Chapter 9 (Strickberger 4th ed.) Cell division, Mendelian Genetics and Sex Determination

INTRODUCTION

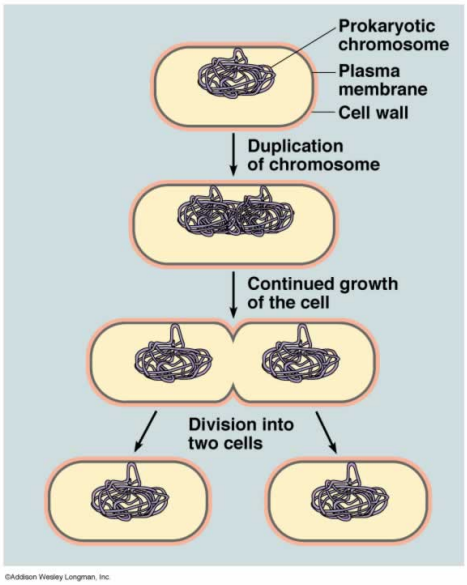
Organism evolution depends on genetic constancy and variability.

> Constancy results from the accuracy of the genetic machinery as it reliably replicates, transcribes, and translates nucleic acids.
>
> Variability results from the inexact maintenance and replication of genetic information, i.e. recombination and production of mutations.

CELL DIVISION

The transmission of biological information is closely linked with cell division so that parental information is passed on to daughter cells.

> Early "cell" division probably allowed membrane-enclosed organisms to grow but not enlarge themselves to the point of structural failure. In other words, they needed to divide so that they wouldn't break.



Early cells likely replicated and divided without protein machinery or rigid cell walls, relying instead on only a lipid membrane.

Current evidence for this possibility:

The vast majority of bacteria have cell walls. However, many bacteria can switch to a wall-free form called the L-form state, which could mirror the structure of early cells.

L-form cells feature increased production of fatty acids in the cell membrane.
Increases the cell's surface area relative to its volume.
Therefore, a simple biophysical change—an imbalance between surface area and volume—underlies L-form cell division.

http://www.youtube.com/watch?v=TY6CokUTeVY

Integral to this process is the **simultaneous duplication of the cell's genetic material**.

In today's prokaryotes (single chromosome) the products of DNA replication each attach to opposite ends of the cell membrane.

Cell elongation occurs, the cell divides, with each new cell taking one new chromosome.

http://www.youtube.com/watch?v=gEwzDydciWc

In eukaryotes, multiple chromosomes result in more complex cell division.

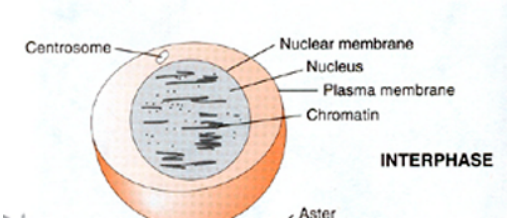
Mitosis – cell division of somatic (body) tissue
Meiosis – cell division of gamete-producing tissue

Mitosis

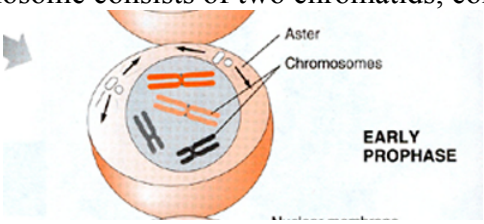
Parent and daughter cells have the same number of chromosomes (for this example, four chromosomes).

Five stages of mitosis…

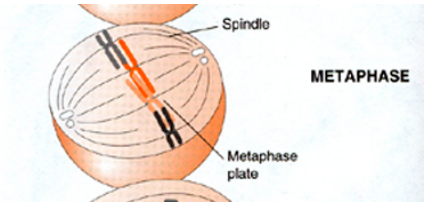
1. Interphase – Cell functioning as "normal", DNA replicates.



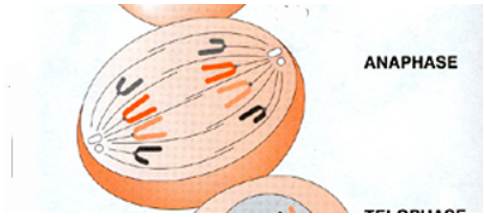
2. Prophase – Each chromosome consists of two chromatids, connected at a centromere.

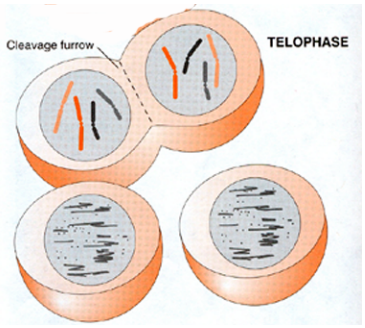


3. Metaphase – The chromosomes line up on a metaphase plate and connect to spindle fibers that attach to opposite poles of the cell.



4. Anaphase – Chromatids separate, each going to one daughter cell.





5. Telephase – A cleavage furrow forms to facilitate completion of cell division.

In mitosis, each cell receives an exact match of the parental genetic material.

In the above example, mitosis began with one cell containing four chromosomes and ended with two cells each containing four chromosomes exactly matching those of the parent cell. **How does this process promote evolution?**

Meiosis – cell division performed by **eukaryotes that reproduce sexually**.

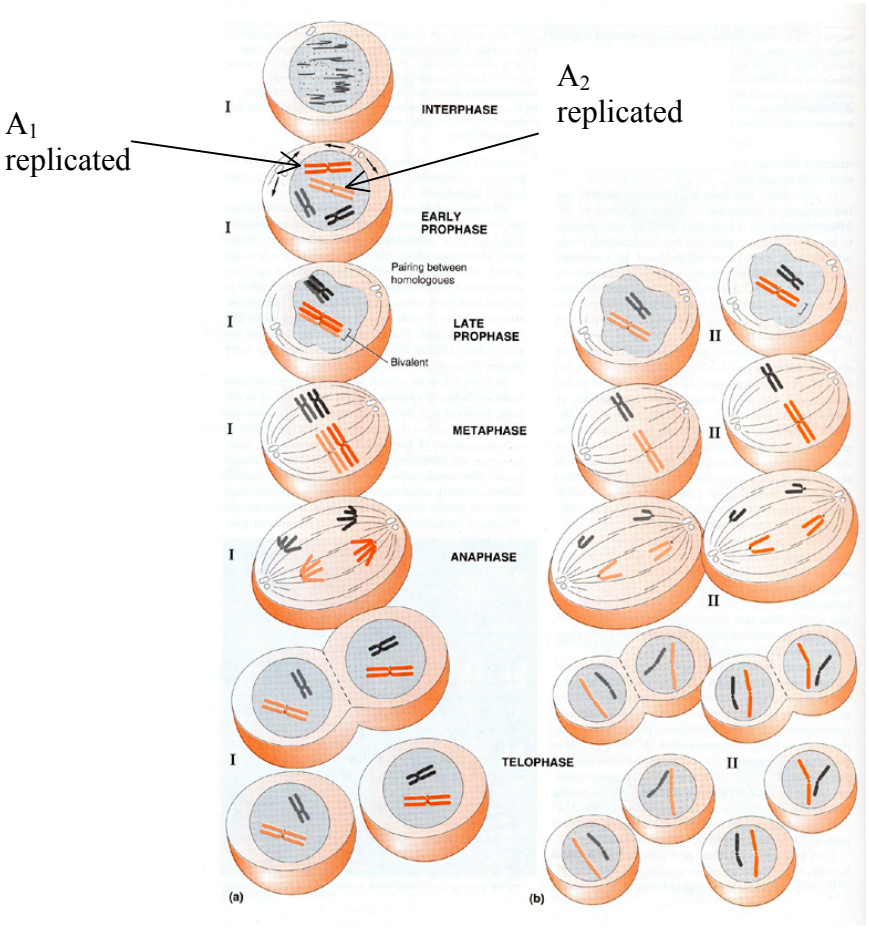
Since all organisms that undergo mitosis also undergo meiosis, it is thought that these two processes evolved at the same time.

Meiosis forms **gametes** (sperm cells/eggs) that contain half of the genetic information found in somatic cells.

A gamete that might contain two kinds of chromosomes (A_1 and B_1 from a male) fertilizes another gamete containing A_2 and B_2 (from a female) to form a zygote.

The zygote contains the full chromosome compliment ($A_1A_2B_1B_2$).

Meiosis will reduce and divide the chromosome compliment to produce new gametes (either A_1B_1, A_1B_2, A_2B_1, or A_2B_2).



The first meiotic division is similar to mitosis, but with an important difference:

Following chromosome replication in prophase, **homologous chromosomes** pair-up; e.g. A_1 with A_2, B_1 with B_2, etc.

The second meiotic division separates the two chromatids of each chromosome in each of the two daughter cells produced by the first meiotic division.

Results in four gametes, each containing one representative of a homologous pair of chromosomes.

Overall, the number of different gametes produced during meiosis is 2^n, where *n* is the number of chromosome pairs.

Two chromosomes – A_1A_2, B_1B_2 can yield A_1B_1, A_1B_2, A_2B_1, A_2B_2.

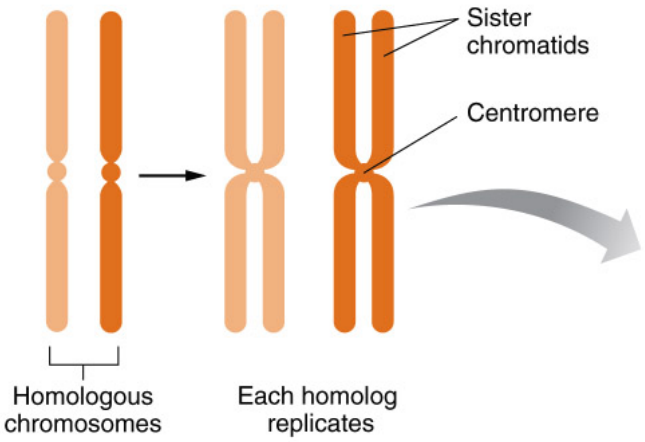
Three chromosomes - A_1A_2, B_1B_2, C_1C_2 can yield $A_1B_1C_1$, $A_1B_1C_2$, $A_1B_2C_1$, $A_1B_2C_2$, $A_2B_1C_1$, $A_2B_1C_2$, $A_2B_2C_1$, $A_2B_2C_2$.

Humans carry 23 chromosome pairs, 2^{23} (more than 8 million) combinations are possible (before genetic exchange).

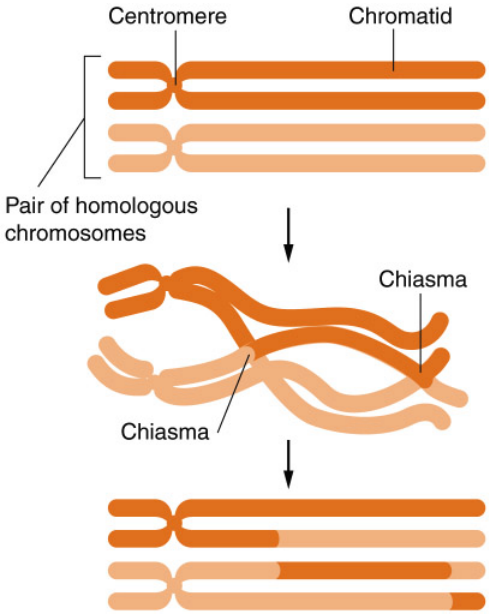
The mechanism of cellular division was most important to evolving eukaryotic organisms that needed to adapt to changing environmental conditions. Why?

Meiosis presents a unique opportunity for genetic diversity.

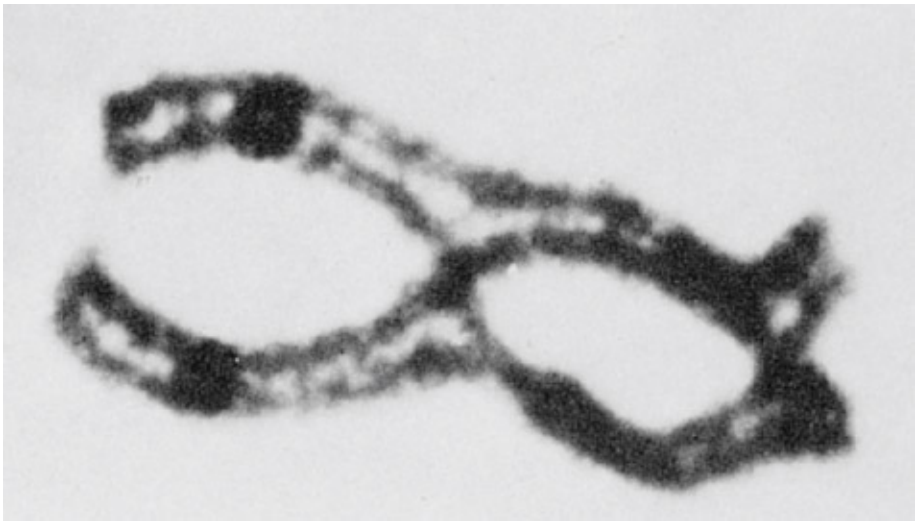
In prophase, pairing of homologous chromosomes following replication is associated with the formation of **chiasmata**, which are locations along the chromosome where an exchange of genetic material can take place.



The formation of chiasmata facilitates **genetic recombination** (or crossing over).



Genetic material is "swapped" between homologous chromosomes to generate different, linear nucleotide sequences on each chromosome.



Pairing and chiasma formation between homologous chromosomes in meiosis.

http://www.youtube.com/watch?v=5x_Rp1mwotQ

Recombination produces altered sequences of genes (alleles) along the length of a chromosome.

Also produces different sequences within genes when recombination occurs "inside" the gene.

MENDELIAN SEGRAGATION AND ASSORTMENT

Early observations by Gregor Mendel helped us to understand the principles of genetics = Mendelian genetics.

Observations were based on the characteristics of pea plants.

Each character of the plant possessed two alternative appearances.

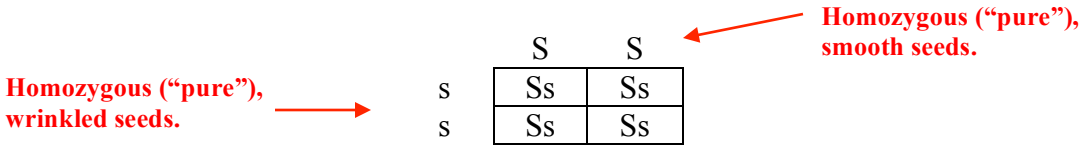
e.g. tall or short plants, smooth or wrinkled seeds, yellow or green seeds

Mendel studied the frequency of traits in many generations of pea plant populations.

…led to two principles:

1. Principle of segregation (principle of non-blending)

When two homozygous (pure) breeding stocks that differ with respect to a given character (smooth vs. wrinkled seeds, for example) are crossed, the first filial generation (F1) carries genes for both traits.



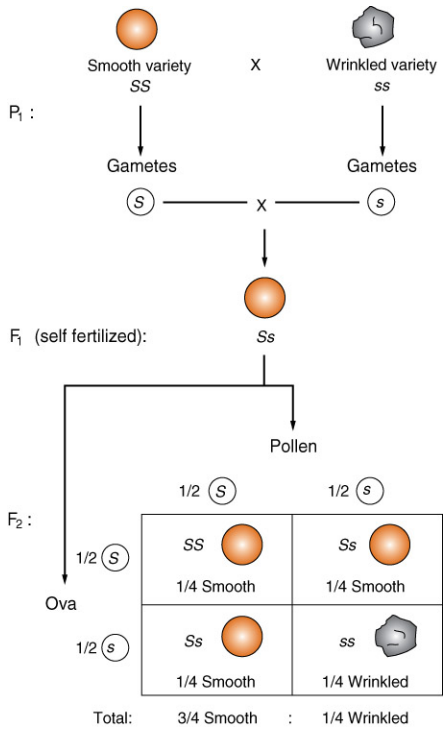
The components of a gene pair are called alleles (e.g. *smooth* is one allele and *wrinkled* is the other; one from one parent the other from the second parent).

S is a dominant allele, **s** is a recessive allele.

Production of gametes (meiosis) in P1 results in segregation of the alleles.

When the gametes unite in F2, a predictable proportion of traits arises because one allele is dominant over a recessive allele.

In short, the protein encoded by the expressed allele (the dominant one in this case), is "stronger" than the protein expressed by the recessive allele.



e.g. *SS* (homozygote) and *Ss* (heterozygote) peas are smooth, while *ss* are wrinkled (smooth dominant over wrinkled).

The term **segregation** describes alleles whose protein products had not been "blended" in the heterozygous individual, but rather were segregated from each other.

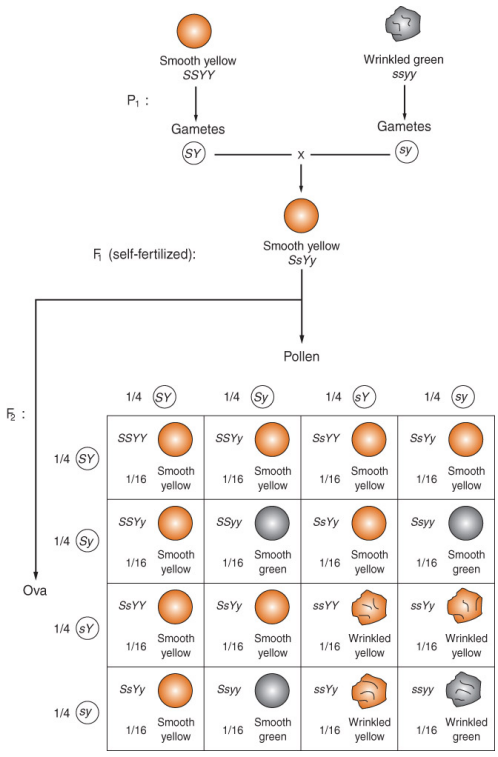
i.e. there was no one individual that was "a little smooth" and "a little wrinkled".

2. Principle of independent assortment (>1 trait)

In crosses involving two different characteristics, the resulting ratios of traits were predictable **if** genes that determined one character had **no effect** on the segregation of genes for the other character.

Genes for different characters segregated **independently** from each other.

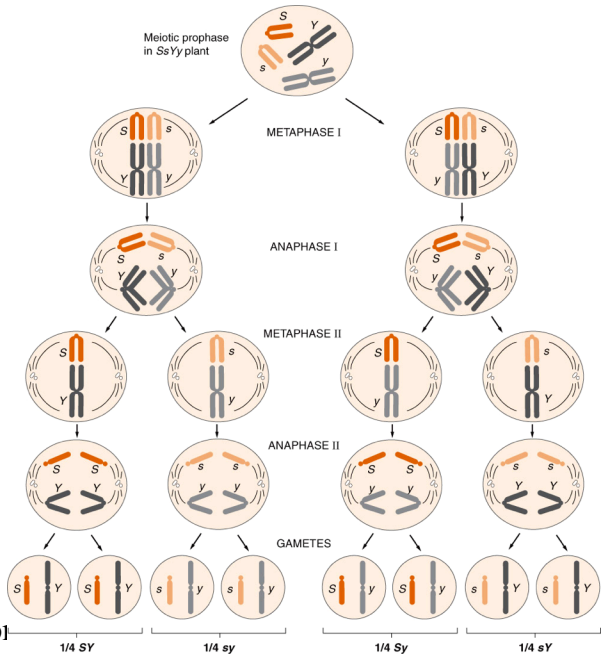
Example: add to the smooth/wrinkled seeds a trait for color.
Y - yellow
y - green



F2 proportions are 9/16 smooth yellow, 3/16 smooth green, 3/16 wrinkled yellow, 1/16 wrinkled green (9:3:3:1 ratio).

These are predictable ratios because each seed shape allele and seed color allele are independent from each other.

By noting these ratios, Mendel was able to determine how genetic components flowed during curing cell division, and eventually how meiosis worked.



DOMINANCE RELATIONS AND MULTIPLE ALLELES

Mendel's observations were based on each gene having only two alleles and displaying complete dominance or recessiveness.

This held true under three conditions:

e.. the phenotypic difference was due to a single gene (not an interaction between different genes, which is called epistasis).

Human obesity, pea flower color and chicken head-combs are thought to arise in part due to interactions between different genes.

2. the genes involved showed either complete dominance or complete recessiveness.
3. the gene only had two alleles for each character.

But what about genes that don't fit these conditions?

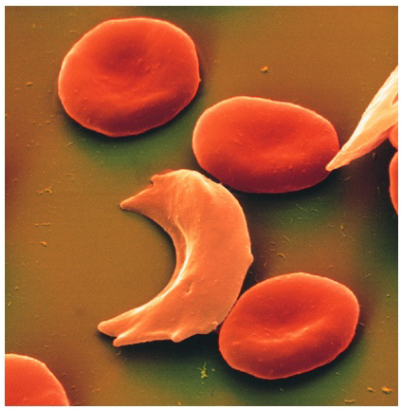
Incomplete dominance can be illustrated by G_1G_1 producing red flowers, G_2G_2 producing white flowers, and G_1G_2 producing **pink** flowers.

G_1G_1 **G_1G_2** **G_2G_2**

Co-dominance - the product of each allele is evident.

What is the evolutionary importance of these relations?

Another example of a co-dominant trait is **sickle cell anemia**: If a person has one normal hemoglobin gene and one abnormal gene, both normal and abnormal hemoglobin is produced.



In general the most advantageous alleles have been selected for through time = **wild type**.

However, many allelic differences, dominance, and interaction effects are possible.

Results in an astronomical amount of potential variability.

e.g. a gene with four alleles (G_1, G_2, G_3, G_4) can produce 10 possible diploid genotypes (G_1G_1, G_1G_2, G_1G_3, G_1G_4, G_2G_2, G_2G_3, G_2G_4, G_3G_3, G_3G_4, G_4G_4).

An excellent example of multiple allele inheritance is human blood type. Blood type exists as four possible phenotypes: A, B, AB, & O.

Three alleles exist for the gene that determines blood type. You only have two of them…why?

ALLELE	CODES FOR
I^A	Type "A" Blood
I^B	Type "B" Blood
i	Type "O" Blood

GENOTYPES	RESULTING PHENOTYPES
I^AI^A	Type A
I^Ai	Type A
I^BI^B	Type B
I^Bi	Type B
I^AI^B	Type AB
ii	Type O

What's going on with "AB" blood?

One hundred such genes (i.e., with four alleles) can produce 10^{100} different genotypic combinations.

Even the simplest organisms contain more than 100 genes!

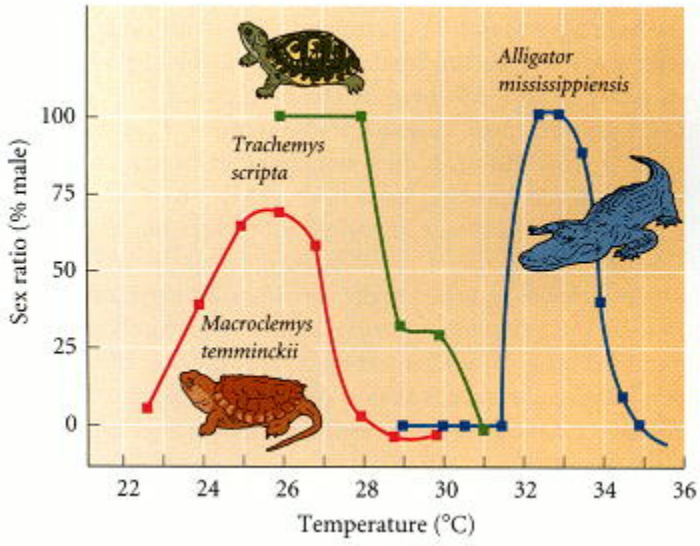
SEX DETERMINATION

Today, the sex of most species (especially mammals) is determined by chromosomal differences, but this has not always been the case.

While most sex determination is driven strictly by genetics, examples exist of **environmental sex determination**, which is thought have evolved 300 million years ago, and before genetic sex determination.

Mostly limited to cold-blooded organisms and plants.

In *Agama agama* (a lizard) the temperature at which eggs are incubated determines the sex of the offspring (warmer = males). The opposite is true in painted turtles.



Temperature-dependent sex determination in three reptile species: the American alligator (*Alligator mississippiensis*), the red-eared slider turtle (*Trachemys scripta elegans*), and the alligator snapping turtle (*Macroclemys temminckii*). (After Crain and Guillette 1998.).

Horsetail plants grown in poor conditions will develop into males (good conditions = females).

Mechanisms of environmental sex determination allow for the possibility of rapid adaptation of sex ratios within a changing environment, but can also make these species vulnerable to extrinsic changes that might lead to significant changes in the sex ratio…so why have it?

Most hypotheses base the existence of EST on **fitness**.

In some lizards (e.g. snow skink) it is advantageous to have a high proportion of females early in the season.

During years when it is warm early in the season, female-biased broods will dominate.

The females will have more time to grow and reach maturity, thereby being fit to reproduce earlier.

In snapping turtles, offspring produced at intermediate temperature (one that produced both sexes) had a much higher propensity to run.

Offspring from either all male-producing temperatures or all female-producing temperatures were more inclined to remain motionless.

Intermediate temperature hatchlings experienced significantly higher predation rates presumably due to their higher visibility while moving (Janzen 1995).

Offspring produced at different temperatures may be better suited to avoid predation.

Environmental sex determination ensured that ratios of males to females coincided with environmental conditions that favored individuals and their ability to eventually reproduce.

However, when warm-blooded mammals arose, sex determination by temperature became problematic. **Why?**

In response, roughly 300 million years ago, the X and Y chromosomes arose from a pair of identical, non sex-determining chromosomes (known as autosomes).

One of the autosomes mutated and acquired the ***SRY* gene**--Sex-determining Region Y.

The "master switch" for creating a male.

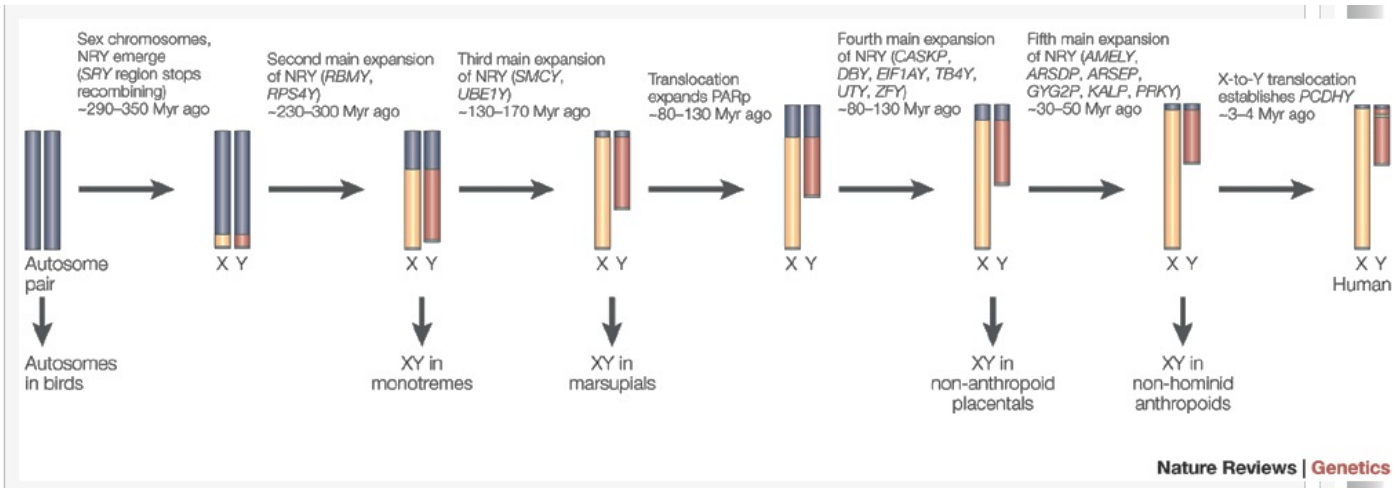
The *SRY*-bearing chromosome became the Y chromosome and its *SRY*-deficient partner became the X chromosome.

We have seen already that recombination is essential to maintaining genetic identity between homologous chromosomes (remember metaphase I in meiosis).

No recombination → no genetic diversity.

Over time, X and Y stopped recombining during meiosis, which resulted in to genetically-distinct "once homologous" chromosomes.

Today, most females have two "X" chromosomes (XX), while males have "X" and "Y" chromosomes (XY).



The human X and Y chromosomes hardly recombine at all, with the exception of a small, homologous region. Why is this important?

The establishment of genetic sexual determination ensured an equal proportion of males and females, and was a significant departure from environmental sex determination.

Isn't this evolutionarily counterintuitive?

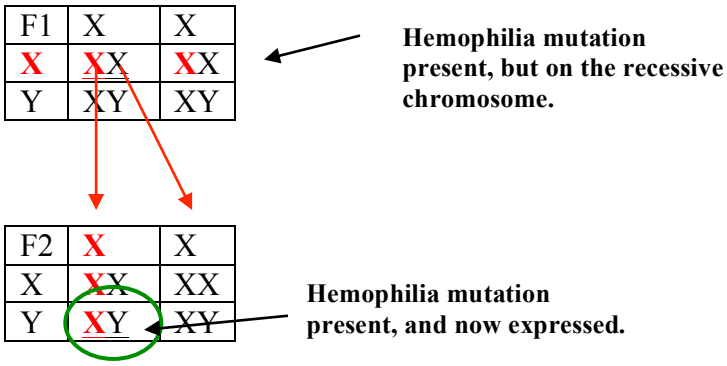
SEX LINKAGE

It was discovered that some genes that had nothing to do with sex determination were localized to specific sex chromosomes.

e.g. hemophilia – localized on the "X" chromosome of mammals.

In males, the **Y chromosome is mostly inactive**, so alleles present on the X chromosome tend to express themselves as "dominant".

Also, such alleles (on the male X chromosome) are often **recessive in females**.



A single hemophilia-producing allele on the X chromosome of male results in hemophilia.

Inherited from the mother (XX, although 1/3 of cases result from mutagens).

Many sex-liked genes identified in humans have also been identified in other mammals.

This conservation suggests a large part of the X chromosome has persisted throughout mammalian evolution (at least 90 million years).

LINKAGE AND RECOMBINATION

The location of certain genes to specific chromosomes allows us to determine the actual "distance" between certain genes, or **linkage relationships**.

Even though genetic exchange occurs during meiotic crossing-over events, certain gene combinations **always seem to remain associated…why?**

While recombination can occur between any two genes on a chromosome, the amount of crossing over is a function of <u>how close the genes are to each other</u> on the chromosome.

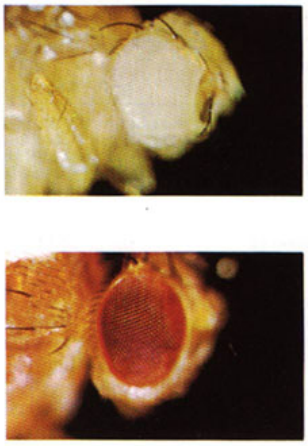
If crossing-over events were completely random, then we would expect to see the combination of any two genes occurring 50% of the time.

However, gene recombinations do not occur this way.

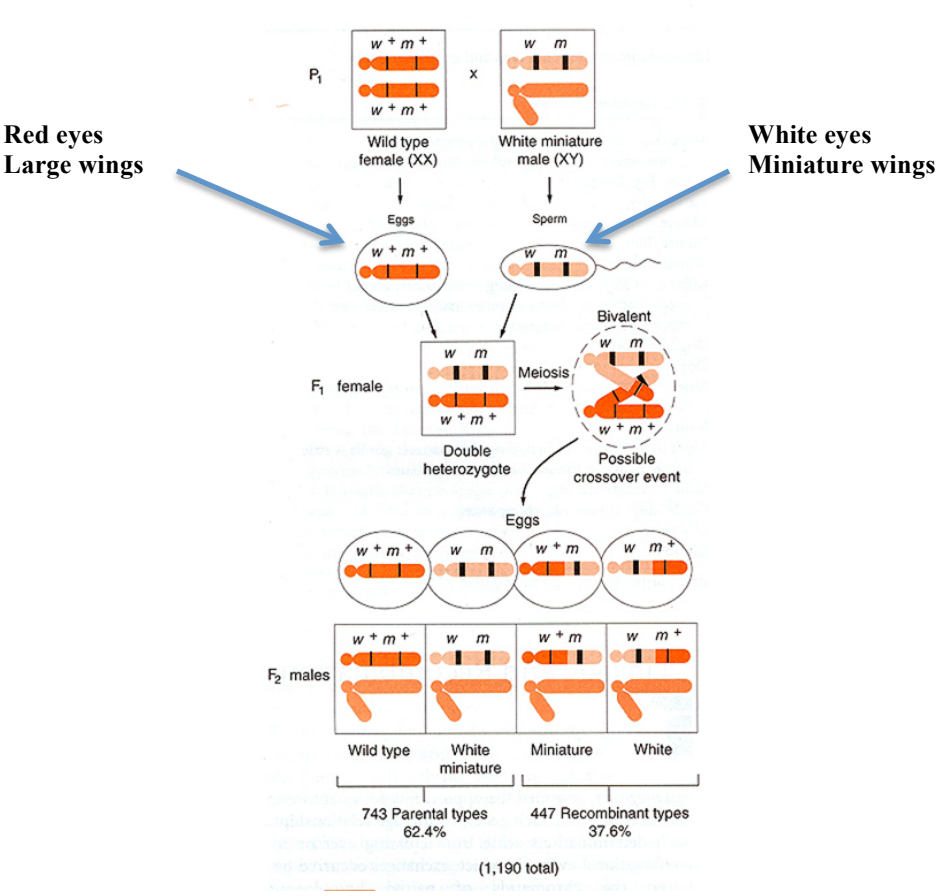
For example, let's look at two drosophila traits; wing size and eye color.

m^+- large wings (wild type)
m- miniature wings

w^+- red eyes (wild type)
w- white eyes



The genes encoding for these two *Drosophila* traits remain associated 62% of the time (i.e. they recombine with other genes 38% of the time).

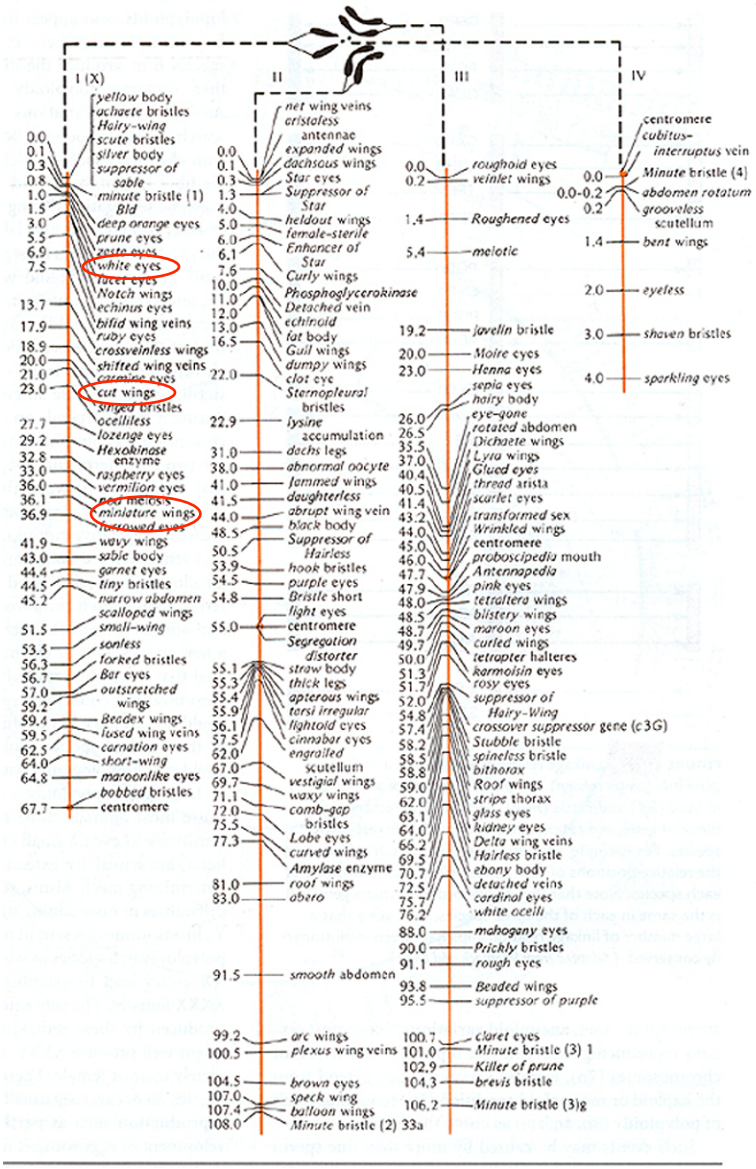


This frequency can provide a measure of linkage distance between genes on the same chromosome.

Greater recombination frequency = greater genetic distance

Therefore, if the recombination frequency between genes for white eyes and cut wings was **half** the frequency of white eyes and miniature wings, then the linkage distance between white and cut was **half** that of white and miniature.

This information can lead to development of **linkage maps** displaying gene loci.



Overall, the ability for genes to recombine results in vast diversity and adaptation potential.