



Mapping complex traits in crosses



PREDICTION:

- If look at many linked markers, you should be able to pinpoint the location of a QTL by where the association is strongest
 - OR by where you'd "PREDICT" it to be strongest
- Can follow "trajectory of association strength" to infer location of the QTL
 - Let's do this with some examples



Example from mapping cross

- You cross tall and short strains together, and then cross the intermediate height F_1 corn
- **NOT** trying to get recombination fractions this time- just look at association of *genotype* and *phenotype* and how strong it is
- You genotype 5 markers and look at how they associate with corn height



Fine localization in crosses

- Look at association of 5 close markers to trait:



- Markers are ~2 cM apart from each other
- Height gene is next to C
- Would you see association of height with E genotype?



Fine localization in crosses

- Look at association of 5 close markers to trait:



EE 3.5'
Ee 3'
ee 2.5'

- Predict some association at E since only ~4 cM away
- What about at D?



Fine localization in crosses

- Look at association of 5 close markers to trait:



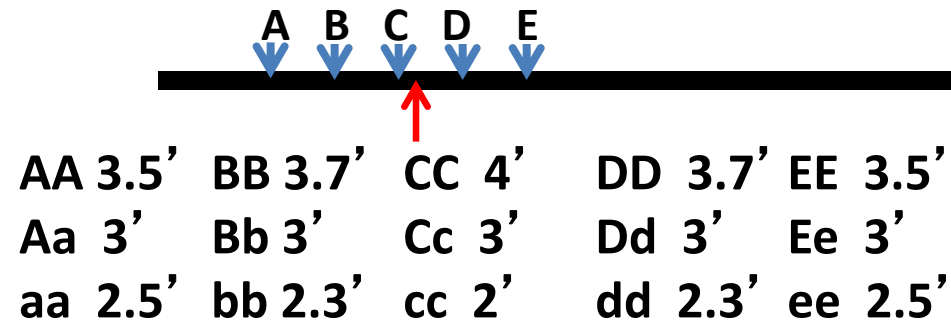
DD	3.7'	EE	3.5'
Dd	3'	Ee	3'
dd	2.3'	ee	2.5'

- Genotypes at D are **more strongly** associated with height



Fine localization in crosses

- Look at association of 5 close markers to trait:



- Predict association strongest when closest to gene affecting trait



Association depicted using “LOD” plot

- Use math (we won't cover) to translate observed & expected associations and identify “likely” position of gene(s) affecting trait of interest.
- High number (>3) means likely effect

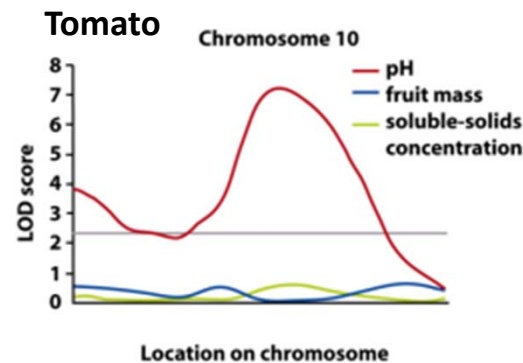
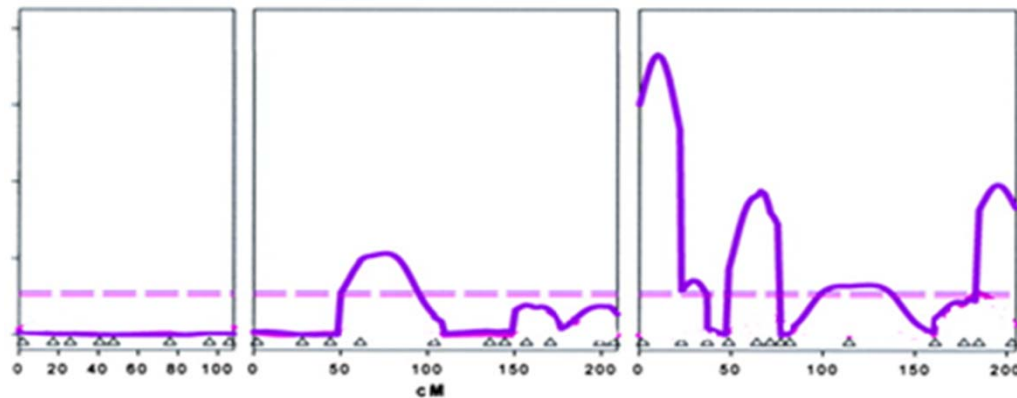


Figure 6-10. Linkage analysis. © 2007 Pearson Education, Inc.

What's different from simple traits?

- Big difference now is that we now have markers in **multiple** regions of genome associated with trait
- Map of QTLs that associate with *Drosophila* mating success:



You try it!

- Infer the location of QTL by trajectories of association...

AA 3.5'	BB 3.7'	CC 3.7'	DD 3.5'
Aa 3'	Bb 3'	Cc 3'	Dd 3'
aa 2.5'	bb 2.3'	cc 2.3'	dd 2.5'

You try it!

- Infer the location of QTL by trajectories of association...

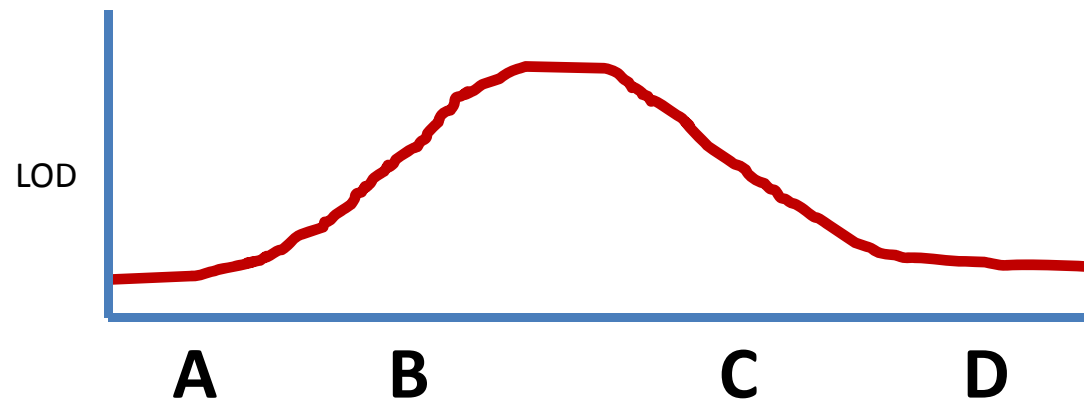
AA 3.5'	BB 3.7'	CC 3.7'	DD 3.5'
Aa 3'	Bb 3'	Cc 3'	Dd 3'
aa 2.5'	bb 2.3'	cc 2.3'	dd 2.5'

- You observed that A and D had *weaker* associations than B and C
- B and C had similar associations
- You inferred the QTL location to be in the middle based on the trajectory A->B and D->C

... but there are dangers...

- Can infer the location of factor by trajectories of association...

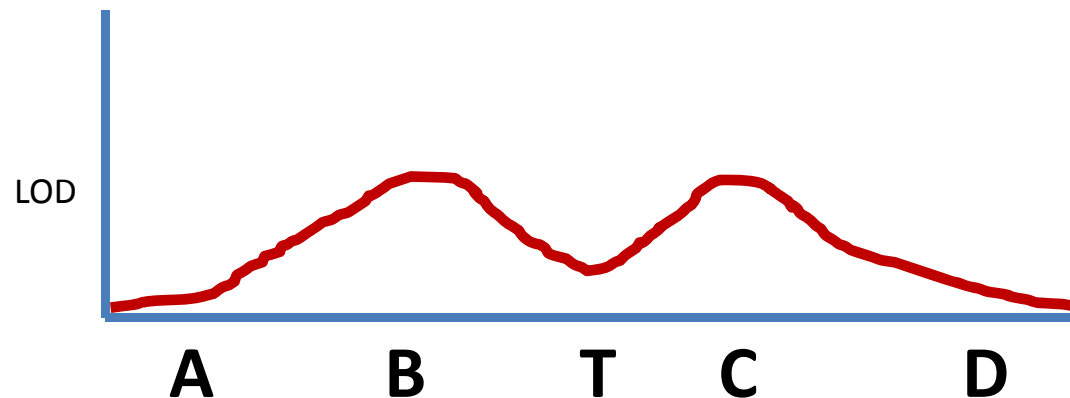
AA 3.5'	BB 3.7'	CC 3.7'	DD 3.5'
Aa 3'	Bb 3'	Cc 3'	Dd 3'
aa 2.5'	bb 2.3'	cc 2.3'	dd 2.5'



... but there are dangers...

- What would adding this “T” marker data imply?

AA 3.5'	BB 3.7'	TT 3.5'	CC 3.7'	DD 3.5'
Aa 3'	Bb 3'	Tt 3'	Cc 3'	Dd
aa 2.5'	bb 2.3'	tt 2.5'	cc 2.3'	dd 2.5'



We don't know what makes the QTL effect...

- May be multiple genes that are close together or a single gene
- **VERY IMPORTANT:** QTL mapping (by cross/ pedigree or by population association study) is not conclusive- it is a **hypothesis** of where one or more genes affecting the trait reside.

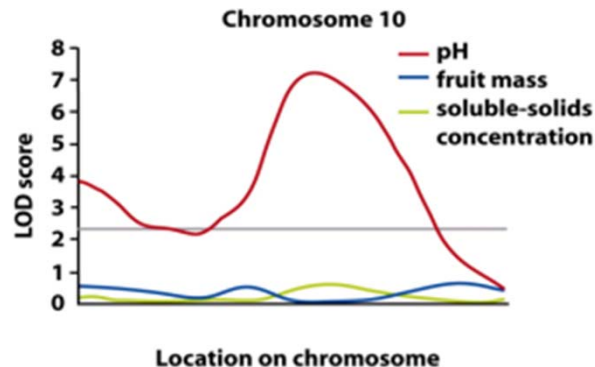


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