Genetics

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Topic 9:

Linkage and Genetic Mapping

Independent assortment

- In Mendel's dihybrid cross, alleles responsible for the two traits assort independently (Law of independent assortment).

- This happens when the two genes are on different chromosomes.

- In this case we have a ratio of 1:1:1:1 for the F1 gametes (for example, 1RY:1Ry:1rY:1ry)

Linkage

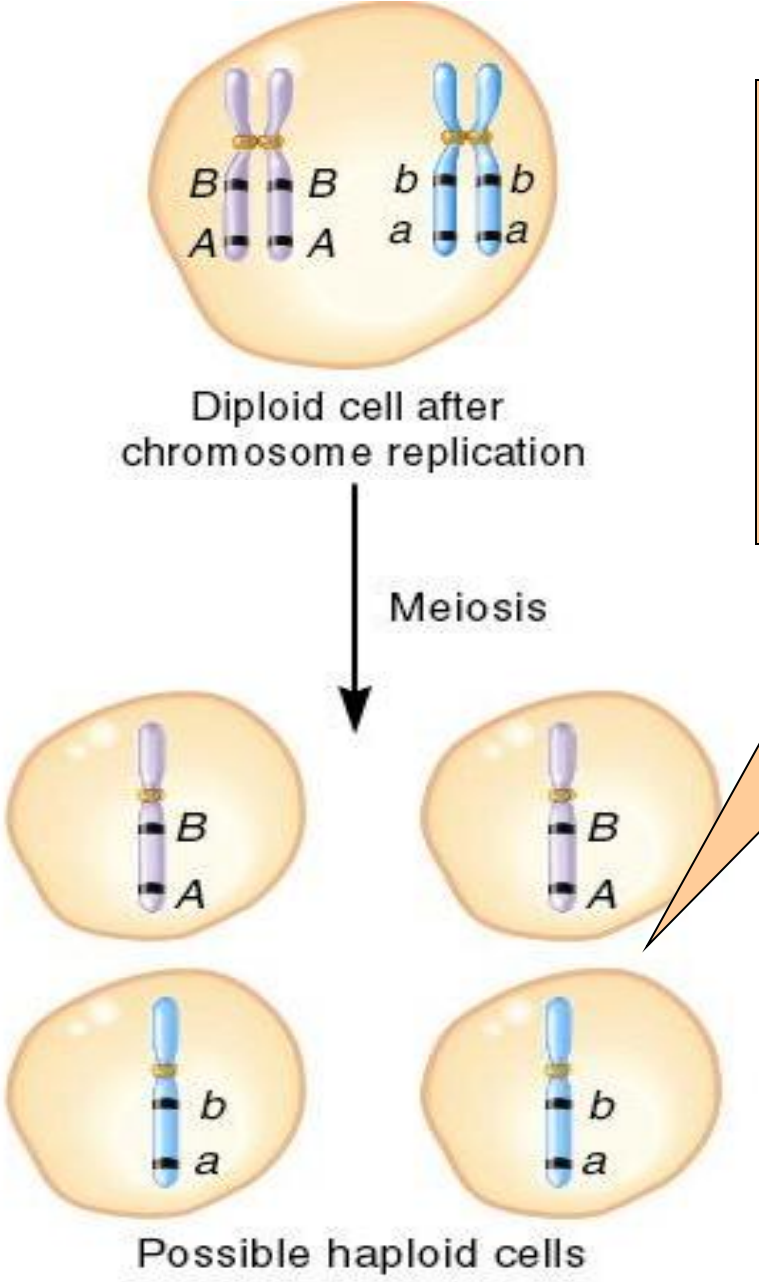
- In eukaryotic species, each linear chromosome contains a long piece of DNA (contains many hundred or even a few thousand different genes)
- Two genes are linked if they occur on the same chromosome (the genes are physically linked to each other).
- Two loci on different chromosomes are not linked, because they are usually separated by independent assortment.
- The term linkage has two related meanings
  1. Two or more genes can be located on the same chromosome
  2. Genes that are close together tend to be transmitted as a unit

- Chromosomes are called linkage groups
  - They contain a group of genes that are linked together

- The number of linkage groups is the number of types of chromosomes of the species
  - For example, in humans
    - 22 autosomal linkage groups
    - An X chromosome linkage group
    - A Y chromosome linkage group
- Genes that are far apart on the same chromosome may independently assort from each other
  - This is due to crossing-over

Crossing Over May Produce Recombinant Phenotypes

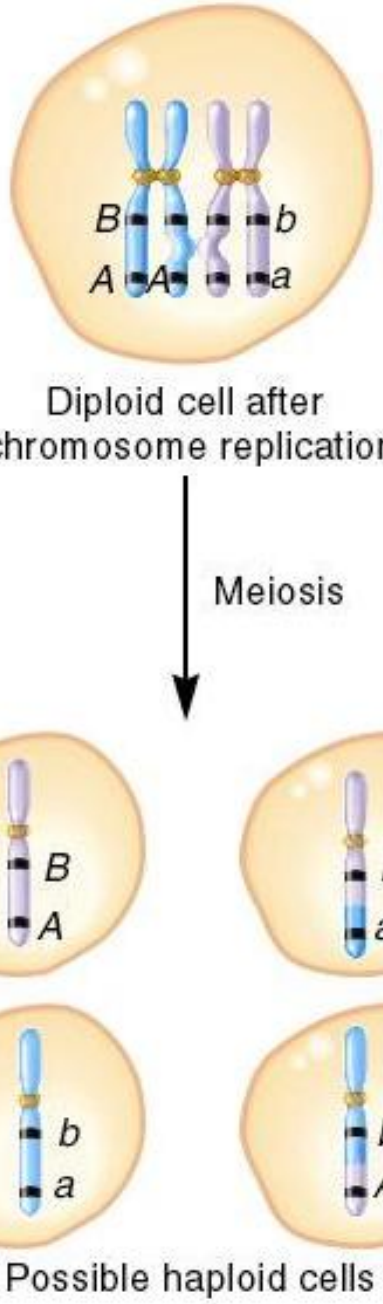
- In diploid eukaryotic species, linkage can be altered during meiosis as a result of crossing over
- Crossing over
  - Occurs during prophase I of meiosis at the bivalent stage
  - Non-sister chromatids of homologous chromosomes exchange DNA segments



The haploid cells contain the same combination of alleles as the original chromosomes

The arrangement of linked alleles has not been altered

ı) Without crossing over, linked alleles segregate together.



These are termed **parental** or **non-recombinant** gametes

These haploid cells contain a combination of alleles NOT found in the original chromosomes

This new combination of alleles is a result of **genetic recombination**

These are termed **nonparental** or **recombinant gametes**

(b) Crossing over can reassort linked alleles.

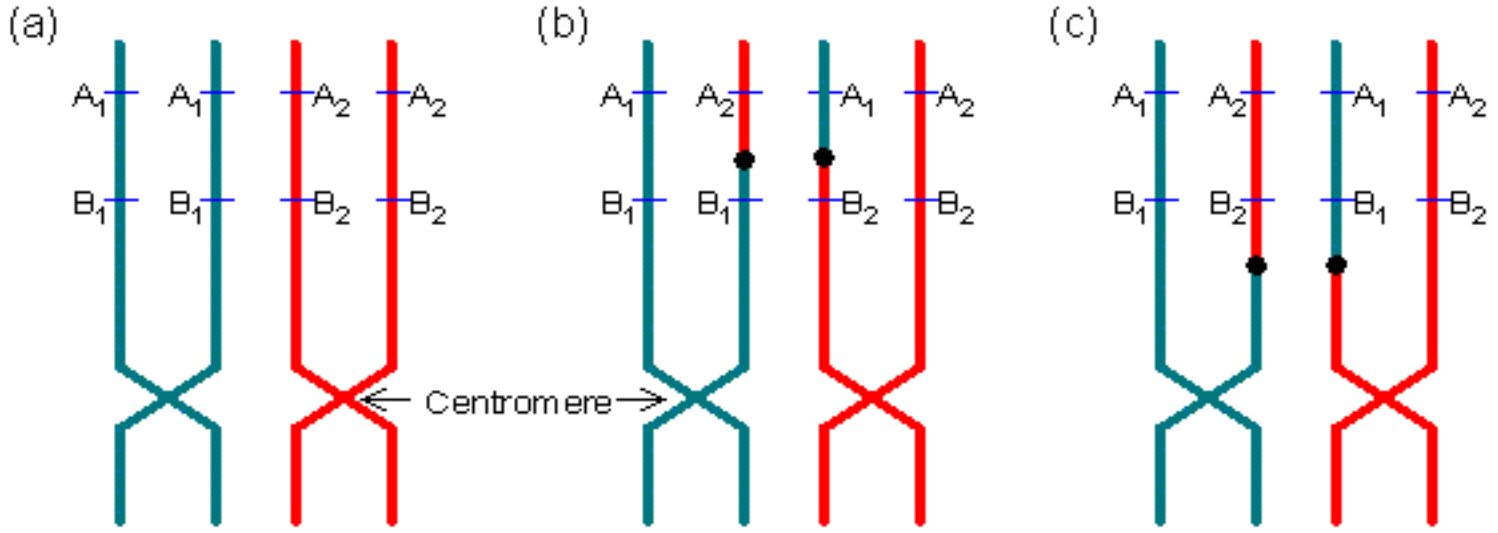


Illustration of recombination between two loci A and B:

(a) Two pairs of sister chromatids align during meiosis. A1 and B1 are located on the same chromosome. A2 and B2 are located on a different chromosome.

(b) DNA crossover leads to recombination if the chiasma is located between the two loci.

(c) DNA crossover does not lead to recombination if the chiasma is not located between the two loci.

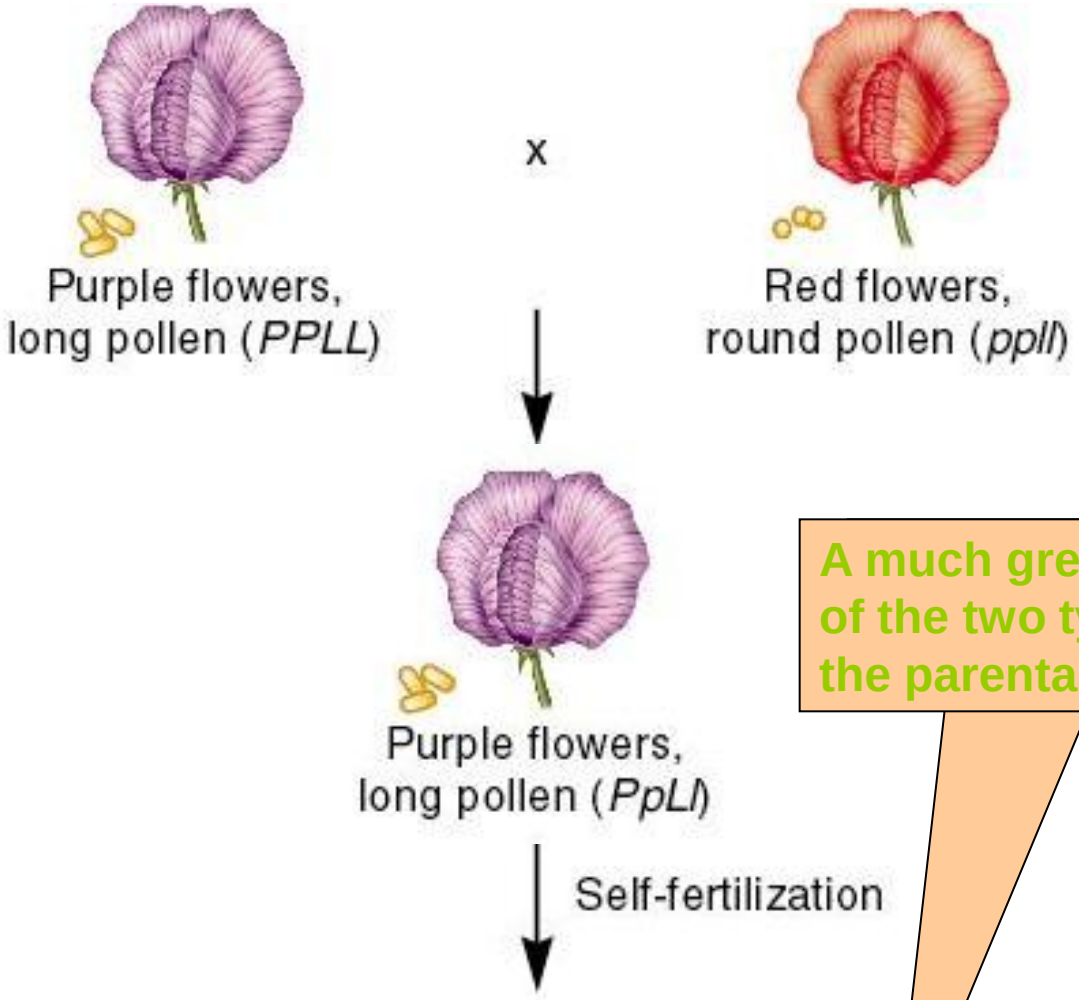
- The gametes carrying A1B1 or A2B2 are called **parental** or (**non-recombinant**) gametes. While the gametes carrying A1B2 or A2B1 are called recombinant gametes because they resulted from recombination during crossing-over.
- **Recombination** is the exchange of alleles between non-sister chromatids due to crossing over and results in new combinations of alleles.
- The **recombination frequency** depends on the distance between the two loci and the position of crossover (the chiasma).
- The closer they are, the less likely the recombination will occur, because recombination occurs only when the chiasma is located **between** the two loci.

Recombination fractions

- A recombination event gives parental type (P) and recombinant type (R) offspring
- Recombination fraction RF = R/(R+P)
- RF is between 0 and 0.5 (0 and 50%)
- The closer together the genes are, the smaller is RF
- RF = 0.5 for unlinked genes (very far apart or on different chromosomes)

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	Rat	Expected number	Ratio
Purple flowers, long pollen	296	15.6	240	9
Purple flowers, round pollen	19	1.0	80	3
Red flowers, long pollen	27	1.4	80	3
Red flowers, round pollen	85	4.5	27	1

Genetic Mapping

- **Genetic mapping (**or **gene mapping)** is to determine the order and distance between genes that are linked to each other on the same chromosome.

- Used for construction of **genetic linkage maps**

- **Genetic maps are useful in many ways:**

1. They allow us to understand the overall complexity and genetic organization of a particular species
2. They improve our understanding of the evolutionary relationships among different species
3. They can be used to diagnose, and perhaps, someday to treat inherited human diseases
4. They can help in predicting the likelihood that a couple will produce children with certain inherited diseases
5. They provide helpful information for improving agriculturally important strains through selective breeding programs

- The units of distance are called **map units (mu)** or sometimes called **centimorgan (cM).**
- One map distance (1 cM) is equivalent to 1% recombination frequency.
- The basis for genetic mapping is that the percentage of recombinant offspring (R) is used to deduce the distance between two genes.
- If two genes are far apart, many recombinant offspring will be produced.

$$\text{Map distance} = \frac{\text{Number of recombinant offspring}}{\text{Total number of offspring}} \times 100$$

Dihybrid Test Cross Mapping

- Figure 5.9, Brooker, provides an example of a testcross involving <u>two genes</u>
  - This cross concerns two linked genes affecting bristle length and body color in fruit flies:

    - *s* = short bristles
    - s^+ = normal bristles
    - *e* = ebony body color
    - e^+ = gray body color

- One parent displays both recessive traits – i.e. it is homozygous recessive for the two genes (*ss ee*)
- The other parent is heterozygous for the two genes ($ss^+ ee^+$)
- The *s* and *e* alleles are linked on one chromosome
- The *s+* and *e+* alleles are linked on the same homologous

(Short bristle, Ebony body) x **(Normal bristles, Gray body)**

(se/se) x (se/s^+e^+)

Offspring:

Short bristles, ebony body (parental)	542
Normal bristles, gray body (parental)	537
Normal bristles, ebony body (recombinant)	76
Short bristles, gray body (recombinant)	75

$$\text{Map distance} = \frac{\text{Number of recombinant offspring}}{\text{Total number of offspring}} \times 100$$

$$= \frac{76 + 75}{542 + 537 + 76 + 75} \times 100$$

= **12.3 map units (cM)**

Interference

- **Positive interference**
  - The first crossover decreases the probability that a second crossover will occur nearby
- **Negative interference**
- Rarely, the outcome of a testcross yields a negative value for interference (the first crossover *enhances* the rate of a second crossover)
- The molecular mechanisms that cause interference are not completely understood, however, most organisms regulate the number of crossovers so that very few occur per chromosome