Cell Biology, Genetics and Evolution

Construction of Linkage Maps and Detection of Linkage

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Construction of Linkage Maps and Detection of Linkage

- ❖Linkage maps, also known as genetic maps, provide a visual representation of the relative positions of genes on a chromosome based on their recombination frequencies.
- ❖These maps are constructed through the study of gene linkage, which involves determining how frequently two genes are inherited together.
- ❖Linkage detection involves identifying whether two or more genes are linked on the same chromosome or not and then calculating the degree of linkage based on recombination data.

1. Detection of Linkage

- **A. Concept of Linkage Detection**
- Gene linkage is detected when two genes tend to be inherited together more frequently than would be expected by random chance.
- This violates Mendel's Law of Independent Assortment.
- Genes on different chromosomes or far apart on the same chromosome assort independently.
- If two genes are physically close on the same chromosome, they do not assort independently and are often inherited together.

1. Detection of Linkage

- **B. Steps in Detecting Gene Linkage**
- **1. Perform a Test Cross:**
- A common way to detect gene linkage is by performing a test cross or dihybrid cross, typically between an individual heterozygous for two genes and an individual that is homozygous recessive for both genes. The offspring of this cross are then analyzed to determine the inheritance patterns of the two genes.
- **Example:** If the parent is heterozygous for genes A and B (genotype AaBb) and the other parent is homozygous recessive (aabb), the expected ratios of offspring phenotypes can reveal if the genes are linked.

1. Detection of Linkage

- **2. Examine Offspring Phenotypes:**
- If the genes are not linked, we expect offspring to show a 1:1:1:1 ratio for four different phenotypic combinations (i.e., equal proportions of parental and recombinant phenotypes).
- If the genes are linked, the parental phenotypes will be more common, while the recombinant phenotypes will be less frequent.

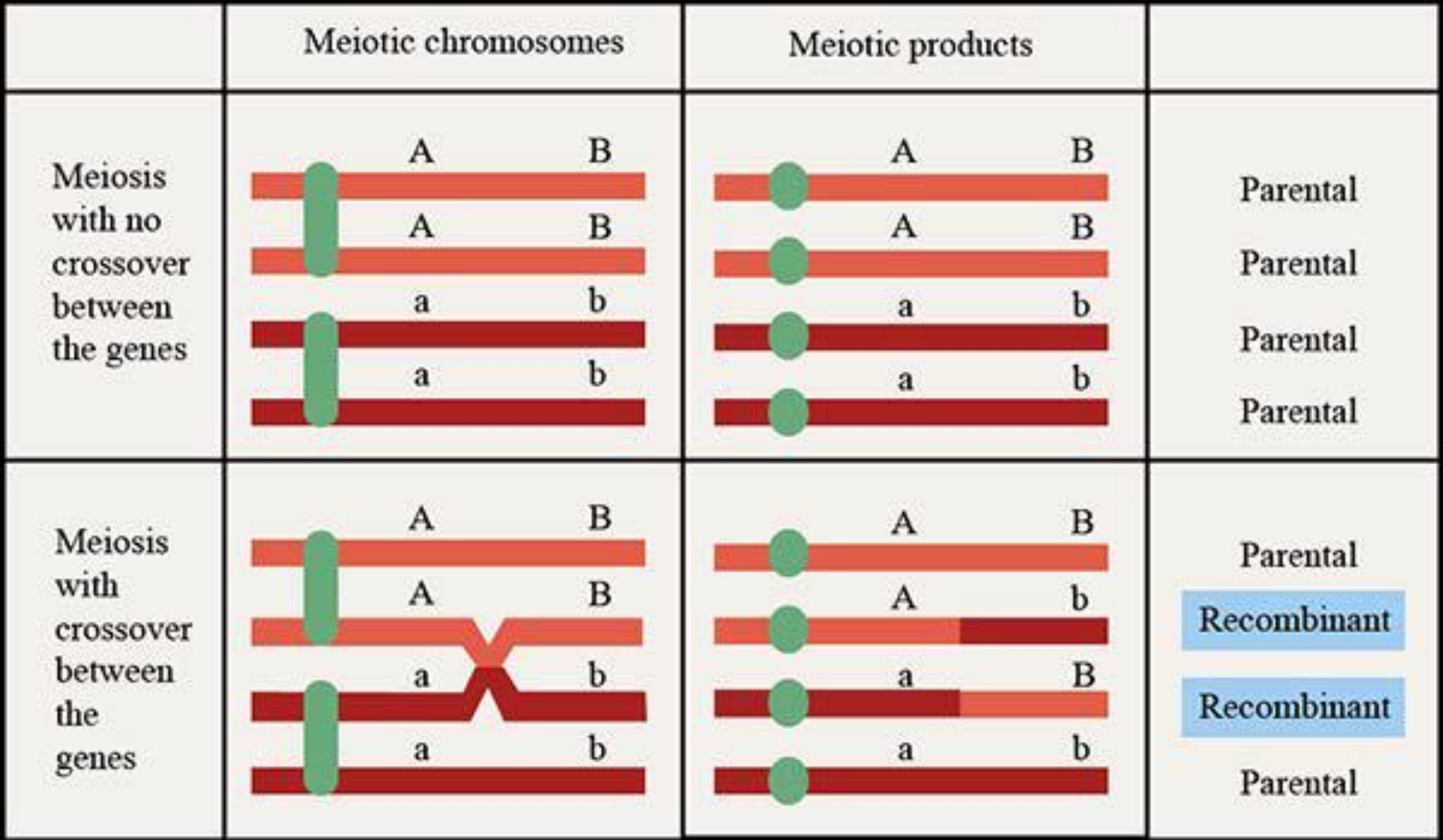
1. Detection of Linkage

❖ 3. Calculate Recombination Frequency:

❖ Recombination frequency (RF) is calculated by dividing the number of recombinant offspring by the total number of offspring and multiplying by 100 to get a percentage.

$$\text{Recombination Frequency (RF)} = \frac{\text{Number of Recombinant Offspring}}{\text{Total Offspring}} \times 100$$

❖ A recombination frequency of 0% indicates complete linkage (no crossing over), while 50% or more suggests independent assortment (genes are either far apart on the same chromosome or on different chromosomes).


Meiotic chromosomes
Meiotic products
Meiosis with no crossover between the genes
A B
A B
a b
a b
A B
A B
a b
a b
Parental
Parental
Parental
Parental
Meiosis with crossover between the genes
A B
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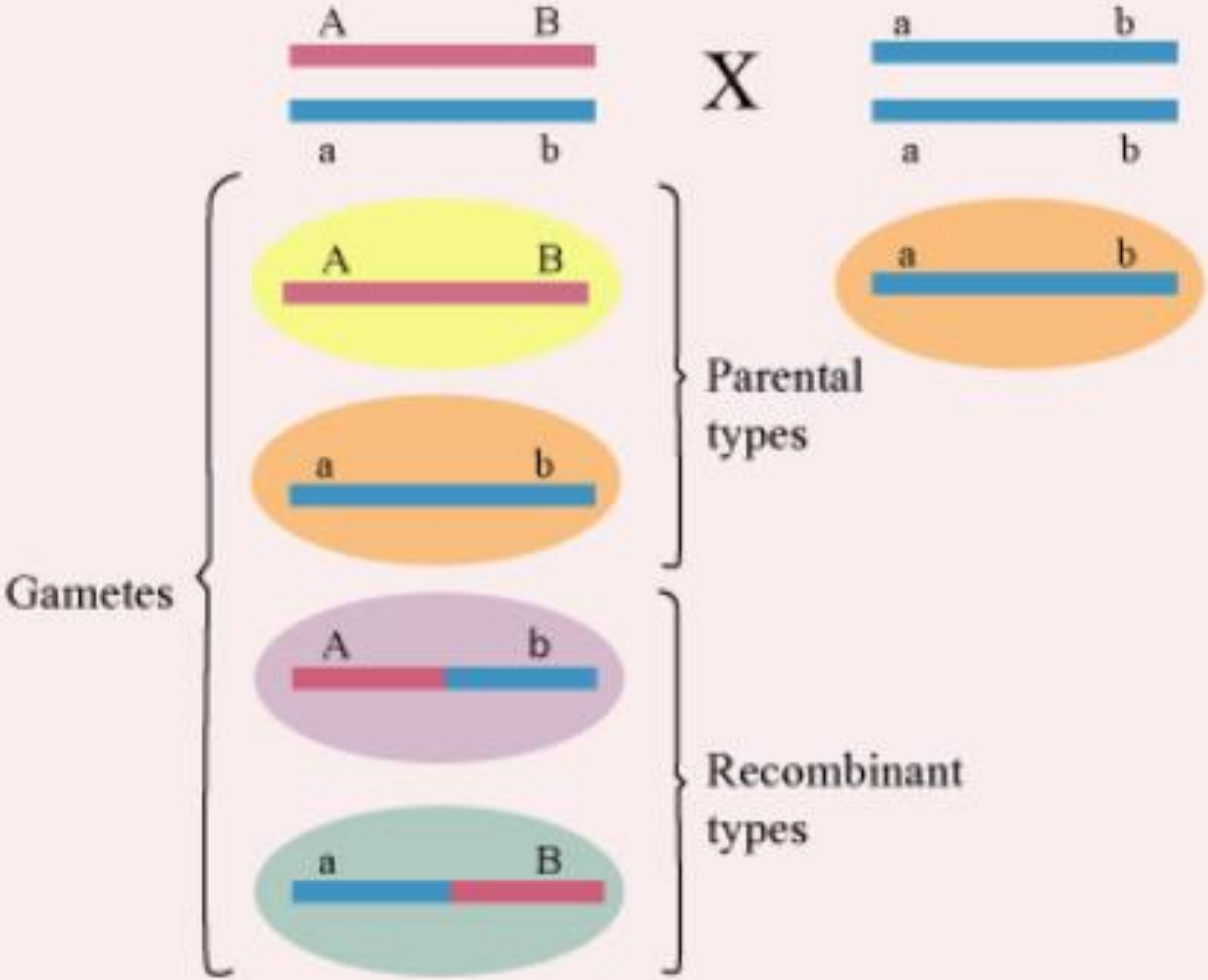
Parental
Recombinant
Recombinant
Parental


A
B
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Parental
types
Gametes
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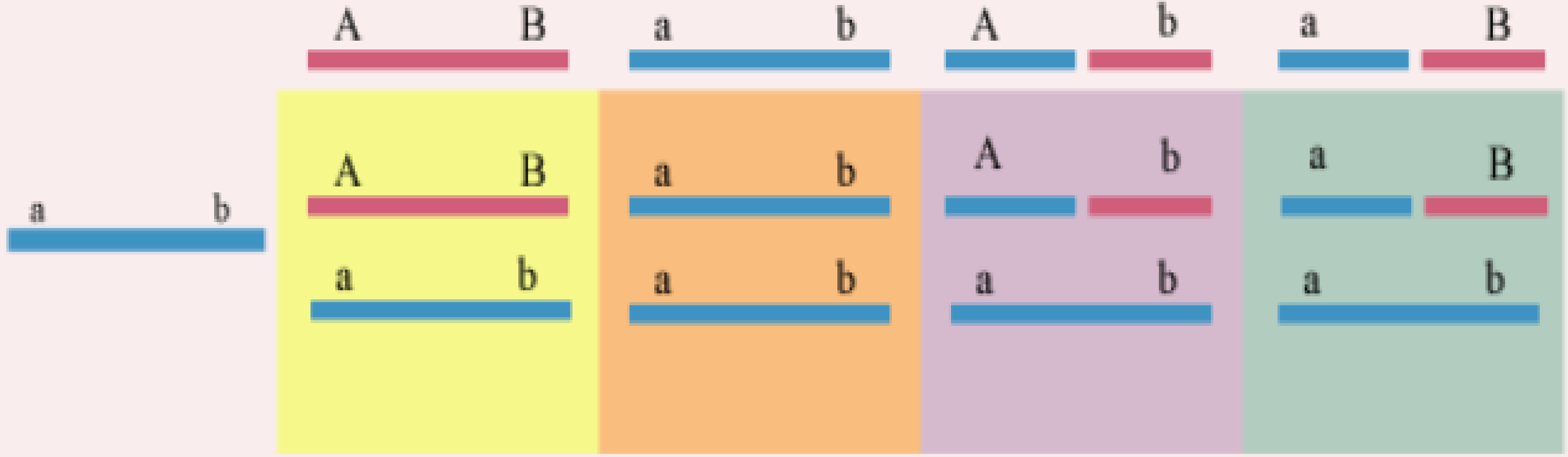
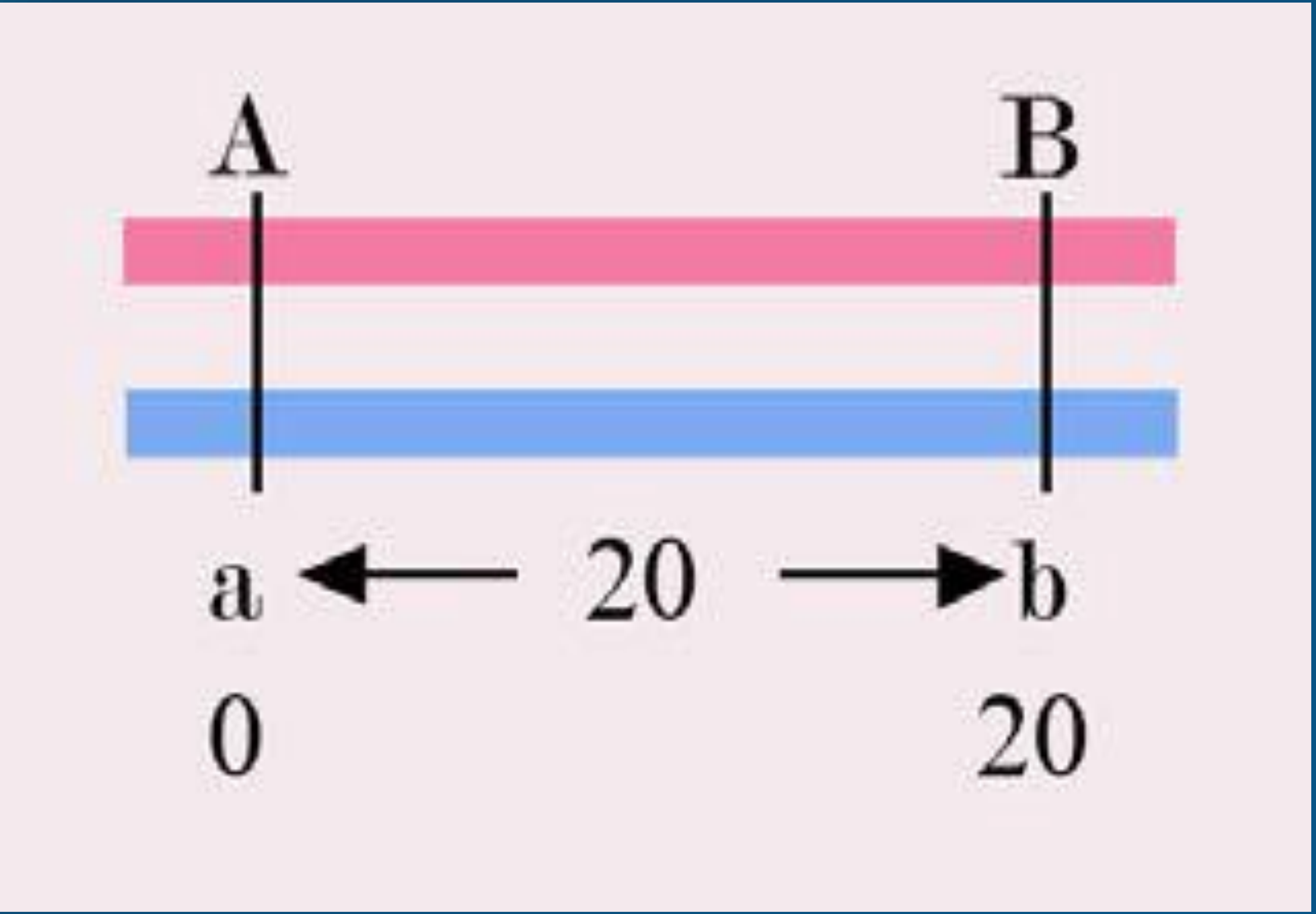
Recombinant
types



Offspring : Parental types (40 + 40 = 80) Recombinant types (10 + 10 = 20)

$$\text{Recombination frequency} = \frac{20}{40 + 40 + 10 + 10} \times 100$$

$$= \frac{20}{100} \times 100 = 20\,\%$$


A
B
a
20
b
0
20

Recombinant Frequency:

- The recombination frequency is directly proportional to the distance between the linked gene loci. Genes can be mapped on a chromosome on the basis of their recombination frequencies.
- If 1% of recombination frequency is equal to 1 unit map distance, the two linked genes A and B with a 20% recombination frequency must be 20 units apart.

1. Detection of Linkage

- **C. Key Indicators of Linkage:**
- **High percentage of parental types:**
- If offspring predominantly exhibit the parental combinations of traits, it indicates that the genes are linked.
- **Low recombination frequency:**
- A recombination frequency significantly below 50% signals that the genes are close to each other on the chromosome, and crossing over between them is infrequent.

2. Construction of Linkage Maps

- Once gene linkage is detected, the next step is constructing a linkage map. A linkage map places genes in order along a chromosome based on recombination frequencies, which serve as a proxy for physical distances between genes.
- **A. Steps in Linkage Map Construction**
- 1. Collect Data from Crosses:
- 2. Determine Recombination Frequencies:
- 3. Convert Recombination Frequencies into Map Units:
- 4. Construct the Genetic Map:
- 5. Check for Double Crossovers:
- **B. Three-Point Test Crosses**

A. Steps in Linkage Map Construction

- **1. Collect Data from Crosses:**
- Perform crosses (usually test crosses) involving multiple genes. For example, a trihybrid cross (three genes) or dihybrid cross (two genes) can be used to determine the inheritance patterns and recombination frequencies between different gene pairs.

A. Steps in Linkage Map Construction

- **2. Determine Recombination Frequencies:**
- Calculate recombination frequencies for each gene pair. Genes that are farther apart will have higher recombination frequencies, while genes that are closer together will have lower recombination frequencies.
- **Example:** If gene A and gene B have a recombination frequency of 12%, and gene A and gene C have a recombination frequency of 7%, This means that gene C is closer to gene A than gene B is.

A. Steps in Linkage Map Construction

- **3. Convert Recombination Frequencies into Map Units:**
- Recombination frequencies are used to determine the map distance between genes. This distance is measured in centimorgans (cM), where 1 cM corresponds to a 1% recombination frequency.
- **Example:**
- A recombination frequency of 12% between two genes suggests that the genes are 12 centimorgans apart on the linkage map.

A. Steps in Linkage Map Construction

- **4. Construct the Genetic Map:**
- Based on the calculated map distances, the genes are positioned in relation to each other on the chromosome.
- The gene order is determined by analyzing the recombination frequencies of different gene pairs and placing genes that have the lowest recombination frequencies closer together.
- **Example:** If genes A, B, and C have recombination frequencies of 12% (A-B), 7% (A-C), and 5% (B-C), the order would be B-C-A, with C being closest to B.

A. Steps in Linkage Map Construction

- **5. Check for Double Crossovers:**
- In cases involving multiple genes, double crossovers can occur, which might affect recombination frequency calculations. Detecting double crossovers helps refine the linkage map by accurately positioning genes.
- To account for double crossovers, adjust the recombination frequency, especially when mapping three or more genes.

B. Three-Point Test Crosses

- Three-point test crosses are often used to determine the order and distances between three genes simultaneously. This type of cross provides more accurate information about gene order and can help detect double crossovers.
- The process involves calculating recombination frequencies between all pairs of genes and determining the gene order based on the lowest recombination frequency.

Thank You!