

Chapter for today: Chap. XII**Major points for the day:**

1. Genes can interact-Epistasis
2. The concept of genetic linkage
3. Sex-linkage versus autosomal linkage

Question from last time: What assumptions about inheritance does Mendelian inheritance make?

Might expect to hear:

- One gene per phenotype; genes are segregate entirely randomly; complete dominance (?); no environmental effects.

None of these factors invalidate Mendelian genetics, but they do reveal that there are phenomena which Mendel did not deal with.

Interactions between genes

One of the features of Mendelian genetics is that each gene has a distinct phenotype which is unaffected by any other gene

- A gene specifies whether the flower will be purple or white
- Another gene specifies if the seed will be green or yellow
- A third specifies if the plant is tall or short

The phenotype of each allele of each gene is unaffected by what alleles are present at other genes.

This independence is not always true, sometimes the genes interact-interactions between distinct genes is called **epistasis**

An example of epistasis is given in the book:

A gene in labradors controls deposition of melanin

- The dominant allele *B* causes deposition of large amounts of melanin
- A recessive allele *b* causes less deposition

A *BB* or *Bb* dog is black, while a *bb* dog is brown

Another gene controls whether or not melanin is deposited at all

- The dominant allele *E* allows deposition
- The recessive allele *e* does not

An *ee* dog is yellow (no melanin) while an *Ee* or *EE* dog has melanin and is not yellow

Combining any combinations of alleles of the *B* gene with *ee* results in a yellow dog rather than a black or brown dog.

- This is *not* dominance since gene *E* and *B* are not allelic (dominance is a relationship between homologous genes)
- However, homozygous recessive mutants of *E* can not express any melanin, and therefore the nature of the *B* genes is irrelevant to coat color

This kind of relationship is called epistasis

In a dihybrid cross between *BB EE* and *bb ee* [What color would they be?] you get:

- 9 Black (combination of at least one *B* and one *E* allele)
- 3 Brown (homozygous *bb* combined with at least one *E* allele)
- 4 Yellow (homozygous *ee* with any alleles of *B*)

Continuous variations in traits

More complicated interactions lead to **continuous variation** in phenotypes:

- Eye color and height are two examples given in the book
- In each case, the phenotype can not be broken down into two clear alternatives
- Instead multiple genes interact to affect the phenotype

Another name for this type of trait is **multigenic**

A special kind of linkage: sex linkage

Because some of the chromosomes have a special role-in determining gender-the genes on those chromosomes have a special kind of linkage called **sex linkage**

- Because there are two such chromosomes in humans and many other animals this linkage can be separated into **X-linkage** and **Y-linkage**
- As it turns out, the Y chromosome has very few genes that cause an observable phenotype, therefore most sex-linkage is in fact X-linkage

Because of the difference in sex chromosomes, sex linked genes segregate differently in males and females.

- Imagine a recessive allele of a gene that is carried on one of the X chromosomes of a particular female. She mates with a male carrying the dominant allele. What are the expected phenotypes of the male and female progeny?
- Remember that all female offspring receive one X chromosome from the father. Since the father's X carries the dominant allele all the female progeny will have the dominant phenotype
- Since all male receive one Y chromosome from their father and an X from their mother, and because genes present on the X are absent from the Y, half of the sons will receive the recessive allele without any dominant allele, and therefore express the recessive phenotype

1:1 segregation in sons with only one phenotype among the daughters is the hallmark of an X-linked gene.

This type of inheritance can be seen in human X-linked traits-here are three examples:

- **Hemophilia**-an inherited form of hemophilia was passed through the family of the British queen Victoria
 - We know that the mutation occurred in Victoria since none of her ancestors showed the disorder
 - Victoria had one hemophiliac son and his normal daughter in turn had a hemophilic son
 - Two of Victoria's daughters had hemophilic sons and hemophilic grandsons (including the heir to the Russian throne, the Crown Prince Alexis)
- **Red-Green color blindness**-the genes for the two proteins which recognize red and green light are located on the X chromosome
 - The two genes are located near to each other and mutations often occur which eliminate one or the other of the pair
 - The fact that they are located on the X means that color blindness is much more common in males **[ask for a show of hands]**
 - **Pattern baldness**-the form of baldness in which hair is lost first from the crown of the head is another X-linked trait

Given that, who should men look at to see whether they are likely to have pattern baldness, their father or the mother's brothers? Why?

Autosomal inheritance

Most of our genes are on the autosomes, so they show autosomal inheritance

- That means that male and female progeny have an equal chance to be affected

Autosomal diseases exist in humans, many of which the book lists.

- They come in two types-dominant and recessive
- Autosomal recessive diseases (such as sickle-cell anemia) must be inherited from both parents (who are often carriers-i.e., Aa types)
- Autosomal dominant diseases (such as Huntington’s disease) are inherited from a single affected parent

Random segregation of markers

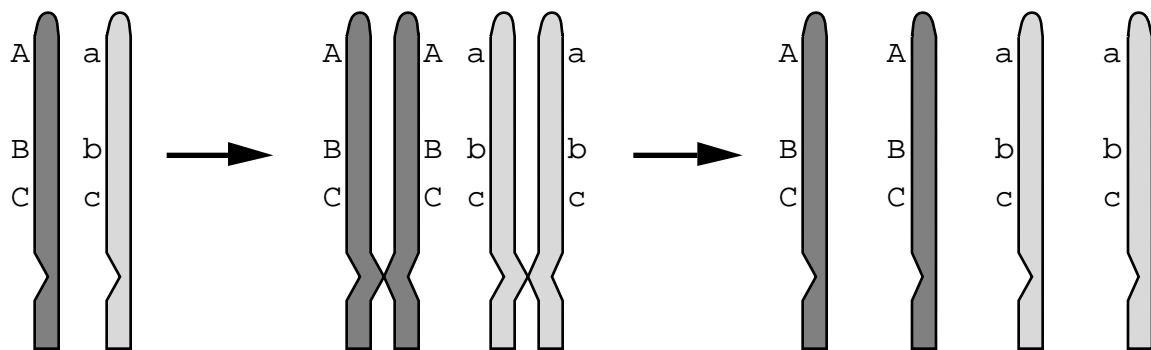
The second thing that Mendelian genetics depends on random segregation of alleles and of genes.

- For each gene pair, the chance of progeny inheriting either is equal (50%)
- Each gene segregates entirely randomly with respect to each other gene

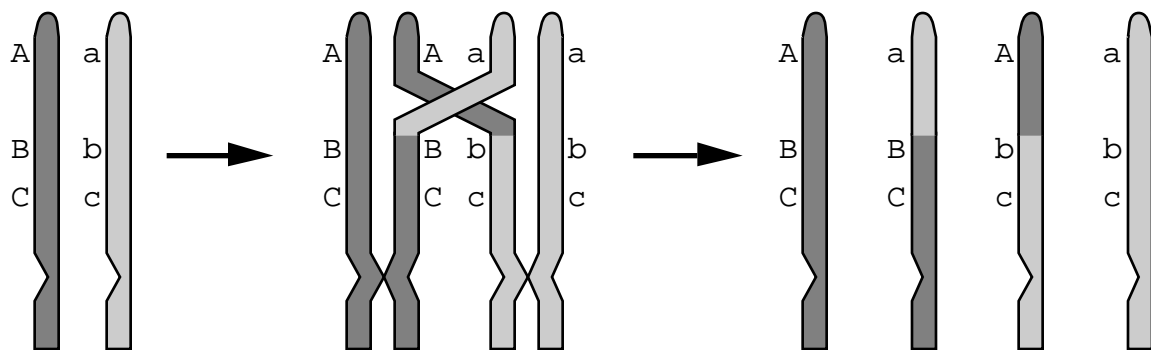
Mendel couldn’t have known, but we know that the genes are located on chromosomes as linear arrays.

- Because they are linked in this way they cannot always segregate entirely randomly
- Physical linkage means that they will tend to segregate together in meiosis

If meiosis occurred without any recombination between non-sister chromatids genes located on the same chromosome would never segregate away from each other:



However, recombination occurs during Prophase I of meiosis, and changes the linkage of genes



- Recombination occurs randomly across the chromosome
- The frequency of recombination is approximately the same across the entire genome

| How might these facts be useful to geneticists?

The relative distance between genes can be determined by the frequency of recombination between them

This relationship was first noted by Thomas Morgan, a fly geneticist from the turn of the century.

- The unit of genetic distance is called a morgan
- 1 percent recombination equals 1/100 of a morgan, or a centimorgan

Using measures of recombination between genes geneticists created maps of entire genomes, including the human genome

The process of recombination between genes is random, but in large populations the number of recombinants are very predictable

That is why the maps are very accurate and very detailed