

Evolution lecture #10 -- **Mendelian genetics, Hardy-Weinberg** -- Nov. 28th, 2007

ch. 14: 251-270 and ch. 23: 454-458 in 7th ed.

ch. 14: 247-266 and ch. 23: 445-449 in 6th ed.

Summary of topics

- Use Mendel's **first law (independent segregation)** to predict genotypes and phenotypes resulting from a given cross
- Genes on different chromosomes assort independently - **Mendel's second law (independent assortment)**
- Apply Mendel's principles to examples with **incomplete dominance** and **codominance** relationships of alleles, and multiple alleles
- Use the method of **gene (allele) counting** to determine allele frequencies when heterozygotes can be distinguished from the homozygote state
- Describe the **Hardy-Weinberg law**, explain the **conditions** that must be met for it to hold true, and determine if a population is in **HW proportions** (including multiple allele cases)
- Use the **HW expectations** to calculate allele frequencies for **recessive/dominant** traits or diseases, estimate the frequency of heterozygous carriers for a recessive trait, and explain why the majority of mutant alleles are carried in heterozygous individuals for rare recessive traits.

Timeline of Mendelian genetics (you do not need to memorize all these, just the three with asterisks)

1858 Darwin and **Wallace** independently propose the mechanism of evolution, natural selection.

***1859 Darwin** published *On the Origin of Species*.

1865 Gregor Mendel discovered the basic laws of genetic inheritance (Mendel's laws were unknown to Darwin).

***1900** Mendel's results are rediscovered, ABO blood group system in humans are discovered and shown to be an example of Mendelian inheritance.

1944 DNA is the genetic material.

***1953 Watson** and **Crick** discover the molecular structure of DNA.

1970 Gene mapping in humans essentially limited to the X chromosome, based on the specific pattern of inheritance.

1983 Genetic linkage of Huntington disease to a chromosomal location.

1989 Cystic fibrosis gene identified.

1990 Human Genome project initiated, a handful of human disease genes had been identified.

1993 The Huntington disease gene identified.

1994 The familial breast/ovarian cancer gene (BRCA1) was identified.

1997 The first cloning of a mammal, a sheep named Dolly.

The future: Documenting genetic variation of human and other genomes at the population level, identifying the genes involved in complex diseases, understanding the genetic basis of development, and much more. Many ethical issues will arise...

Overview of Mendelian genetics

Gregor Mendel, 1865: discovered basic laws of genetics by focusing on *particulate* inheritance, going against previous approaches to heredity that focused on quantitative characters.

gene: sequence of DNA coding for a protein (or in some cases, part of a protein)

allele: a variant of a single gene, inherited at a particular genetic locus (A and a)

genotype: the genetic constitution of an individual; in diploid individuals it is the set of two alleles at a locus possessed by an individual (AA, Aa, and aa)

phenotype: an observable trait in an organism; it can be determined by genotype and environment and interaction between the two (see Fig. 14.6 (7th) (Fig. 14.5 6th))

homozygote: individual having two copies of the same allele at a genetic locus (AA and aa)

heterozygote: individual having two different alleles at a genetic locus (Aa)

dominant: an allele A is dominant if the phenotype of the heterozygote Aa is the same as that of the homozygote AA, but differs from the homozygote aa

recessive: an allele a is recessive if the phenotype of the homozygote aa differs from that of the heterozygote Aa and the homozygote AA, which are the same.

Mendel's life and work: lonely life in a monastery in Brno, in current Czech Republic. Peas and bees, and financial headaches eased by beer...

Mendel's Experimental, Quantitative Approach

Advantages of pea plants for genetic study:

- There are many varieties with distinct heritable features, or characters (such as color); character variations are called traits
- Mating of plants can be controlled
- Each pea plant has sperm-producing organs (stamens) and egg-producing organs (carpels)
- Cross-pollination (fertilization between different plants) can be achieved by dusting one plant with pollen from another

In a typical experiment, Mendel mated two contrasting, true-breeding varieties, a process called hybridization:

- The true-breeding parents are the P generation
- The hybrid offspring of the P generation are called the F₁ generation
- When F₁ individuals self-pollinate, the F₂ generation is produced

- When Mendel crossed contrasting, true-breeding white and purple flowered pea plants, all of the F₁ hybrids were purple
- When Mendel crossed the F₁ hybrids, many of the F₂ plants had purple flowers, but some had white
- Mendel discovered a ratio of about three to one, purple to white flowers, in the F₂ generation
- Mendel reasoned that only the purple flower factor was affecting flower color in the F₁ hybrids
- Mendel called the purple flower color a dominant trait and white flower color a recessive trait
- Mendel observed the same pattern of inheritance in six other pea plant characters, each represented by two traits
- What Mendel called a “heritable factor” is what we now call a gene

Mendel's Model:

- Mendel developed a hypothesis to explain the 3:1 inheritance pattern he observed in F₂ offspring
- Four related concepts make up this model (below)
- These concepts can be related to what we now know about genes and chromosomes

- **The first concept** is that alternative versions of genes account for variations in inherited characters
- For example, the gene for flower color in pea plants exists in two versions, one for purple flowers and the other for white flowers
- These alternative versions of a gene are now called alleles
- Each gene resides at a specific locus on a specific chromosome

- **The second concept** is that for each character an organism inherits two alleles, one from each parent
- Mendel made this deduction without knowing about the role of chromosomes
- The two alleles at a locus on a chromosome may be identical, as in the true-breeding plants of Mendel's P generation
- Alternatively, the two alleles at a locus may differ, as in the F₁ hybrids

- **The third concept** is that if the two alleles at a locus differ, then one (the dominant allele) determines the organism's appearance, and the other (the recessive allele) has no noticeable effect on appearance
- In the flower-color example, the F₁ plants had purple flowers because the allele for that trait is dominant

- **The fourth concept**, now known as the law of segregation, states that the two alleles for a heritable character separate (segregate) during gamete formation and end up in different gametes
- Thus, an egg or a sperm gets only one of the two alleles that are present in the somatic cells of an organism
- This segregation of alleles corresponds to the distribution of homologous chromosomes to different gametes in meiosis
- Mendel's segregation model accounts for the 3:1 ratio he observed in the F₂ generation of his numerous crosses
- The possible combinations of sperm and egg can be shown using a Punnett square, a diagram for predicting the results of a genetic cross between individuals of known genetic makeup
- A capital letter represents a dominant allele, and a lowercase letter represents a recessive allele

test cross: a testcross is designed to reveal the genotype of an organism that exhibits a dominant trait, such as purple flowers in pea plants. Such a plant could be homozygous or heterozygous for the dominant allele. To reveal the genotype of the purple flower it is crossed to a homozygous recessive white flowered plant (Fig. 14.7 (7th) (Fig. 14.6 6th)).

If the purple parent plant is homozygous, all the offspring will be heterozygous and hence purple; if the purple parent plant is heterozygous, half the offspring on average will be heterozygous and purple, and the other half will be homozygous for the recessive trait and hence white.

To summarize:

Mendel's law of segregation (first law): states that a simple genetic trait is determined by a pair of separable factors (now called alleles of a gene), one inherited from each parent, and when an individual produces an egg or sperm cell, only one or the other of this gene pair is randomly transmitted (alleles segregate randomly) (Figs. 14.5, 14.9, and 14.14 (7th) (Figs. 14.4, 14.8, and 14.14 (6th))).

The important feature of Mendelian inheritance is that although a recessive allele is hidden in heterozygous individuals by the dominant allele, it is not lost to the population. The heterozygote Aa individual produces on average 1/2 A and 1/2 a gametes.

Previous to this, blending inheritance was the most commonly believed pattern of inheritance; but under blending inheritance genetic variation is halved each generation.

The Law of Independent Assortment (second law)

- Mendel derived the law of segregation by following a single character
- The F₁ offspring produced in this cross were monohybrids, individuals that are heterozygous for one character
- A cross between such heterozygotes is called a monohybrid cross
- Mendel identified his second law of inheritance by following two characters at the same time

- Crossing two, true-breeding parents differing in two characters produces dihybrids in the F₁ generation, heterozygous for both characters
- A dihybrid cross, a cross between F₁ dihybrids, can determine whether two characters are transmitted to offspring as a package or independently
- Using a dihybrid cross, Mendel developed the law of independent assortment
- The law of independent assortment states that each pair of alleles segregates independently of other pairs of alleles during gamete formation
- Strictly speaking, this law applies only to genes on different, nonhomologous chromosomes
- Genes located near each other on the same chromosome tend to be inherited together

An aside on probability:

- Ranges from 0 to 1
- Probabilities of all possible events must add up to 1
- Rule of multiplication: The probability that independent events will occur simultaneously is the product of their individual probabilities.
- Rule of addition: The probability of an event that can occur in two or more independent ways is the sum of the different ways.

Solving Complex Genetics Problems with the Rules of Probability

- We can apply the rules of multiplication and addition to predict the outcome of crosses involving multiple characters
- A dihybrid or other multicharacter cross is equivalent to two or more independent monohybrid crosses occurring simultaneously
- In calculating the chances for various genotypes, each character is considered separately, and then the individual probabilities are multiplied together

To summarize:

Mendel's law of independent assortment (second law): states that alleles of different genes assort independently. This is the case if the genes are unlinked (on different chromosomes) or separated by a recombination fraction of 50% on the same chromosome.

Inheritance patterns are often more complex than predicted by simple Mendelian genetics

- The relationship between genotype and phenotype is rarely as simple as in the pea plant characters Mendel studied
- Many heritable characters are not determined by only one gene with two alleles
- However, the basic principles of segregation and independent assortment apply even to more complex patterns of inheritance

Extending Mendelian Genetics

- Inheritance of characters by a single gene may deviate from simple Mendelian patterns in the following situations:
- When alleles are not completely dominant or recessive
- When a gene has more than two alleles
- When a gene produces multiple phenotypes
- Some traits may be determined by two or more genes

incomplete dominance: the heterozygote AB has a phenotype intermediate to that of the two homozygotes AA and BB. For instance, in snapdragons red flowers and white flowers represent the two homozygous phenotypes, while the heterozygote has pink flowers.

E.g., a cross of a red (RR) by white (WW) flowers will result in all the offspring being pink (RW) (Fig. 14.10 (7th) (Fig. 14.9 6th)).

codominance: the heterozygote AB has a phenotype distinguishable from both homozygotes AA and BB, and both alleles are separately manifest in the phenotype. One example is the so-called MN blood group in humans, where the homozygote MM and NN phenotypes each express one type of molecule on the cell surface, whereas the heterozygote MN individuals express both types of molecule.

multiple alleles: a group of individuals may have more than two different alleles for a given gene. (Any one individual has only two alleles, which may be the same or different, one inherited from their mother, the other from their father.)

E.g., the ABO blood group system in humans is determined by a set of 3 alleles, denoted A, B, and O. The A and B alleles are codominant, while both these are dominant to the O allele, giving rise to 4 blood group phenotypes A (genotypes AA and AO), B (genotypes BB and BO), AB (genotype AB), and O (genotype OO) (Table 14.2 (7th) (Fig. 14.10 6th)).

Some genes of the HLA (human leukocyte antigen system) which is involved in the immune response have over 200 alleles. Organ transplants have a much higher success rate when donor and recipient are matched for their HLA genes, but the high level of variation makes this difficult.

polymorphic: a genetic locus is polymorphic if it has 2 or more different allelic forms.

At the population level there can be more than 2 alleles at a gene, even though a single individual has a maximum of 2 different alleles, e.g., consider the ABO blood group system with 3 alleles A, B, and O.

pleiotropy

- Most genes have multiple phenotypic effects, a property called pleiotropy
- For example, pleiotropic alleles are responsible for the multiple symptoms of certain hereditary diseases, such as cystic fibrosis and sickle-cell disease

epistasis

- In epistasis, a gene at one locus alters the phenotypic expression of a gene at a second locus
- For example, in mice and many other mammals, coat color depends on two genes
- One gene determines the pigment color (with alleles B for black and b for brown)
- The other gene (with alleles C for pigment color and c for no pigment color) determines whether the pigment will be deposited in the hair

polygenic inheritance

- Quantitative characters are those that vary in the population along a continuum
- Quantitative variation usually indicates polygenic inheritance, an additive effect of two or more genes on a single phenotype
- Skin color in humans is an example of polygenic inheritance

Nature and Nurture: The Environmental Impact on Phenotype

- Another departure from Mendelian genetics arises when the phenotype for a character depends on environment as well as genotype
- The norm of reaction is the phenotypic range of a genotype influenced by the environment
- For example, hydrangea flowers of the same genotype range from blue-violet to pink, depending on soil acidity
- Norms of reaction are generally broadest for polygenic characters
- Such characters are called multifactorial because genetic and environmental factors collectively influence phenotype

Integrating a Mendelian View of Heredity and Variation

- An organism's phenotype includes its physical appearance, internal anatomy, physiology, and behavior
- An organism's phenotype reflects its overall genotype and unique environmental history

• Overview of different types of genetic variation:

phenotypic polymorphisms: qualitative differences in phenotype can be used as a genetic polymorphism, e.g., shell color and pattern forms in snails. (One must demonstrate that the trait has a genetic basis, and determine the number of genes involved.)

antigenic polymorphisms: sequence differences in a molecule can be detected by antibodies specific to each molecule, e.g., the ABO blood group system, and original typing of the HLA system and major histocompatibility complexes (MHCs) in other species (these are now typed by molecular methods).

chromosome markers: heritable variations in chromosome morphology.

electrophoretic polymorphisms: many proteins can be shown to be polymorphic by agarose or starch gel electrophoresis due to differences in electric charge or molecular weight at the protein (amino acid) level. This method was used extensively in the late 1960's and the 1970's. Not all mutations can be detected with this technique.

DNA polymorphisms: RFLP's, minisatellites (VNTR's—variable number of tandem repeats), microsatellites, SNP's (single nucleotide polymorphisms), indels (insertions/deletions).

The Hardy-Weinberg Theorem

- The Hardy-Weinberg theorem describes a population that is not evolving
- It states that frequencies of alleles and genotypes in a population's gene pool remain constant from generation to generation, provided that only Mendelian segregation and recombination of alleles are at work
- Mendelian inheritance preserves genetic variation in a population

• **Gene (allele) counting**

gene (allele) counting with incomplete dominance or codominance: When heterozygotes can be distinguished from the homozygous states (e.g., with incomplete dominance or codominance) allele frequencies are obtained by the method of gene (allele) counting.

In a 2 allele system with alleles denoted A and B,

$$f(A) = f(AA) + f(AB)/2, \quad f(B) = f(AB)/2 + f(BB), \quad \text{with } f(A) + f(B) = 1,$$

where $f(AA)$ is the frequency of homozygous AA individuals, $f(AB)$ of heterozygous AB individuals, etc.

Note that no assumption of Hardy Weinberg is required.

For the observed genotype values:

Genotypes	AA	AB	BB	
Observed	50	40	10	Total: 100
Frequencies:	0.50	0.40	0.10	

$$f(A) = 0.5 + (0.4)/2 = 0.7, \quad f(B) = (0.4)/2 + 0.10 = 0.3, \quad \text{check } f(A) + f(B) = 1.$$

These calculations can be done using observed numbers of genotypes (Fig. 23.4 (7th) (Fig. 23.3 6th)):

Genotypes	AA	AB	BB	
Observed	N_{AA}	N_{AB}	N_{BB}	Total: N_{total}

$$f(A) = (2N_{AA} + N_{AB})/2N_{total}, \quad \text{and } f(B) = (N_{AB} + 2N_{BB})/2N_{total}.$$

• **Hardy Weinberg**

Observed genotype frequencies in a population: consider the following examples of genotype frequencies for the $\Delta 32$ variant of the CCR5 gene, which protects against progression to AIDS, the MN blood group system, and the gene for cystic fibrosis (cc individuals are affected, Cc individuals are carriers).

CCR5 $\Delta 32$ variant in a French population

genotypes:	A/A	A/ $\Delta 32$	$\Delta 32/\Delta 32$	
observed numbers	795	190	15	Total: 1,000

MN blood group system in an Egyptian population

genotypes:	MM	MN	NN	
observed numbers	278	489	233	Total: 1,000

Cystic fibrosis in a European population

genotypes:	CC	Cc	cc	
observed numbers	9,596	400	4	Total: 10,000

Why do we see these particular genotype frequencies, is there some relationship between allele frequencies and the genotype frequencies, why are the heterozygote frequencies so much larger than the homozygous frequencies for $\Delta 32/\Delta 32$ and cc ?

In fact, each of these three examples have genotype frequencies close to those expected given their allele frequencies and random mating and some other assumptions described below under Hardy Weinberg.

Hardy Weinberg assumptions: Mendelian genetics was rediscovered in the early 1900's. The principle which is the foundation of population genetics—the Hardy-Weinberg law—was derived independently in 1908 by an English mathematician Hardy and a German physician Weinberg.

The geneticist Punnett brought to the attention of Hardy a remark of Yule (also a geneticist)—Yule is reported to have suggested as a criticism of the Mendelian position that if brachydactyly (short fingeredness) is dominant “in the course of time one would expect, in the absence of counteracting factors, to get 3 brachydactylous individuals to 1 normal.” Of course we now understand that Yule is confusing the Mendelian 3:1 ratio in an F1 cross ($Aa \times Aa$ gives $3A- : 1aa$) with population features.

The importance of the Hardy-Weinberg law is that if there are no counteracting forces, then the frequencies of alleles do not change in a population.

In other words, variation in a population, under a Mendelian system, tends to be maintained. We contrast this to the previously believed blending inheritance where genetic variation is decreased each generation.

Basically we want to consider whether or not Mendelian segregation causes changes in the genetic structure of a population.

We want to consider the effect of this factor acting in isolation from all other possible factors, so we assume:

- (1) random mating
- (2) mutation and migration rates are negligible
- (3) no selection
- (4) segregation according to Mendelian rules
- (5) a very large population, in essence, an infinitely large population

[Departures from these assumptions yields *evolution in gene frequencies*, the subject of the next two lectures]

HARDY-WEINBERG PRINCIPLE

IF in a large (etc) population:
p is the proportion of allele A
and q is the proportion of allele a

($p+q=1$) ie if we know one we can calculate the other.
Then after 1 generation of random mating the genotypes will attain and remain at the following frequencies:

GENOTYPE	FREQUENCY
AA	p^2
Aa	$2pq$
aa	q^2

The gene frequencies will not change from one generation to the next.

Hardy Weinberg equilibrium: We consider a 2 allele system with
 $p = f(A)$, $q = f(B)$ in the parental generation, so that $p + q = 1$.

Under the assumptions listed above, in the offspring:

$$f(AA) = p^2, f(AB) = 2pq, f(BB) = q^2,$$

and these are referred to as Hardy Weinberg proportions (HWP) or Hardy Weinberg equilibrium (see Fig. 23.4 (7th) (Fig. 23.3 6th)).

Note that in the offspring generation $f(A) = p$, $f(B) = q$. (Variation is maintained.)

Thus, allele frequencies do not change under the conditions of Hardy Weinberg, and genotype frequencies (proportions) are predicted from allele frequencies.

Hardy Weinberg proportions for a given allele frequency p of allele A (hence frequency q (= 1 - p) for allele B) -- there is only one genotype distribution in exact HWP.

Composition of an equilibrium population: for a range of allele frequencies, the HWPs are given below:

A	B	AA	AB	BB
p	q	p^2	$2pq$	q^2
.1	.9	.01	.18	.81
.2	.8	.04	.32	.64
.3	.7	.09	.42	.49
.4	.6	.16	.48	.36
.5	.5	.25	.50	.25

Note that for a 2-allele system, the maximum heterozygosity under HWP occurs when the 2 alleles have equal frequency of 1/2.

{Example given from Budgie breeding}

Deviations from Hardy Weinberg proportions: Given any sample is of finite size, we do not expect the genotype frequencies to be in exact HWP.

In the example above on determining allele frequencies by gene (allele) counting where we have $f(A) = p = 0.7$, $f(B) = q = 0.3$, the expected genotype frequencies under HWP are 0.49, 0.42, and 0.09, which deviate slightly from the observed values of 0.50, 0.40, and 0.10.

Using statistical testing one can show that such a small deviation is well within the range expected with this sample size (the statistical test is termed a chi-square goodness of fit, and is not covered in this course).

Another example of an observed sample with a close fit to HWP is

<u>genotype values:</u>	<u>CC</u>	<u>CD</u>	<u>DD</u>	
	35	50	15	Total: 100
Frequencies:	0.35	0.50	0.15	$f(C) = 0.6$, $f(D) = 0.4$, and
Expected HWP:	0.36	0.48	0.16	

An example with the same allele frequencies, but large (statistically significant) deviation from HWP is:

<u>genotype values:</u>	<u>EE</u>	<u>EF</u>	<u>FF</u>	
	56	8	36	Total: 100
Frequencies:	0.56	0.08	0.36	$f(E) = 0.6$, $f(F) = 0.4$, and
Expected HWP:	0.36	0.48	0.16	

One would need to investigate the possible reasons in this case for the large deviation from HWP (deficiency of heterozygotes, excess homozygotes), e.g., selection, inbreeding (**more next lectures!**)

Hardy Weinberg equilibrium for multiple alleles: For a gene with multiple alleles, labeled A_1, A_2, \dots, A_k , with frequencies p_1, p_2, \dots, p_k ,

the expected HWP for the homozygote A_1A_1 is $(p_1)^2$, and, for the heterozygote A_1A_2 is $2p_1p_2$, etc.

The total number of expected homozygotes under HWP is $F = \sum p_i^2$, and heterozygotes is $H = 1 - F$, termed the gene diversity index.

• Recessive traits and the square root formula

estimation of allele frequency for recessive trait, the square-root formula: Many traits of interest are not codominant or incompletely penetrant, but we may be interested in estimating the allele frequencies in this case, and the proportion of individuals heterozygous for a recessive trait (called carriers).

To do this, we **assume** HWP in the population, and then using the fact that the expected frequency of homozygotes for the recessive trait is $f(aa) = q^2$, we estimate the allele frequency of the recessive trait by $q = f(a) = [f(aa)]^{1/2}$.

Note that we cannot test whether the population is in HWP, we have used this information to obtain our estimate of the allele frequencies.

carrier frequencies:

We can also use the assumption of HWP to estimate how many carriers for the trait (heterozygotes) there are in the population, i.e., we estimate $2pq$, using our estimate of q (and hence $p = 1 - q$), above.

rare recessive traits: the majority of mutant alleles are carried in heterozygotes for rare autosomal recessive traits (frequency $\sim 2q$), and most affected individuals result from heterozygote by heterozygote matings.

The following examples of carrier frequencies in rare autosomal recessive traits are given for illustration, you do not need to memorize the details.

cystic fibrosis: Among Caucasians, one of the most frequent recessive diseases is cystic fibrosis, characterized by malfunction of the pancreas and other glands. (The gene for cystic fibrosis was identified in 1989.) The incidence of the condition is about 1/2,500 individuals, thus $q^2 = 0.0004$, and our estimate of $q = 0.02$, and the estimate of carriers is $\sim 4\%$.

sickle cell anemia: Among African Americans, sickle cell anemia is the most common recessive disease, with an incidence of approximately 1/400 individuals. In this case, $q^2 = 0.0025$, the estimate of $q = 0.05$, and the estimate of carriers is $\sim 9.5\%$ (heterozygous carriers of the disease show no ill effects except in conditions of oxygen stress). In parts of West Africa about 1/100 individuals have sickle cell anemia, and $\sim 18\%$ are carriers. The high frequency of the allele is due to an advantage to heterozygous individuals in malarial environments.

Tay Sachs: Among descendants of Ashkenazi Jews who settled in Eastern and Central Europe the recessive condition Tay Sachs disease occurs with an incidence of $\sim 1/4,000$, thus $q^2 = 0.00025$, the estimate of $q = 0.016$, and of heterozygous carriers is $\sim 3.2\%$. Individuals with Tay Sachs disease lack the enzyme hexosaminidase A. It is a tragic illness which leads to death by age 3 or 4 years. Carrier status screening is possible, and is performed each year on campus. If a couple are both carriers then prenatal diagnosis can be performed. Among the non-Jewish population of North America the incidence of Tay Sachs is about 1 in 500,000 births, with $q = 0.0014$.

CALCULATIONS to practice:

MENDELIAN GENETICS

- GIVEN parental phenotypes CALCULATE offspring genotypes, phenotypes and proportions.
- GIVEN offspring genotypes CALCULATE parental genotypes.
- GIVEN offspring phenotypes CALCULATE possible adult phenotypes or vice versa. (Pedigree charts)

HARDY WEINBERG

- GIVEN allele frequencies CALCULATE genotype or phenotype frequencies.
- GIVEN phenotype or genotype frequencies CALCULATE allele frequencies.

Questions relating to lecture on Mendel and Hardy Weinberg

1. Do self quiz questions #'s 3, 5, 6, 9, 14, and 15 on pages 272-273 of the textbook (7th edition) (questions #'s 1, 4, 6, 7, 8, 11, 16, and 17 on pages 267-268 of the 6th edition of the textbook).
2. Do self quiz questions #'s 1-3 on page 471 of the textbook (7th edition) (questions #'s 1-3 on pages 462-463 of the 6th edition of the textbook).
2. Calculate the expected genotype frequencies under Hardy Weinberg for the three examples given above of:
CCR5 Δ 32 variant in a French population
MN blood group system in an Egyptian population
Cystic fibrosis in a European population.