Biology 3A Laboratory
Mendelian, Human and Population Genetics

OBJECTIVE

- To be able to follow alleles through meiosis and determine gametes.
- To study the principles of inheritance.
- To understand the basic types of inheritance patterns in humans and other multicellular organisms.
- To solve genetic problems involving monohybrid, dihybrid and trihybrid crosses.
- To solve genetic problems when the genotype of the parents or offspring are known and unknown.
- To observe and record some phenotypes which occur in humans.
- Calculate Hardy-Weinberg equation.

INTRODUCTION

Genetics is the branch of biology that examines the inheritance of traits and how these traits are passed from one generation to the next. Much of what we know about genetics today stems from Gregor Johann Mendel's studies of pea plants during the 1860's. Mendel has been credited with the founding of genetics. The significance of his investigations, however, were not recognized until well after his death. Through his work with pea plants, Mendel was able to observe and track individual characteristics and employ simple mathematical models in predicting the outcomes of his investigations. His conclusions can be summarized as four "laws" of heredity:

1. **Law of Unit Character**: characteristics are inherited as separate units.

2. **Law of Dominance**: for some characteristics, the presence of one gene (the dominant gene) will mask the presence of another gene (the recessive gene), resulting in the expression of the dominant gene.

3. **Law of Segregation**: all cells in the body contain a pair of characteristics (genes). During gamete formation in the reproductive cells, each gamete will only receive one member of each pair.

4. **Law of Independent Assortment**: during gamete formation, a pair of genes for a particular characteristic will be inherited independently of other genes that code for any other characteristic(s).

Although Mendel's experiments with pea plants paved the way for understanding the mechanisms involved in heredity, it wasn't until the discovery of chromosomes and the meiotic process that inheritance become more clearly understood.

If you recall, all **diploid (2n)** cells in your body contain a complete (two) set(s) of **homologous chromosomes**. This complete set of chromosomes is composed of a maternal and paternal pair. Each pair of homologous chromosomes contains **genes** that determine specific traits by coding for the production of a specific protein. Each gene also has a specific location (**locus**) on a specific chromosome and may have several versions/forms called **alleles**. For example, in pea plants, height is governed by a single gene which can have two versions, *T* and *t*. Every diploid cell has two copies of one gene which make up the homologous pair of chromosomes that determine a particular trait. These two alleles could be either the same (**homozygous**) or different (**heterozygous**). In either case, these alleles together will determine an organism's genetic make-up (**genotype**).

A. UNDERSTANDING MEIOSIS & CHROMOSOME SEGREGATION

After **meiosis** (sexual reproduction), the genetic traits of an organism are segregated and readied to be passed from parent to offspring. When sexually reproducing organisms undergo meiosis, they produce **gametes** that are **haploid (n)**. Haploid cells include sperm and ovum (unfertilized egg) that have half the number of chromosomes as the original precursor cell. When humans undergo meiosis, this means that the sperm or ovum will contain 23 chromosomes as opposed to the 46 chromosomes found in diploid cells. So, in order to maintain a constant number of chromosomes in successive generations, a reduction in chromosome number between successive fertilizations (fusion of the male and female gametic nuclei) is necessary and is accomplished through meiosis. Recall from the lecture material that meiosis in the female is called **oogenesis** and in the male, **spermatogenesis**. In this exercise, you will review your understanding of the meiotic process by diagramming the separation of chromosomes in an organism with a diploid number of 4.

Procedure:

1. Prior to drawing and labeling the meiosis diagram in your worksheet, practice/go over the meiotic process. If you need assistance, please ask your laboratory instructor.
2. Make sure that you understand the following terms before you begin: chromatin, chromosome, chromatid (sister chromatids) and centromere.
3. Assume a diploid number of 4 for this organism. This means that this organism will have inherited 2 chromosomes from the mother and 2 chromosomes from the father. Let the red colored chromosomes represent the maternal set and the yellow colored chromosomes represent the paternal set.
4. Here's what you'll have: one long yellow chromosome, one long red chromosome, one short yellow chromosome and one short red chromosome. This will give you four chromosomes (2n = 4).
5. Place the four chromosomes on the meiosis board in the large cell located at the top of the board. This cell is in interphase. Using the four remaining chromosomes to the side of the board, demonstrate DNA replication (synthesis).
6. You should now have four duplicated chromosomes (each chromosome should now be composed of two sister chromatids attached at the centromere) in the large cell.
7. Using the duplicated chromosomes, complete meiosis I and then meiosis II.
8. Have your instructor sign off after you have demonstrated the meiotic process.

B. Importance of sample size in probability

Before we begin to predict the possible outcomes of genetic crosses, you must first understand probability, which is the chance of an event occurring out of the total number of possible events. For example, if you flip a coin, there is a one in two chance (50%) of the coin coming up heads for a two sided coin. Another example that you may be familiar with is the rolling a die. There is only one chance for rolling a "six" on a six-sided die.

Often times, you will need to combine two or more probable events. The total probability of two independent events occurring simultaneously is equal to the product of their individual probabilities. For example, the probability of two successive coin flips coming up "heads" is equal to the product of their individual probabilities. Remember that the probability for coin flip coming up heads is ½, thus, the probability for two successive coin flips coming up "heads" would be: ½ x ½ = ¼ . If you were at Las Vegas playing craps and wanted to determine the probability of rolling a hard six (two six's), this probability would be: 1/6 x 1/6 = 1/36.

With all of these events, it is important to remember that chance has no memory. That is, each time you roll a pair of dice, there is a 1/36 chance of rolling two six's. As we increase the number of rolls, we will come closer to the probable ratios. The same will apply to flipping coins. For each time you flip a coin, there is 50% chance of the coin coming up "heads" or "tails". The more time you flip, the closer you'll come to the 50:50 ratio for coin flips. It is less likely for you to toss heads a hundred times in a row, than heads ten times in a row. If you think about this, Mendel did thousands of crosses with peas.

Procedure:

1. Obtain a coin and toss it 100 times, recording the number of heads and tails.
2. Record your group's data on the spreadsheet before you leave class.
3. Calculate the % deviation for your groups probability using the following equation:

$$\frac{|\text{expected \# H} - \text{actual \# H}| + |\text{expected \# T} - \text{actual \# T}|}{\text{Total number of tosses}} \times 100$$

C. Chi-Square "Goodness of Fit" Test

Chi-square is a statistical test commonly used to compare **observed values** with **expected values** based on a specific hypothesis. For example, if you expected 10 of 20 (50%) offspring from a cross to be male and the actual observed number was 8, then you might want to test the "goodness to fit" between the observed and expected. Were the deviations (differences between observed and expected) the result of chance, or were they due to other factors? As with the other statistical test we have used, chi-squared tests the null hypothesis, which states that there is no significant difference between the expected and observed result. For our work the level of significance will be $p \leq 0.05$. Chi-squared calculations require that you use only numerical values, not percentages or ratios.

In this lab we will test the coin flipping data that you obtained and the data from the entire class. You first need to put together a chi-squared data table for each data set.

	Observed	**Expected**
Heads	**30**	**25**
Tails	**20**	**25**

After you have inserted your observed values, add your number of heads and tails. Into the expected cells insert the total number of measurements divided by two. You then can use any of the on-line chi-squared tests to find the p value for this data set. The p value will be the measure of "goodness of fit." The p value answers this question: What is the probability of observing such a large discrepancy (or larger) between observed and expected values? A small p value is evidence that the data are not sampled from the distribution you expected. If the p value is less than 0.05, there is a statistically significant difference.

Note: The chi-square test is more commonly used in a very different situation -- to analyze a contingency table. This is appropriate when you wish to compare two or more groups, and the outcome variable is categorical. For example, compare the number of animals with white fur in two different habitats. If you want to do this, you should use a "contingency table" calculation.

D. Types of Inheritance Patterns

There will be two basic types of genetic problems that you will solve: one in which you know the genotypes of the parents and will be able to predict the genotypes and phenotypes of the offspring; and the other, you know the genotypes of the offspring and must figure out the genotypes and phenotypes of the parents. To do these problems, you will be required to use a bit of logic and data analysis. A helpful tool in solving genetic problems is the **Punnett square**. The Punnett square is a box of squares in which the various combinations of genes from any two parents are used to determine the possibilities for the offspring. The upper, horizontal axis shows the possible gametes for one parent and the left, vertical axis shows the possible gametes for the other parent. You will use the Punnett square to solve **monohybrid** crosses, where you track a single characteristic, disregarding the inheritance pattern of other genes; and **dihybrid** crosses, where you track two inherited characteristics, disregarding the inheritance pattern of other genes. There are four basic steps in solving genetic problems:

1. Write down the phenotypes and determine the genotypes (from information given).

2. Figure out the number of different gametes that can be produced.

3. Set up your Punnett square and place the parents' genotypes on the outside of the Punnett square.

4. Determine the genotypes and phenotypes of the offspring.

<u>Complete Dominance</u>:
Most of the characteristics that Mendel observed in pea plants exhibited complete dominance. For example, the alleles that code for stem length in pea plants come in two versions: long stems (*T*) and short stems (*t*). The long stem allele is **dominant** over the short stem (**recessive**) allele. A pea plant with two *T* alleles would have the genotype *TT* (**homozygous dominant**). A pea plant with two *t* alleles would have the genotype *tt* (**homozygous recessive**). A pea plant that has one of each allele version would have the genotype *Tt* (**heterozygous dominant**). In order for a recessive trait to be expressed, the organism must be homozygous recessive and have the recessive allele on both chromosomes that they receive from the parents. These same types of problems can be applied to many living organisms.

Problem: Long stems are dominant over short stems in pea plants. A pea plant that is homozygous dominant for long stems is crossed with a pea plant that has short stems. What are the types of offspring could be produced from this cross?

Solution: Remember to write down what you know from the given information.

T = long stems
t = short stems

1. Genotypes of the parents (**P generation**): TT x tt

2. What are the gametes possible from the parents?
   TT → T and T; tt → t and t

3. Set-up the Punnett square.

	T	T
t	Tt	Tt
t	Tt	Tt

Fill in the box by cross-multiplying the alleles of each parent.

4. Calculate the expected genotypic and phenotypic ratios of offspring (**F_1 generation, children – first offspring**):

   Offspring: 100% Tt → all long stemmed

Problem: Astigmatism (A) is dominant over normal vision (a). What is the probability of having an offspring with and without astigmatism if both parents have astigmatism? Both parents each had one parent with normal vision.

Solution:

1. Genotypes of the parents: Aa (astigmatism) x Aa (astigmatism)

Rationale: We know that both parents are dominant (A?) for astigmatism and are heterozygous because both parents had a parent with normal vision (aa) and could only pass on an *a* allele, therefore the genotype of the parents in question are Aa.

2. Gametes possible:
   Since both parents are heterozygous, they will both produce gametes: Aa → A and a.

3. Set-up the Punnett square.

	A	a
A	AA	Aa
a	Aa	aa

4. Calculate the expected genotypic and phenotypic ratios of offspring:

   Offspring Genotypes: 1 AA; 2 Aa; 1 aa → **1:2:1 genotypic ratio**

   Offspring Phenotypes: 3 Astigmatism and 1 normal vision → **3:1 phenotypic ratio**, thus 75% chance of having children with astigmatism and a 25% chance of having children with normal vision.

Incomplete Dominance:
There are instances when characteristics observed produce two extremes and an intermediate blend. This intermediate blend is called **incomplete dominance**. The inheritance of two identical

alleles (dominant or recessive) will result in the extreme conditions, but inheritance of both alleles (dominant and recessive) will result in the intermediate condition. When solving genetic problems that involve incompletely dominant characteristics, the heterozygous condition will be a blend of the two extremes. For example, in snapdragons, red flowers (RR) are incompletely dominant over white flowers (rr). A snapdragon with the genotype Rr, would result in an intermediate color, pink.

Problem: A red snapdragon is crossed with a pink flowered snapdragon. What are the possible genotypes and phenotypes of the cross? Will there be any white flowers produced?

1. Genotypes of the parents: RR (red) x Rr (pink)
2. Gametes possible: RR → R and R; Rr → R and r
3. Set-up the Punnett square.

	R	R
R	RR	RR
r	Rr	Rr

4. Calculate the expected genotypic and phenotypic ratios of offspring (**F_1 generation, children**):
   Offspring Genotypes: 2 RR & 2 Rr → 1:1 genotypic ratio
   Offspring Phenotypes: 50% red and 50% pink → 1:1 phenotypic ratio

Dihybrid Cross – Tracking Two Characteristics:
In a dihybrid cross, two characteristics are tracked while the inheritance pattern of all other characteristics is disregarded. These crosses are more complicated than monohybrid crosses. The same principles apply; however, the number of allelic combinations is increased. To determine the number of gametes that are required for dihybrid crosses, use the following formula: $\mathbf{2^n}$, where **n = the number of allelic pairs that are heterozygous**. By using this formula, you will only be producing the unique gametes, not duplicates. This formula could also be used in a monohybrid cross in determining the number of gamete(s) for tracking one characteristic. If an individual is homozygous, n = 0, and the number of unique gametes is $2^0 = 1$. If there is one heterozygous characteristic, n = 1, and the number of unique gametes is $2^1 = 2$. If there are two heterozygous characteristics, n = 2, and the number of unique gametes is $2^2 = 4$.
For example, if the genotype for an organism is TtYY, there is only one heterozygous pair, Tt. By using the formula, $2^1 = 2$, there will be two unique gametes. **Remember**, for every potential gamete produced during meiosis**, THERE MUST BE ONE ALLELE FOR EACH CHARACTERISTIC IN THAT GAMETE**. The unique gametes from the genotype TtYY are TY and tY. Notice that one member from each pair is present in a gamete.

Problem: In pea plants, long stem (T) is dominant to short stems (t) and yellow seeds (Y) are dominant to green seeds (y). If a homozygous long stemmed, yellow seed pea plant was crossed with a short stemmed, green seed pea plant, what types of offspring would result?

1. Genotypes of the parents: TTYY (long, yellow) x ttyy (short, green)
2. Gametes possible: TTYY ($2^0 = 1$) → TY; ttyy ($2^0 = 1$) → ty
3. Set-up the Punnett square.

	TY
ty	TtYy

4. Calculate the expected genotypic and phenotypic ratios of offspring (**F_1 generation, children**):
   Offspring Genotypes: TtYy
   Offspring Phenotypes: 100% long stemmed with yellow seeds

Problem: If the F_1 generation of the above cross were mated, what are the genotypes and phenotypes of the offspring that would result?

1. Genotypes of the parents: TtYy (long, yellow) x TtYy (long, yellow)

2. Gametes possible: TtYy ($2^2 = 4$) → TY, Ty, tY and ty for both parents

3. Set-up the Punnett square.

	TY	Ty	tY	ty
TY				
Ty				
tY				
ty				

4. Calculate the expected genotypic and phenotypic ratios of offspring (**F_2 generation, grandchildren**):

Offspring Genotypes:		Offspring Phenotypes:
T_Y_	-	Long stemmed with yellow seeds = 9
T_yy	-	Long stemmed with green seeds = 3
ttY_	-	Short stemmed with yellow seeds = 3
ttyy	-	Short stemmed with green seeds = 1

Note: A cross between two totally heterozygous individuals will result in a **9:3:3:1 phenotypic ratio** in a dihybrid cross.

<u>Sex-Linked (X-Linked) Characteristics</u>:
The characteristics that we have examined thus far are referred to as somatic characteristics. The genes for these characteristics in humans are located on chromosomes 1 – 22 and on the portion of the X chromosome that will be paired with another X chromosome or a portion of the Y chromosome. In humans, like the fruit fly (*Drosophila melanogaster*), females are XX and males are XY. The larger X chromosome carries a variety of genes while the smaller Y chromosome only carries a few genes that determine maleness. Characteristics that are located on the X chromosome are called sex-linked because their inheritance is linked with sex determination. The following are the possible genotypes and phenotypes for females and males in relation to the sex chromosomes:

For example: A = normal gene; a = gene associated with a disorder

Genotype	Phenotype	Genotype	Phenotype
X^AX^A	normal female	X^AY	normal male
X^AX^a	normal female (carrier)	X^aY	sex-linked disorder
X^aX^a	sex-linked disorder		

Notice that the gene associated with the sex chromosomes is located **<u>on the X chromosome</u>** and is written as a superscript. There is no gene associated with the Y chromosome that will pair up with the X chromosome.

A few sex-linked disorders that we will examine include: colorblindness, the inability to distinguish certain colors (red-green, etc.); hemophilia, the inability to clot blood due to the body's inability to produce one or more of the thirteen clotting factors; and Duchenne's muscular dystrophy.

Problem: Hemophilia is sex-linked blood clotting disorder carried on the X chromosome. Two individuals that are normal for blood clotting marry. The woman's father had hemophilia. What are the possible genotypes and phenotypes if they have children?

1. Genotypes of the parents: X^AY x X^AX^a

2. Gametes possible: X^AY ($2^1 = 2$) → X^A and Y; X^AX^a ($2^1 = 2$) → X^A and X^a

3. Set-up the Punnett square.

	X^A	X^a
X^A	X^AX^A	X^AX^a
Y	X^AY	X^aY

4. Calculate the expected genotypic and phenotypic ratios of offspring (**F_1 generation, children**):

Offspring Genotypes:	Offspring Phenotypes:
X^AY	Normal male
X^aY	Hemophiliac male
X^AX^A	Normal female
X^AX^a	Normal female – carrier of the hemophilia gene

<u>Multiple Alleles</u>

For the genes that we have discussed thus far, there have only been two different alleles. However, there are some genes that have more than two alleles that determine the phenotype. In these cases where there are three or more alleles (multiple alleles) for a given gene there is usually a dominance hierarchy.

The multiple allele that you are most likely familiar with is the human ABO blood grouping. In this case, alleles for A and B blood are also **codominant** to each other and are both dominant over the O allele (recessive). Others that show multiple alleles include: rabbit or rodent hair colors (4 – 6), E color locus in chickens (12+), color patterns in cows (3 – 4), Mallard ducks (3), etc.

The alleles for the human ABO blood group are: I^A = A allele; I^B = B allele and I^O or i = O allele. These result in the following genotypes and phenotypes:

Phenotype – Blood type	Genotypes
A	I^AI^A, I^AI^A or I^Ai
B	I^BI^B, I^BI^B or I^Bi
O	I^OI^O or ii
AB	I^AI^B

<u>Sex-influenced traits</u>

Unlike sex-linked traits, sex-influenced traits are not carried on the X chromosome. These are genes that express certain given phenotypes only if the individual is a certain sex. These differences arise due to differing amounts of sex hormones produced by males versus females. One example of a sex influenced trait in humans in pattern baldness. The gene for baldness is dominant in the male and recessive in the female. The heterozygous genotype (Bb) expresses the phenotype baldness in males but not in women. This would help explain why there are more males that are bald versus females. The easiest way to understand this type of problem is to do them like a dihybrid cross where sex is one gene and pattern baldness is the other gene.

Polygenic Inheritance

Many human traits, such as eye color, height, intelligence, body form and skin color, are not the result of a single gene. These traits are often the result of several pairs of genes that interact to affect the phenotype (the added affect of two or more genes on a phenotype). For example, there are at least three genes that affect skin color which will result in numerous genotypes and phenotypes which often form a continuum. The more dominant alleles (capital letters) possessed by an individual the darker the skin color (AABBCC). The more recessive alleles possessed by an individual the lighter the skin color (aabbcc).

E. HUMAN GENETICS

The human genome, the genetic make-up of an individual or the genetic make-up of an entire species, has been estimated to have between 80,000 to 150,000 inheritable genes that code for the characteristics of an individual. However, the Human Genome Project, which began in 1990, has analyzed 3 billion base pairs and discovered that there are 30,000 to 35,000 genes that help make up a human individual. This massive undertaking included worldwide commitment to identifying, cataloging and analyzing the entire human genome in an attempt to understand and provide possible cures for human genetic diseases.

In this section, you will observe and record the phenotypes of a few of these known human characteristics. In the process, you will deduce the genotype that codes for your phenotype. Most of these characteristics that you will observe today operate with only two alleles. One of these alleles will be dominant and mask the expression of the recessive allele, unless the individual has both recessive alleles present. These genes are located on your autosomes, chromosomes 1 – 22, and the portion of the X chromosome that will be paired up. Remember from the last section, that the unpaired portion of the X chromosome is known as sex-linked characteristics.

Somatic Characteristics

1. **PTC**: the ability to taste phenylthiocarbamine (PTC) is dominant (TT or Tt) over those that can not taste it (tt). Those that taste PTC will taste very bitter. Place the PTC strip on the back of your tongue.
2. **Sodium Benzoate**: the ability to taste a salty taste is produced by a dominant allele (B). Those who can not taste it are recessive (bb).
3. **Hair type**: Is your hair naturally curly (CC), wavy (Cc) or straight (cc)?
4. **Hair color**: Dark hair (DD or Dd) is dominant over light colored hair (dd).
5. **Widow's peak**: Does your forehead hairline form a point in the center? This is produced by a dominant gene (WW or Ww) and the straight hairline is (ww).
6. **Eyebrows**: bushy eyebrows are dominant (BB or Bb) over fine eyebrows (bb). NOTE: prior to plucking.
7. **Eye color**: non-blue (EE or Ee) eye color is dominant over blue eyes (ee).

8. **Eyelashes**: long eyelashes (LL or Ll) are dominant over short eyelashes (ll). Long eyelashes are those that are > 1 cm length.
9. **Freckles**: the presence of freckles (FF or Ff) is dominant to no freckles (ff).
10. **Nose profile**: a large convex nose profile (NN or Nn) is dominant over the straight nose profile (nn).
11. **Earlobes**: free (or unattached to the sides of the head) earlobes (UU or Uu) are dominant over attached earlobes (uu).
12. **Lip thickness**: thick lips (AA or Aa) are dominant over average and thin lips (aa).
13. **Tongue roller**: the ability to roll into U shape (RR or Rr) is dominant over non-rollers (rr).
14. **Mid-digital hair**: the presence of hair on the dorsal surface of the middle section of the digits (II – V) is due to the dominant allele (H). Absence of hair is recessive allele (h).
15. **Bent little finger**: the distal phalanx V which is bent laterally towards digit IV is due to the dominant allele (B). A straight phalanx is produced by the recessive allele (b).
16. **Hand clasp**: with the hands folded together and the fingers intertwined, is the right thumb over the left thumb or left thumb over the right thumb? Left over right is dominant (L) to right over left (l). Remember, the hand position must feel natural.
17. **Foot arch**: a high arch is produced by a dominant allele (A) and a low arch or "flat feet" is produced by its recessive allele (a).
18. **Hitch-hiker's thumb (double-jointed)**: hyperextensibility of the thumb at an angle greater than 50^o is dominant (H) to the normal extension of less than 50^o (h).
19. ***Palmaris longus* muscle tendon**: the presence of the *palmaris longus* muscle tendon is recessive (aa) to those that have tendon absent (A).

Procedure:

1. Using the above somatic characteristics, fill in the data table in your worksheet regarding your phenotype and possible genotype.
2. After you have completed your data table, make comparisons with two other members in your lab: one of the same ethnicity and one of a different ethnicity.

G. Population Genetics

During 1908, G. H. Hardy, an English mathematician, and G. Weinberg, a German physician, independently solved why genetic variation exist in populations. They discovered that sexual reproduction alone will do nothing to change the frequencies of alleles in population. Meaning that dominant alleles will not replace recessive alleles as long as populations met the following five conditions:

1. Population size is very **<u>large</u>** so that random chance events will not affect allelic frequencies.
2. Mating between members of the population occur at **<u>random</u>**.
3. There must be no **<u>net mutation</u>** of one allele to the other allele.
4. There is **no gene flow** between populations due to immigration or emigration.
5. There must be **no natural selection** against either allele.

If all five conditions are perfectly met, the frequency of each allele will remain exactly the same from generation to generation. Because these proportions are not changing, the population is considered to be in **Hardy-Weinberg equilibrium**.

Suppose that the frequency of *A* allele is X, and there are two alleles for this gene. The frequency of the second allele, *a*, has to be equal to 1 – X because the sum of the two alleles must be 100% or a frequency of 1. The chance of getting the genotype *AA* is the chance of getting one *A* allele times the chance of getting a second, X^2. To avoid confusion, the frequency of the dominant allele is called *p*, so the frequency of the recessive allele is called *q*. For any gene that has two alleles, *p* plus *q* must always equal 1 ($p + q = 1$). The chance of getting the *AA* genotype is p^2. The of getting the *aa* genotype is q^2. The heterozygous genotype can be formed by getting a recessive and a dominant allele ($q \times p$) or the dominant and recessive allele ($p \times q$). Therefore, the chance of the heterozygous genotype, *Aa*, is $qp + pq$ or $2pq$. Knowing this, one can make predictions regarding genotypic frequencies for successive generations of a population in Hardy-Weinberg equilibrium once *p* and *q* are known. The following equation is the binomial expansion of $(p + q)^2$.

p = frequency of the dominant allele	Frequency:	p^2 +	$2pq$ +	q^2
q = frequency of the recessive allele	Genotype:	AA	Aa + aA	aa

If more than two alleles are involved, more unknowns can be added and each term will represent the frequency of a corresponding genotype.

The frequency of phenotypes can then be stated once the frequencies of the genotypes are known:

Dominant phenotype (A-): AA + Aa → $p^2 + 2pq$

Recessive phenotype (aa): q^2

Because the frequencies of the dominant and recessive phenotypes must also add up to 1, the second frequency is known as soon as one or the other is calculated.

The Hardy-Weinberg Law is very useful because deviations from the Hardy-Weinberg frequencies indicate the effects of selection, non-random mating or other factors that influence the genetic make up of the population.

For this experiment, your lab section will constitute a **population** of organisms of the same species that occur in the same area that interbreed or share a common **gene pool**, all the alleles at all gene loci of all the individuals in the population. We will calculate Hardy-Weinberg from our data regarding PTC and sodium benzoate tasting.

In actual populations, it is usually not possible to tell genotypes of all the individuals, especially dominant phenotypes. We will not be able to differentiate homozygous dominant (AA) individuals from heterozygous dominant individuals (Aa). The phenotype that is easily observed or measured is the recessive phenotype ($aa = q^2$). Once the recessive frequencies are determined, we can calculate the dominant frequencies since all frequencies must add up to 1 ($p^2 + 2pq + q^2 = 1$ and $p + q = 1$).

Procedure:

1. Obtain a control, PTC and sodium benzoate taste paper from your instructor.
2. Make sure that your mouth does not have the flavors from other items (gum, candy, cigarettes, etc.).
3. Taste each paper as instructed by your instructor.
4. Record the data for you and the others in class on your worksheet.
5. Input final numbers on the computer before you leave class so that we can increase our sample size.