HOS 6236 Molecular Marker Assisted Plant Breeding

Fall 2017

Last Class:

Linkage mapping construction

Todays Class:

Linkage phase, QTL analysis basic, project questions

Developing a Linkage Map

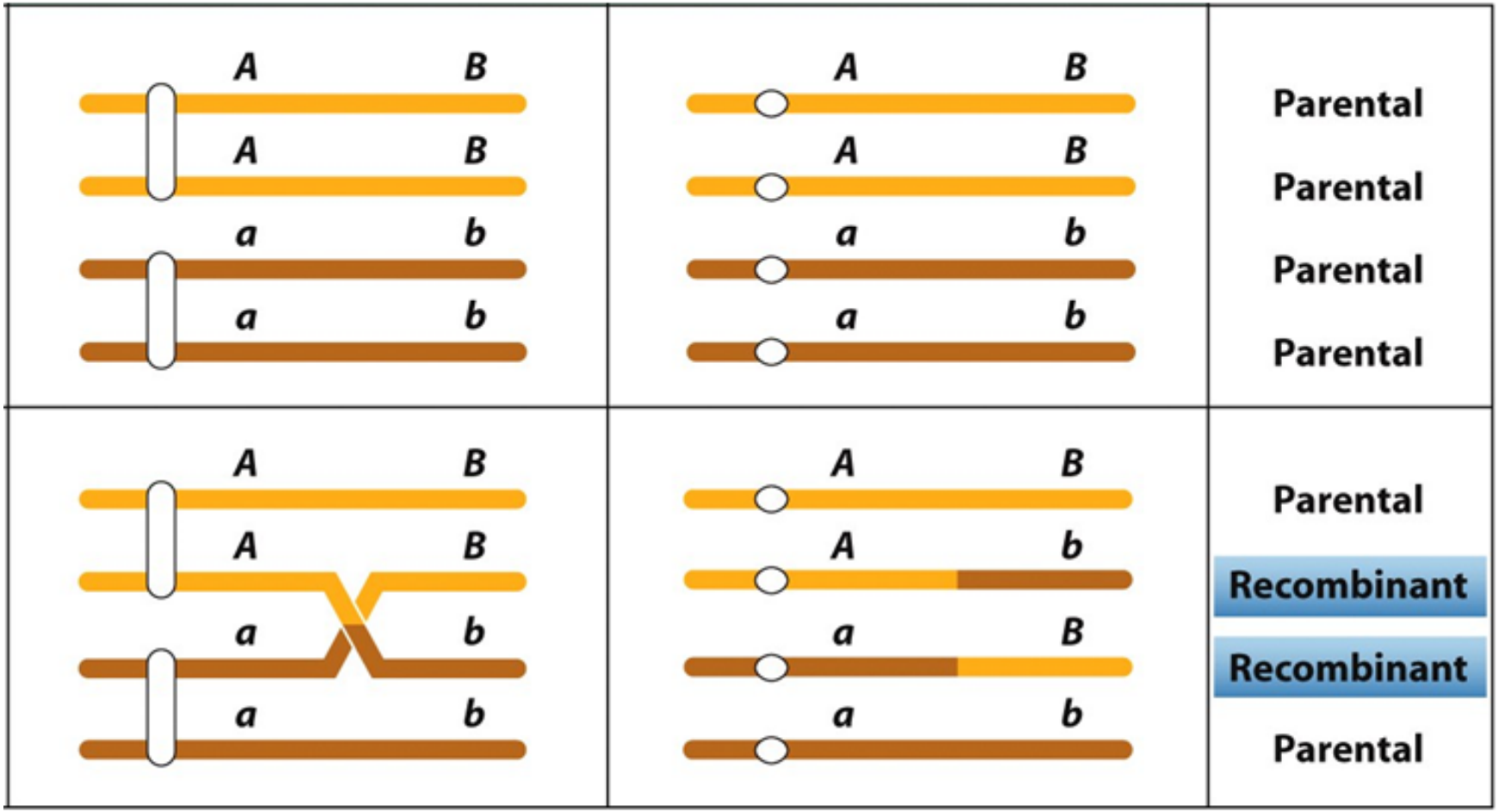
1. Develop or identify a “mapping” population and determine sample size

2. Genotype entire population with appropriated molecular markers (Dom or Co-dom)

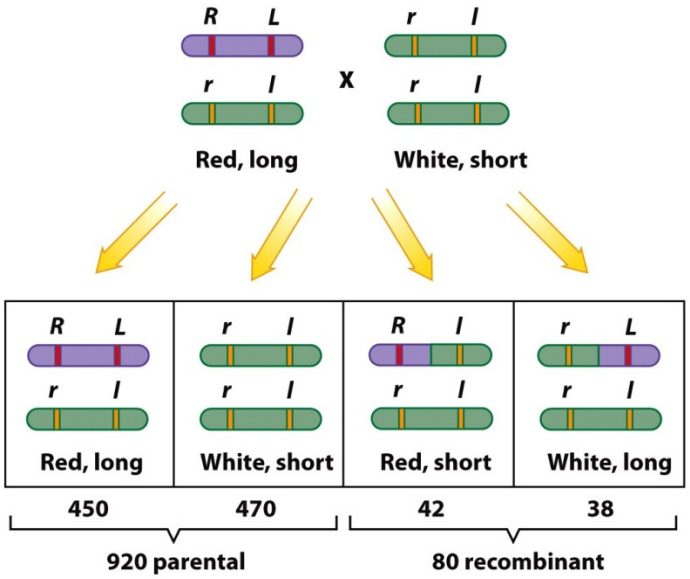
3. **Perform Linkage analyses – filter markers, test segregation, calculate recombinations, establish linkage groups, estimate map distances, determine map order (software)**

Linkage Map – recombination

- Mapping is simple determine what individuals are recombinant

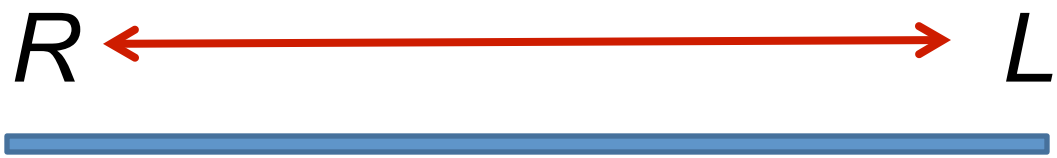


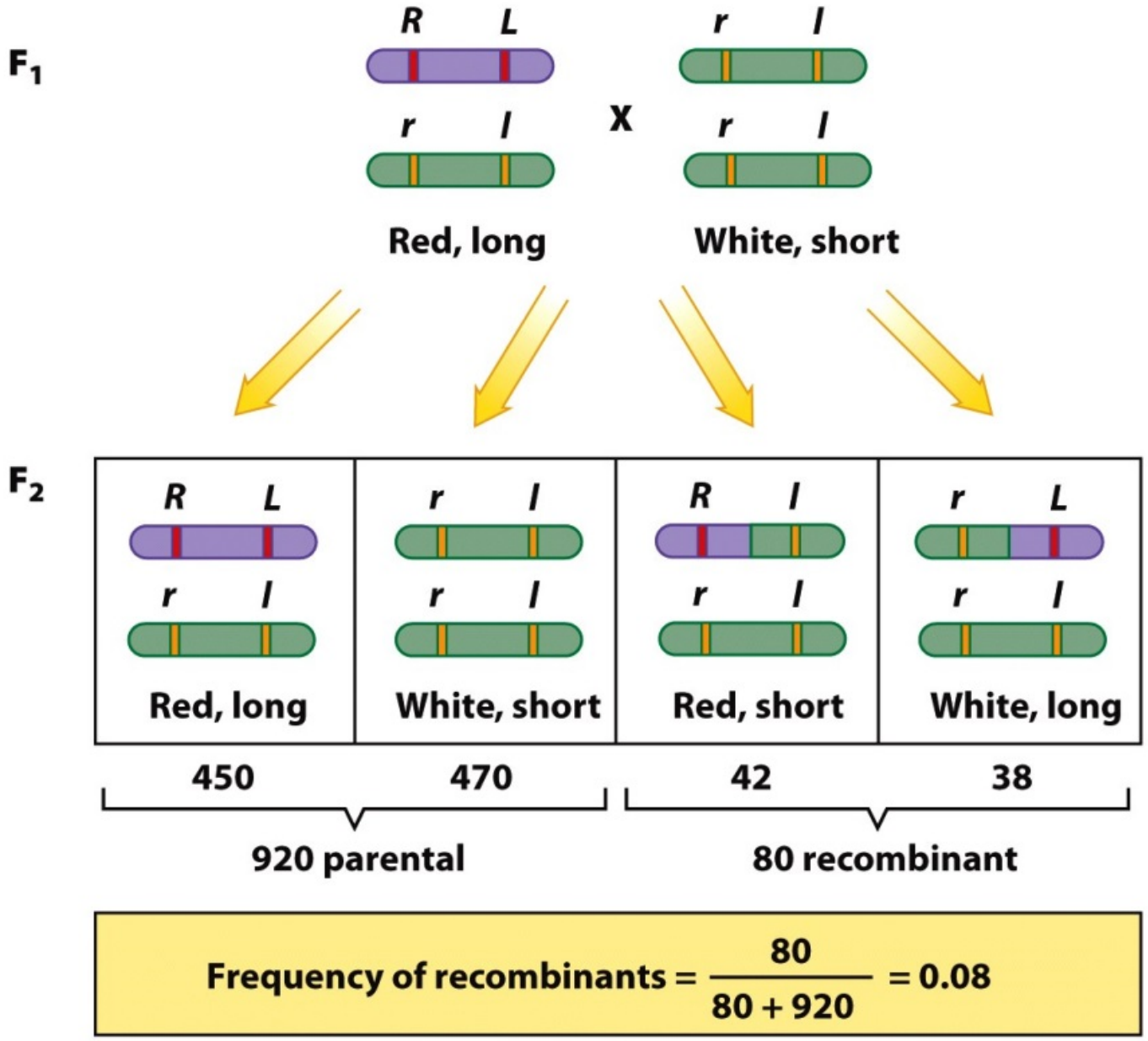
Griffiths et al, Introduction to Genetic Analysis, 10th Ed. W. H. Freeman and Company, 2011



What would the recombination fraction (r) be?

How many cM apart would these genes be?




F1
R L
r l
X
r l
r l
Red, long
White, short
F2
R L
r l
Red, long
r l
r l
White, short
R l
r l
Red, short
r L
r l
White, long
450
470
42
38
920 parental
80 recombinant
Frequency of recombinants = 80 / 80 + 920 = 0.08

Linkage Phase

- Linkage phase is the arrangement of alleles on the parental chromosomes.

Parent 1 AABB

Parent 2 aabb

Allele A is in coupling with allele B

Linkage Phase

- Linkage phase is the arrangement of alleles on the parental chromosomes.

Parent 1 AAbb

Parent 2 aaBB

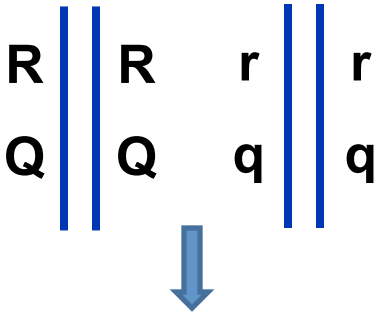
Allele A is in repulsion with allele B

But why does it matter???

Coupling vs. Repulsion in F2

- Depending whether markers are in coupling or repulsion will be the progeny type that we consider as recombinant.

- For the same pair or markers it will change the map distance if coupling vs. repulsion.



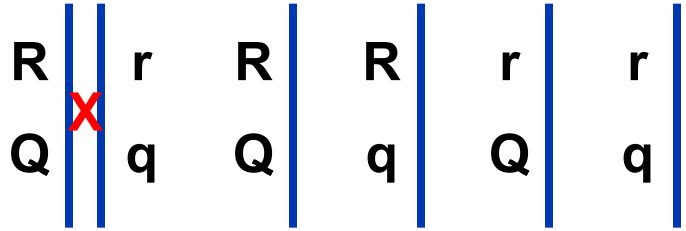
RRQQ x rrqq

Parents in coupling

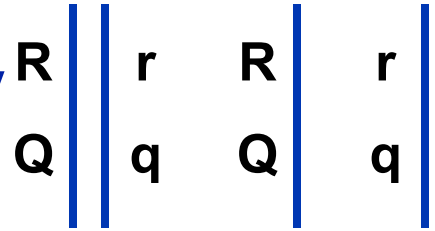
	RQ	Rq	rQ	rq
RQ	RRQQ	RRQq	RrQQ	RrQq
Rq	RRQq	RRqq	RrQq	Rrqq
rQ	RrQQ	RrQq	rrQQ	rrQq
rq	RrQq	Rrqq	rrQq	rrqq

9 : 3 : 3 : 1

F1 unlinked (r = 0.5)

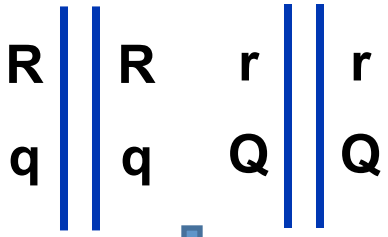


F1 completely linked (r = 0)



	RQ	RQ	rq	rq
RQ	RRQQ	RRQQ	RrQq	RrQq
RQ	RRQQ	RRQQ	RrQq	RrQq
rq	RrQq	RrQq	rrqq	rrqq
rq	RrQq	RrQq	rrqq	rrqq

12 : 0 : 0 : 4



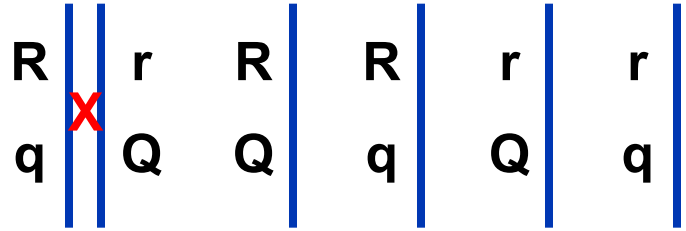
RRqq x rrQQ

Parents in repulsion

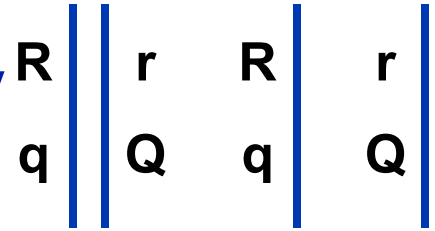
	RQ	Rq	rQ	rq
RQ	RRQQ	RRQq	RrQQ	RrQq
Rq	RRQq	RRqq	RrQq	Rrqq
rQ	RrQQ	RrQq	rrQQ	rrQq
rq	RrQq	Rrqq	rrQq	rrqq

9 : 3 : 3 : 1

F1 unlinked (r = 0.5)



F1 completely linked (r = 0)



	Rq	Rq	rQ	rQ
Rq	RRqq	RRqq	RrQq	RrQq
Rq	RRqq	RRqq	RrQq	RrQq
rQ	RrQq	RrQq	rrQQ	rrQQ
rQ	RrQq	RrQq	rrQQ	rrQQ

8 : 4 : 4 : 0

Coupling vs. Repulsion in F2

- Markers in coupling:
  - Segregation ratios are very different when comparing linked and unlinked situations

12 : 0 : 0 : 4 vs. 9 : 3 : 3 : 1

- Markers in repulsion:
  - Segregation ratios are very similar when comparing linked and unlinked situations

8 : 4 : 4 : 0 vs. 9 : 3 : 3 : 1

QTL analysis

- A Quantitative Trait Loci (QTL) is a portion of the genome which contains gene(s) that control the phenotypic variation of a given trait.

- A QTL analysis is an analysis to find these QTLs.

Why QTL analysis?

- Analysis of QTL will determine whether:
  - The **number** of genes/QTLs control variation of a trait
  - The **amount** of variation each gene/QTL contributes (major genes?)
  - The **location** of the genes/QTL on the genome; one chromosome or the whole genome.

What do I need to perform a QTL analysis?

- A Quantitative Trait Loci (QTL) is a portion of the genome which contains gene(s) that control the phenotypic variation of a given trait.

- These analyses require populations **genotyped and phenotyped.** The location of markers in the genome is also needed.

- Statistics methods are used to study whether a marker is associated with the phenotypic trait (correlation)

Steps for a QTL analysis

1. Create or find a suitable population
2. Genotype with molecular markers
3. Use markers to build a linkage map
4. Phenotype for trait of interest (and more)
5. Use the linkage map with the phenotypic data to determine whether markers are correlated to traits; Number of QTLs, the amount of variation and position on genome

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Phenotypic traits and QTLs

- In order to find QTLs you need to have a population where the trait is segregating.
- Meaning variation of phenotypic trait should be observed in the population used.
- The most contrasting the parents (assuming a genetic additive mode of action) the most variation will be observed in the segregation population (QTL mapping population).
- Measuring other traits