# (2) Quantitative trait loci and genetic maps

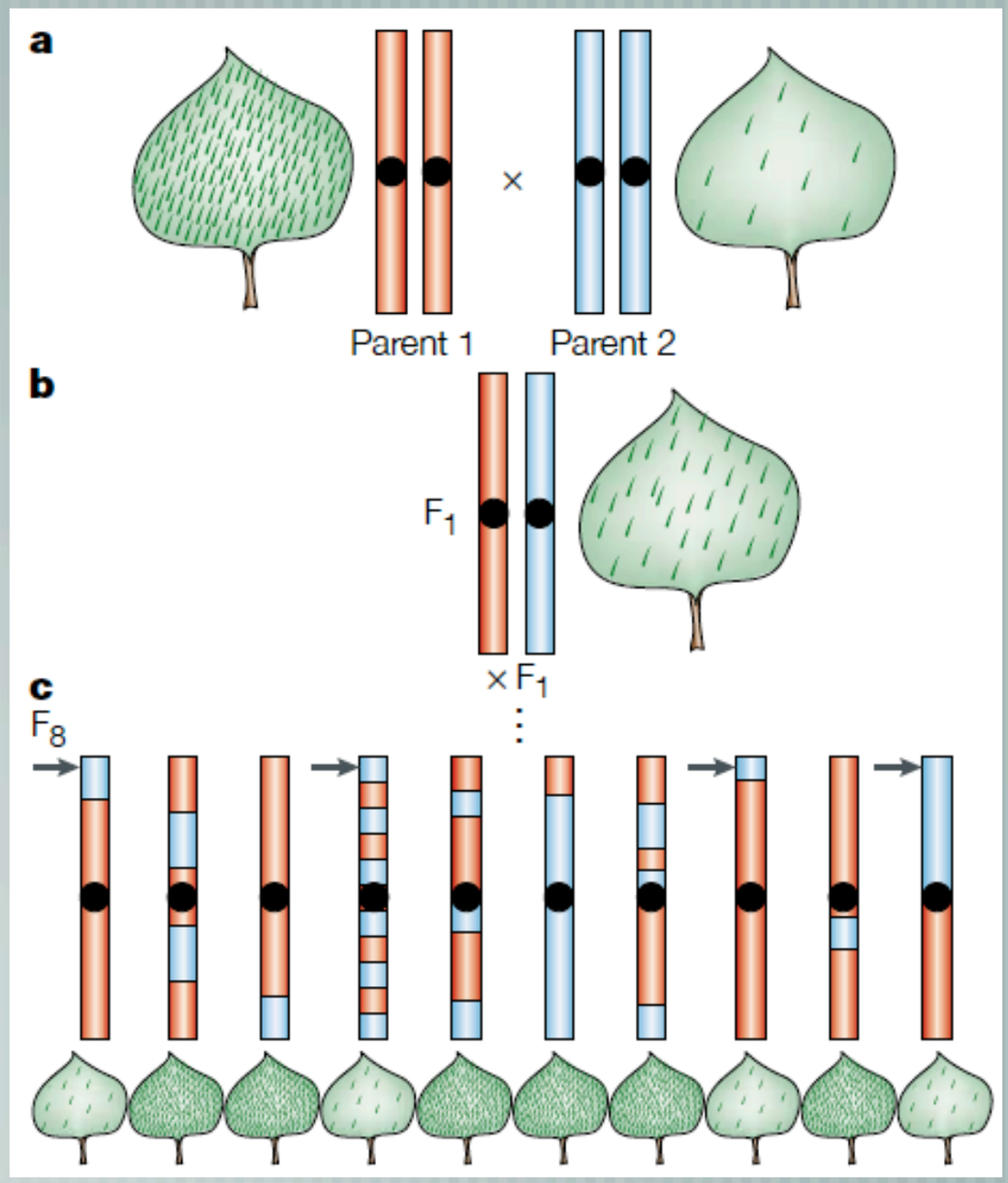
060313
1400:1700

By the end of this lecture you should be able to explain:

- The four main types of information you need to for QTL analysis
- Why understanding recombination & genetic linkage is important for localising genes that control traits
- What a marker-trait association is

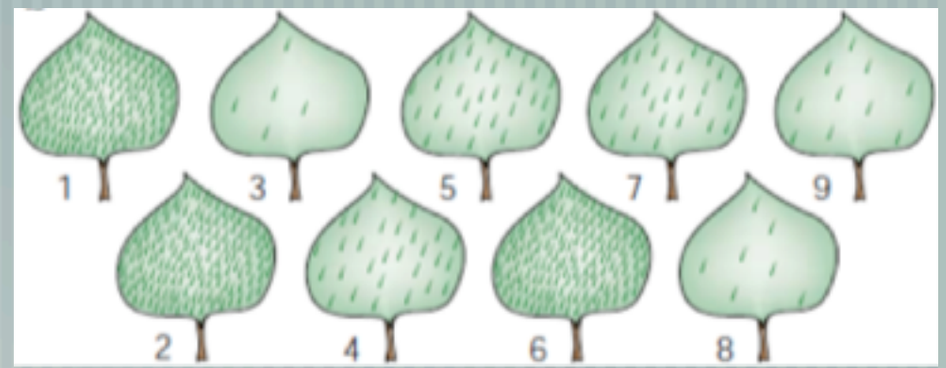
# Objectives of QTL analysis

- The statistical study of the alleles that occur at a locus and the phenotypes (traits) that they produce
- Methods developed in the 1980s
- Next-gen sequencing = enabling
- Rapid, genome-wide analysis possible
- Better statistical methods



# What you need for QTL analysis:

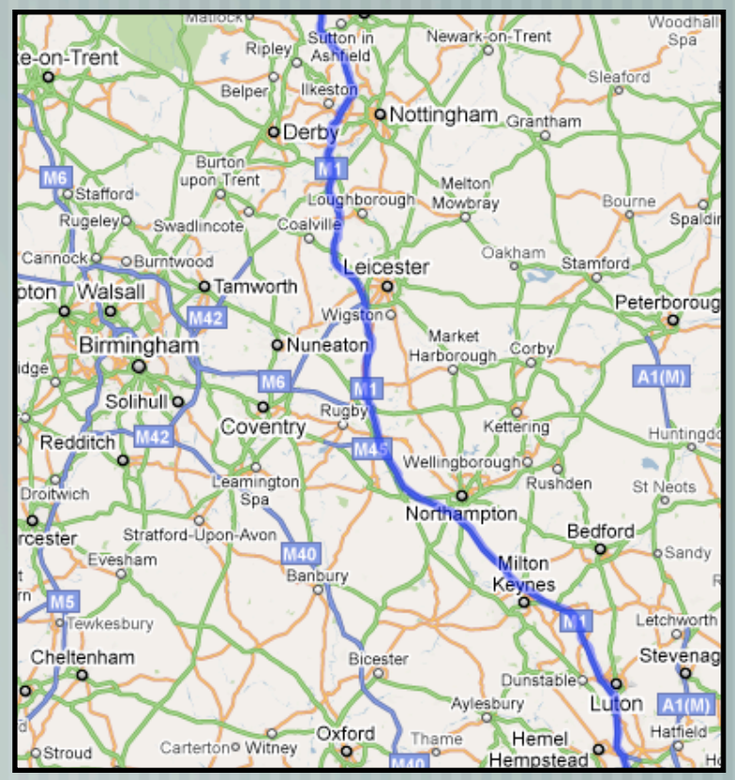
- (i) A large population of individuals that you can score
  - variation in phenotype
  - population designed using parents with contrasting phenotypes



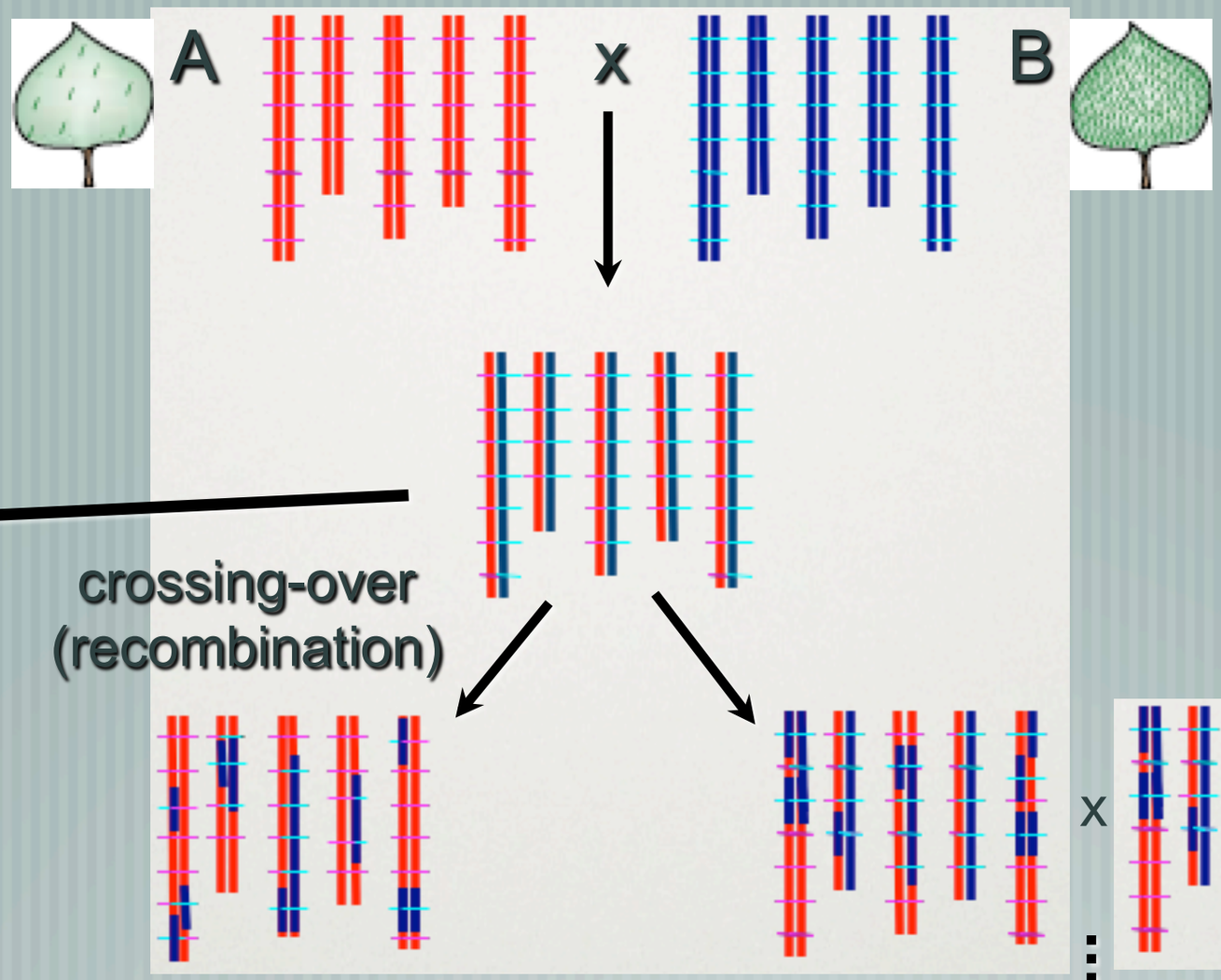

- (ii) Markers over the genome to pinpoint QTL location

- (iii) A way to identify which markers from each parent have been inherited by the progeny

- (iv) A map of the genome to find out where you are



# (i) Mapping lines




Parents = Homozygous

F1 = Heterozygous at all loci

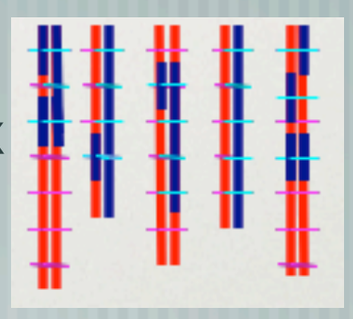
F1 microspore culture of male gametes

DH population (homozygous)

crossing-over (recombination)



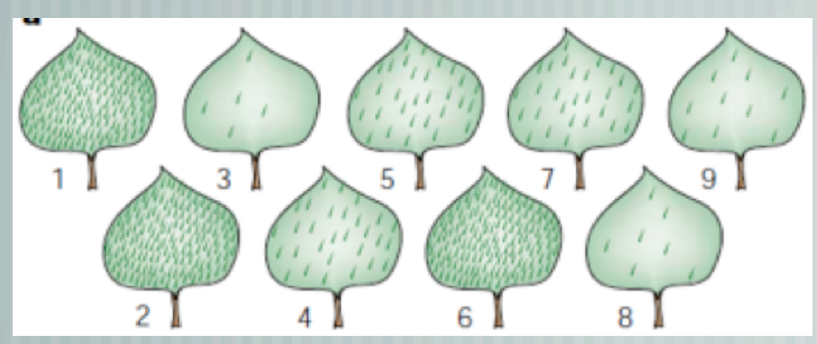
x

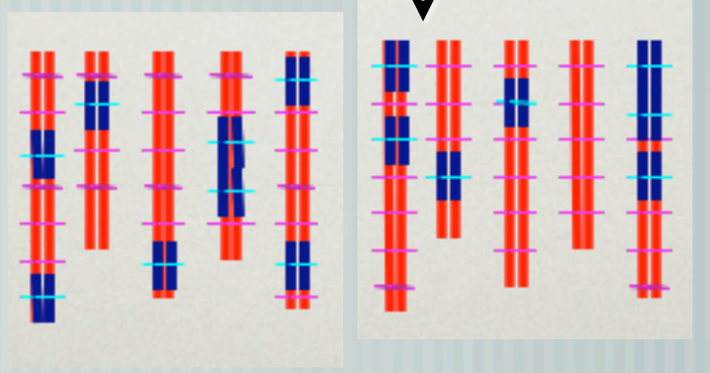


F2 = Heterozygous at some loci

Many different individuals are obtained & separately selfed to develop RILs

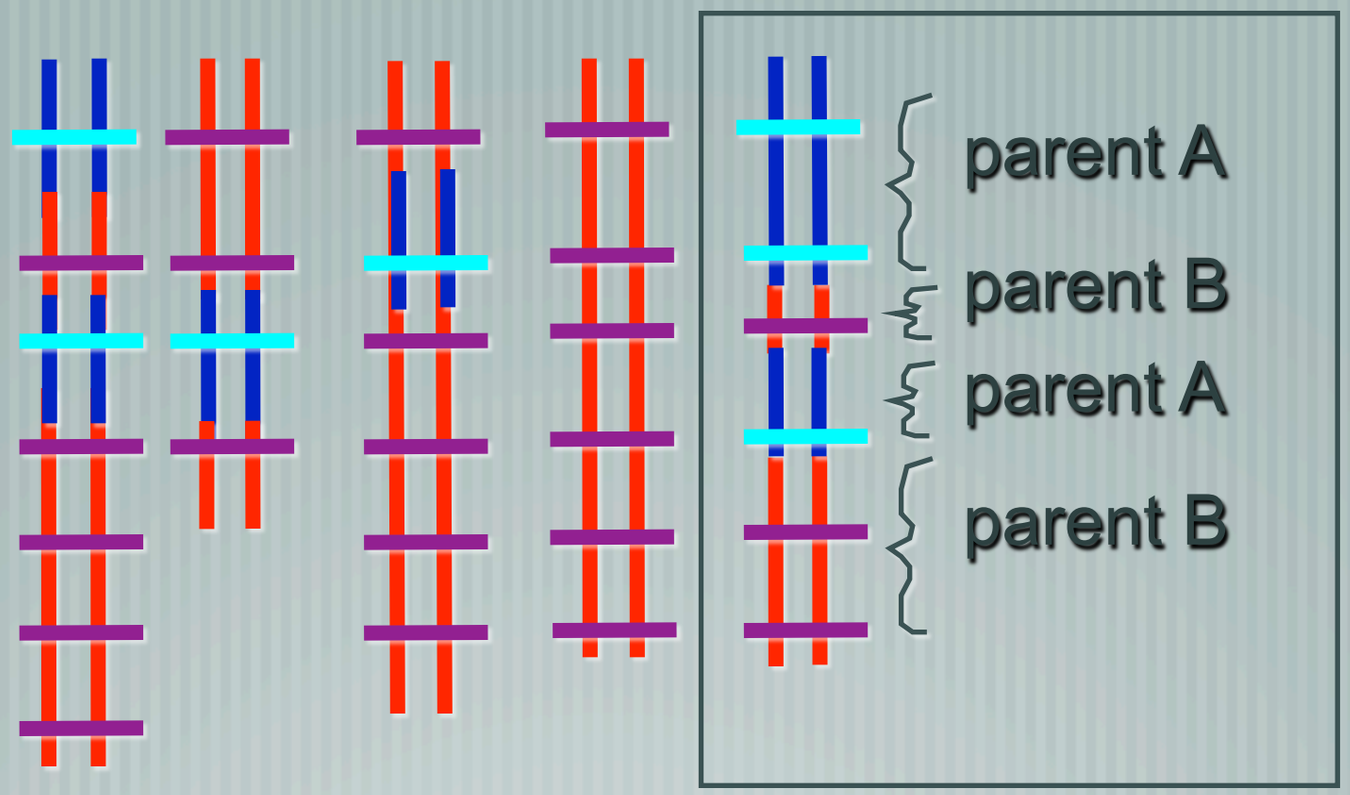
x5



F7 RILs = Homozygous at all loci & heterogeneous

# (ii) Genetic markers




- Most common: molecular markers (DNA sequence differences)
- What else could you use?

GAATTC GATTTC

# (iii) A way to distinguish molecular markers

GAATTC

GATTTC

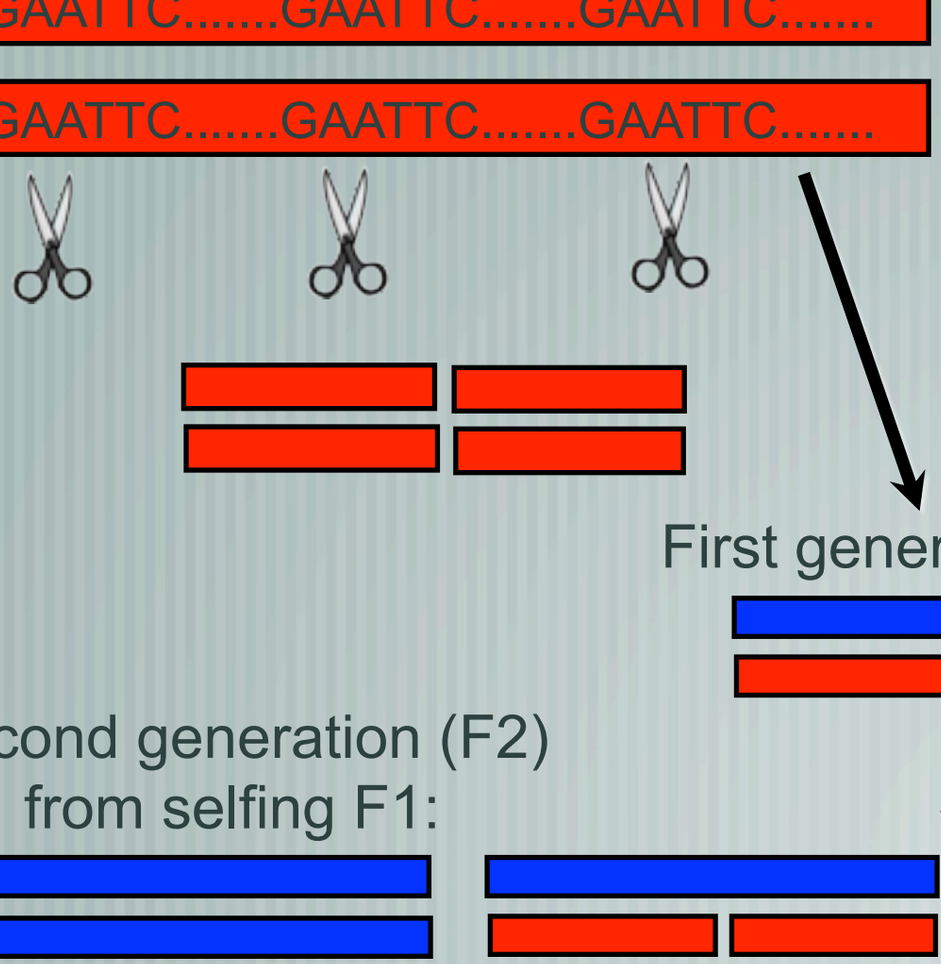
- Restriction enzymes e.g. EcoRI cut DNA only at a specific recognition sequence
- Compare restriction patterns:

Parent A

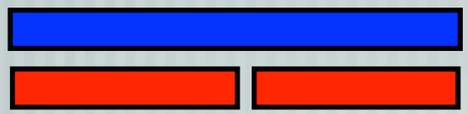
.....GAATTC.....GAATTC.....GAATTC.....

Parent B

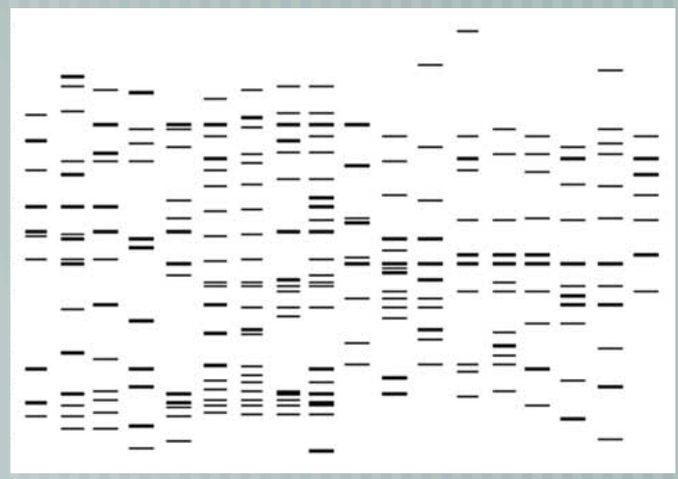
.....GAATTC.....GATTTC.....GAATTC.....



First generation (F1)

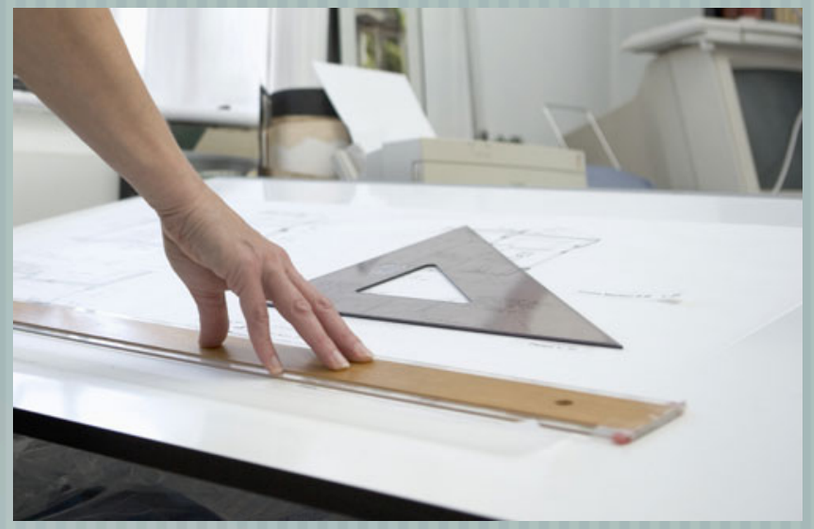


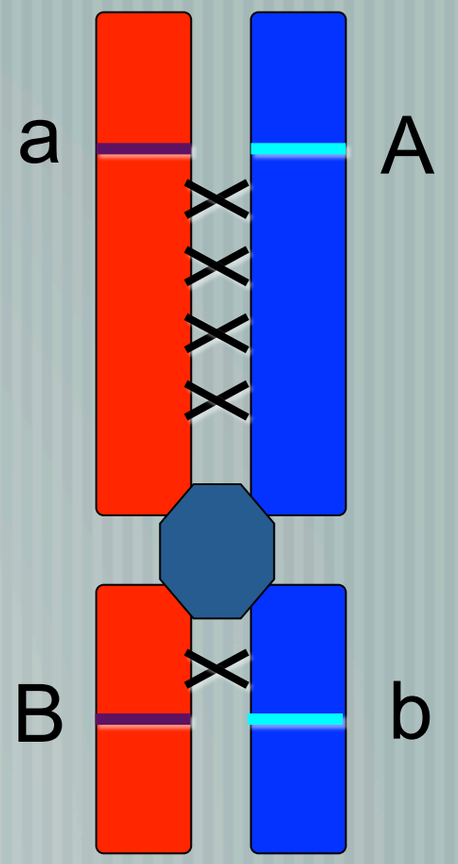
Second generation (F2) from selfing F1:



# (iv) Genetic map

- Physical map: lays out the sequence information and annotates it: promoters, genes etc.





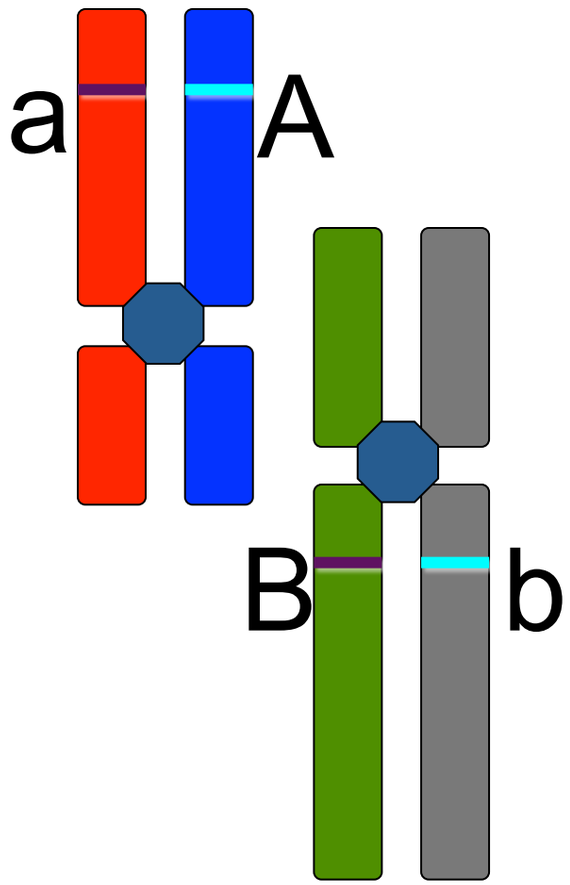

- Linkage map:

order of genetic markers and relative distances from each other

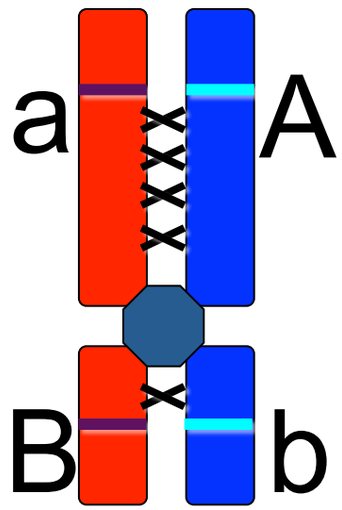
- based on meiotic recombination (crossing over) between chromosomes

  - Link genetic map to physical map

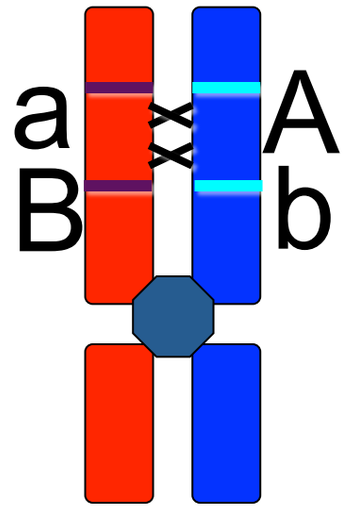
# Genetic linkage is related to recombination frequency



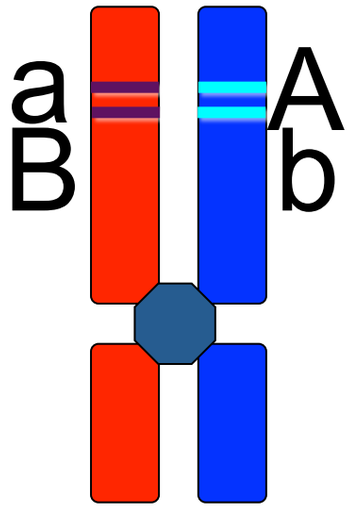

Rf = 0.5 (50%)
= no linkage




More recombination
so Rf = high ( ≤0.5 )
= weak linkage



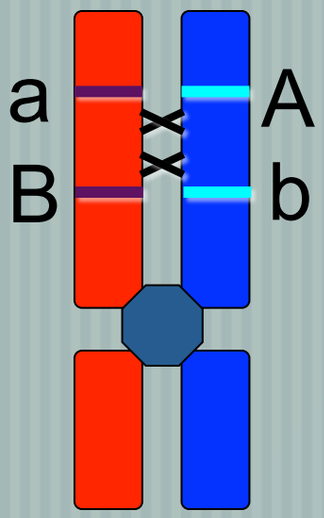

Some recombination
so Rf = medium
= quantifiable linkage




Little recombination
so Rf = small
= tight linkage

Rf = recombination frequency

# Map distances and genetic linkage




- Recombination frequency of 0.01 (1%) = a genetic map unit of 1 cM
- Recombination events occur randomly, once or twice per chromosome
- Linkage map made by characterising the recombination events that have taken place in a cross between two parental genotypes
- Assumes that linkage is the only cause of non-independence between markers and that segregation is Mendelian
- Haldane mapping function adjusts map distance to account for double crossovers that go undetected
- Kosambi mapping function also adjusts for crossover interference

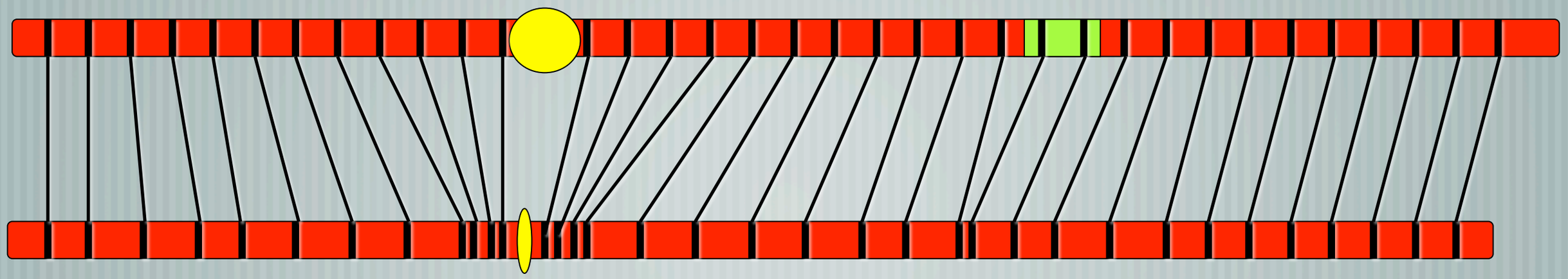
# Linkage groups are the basis of genetic maps

These should theoretically correspond to chromosomes, but if...

- Chromosomes very long
- Recombination frequency very high
- Mapping populations are not large enough

  ...one chromosome can statistically “break” into several linkage groups

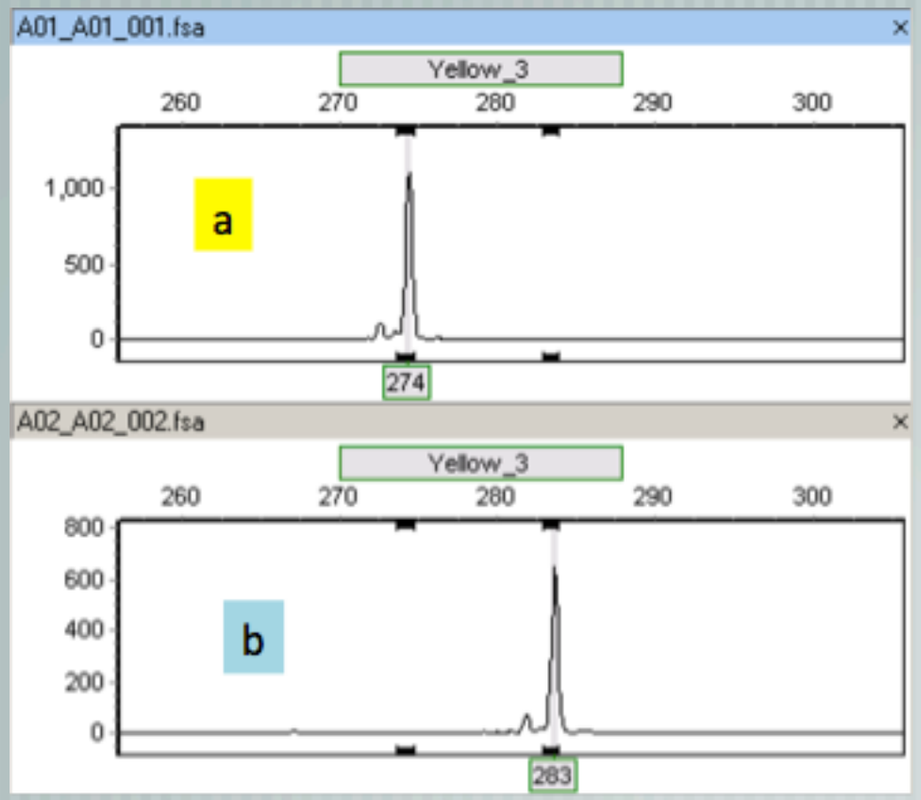
- Also, centromeres and heterochromatin have supressed recombination

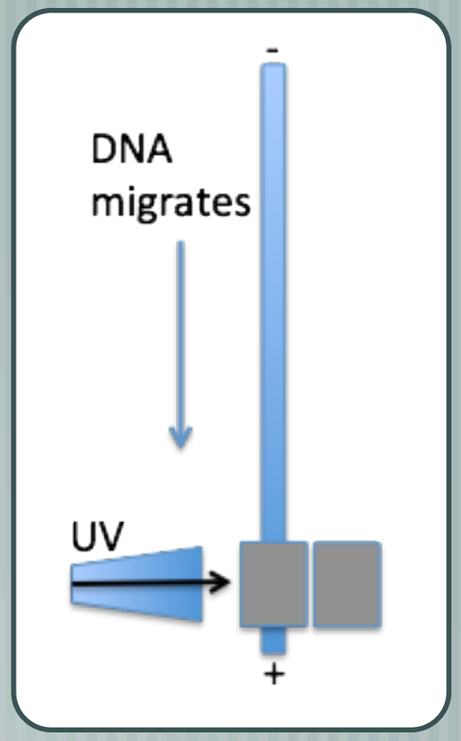


# Making a map: Selecting markers

- Are the markers

polymorphic between the parental lines?

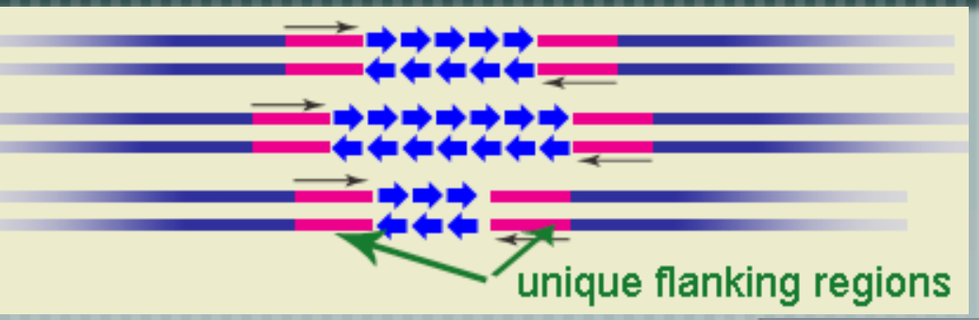


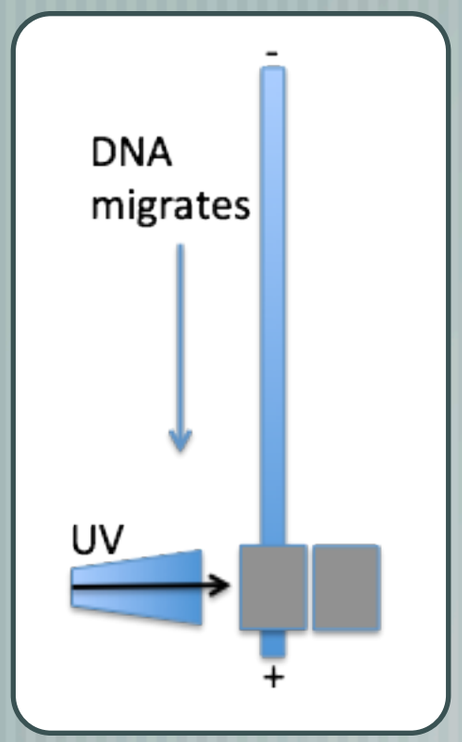

Marker 1 parental genotypes

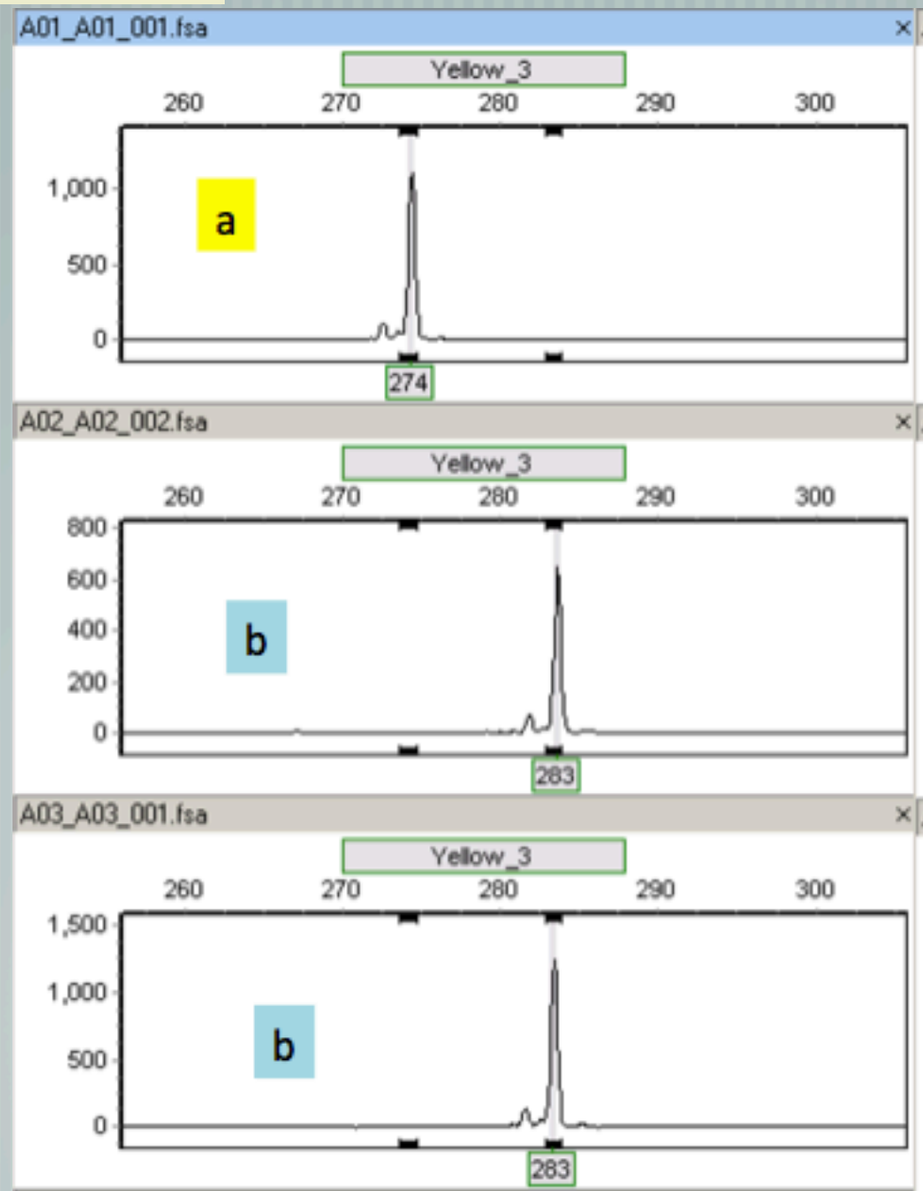
- P1 274 bp
- P2 283 bp

# Making a map: scoring genotypes




- The number of SSRs is highly variable among individuals



# Making a map: scoring genotypes

**Raw data matrix**

| | | Lines | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | DH01 | DH02 | DH03 | DH04 | DH05 | DH06 | DH07 | DH08 | DH09 | DH10 |
| Markers | A | a | a | a | b | a | b | b | b | a | b |
| | B | b | a | b | b | a | a | a | a | b | b |
| | C | a | b | b | b | a | a | a | a | b | b |
| | D | a | b | a | b | b | a | a | b | b | a |
| | E | a | a | b | a | a | b | b | b | a | b |
| | F | a | b | b | a | a | b | b | a | b | a |
| | G | b | a | b | a | a | b | a | a | b | b |
| | H | a | b | b | a | a | b | b | a | a | b |
| | I | a | b | a | b | b | a | a | a | b | b |
| | J | a | b | b | a | b | b | a | a | b | a |

# An example by hand

**Raw data matrix**

| Markers | Lines | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | DH01 | DH02 | DH03 | DH04 | DH05 | DH06 | DH07 | DH08 | DH09 | DH10 |
| A | a | a | a | b | a | b | b | b | a | b |
| B | b | a | b | b | a | a | a | a | b | b |
| C | a | b | b | b | a | a | a | a | b | b |
| D | a | b | a | b | b | a | a | b | b | a |
| E | a | a | b | a | a | b | b | b | a | b |
| F | a | b | b | a | a | b | b | a | b | a |
| G | b | a | b | a | a | b | a | a | b | b |
| H | a | b | b | a | a | b | b | a | a | b |
| I | a | b | a | b | b | a | a | a | b | b |
| J | a | b | b | a | b | b | a | a | b | a |

**Chart 1**

Score recombination frequencies, i.e. 4 recombinations in 10 lines is 4/10 = 0.4, and fill in the chart

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| J | 0.8 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.4 | 0.4 | 0.4 | 0 |
| I | 0.6 | 0.4 | 0.2 | 0.2 | 0.8 | 0.6 | 0.6 | 0.6 | 0 | 0.4 |
| H | 0.4 | 0.6 | 0.4 | 0.8 | 0.2 | 0.2 | 0.4 | 0 | 0.6 | 0.4 |
| G | 0.6 | 0.2 | 0.4 | 0.8 | 0.4 | 0.4 | 0 | 0.4 | 0.6 | 0.4 |
| F | 0.6 | 0.6 | 0.4 | 0.6 | 0.4 | 0 | 0.4 | 0.2 | 0.6 | 0.2 |
| E | 0.2 | 0.6 | 0.6 | 0.8 | 0 | 0.4 | 0.4 | 0.2 | 0.8 | 0.6 |
| D | 0.6 | 0.6 | 0.4 | 0 | 0.8 | 0.6 | 0.8 | 0.8 | 0.2 | 0.4 |
| C | 0.6 | 0.2 | 0 | 0.4 | 0.6 | 0.4 | 0.4 | 0.4 | 0.2 | 0.4 |
| B | 0.6 | 0 | 0.2 | 0.6 | 0.6 | 0.6 | 0.2 | 0.6 | 0.4 | 0.6 |
| A | 0 | 0.6 | 0.6 | 0.6 | 0.2 | 0.6 | 0.6 | 0.4 | 0.6 | 0.8 |
| | A | B | C | D | E | F | G | H | I | J |

Chart 1

- Determine all pairwise recombination frequencies (each marker with every other marker)

# Determining map order: example continued

**Chart 1**

Score recombination frequencies, i.e. 4 recombinations in 10 lines is 4/10 = 0.4, and fill in the chart

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| J | 0.8 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.4 | 0.4 | 0.4 | 0 |
| I | 0.6 | 0.4 | 0.2 | 0.2 | 0.8 | 0.6 | 0.6 | 0.6 | 0 | 0.4 |
| H | 0.4 | 0.6 | 0.4 | 0.8 | 0.2 | 0.2 | 0.4 | 0 | 0.6 | 0.4 |
| G | 0.6 | 0.2 | 0.4 | 0.8 | 0.4 | 0.4 | 0 | 0.4 | 0.6 | 0.4 |
| F | 0.6 | 0.6 | 0.4 | 0.6 | 0.4 | 0 | 0.4 | 0.2 | 0.6 | 0.2 |
| E | 0.2 | 0.6 | 0.6 | 0.8 | 0 | 0.4 | 0.4 | 0.2 | 0.8 | 0.6 |
| D | 0.6 | 0.6 | 0.4 | 0 | 0.8 | 0.6 | 0.8 | 0.8 | 0.2 | 0.4 |
| C | 0.6 | 0.2 | 0 | 0.4 | 0.6 | 0.4 | 0.4 | 0.4 | 0.2 | 0.4 |
| B | 0.6 | 0 | 0.2 | 0.6 | 0.6 | 0.6 | 0.2 | 0.6 | 0.4 | 0.6 |
| A | 0 | 0.6 | 0.6 | 0.6 | 0.2 | 0.6 | 0.6 | 0.4 | 0.6 | 0.8 |
| | A | B | C | D | E | F | G | H | I | J |

**Chart 2**

Identify adjacent markers on the basis of low recombinaiton frequency and assign to one of 2 groups - Hint: there are 5 markers per group

| Marker | Adjacent markers | | Group |
|---|---|---|---|
| A | E | | 1 |
| B | C | G | 2 |
| C | B | I | 2 |
| D | I | | 2 |
| E | A | H | 1 |
| F | H | J | 1 |
| G | B | | 2 |
| H | E | F | 1 |
| I | C | D | 2 |
| J | F | | 1 |

**Charts 3 and 4**

For each group place the markers in the correct order and fill in the recombination frequencies

**Group 1**

| | | | | | |
|---|---|---|---|---|---|
| A | 0.8 | 0.6 | 0.4 | 0.2 | 0 |
| E | 0.6 | 0.4 | 0.2 | 0 | 0.2 |
| H | 0.4 | 0.2 | 0 | 0.2 | 0.4 |
| F | 0.2 | 0 | 0.2 | 0.4 | 0.6 |
| J | 0 | 0.2 | 0.4 | 0.6 | 0.8 |
| | J | F | H | E | A |

**Group 2**

| | | | | | |
|---|---|---|---|---|---|
| D | 0.8 | 0.6 | 0.4 | 0.2 | 0 |
| I | 0.6 | 0.4 | 0.2 | 0 | 0.2 |
| C | 0.4 | 0.2 | 0 | 0.2 | 0.4 |
| B | 0.2 | 0 | 0.2 | 0.4 | 0.6 |
| G | 0 | 0.2 | 0.4 | 0.6 | 0.8 |
| | G | B | C | I | D |

Chart 2

- Identify closely linked markers

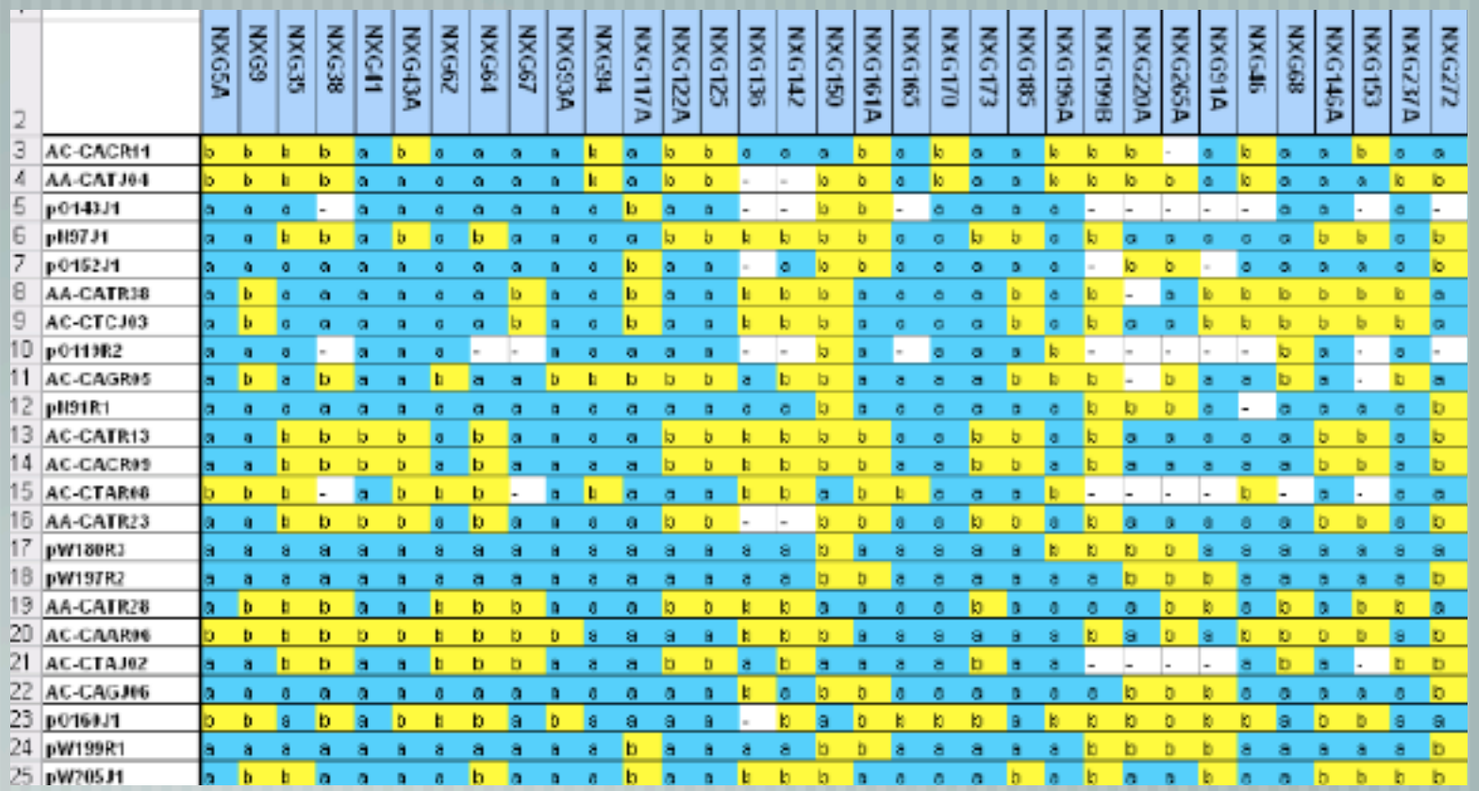
Charts 3 and 4

- Determine the order of markers for each linkage group

# Determining map order: LOD scores

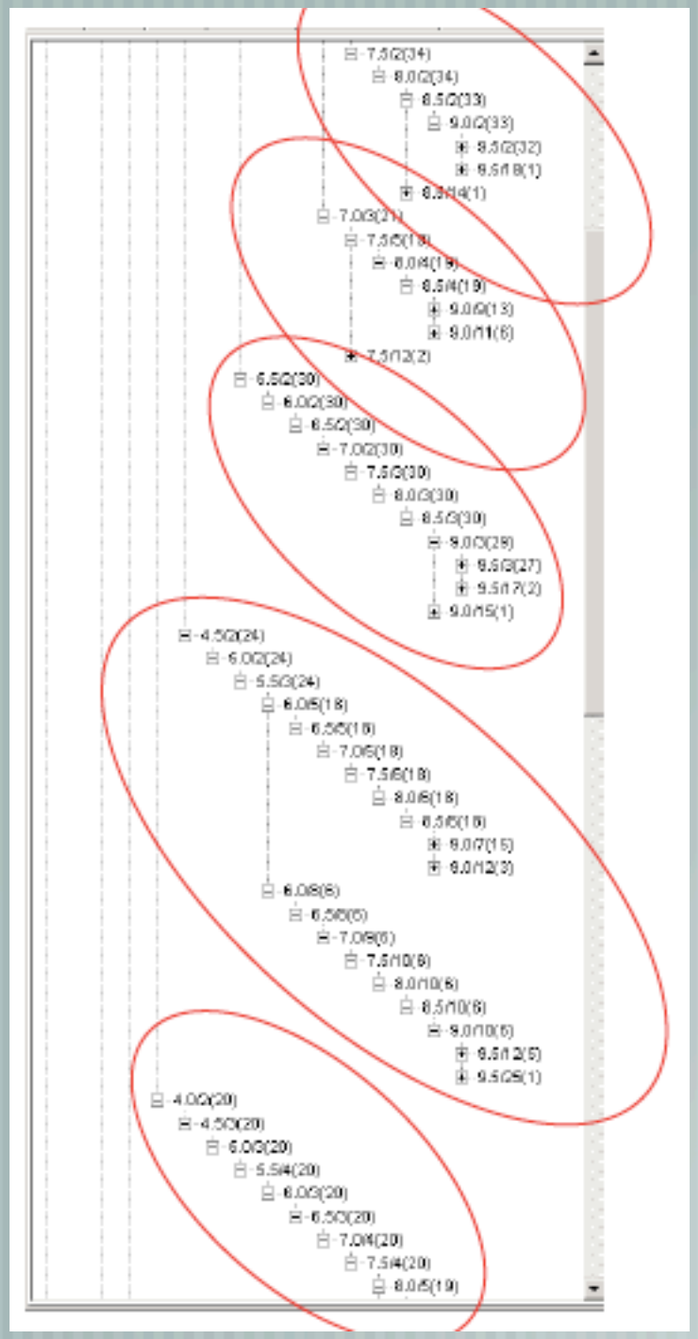
- LOD score: likelihood of the observed linkage
- Statistical analysis of +/- of 100s of markers in (F7) progeny population (parental genotypes)

$$LOD = \log_{10} \frac{(1-\theta)^{NR} \times \theta^{R}}{0.5^{(NR+R)}}$$

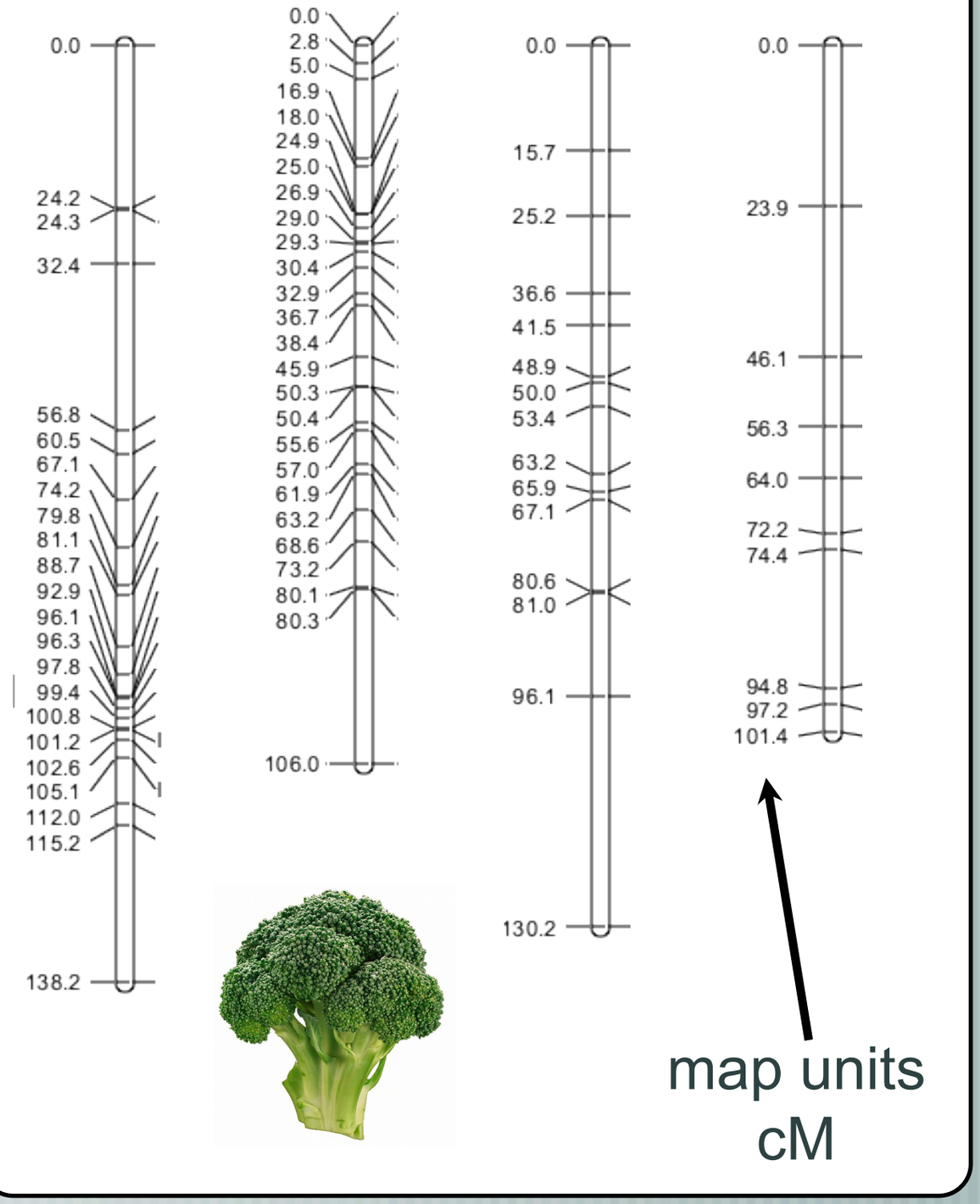



- NR = number of non-recombinant offspring; R = number of recombinant offspring
- Theta = recombinant fraction = R / (NR + R)
- Mapping software e.g. Mapmaker, JoinMap

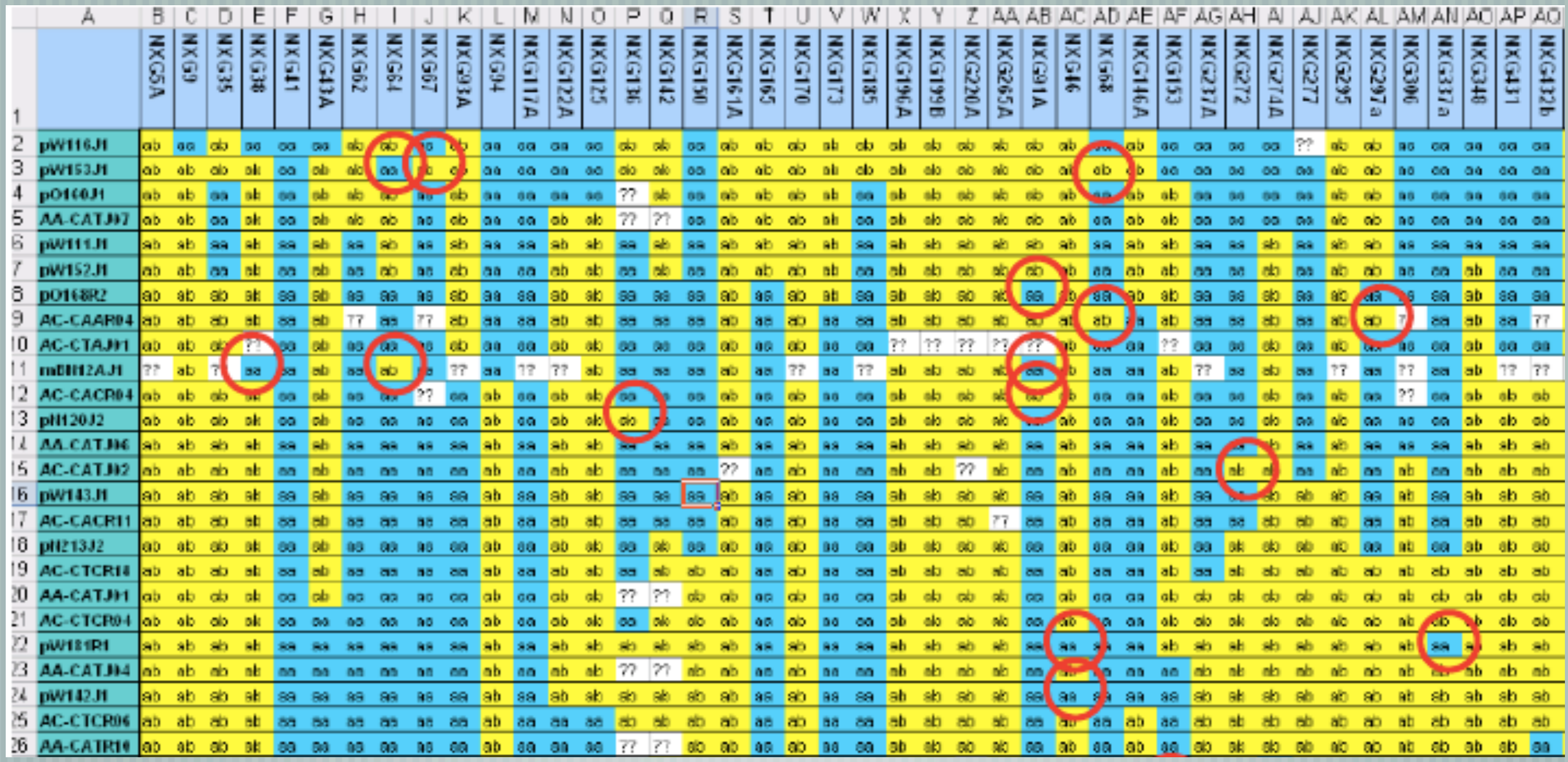
# Create linkage groups -> Linkage (genetic) map



Increasing LOD score

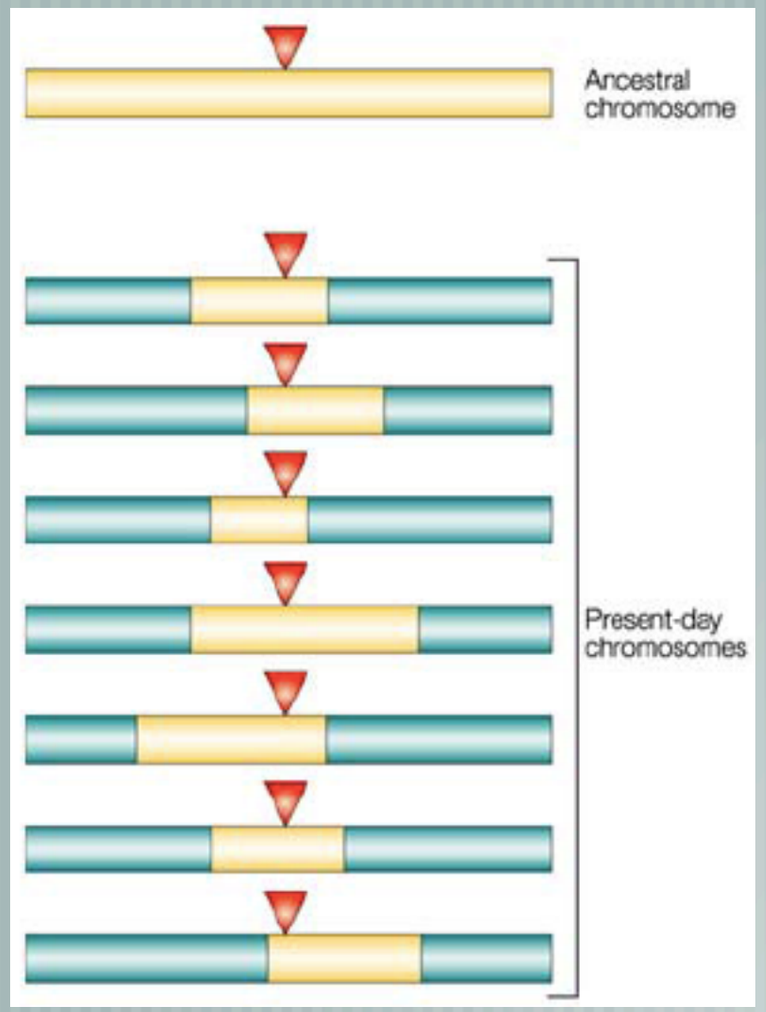


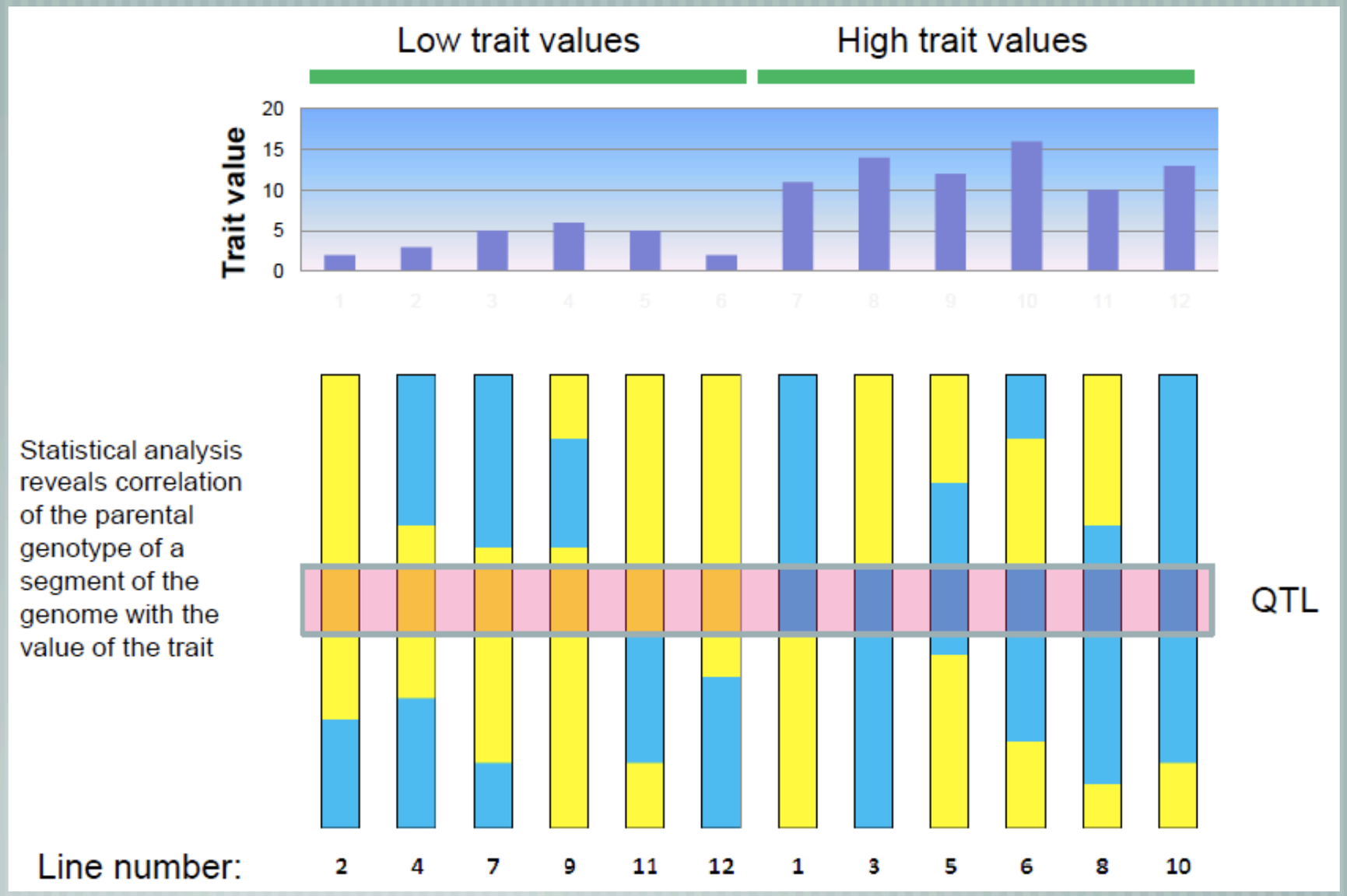
# Map sorted genotype data = graphical genotypes



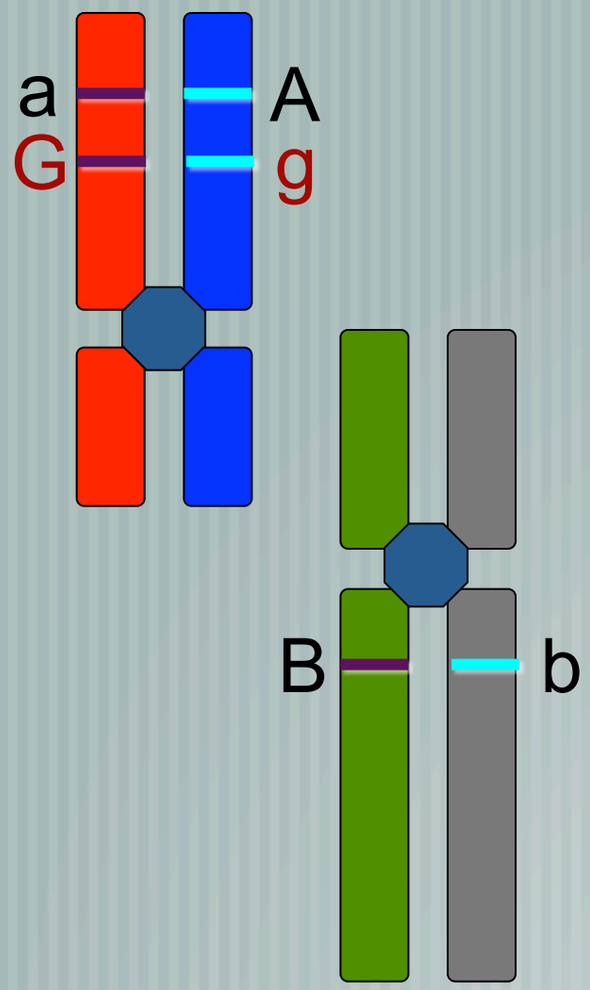
- Format and check the data
- Calculate all pairwise recombination frequencies
- Assign markers to linkage groups then map markers within each linkage group

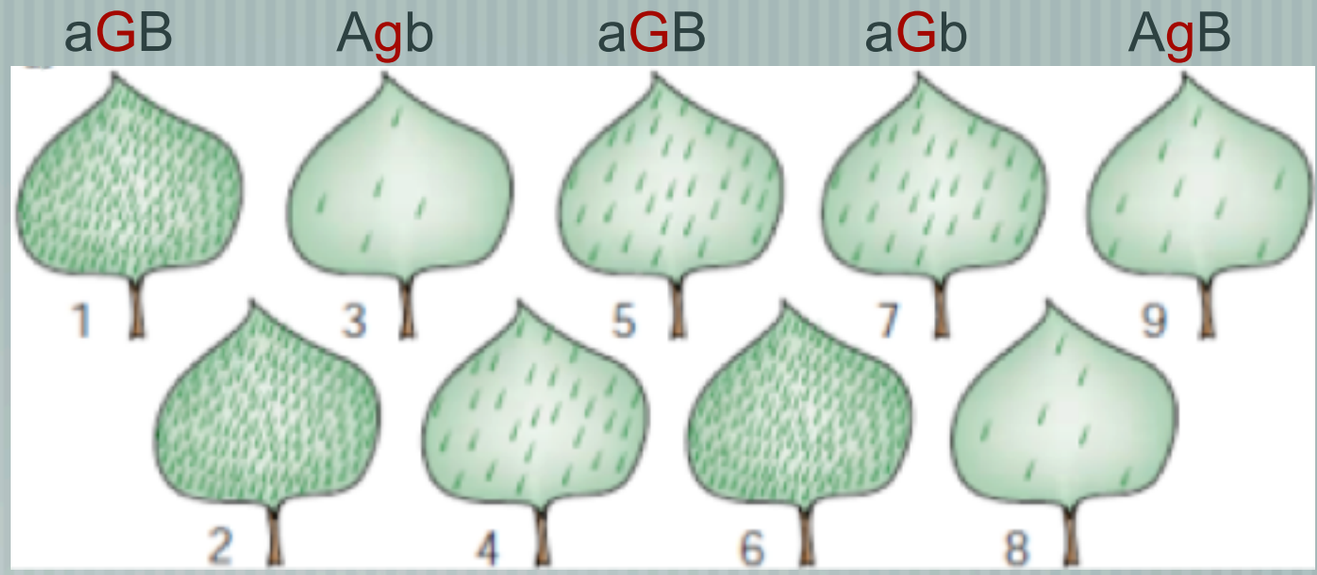
# Quantitative trait loci analysis & association mapping



# Association of phenotypes with markers



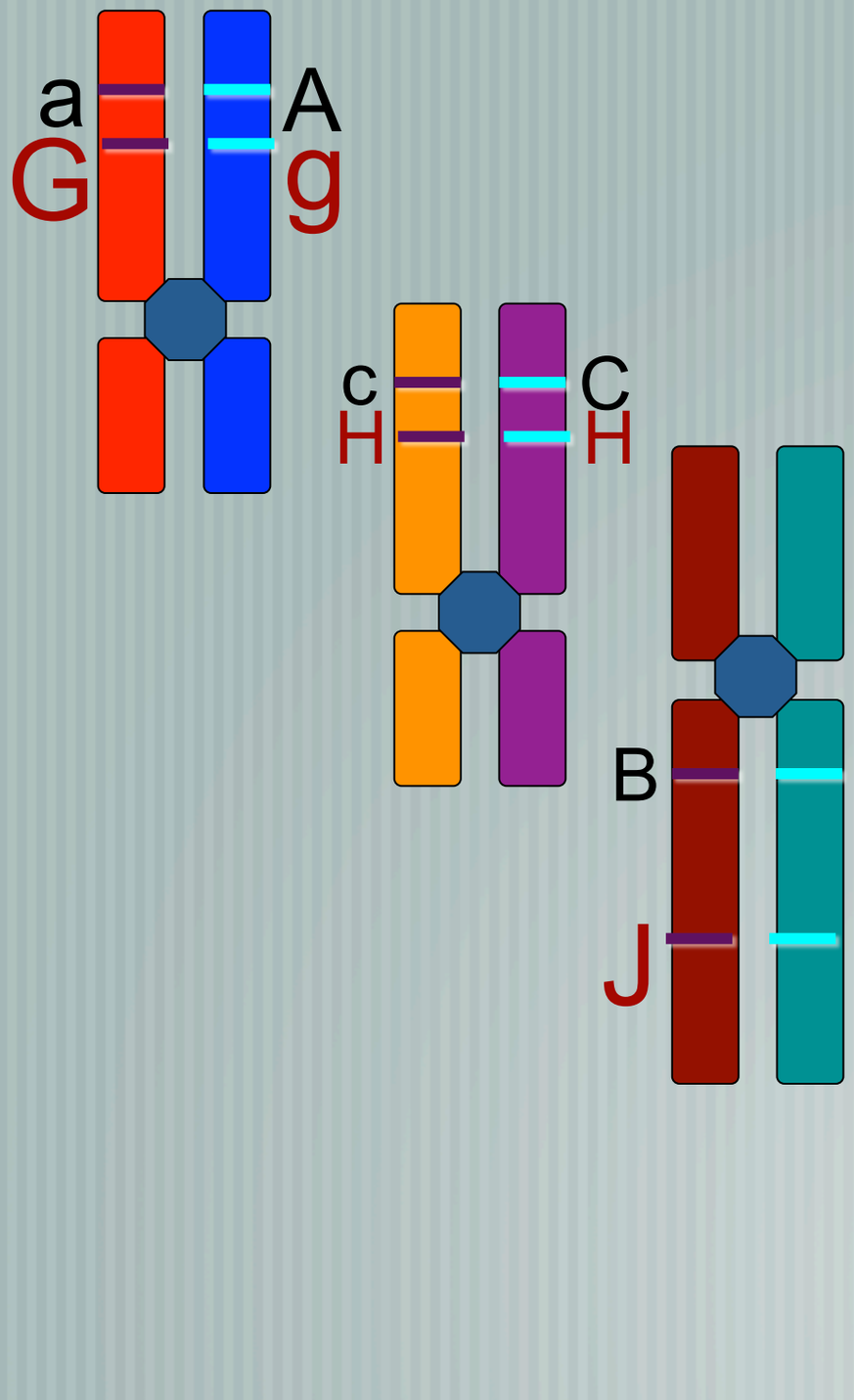

| | |
|---|---|
| aGB | AgB |
| aGB | AgB |
| aGb | Agb |
| aGb | Agb |
| aGb | |

A/a and B/b = molecular scores

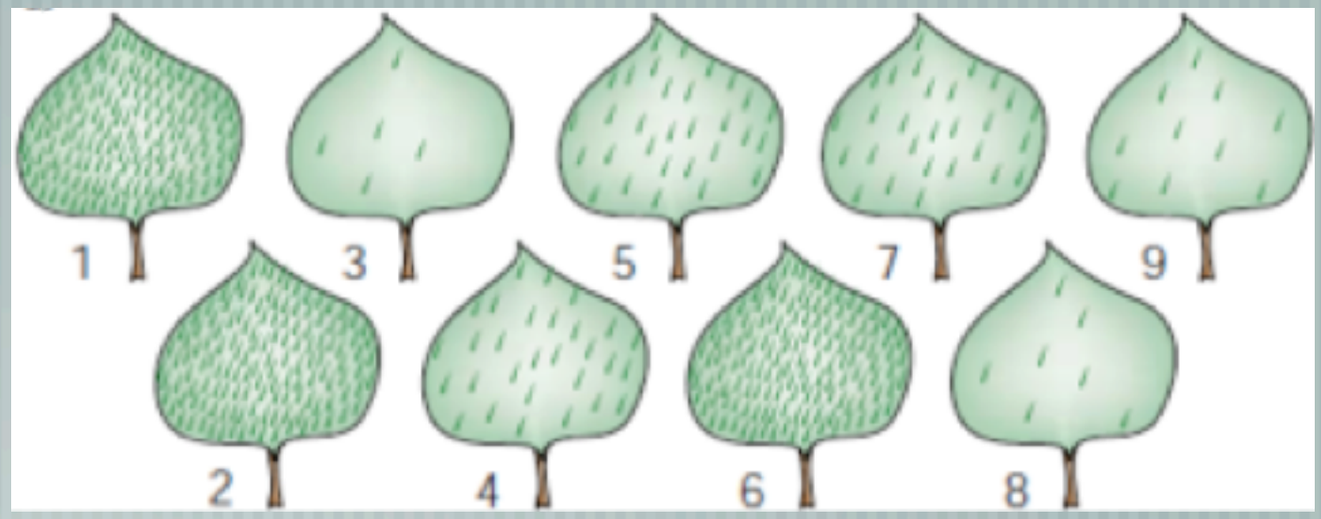
G/g = phenotypic score

- Results from marker A/a: suggests that the gene is very close to the marker
- Results from marker B/b: suggests that the gene is not linked to the marker

# Have to consider multiple loci




aGcH BJkD | AgcH bjkd | AgcH BJKD | AgcH BJkd | aGcH bjkd




AgcH BJkD | aGcH bjkD | aGcH BJKd | AgcH bjkD

AgcH BJkd | AgcH BJkD | aGcH bjkD | aGcH bjkd

AgcH BJKD

AgcH bjkd | AgcH bjkD | aGcH BJkD | aGcH BJKd

# Input data for QTL analysis:

map

| | | |
|---|---|---|
| AC-CTCE02 | 1 | 0 |
| pIH106E1N | 1 | 17.1 |
| pW239E2 | 1 | 30.4 |
| pO52E3 | 1 | 36.3 |
| pIH129E1N | 1 | 48.6 |
| pIH53E2 | 1 | 53.3 |
| pW216J1 | 1 | 91.6 |
| pR85E1 | 1 | 104.7 |
| pW116E1 | 2 | 0 |
| pIH121E1 | 2 | 41.7 |
| pIH102E2 | 2 | 48.4 |
| pIH108E2 | 2 | 58.8 |
| pIH63E1 | 2 | 68.2 |
| pR72J1 | 2 | 79.3 |
| pO120E1 | 2 | 88.6 |
| pW141E1 | 2 | 104.7 |
| pO115E2 | 2 | 109.8 |
| AC-CTAE03 | 2 | 115.6 |
| pW116J1 | 3 | 0 |
| pW153J1 | 3 | 7.5 |
| LEW6E1 | 3 | 15.8 |
| pIH102E1 | 3 | 20.4 |
| pW111J1 | 3 | 30.5 |
| pW112E1 | 3 | 43.3 |
| pW143J1 | 3 | 54.2 |
| pH213J2 | 3 | 62.4 |
| pW172E2 | 3 | 72.1 |
| pH207E1 | 3 | 83.6 |
| pR6E1 | 3 | 93.7 |
| pH56E1 | 3 | 100.1 |
| flower | 3 | 113.2 |
| pW225E1 | 3 | 121.2 |
| pO43E1 | 3 | 130.5 |
| AA-CATE02 | 3 | 140.1 |
| pW177E1 | 4 | 0 |
| pW143E2 | 4 | 15 |
| pO171J1 | 4 | 23.2 |
| pIH64E1 | 4 | 31 |
| pH202E1 | 4 | 40.2 |
| pO98E1 | 4 | 74.7 |
| pW139E1 | 4 | 89.6 |
| pR113E3 | 4 | 110.9 |
| pW143E1 | 4 | 121.1 |
| pH21E2 | 5 | 0 |
| pO92J1 | 5 | 8.6 |

marker data matrix

| AC-CTCE02 | pIH106E1N | pW239E2 | pO52E3 | pIH129E1N | pH53E2 | pW216J1 | pR85E1 | pW116E1 | pH121E1 | pH102E2 | pH108E2 | pH63E1 | pR72J1 | pO120E1 | pW141E |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 208 | 88 | ! | | | | | | | | | | | | | |
| 1 | 1 | ! | 1 | 1 | 4 | 1 | 1 | 1 | ! | 1 | 1 | 3 | 3 | 3 | ! |
| 1 | 1 | ! | 1 | 3 | 3 | 1 | 1 | 3 | 3 | 1 | 1 | 1 | 1 | 1 | 3 |
| 1 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| 4 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | ! | 1 | 4 | 3 | 3 | 3 | 3 |
| 1 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| 1 | 1 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | ! | 1 | 1 | 1 | 1 | 1 | 1 | ! |
| 1 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 |
| 1 | 4 | ! | 1 | 1 | 1 | 1 | 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 1 | ! | 1 | 1 | 3 | 3 | 3 | ! |
| 3 | 3 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 4 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 1 | ! | 1 | 4 | 1 | 1 | 1 | 3 |
| 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 3 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | ! |
| 1 | 1 | ! | 1 | 1 | 1 | 1 | 1 | ! | ! | 1 | 1 | 3 | 3 | 3 | 3 |
| 3 | 3 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 4 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 1 | ! | 1 | 4 | 1 | 1 | 1 | 3 |
| 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 3 | 3 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 3 | 1 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 1 | 3 | 3 | 3 | 3 | 3 | 1 | 1 | 4 | 3 | 3 | 3 | 3 | 1 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 4 | 3 | 3 | 3 | 3 |
| 3 | 3 | 3 | 1 | 1 | 1 | 1 | 3 | 1 | ! | 1 | 3 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 1 | 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | ! |
| 1 | 1 | ! | 4 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 3 | 1 | ! | 1 | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 1 | 1 | ! |
| 1 | 1 | ! | 1 | 3 | 3 | 1 | 1 | 3 | ! | 1 | 1 | 1 | 1 | 1 | ! |
| 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 |
| 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 |
| 3 | 3 | ! | 1 | 1 | 1 | 1 | 1 | ! | ! | 3 | 3 | 3 | 1 | 1 | ! |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 3 | 3 | 3 | 3 | 3 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| 1 | 1 | ! | 4 | 1 | 1 | 1 | 1 | 4 | 3 | 3 | 3 | 3 | 3 | 3 | 4 |
| 3 | 1 | 3 | 1 | 1 | 1 | 3 | 3 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 3 |
| 1 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 1 | 3 | 3 | 3 | 3 | 3 | 3 | ! |
| 3 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 1 | ! | 1 | 1 | 3 | 3 | 3 | 3 |
| 4 | 1 | ! | 1 | 1 | 1 | 1 | 1 | 3 | 3 | 3 | 4 | 3 | 3 | 1 | ! |
| 1 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| 4 | 1 | ! | 1 | 1 | 1 | 3 | 3 | 1 | ! | 1 | 3 | 3 | 3 | 3 | 3 |
| 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |

trait data matrix

| bdNO | bdFlNO | 5mmbd | 5mmbdsy | 5mmbdstGy | | 10mmbdst | 10mmbdsy | |
|---|---|---|---|---|---|---|---|---|
| 26.50 | 30.00 | 3.15 | 3.50 | 0.89 | 4.20 | 6.00 | 0.70 | 8.0 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 30.67 | 32.67 | 3.30 | 3.33 | 1.00 | 6.67 | 5.67 | 1.18 | 9.1 |
| 34.50 | 38.00 | 3.25 | 3.75 | 0.87 | 6.45 | 6.25 | 1.03 | 10.0 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 38.00 | 42.33 | 3.43 | 3.00 | 1.14 | 6.10 | 5.67 | 1.07 | 11.3 |
| 33.50 | 35.00 | 3.40 | 4.00 | 0.85 | 6.70 | 6.50 | 1.03 | 9.0 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 33.50 | 44.00 | 3.40 | 3.75 | 0.92 | 6.80 | 6.25 | 1.06 | 9.0 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 51.33 | 59.00 | 3.27 | 3.50 | 0.93 | 7.47 | 6.83 | 1.09 | 9.5 |
| 25.50 | 30.50 | 3.30 | 3.50 | 0.94 | 6.45 | 6.25 | 1.04 | 9.5 |
| 36.50 | 43.00 | 3.00 | 3.00 | 1.00 | 5.25 | 5.75 | 0.91 | 10.5 |
| 14.00 | 20.67 | 3.10 | 3.33 | 0.97 | 5.03 | 6.25 | 0.84 | 10.6 |
| 40.67 | 43.00 | 3.30 | 4.17 | 0.80 | 6.13 | 6.67 | 0.92 | 9.0 |
| 31.33 | 32.67 | 3.43 | 3.67 | 0.94 | 6.43 | 6.17 | 1.04 | 9.0 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 30.33 | 21.67 | 3.60 | 3.67 | 0.98 | 6.23 | 7.00 | 0.89 | 9.5 |
| 45.00 | 47.00 | 3.50 | 3.75 | 0.93 | 7.20 | 6.25 | 1.16 | 9.5 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 37.67 | 44.00 | 3.10 | 3.50 | 0.88 | 5.60 | 6.00 | 0.93 | 8.6 |
| 37.50 | 47.00 | 3.15 | 3.50 | 0.90 | 6.50 | 6.00 | 1.09 | 9.0 |
| 22.00 | 30.67 | 3.33 | 3.75 | 0.90 | 6.07 | 5.67 | 1.08 | 9.0 |
| 30.33 | 37.00 | 3.03 | 3.67 | 0.83 | 6.10 | 6.50 | 0.94 | 8.8 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 41.00 | 48.33 | 2.90 | 3.50 | 0.84 | 5.97 | 7.00 | 0.85 | 9.1 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 41.00 | 50.33 | 3.53 | 3.50 | 1.01 | 5.60 | 5.50 | 1.02 | 7.6 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 38.00 | 43.50 | 3.15 | 3.25 | 0.97 | 6.80 | 6.50 | 1.04 | 10.2 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| -999 | -999 | -999 | -999 | -999 | -999 | -999 | -999 | -99 |
| 38.00 | 40.33 | 3.37 | 4.00 | 0.93 | 7.03 | 6.83 | 1.03 | 9.1 |
| 48.67 | 54.67 | 2.90 | 3.50 | 0.83 | 5.33 | 6.00 | 0.89 | 9.1 |
| 24.50 | 27.50 | 3.20 | 4.00 | 0.79 | 6.45 | 7.75 | 0.83 | 9.5 |

# To map a quantitative trait (QTL analysis):

1. Make a suitable population
2. Genotype individuals - generate linkage map

3. Collect phenotypic measurements
   - Evaluate in uniform environment,
   - Evaluate in multiple environments
   - Data transformation (approach normal distribution)

Look at correlations between traits, transgressive segregation?

design your experiment, e.g. DEW

4. Look for trait-marker associations

5. Estimate the effects of the QTLs on the quantitative trait:
   - many genes with small effect each or few genes with large effect each?
   - their effects on the trait: is gene action additive or dominant?
   - their positions in the genome: linkage and association, epistasis
   - their interaction with the environment

6. Identify candidate genes underlying the QTL and thus the trait

Variation in a trait in a population is caused by Genetic and Environmental contributions

$V_P = V_G + V_E$

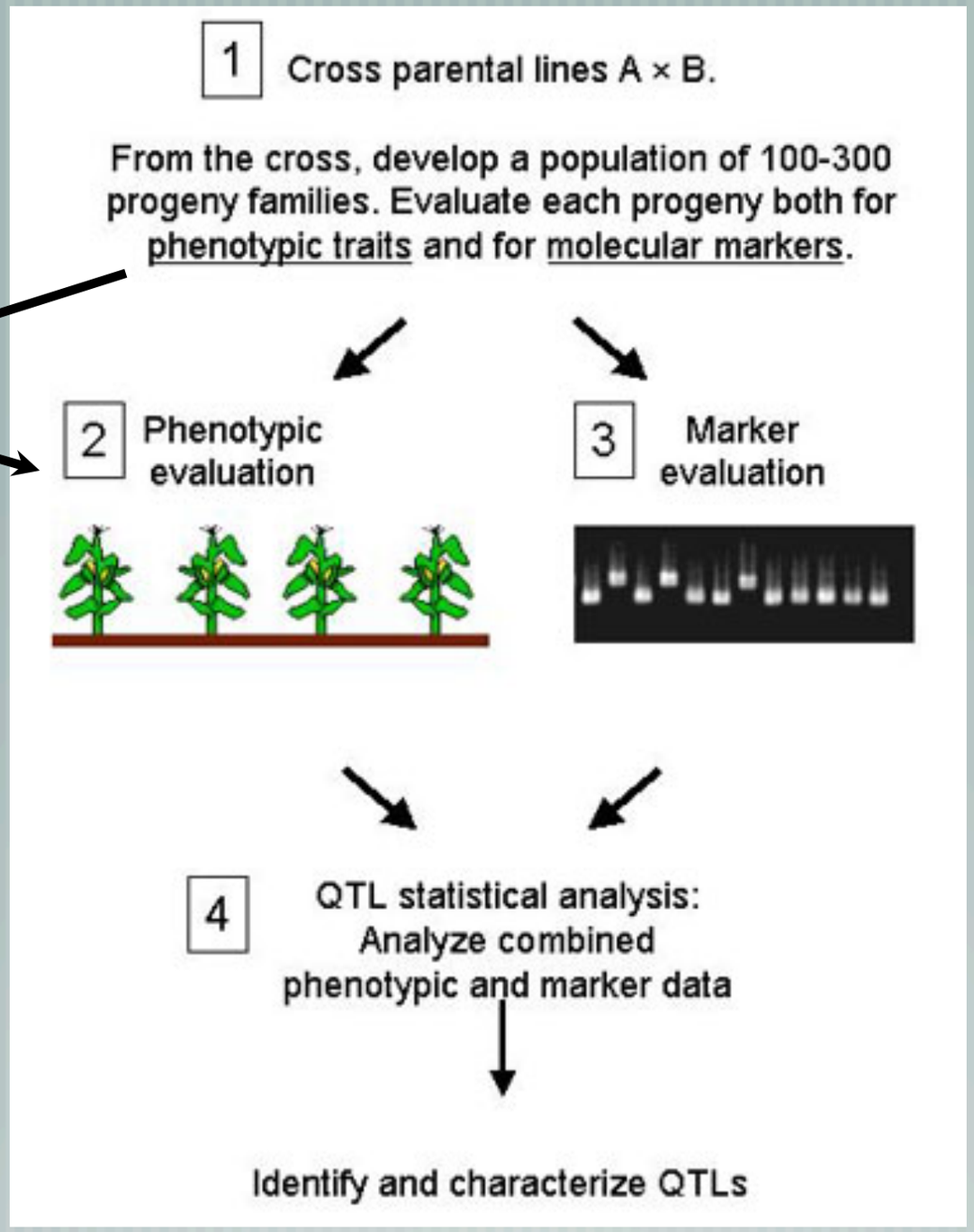
Variation due to genetical causes is the heritability of the trait

$h^2 = V_P/V_G$

broad sense heritability
h2b = VG/(VG+VE)

# To map a quantitative trait (QTL analysis):

design your experiment, e.g. DEW




Variation in a trait in a population is caused by Genetic and Environmental contributions

$V_P = V_G + V_E$

Variation due to genetical causes is the heritability of the trait

$h^2 = V_P/V_G$

# Next time:
# (3) QTL and GWAS methods

By the end of this lecture you should be able to explain:

- Some of the principles underlying the statistical analysis of QTLs
- Under what conditions particular methods are suitable
- The core differences between QTL analysis and GWAS