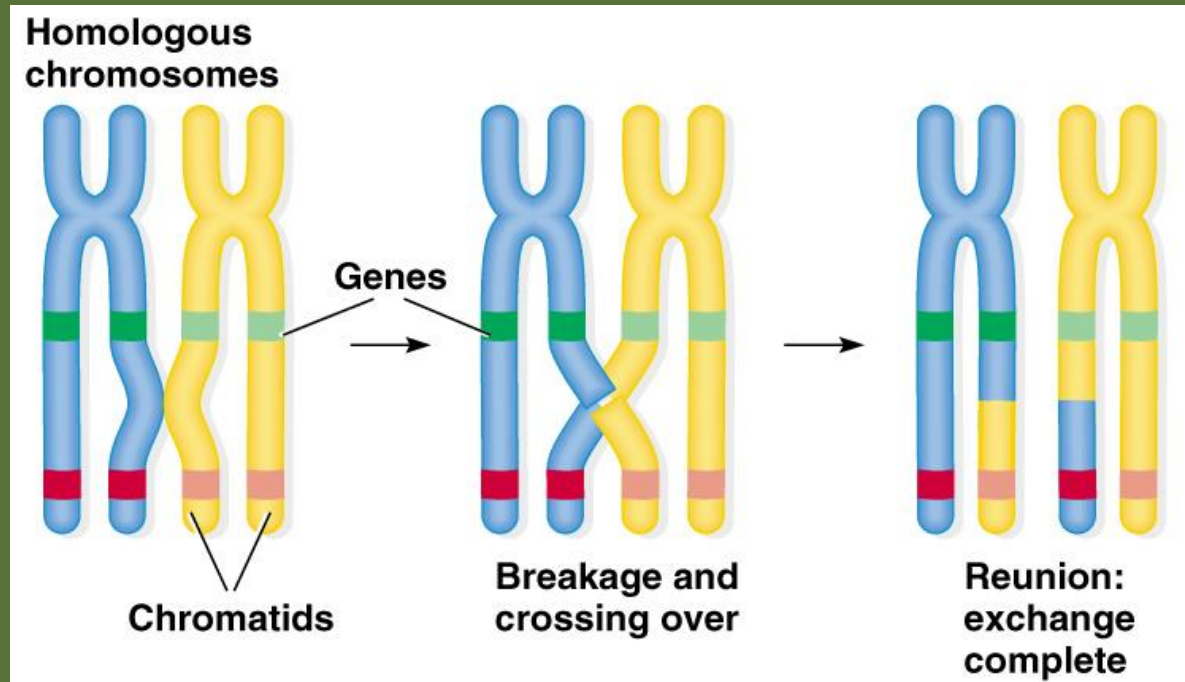


Linkage & Crossing over



Linkage

- Hereditary units or genes which determine the characters of an individual are carried in the chromosomes and an individual usually has many genes for the determination of various different characters.
- As there are more genes than the chromosomes, it can be expected that each chromosome contain more than one gene

- The genes for different characters may be either situated in the same chromosome or in different chromosomes.

When the genes are situated in different chromosomes,

1. The characters they control appear in the next generation either together or apart, depending on the chance alone.
2. They assort independently according to the Mendel's law of independent assortment.

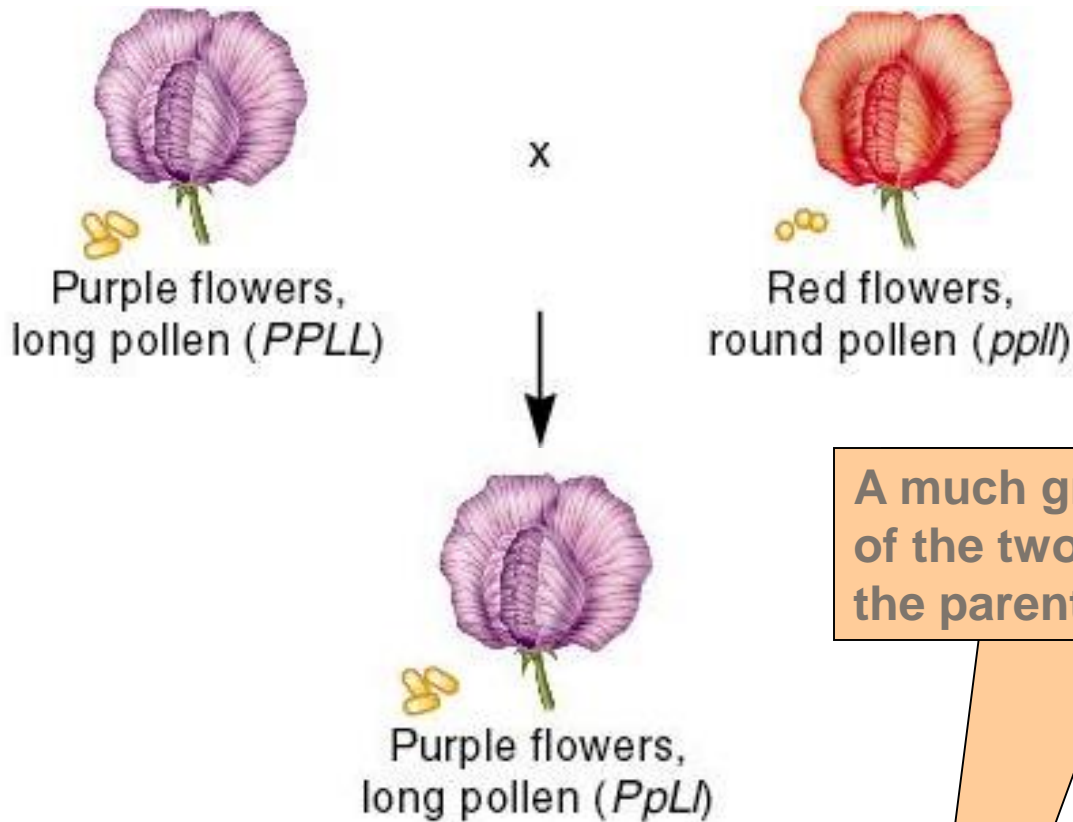
But if the genes are situated in the same chromosome and fairly close to each other,

- They tend to be inherited together

This type of coexistence of two or more genes in the same chromosome is known as **linkage**

Bateson and Punnett Discovered Two Traits That Did Not Assort Independently

- In 1905, William Bateson and Reginald Punnett conducted a cross in sweet pea involving two different traits
 - Flower color and pollen shape
- This is a dihybrid cross that is expected to yield a 9:3:3:1 phenotypic ratio in the F_2 generation
 - However, Bateson and Punnett obtained surprising results



A much greater proportion of the two types found in the parental generation

F_2 offspring	Observed number	Ratio	Expected number	Ratio
Purple ,Long	296	7	240	9
Purple, Round	19	1	80	3
Red, long	27	1	80	3
Red, Round	85	7	27	1

- They suggested that the transmission of the two traits from the parents was somehow coupled
 - The two traits are not easily assorted in an independent manner
- However, they did not realize that the coupling is due to the linkage of the two genes on the same chromosome

Morgan Provided Evidence for the Linkage of Genes

- The first direct evidence of linkage came from studies of Thomas Hunt Morgan
- Morgan investigated several traits that followed an pattern of inheritance
- An experiment involving following traits
 - Body color
 - Wing length
 - Eye color



Linked genes sorted on
chromosomes

Thomas H. Morgan

Morgan experimental results from *Drosophila* in 1919.

P1: Gray, Vestigial x Black, long
 b^+vg/b^+vg bvg^+/bvg^+

Gametes: b^+vg bvg^+



F1: All gray, long (b^+vg/bvg^+)

Test cross : Male:gray long x Female:Black,Vestigial
 b^+vg/bvg^+ bvg/bvg

Gametes:



Test cross ratio,

• Gray, Vestigial

$b^{+}vg/bvg$

1

:

Black, Long

bvg^{+}/bvg

1

Only two type of progenies are possible .
However four types of phenotypes were
obtained.

Morgan experimental results from *Drosophila* in 1919.

P1: Gray, Vestigial x Black, long

b^+vg/b^+vg

bvg^+/bvg^+

Gametes:

b^+vg

bvg^+



F1: All gray, long (b^+vg/bvg^+)

Test cross : Female:gray long Male:Black,Vestigial

b^+vg/bvg^+

bvg/bvg

Gametes:

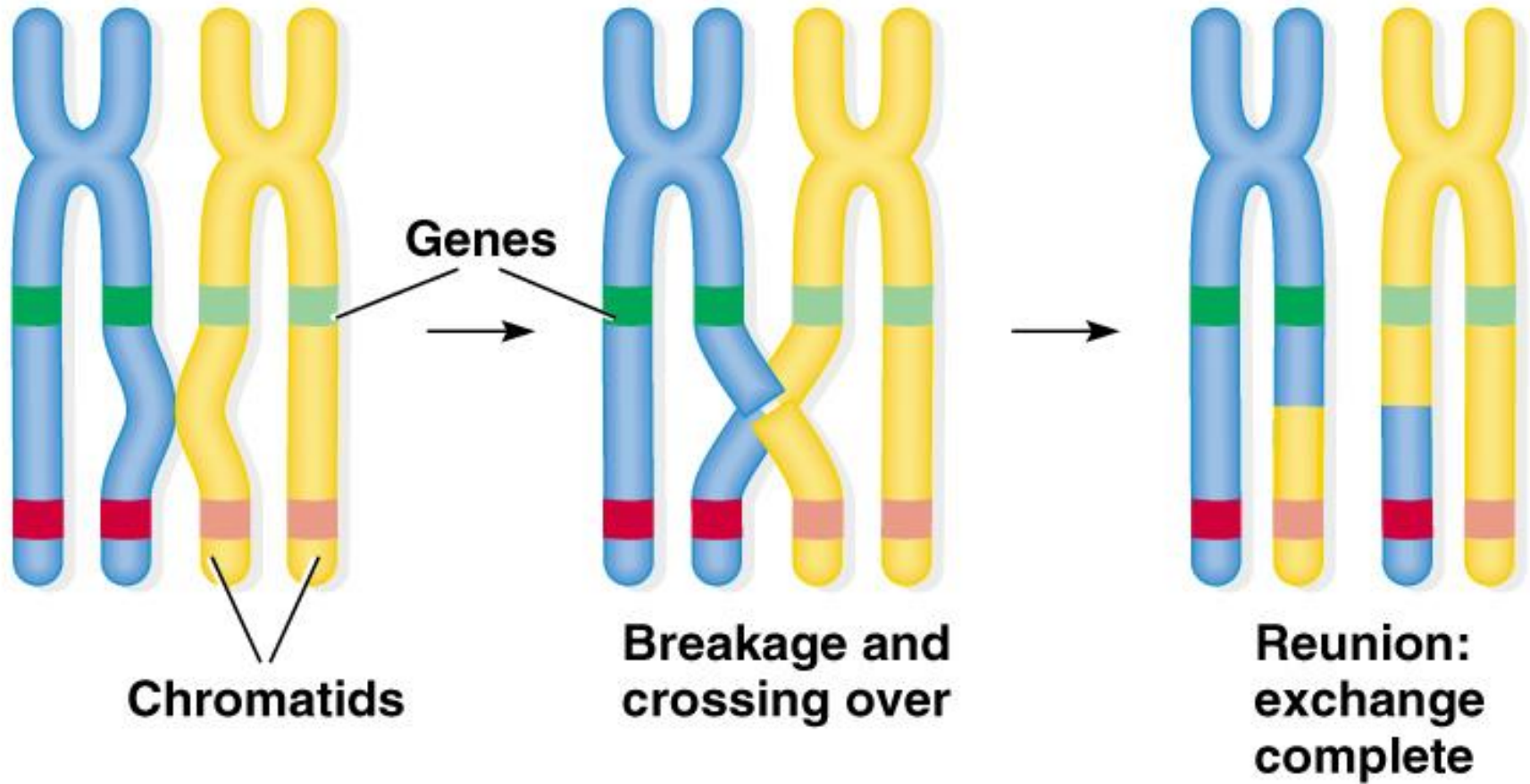
b^+vg

bvg^+

bvg

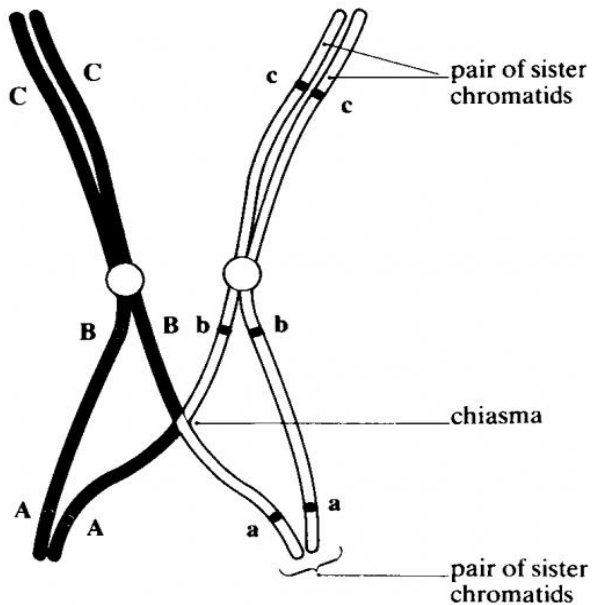
Mechanism of crossing-over gives rise to recombinant (non-parental) genotypes and phenotypes for linked genes.

Homologous chromosomes

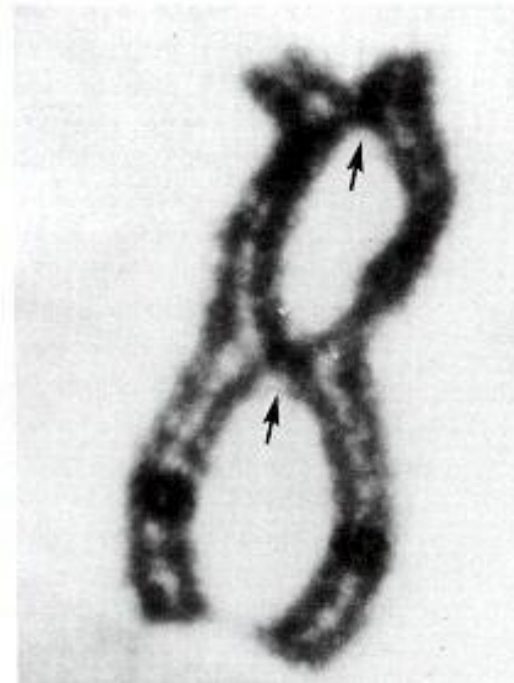


Some basics terminology about crossing-over:

1. Chiasma (pl. chiasmata) is the site where crossing-over occurs.
2. Crossing-over is a reciprocal exchange of DNA, involving breaking and rejoining of homologous chromatids.
3. Crossing-over leads to recombination between linked genes and produces novel genetic variation.



(c) *crossing over during prophase 1*



b^+vg

bvg^+

Non cross
over

b^+vg^+

bvg

Recombinants

Test cross ratio

Gray, vestigial	41.5%
Black, long	41.5%
Gray, long	8.5%
Black, vestigial	8.5%

**But this
nonparent
combination
was rare**

Parents

Coloured & full ×

Colourless & shrunken

CS/CS

cs/cs

Gametes

CS

×

CS

↓

F₁

CS/cs

Coloured & full

Test Cross

Cs/cs

X

cs/cs

Gametes

cs

Result:

CS

CS/cs

– Coloured & full 48.2%

Cs

Cs/cs

– Coloured & shrunken 1.8%

cS

cS/cs

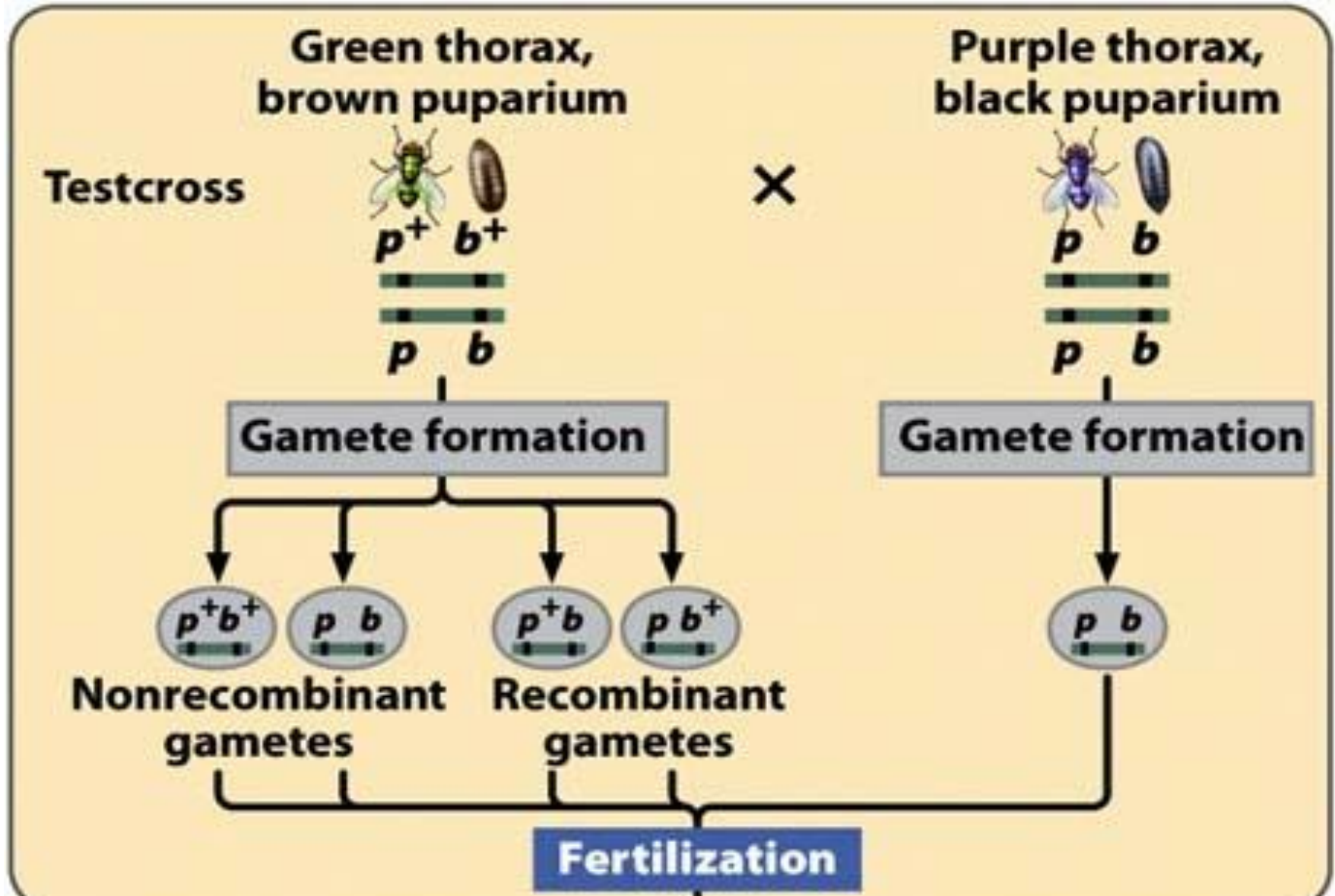
– Colourless & full 1.8%

cs

cs/cs

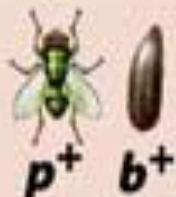
– Colourless & shrunken 48.2%

Using test crosses to analyze crossing over



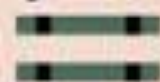
Fertilization

Green thorax, brown puparium



p b

Purple thorax, black puparium



p b

Green thorax, black puparium



p b

Purple thorax, brown puparium



p b

Progeny number

40

40

Nonrecombinant progeny

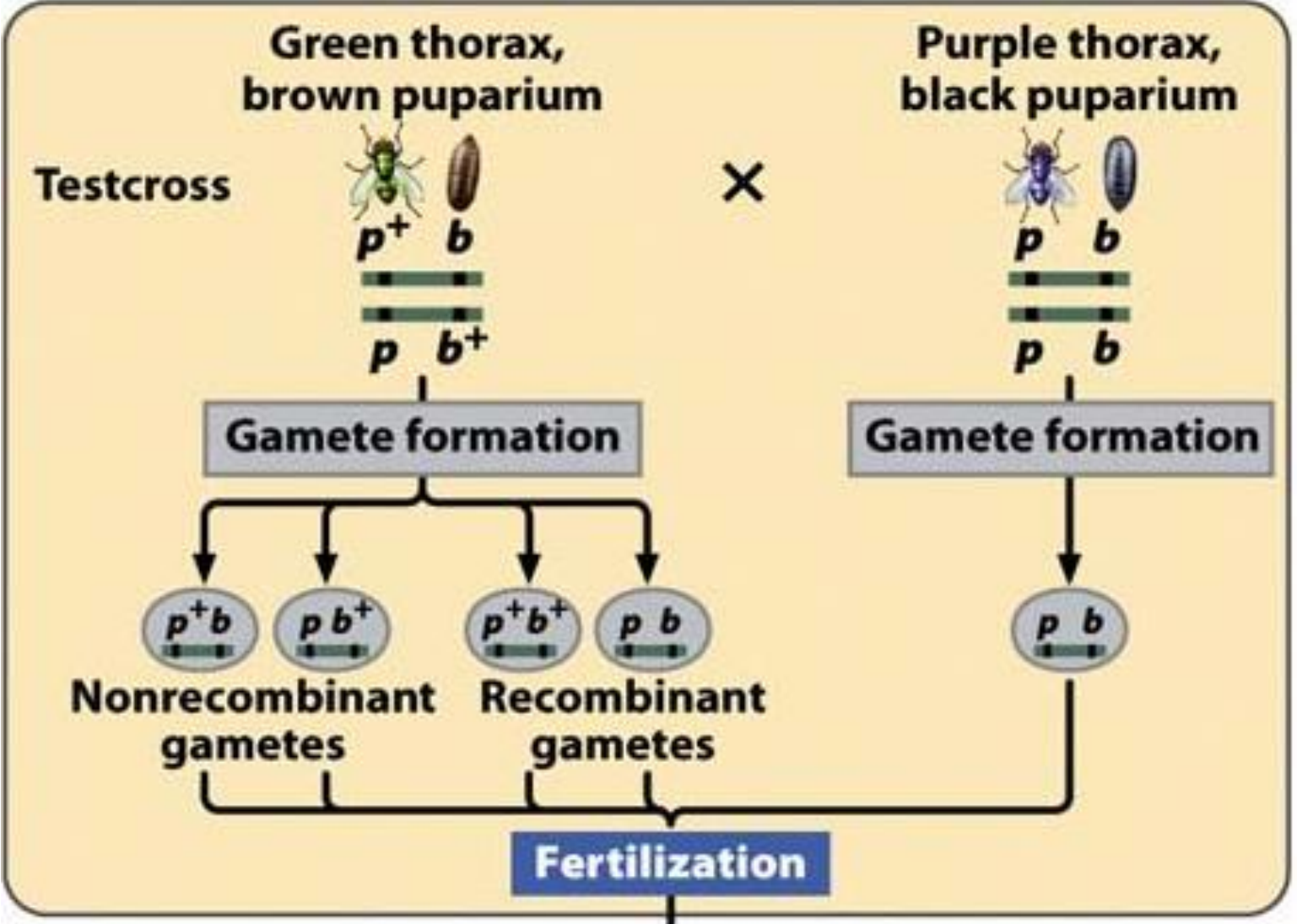
10

10

Recombinant progeny

Coupling

- Coupling (cis arrangement) refers to the condition of having both dominant alleles on the one homologue and both recessive alleles on the other homologue.



**Green
thorax,
black
puparium**



p^+ b



p b

**Purple
thorax,
brown
puparium**



p b^+



p b

**Green
thorax,
brown
puparium**



p^+ b^+



p b

**Purple
thorax,
black
puparium**



p b



p b

**Progeny
number**

40

40

**Nonrecombinant
progeny**

10

10

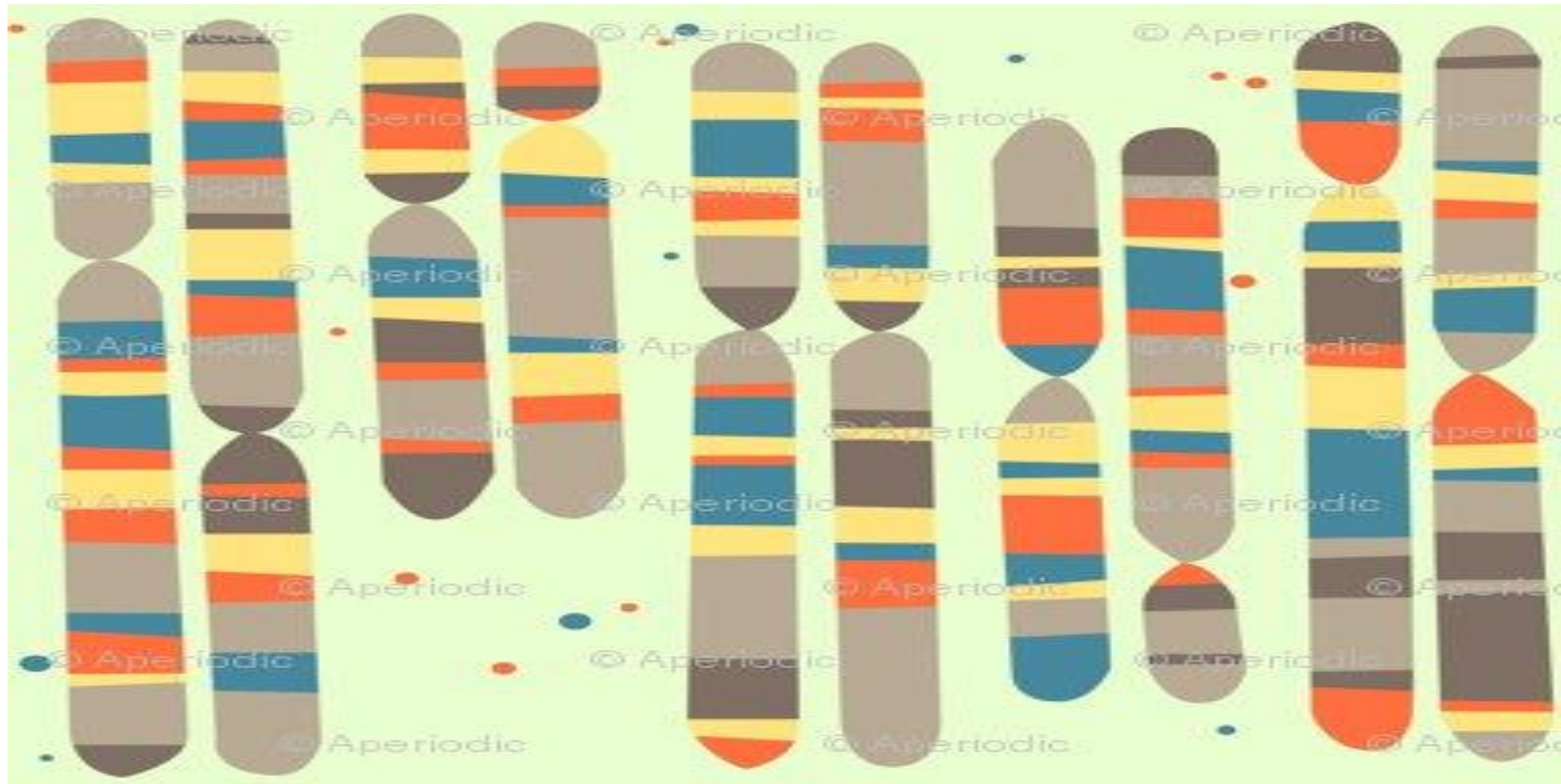
**Recombinant
progeny**

Repulsion

Repulsion ('trans' arrangement) refers to the condition of having one dominant and one recessive allele on the each homologue.

The arrangement (coupling or repulsion) determines the relative numbers of different phenotypes in the offspring.

Gene Mapping



- Technique originated by Alfred Sturtevant, one of Morgan's students.
- Assumes that frequency of crossing over (called recombination rate) is a function of distance between genes.
- The farther apart the loci are, the more often crossing over *between* them happens.
- The map distance between two genes then is calculated from the frequency of crossing over.

Two-point cross

- 2-point cross is a dihybrid test cross designed to determine the map distance between two linked genes.

Procedure

- Set up a test cross with a double heterozygous parent and a homozygous recessive parent. Done this way, recombination (crossing over) is only detected in the heterozygous parent.
- Determine which gametes from the heterozygous parent are recombinant (resulted from crossing over).
- Calculate the recombination rate (r)
- Calculate the map distance ($r \times 100\%$)

Green
thorax,
black
puparium



p^+ b



p b

Purple
thorax,
brown
puparium



p b^+

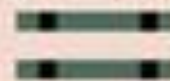


p b

Green
thorax,
brown
puparium



p^+ b^+



p b

Purple
thorax,
black
puparium



p b



p b

Progeny
number

40

40

Nonrecombinant
progeny

10

10

Recombinant
progeny

- $r = (10 + 10) / 100 = 0.2$
- $(0.2)(100) = 20$ map units
- So the loci b and p are 20 map units (mu) apart.

- **Example: suppose there are three genes a, b, and c.**

2-point crosses determine that the map units between genes are:

a - b distance = 20 map units

a - c distance = 8 map units

b - c distance = 12 map units

Three point cross

- Building a 3 gene map can also be done with a single test cross (3-point cross)
- This is a test cross between a heterozygous trihybrid and completely homozygous recessive parent.

wild type

$\frac{b^+ \quad c^+ \quad pr^+}{b^+ \quad c^+ \quad pr^+}$

black, curved, purple

$\frac{b \quad c \quad pr}{b \quad c \quad pr}$

X



F₁ (wild type)

$\frac{b^+ \quad c^+ \quad pr^+}{b \quad c \quad pr}$

black, curved, purple

$\frac{b \quad c \quad pr}{b \quad c \quad pr}$

X

Test
Cross

Phenotype	Gametes of F ₁	Number of offspring
wild type	b ⁺ c ⁺ pr ⁺	5701
black	b c ⁺ pr ⁺	367
curved	b ⁺ c pr ⁺	1412
purple	b ⁺ c ⁺ pr	60
black, curved	b c pr ⁺	72
black, purple	b c ⁺ pr	1383
curved, purple	b ⁺ c pr	388
black, curved, purple	b c pr	5617

1. Rearrange data , so that reciprocal gametes are paired up.
2. The 4 pairs of gametes represent different behaviors of bivalents during meiosis
 - **Non-recombinant - no crossing over occurred**
 - **Single crossover I - One crossover occurred between middle gene and one end.**
 - **Single crossover II - One crossover occurred between middle gene and the other end.**
 - **Double crossover - Two crossovers occurred on the same chromatid at the same time.**
3. Calculate the frequency of each crossover type
4. Determine the order of genes on the chromosome
5. Determine map distances of the two intervals
6. Calculate the map units for the two intervals
7. Diagram the genetic map

Procedure

1. In calculating map distances on the chromosome is to see from the observed data, the parental combinations. This can be obtained by looking at the largest numbers among the test cross progeny. then the lowest number has to be looked into, these are double cross overs.
2. Second step is to find out the gene sequence. This can be done, by taking the parental combinations and by drawing two chromosomes with the given sequence with the given sequence in the problem then make a expected double cross over and compare with double cross over given in the problem. If it similar- expected gene sequence is correct. If not rearrange the genus on the parental combinations

3. The third step is to obtain crossing over at region I. this is done by putting one single cross over b/w the region I in the diagram with parental combinations.
4. The fourth step is to obtain crossing over at region II. this is done by putting one single cross over b/w the region II in the diagram with parental combinations.

Gametes	Number	Frequency	Type
b ⁺ c ⁺ pr ⁺	5701	0.755	Non-recombinant
b c pr	5617		
b ⁺ c pr ⁺	1412	0.186	Single crossover [Yellow box]
b c ⁺ pr	1383		
b ⁺ c pr	388	0.05	Single crossover [Yellow box]
b c ⁺ pr ⁺	367		
b ⁺ c ⁺ pr	60	0.009	Double crossover
b c pr ⁺	72		
Total	15000		

Interference and coincidence

- Independent crossing over assumes that when two events are independent, the probability of their simultaneous occurrence is the product of their separate probabilities.
- **In above example; expected DCO is,
 $18.6 \times 5 = 0.93$**

But in actual DCO is 0.009. It seems that the occurrence of crossing over at one point in the chromosome decreases the probability of its occurrence elsewhere in the same chromosome it known as Interference.

- An inverse measure of interference is called Coincidence.
- It is defined as the ratio of observed double cross overs to the expected DCO.

$$\text{Coefficient of coincidence} = \frac{\text{Observed DCO}}{\text{Expected DCO}}$$

Example 02- Bridges crossed crossveinless(cv) to echinus(ec) and cut wing (ct)

Genotypes	Number
Cross veinless	2207
Echinus, cut	2125
Echinus, crossveinless	273
cut	265
echinus	217
Crossveinless, cut	223
Wild type	5
Echinus,crossvein less,cut	3
	5318