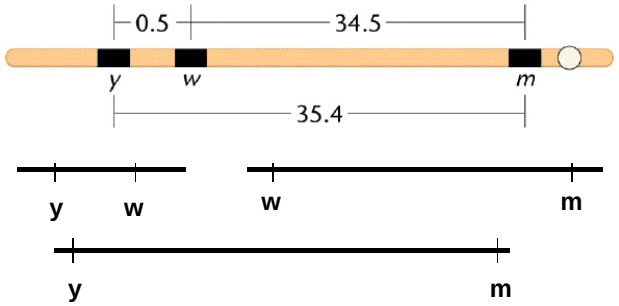
Given the following cross examining two genes (A and B) that are 40 cM apart, what would be the expected number of different phenotypes seen in 100 progeny in the testcross?

Parents	**AAbb**	**x**	**aaBB**
F1		**AaBb**	
Test Cross the F1	**AaBb**	**x**	**aabb**

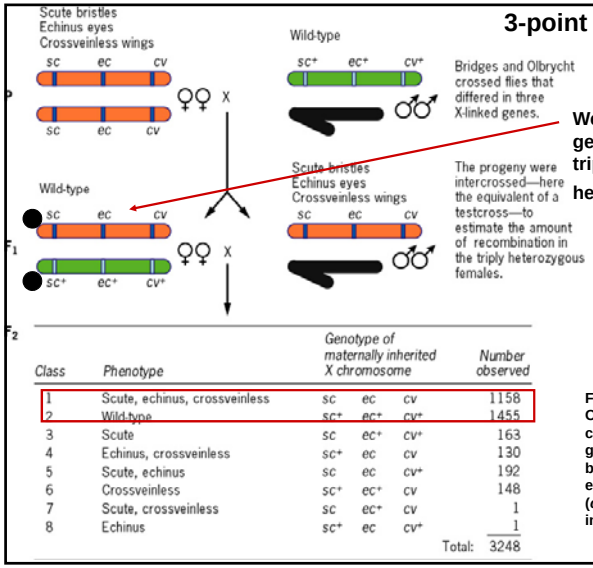
	A	B	C	D	E
AaBb	40	30	20	20	10
Aabb	10	20	80	30	40
aaBb	10	20	80	30	40
aabb	40	30	20	20	10

Recall, Sturtevant needed multiple crosses to map his 3 ge



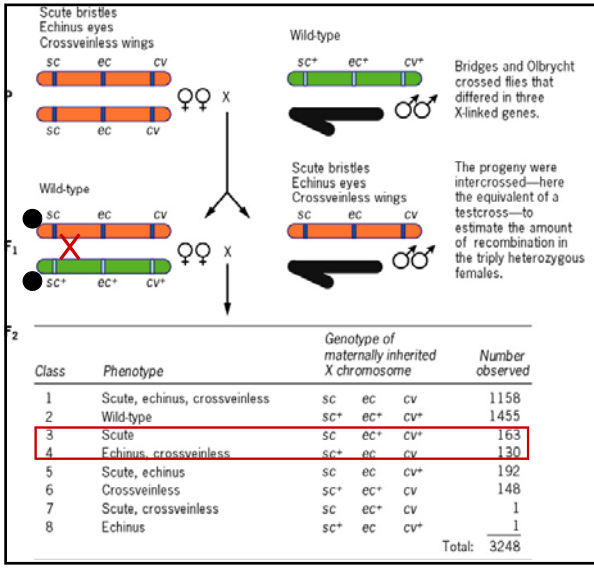
This can be done more efficiently and accurately

3-point Crosses



Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc+	ec+	cv+	1455
3	Scute	sc	ec+	cv+	163
4	Echinus, crossveinless	sc+	ec	cv	130
5	Scute, echinus	sc	ec	cv+	192
6	Crossveinless	sc+	ec+	cv	148
7	Scute, crossveinless	sc	ec+	cv	1
8	Echinus	sc+	ec	cv+	1
				Total:	3248

Fig. 8.13 Bridges and Olbrycht's three-point cross with the X-linked genes *sc* (*scute* bristles), *ec* (*echinus* eyes), and *cv* (*crossveinless* wings) in *Drosophila*.



Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
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2	Wild-type	sc+	ec+	cv+	1455
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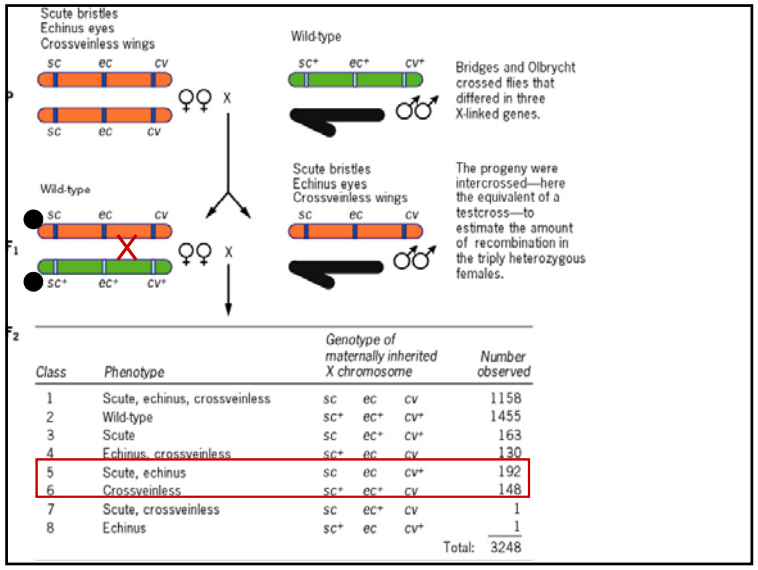
4	Echinus, crossveinless	sc+	ec	cv	130
5	Scute, echinus	sc	ec	cv+	192
6	Crossveinless	sc+	ec+	cv	148
7	Scute, crossveinless	sc	ec+	cv	1
8	Echinus	sc+	ec	cv+	1
				Total:	3248



Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc+	ec+	cv+	1455
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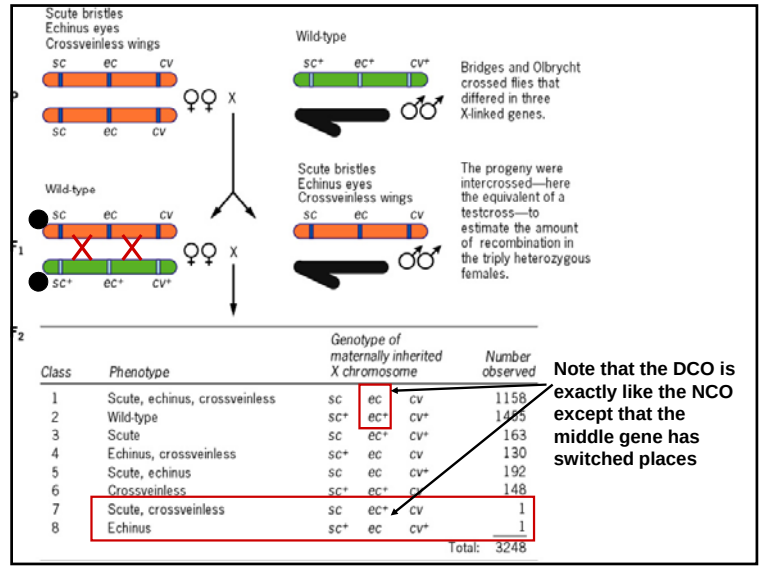
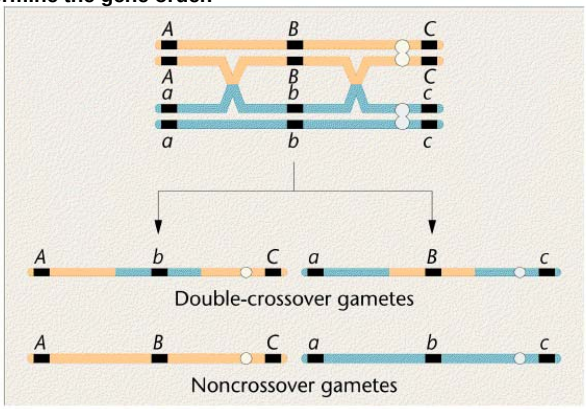
6	Crossveinless	sc+	ec+	cv	148
7	Scute, crossveinless	sc	ec+	cv	1
8	Echinus	sc+	ec	cv+	1
				Total:	3248



Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc+	ec+	cv+	1455
3	Scute	sc	ec+	cv+	163
4	Echinus, crossveinless	sc+	ec	cv	130
5	Scute, echinus	sc	ec	cv+	192
6	Crossveinless	sc+	ec+	cv	148
7	Scute, crossveinless	sc	ec+	cv	1
8	Echinus	sc+	ec	cv+	1
				Total:	3248

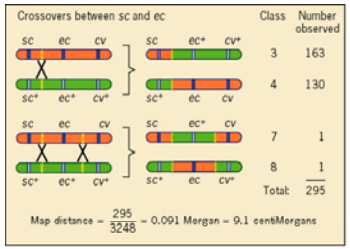
Note that the DCO is exactly like the NCO except that the middle gene has switched places

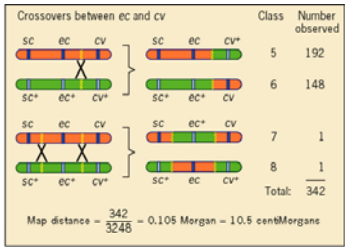
Middle gene is always the one that switches places when you compare NCO with DCO categories!! You can use this to determine the gene order.



Once you have taken the NCO group and put the genes in the correct order, it is routine to find distances. Here one NCO chromosome is sc – ec – cv, while the other is sc⁺ - ec ⁺ - cv ⁺.

Note: the dominant + will not always all be on the same chromsome!





Calculation of genetic map distances from Bridges and Olbrycht's data.

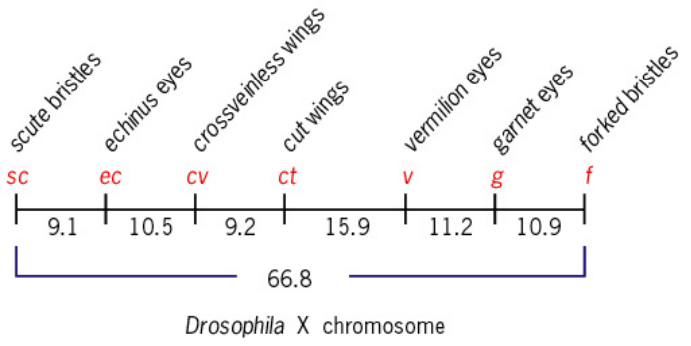


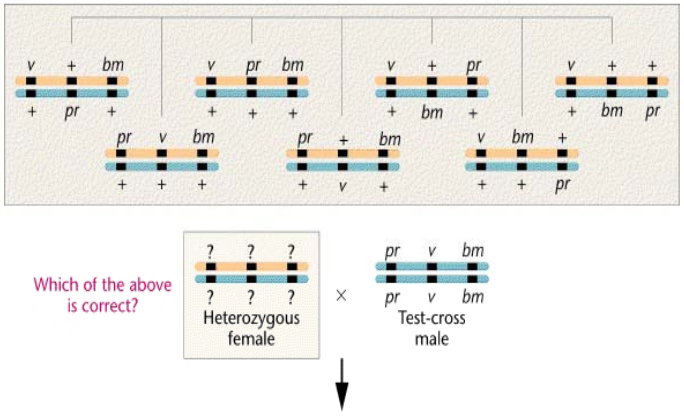
Fig 8.15 Bridges and Olbrycht's map of seven X-linked genes in *Drosophila*.

F1		A B C / a b c	A B c / a b C	A C B / a c b
Test Cross Progeny				
ABC	abc	No COs	SCO (B -C)	NCO
Abc	aBC	Single (A - B)	DCO	SCO (A - C)
ABc	abC	Single (B - C)	NCO	DCO
AbC	aBc	Double CO	SCO(A - B)	SCO (C - B)

Both the orientation of the alleles (which chromosome has the dominant or recessive alleles) and the order of the genes can vary!

Now we work in the reverse direction. Start with progeny and predict parent!!

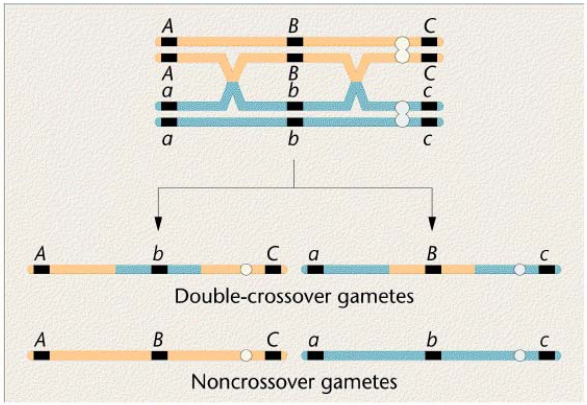
(a) Possible allele arrangements and gene sequences in a heterozygous female



(b) Actual results of mapping cross

Phenotypes of offspring		
+	v	bm
pr	+	+
+	+	bm
pr	v	+
+	v	+
pr	+	bm
pr	v	bm
+	+	+

What did the heterozygous parent look like?
pr+ v bm on one chromosome and pr v+ bm+ on the other.
What's order?? Must compare NCO and DCO classes to see which alleles switched places



pr is the "odd man out" so it must be in the middle

pr+ v bm	pr v+ bm+	parental
pr v bm	pr+ v+ bm+	DCO

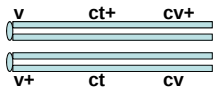
F1 **v⁺v cv⁺cv ct⁺ct** X test cross parent (triple recessive) **vv cvcv ctct**

v	cv+	ct+	580
v+	cv	ct	592
v	cv	ct+	45
v+	cv+	ct	40
v	cv	ct	89
v+	cv+	ct+	94
v	cv+	ct	3
v+	cv	ct+	5
			1448

1) Which are parental classes?
2) Which are dco classes?

3) What is the gene order? "odd man out method" (Method 2)
Compare either parental class with either dco class e.g.
v cv+ ct+
v cv+ ct
Which locus is odd man out? (ct)
Therefore ct is in middle, order is (v ct cv)

Draw the F1
Parental classes
but in the correct order



4) Which sco class represents co v-ct?
Which sco class represents co ct-cv?

5) What are the distances between genes?

v	ct	89+94+3+5 = 191	191/1448 = 0.132 = 13.2%
ct	cv	45+40+3+5 = 93	93/1448 = 0.064 = 6.4%

6) Does the frequency of dco class equal that predicted from sco x sco?

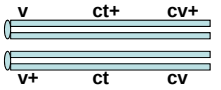
Expected 0.132 x 0.064 = 0.0084; 0.0084 x 1448 = 12
Obs = 8
Generally fewer obs. dco than expected.
7) **Coef of coincidence** = obs/exp = 2/3
Interference = 1- obs/exp = 1/3
The Interference is the proportion of the DCO that are missing (we expected 4 more than we found. This tends to be high when markers are close and a CO in one region "interferes" with a CO in a neighboring region! WHY??

WHAT IF THEY WERE ALL OUT OF ORDER? HOW CAN YOU DECIDE WHICH GENOTYPES GO TOGETHER?

F1 **v⁺v cv⁺cv ct⁺ct** X test cross parent (triple recessive) **vv cvcv ctct**

v	cv+	ct+	580	
v+	cv+	ct	40	
v+	cv+	ct+	94	
v+	cv	ct	592	
v	cv	ct+	45	
v	cv+	ct	3	**Same Same Diff**
v	cv	ct	89	
v+	cv	ct+	5	**Diff Diff Same**
			1448	

Draw the F1
Parental classes
but in the correct order



What do the chromosomes of the F1 look like?

Aa Bb Cc x aa bb cc

A B C	80
A B c	180
A b C	20
a B C	290
A b c	310
a B c	30
a b C	190
a b c	75

Which orientation of the chromosomes in the F1 AaBbCc parent is correct?

A

B

C

D

E

What do the chromosomes of the F1 look like?

Aa Bb Cc x aa bb cc

A B C	20
A B c	180
A b C	290
a B C	70
A b c	80
a B c	310
a b C	190
a b c	30

Which orientation of the chromosomes in the F1 AaBbCc parent is correct?

A

B

C

D

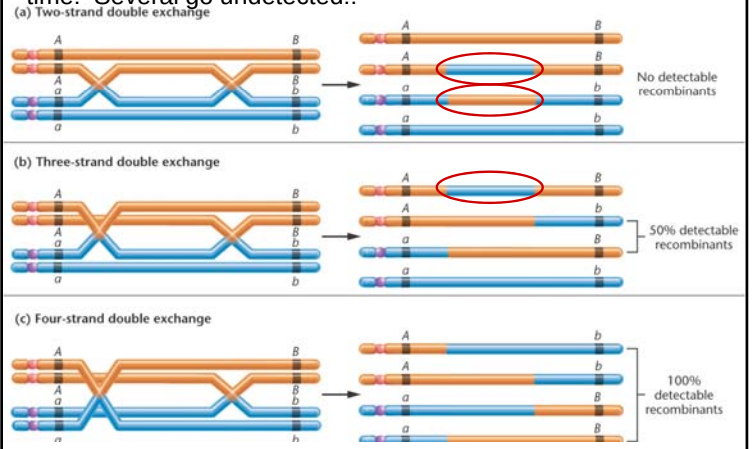
E

Two Reasons Why Recombination Frequency is Not Linear with Physical Distance

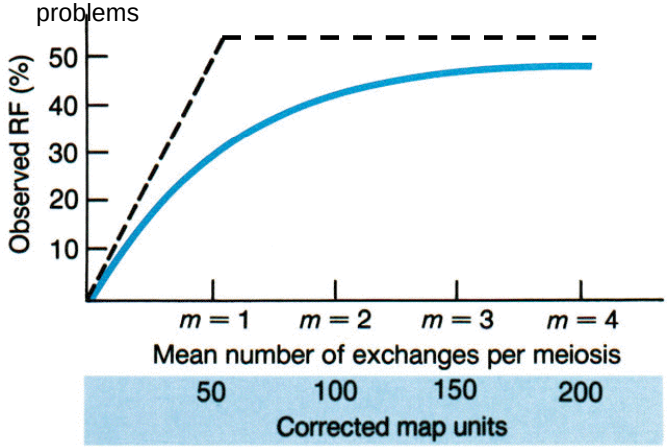
1) "Interference"… when markers are close, one crossover in a region makes it physically difficult to have another close-by in that same region!

2) Also, the further apart genes are the more likely that cryptic crossovers will go undetected.

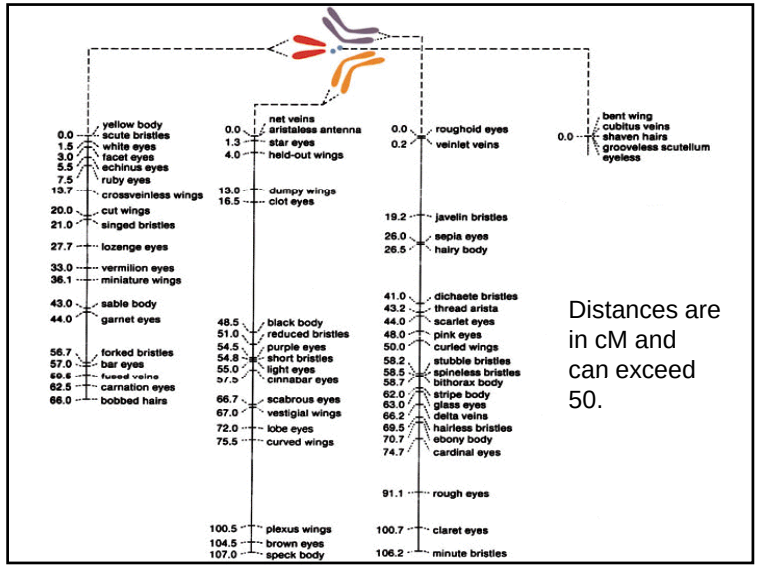
Cryptic crossovers: as distance increases, more and more crossovers, but still can only detect recombinants 50% of the time! Several go undetected!!



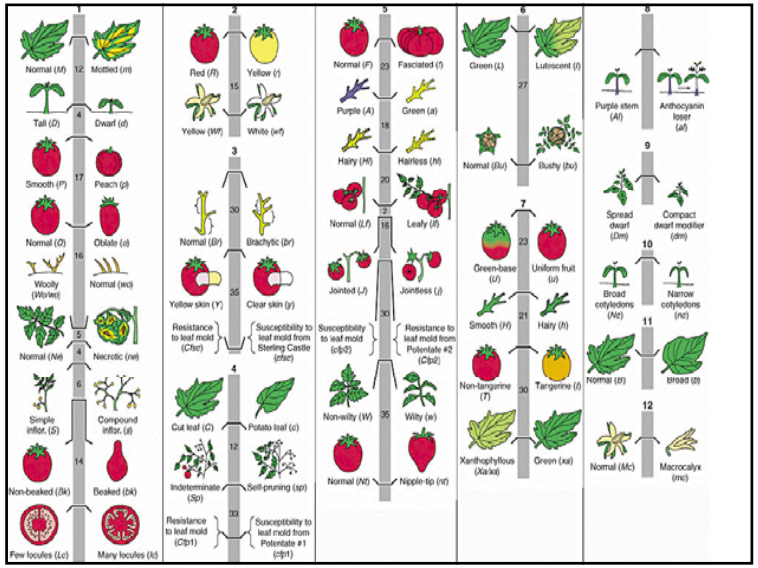
Mapping Functions solve some of these problems

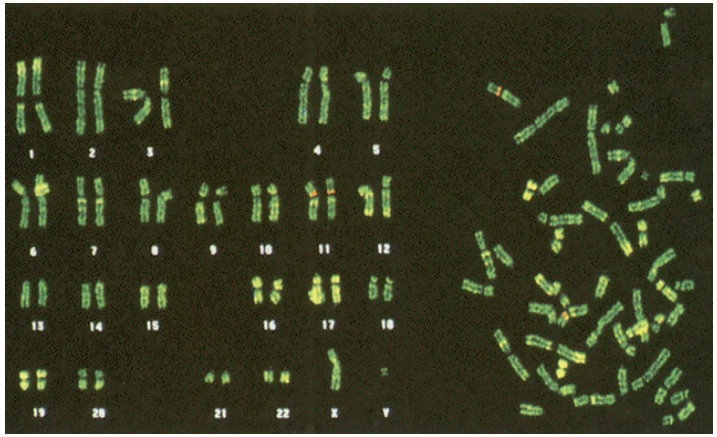


CentiMorgans cM

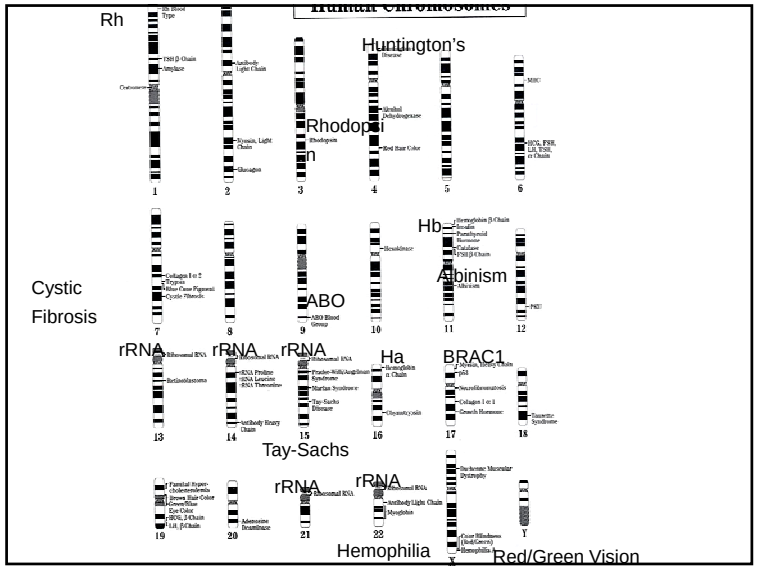


Distances are in cM and can exceed 50.



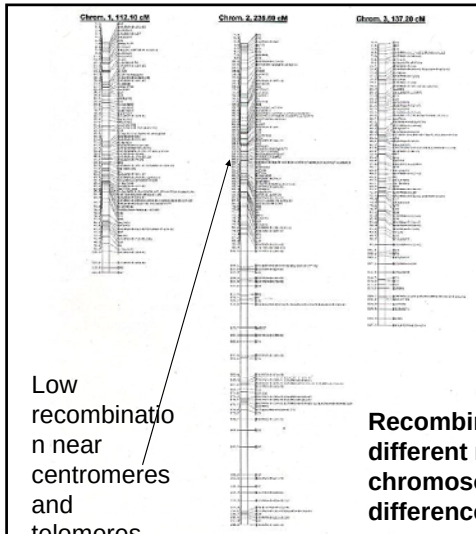


Merging of the "cytological" and the "transmission" (Mendelian) approaches to the study of inheritance!



Recombination Rates differ among species!!

In Sunflower (Mbp)	1 cM	=	1.5 million base pairs
In Humans	1 cM	=	1.0 Mbp
In Corn	1 cM	=	1.0 Mbp
In Tomato	1 cM	=	0.5 Mbp (500,000 bp)
In Drosophila	1 cM	=	50,000 bp
In Yeast	1 cM	=	4000 bp

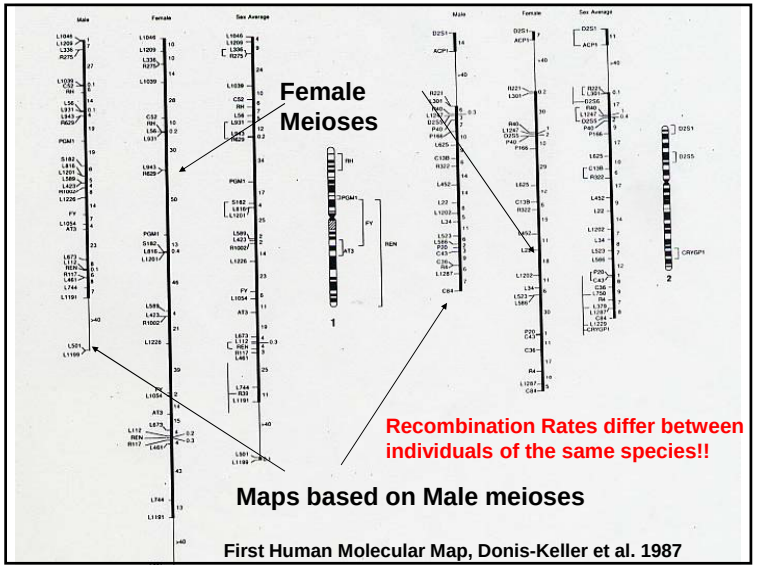


First 3 chromosomes of the lettuce map

Low recombination near centromeres and telomeres

Recombination rates vary in different regions of a chromosome (10X - 100X difference)

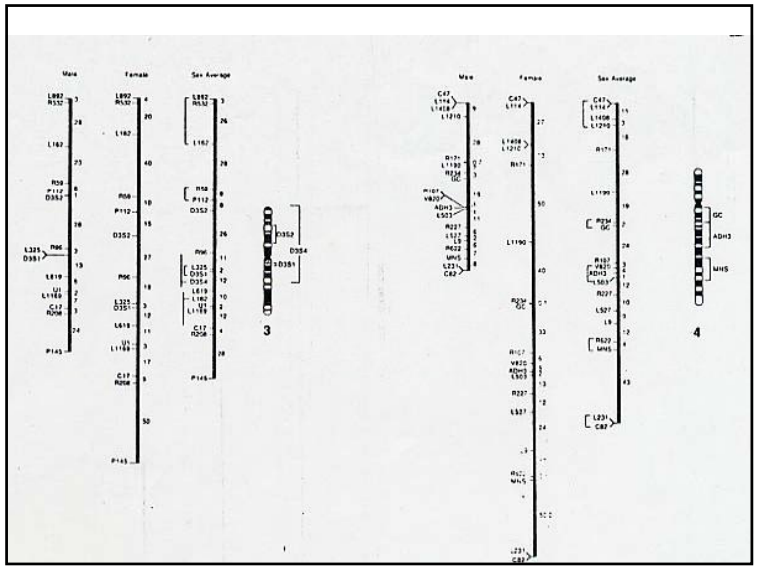
Kesseli et al. 1994; Truco et al. 2007

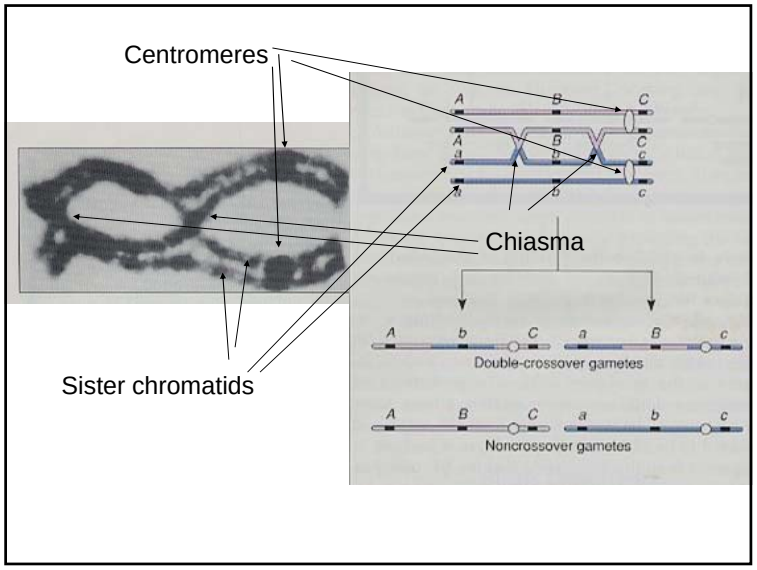


Recombination Rates differ between individuals of the same species!!

Maps based on Male meioses

First Human Molecular Map, Donis-Keller et al. 1987





What is the importance of recombination?

It generates variation that is essential for the survival of all species!!

Plymouth Gentian

Sabatia kennedyana

Lelia Orrell
unpublished

The Compositae Genome Project

Easy to grow crops in monoculture, but…..

http://compgenomics.ucdavis.edu/

Monoculture Corn field devastated by Bacterial Wilt disease

Southern Corn Blight wiped out 60% of the US crop in the 1960s, because all the corn was derived from the same genetic stock.

Playing with numbers:

How many genes in the human genome?

25-35,000

How much variation can we create with a few genes each with a couple of variants?

If only 200 of the 30,000 genes were variable (2 alleles each) how many combinations of these different traits could we make in a gamete?

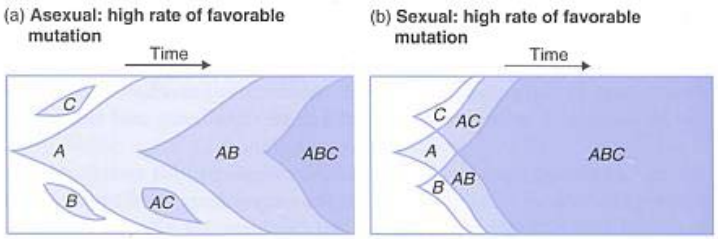
2^{200} = ?

1,600,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000

total # of humans that EVER lived is 13,000,000,000!!

Evolutionary Importance of Recombination

Generate variation, new combinations of alleles.



A, B, C represent favorable mutations.

Figure a) Mutations occur regularly, but the only way all three can get into a single individual creating the most fit individual is for the new mutation to occur in an individual that already carried the preexisting good mutation.

Figure b) Mutations occur in separate individuals, but through **sexual reproduction and recombination**, can quickly become established in a single individual.