**Module 6: Population Changes Over Time in Living Systems**

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**6.1. Introduction to the Module**

One important feature of living systems is the presence of variation among its components. Charles Darwin observed this, and he realized the importance of variation with respect to changes that take place in populations over time, allowing adaptation and evolution to take place.

Variation is a fact of life, and we only need to look at ourselves as examples. In populations within living systems, it is typical for some traits to occur more than others. In humans, for instance, baldness is a phenomenon where individuals lose hair as they grow older. However, not everyone grows bald. Another example, albinism, is a condition where individuals have significantly reduced level of melanin pigments in their tissues, most notably in the epidermis. Nevertheless, not everyone has this condition. A third example is polydactyly, where afflicted individuals have extra fingers or toes. As with the previous examples, this condition is not present in all individuals in a population.

This module will try to explain why traits are not expressed at equal frequencies as well as the underlying mechanisms that lead to such differences. The implications of such mechanisms will also be discussed within the context of adaptation and evolution in living systems.

**6.2. Learning Outcomes**

At the end of this module, the student should be able to:

1. compute for allelic and genotypic frequencies
2. explain how allelic and genotypic frequencies and the traits they control change over time
3. relate biological concepts of change and adaptation in living systems to social and cultural systems

**Reading Assignment 1**

Read Sections 13.6-13.10 of Campbell et al.’s (2003) Biology: Concepts and Connections (or any later versions) and answer the following guide questions:

1. How do you distinguish species based on the Biological Species Concept?
2. According to Charles Darwin, how do populations change?
3. When does a member of a population become a part of the gene pool?

**6.3. Gene Pool**

Recall from your High School Biology that a gene is the basic unit of inheritance and facilitates the transfer of traits from one generation to the next through the information stored in the DNA. Genes may come in different or alternative forms called alleles, and depending on the number of types of alleles, different traits may be expressed (Campbell et al. 2003).

In albinism, a single gene pair controls the trait. There are two types of alleles available for this trait, the dominant allele *A* and the recessive allele *a.* If an individual inherits two dominant alleles (*AA*, termed homozygous dominant) or a dominant allele and a recessive allele (*Aa*, termed heterozygous dominant), then the person will have normal skin pigmentation. Otherwise, if two recessive alleles are inherited (*aa,* termed homozygous recessive), then the person becomes an albino. These allelic combinations are what we call genotypes, while the traits they express, whether normal or albino, are what we call phenotypes.

In polydactyly, the condition of having extra digits is due to the presence of the dominant allele *P*; therefore, an individual who is homozygous dominant (*PP*) or heterozygous dominant (*Pp*) will exhibit the condition whereas those who are homozygous recessive (*pp*) will have the normal number of digits.

Baldness is an interesting human trait because it seems to occur at a higher frequency in males than in females. It is believed that this condition is controlled by a single gene pair. However, its expression varies between the two sexes. In males, those that have at least one dominant allele (*BB* or *Bb*) will manifest the trait while those that are homozygous recessive (*bb*) will be normal. In the case of women, however, it takes two dominant alleles (*BB*) for the trait to manifest itself; otherwise, the individual will have normal hair growth. The difference is believed to be due to the difference in the level of testosterone between men and women; because testosterone level is significantly lower in females, the trait is not expressed if there is only one dominant allele present. This is an example of a sex-influenced trait (Enger et al. 2005).

When we consider all the genes in every individual in a population at any given time, what we have is population’s gene pool (Campbell et al. 2003). The available alleles present in the population therefore determine the frequency of genotypes and phenotypes in that population. We can simplify the principle of the gene pool by focusing on the alleles for a particular trait. If the frequency of the genotypes are known, we can actually compute for the allelic frequencies, and vice versa.

Example:

In a given population where albinism is present, the frequency of the genotypes are as follows: *AA*=300; *Aa*=600; *aa*=100. We can characterize the gene pool of this population with respect to the albino gene by assuming that each individual carries a pair of alleles for the trait. If there are 1000 individuals in this population, then we can assume that there are 2000 alleles for the trait. But how many *A* and *a* alleles are there in the population? To solve for the allelic frequencies, we refer to the genotypic frequencies. If we compute for the *A* allele, we need to identify first which individuals carry this allele and how many do they carry. For the *AA* genotype, there are 300 individuals, each carrying two *A* alleles, giving a total of 600 *A* alleles. For the *Aa* genotype, there are 600 individuals, each carrying just one *A* allele, for a total of 600 *A* alleles. This gives a total of 1200 *A* alleles in the population over 2000 total alleles, or a frequency of 0.6. Implicitly, the frequency of the *a* allele is 1 – 0.6 = 0.4.

**Activity 1 (15 minutes)**

Group yourselves into three or four and, as a seatwork, answer the following set of problems:

1. In a population of 1000 individuals, 180 have kinky hair, 360 have wavy hairy, and the rest have straight hair. Let us assume that hair type is governed by a pair of alleles, and there are two types of alleles, *S* (kinky) and *s* (straight), with the heterozygote condition being wavy. Compute for the allelic frequencies for hair type in the population.
2. Albinism is a rare genetic condition, occurring in only one in every 17,000 to 22,000 individuals in the world (Campbell et al. 2003; Gronskov et al. 2007). Conduct a library or online research and answer these questions:
3. What can you conclude about the allelic frequency of the *a* allele globally?
4. Where do you think the *a* allele would be more commonly found, among the heterozygotes (*Aa*) or the homozygote recessives (*aa*)? Why do you say so?
5. What happens to an individual who is albino (*aa*) or who has very low or lacks melanin pigments in the hair, skin and eyes?
6. Based on your answer in c, how would you explain the frequency of the *a* allele?

**Reading Assignment 2**

Still on the same text as the first reading assignment (Sections 13.6-13.10 of Campbell et al.’s (2003) Biology: Concepts and Connections), answer the following guide questions:

1. What are the assumptions of the Hardy-Weinberg Equilibrium model that makes populations unchanging?
2. What are the implications if the gene frequencies do not change?

**6.4. The Hardy-Weinberg Equilibrium**

Let us now look at gene frequencies in populations over several generations. The frequencies of alleles for specific traits affect the frequencies of genotypes in the population, so when the allelic frequencies change in generations over time, the genotypic frequencies likewise change. Such changes in populations could lead to diversification of the members of the said population towards specific directions. In order to understand what mechanisms are involved that cause the change in the allelic frequencies over time, a real population must be compared with an idealized population where the allelic frequencies do not change. This concept of an ideal population is best described by the mathematical concept called the Hardy-Weinberg principle, which was independently developed by Godfrey Hardy and Wilhelm Weinberg in 1908. A population at Hardy-Weinberg equilibrium assumes the following: (1) the population is large; (2) every individual has the capacity to reproduce; (3) mating/pairing is random or panmitic; (4) there is no mating/pairing between generations; (5) the allelic frequencies between males and females are the same; (6) there is no mutation; (7) there is no selection; and (8) there is no migration. If all these assumptions are in effect, then the allelic frequencies should not change from one generation to the next, and the genotypic frequencies are determined by the allelic frequencies. When these assumptions are met, then the population is said to be in Hardy-Weinberg equilibrium (Burns & Bottino, 1989). Such a population’s genotypic and allelic frequencies can be best described by the following equation:

*p2 + 2pq + q2 = 1*

where *p2*=frequency of the homozygous dominant

 *2pq*=frequency of the heterozygous dominant

 *q2*=frequency of the homozygous recessive

 *p*=frequency of the dominant allele

 *q*=frequency of the recessive allele

If we get the square root of the equation and do away with the negative root for the moment since there is no such thing as a negative allelic frequency, then the equation can also be simplified as:

*p* + *q* = 1

where *p* = 1 – *q*

 *q* = 1 - *p*

Consequently, if the population is at Hardy-Weinberg equilibrium, then the allelic frequencies could easily be determined once the genotypic frequencies are known. Take note that in many instances, the homozygous dominants and heterozygous dominants could not be distinguished if they exhibit the same phenotype, as in the case of albinism. However, if the homozygous recessive phenotype is known, then the other genotypic and allelic frequencies can be inferred.

**Activity 2: (20 minutes)**

Group yourselves into three or four and, as a homework, answer the following set of problems:

1. In a population at Hardy-Weinberg equilibrium, 190 out of 1000 individuals have polydactyly. Note that the trait is dominant.
2. What is the frequency of the dominant and recessive alleles?
3. How many are expected to be heterozygotes for the trait?
4. How many are expected to be homozygous dominant?
5. Galactosemia is a recessive disorder characterized by the accumulation of galactose in tissues that leads to mental retardation and eye and kidney damage (Campbell et al. 2003). In a population with 1000 individuals and at Hardy-Weinberg equilibrium, the frequency of individuals with galactosemia is 4%.
6. What are the frequencies of the dominant and recessive alleles?
7. What is the expected frequency of the homozygous dominant in the population?
8. What would be the expected frequency of the heterozygous dominant after five generations?
9. Consider your university campus student population. Do you think this population is at Hardy-Weinberg equilibrium? Do you think the gene and genotypic frequencies within your gene pool remain constant across all batches at any given time? Evaluate by testing if each assumption of the Hardy-Weinberg equilibrium model is valid.

**6.5. Factors that Change Populations Over Time**

**Reading Assignment 3**

Read Sections 13.11-13.21 of Campbell et al.’s (2003) Biology: Concepts and Connections and answer the following guide questions:

1. How do new variations arise?
2. What does Darwin mean by an organism’s fitness?
3. What happens to the gene pool of a species if it becomes endangered?

It is very rare to find a real population at Hardy-Weinberg equilibrium. In fact, scientists doubt if they truly exist. However, having a model can be quite useful in order to understand what goes on in real populations by identifying which assumptions are being violated, which in turn could account for the changes in gene frequencies.

**Activity 3 (30 minutes)**

Working in groups of three or four, you will test the Hardy-Weinberg equilibrium by simulating a population using colored beads.

Materials

* 50 beads of one color
* 50 beads of another color
* Paper or plastic bag

In humans, sickle cell anemia is controlled by a single pair of alleles. People who are homozygous recessive (*ss*)will develop sickle cell anemia due to a mutation that results in misshapen red blood cells while those who are homozygous dominant (*SS*) or heterozygous dominant (*Ss*) are normal.

Let us assume that the bag of beads represents the gene pool for the sickle cell gene in a hypothetical human population. Each bead is regarded as a single allele carried by either the sperm or the egg and the two colors represent the *S* and *s* alleles. Each group will be given a bag containing 100 beads of two colors, with 50 beads of each color. This population will therefore have the following allelic frequencies: *S* = 0.5; *s* = 0.5. In turn, each genotype is represented by a pair of beads; designate two beads of one color as *SS*; two beads of the other color as *ss*; and two beads with contrasting color as *Ss.* Following the Hardy-Weinberg equation *p2 + 2pq + q2 = 1*, we would expect the population to have the following genotypic frequencies: *SS* = 0.25; *Ss* = 0.5; *ss* = 0.25.

1. Simulation of a Population at Genetic Equilibrium
2. Without looking, randomly remove two beads from the bag. This represents one diploid individual in the next generation. Record the genotype (*SS, Ss, ss*) of the individual formed from these two beads.
3. Return the beads to the bag and shake the bag to reinstate the gene pool. By replacing the beads each time, the size of the gene pool remains constant and the probability of selecting any allele should remain equal to its frequency. This is called sampling with replacement.
4. Repeat this procedure (select two beads, record the genotype of the new individual, and return the beads to the bag) until you have recorded the genotypes for 50 individuals who will form the first generation of the population. Designate this as the generation 1.
5. Using the same beads, repeat the process for the next two generations until you have 50 individuals for each generation. Designate these generations as generations 2 and 3, respectively.
6. Based on the number of individuals per genotype, compute for the genotypic frequencies (*p2*, *2pq*, and *q2*)for each generation by dividing the observed number with 50. Likewise, calculate the allelic frequencies (*p* and *q*) for each generation by obtaining the sum of the number of each allele from all three genotypes and divide it by 100. Write your data in Table 6.1.
7. What do you notice about the frequencies of *S* and *s* alleles for generations 1 to 3? Are they each close to 0.5, or are they considerably different?
8. If you continue doing this for another 10 generations, what would you expect the values of the allelic frequencies to be? What about the genotypic frequencies?
9. Simulation of Natural Selection
10. Return the beads again to the bag and shake the bag to reinstate the gene pool. This time, however, the *ss* genotype, which leads to sickle cell anemia in humans, will be selected against and will no longer be counted in the next generation. Similar with the above procedures, remove two beads from the bag, take note of the genotype, and return the alleles in the bag. However, every time the *ss* genotype is obtained, this count will not be tallied and the beads will not be returned to the bag. Repeat this procedure until you have 50 individuals. Designate this as generation 4.
11. Repeat step 8 to generate generations 5, 6, 7, and 8. Make sure that you do not include anymore all the beads that you have discarded in the previous populations. Record the number of diploid individuals for each genotype in Table 6.2. Take note that you now have only 2 genotypes; do not report the *ss* genotype in Table 6.2. The sum of all tallied individuals should still total 50.
12. What do you notice about the frequencies of *S* and *s* alleles for generations 4 to 8? Are they each close to 0.5, or are they considerably different? Do you notice any trend?
13. If you continue doing this for another 10 generations, what would you expect the values of the allelic frequencies be? How would the genotypic and allelic frequencies compare with those of generations 1 to 3?

Table 6.1. Population at Hardy-Weinberg Equilibrium

|  |  |  |
| --- | --- | --- |
| Generation | Genotypes | Alleles |
| *SS* (p2) | *Ss* (2pq) | *ss* (q2) | *S* (p) | *s* (q) |
| 1 |  |  |  |  |  |
| 2 |  |  |  |  |  |
| 3 |  |  |  |  |  |

Table 6.2. Population Undergoing Natural Selection

|  |  |  |
| --- | --- | --- |
| Generation | Genotypes | Alleles |
| *SS* (p2) | *Ss* (2pq) | *ss* (q2) | *S* (p) | *s* (q) |
| 4 |  |  |  |  |  |
| 5 |  |  |  |  |  |
| 6 |  |  |  |  |  |
| 7 |  |  |  |  |  |
| 8 |  |  |  |  |  |

The simulation that we have just done demonstrates the phenomenon called natural selection, which affects allelic and genotypic frequencies over time. It should be noted that the environment determines which trait will be favored in the population, depending on the advantage it poses to the individual, which we call its fitness value. Therefore, an allele that has a higher fitness value within an environmental context will make the individual that carries it to have a greater chance of surviving and reproducing, which then increases the chance of that allele to be passed on and propagate through many offspring and through several generations. Through time, this selective reproductive success will lead to changes in the gene frequencies in the populations and a change in the frequency of traits expressed. Eventually, there will be enough changes to arise for the population to diversify and lead to new species. This process shows how populations adapt through changing environments and ultimately evolve. In other words, the basic unit of evolution is the population.

It was Charles Darwin and Alfred Russel Wallace who espoused evolution by natural selection. Darwin expounded on the concept when he published his book, *On the Origin of the Species by Means of Natural Selection*, which was based on his travels, particularly to the Galapagos Archipelago.

**Activity 4 (30 minutes; to be done outside class hours)**

If there is enough time, go to the link provided on the British peppered moth, *Biston betularia* (link: <http://peppermoths.weebly.com/>) where you will learn more about natural selection in a real world example. Then go to this video link by Paul Andersen where he further elaborated on natural selection (video link: <https://www.youtube.com/watch?v=R6La6_kIr9g>). Afterwards, answer the following questions:

1. The British peppered moth have two color morphs. What are these morphs and what are their genotypes?
2. What was the selection pressure exhibited on the British peppered moth during the industrial revolution that led to a change in its gene pool?
3. What is the most important source of variation in a population, which generates novel genes?
4. List down the important elements that must be present in a population in order for natural selection to occur.

**Activity 5 (30 minutes; to be done outside class hours)**

Natural selection is not the only factor that affects gene frequencies over time. As a thought experiment, imagine doing the same bead simulation in Activity 3. However, what do you think will happen to the allelic frequencies over several generations if you:

1. reduce the sample size to five individuals per generation?
2. add 50 beads of one color to the mix or remove 25 beads of one color and 5 beads of another color?
3. intentionally choose only beads of one color?

The scenarios depicted above are just three other factors that change allelic frequencies, and these are genetic drift, gene flow, and non-random mating, respectively. Can you cite real life scenarios which exhibit these processes?

It should then be apparent to you that changes in gene frequencies is a combination of many factors. These are natural selection, mutations, genetic drift, gene flow, and non-random mating.

**Activity 6: Application (1 hour; to be done outside class hours)**

Gonorrhea is a sexually transmissible disease (STD) caused by the bacterium *Neiserria gonorrhoeae*. In the 1940’s, penicillin was introduced as an antibiotic to treat gonorrhea. In particular, the drug inhibits the formation of new cell walls in dividing bacterial cells, making new cells vulnerable to the human body’s defenses. However, a new strain of *Neiserria gonorrhoeae* was found that is capable of breaking down penicillin, making this strain resistant. The emergence of this new strain has been associated with instances of non-strict compliance of certain patients on the use of penicillin as well as the improper administration of the drug. Based on the information given,

1. develop a hypothesis that could explain the rise of this new, penicillin-resistant strain.
2. formulate a strategy that could help control this new strain.

**6.6. Evolution in Other Systems**

The concept of evolution need not be restricted to biological systems. In fact, social and cultural systems may also behave in similar ways. One very good example is the evolution of mobile or cellular phones. From the bulky, brick-like configurations in the 1970’s and 1980’s to the smart phones that we have today, we see the changing marketability of various versions of the mobile phone depending on the features they carry. If we consider these features as ‘traits’ and consumer preference as the ‘environment that acts on these traits,’ then it is unsurprising why phones evolve the way they do. Could you name some of these features that changed the way cell phones look through the years?

**Activity 7 (1 hour; to be done outside class, then conduct a group report)**

In groups of three or four, cite and discuss an example of evolution in consumer products, art, fashion, and services. Your group will then share what you have discussed in class.

**6.7. Summary**

Populations constantly change. This can be seen in the changes in the gene frequencies of the populations’ gene pools; otherwise, the population is said to be at Hardy-Weinberg equilibrium. When variations within populations diverge enough, new species may arise. It is therefore important to remember that populations are the basic unit of evolution, which is defined as the change in gene frequencies over time. There are many factors that affect the gene frequencies and ultimately influence evolution.

In a given population, mutations and immigrants bring novel variations or genes in to the population’s gene pool while emigrants remove genes from the gene pool. Within the population itself, sexual reproduction produces new individuals with different combinations of alleles, depending on what is available in the gene pool. In the succeeding generations, the gene frequencies may be affected depending on the environmental factors that influence reproductive success. These include which individuals can survive based on the fitness value of the traits they possess, the capacity of the individuals to reproduce, and whether their ability to find mates (Enger et al. 2005). These processes that influence evolution are summarized in Figure 6.1.



Figure 4.1. Processes that cause changes in gene pools that lead to evolution (Adapted from Enger et al. 2005).

**6.8. Assessment**

**Multiple Choice**

1. In a population at Hardy-Weinberg equilibrium, the frequency of the homozygote recessive is 0.09. What is the frequency of the heterozygote?
2. 0.09
3. 0.21
4. 0.30
5. 0.42
6. 0.49
7. All of the following are criteria for maintaining a Hardy-Weinberg equilibrium involving two alleles EXCEPT
8. populations must be large.
9. the genotypic frequencies are equal.
10. there is no gene flow.
11. there is no mutation.
12. there is random mating.
13. One important premise in Darwin and Wallace’s theory of evolution by natural selection is that
14. change occurs by big steps called mutations.
15. characteristics acquired during the lifetime of an individual modify genes.
16. hybridization between existing species accounts for the origin of new species.
17. individuals of every generation vary in their ability to survive under prevailing conditions.
18. the direction of evolution is always from simple to complex.
19. Natural selection is sometimes referred to as ‘survival of the fittest.’ By ‘fitness,’ we ultimately mean an individual’s
20. ability to gather food.
21. ability to outcompete other individuals.
22. ability to survive in harsh environments.
23. number of viable, fertile offspring it can produce.
24. rate of mutation.
25. In the bead simulation activity, a population has an allelic frequency of 0.5 each for two alleles for a given trait. You then randomly sample three individuals from the population, and you obtained two homozygous recessives and one heterozygote. Using only the beads from these three individuals, you set up a new population of fifty individuals by sampling with replacement. What you have simulated is called the Founder effect, a phenomenon where a small set of a population which carries a set of alleles that happens to differ from allelic frequencies of the original population moves to a new area and establishes a new population through time. The change in allelic frequencies is largely due to
26. gene flow.
27. genetic drift.
28. rutations.
29. natural selection.
30. random mating.

**Adapted with modifications from:**

Enger ED, Ross FC, Bailey DB. 2005. Concepts in Biology, 11th ed. McGraw-Hill Higher Education.

Morgan JG, Carter MEB. 1993. Investigating Biology: A Laboratory Manual for Biology. California: The Benjamin/Cummings Publishing Co., Inc.

**References**

Burns GW, Bottino PJ. 1989. The Science of Genetics, 6th ed. McMillian.

Campbell NA, Reece JB, Mitchell LG, Taylor MR. 2003. Biology: concepts and connection, 4th ed. Benjamin Cummings.

Enger ED, Ross FC, Bailey DB. 2005. Concepts in Biology, 11th ed. McGraw-Hill Higher Education.

Gronskov K, Ek J, Brondum-Nielsen K. 2007. Oculocutaneous albinism. Orphanet Journal of Rare Diseases. 2: 43.