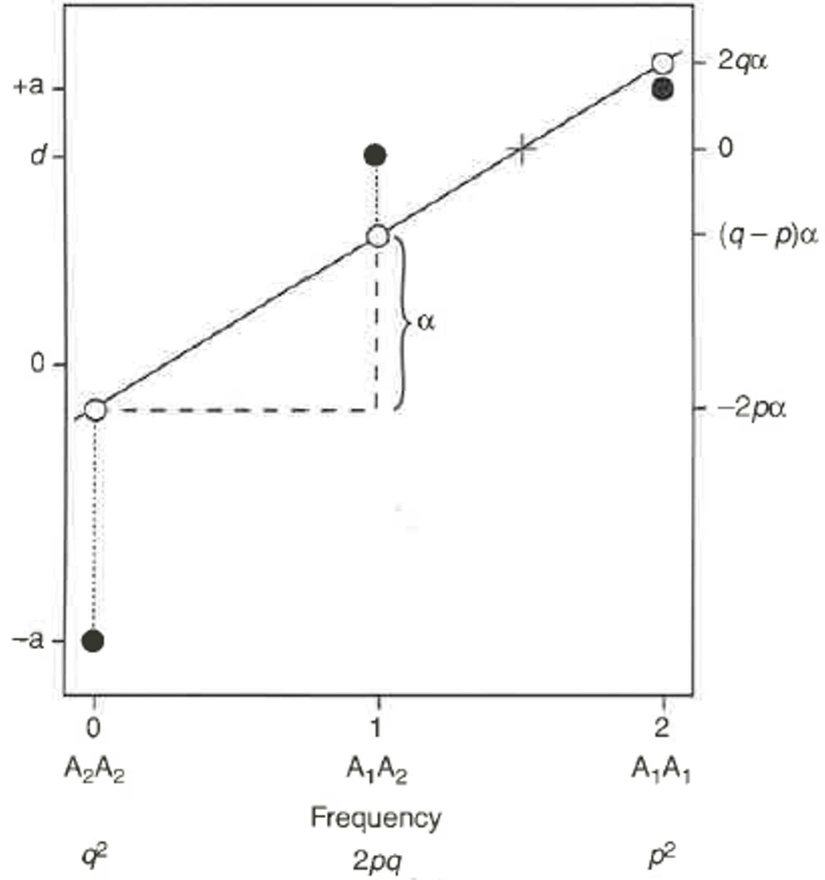
Effects for each marker

Genomic selection

GS uses all molecular markers to predict genomic estimated breeding values **(GEBV).**

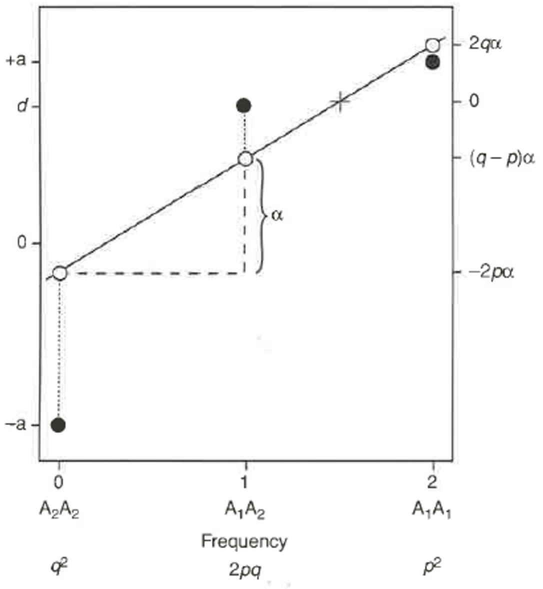
Genotype	Breeding value
A1A1	$2\alpha_1 = 2q\alpha$
A1A2	$\alpha_1 + \alpha_2 = (q - p)\,\alpha$
A2A2	$2\alpha_2 = -2p\alpha$

$$GEBV = \sum_{i}^{p} Z_i\,\alpha_i$$



Falconer & Mackay p 115,117

Genomic selection



Falconer & Mackay p 115,117

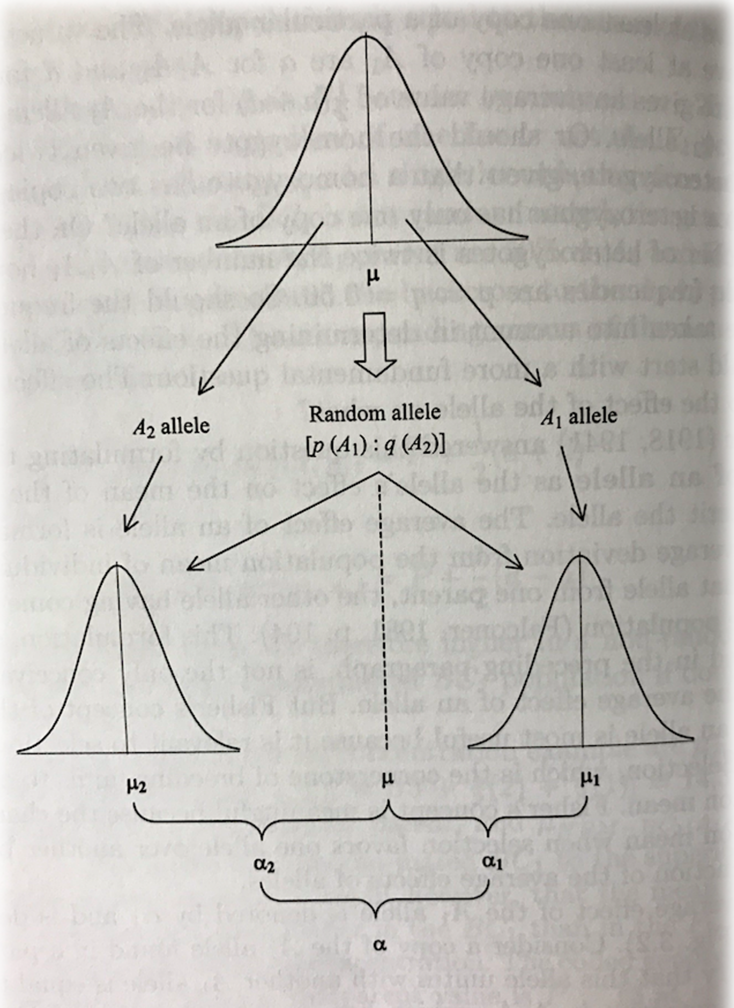


FIGURE 3.2. Average effects of alleles.

Bernardo 2020

Average effects of the al

$$\alpha_1 = q[a + d(q - p)] \qquad \alpha_2 = -p[a + d(q - p)]$$

Average effects of gene supstit

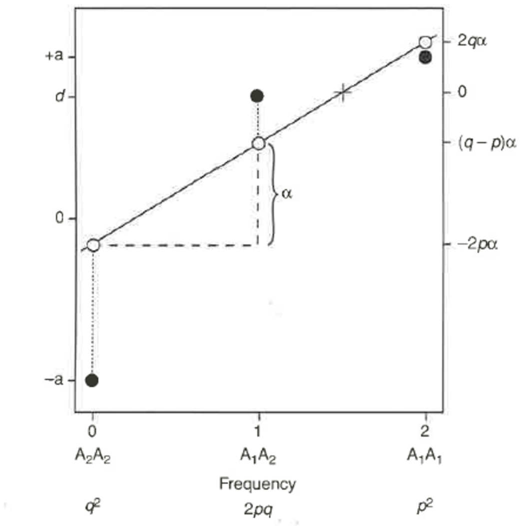
$$\alpha = \alpha_1 - \alpha_2 = \mathrm{a} + \mathrm{d}(\mathrm{q} - \mathrm{p})$$

$$GEBV = \sum_{i}^{p} Z_i \, \alpha_i$$

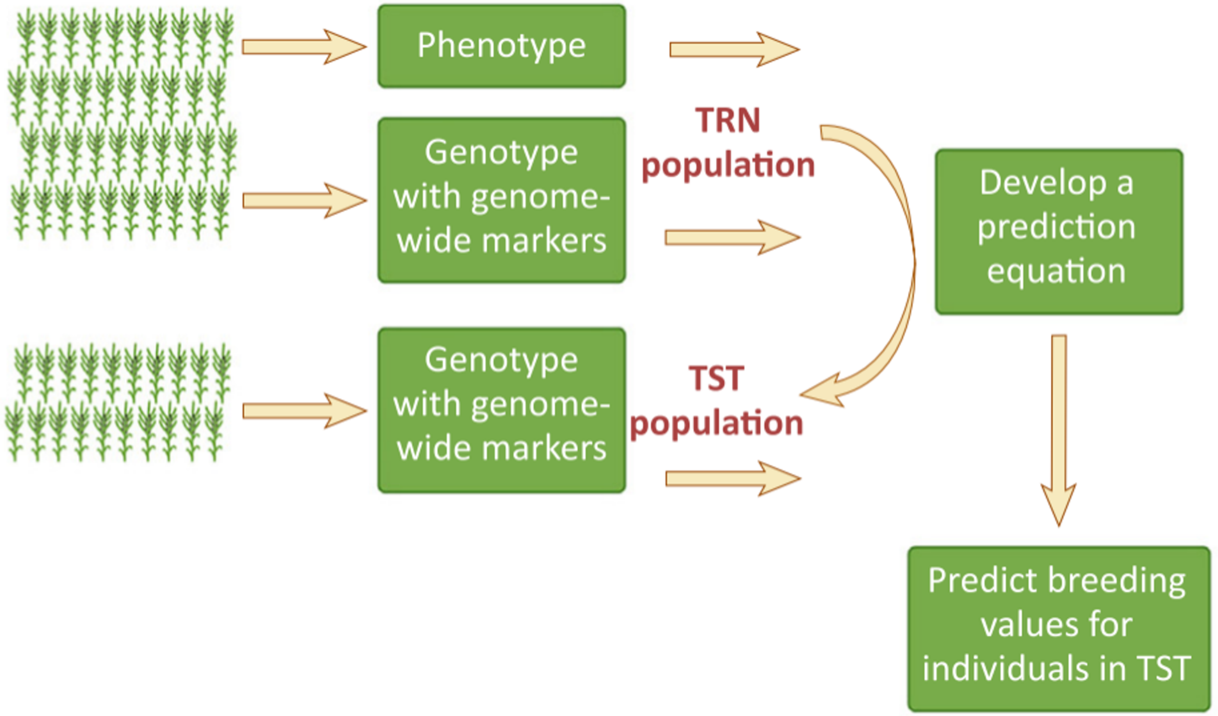
Genomic selection

- GS uses all molecular markers to predict genomic estimated breeding values **(GEBV).**

- GS combines molecular and phenotypic data in a training population to obtain the GEBV of individuals in a testing population that have been genotyped but not phenotyped.



$$GEBV = \sum_{i}^{p} Z_i \, \alpha_i$$



Phenotype

TRN population

Genotype with genome-wide markers

Develop a prediction equation

TST population

Genotype with genome-wide markers

Predict breeding values for individuals in TST

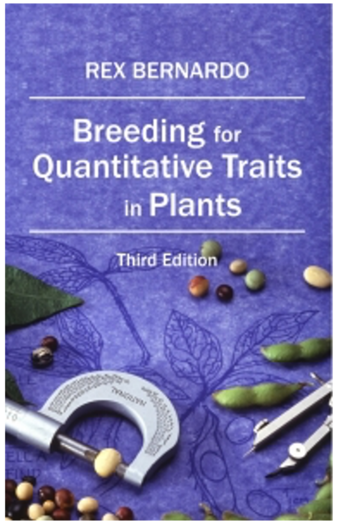
Crossa et al 2017

Genomic selection

- Are interested in go deeper in GS basic model?

$$GEBV = \sum_{i}^{p} Z_i \alpha_i$$

University of Minnesota


REX BERNARDO

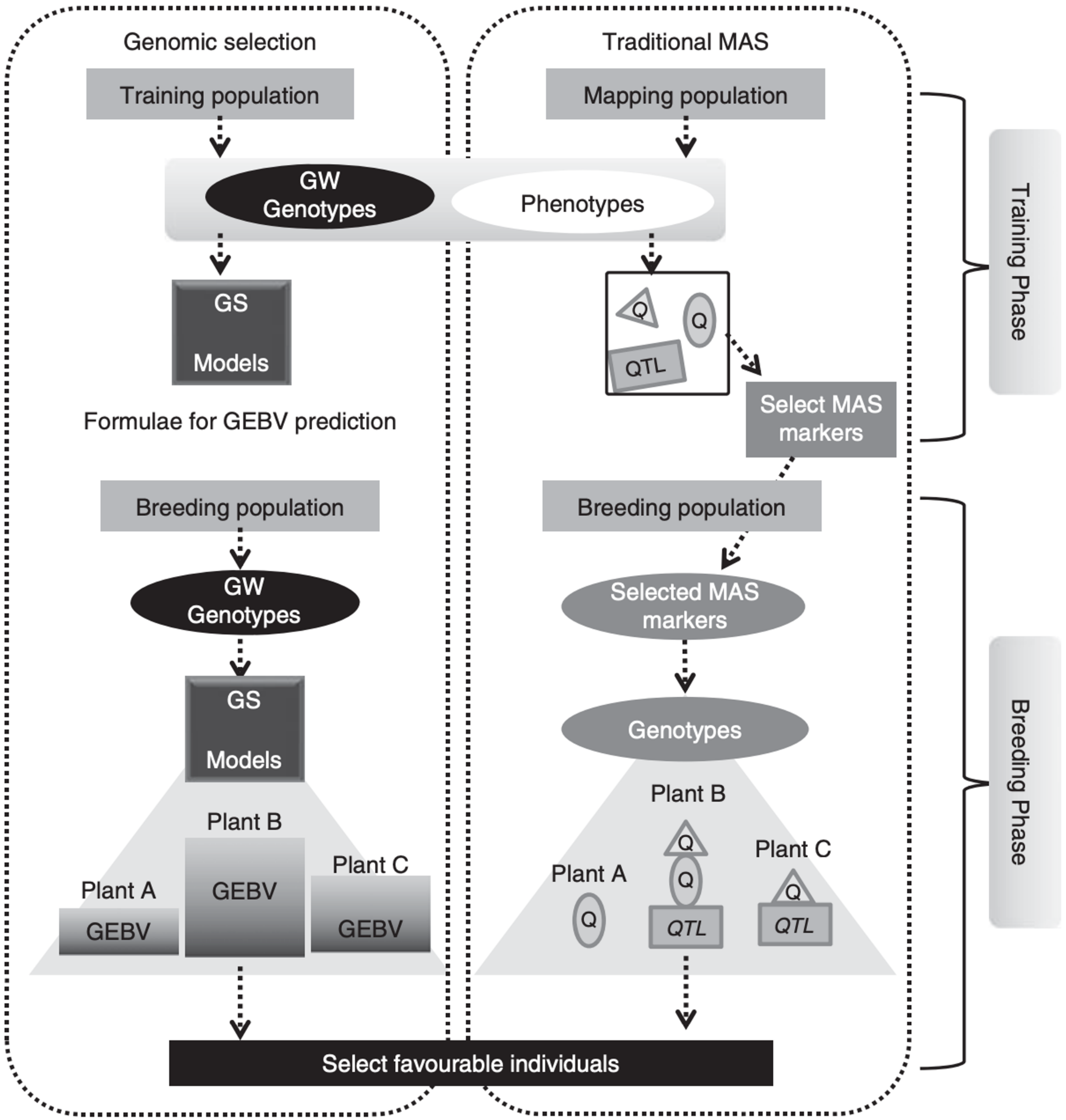
Breeding for Quantitative Traits in Plants

Third Edition

https://www.youtube.com/watch?v=O7KYlSOZhZo&t=1939s

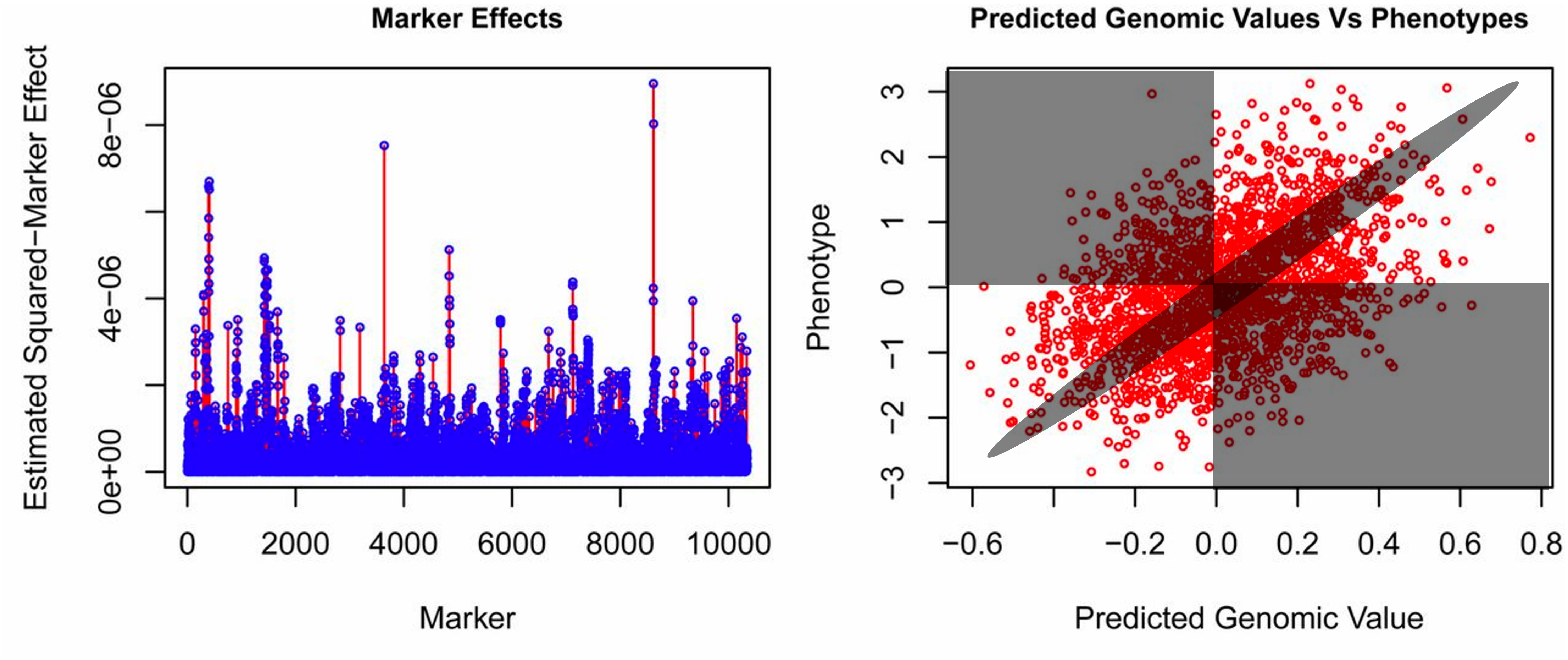
MAS vs GS

Schemes of GS and traditional MAS for the selection of quantitative traits (right).



Nakaya and Isobe 2021

Framework for GS



Perez and Gustavo de los Campos (2014)

GS is not the solution of all our problems

…but it is helpful

- Reduce breeding cycle
- Increase selection intensity
- Increase genetic variance
- Reduce costs

$$\Delta G_{year} = \frac{i \; r_{AI} \; \sigma_A}{L}$$

i = Selection intensity

r_{AI} = Accuracy

σ_A = Genetic standard deviation

L = Generation interval