HOS 6236 Molecular Marker Assisted Plant Breeding

Fall 2017

Last Class:

Breeding values and Molecular markers review

Todays Class:

Linkage mapping

Linkage Map - rationale

What is a linkage map?

A linkage map (or genetic map) is a figure depicting the relative position of markers along linkage groups.

And why do we need one? Better sequence the genome, right?

Interest in one gene position
Associate markers to phenotypic traits
As a reference for a physical map

Linkage Map - rationale

Why “linkage map”?

Think the law of independent assortment: genes for different traits segregate independently from each other during gamete formation.

Right?

Nope, genes in the same chromosome are linked, and tend to stay that way when passed to future generations

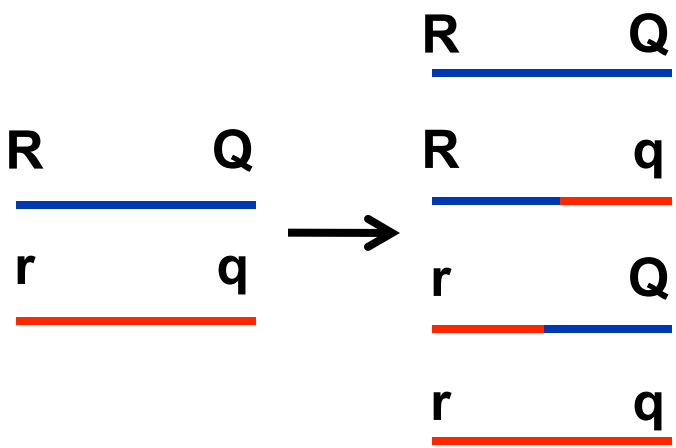
Crossing-over breaks this linkage.

Linkage Map - rationale

The further two genes are in the chromosome the higher the probability that crossing-over (recombination) will occur and then break the linkage between genes.

Linkage mapping takes advantage of these events. Tracks and maps the recombination that brake the linkage. There the name linkage mapping.

Linkage Map - recombination



	Independent	Linked	Complete Linkage
R Q	1/4	> 1/4	1/2
R q	1/4	< 1/4	0
r Q	1/4	< 1/4	0
r q	1/4	> 1/4	1/2

Linkage Map

What do we need to do a linkage map?

A **mapping population** genotyped with polymorphic **molecular markers**.

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 - populations

A population needs to be created or identified.

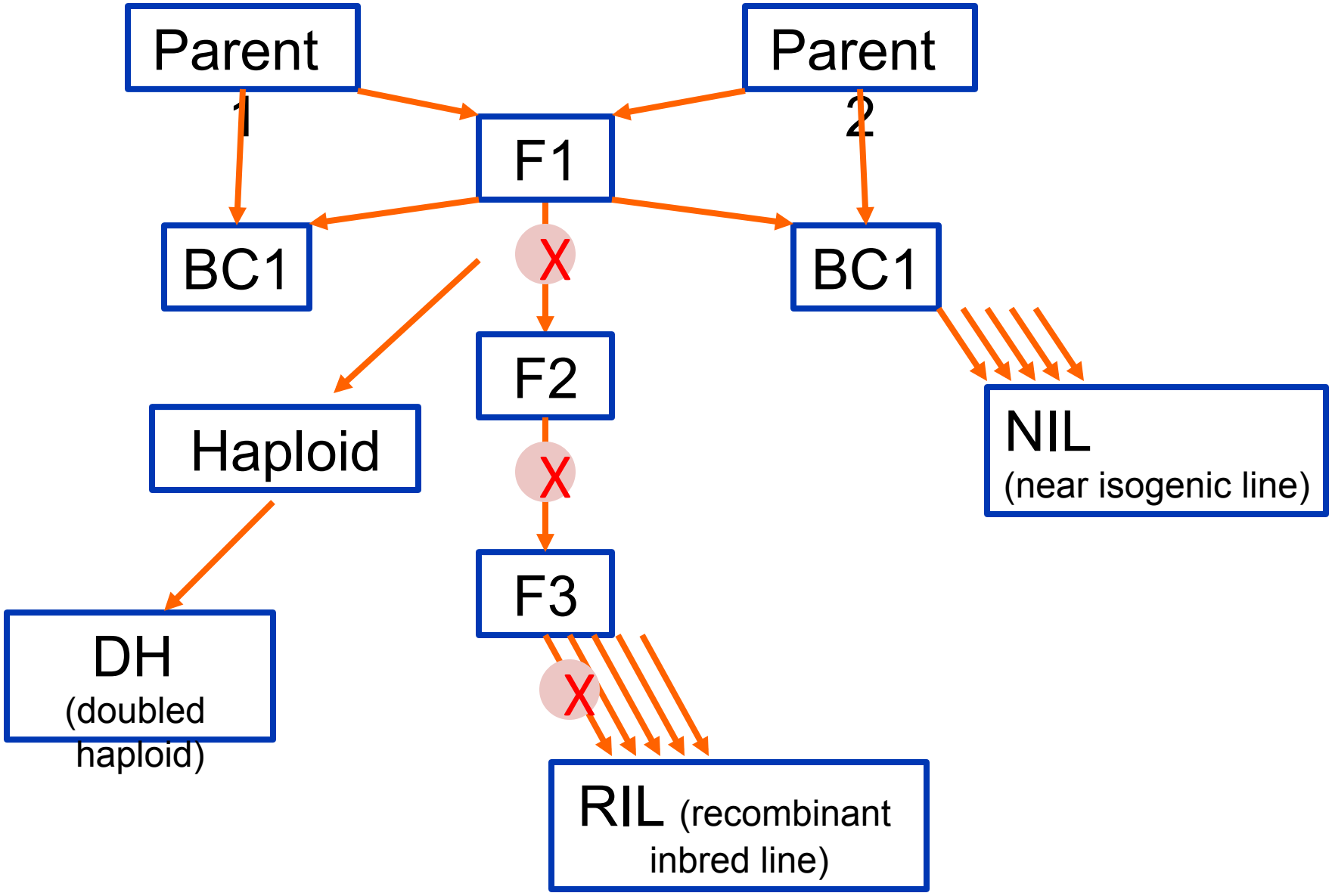
Right parents are critical for success

- Marker polymorphism
- Low levels of marker distortion
- Type of population (pedigree)

Types of “mapping” populations are:

F2, BC1, DH, RILs, and NILs

Linkage Map – types of populations



Linkage Map – populations segregation ratios inbreds

Population types commonly used for inbred crops:

Population	Marker Expression Pattern	Ideal Segregation Ratio
BC1	Dominant or Co-dominant	1:1
F2	Co-dominant	1:2:1
F2	Dominant	3:1
DH	Dominant or Co-dominant	1:1
RIL	Dominant or Co-dominant	1:1

Linkage Map – heterozygous outbred crops

Better segregation for F2 or BC1 type of populations

Different from inbred populations there will be mixed segregation ratios in the mapping populations. Why?

Linkage Map – populations segregation ratios heterozygous parents

Heterozygous Parents

A b C D E f G

A B c d E f g

X

A b C D E f G

a B C d e f g

Heterozygous F1

- Like F2 for loci B, D, G
- Like BC1 for loci A, C, E
- No segregation for F

Linkage Map – populations size

The larger the population, better the map (Ferreira et al 2006) F2, BC, RILs and DH. Simulation from 50-1000 ind:

Lowest number of individuals (50) provided several fragmented linkage groups and inaccurate locus order.

More accurate maps with RIL and F2 with co-dominant markers. F2 with dominant marker was less accurate.

For all population types, a total of **200 individuals** were required to construct reasonably accurate linkage maps.

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Linkage Map – Molecular Markers

Many types of molecular markers exist (check molecular marker review on week 2). The best markers are:

Reliable/Repeatable
Highly polymorphic
Informative
Type - dominant vs co-dominant

Linkage Map − Molecular Marker Density

In general, marker density depends on:

- Objective of the linkage map
- Number of individuals in mapping pop
- Genome size of population