

Bio 97

Linked genes

Mendel's Laws & the Chromosome Theory - I

- Homologous pairs of chromosomes contain the same genes (excpn: X and Y)
- Information is often non-identical = alleles
- Homologous chromosomes segregate at meiosis I
--> The two alleles of a given gene " " " "

Mendel's Laws & the Chromosome Theory - II

- Homologous pairs of chromosomes line up randomly (with respect to other pairs of homologs) at Meiosis I.

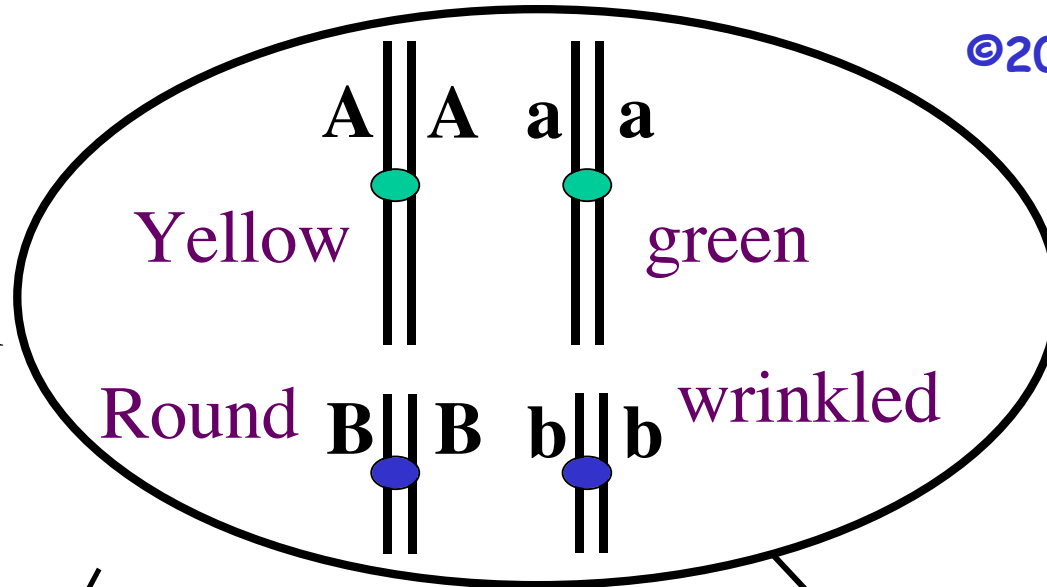
--> Alleles of genes on different chromosomes assort independently

Show movie

Independent Assortment of Chrms

©2000 Lee Bardwell

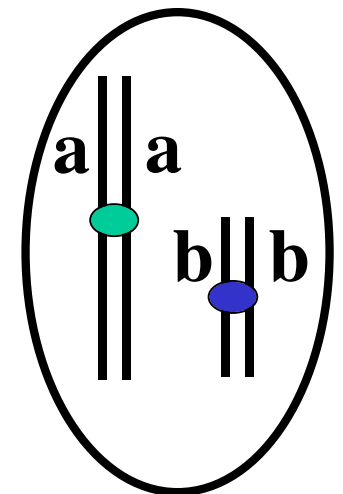
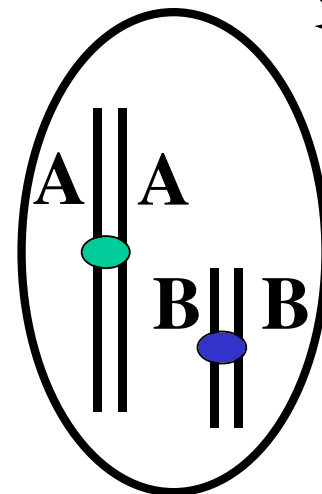
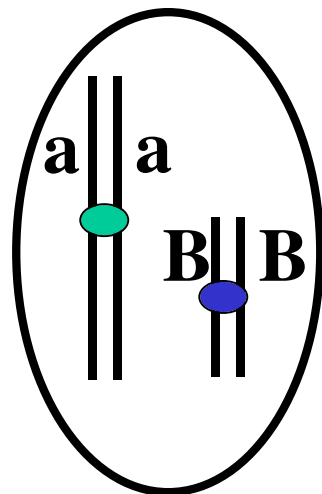
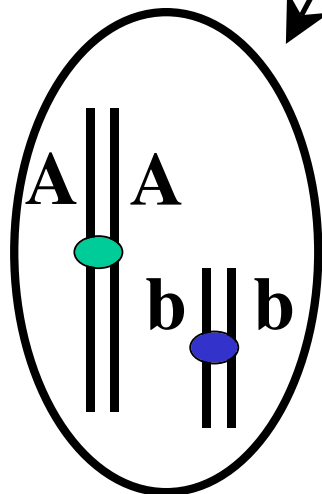
Stem cell
after chrm
replication

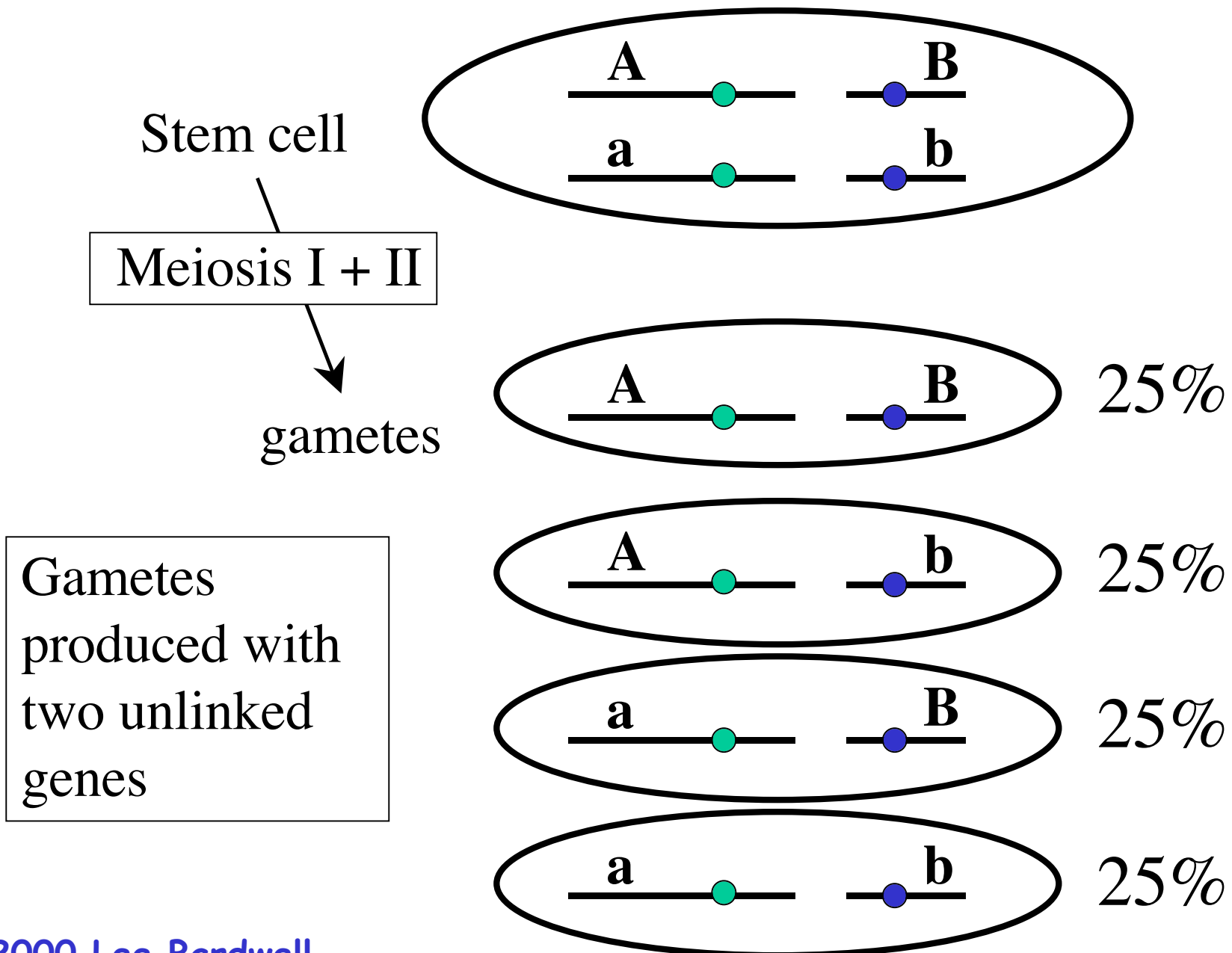


Half of the time

MEIOSIS I

Half of the time





Independent assortment F1 x F1

AaBb × AaBb

meiosis

meiosis

AB

Ab

aB

ab

AB

Ab

aB

ab

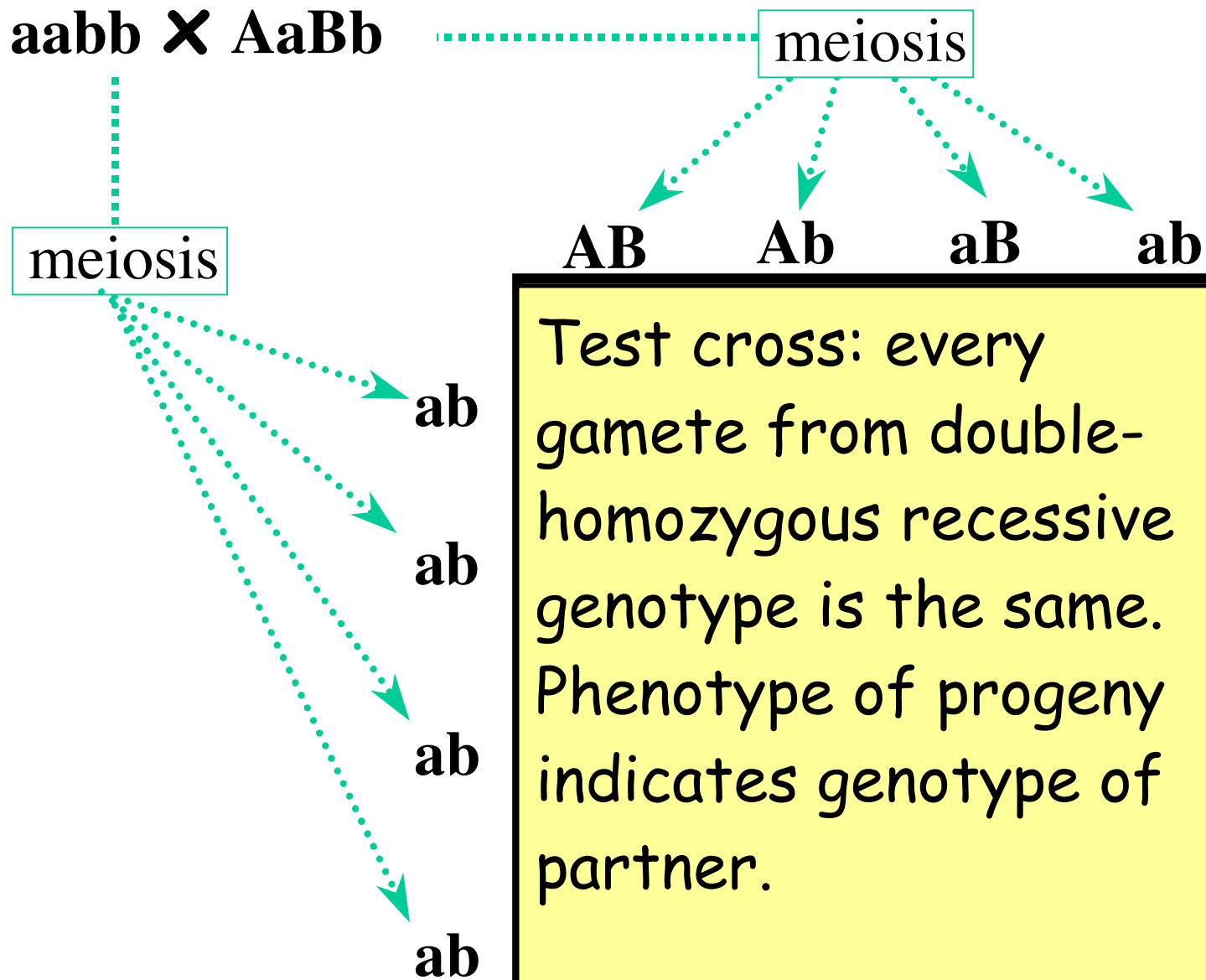
	AB	Ab	aB	ab
AB	<u>A</u> <u>B</u>	<u>A</u> <u>B</u>	<u>A</u> <u>B</u>	<u>A</u> <u>B</u>
Ab	<u>A</u> <u>B</u>	<u>A</u> <u>b</u>	<u>A</u> <u>B</u>	<u>A</u> <u>b</u>
aB	<u>A</u> <u>B</u>	<u>A</u> <u>B</u>	<u>a</u> <u>B</u>	<u>a</u> <u>B</u>
ab	<u>A</u> <u>B</u>	<u>A</u> <u>b</u>	<u>a</u> <u>B</u>	<u>a</u> <u>b</u>

round,
yellow

wrinkled,
green

Indep. Assort. in a Test Cross

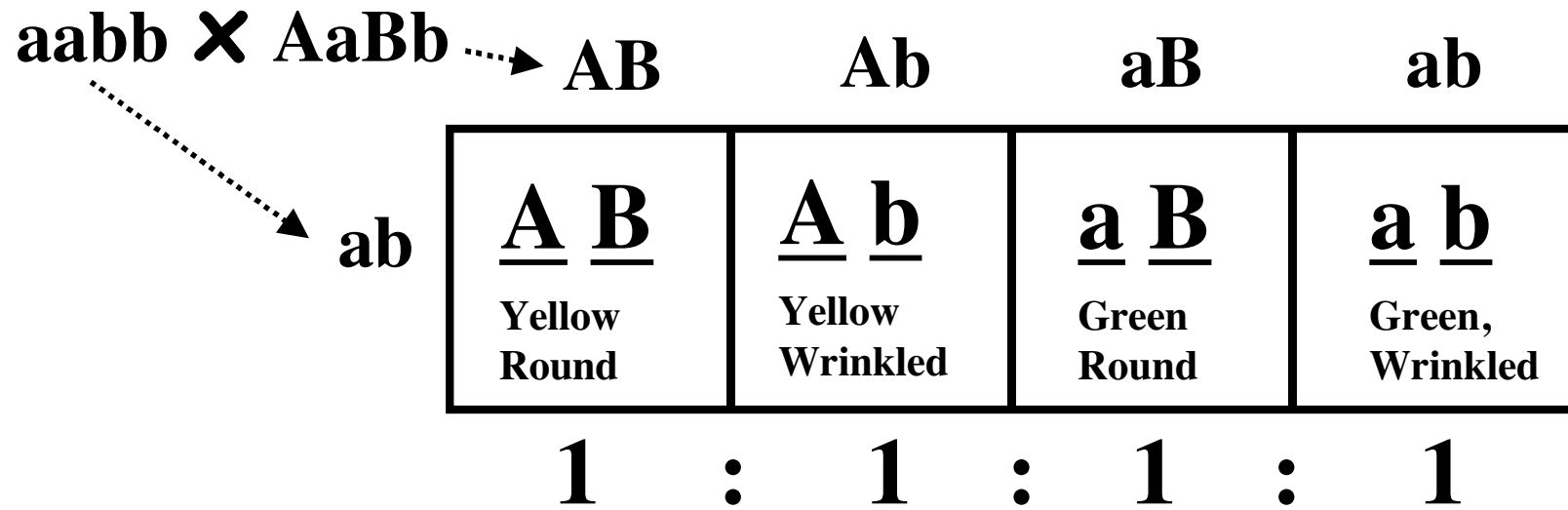
aabb × AaBb



Test cross: every gamete from double-homozygous recessive genotype is the same. Phenotype of progeny indicates genotype of partner.

Test cross: dihybrid heterozygote

- genes are unlinked



CAPITALS = dominant
small = recessive
Underline = phenotype
 Not underlined = genotype

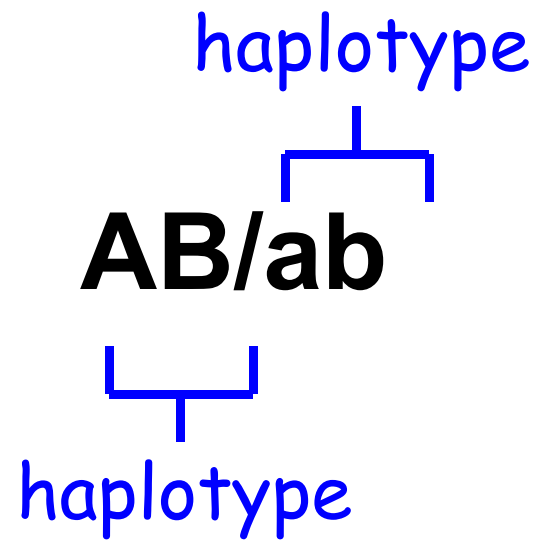
Here A and a are two alleles
 of a gene controlling seed color
 B and b are two alleles
 of a gene controlling seed shape

But wait...

If we have 30,000 genes, and only 23 chrms (haploid set), then all our genes can't segregate independently

T.H. Morgan, in 1910, sets out to test the hypothesis that some genes should show a segregation pattern indicating they are linked

(= on same chrm) ©2000 Lee Bardwell

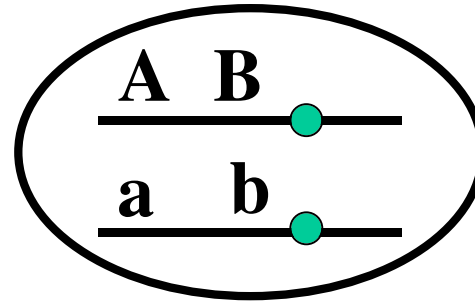


The allelic configuration of multiple loci on a single chromosome.

haplotype

AB/ab

haplotype



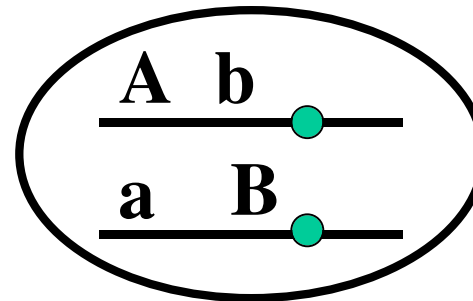
Yellow,
Round
diploid cell

Recessive alleles are cis

haplotype

Ab/aB

haplotype



Yellow,
Round
diploid cell

Recessive alleles are in trans

Three test crosses:

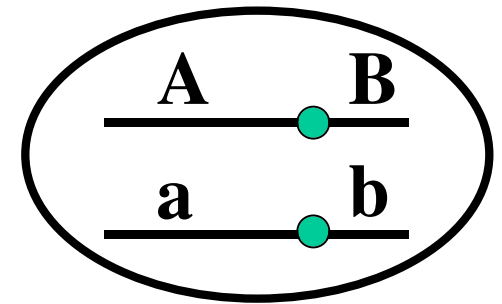
of green wrinkled to Yellow Round

1. $aabb \times AaBb$ (no linkage)

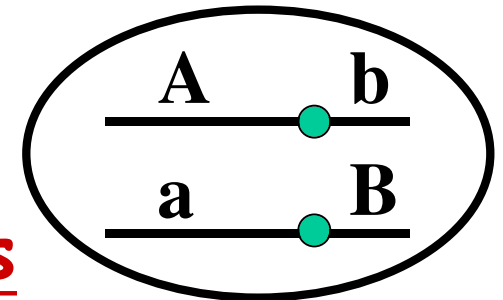
green
wrinkled

Yellow
Round

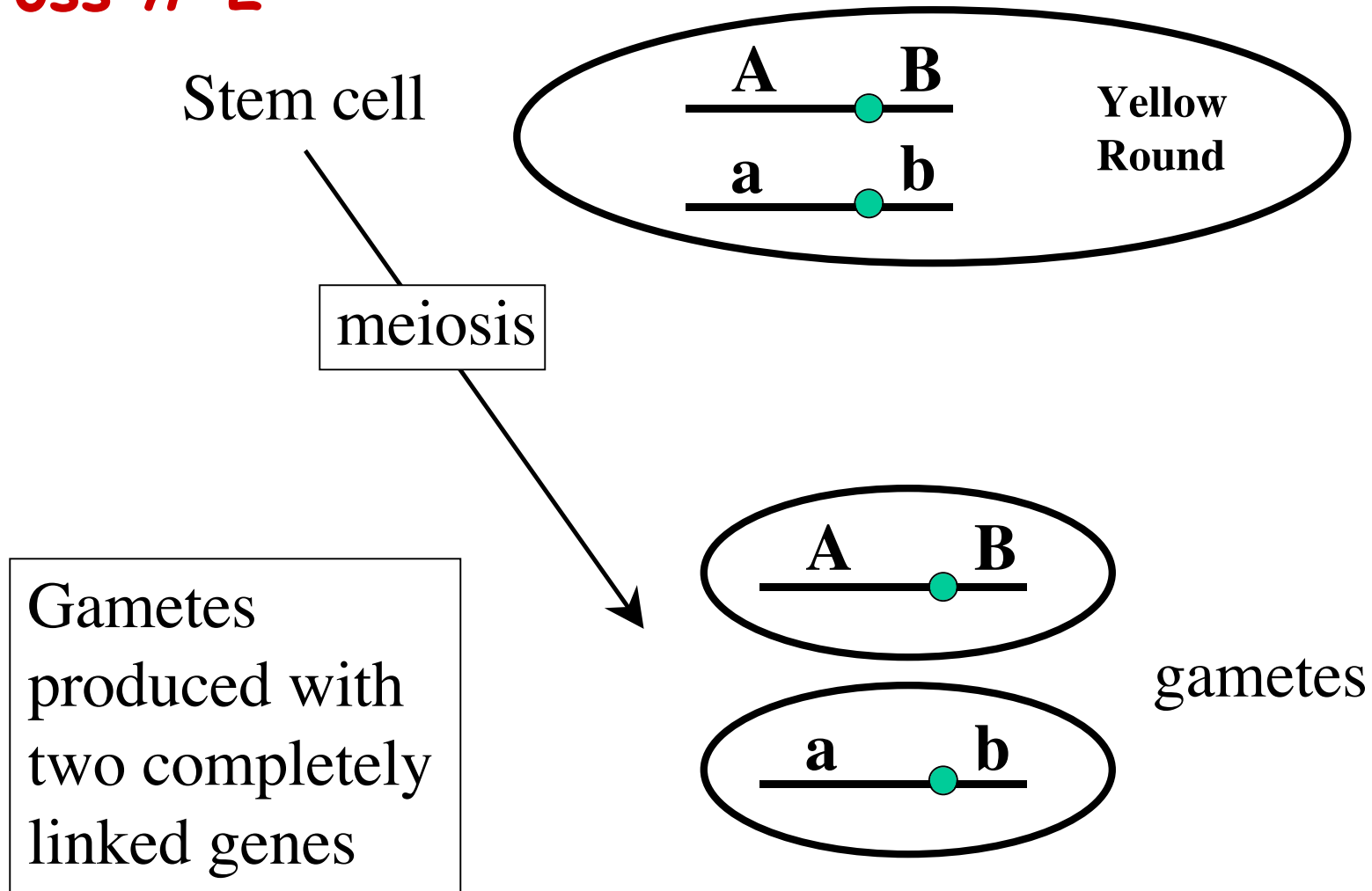
2. $ab/ab \times AB/ab$ (linked)
Recessive alleles are cis



3. $ab/ab \times Ab/aB$ (linked)
Recessive alleles are in trans

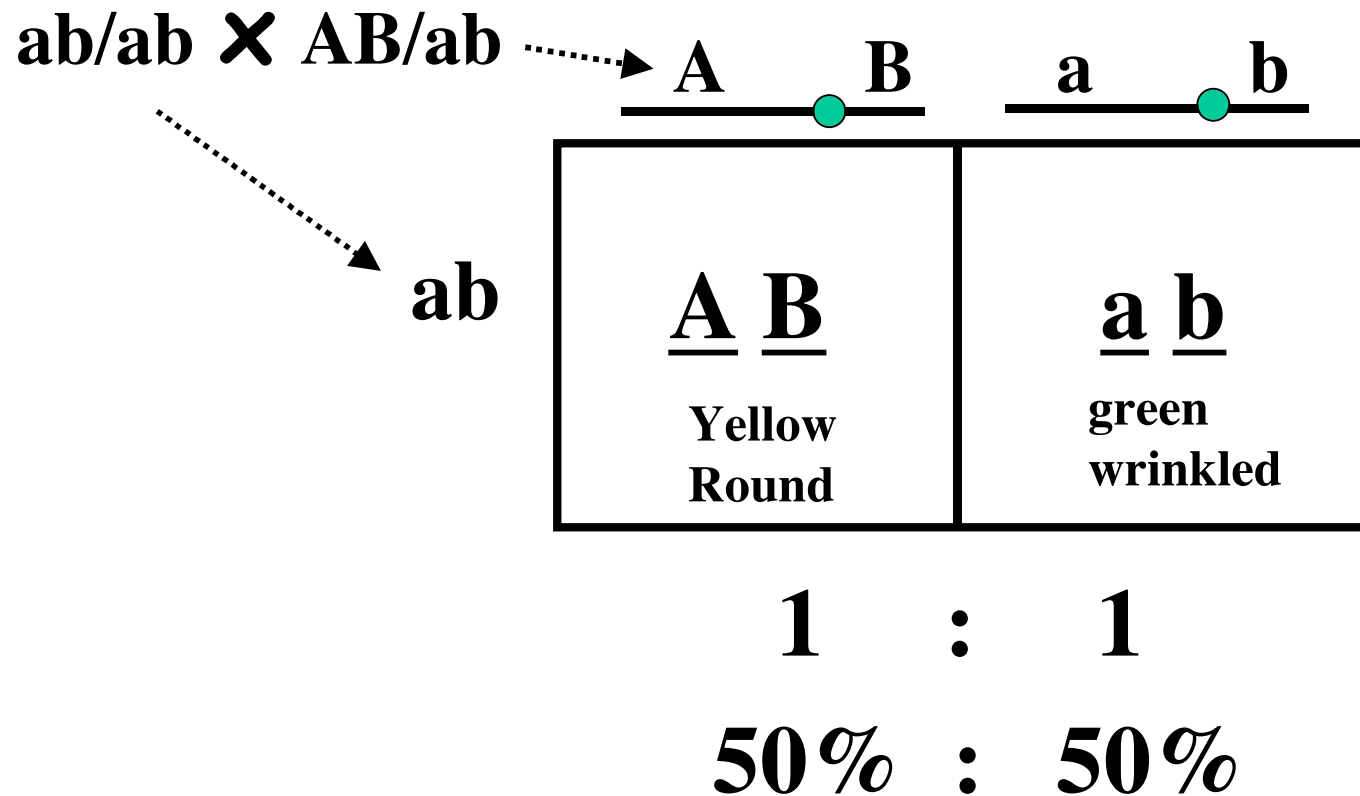


Cross # 2

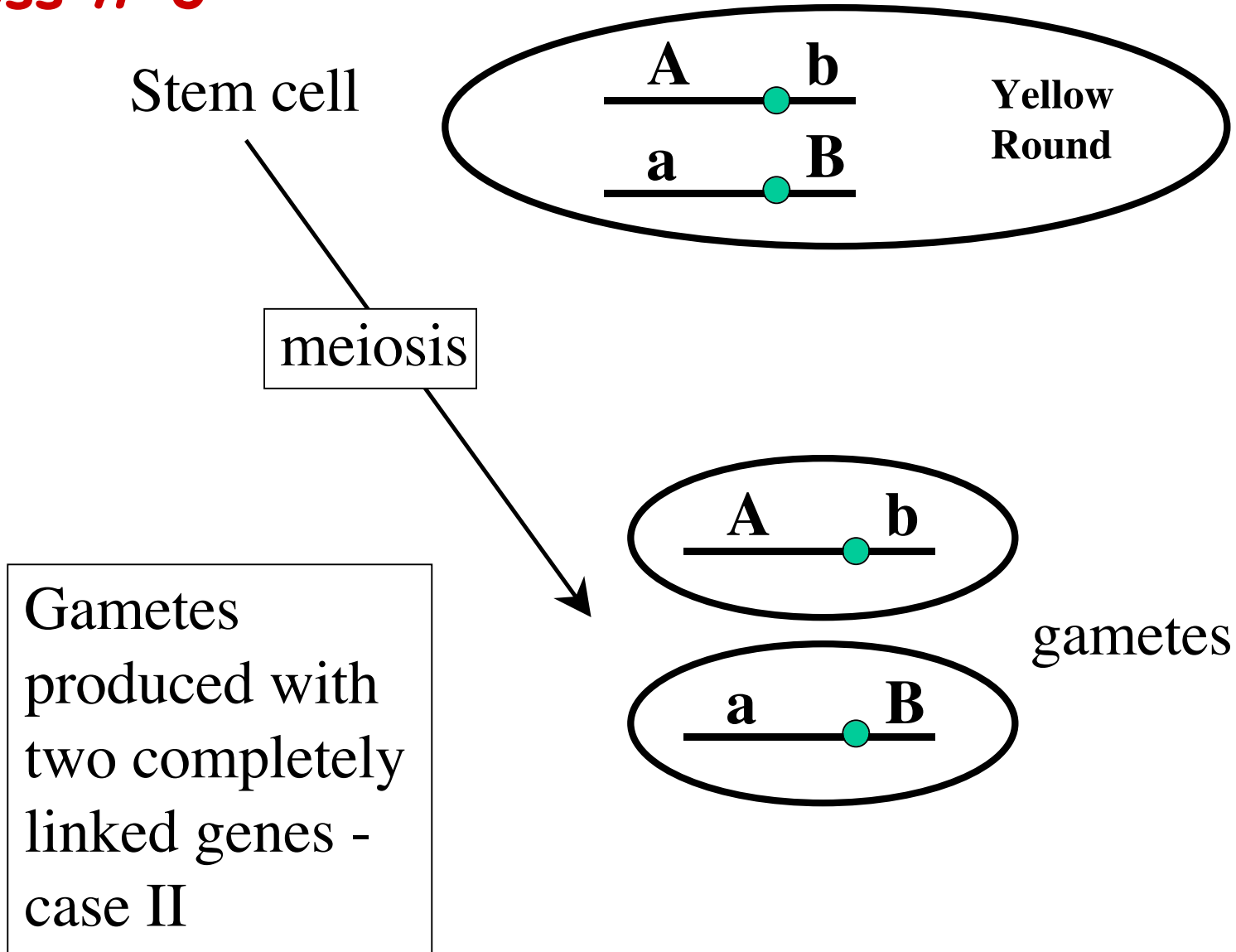


Test cross: dihybrid heterozygote

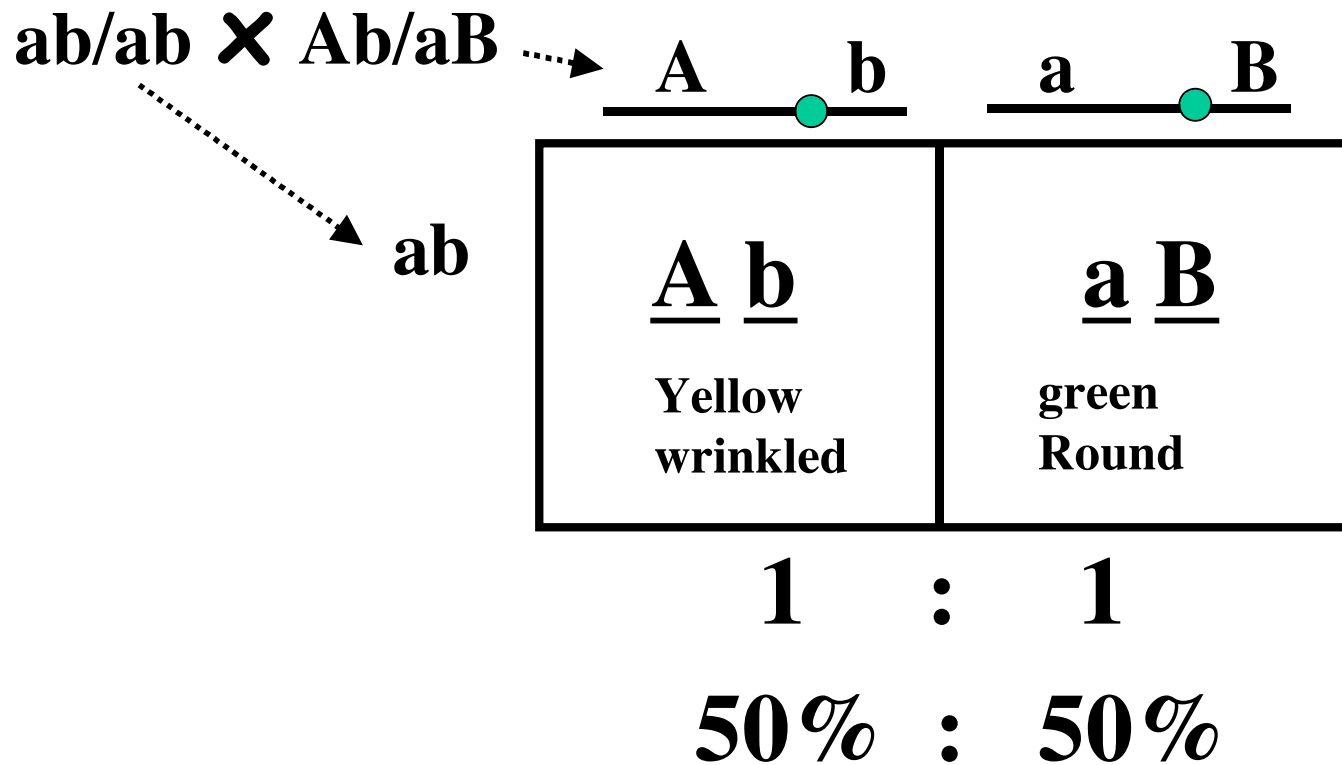
- genes are completely linked



Cross # 3



Test cross: dihybrid heterozygote
 - genes are completely linked



The expectation

Phenotypes: AB : Ab : aB : ab

aabb X AaBb

1 : 1 : 1 : 1

Unlinked

ab/ab X AB/ab

1 : 0 : 0 : 1

ab/ab X Ab/aB

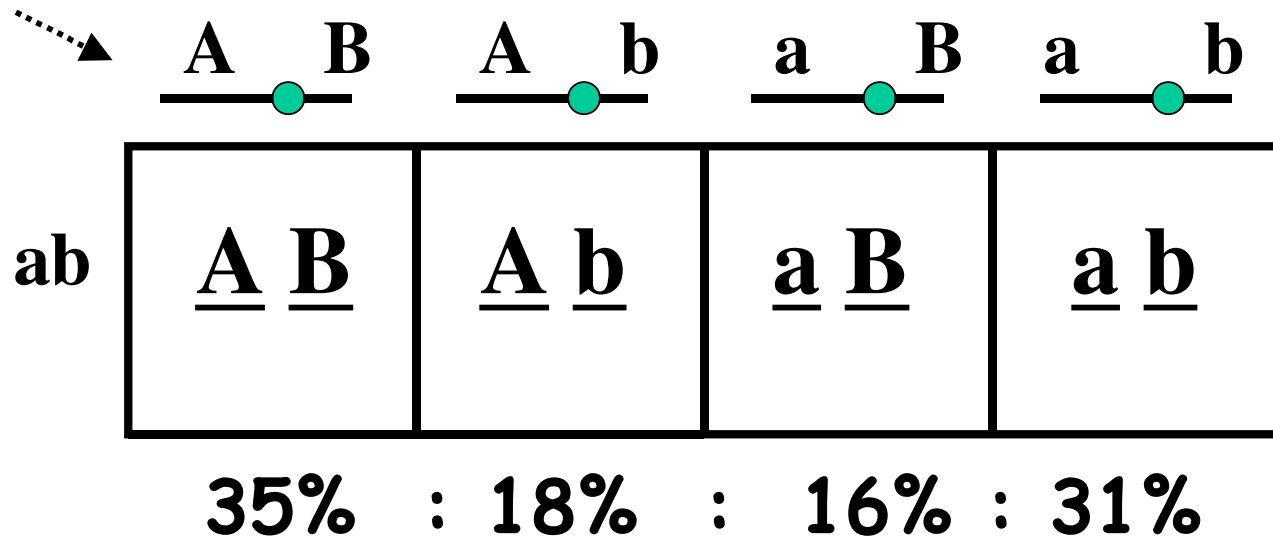
0 : 1 : 1 : 0

Morgan's
cross

Assuming
complete linkage

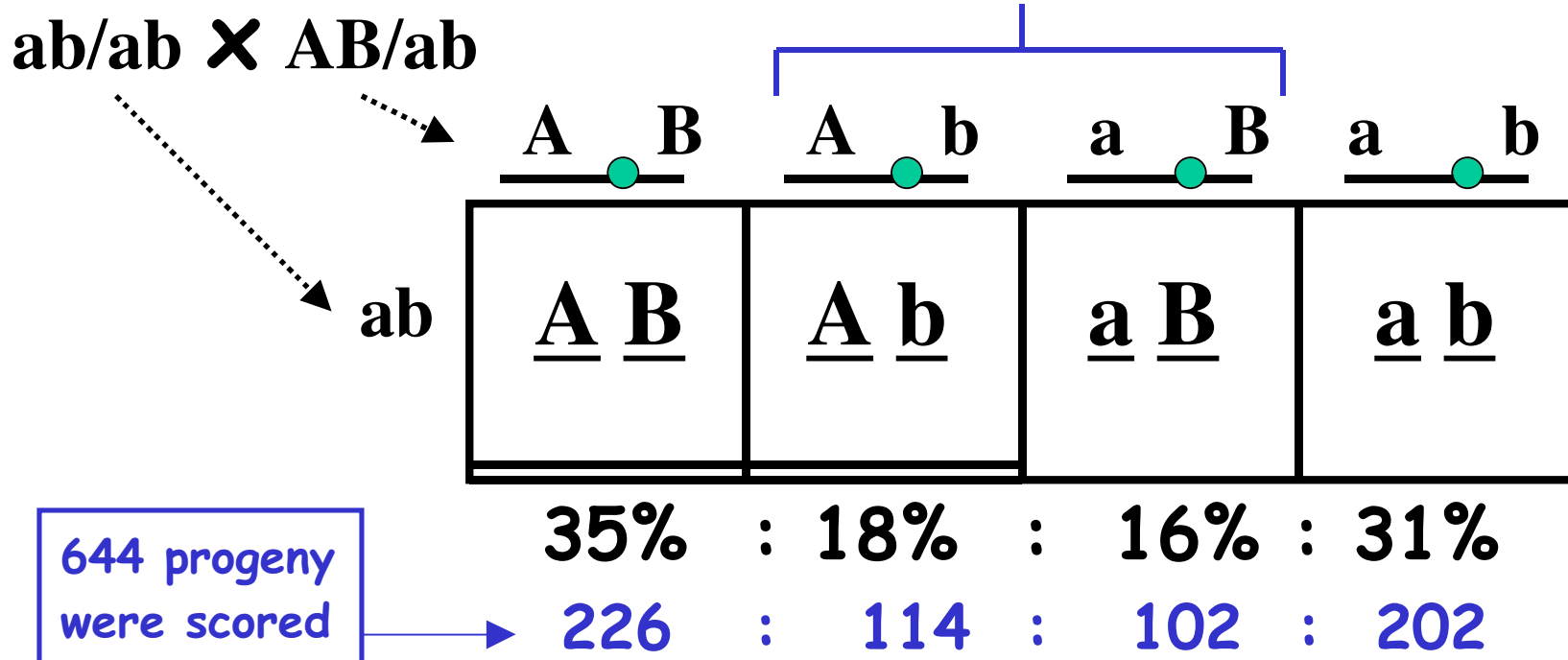
The Result

$ab/ab \times AB/ab$



- Inconsistent with independent assortment
- Inconsistent with complete linkage
- What's going on?

Non-parental chrms



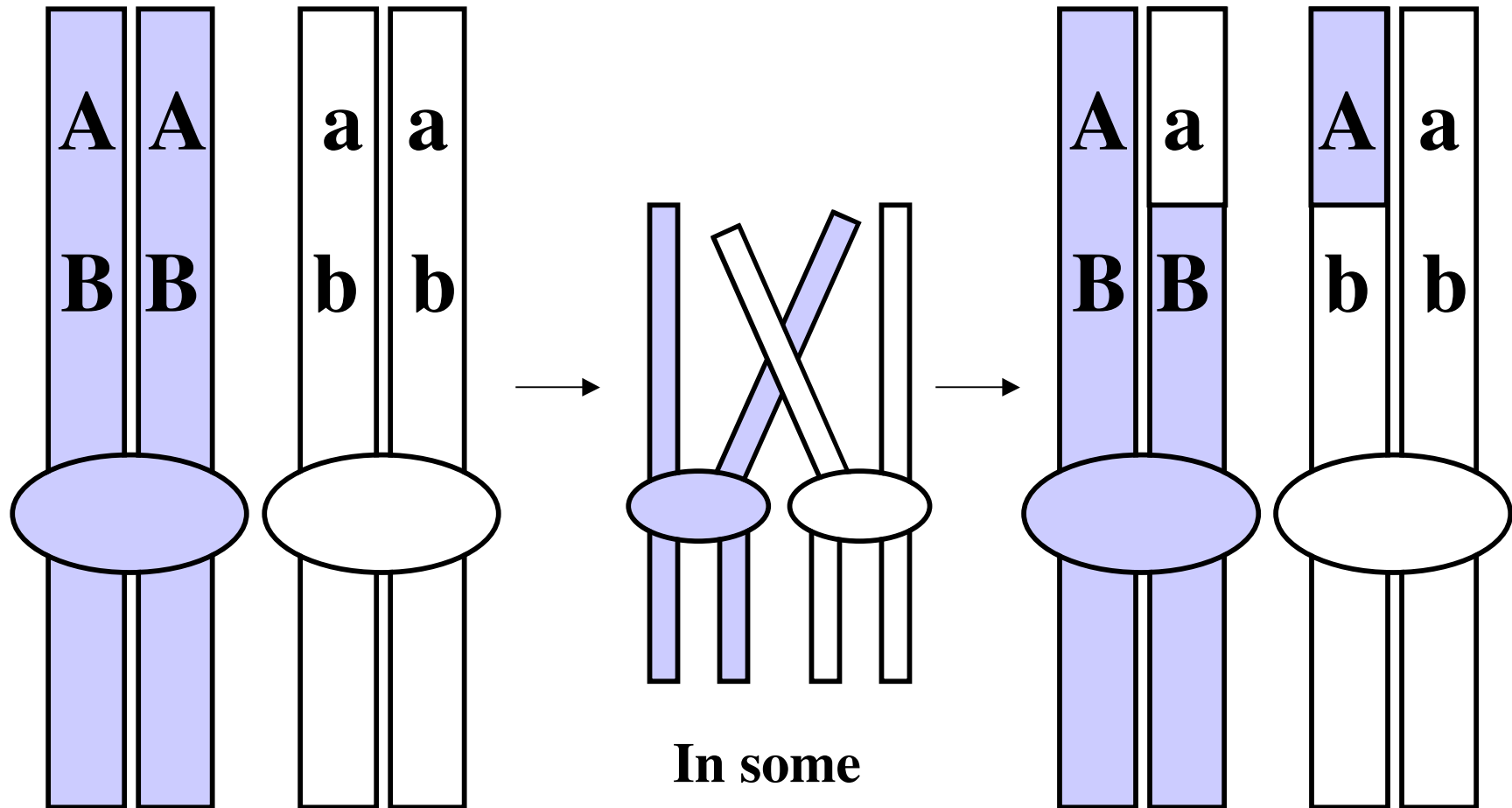
Somehow, chromosomes got into the progeny that didn't come from either parent.

Where did these chrms come from ?!?

Infidelity? **NO** Aliens? **NO**

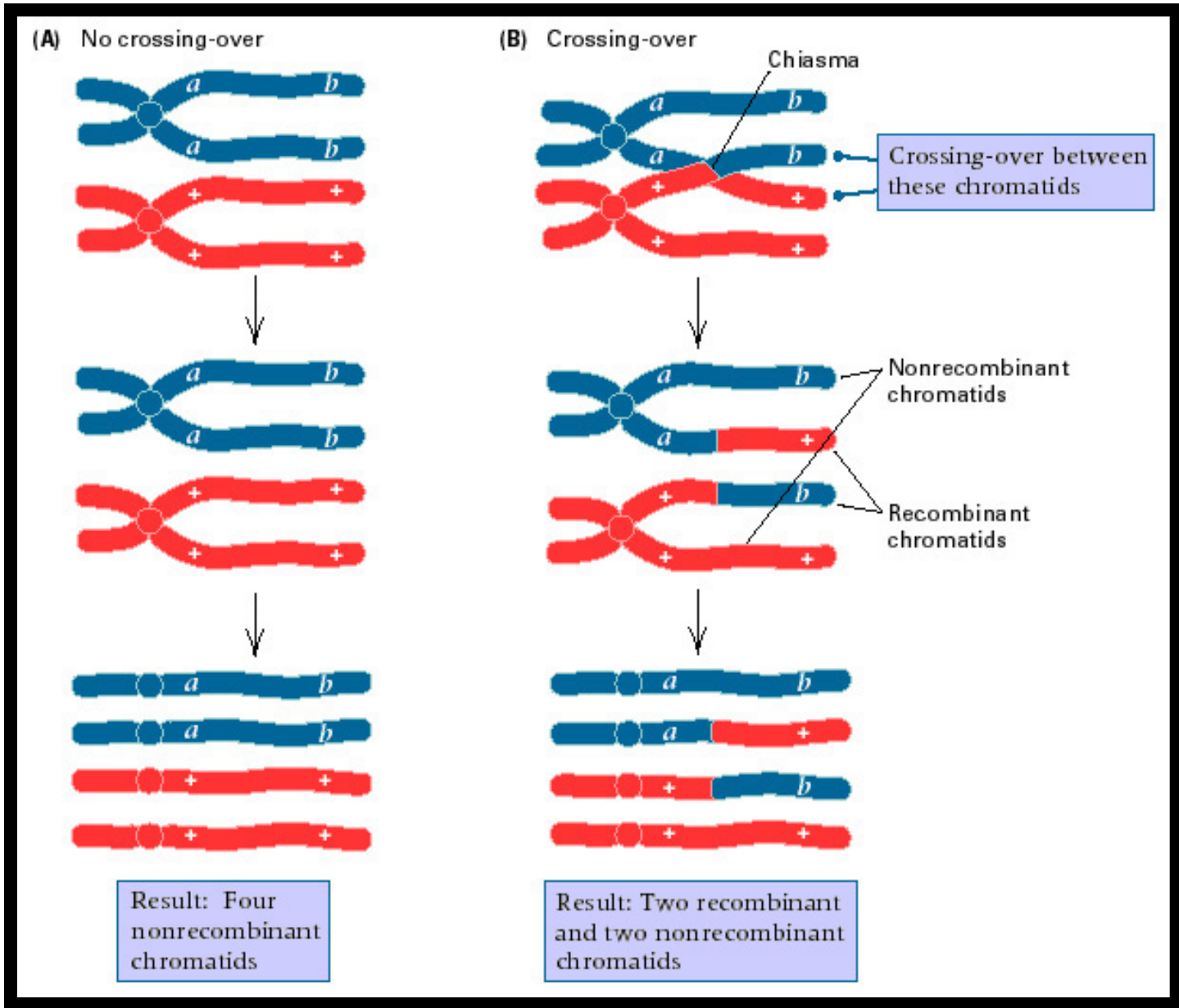
Statistical fluctuation? **NO**

Non-parental haplotypes in progeny --> meiotic recombination (crossing-over)



Paired homologous
chrms in prophase of
meiosis I

In some
fraction of
meioses



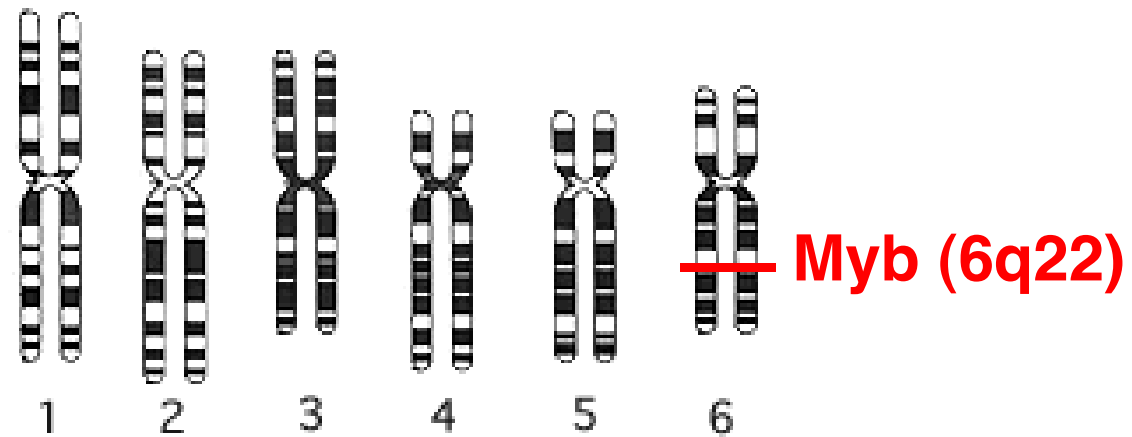
H&J Fig 4.4

Recombination = Crossing-over

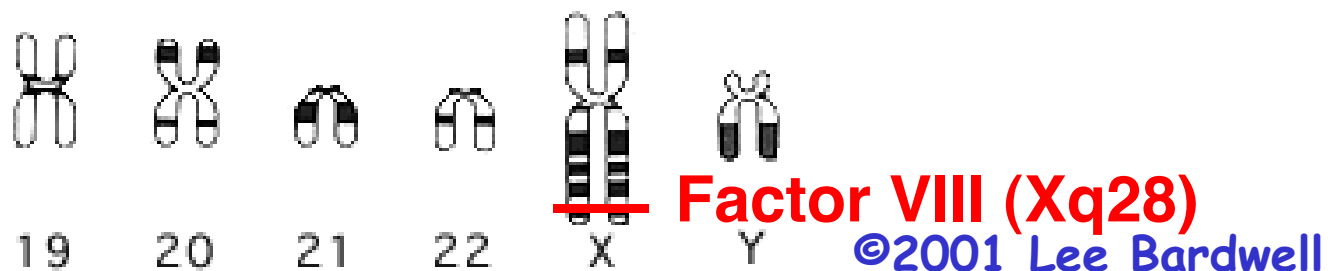
- Non-parental chromosomes (or haplotypes) are result of recombination = crossing-over = physical exchange of segments between homologous chrms
- Occurs ~ 1-3 times/chr, on average
- Occurs during synapsis of meiotic prophase I
- chiasma = cross-shaped configuration caused by breakage and rejoining of chromatids
- Catalyzed by enzymes (= proteins = "the recombination machinery")
- Greatly increases the number of possible genotypes in progeny
- Enables genetic mapping

Bio 97 2004 Lecture 5b

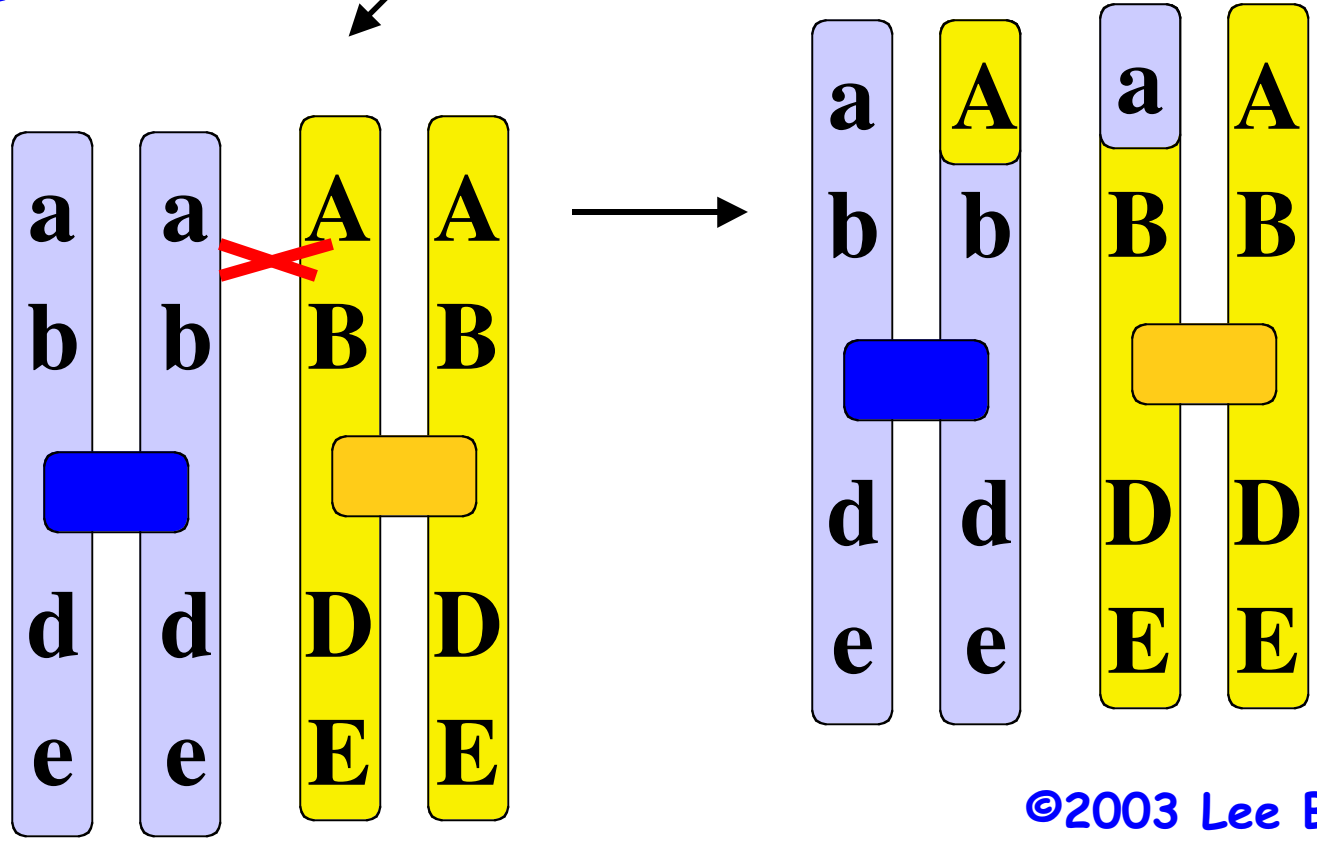
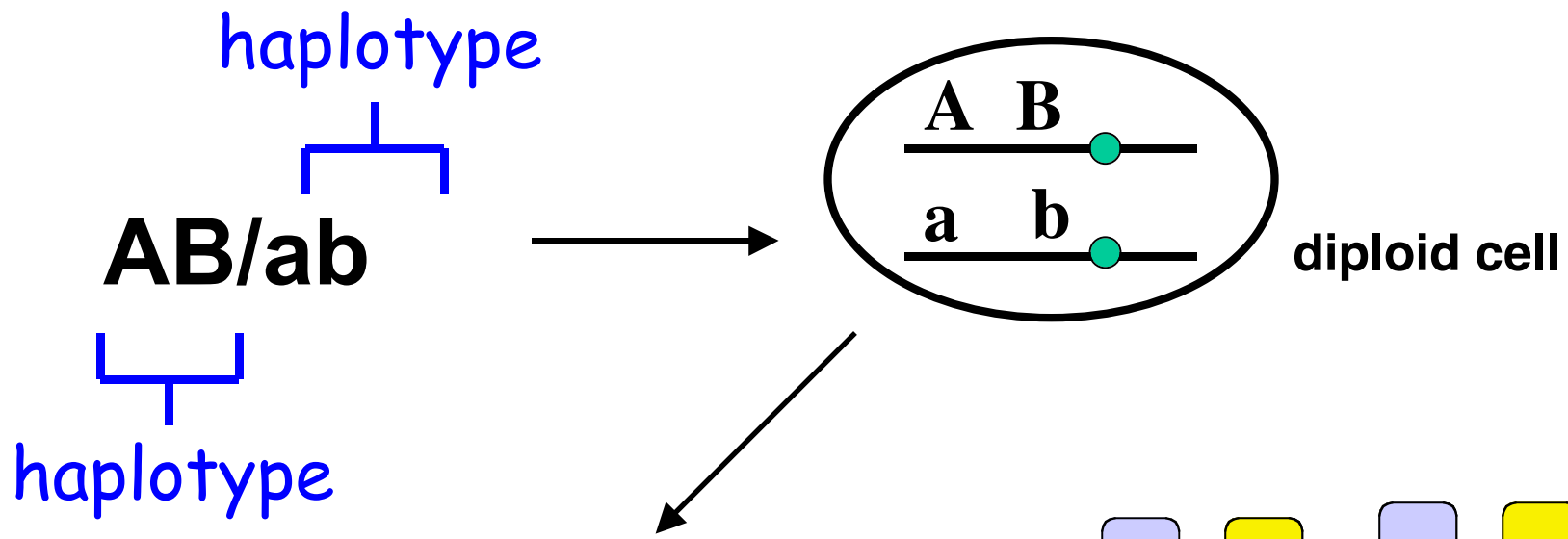
Gene Mapping



Each gene occurs at a specific site, or locus, on a chromosome.

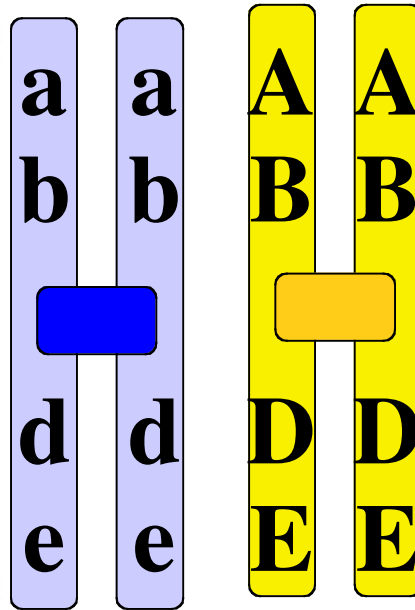


The probability of crossing over between two genes (or loci) is roughly proportional to their distance apart on the chromosome.

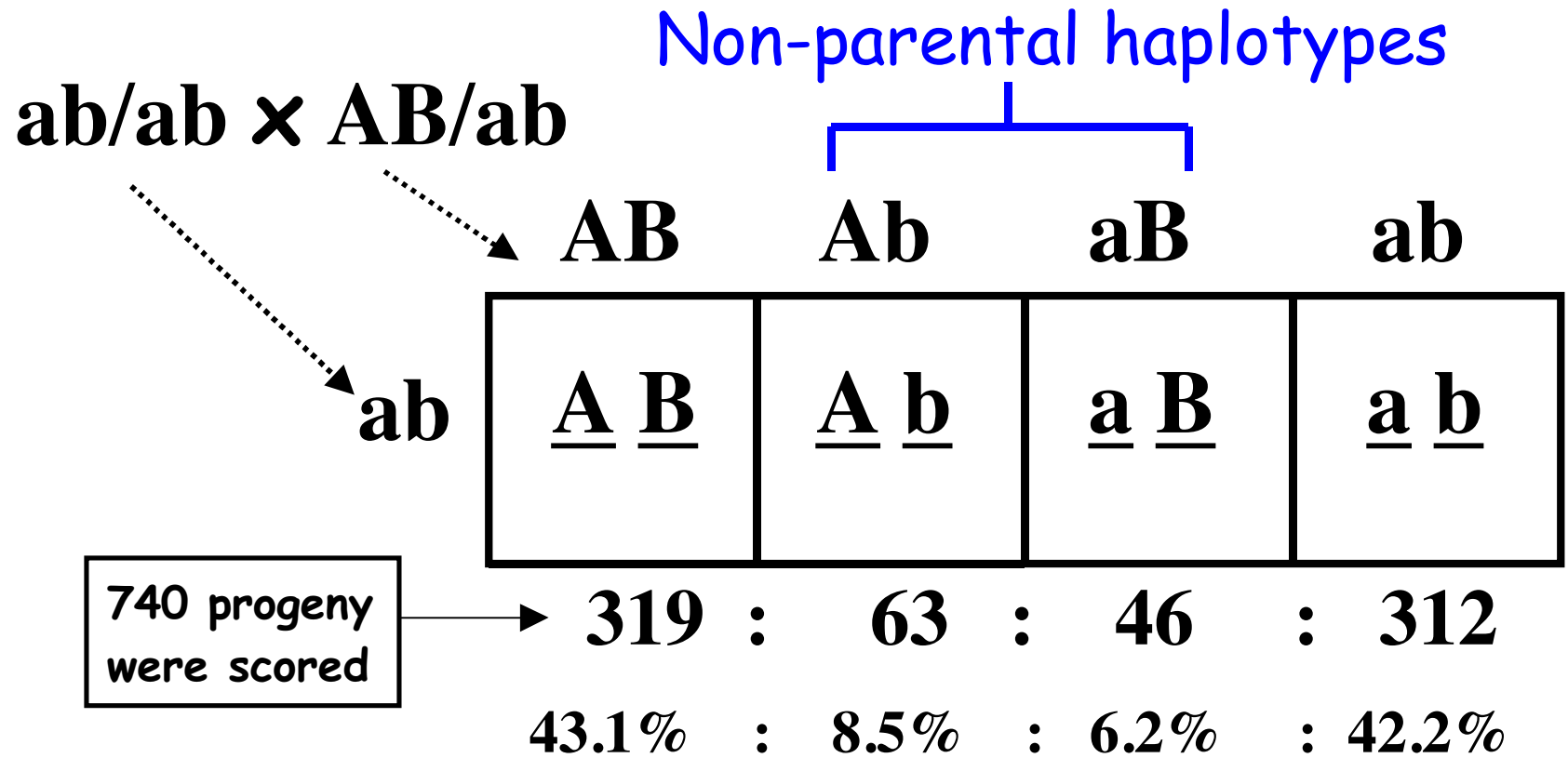


(b)

To separate *a* and *b*,
crossover must occur
in this narrow stretch



To separate *a* and *e*,
crossover can occur
anywhere in this
stretch



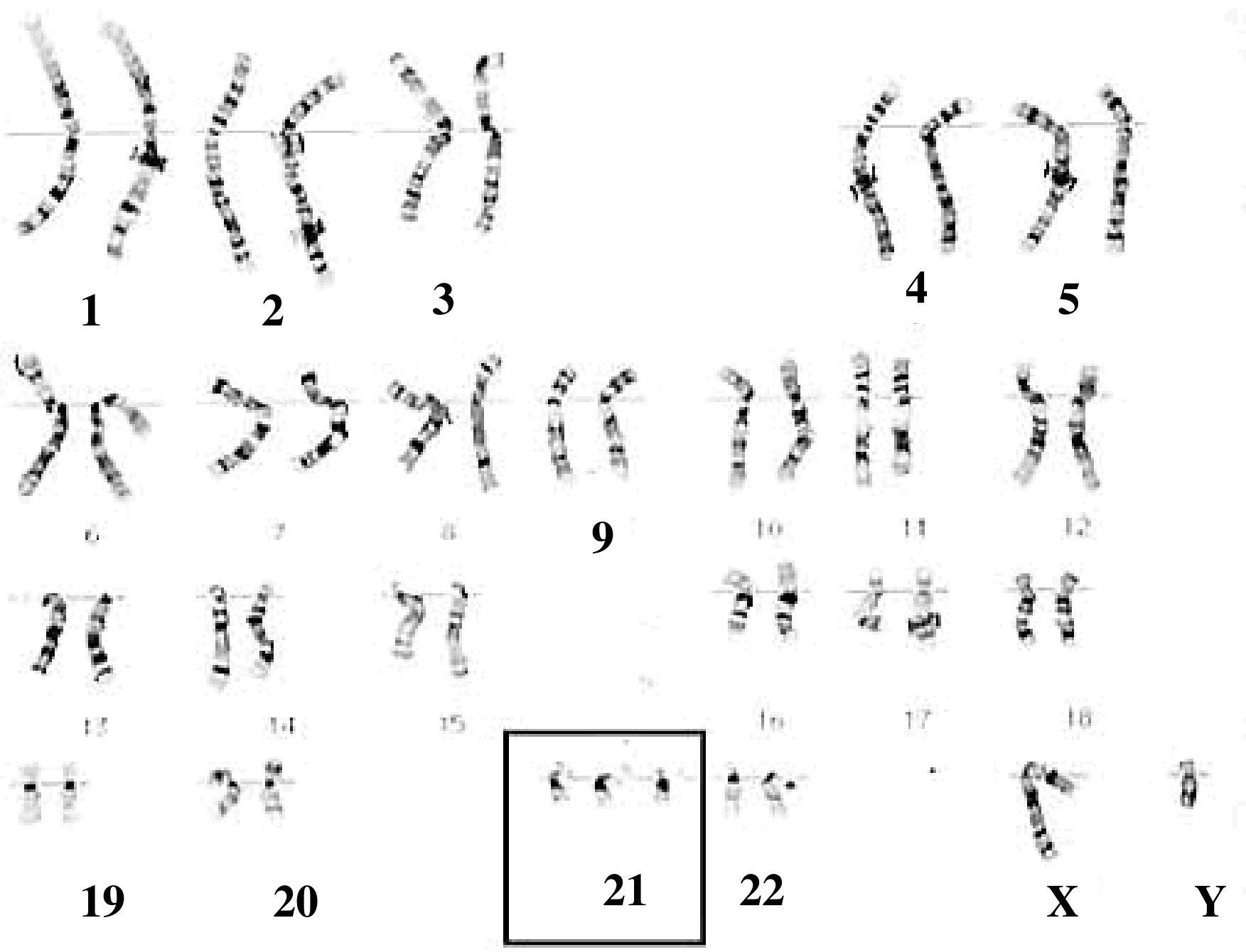
14.7% recombination

1% recombination
=
1 centiMorgan (cM)
=
1 map unit
~
1 million base pairs

Definition of linkage

**Linked genes
exhibit less than 50%
recombination
(that is, they are less
than 50 cM apart)**

(Human Chrm 9 is ~ 200 cM)



1

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

X

Y

ab/ab × AB/ab:	39% AB	11% Ab	11% aB	39% ab
ad/ad × AD/ad:	42% AD	8% Ad	8% aD	42% ad
bd/bd × BD/bd:	41% BD	4% Bd	4% bD	41% bd

Ar 22 cM **Be**

Ar 16 cM **Du**

Be 8 cM **Du**

Map: which gene is in the middle?

Be ——— Ar — Du = Du — Ar ——— Be

Be ——— Du — Ar = Ar — Du ——— Be

Ar ——— Be — Du = Du — Be ——— Ar

Ar 22 cM Be

Ar 16 cM Du

Be 8 cM Du

Alfred H. Sturtevant

“The linear arrangement of
sex-linked factors in
Drosophila, as shown by
their mode of association”

J. Exp. Zool., 1913

Work done while he was an undergraduate
In T.H. Morgan's lab

$$\text{Be} \xrightarrow{8 \text{ cM}} \text{Du} \xrightarrow{16 \text{ cM}} \text{Ar}$$

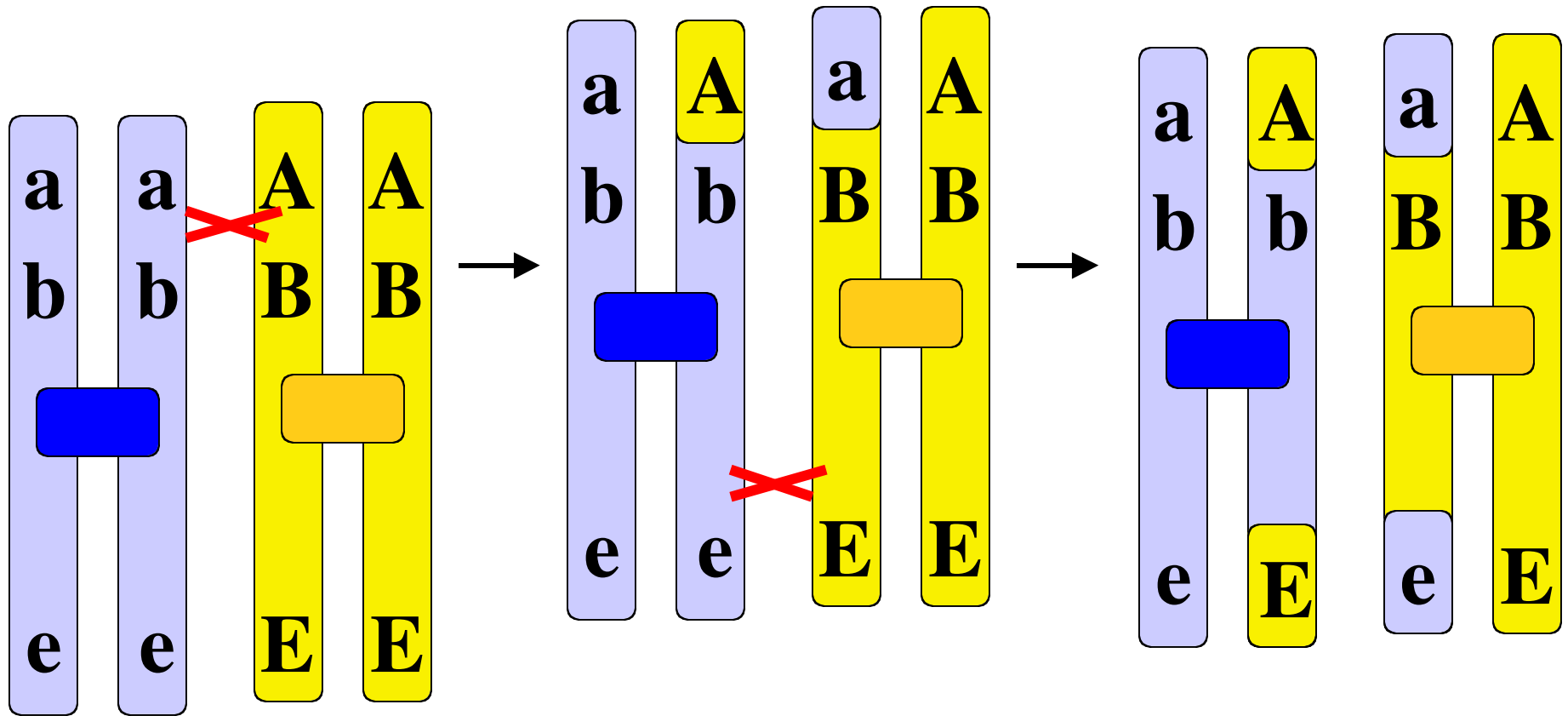
=

$$\text{Ar} \xrightarrow{16 \text{ cM}} \text{Du} \xrightarrow{8 \text{ cM}} \text{Be}$$

$$\text{Be} \xrightarrow{22 \text{ cM}} \text{Ar} \quad ?$$

Why don't the numbers add up?

Double-crossovers cause an under-estimation of the distance between two loci.



0 crossover result: 2 ae gametes, 2 AE gametes

2 crossover result: 2 ae gametes, 2 AE gametes